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AZƏRBAYCAN RESPUBLİKASI
ELM VƏ TƏHSİL NAZİRLİYİ

EGE
TARIMSAL

ABSTRACT E-BOOK

2nd MİRZA GÖKGÖL INTERNATIONAL PLANT GENETIC RESOURCES SYMPOSIUM

ORGANIZED BY THE GENETIC RESOURCES INSTITUTE,
MINISTRY OF SCIENCE AND EDUCATION OF THE REPUBLIC OF AZERBAIJAN,
AND THE AEGEAN AGRICULTURAL RESEARCH INSTITUTE,
MINISTRY OF AGRICULTURE AND FORESTRY OF THE REPUBLIC OF TÜRKİYE

AUGUST 19-22, 2025, GANJA, AZERBAIJAN

2nd MİRZA GÖKGÖL INTERNATIONAL PLANT GENETIC RESOURCES SYMPOSIUM

GANJA, AZERBAIJAN, AUGUST 19-22, 2025

2-Cİ MİRZƏ GÖKGÖL BEYNƏLXALQ BİTKİ GENETİK EHTİYATLARI SİMPOZİUMU

GƏNCƏ, AZƏRBAYCAN, 19-22 AVQUST 2025-ci il

ORGANIZED BY THE GENETIC RESOURCES INSTITUTE OF THE MINISTRY OF SCIENCE AND EDUCATION OF THE REPUBLIC OF AZERBAIJAN, AND THE AEGEAN AGRICULTURAL RESEARCH INSTITUTE, MINISTRY OF AGRICULTURE AND FORESTRY OF THE REPUBLIC OF TÜRKİYE

ABSTRACT E-BOOK

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2nd MİRZA GÖKGÖL INTERNATIONAL PLANT GENETIC RESOURCES SYMPOSIUM

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CONTENTS

PREFACE

Dear Colleagues,

We are honored to invite you to the ***2nd Mirza GÖKGÖL International Plant Genetic Resources Symposium,*** which will be held in the ancient Turkic city of Ganja, Azerbaijan, from August 19 to 22, 2025.

The symposium is jointly organized by the Genetic Resources Institute of the Ministry of Science and Education of the Republic of Azerbaijan and the Aegean Agricultural Research Institute (AARI) under the General Directorate of Agricultural Research and Policies (TAGEM), Ministry of Agriculture and Forestry of the Republic of Türkiye. It will be hosted by the Azerbaijan State Agricultural University and the Scientific Research Institute of Plant Protection and Technical Crops of the Ministry of Agriculture of the Republic of Azerbaijan.

The symposium aims to bring together scientists working on plant genetic resources for food and agriculture including landraces, heirloom seeds, cultivated species, their wild relatives, and wild species of economic importance. It will provide a platform for presenting scientific studies, sharing knowledge and experience, and strengthening international collaboration.

We look forward to meeting you in Ganja, the homeland of the great Nizami Ganjavi.

With kind regards,

On behalf of the Symposium Organizing Committee

Professor Zeynal Akparov

Symposium Chair

Director of the Genetic Resources Institute MSE RA

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INVITED SPEAKERS’ ABSTRACTS

Mirza Gökgöl's Contributions to the Science of Plant Genetic Resources

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Abstract: Despite his significant contributions to the science of plant genetic resources in the 20th century, Professor Mirza Gökgöl remains relatively unknown to the international scientific community.

He was born in the ancient city of Ganja, Azerbaijan in 1897, and completed his studies at Ganja Male Gymnasium (1906–1915). He then pursued higher education at the Novo-Aleksandrovsky Institute of Agriculture and Forestry in Kharkiv (1916–1917), but returned home early due to the Russian Revolution in 1917.

Mirza Hacizade was among the 100 students sent abroad by the Azerbaijan Democratic Republic (1918–1920) to study. In early 1920, he began studying at the Portici Agricultural Lyceum in Naples, Italy, and later transferred to the Berlin Higher Agricultural School in November of the same year. Under the mentorship of prominent geneticists Erwin Baur (1875–1933) and Kurt Opitz (1877–1958), he completed his education in breeding and seed science by 1924. He also received a diploma under the supervision of Elisabeth Schiemann.

In June 1925, Mirza Hacizade passed his diploma exam and completed his PhD dissertation by December 1926, earning a Doctor of Philosophy degree with the signature of Professor Aereboe. Although he applied to the Soviet embassy in Berlin for a visa to return to Azerbaijan, he received no response and continued to work as a breeder-scientist in Germany.

In 1926, when Turkish Minister of Agriculture Sabri Toprak visited Germany, he offered Erwin Baur a position in Turkey as a breeder-scientist. However, Baur recommended his student Mirza instead. Although Sabri Toprak intended to sign an official contract with Mirza, the young scientist, identifying himself as a Turk, chose to work without a contract and moved to Turkey in 1926. That same year, he established and began work at the Breeding and Seed Station at the Halkalı Agricultural Institute in Istanbul.

In 1931, the station was relocated to the Yeşilköy district and transformed into the Yeşilköy Agricultural Research Institute.

In accordance with Turkey's Surname Law, Mirza Hacizade adopted the surname "Gökgöl" on December 17, 1934, named after the Gökgöl region near Ganja, to which he had deep emotional ties.

He remained deeply connected to his homeland of Azerbaijan, especially the city of Ganja, which he held in high esteem. Over the course of 35 uninterrupted years (30 of them as director), Mirza Gökgöl turned the institute into one of Turkey's most prestigious scientific research centers. After retiring in 1961, he continued teaching at various universities.

His rich scientific legacy in Turkey is reflected in the first systematic research conducted in the field of wheat breeding and genetics. Between 1929 and 1955, he carried out extensive studies on identifying traditional local wheat varieties grown in various regions of Türkiye and

assessing their economically significant traits. Based on this work, he selected the most promising genotypes and used them to develop new varieties.

He collected more than 18,000 local wheat samples, conducted comprehensive research on their morphological and biological traits, and, through selection, developed 256 new wheat varieties. The first varieties he developed were the Karagılçık durum wheat and the Zafer barley.

Approximately 4,500 herbarium specimens, mainly belonging to the genus Triticum, are currently preserved at the Aegean Agricultural Research Institute in Menemen, Izmir. Mirza Gökgöl demonstrated that Turkey possesses a vast wealth of wheat genetic diversity and that there is no need to import foreign genetic material for breeding purposes.

Thus, Professor Gökgöl laid the scientific foundation for developing high-yield, disease- and pest-resistant plant varieties, adapted to local conditions and climate, by comprehensively evaluating the collected genetic resources and applying them across different ecological zones of the country.

The distinguished scientist also conducted extensive research on potato, maize, tobacco, millet, flax, poppy, soybean, alfalfa, sunflower, chickpea, lentil, and other forage, grain, and industrial crops. His first works on vegetable crops were initiated in Yeşilköy.

One of the most significant expeditions within Turkish territories was carried out jointly with Professor P.M. Zhukovsky from the All-Union Institute of Plant Industry, named after N.I. Vavilov. Gökgöl also engaged in scientific debate with the great Russian scientist and academician Nikolai Vavilov on his “Centers of Origin of Cultivated Plants” theory.

Vavilov believed that high morphological diversity in a region indicated its genetic center of origin and proposed in 1926 that diploid wheat originated in Western Asia (Anatolia), tetraploid wheat in Ethiopia, and hexaploid wheat in the Pamir plateau and the foothills of the Himalayas.

Mirza Gökgöl challenged this theory, asserting that the origin of wheat could not be in multiple regions, but rather in a single genetic center – Western Asia. He scientifically proved that this center included Anatolia, the South Caucasus, Iraq, and Western Iran. After the publication of these findings in May 1939, Vavilov himself acknowledged Gökgöl’s perspective as worthy of recognition.

Gökgöl published the results of his research on cereal crops in nearly 300 scientific articles, 37 monographs, including his two-volume fundamental work “The Wheats of Turkey”.

Of the 43 works he published between 1930 and 1965, nine were written in German and one in French. He also translated three major books by Erwin Baur into Turkish and published 34 university textbooks.

His doctoral dissertation, written in German and published in Istanbul in 1930, titled “The Relationship Between Climatic Conditions and Wheat Yield and Quality” (138 pages), holds special significance.

His 1955 book published in Ankara, “Key to the Classification of Wheats,” is also of great importance. It served as a fundamental resource for the systematic classification of wheat not only in Turkey but also in the Middle East and the Caucasus.

He conducted experimental studies on wheat at the International Institute of Agricultural Sciences in Paris and collaborated with institutions in France, Switzerland, and other countries. Among many renowned scientists, he also maintained close academic cooperation with prominent Azerbaijani scholar Academician Imam Mustafayev.

His scientific legacy reflects the idea of transboundary cooperation in the exchange of genetic resources and joint research projects—making him one of the early pioneers of scientific diplomacy.

His contributions also significantly supported the education and training of young breeders and geneticists at universities and research institutes.

In addition to university teaching, Gökgöl prioritized the training of young researchers at experimental stations. He actively participated in establishing breeding and experimental fields in various regions and organizing scientific oversight.

Mirza Gökgöl had a direct influence on shaping Turkey's agricultural policy based on scientific principles, organizing the seed system, and applying breeding achievements to increase productivity.

He was one of the first to formulate scientific concepts for the conservation and sustainable use of plant genetic resources.

His legacy remains highly relevant today, as the classification systems, breeding methods, and agrobiological approaches he developed serve as a bridge between classical genetics and modern biotechnology, offering a valuable heritage for the advancement of global plant breeding and genetics.

His father, merchant Mashadi Yusif Bey, and mother, Mashadi Yagut Khanum, a housewife, had three children:Mirza Bey (1897–1981, Istanbul),Majid Bey (1899–1930, Uzbekistan),Mahtavan Khanum (~1900–1970, Mashhad)

After Yusif Bey's death in 1901, Yagut Khanum married her late husband's nephew, Mukhtar Hacizade, and had three more children:Aslan Bey (1905–1930, Ganja), Shola Khanum (1907–1979, Baku), Islam Gökgöl (1908–1987, Ankara). These three were Mirza Gökgöl's maternal half-siblings.

Due to Soviet repressions, the Hacizade family was exiled, their property confiscated, and Mashadi Yusif Bey's estate was destroyed.

In 1929, in Istanbul, Mirza Gökgöl married Zohra Khanum, the daughter of Nasib Bey Yusifbeyli (1881–1920), the second Prime Minister of the Azerbaijan Democratic Republic. The couple had four children. After their marriage, Nasib Bey's wife, Shafiqa Khanum, also lived with them in the Kabataş district of Istanbul.

Shafiqa Khanum was the daughter of Ismail Gasprinski, a pioneer of the Crimean Tatar national awakening movement, renowned publicist, and editor-in-chief of the journal Alem-i Nisvan.

Mirza Gökgöl never severed his ties.

In 1968, he visited Baku with his wife Zohra Khanum, where he delivered lectures in various scientific circles.

However, the Soviet security services did not permit him to visit his birthplace, the city of Ganja, or to say farewell to Lake Göygöl.

Finally, in 1969, he made a second trip to Azerbaijan with his wife — this would be his last visit to his homeland. They visited Quba and Ganja.

In Ganja, he visited the site of his ancestral home and the grave of his brother. With this visit, Gökgöl was able to partially ease the deep longing for his homeland that he had carried throughout his life.

Keywords: Mirza Hacızade Gökgöl, Plant Genetic Resources, Türkiye's wheat

Tagem's Biodiversity Conservation Strategies

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Abstract: Biodiversity and genetic resources have become increasingly important topics in international policy development in recent years, and maintaining the natural equilibrium is essential for sustaining life on Earth. In Türkiye, *ex situ* and *in situ* conservation programs are implemented by 32 research institutes operating under the General Directorate of Agricultural Research and Policies (TAGEM) of the Ministry of Agriculture and Forestry, with the aim of conserving, ensuring long-term preservation, enabling sustainable use, supporting scientific research, and transferring the country's genetic resources to future generations. Through gene banks and related facilities established for this purpose, the collection, conservation, documentation, molecular and morphological characterization, regeneration, and provision of plant, animal, aquatic, and microbial genetic materials to research institutions are carried out. In parallel, Türkiye actively participates in international agreements and programs to which it is a Party or is likely to become a Party, in order to define its national position regarding biodiversity and genetic resources. Türkiye hosts two seed gene banks in which plant genetic resources are preserved: the National Seed Gene Bank located at the Aegean Agricultural Research Institute in İzmir, and the Türkiye Seed Gene Bank located at the Field Crops Central Research Institute in Ankara, containing over 122,000 seed accessions in total. Additionally, approximately 10,000 living accessions of 107 species (grapevine and fruit species) are maintained in 18 field gene banks across different institutes. The collections preserved in the seed gene banks include landraces, wild relatives and intermediate forms, other wild species of economic importance, as well as endemic plant species. Materials conserved in these gene banks are actively used in plant breeding through advanced biotechnological tools, particularly for developing new varieties tolerant to biotic and abiotic stress under global climate change. At the Geophyte Research Center established within the Atatürk Horticultural Research Institute, approximately 1,000 geophyte species represented by around 7,000 populations of bulbous and tuberous ornamental plants are conserved. In addition, various plant herbaria, fungaria, and multiple databases supporting the documentation of plant genetic resources are also maintained in different institutions. For the conservation of animal genetic resources, the National Domestic Animal Genetic Resources Strategy has been developed, and both institute-based and on-farm conservation programs are being implemented. Within this scope, genetic materials belonging to 31 native domestic animal breeds, including 7 cattle, 19 small ruminant, and 5 horse breeds, are conserved. Twelve high-risk breeds (4 cattle, 4 sheep, 1 goat, 2 chicken, and 1 honey bee) are currently under active conservation in six research institutes of the Ministry. To ensure the conservation and sustainable management of aquatic biodiversity in Türkiye, the National Aquatic Genetic Resources Gene Bank and Biotechnology Center has been established in Trabzon. The center provides the infrastructure for the *in vivo* preservation of sperm, tissue, and DNA samples, as well as the *in vivo* conservation of certain endemic and commercially valuable species. As the smallest living units, microorganisms form essential components of biodiversity and ecosystems and hold significant potential for utilization. Phenotypic and genotypic analyses are planned to be performed on microorganisms isolated by the institutes during their research activities, and these strains will be incorporated into culture collections in line with a defined national policy framework. Additionally, the Dairy Products Gene Bank within the Food and Feed Control Central Research Institute conserves nearly 1,000 microbial strains isolated from yoghurt, cheese, and other dairy products.

Keywords: Biodiversity, genetic resources, gene banks, *ex situ* conservation, *in situ* conservation, Türkiye, Tagem, sustainable use, genetic diversity, preservation

Challenges and Opportunities for PGR Conservation and Use: Time to Choose an Improved Way Forward

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Abstract: Historically, genebanks have been the providers of plant genetic resource (PGR) conservation, and meeting the needs of germplasm users. PGR populations were sampled, dried, and stored in commercial freezers and users made selection from what was conserved. To promote resource utilization, germplasm was characterized and evaluated, facilitating user selection and application. The ultimate goal being to develop new, improved cultivars with enhanced quantitative and qualitative traits. This approach was effective in maintaining production and preventing harvest shortfalls, even as the human population grew toward and even beyond the earth's carrying capacity. Today, however, the situation has significantly changed. Today in 2025, the global population is 8.21 billion, 733 million people suffer from malnutrition, that 1 in 11 people worldwide and 1 in 5 in Africa in 2023. To meet the demands of the 2050 population, food supplies must increase by 60% globally and 100% in developing countries. Meanwhile, climate change is expected to reduce agricultural productivity by approximately 2% each decade this century. Although Sustainable Development Goal 2 aims at NO HUNGER by 2030, current reviews suggest this target will not be achieved. In the light of these challenges, continuing with the current practices appears unviable and irresponsible. We must review the foundations of PGR conservation and utilization, rethink core principles, to ensure a continuous flow of greater diversity is available as a basis for improved crop varieties. Understanding current conservation and use practices, deconstructing existing paradigms, and rebuilding more effective and efficient systems are crucial steps toward securing humanity's future food security, and existence. Key issues to address include: (1) critically evaluating the standard model for PGR conservation and use; (2) defining clear goals for PGR practice; (3) establishing *in situ* conservation applications; (4) integrating e*x situ* and *in situ* applications; and (5) expanding the adoption of conserved PGR by germplasm users such as plant breeders, farmers, researchers, and other stakeholders. It is argued that the traditional model for PGR conservation is overly simplistic. Genebanks, or genetic resource centres, should play a broader role beyond simple curating of *ex situ* collections and responding to user requests. Their responsibilities in the 21st century should include providing leadership in PGR conservation, planning (including threat assessments), characterization, evaluation, policy development, information management, research, training, capacity building, and engaging with diverse PGR users and the wider biodiversity community, considering societal, economic, and humanities perspectives. For PGR users and humanity at large, addressing current challenges and leveraging available opportunities is vital to ensuring greater diversity availability, sustainable food production, long-term food security, and even the future for humankind.

Keywords: PGR, germplasm, genebank, *in situ* conservation, *ex situ* collections

Wild Relatives of Wheat in Türkiye: Taxonomy, Diversity, and Conservation Perspectives

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Abstract: This study investigates the taxonomy, diversity, and conservation of wild relatives of wheat (tribe Triticeae) occurring in Türkiye, a key region in the evolutionary history of cereal crops. Through extensive field studies and taxonomic analyses, the research maps the distribution of target species, assesses their genetic variability, and evaluates major anthropogenic and environmental threats.

Wild relatives constitute an essential genetic reservoir for the improvement of cultivated wheat, offering adaptive traits such as drought tolerance, salinity resistance, and pest resilience. Türkiye represents a primary center of diversity for the genus ***Aegilops***, comprising 17 species and plays a central role in global wheat conservation efforts. However, habitat degradation caused by agricultural expansion, deep ploughing, herbicide use, grazing mismanagement, and climatic instability combined with insufficient monitoring of existing Gene Management Zones (GMZs) continues to endanger these taxa.

To ensure long-term preservation, the study recommends establishing new GMZs in underrepresented regions, conducting recurrent germplasm collections, initiating long-term ecological monitoring, and strengthening community-based conservation and education programs. Integrating scientific research with participatory management is vital for maintaining Türkiye's unique wild wheat diversity and securing the genetic foundation of future global food production.

Keywords: Triticeae, ***Aegilops***, wheat relatives, biodiversity, genetic resources, conservation, Türkiye

Utilization of Wheat Landraces in Breeding and Their Changing Status in Farmers' Fields and Breeding Programs: The Case of Türkiye

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Abstract: Wheat is a staple crop in Türkiye, cultivated on approximately 7.5 million hectares with over 20 million tons of annual production. Despite the availability of many modern varieties, wheat landraces (WLRs) are still grown, particularly in remote areas, which is a unique situation in the world. These landraces, carried out by generations, not only provide income to farmers but also serve as a valuable source of genetic diversity for wheat breeding. The use of WLR's in Türkiye's breeding programs can be categorized into three main phases. The first phase, starting in the 1930s, called direct selection: Landrace populations were collected, pure lines were selected from those populations, selected ones tested, and successful lines were released as varieties. The varieties developed by this method remained in production until the mid-1970s especially in rainfed condition. In the second phase, beginning in the late 1930s, WLRs were used as parents in crosses, contributing to variety development until the early 1990s. In the third phase, WLRs have mostly contributed indirectly appearing in pedigrees as secondary parents or as sources of specific traits such as quality, disease resistance or nutritional value. The International Winter Wheat Improvement Program (IWWIP) is a joint program between Türkiye, CIMMYT, and ICARDA operating in Türkiye since 1986. Between 2009 and 2014, IWWIP collected over 1,700 WLRs from across the country. These were characterized and deposited in Türkiye's national genebank. Similar collections were made in some other countries. Comparative studies of WLRs from Türkiye, Iran, Uzbekistan, Tajikistan, and Afghanistan revealed that Turkish and Iranian landraces show significant overlap, while both differ markedly from Uzbek, Tajik and Afghan WLRs. This study presents the historical and ongoing contributions of Turkish WLRs to wheat breeding, highlights their genetic distinctiveness in regional comparisons and current status in the farmers' fields.

Keywords: Wheat landraces, breeding, genetic difference

ORAL PRESENTATIONS

Results of the Evaluation of Genetic Resources of Grapevine (Vitis vinifera L.) in Azerbaijan

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Abstract: The aim of the study is to determine, collect, perform ampelographic description, evaluate, and utilize in breeding the genetic resources pertaining to the subspecies of grapevine ***Vitis vinifera* ssp. *sylvestris*** C.C. Gmel. and ***Vitis vinifera* ssp. *sativa*** DC., which are widespread in Azerbaijan. The materials of the study were lianas and fruits of local grape varieties and wild forms. Ampelographic description of grape varieties and wild forms was carried out on the basis of modern methods, the coordinates of the areas where the samples were found were determined using GPS, and photographs were taken with a digital camera. As a result of the research, the main distribution areas of the identified grape samples were established, along with their phytocenotic characteristics and uvological indicators. Significant differences between local varieties and wild samples were also detected. It was determined that wild grapevine in Azerbaijan is found at elevations ranging from 12 meters above sea level to 2000 meters. It occurs on mountain slopes, in forests, near rivers, and in other locations. Varieties of folk selection and wild-growing forms of grapes were identified and collected, their ampelographic descriptions were carried out, and an assessment of morphological, biomorphological, economic and technological characteristics was given. New grape varieties "Alindja," "Nakhchivan Muscati" and "Nargizi" developed through long-term breeding work, have been registered by the Agency for Agricultural Services under the Ministry of Agriculture of the Azerbaijan Republic. The conducted research revealed that the conservation status of natural reserves of wild grapevine is at a low level, and the total cultivated areas and the number of local grape varieties are decreasing annually. Therefore, it is highly relevant to establish new ex situ collections of wild and cultivated grapevine samples with valuable biological and economic traits and unique genes, ensure their reliable protection, and utilize them in breeding new varieties, scientific research across various fields, and agriculture.

Keywords: Grape, variety, wild, genetic resources

Flora Biodiversity of Zangilan District

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Abstract: Zangilan district, located in the southwest of Azerbaijan, borders the Republic of Armenia to the west and north-west, and the Islamic Republic of Iran to the south and southeast. The area has a complex geomorphological relief, fascinating nature, and rich biodiversity as part of the Lesser Caucasus ecosystem. Monitoring was conducted on the main plant groups distributed here, including along the Hakari River basin. The territory is very suitable for the preservation of rare relict and endemic species. Currently, 20-22 percent of the region's territory is covered with forest, and 24% has been destroyed by the Armenian invaders. Semi-deserts with wormwood (Artemisetum) and steppes with Stipetum are characteristic of the Zangilan region. ***Astragalus zangelanus*** **Grossh.,** ***Centaurea karabajhensis*** **Sosn.,** ***Tulipa karabachensis*** **Grossh.,** ***Pyrus zangezura*** **Maleev.,** are native to Karabakh only. ***Platanus orientalis*** **L.,** ***G.arachina*** **(Tautv) Grossh.,** ***G. robur, G. longipes*** **Menitskii,** ***Celtis caucasica*** **Willd,** ***Pinus kochiana*** **Klotzsch.,** ***C. orientalis,*** can be found on the dry stony slopes of the region. ***P. mutica, Acer iberica, Ulmus arachina, Pyrus salicifolia, Juniferus*** *foetidissima* Uilld., from xerophytic shrubs ***Atraphaxis spinosa, Lonicera iberica, Cerasus microcarpa, Ephedra intermedia*** **Schrenk Et. C. A. Mey.,** ***Punica granatum*** **L.,** ***Mosquito rose*** **Sosn.,** ***Crataegus caucasica*** **C.Koch.,** ***Jasminum fruticans, Rhamnus pallasii, Paliurus spina-christi*** are naturally distributed. The main families of ***Asteraceae, Rosaceae, Fabaceae, Lamiaceae, Brassicaceae,*** **and** ***Poaceae*** occupy a prominent place in the flora of Zangilan. ***Geranium sanguinetum, Sambucus nigra, Melissa oficinalis, Valeriana oficinalis, Setaria viridis, Frangula alnus, Laamium album, Potentilla argentea, Euphorbia iberica, Primula macrochalus, Scutellaria orientalis, S. sevanensis, Iris camillae, Alchimilla amicta***, and other species are found in various meadow phytocenoses. Arctic-Tertiary relics of Hekari river Basin include species like ***Parmelia borreri, P. omphalodes, Bilimbia pulchra, Lecidea elata, Bacidia muscorum, Lecidea a, Aspicilia alpina, A. pleiocarpa, Hypogimnia vellata, Lecanora badia, Acarosporpa badiofusca, Solorina saccata, S. bispora, Cetraria cuculata, C. nivalis, Thelidium papulare, Caloplaca tetrospora, Stereocolon alpinum, Ochrolechia tetraspora, Rhizocarpon alpicola,*** etc. Considering the rich diversity of Zangilan's flora, monitoring and conducting field studies should be the main topics of research due to the increasing activity of invasive plant species that cause the loss of biodiversity.

Keywords: Flora, biodiversity, Zangilan district

Flora Biodiversity and Natural Plant Resources of the Lachin Turshsu Environment

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Abstract: Lachin is one of the regions located in the southwest of Azerbaijan, rich in natural resources and with diverse relief features. The Turshsu area is especially distinguished by its clean water, mineral springs and vegetation. In this article, the flora biodiversity and natural plant resources of the Turshsu area of Lachin district are initially investigated, rare and endemic species are noted, and their ecological and economic significance is evaluated. The Turshsu area is located in the mountainous part of Lachin district, mainly at altitudes of 1400–1800 m. Its cool and humid climate in summer and snow cover in winter create conditions for the formation of a specific flora of this zone. As a result of floristic observations conducted around Turshsu, more than 250 higher plant species have been recorded. Among them, representatives of families such as Asteraceae, Fabaceae, Lamiaceae, etc. predominate. Relict and endemic species have also been found in the area, including ***Betula litwinowii, Juniperus polycarpos, Iris acutiloba***, and Daphne mezereum. Subalpine and alpine phytocenoses, high mountain meadows, forest areas and hydrophilic shrub landscapes formed around the valleys in the area. Broad-leaved forests have formed in these zones. The main forest-forming species include ***Quercus iberica***-Iberian oak, ***Carpinus orientalis***-Oriental beech, Acer campestre-Common poplar and Fagus orientalis-Oriental hazelnut, etc. Rare and relict tree species such as Juniperus polycarpos-Long-leaved juniper and Betula litwinowii-Litvinov birch have also been found in some parts of the area. In the underforest area, shrubs of the Rubus, Rosa, Cornus, Berberis and Crataegus genera are widespread. Forest cover plays an important role in both protecting soils from erosion and ensuring the stability of the ecosystem. Hydrophilic shrubby plant associations are widespread in the Turshsu area, near running water sources and along the edges of valleys. These phytocenoses are mainly characterized by species such as ***Populus, Salix, Alnus, Cornus sanguinea***.

Keywords: Turshsu, herbarium, phytocenosis, ecological buffer, floristics

Distribution Area Characteristics of Anatolian Phoenix theophrasti (Datça Date Palm) Populations

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Abstract: The ***Phoenix theophrasti*** (Datça date palm), a Tertiary relict, is distributed along the Aegean-Mediterranean coast of Türkiye and from the Greek island of Crete. Genetically, the Datça date palm is the closest wild relative of the Phoenix dactylifera (date palm), which is traded and consumed globally today. The primary focus of this study is to determine the ecological characteristics of the Turkish populations of this Tertiary relict palm species and to develop conservation strategies accordingly. This study identified five populations of the species in Türkiye (from south to north, Antalya-Finike, Antalya-Patara, Muğla-Datça/Hurmalıbük, Muğla-Datça/Eksere, and Muğla-Bodrum/Göltürkbükü). Habitat characteristics of the populations were determined by field observations according to the EUNIS habitat classification. Soil physical and chemical properties of these populations were determined using standard analysis methods, and local climatic characteristics were determined using data loggers placed in each population. Statistical analyses were used to determine the relationships among the populations based on the data. According to the EUNIS habitat classification system, Datça date palm populations are known as "G2.53 - Anatolian Phoenix theophrasti groves." The populations are distributed around Mediterranean-type temporary (seasonally) running waters. The study determined that five populations of Datça date palms inhabit sandy loam and loamy soils. pH ranged from neutral to moderately alkaline, and salinity ranged from 0.475 to 1.520 (dS/ml). This finding was consistent with the basin soil inventory. Organic matter (%) ranged from 5 to 6.88, indicating that the species prefers humus-rich soils. In terms of CaCO3 (%), all populations except the Patara population were found to inhabit low-calcareous soils. The Patara population was found to inhabit very calcareous soils (22.32-29.4%). Three years of climatic data recorded from the populations indicated that the species has a climate preference between Mediterranean and subtropical climates, and that there were no significant differences among the populations except for maximum relative humidity values. This study was supported by TÜBİTAK under project number 116Z288. We believe that the soil and climatic data identified will contribute to the ex situ conservation of the species. According to the same project data, P. theophrasti (Datça date palm) populations, represented by 307 adults in Türkiye, should be rapidly enriched and their numbers increased through ex situ conservation and recovery efforts to ensure their survival into the future. Furthermore, awareness of the species' use in landscaping and in local gardens should be raised among local governments in areas where the species is distributed, and these efforts should be supported by national and international project resources.

Keywords: ***Phoenix***, Arecaceae, date, EUNIS, habitat, soil, conservation

Investigation of Wild Plant Diversity in Azerbaijan: Collection and Taxonomic Evaluation

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Abstract: Azerbaijan's rich and unique wild flora represents a primary source of genetic diversity and a crucial reservoir for plant breeding. Considering that wild relatives of crops often possess resistance to diseases and tolerance to climatic fluctuations, their study and conservation are of great importance for food and agricultural security. The main objective of this research was to investigate, collect, and taxonomically evaluate the diversity of wild plant species distributed across different ecological conditions. The study was conducted between 2014 and 2024 in the regions of Qakh, Balakan, Zagatala, Khizi, Altiaghaj, Masalli, Jalilabad, Lankaran, Astara, Lerik, Yardimli, Goygol, Dashkasan, Goranboy, Tovuz, Gadabay, Ganja, Quba, Qusar, Barda, Aghjabadi, Beylagan, Fuzuli, Shusha, and Jabrayil. The research material consisted of plant collections gathered from various habitats. During field expeditions, wild plant species occurring under diverse ecological conditions were observed, and more than 3,000 herbarium specimens and over 150 seed samples were collected and preserved. The priority names of the studied species were verified based on the multi-volume Flora of Azerbaijan, the book Plants of Azerbaijan, as well as through international plant nomenclature databases (IPNI, WFO, CWR, Green Global). As a result of the investigations, more than 100 wild relatives of crops were identified and assessed as potential donors for breeding programs. Special attention was given to species belonging to the genera ***Aegilops, Allium, Avena, Asparagus, Brassica, Corylus, Crataegus, Hordeum, Lathyrus, Malus, Medicago, Onobrychis, Prunus, Pyrus, Rosa, Sorghum, Trifolium, Vicia*** and others. The collected data demonstrate that the systematic study and conservation of wild species hold strategic significance, particularly for their future utilization in agriculture and food security. This research contributes to the scientific understanding of Azerbaijan's wild plant diversity and supports the sustainable management of its genetic resources.

Keywords: Species, wild plant diversity, collection, taxonomic evaluation, genetic resources

Genetic Resources and Diversity of Cotton (Gossypium ssp.) in Azerbaijan

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Abstract: Cotton is one of the economically important industrial crop in Azerbaijan. Production of cotton provides income for more than 250 million people worldwide by employing almost 7% of all labor in developing countries. The oil obtained from the seeds is used for food, and the oilcake is used as a high-protein feed for livestock. Its fiber serves as a raw material for the textile industry. In addition to productivity and fiber quality, disease resistance is a very important goal for cotton cultivation. The National Genbank has 1518 cotton accesions of diverse origin. Local cotton collection is consisted of ***G.arboreum*** (2 accsesions), ***G.barbadense*** (118 accesions), ***G.hirsutum*** (1396 accesions), ***G.thurberi*** (1 accesion), ***G.tricuspidatum*** (1 accesion). Out of 936 accessions, 2 are in long-term, and 934 are in mid-term conservation. In addition to seed rehabilitation, we are conducting the collection of characteristic data based on international descriptors. The characteristic data includes productivity, fiber yield, 12 parameters of cotton fiber etc. Currently, the Central Database of the National Genebank contains characteristic data for 354 accesions for 17 traits. As a result of hybridization, physical and chemical mutagenesis carried out by geneticists and breeders of the Institute for many years, a rich collection of cotton genotypes has been created. Along with amphidiploid species, diploid, triploid, complex hexaploid species are stored in the collection. In addition to cytogenetic diversity, diversity according to biomorphological traits - dwarfism, semi-dwarfism, compact forms, color diversity in different spectra of brown in the color of leaves and fiber has also been created.

Keywords: Cotton, ***G.hirsutum***, Genbank

Formation of the VIR Aromatic and Medicinal Crops Collection

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Abstract: Medicinal and aromatic plants (MAPs) are a source of biologically active compounds used in medicine, cosmetics, functional foods, and the production of natural dyes. The collection of the VIR MAPs began forming in the 1930s, with sorrel and asparagus being the first crops introduced. The VIR MAPs collection includes 5 003 accessions, representing 118 genera, 237 species, subspecies, local forms, cultivars, and hybrids belonging to 36 families. The collection includes aromatic crops, rare leafy greens, rare root vegetables, a group of perennial vegetable crops, and medicinal plants. The most widely represented families are Lamiaceae (28.4%) and Asteraceae (17.3%). In recent years, the collection has been actively expanded. VIR expeditions cover vast regions of Russia, Central and Middle Asia, and Transcaucasia - traditional cultivation zones for many rare greens and aromatic crops, such as basil, savory, garden cress, and tarragon. Of particular value are landrace, breeding cultivars, and accessions collected during expeditions. The collection has been enriched with modern breeding varieties of diplotaxis, arugula, lavender, basil, and leaf chicory from Russia, Germany, the Netherlands, Romania, and Vietnam. Research on the collection has been ongoing since the 1930s, focusing on phenological growth stages, biological characteristics, morphological traits, biochemical parameters, plant physiology, breeding and seed production methods, cultivation techniques. Studies have included rare crops for most Russian regions, such as coriander, garden cress, endive and witloof chicory, asparagus, rhubarb, savory, okra, scorzonera, lemon balm, as well as traditional crops like sorrel and horseradish. In recent years, active research has been conducted on morphological, phenological, and biochemical traits of collection accessions, particularly garden cress and arugula under different growing conditions (open field, green houses, artificial lighting), ecological and geographical studies of basil, root chicory, St. John’s wort, and nigella, biochemical analyses of mint, nigella, endive, basil, edible chrysanthemum, Malabar spinach, and St. John’s wort.

Keywords: Collection, medicinal and aromatic plants, gene bank, diversity, variability

VIR Vegetable and Cucurbit Crops Genetic Resources

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Abstract: 103 years old Russian collection of vegetable and cucurbit genetic resources, stored in N.I.Vavilov Institute (VIR), consists of 53177 germplasm accessions of different status (5.5% - wild species and primitive forms, 34% - landraces, 49% - breeding cultivars, 11.5% - genetic material) from 98 countries, belonging to 32 botanical families, 148 genera, 610 species, and reflects natural diversity of worldwide wild and cultural plants in evolutional aspect quite complete. Main directions of vegetable collection composition increasing: introduction new for Russia crops and cultivar types; collection the wild species and landraces, including large diversity of medicinal plants, with high level of resistance to biotic and abiotic stresses, valuable biochemical composition, decorative characters. VIR organized totally 442 expeditions to collect vegetable genetic resources, 30 from them for the last 15 years; during annual collection missions VIR collects 400-450 new vegetable accessions per year. Regeneration of collection includes 8500 accessions per year, characterization and complete evaluation for morphological and biological traits using the VIR descriptors and standardized research methodics – 2600 accessions at 11 experimental stations in the different ecogeographic zones of Russian Federation. The main goals of vegetable PGR evaluation at VIR: productivity, precocity (generally to move the crops to the Northern regions of Russia), availability for city-farming, resistance to diseases and pests, taking into account the increase in their number, biochemical composition, including value for functional nutrition, dwarfism, portioning, original shape and colour, etc. VIR develops the genotyping of biodiversity, search of the target genes. As result, the trait and genetic collection are being replenished annually.

Keywords: VIR vegetable collection, status, activities

Azerbaijan's Plant Genetic Wealth in the Works of Nizami Ganjavi

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Abstract: National Leader of the Azerbaijani people, Haydar Aliyev, while speaking about the universality of the works of the great Azerbaijani poet Nizami Ganjavi and the scientific essence of his 'Khamsa', said: " These works don't just consist of poem, all of them has a big science, a big philosophy, big thoughts. That is why he and also his works still are in the life." The great poet of Azerbaijan Nizami Ganjavi , in his works, delicately reflected not only national-spiritual and universal values but also rich natural landscapes, the true artistic beauty of the local flora and fauna, and their genetic diversity. The genetic diversity of cultivated plants reflected in his poetic legacy is depicted like a mirror of the nature of Azerbaijan's geographically rich regions. Especially in the poems included in the "Khamse" (such as "Yeddi Gozal", "Iskandarnama", "Layla and Macnun" and "Sirler Khazinesi"), the reader encounters the rare plants, fruits, mountain streams and forests of the fertile Azerbaijani lands. For Nizami, the valuable plant genetic resources unique to the nature of Azerbaijan are not merely an aesthetic background but a living organism that gives spiritual pleasure to humans. The fruit orchards, unique flowers, and wildlife described in his works are a reference to the local species that form Azerbaijan's genetic diversity and ecosystem. For example, the depiction of the diversity of plants such as pomegranate, grape, saffron, and basil serves both as a folkloric element and as a portrayal of the genetic uniqueness of these plants in the nature of Azerbaijan. In "Yeddi Gozal" – the narcissus blooming in the gardens of Ay Kız and Shahrevser, the zodiac flowers, and the saffron spreading fragrance are depicted in such a way that the reader senses the unique genetic code of these plants passed down from generation to generation. In the poem "Layla and Macnun", it is emphasized that the mulberry tree, which awaken love in Majnun in the desert, are not only symbolic but also rooted in the genetic memory of this land. Likewise , in the masnavi "Iskandarnama", the seasonal harmony of Azerbaijan's nature reveals that Nizami, the author of the "Khamsa", was also one of the greatest naturalists. Such aristic representation of Azerbaijan's local flora also demonstrates, from a scientific perspective, that it is a highly valuable resource. Nizami's poetic language, which conveys the harmony between nature and humanity, unites universal values with love for the homeland and biological sustainability within the same theme. The saffron, basil, pomegranate, and other plants mentioned in the poet's works are not only spiritual symbols but also living resources of the national gene pool shaped over centuries. Nizami's attention to this field provides strong inspiration today for the preservation of genetic diversity, the protection of rare species and the environment, as well as the safeguarding of food security. In conclusion, the works of Nizami Ganjavi are not only a literary treasure but also a scientific and artistic insight into the genetic resources of Azerbaijan's nature. This legacy conveys to future generations the necessity of preserving both national identity and natural wealth.

Keywords: Azerbaijan, Nizami Ganjavi , nature, plant, genetic wealth

ICARDA's RegionalHhub for CWR Regeneration and Characterization - Strengthening Conservation of CWANA Agrobiodiversity Through Partnerships and Innovation

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Abstract: Conservation and sustainable use of CWR is not just important – it is urgent. The climate change implications threatening food security, are particularly in fragile and vulnerable drylands. ICARDA's new initiative, is using its assets to remove bottle necks in national genebanks that cause limited availability of CWR for sustainable use. Being at the forefront on plant genetic resources conservation, ICARDA Genebank holds a pivotal role in conserving, managing and utilizing the CWR. The activities expand from collecting novel diversity of CWR using GAP analysis and continue to regeneration of the accessions following innovative protocols related to seed germination, maintenance of genetic integrity, identification of valuable traits, and seed processing. Furthermore, using salient tools to seek adaptive traits, selected CWR are entered into the pre-breeding pipeline, where advanced technologies, such as speed-breeding combined with genotyping will enhance ICARDA efforts to derive unique germplasm with better adaptation to major biotic and abiotic stresses. While ICARDA Genebank conserves one of the largest CWR collections acquired (collection missions or donations) through decades of collaboration with national partners mainly across CWANA region, however, critical gaps remain. More valuable CWR diversity is conserved in national collections or awaiting to be sampled from in situ. In many of these national collections, regeneration and characterization of CWR is often the most challenging core activity, quite justifiably. Fortunately, ICARDA has accumulated over the years capacities in facilities, specialized equipment and tools, expertise, specialized knowledge, customized protocols, and advanced technologies that has allowed us to deal efficiently and effectively with the difficult wild species. We are presenting ICARDA's role as a regional hub for services and knowledge sharing for CWR regeneration and characterization, with the aim of increasing collaboration and complementarity, and increasing regional impact of CWR conservation and sustainable use.

Keywords: Crop Wild Relatives (CWR), regional hub, regeneration & characterization, CWANA, Genebank

Plant Genetic Resources of Azerbaijan

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Abstract: The high diversity of soil and climatic conditions in Azerbaijan has led to the development of a rich vegetation cover. As a result of serious fundamental research and international expeditions, it has been established that Azerbaijan is one of the centers of origin and domestication for many cultivated plants. Among the approximately 5,000 higher plant species in the natural flora, more than 40% are wild ancestors and relatives of cultivated plants, and 5% are currently cultivated in domesticated form. The basis of the country's food and agricultural system consists of modern varieties, ancient landraces, and forms. Secondary and underutilized species, wild ancestors of cultivated plants, other wild species used for food purposes, as well as intraspecific and interspecific diversity, are also considered part of plant genetic resources. The main agricultural crops include:cereals (wheat, barley, rye, emmer, etc.),grain legumes (chickpea, lentil, grass pea, beans, etc.),vegetables and melons (tomato, eggplant, watermelon, melon, squash, etc.), forage legumes (alfalfa, sainfoin, etc.),fruits (apple, pear, apricot, plum, quince, pomegranate, fig, almond, walnut, hazelnut, etc.), grapes and technical crops (cotton, sugar beet, tobacco, etc.). In the flora of Azerbaijan, 1,227 species (from 53 families and 172 genera) can be classified as wild ancestors of cultivated plants (excluding ornamental and medicinal plants). Azerbaijan is considered a center of origin for many of these plants, including: some wheat species (***Triticum boeoticum***, ***T. spontaneum***, ***T. urartu***, ***T. araraticum***, etc.), barley species, especially (***Hordeum spontaneum***, ***H. bulbosum***, ***H. geniculatum***, ***H. violaceum***, etc.), 9 species of goatgrass (***Aegilops kotschyi***, ***A. tauschii***, ***A. umbellulata***, etc.), 5 species of rye (***Secale vavilovii***, ***S. anatolicum, S. segetale***, etc.). Numerous forage plants (***Medicago***, ***Onobrychis***, ***Vicia***, ***Pisum***, etc.), fruit and vegetable crops can also be mentioned. Global environmental changes and anthropogenic factors have intensified genetic erosion, placing biological diversity at serious risk. The risk of losing highly valuable genetic diversity specifically traditional varieties created by local people and their wild ancestors is high. Such local varieties and forms are rapidly disappearing and being forgotten.
Therefore, the collection, restoration, conservation, involvement in modern research, and establishment of a new management and coordination system for genetic resources is urgently needed. For this purpose, in 2003, the Genetic Resources Institute was established on the basis of the Institute of Genetics and Selection and in 2005, for the first time, a Genebank with medium- and long-term storage and research capacity was created. In 2011, the Law of the Republic of Azerbaijan on the Conservation and Efficient Use of Genetic Resources of Cultivated Plants was adopted by the National Assembly of the Republic of Azerbaijan. To strengthen activities in the field of plant genetic resources (PGR) and ensure the implementation of this law, the Cabinet of Ministers of Azerbaijan assigned the Genetic Resources Institute as the National Coordinating Institution for the conservation and efficient use of cultivated plant

genetic resources by Resolution № 259 in 2012. The genebank at the Institute was granted the status of the National Genebank. According to the law, the National Genebank is a national treasure of the Republic of Azerbaijan and is classified as a state-protected natural object with all its property. At the beginning of 2013, to further strengthen PGR activities at the state level, a Scientific-Technical Council – Management Committee was created under the Cabinet of Ministers, involving various government institutions. Within this structure, specialized expert councils and working groups on priority directions operate as part of the national PGR management system. The National Genebank preserves 15,003 samples of plant genetic resources, including 892 species and 367 intraspecific taxa., belonging to 117 families and 460 genera. By crop type: 6,073 cereals, 2087 legumes, 811 medicinal plants, 789 forage crops,1,650 industrial crops, 930 vegetables, 2,659 fruit crops. By biological status: 4,179 scientific varieties, 2,524 landraces, 5,198 research materials, 2989 wild relatives. A selected and globally important part of the national collection is duplicated and preserved in the Svalbard Global Seed Vault (Spitsbergen Island) and in international genebanks, including: CIMMYT (***Triticum durum*** **Desf**. – 510 samples, ***Triticum aestivum*** **L.** – 369, **Zea mays L.** – 200); ICARDA (***Hordeum*** (***distichon, vulgare***) **L.** – 194, ***Lathyrus sativus*** **L.** – 67, ***Lens culinaris*** (***esculenta, ervoides***) **L.** – 40, ***Vicia faba*** **L**. – 14); ICRISAT (***Sorghum bicolor*** **(L.) Moench** – 11, ***Cicer arietinum*** **L.** – 65); CIAT (***Phaseolus vulgaris*** **L.** – 73); IITA(***Vigna*** (***unguiculata, radiata, sinensis***) L. – 20); KEW (UK): 511 accessions of crop wild relatives. Currently, breeding work is carried out based on comprehensive scientific foundations using an ecosystem approach. In the context of global climate change, long-term experimental data is analyzed, and agro-ecological forecasting models are developed. Based on scientifically grounded forecasts, new plant varieties with relevant traits are created for each region. The use of plant genetic resources in breeding programs has reached a significantly higher level. The improvement of conservation and utilization efforts also depends on well-organized and efficiently managed information systems. A National Network and National Information System have been established to collect, analyze, and seamlessly transmit all information related to PGR. This information system has been integrated into international platforms, including FAO, EURISCO, GENESYS, and others.

Keywords: Azerbaijan plant genetic resources, management system of PGR, National Gene Bank

NARO Genebank, Japan

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Abstract: NARO Genebank is the lagest genebank in Japan for agriculture, conserving genetic resources of plants (24 thousand accessions), microorganisms (37 thousand accessions) and animals (2 thousand accessions). Ministry of Agriculture, Forestry and Fisheries, Japan, started the genebank in 1985, and currently the Research Center of Genetic Resources, National Agriculture and Food Research Organization (NARO), organizes it as a center-bank, responsible for its management in collaboration with a network of sub-banks all over Japan. We have two seed storages in Tsukuba, Japan, for mid-term and long-term conservation in duplication. The operation of the seed storages is automated: upon orders by operators on computer, automatic machines take out the seeds of request. According to standard procedures of genebanks, germination rates of conserved seeds are tested basically every five years. If necessary seeds are renewed and multiplied in the field, then divided into the two storages. Recently, we are developing and implementing cryopreservation tecnhiques for various plant genetic resources which needs vegetative propagation, such as potatoes and fruit trees, to avoid risks of loss due to pests or climate changes and also to reduce costs of conservation. Core collections have also been developed in NARO Genebank. They are a small subset of specific crops representing the whole genetic diversity and used as tools for breeding and diversity researches of plant genetic resources. In addition to the collection of plant genetic resources in Japan, we collaborate with foreign countries, such as Vietnam, Cambodia, Laos, Kyrgyz and Uzbekistan to conduct joint research projects on plant genetic resources.

Keywords: Genebank, cryopreservation, international collaboration

Studies of National Seed Gene Bank

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Abstract: Protecting our biodiversity and genetic resources today and transferring them to the future is crucial for the sustainable use of our biodiversity and genetic resources. One of the most effective conservation methods is *ex situ* conservation under gene bank conditions. This article summarizes the activities of the National Seed Gene Bank in the *ex situ* conservation of plant genetic resources. The National Seed Gene Bank has long been conducting its activities according to international standards in monitoring, resource collection, preservation, and information management for the protection and conservation of plant genetic resources. The National Seed Gene Bank began its collection and preservation efforts in 1964 within the Aegean Agricultural Research Institute. It has continued its work to international standards since 1974. The National Seed Gene Bank's activities ensure the long- and medium-term conservation of orthodox-type seeds of local varieties, wild relatives of cultivated plants, and other wild species found in the Turkish flora. For this purpose, seed collections obtained from annual collection programs are preserved in the Seed Gene Bank in two sets: active and base collections, in cold rooms at 0°C and -18°C, respectively. The viability of each seed sample is periodically monitored in the gene bank. The total number of materials in the National Gene Bank collection is approximately 60,000 seed samples, representing approximately 3,090 species. All of the preserved seed samples are of Turkish origin. The Turkish Seed Gene Bank, operating under the Field Crops Central Research Institute, maintains backups of the base collections in the National Gene Bank. The gene bank collections are used by researchers free of charge for research and plant breeding purposes within the scope of the project, in accordance with a material transfer agreement. Additionally, the National Gene Bank maintains more than 37,000 herbarium specimens at the IZ Herbarium.

Keywords: National Seed Gene Bank, *ex-situ* conservation, genetic resources

Collection, Conservation, Study, and Utilization of Plant Genetic Resources in Uzbekistan: a Century of Progress

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Abstract: Uzbekistan's rich biodiversity, encompassing over 4,500 plant species with a significant proportion of endemics, underscores the critical importance of conserving and utilizing its plant genetic resources. The National Gene Bank leads these conservation efforts, managing the systematic collection, preservation, and study of these valuable resources for current and future generations. This study draws on comprehensive data from the National Gene Bank's archives, electronic databases, and expedition materials, following established methodological guidelines from FAO and Bioversity International. The research methodology ensures standardized approaches to genetic resource documentation and analysis. Over the past century, the Scientific Research Institute of Plant Genetic Resources has systematically amassed an impressive collection of over 44,000 accessions representing 103 distinct crop species through extensive national and international expeditions and collaborative partnerships. The National Gene Bank currently maintains this substantial collection, which includes cereals (21,969 accessions), technical crops (11,068), vegetables and melons (5,755), fruit crops (2,985), and grapes (1,812). This collection represents a rich repository of unique and endangered forms, ancient local varieties, and wild relatives of cultivated plants sourced from numerous countries worldwide. The genetic resources are strategically preserved using dual conservation approaches: a Medium-Term Seed Gene Bank housing 38,753 accessions and a Field Gene Bank maintaining 5,002 living collections. These comprehensive conservation efforts have yielded significant practical outcomes, resulting in the successful development, release, and official approval of 312 improved varieties across cereals, legumes, fruits, vegetables, melons, technical crops, and grapes. This achievement demonstrates the tangible benefits and practical applications of genetic diversity conservation for advancement.

Keywords: Genetic diversity, gene bank, breeding, conservation, endemic species

Using Prospects of Ozonization Technology for Fumigation of Plant Seed Samples in Genebank Conditions

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Abstract: Prospects of ozonization technology for the safe and long-term storage of seed samples in genebank were identified. Tests were conducted to inactivation of harmful spores on the seed surface without breaking the dormancy by short-term exposure to a slightly higher concentration of an Ozone-Air Mixture (OAM) for fumigation under genebank conditions. Germination was determined on the 1st, 3rd and 7th days after seed processing at a concentration of 700-3000 ppm for 10, and 20 minutes. Based on the obtained results, the efficiency of using OAM was determined with an exposure of 10 and 20 minutes (700 ppm x 20 min on wheat, 1200 ppm x 10 min on chick pea, 800 ppm x 20 min on corn, 3000 ppm x 10 min on cotton) for fumigation, since it does not cause the breaking of the seeds dormancy. At the concentration of OAM corresponding to the seed size and 10, 20 minutes of exposure time, the viability of the bread wheat variety Azametli 95 compared to the control was 30% on the 1st day, 15% less on the 3rd day, and the germination on the 7th day was 1% more (96%), for the corn variety Zagatala-68 on the 1st day 31%, on the 3rd day 29%, on the 7th day 2% less (92%), for the cotton variety Ganja 110 on the 1st day 21%, on the 3rd day 14%, on the 7th day 2% less (95%), and for the chickpea variety Sultan on the 1st day 15%, on the 3rd day 4% less, on the 7th day was the same (94%). As a result of the conducted studies on the effectiveness of using OAM in fumigation of seeds of crops stored in gene bank conditions, the ozonization dose for various species was clarified by the mass fraction of the seed coat and method for processing was developed.

Keywords: Genebank, fumigation, seed, germination percentage

The Effect of Phytohormone Complex on Hard Wheat Samples Stored Long-Term in Genbank Conditions

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Abstract: The aim of this study was to evaluate the effectiveness of auxin and kinetin phytohormones in reducing the risk of genetic damage that occurs during long-term seed storage in cooling chambers, using soft wheat samples from the National Genebank collection. The research material consisted of seeds of 10 durum wheat (***Triticum durum*** **Desf**.) varieties (Qizil bughda, Birlik, Jafari, Sevinj, Aran dani, Qaraqilçiq, Sari bughda, Qara bughda, Agh bughda, and Shirvan bughda) that had been stored long-term in the National Genebank. To ensure genetic stability, a mixture of auxin and kinetin was applied (each at a concentration of 10^{-2} mg/ml), and the functional state of the seeds was assessed based on germination capacity, cell division dynamics, and the frequency of chromosomal aberrations. When rootlets reached a length of 11–13 mm, they were fixed in Carnoy’s solution (3:1 alcohol to glacial acetic acid) and stained with acetocarmine. Chromosomal aberrations and mitotic activity were analyzed using the anaphase–telophase method on temporary preparations. As a result of natural aging, the frequency of chromosomal aberrations increased (6.0–8.0%), seed germination declined (62.0–75.0%), and mitotic activity decreased (8.0–11.0%). Treatment with auxin and kinetin significantly improved both germination percentage and mitotic activity of meristematic cells, while also reducing the frequency of chromosomal aberrations with high statistical confidence (Student’s criterion, $p < 0.001$). The strongest positive effect of phytohormones was observed in the Shirvan bughda variety (germination 90.0%, mitotic index 15.75%). The lowest frequency of chromosomal aberrations after treatment was recorded in the Sevinj variety (2.20%). These findings demonstrate that the auxin–kinetin phytohormone complex plays an effective role in maintaining genetic stability and restoring seed viability. This approach may be recommended as a promising method for the preservation of plant genetic resources.

Keywords: ***Triticum durum***, genetic stability, germination capacity, phytohormones, chromosomal aberrations

Callus Induction of Hyphaene thebaica L.: a Step Toward Conservation of a Rare and Endangered Medicinal Plant

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Abstract: ***Hyphaene thebaica L***. (doum palm) is a rare and endangered medicinal plant with significant ethnobotanical value across arid and semi-arid regions. Despite its diverse pharmacological properties, including antioxidant, antidiabetic, and antimicrobial activities, its propagation is hindered by poor seed germination, overexploitation, and habitat degradation. This study aimed to establish an efficient in vitro callus induction protocol as a foundational step for mass propagation and ex situ conservation.

Explants derived from female and male inflorescence and root tip were cultured on Murashige and Skoog (MS) medium supplemented with varying concentrations of auxins (2,4-D, NAA) and cytokinins (BAP, kinetin). Among the treatments, MS medium supplemented with 10.0 mg/L 2,4-D and 3 mg/L 2ip showed the highest callus induction frequency and biomass accumulation. Calli were friable, pale-yellow, and maintained sustained proliferation upon subculturing. Histological examination confirmed the presence of actively dividing meristematic cells, indicating potential for further organogenic or embryogenic differentiation.

The established protocol serves as a preliminary but critical step toward the development of complete regeneration systems for ***H. thebaica***, contributing to its conservation and potential use in future biotechnological and pharmacological studies. These findings underscore the importance of tissue culture techniques in preserving endangered medicinal plant species with high therapeutic potential.

Keywords: ***Hyphaene thebaica***, callus induction, medicinal palm, plant tissue culture, biotechnology

History, Analysis and Importance of the Collection of Cereal Gene Pools

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Abstract: The gene pool is understood as the entire diversity of elementary traits (characters) within a set of any individuals. A gene pool refers to the combination of all the genes (including alleles) present in a reproducing population or species. The main goal of the research is to collect the gene pool of grain and leguminous plants, study their biological characteristics, select the best forms and use them as starting material for breeding work. The methodology of the research work was based on the generally accepted “Methodology of Breeding Work”. In order to theoretically substantiate the results obtained, we set the task of collecting and analyzing wild and cultivated forms of grain plants, studying the varietal differences of plants grown under the same agrotechnical conditions. In order to achieve the set goal, the selected forms were tested in the experimental field of the laboratory, and phenological observations, plant and spike analyses were conducted on them. In this research work, we conducted research in the collection field planted in the experimental field to study the gene pool of wheat species. We studied the species, species diversity, varieties and hybrids there. Therefore, we compiled a program in accordance with the general methodology for the comparative study and evaluation of cultivated plant species and conducted research on its basis. First, we studied the botanical description of the wheat plant, its distribution area, and its importance for the national economy, then we studied the soil-climatic conditions of the zone, the description of important wheat species, the gene pool of tetroploid, durum wheat, rice, polonicum, Turan wheat, etc. turgidium, their distribution, importance and use in plant breeding. Phenological observations are carried out on our wild and cultivated wheat species and varieties, their use in breeding work is determined.

Keywords: Gene pool, wheat, spike, ear, grain

Key Trends in Studies on Genetic Diversity and Origin of Plants in Genome and Post-genome Era

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Abstract: One of the main causes of the diversity of the living world is the genetic diversity of organisms. On our planet, plants are the most diverse group of organisms. To date, more than 380000 plant species have been described. Over the past 25 years, the genetic diversity of plants has been studied in various areas, including the following main areas.

Genomics and pan-genomics. Since 2000, beginning of the plant genome era, over 4600 plant genomes from more than 1480 plant species have been published. Now, the Ten Thousand Plant Genome Project (10KP) aims to sequence the genomes of 10,000 plants. It has been shown that there are numerous differences between the genomes of individuals of the same species, from single nucleotide polymorphisms to large-scale rearrangements, and in many cases they lead to serious functional changes. The presence or absence of certain genes or genomic regions among different genotypes of a species is one of the important manifestations of intraspecific genomic variation in plants. However, over the last 25 years, the questions "How many genes does a genome have?" and "How many different proteins are synthesized in a cell?" are still unanswered. Moreover, a study of a single genome (genomics) is no longer sufficient. Now, within a species, pan-genomics studies are coming to the fore.

Transcriptomics and gene expression regulation. Transcriptome analysis allows us to obtain important knowledge about the genetic diversity, origin and evolutionary history of plants by revealing patterns of coordinated or differential expression of genes depending on the course of ontogenesis and environmental factors, molecular markers associated with certain traits and evolutionary lines. Research in this area is divided into various sub-areas, as determination of gene expression patterns (including RNA-Seq) and molecular markers (for example, SNP spectrum) and patterns of adaptive evolution, phylogenomics, comparison of cultivated and wild populations, etc. The genetic diversity of plants is largely ensured by gene regulation mechanisms. These mechanisms can greatly contribute to the emergence and evolution of new traits and even species of plants by regulating gene expression. The main role in this process belong to the transcription factors (TF) and their binding sites (TFBS) in DNA (enhancers, silencers and other TFBSs). Thus, in tissues and cells, depending on the course of ontogenesis, intercellular/organ signals and environmental factors, there are gene regulation networks.

Proteomics. The study of proteins at the whole organ/tissue/cell scale, in various stress situations and pathological conditions, also provides important information about the genetic diversity, origin and evolution of plants, and the molecular participants and mechanisms of adaptation to a changing environment.

Over the past 20 years, we (my colleagues and I) have been conducting research in all 3 directions mentioned above using bioinformatics analysis tools. During this time, a number of bioinformatics methods have been developed to search for promoters (transcription start sites, TSS), TFBSs and other regulatory elements in plants, where the promoter search tools, TSSP-TCM and TSSPlant, are based on the Artificial Intelligence approach, as Support Vector Machine and Neural Network, respectively. Moreover, a number of important results have been obtained on intracellular (chloroplast-nucleus, mitochondria-nucleus) gene/DNA transfer, potential promoter (TSS) sequences of whole genomes, non-coding RNA sequences of genomes, and the synthesis of alternative proteins (polypeptides) based on the same mRNA. These studies are currently ongoing.

Keywords: Plant genetic diversity, genomics, pan-genomics, transcriptomics, proteomics

Uploading the National Collection to the Genesys PGR Platform: Benefits and Usage Guidelines

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Abstract: The conservation and management of the genetic diversity of agricultural crops is a fundamental component of global food security. Genebanks are specialized infrastructures established for this purpose, which not only conserve seed samples, also hold data on plant accessions maintained in national and international collections across different countries. One of the globally significant platforms in this field is Genesys-the online platform where information on PGR for Food and Agriculture conserved in Genebanks worldwide is made available. This article provides a detailed analysis of the process of uploading data to the Genesys platform, its scientific and practical significance, as well as usage procedures. Since 2004, the Genetic Resources Institute has established an information system on PGR. The central database of this system contains passport descriptor data on plant diversity collected and conserved in the national *ex situ* collections inventoried across the country. These data follow the international MCPD (Multi-Crop Passport Descriptor) standard, which integrates information on taxonomy, geography, storage, regeneration, exchange, and etc. breeders, and donors involved in these activities. Efforts to enhance the Central Database (CDB) – the National PGR Information System – through data refinement, structural analysis, updates, and modernization are ongoing. The Genesys plays a crucial role in conserving and sharing genetic diversity. Uploading data to this platform not only facilitates its use, but also opens new opportunities for the international scientific collaboration. Initially, the data are harmonized according to MCPD. The platform accepts data files in CSV or JSON formats, and integration processes can also be conducted via API. Once the uploaded data is verified by the system, it becomes publicly accessible. Researchers gain rapid access to the information on genetic materials, locally collected data is delivered to the global scientific community, ensuring transparency, equal opportunities in the use of genetic resources.

Keywords: Genesys, plant genetic resources, Genebank

Conservation and Utilization of Vegetable Genetic Resources of Türkiye

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Abstract: Türkiye is very important in terms of plant genetic resources and genetic diversity. Our country overlaps with the Near East and Mediterranean Vavilov centres of plant diversity, ın addition, due to ecological and topographic differences, plant diversity is quite high. The fact that our country is a bridge between Asia, Europe and Africa has enabled many plant species to spread in Turkey since ancient times. Türkiye is very rich in genetic resources and provides raw material for world agriculture. But plant diversity is decreasing and disappearing due to many reasons such as the replacement of local varieties by new registered varieties, new clear land, urbanization, natural disasters such as fires and erosion, etc. A plant genetic resources collection program has been carried out throughout Türkiye by the Aegean Agricultural Research Institute since 1963, and the collected material has been preserved in the National Seed Gene Bank. Today, there are 57,767 materials (3090 species) in the Aegean Agricultural Research Institute National Gene Bank. And these materials include 11,340 vegetable genetic resources collected from every region of our country. In the studies on vegetable genetic resources carried out at the Institute, primarily the survey/collection of new vegetable genetic resources, multiplication/regeneration, characterization and utilisation, and conservation are carried out. In addition, vegetable genetic resources are used extensively in both open pollinated and hybrid variety breeding studies carried out at the Institute. As a result of these studies, many varieties of tomato, pepper, eggplant, melon, lettuce and okra have been developed using these materials.

Keywords: Vegetable genetic resources, regeneration, conservation, characterization, National Seed Gene Bank

Evaluation of The Collection of Rye Inbred Lines Based on Quantitative Traits

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Abstract: This study aimed to investigate the quantitative traits of local and introduced rye inbred lines (**S. *cereale* L., S. *segetale* Roj**.). The plant material consisted of 186 4th generation inbred lines. The accessions were evaluated for nine agronomically important traits: heading date (HD), flowering date (FD), maturing date (MD), plant height (PH), peduncle length (PL), spike length (SL), spikelets number (SN), grain number (GN), and thousand-grain weight (TGW). For data analysis, one-way ANOVA, Pearson correlation and cluster analysis (Euclidean distance, Ward's method) were performed using SPSS software. The phenotypic variability among the inbred lines was assessed using the coefficient of variation (CV). A wide range of variability was observed for all traits in the inbred lines collection. Highest CV was recorded for GN (86.52%) and TGW (36.7%), indicating substantial phenotypic diversity. Accessions were divided into two groups with low and high values, and a traits collection was established from the high-value accessions. Promising lines with the majority of favorable traits were selected from this collection. ANOVA revealed highly significant differences ($P<0.001$) among the groups for all traits, with highest variation for GN ($F=516.5$) and FD ($F=491.7$). Pearson correlation indicated TGW had significant positive correlations of varying strength with all traits, while PH correlated positively with all except phenological traits. The strongest correlations were observed between HD–FD (0.85), FD–MD (0.69), PH–PL (0.67), SL–SN (0.72), and a weak negative correlation between MD and GN (-0.15). The accessions were grouped into three main clusters, comprising 55.38%, 11.29% and 33.33% of the genotypes, respectively. Cluster II showed high phenotypic similarity, while clusters I and III exhibited internal variation. The observed phenotypic variability in the collection demonstrates substantial genetic diversity in key quantitative traits, providing a foundation for breeding and molecular research to improve agronomic performance in rye, wheat, and triticale.

Keywords: Rye, secale, inbred lines, quantitative traits, correlation analysis

Evaluation of Selection Potential in Synthetic Hexaploid Wheat Genotypes

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Abstract: Research has determined that synthetic hexaploid bread wheat (SHW) possess numerous resistances to various biotic and abiotic stresses. Compared to common wheat, SHW has a richer composition, characterized by higher levels of protein, lysine, starch, and B-group vitamins. Furthermore, it has been confirmed to have a higher yield potential. The main objective of our research is to determine the biomorphological and quality indicators of 68 SHW samples and recommend their use in breeding science. Based on a three-year analysis of the structural elements of samples cultivated at the Absheron Research Base (ARB) of the Institute of Genetic Resources, the average indicators were calculated for the following traits: PH, PL, STRL, SL, SPS, FLL, MG. Based on records taken from the analysis of SHW grown under irrigated conditions, a correlation was calculated between the morphological traits and the results of the biochemical analysis. Although a highly significant dependence was found between PH, PL and a significant dependence with SL, no dependence was found among the plant's biochemical indicators. Furthermore, no correlation was recorded between the biomorphological traits PL, FLL, MG, SPS and the biochemical values. Although no correlation was determined between the STRL trait and protein or lysine, a significant dependence with tryptophan (0.301*) was revealed. Additionally, a negative highly significant dependence (-0.369**) was recorded only between the SL trait and the lysine biochemical indicator. A negative highly significant dependence exists between SHW protein and both lysine and tryptophan. The genotypes were grouped into 6 clusters. At the ARB, the average grain protein content ranged from 11.8% to 15.6%, lysine content from 1.50% to 2.48%, and tryptophan content from 0.49% to 0.87%. Based on this, 15 genotypes were selected for high protein content, 16 for lysine, and 8 for tryptophan.

Keywords: Synthetic hexaploid wheat, biomorphology, protein, lysine, tryptophan

Evaluation of Biomorphological and Biochemical Indicators of Lentil (Lens culinaris Medik.) Variety Samples

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Abstract: Leguminous crops, which form a major part of agricultural cultivation, play an important role in meeting the population’s demand for food and related products. The production of high-quality plant protein is one of the current global issues. The main purpose of our research was to evaluate the biomorphology, biochemical indicators, and storage proteins of 46 lentil samples preserved in the National Genebank—1 of Azerbaijani origin and 45 introduced from ICARDA. Based on three years of analysis conducted at the Absheron experimental base of the Genetic Resources Institute of the Azerbaijan National Academy of Sciences, average values were calculated. In the clustering analysis, the number of pods and seeds per plant was prioritized, allowing the samples to be grouped. The first group can be evaluated as tall and medium-yielding, the second group as tall and high-yielding, the third group as short and low-yielding, the fourth group as tall and high-yielding, and the fifth group as short and high-yielding. It was determined that 21.7% of the samples were high-yielding, 45.7% medium-yielding, and 32.6% low-yielding. In our samples, the determination of protein and essential amino acids lysine and tryptophan was carried out; 7 samples stood out for high protein content, and 5 for lysine and tryptophan. Protein content ranged from 23.5% to 30.4%, lysine (mg/100g) from 644 to 974 mg, and tryptophan (mg/100g) from 170 to 242 mg. For the first time in Azerbaijan, electrophoretic analysis of leguminous crops was carried out using a modified ACID-PAGE method with protein markers. Across all zones, 24 spectra and 55 patterns were identified. Cluster analysis was used to determine genetic distances between lentil genotypes based on globulin storage protein polymorphism. Genetic distance among the studied lentil genotypes was established.

Keywords: Lentil, protein, lysine, tryptophan, globulin

Agro-morphological Characterisation of Wild Chickpea Genotypes to Improve Genetic Resources in Türkiye

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Abstract: Wild chickpea resources possess significant genetic diversity and resilience against stress factors. However, due to environmental changes and overgrazing, these wild genetic resources are at the risk of extinction. This study aims to identify and conserve wild chickpea genotypes of Türkiye and prepare them for breeding programs. This study utilized 29 wild chickpea genotypes including 3 species (***Cicer echinospermum***, ***Cicer pinnatifidum***, ***Cicer reticulatum)*** from the National Seed Gene Bank collection at the Aegean Agricultural Research Institute. Agro-morphological traits showing high-heritability were observed for characterization, using IPGRI and UPOV descriptor lists. Traits were analyzed using Principal Component Analysis (PCA) and cluster analysis. Canopy height and canopy width changed between 20-30 cm and 32-51 cm successively. Seed length was changed between 3,9-5,9 mm, while seed width was between 3-4,1 mm. Single plant yield changed between 4,3-5,6 g. In this study, three main components described 75% of the variation in the population. Three groups were formed based on the traits that constitute the first and second main components. The first group (***Cicer reticulatum***) stood out in terms of yield, single-plant yield, and number of seeds per plant, while the second group (***Cicer pinnatifidum***) consisted of early season and small-grain genotypes. The third group (***Cicer echinospermum***) consisted of large seed and late-season genotypes. No significant variation was observed among the species in terms of the traits comprising the second and third principal components, resulting in a single large group. Traits representing variation in both principal components received average values. Two main groups were formed based on the characteristics of the first and third main components. The first group consisted of the species ***Cicer reticulatum*** and ***Cicer echinospermum***, while the second group consisted of the genotypes ***Cicer pinnatifidum***. The second group differed from the other two species in terms of earliness, small grain size, and branch number. While ***Cicer echinospermum*** and ***Cicer reticulatum*** exhibited similar traits, ***Cicer pinnatifidum*** was distinct in terms of the traits examined. Genotypes of ***C. pinnatifidum*** showed lower yield and earlier maturity, whereas the other two species differed in first pod height and number of branches. In conclusion, Cicer pinnatifidum genotypes stood out for their earliness. Since earliness is a desirable trait in drought tolerance studies, these genotypes can be evaluated in this program. Cicer reticulatum genotypes differed from the other two species in terms of high yield and yield components and can be evaluated in this respect. ***Cicer echinospermum*** genotypes were larger and later than the other two species. Wild chickpea genetic resources are endangered due to overgrazing and environmental factors. Genetic resource collection and conservation efforts should continue in a systematic manner. Due to changing climatic conditions and increasing drought, chickpea breeding programs should be revised to prioritize drought resistance, and wild chickpea genotypes should be used for this purpose.

Keywords: Wild chickpea, ***Cicer echinospermum***, ***Cicer reticulatum, Cicer pinnatifidum***

Alleles of Vegetable Brassica oleracea Improve the Earliness of Spring Oilseed B. napus

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Abstract: The oilseed ***Brassica napus*** is a long-day plant. In this crop, the earliness of flowering is an important breeding objective, and this is even more important for extending its cultivation in the regions where day length in crop season is short. Previously, we have demonstrated that an allele of Chinese kale (***B. oleracea var. alboglabra***) located at about 41 Mb region of C1 chromosome contributes to earliness of flowering in spring B. napus under both long- (16-18 h photoperiod) and short-day (10 h photoperiod) conditions. To identify additional early-flowering alleles in ***B. oleracea***, we evaluated a spring ***B. napus*** population, carrying genome contents of six vegetable ***B. oleracea***, under short-day (10 h photoperiod) and field (16 h day length) conditions. The coefficient of correlation between these two growth conditions for flowering time suggests that a different genetic control is involved in the control of this trait under these two growth conditions. Based on the field experiment, we detected two QTL from C2 and C5 chromosomes affecting flowering time. Evaluation of this population at 10 h photoperiod condition disclosed three QTL from C1, C5 and C9 chromosomes. Among these, the C5 QTL affected flowering time under both 10-h and field conditions; the early-flowering allele of this QTL was introgressed from B. oleracea cabbage cv. Bindsachsener. We further confirmed these QTL by testing SSR markers from the QTL regions and analyzing their association with flowering time. Expression analysis of the genes from the C5 and C9 chromosomes in leaves and shoot apex at night (dark) and morning (light) revealed that increased expression of CO (BnaC05g22130D, BnaC0941980D), DNF (BnaC05g39320D), PHYA (BnaC05g45140D), SOC1 (BnaC09g29450D) and TEM1 (BnaC09g49240D) might have played a role in the earliness of flowering under the short-day condition. Thus, the knowledge gained, and the germplasm developed from this research can be used to improve the earliness of oilseed ***B. napus.***

Keywords: ***Brassica***, earliness, genomics, molecular breeding

Pre-Breeding Research of Wheat Genetic Diversity in the South-East of Kazakhstan

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Abstract: Winter wheat is a socially and economically important cereal crop in Kazakhstan, cultivated on an area of ≈ 617.0 thousand hectares, mainly in the South and South-East (https://stat.gov.kz/ru/industries/business-statistics/stat-forrest-village-hunt-fish/spreadsheets//). Monitoring of crops biodiversity as part of pre-breeding research is the genetic basis for improving desired traits and identification of promising genotypes. The purpose of the research was the monitoring of the wheat genetic diversity at the level of species, variety, gene (pre-breeding research). As research material was used the collection accessions of commercial varieties and lines of international (CIMMYT/ICARDA) and national breeding (3020 accessions). The commercial winter wheat variety Steklovidnaya 24 was used as standards. The research methodology was based on guidelines, standards and protocols for the study, characterization and support of genetic resources of cereal crops. Phenotyping covered the traits of adaptability (PBH - period before heading, days from 01.01), resistance to diseases (types of rust, common bunt), productivity and its structure (PH - plant height, cm; GWE - grain weight per ear, g; W1000 - weight of 1000 kernel, g), physiological indicators of productivity (NDVI, chlorophyll). As a result of the research, two accessions of the international nursery 23IWWYT-IR (CIMMYT) were selected - SY SUNRISE (USA-SYNGENTA) and OVERLAND FHB1-10 (USA-UNL) with productivity (7.4 and 7.3 t/ha). On an artificially created infectious background, were selected 6 accessions for breeding to resistance to rust (yellow, leaf and stem) and common bunt. 46.2% of the accessions had a high chlorophyll level (623-696), with a high (0.71-0.8 - 44.9%) and average (0.64-0.7 - 46.4%) value of the plant biomass index (NDVI). The work on genotyping of a spring bread wheat collection using SSR markers of the VRN-A1, VRN-B1, VRN-D1, PPD-A1, PPD-B1, PPD-D1 genes was carried out, which allowed determining the allelic state for each studied DNA marker. The results can be used in creating wheat varieties carrying the necessary alleles of the vernalization and photoperiod genes using marker-assisted selection.

Keywords: Wheat, genetic diversity, pre-breeding, productivity, resistance

Evaluation of Frost Resistance on Hybrids of Wheat-Rye Substitution Lines With Common Wheats in the Conditions of Absheron Peninsula

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Abstract: Frost resistance is one of the most important adaptive traits in plant breeding. Our study aimed to evaluate the frost resistance of segregating populations (F3 – F4) of late hybrid combinations derived from the cross of the 4 wheat-rye substitution lines (378/3SD, 384/1D, 384/2D) with 9 common wheats using a 9-point scale and to analyze their relation to developmental stages based on the BBCH code. The evaluation was conducted after several consecutive days of frosty weather (ranging from 0 °C to - 5 °C) in early February 2025 at the experimental field of our institute in the Absheron region (Azerbaijan). A total of 234 hybrid combinations were evaluated, and frost resistance scores ranged from 5 to 9. The highest scores (9 points) were recorded in hybrid combinations such as 378/3SD × Bezostaya-100, TG-3 × 378/3SD, 384/1D × Rumeli, and 384/2D × Bezostaya-100 (BBCH 26-29). In contrast, some hybrids involving T. aestivum cv. Ch. Spring and cv. Absheron as parents exhibited reduced frost resistance (5–6 points, BBCH 31-32). Parental lines such as cv. Bezostaya-100, cv. Rumeli, common wheat lines TG-3, and 626AO (mostly winter types) positively influenced the hybrids' cold tolerance. There was an inverse relationship between frost resistance and the BBCH stage. As well as, the data revealed a potential correlation between R/D chromosome substitutions and frost resistance. Lines with multiple substitutions, such as 378/3SD (1R/1B, 2D/2R, 3D/3R, 6D/6R) and 383/1SD (1R/1D, 2R/2D), demonstrated high and stable frost resistance (scores of 9 to 7), particularly in early BBCH stages. In contrast, lines with a single substitution, like 384/1D and 384/2D (both 1R/1D), also showed high resistance in early stages, but resistance declined more sharply in later stages (BBCH 31). This suggests that rye chromatin, especially chromosome 1R, enhances cold tolerance, and multiple substitutions may contribute to broader, more durable field resistance.

Keywords: common wheats, wheat-rye substitution lines, frost resistance

Effect of Drought Stress on Some Physiological and Biochemical Parameters of Wheat Genotypes

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Abstract: Wheat production in Semi- Arid regions of the world is limited mainly by drought and high temperatures. In Azerbaijan, wheat is the main cereal crop in terms of cultivation area and consumption. Lack of water and high temperatures during heading-flowering and grain ripening growth stages of wheat negatively effect on grain yield. We aimed to study the effect of drought stress on some physiological, biochemical parameters of field grown wheat genotypes. Gas exchange parameters measured by using Li-6400 XT Portable Photosynthesis System (Li-COR Biosciences, USA). Leaf, stem, spike area was measured by using Li-3100C Area Meter. Dry mass was determined after oven drying of plant samples at 105oC for 24h. The Chlorophyll a, b and carotenoids were determined in 96% of ethanol at 664, 648, 470nm. Determination of proline was followed by method of Bates et al. (1973). The method given by Çakmak and Horst (1991) was followed for malondialdehyde estimation in leaf. Stomatal conductance, net photosynthesis rate, transpiration rate decreased significantly in response to water deficiency. The intercellular CO2 concentration in leaf increased under drought condition. Water deficiency slowed the growth and dry matter accumulation of assimilating organs (leaf, stem and spike) of wheat genotypes and accelerated the outflow of photo assimilates from vegetative organs into grains. The contents of Chl a, b and carotenoids decreased under water deficiency. The relative water content of flag leaf was about 80% under irrigation, while 65-70% under water deficiency during post anthesis grain formation stage of wheat. Proline and malondialdehyde contents in leaves increased in response to water deficiency. After re-hydration, the contents of proline and malondialdehyde decreased. The content of hydrogen peroxide increased in leaves of wheat genotypes under water deficiency. Catalase activity in leaves increased in the range of 26-112% under drought stress conditions. Water deficiency negatively affected the grain yield and structural components of yield of wheat genotypes. On the calculated indices of stress tolerance wheat genotypes were differentiated as drought tolerant and drought sensitive.

Keywords: Wheat, drought, gas exchange, chlorophyll, proline

Evaluation of Transgressive Segregation in the F_2 Generation Derived from Reciprocal Crosses Between Bread Wheat and Haynatriticum

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Abstract: The development of new and high-yielding genotypes in plant breeding fundamentally relies on genetic variation. Among the mechanisms contributing to this variation, transgressive segregation, defined as the emergence of F_2 individuals with trait values that exceed the phenotypic range of the parents, plays a significant role. In the present study, transgressive variation was evaluated in the F_2 generation derived from crosses between a local bread wheat cultivar (***Triticum aestivum*** **cv**. Absheron) and ***haynatriticum*** amphiploid (***Triticum turgidum/Haynaldia villosa***). The aim was to assess the genetic potential of the resulting hybrids for breeding purposes by determining the frequency and magnitude of transgressive individuals based on key morpho-agronomic traits. Transgression parameters were calculated using the method proposed by Voskresenskaya and Shpota. Analysis of the two reciprocal crosses revealed that the combination ***T. turgidum/H. villosa*** × ***T. aestivum*** **cv**. Absheron exhibited greater transgressive variation across multiple traits. For instance, the trait plant height showed a positive transgression magnitude of 7.73% and a frequency of 4.88%. The highest levels of positive transgression were observed in spikelet density (54.20%) and thousand kernel weight (23.44%), both of which are considered critical traits in relation to grain development and yield potential. In contrast, in the reciprocal combination ***T. aestivum*** **cv**. Absheron × ***T. turgidum/H. villosa***, positive transgression was either not observed or was present at minimal levels. For example, the plant height trait exhibited a negative transgression of –0.52%, with no individuals exceeding the parental maximum. Overall, the results demonstrate that using ***T. turgidum/H. villosa*** as the maternal parent leads to greater transgressive potential in the F_2 generation, thereby offering more opportunities to identify superior genotypes for selection. Conversely, when bread wheat was used as the maternal parent, transgressive expression among the traits was largely absent or weakly expressed.

Keywords: Transgression, bread wheat, haynatriticum

Study of Genetic Diversity and Population Structure, and Selection of Beans

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Abstract: The genetic diversity of food legumes plays an important role in ensuring food security and sustainable agricultural development in the modern era. At present, this genetic diversity is crucial not only for meeting current demand but also for addressing future needs and for creating new varieties through breeding. Therefore, special attention is paid to studying the potential of the gene pool in terms of biological and economic indicators to expand the genetic base. For this purpose, traditional varieties and forms, modern selection varieties, and foreign materials are being collected to enrich the gene pool of legumes. Currently, a rich collection of these plants has been created in the national gene bank. Beans occupy one of the dominant places among food legumes and are distinguished by their polymorphism. The greatest diversity is in the color, shape and size of bean seeds. Proper organization of breeding work, rich and diverse initial material, their comprehensive study and correct selection of initial material are important conditions for the creation of a new variety. The composition of bean collection samples is 60.0% local variety-population, 38.4% foreign material, 1.6% hybrid forms. In the republic, they are cultivated in very limited areas, mainly in subsistence areas, subsidiary farms, and small farms. On the one hand, this is due to the fact that, despite the sufficient form diversity of the bean plant, there are few varieties that allow its cultivation in the open field, and on the other hand, their economic importance has not been fully studied. The study of the genetic diversity and population structure of beans plays a key role in its selection, protection and sustainable agriculture. On the other hand, local varieties are part of the traditional agricultural culture of the people and their preservation is also important from the point of view of ethnobotany.

Keywords: Genetic diversity, bean, plant gene pool, variety

Utilization of Eggplant Genetic Resources in Breeding

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Abstract: Eggplant (***Solanum melongena***) is a major vegetable crop with great potential for genetic improvement owing to its large and mostly untapped genetic diversity. Türkiye is the 4th country with the highest production amount among the world's eggplant producing countries. Germplasm banks worldwide hold more than 19 000 accessions of eggplant and related species, most of which have yet to be evaluated. Also, 466 eggplant accessions collected from different geographical regions of Türkiye are conserved in the AARI National Seed Gene Bank. Nonetheless, eggplant breeding using the cultivated S. melongena gene pool has yielded significantly improved varieties. To overcome current breeding challenges and for adaptation to global climate change, tolerance to abiotic stress and resistance to biotic stress, a qualitative leap forward in eggplant breeding is necessary. There are approximately 120 registered eggplant varieties developed by research institutes and the private sector in Türkiye, consisting of hybrid, open-pollinated and rootstock varieties according to Variety Registration and Seed Certification Center records. Accordings to records, 90% of the registered varieties are hybrid varieties and 10% are open pollinated varieties. While 100% of the eggplant varieties grown in greenhouses are hybrids, there is a great diversity in the open field. Especially in open field eggplant cultivation, open-pollinated and local eggplant varieties are used, and in some Anatolian regions there are famous local eggplant varieties and landraces that are identified with their location. At the Aegean Agricultural Research Institute, vegetable genetic resources are used extensively in both open-pollinated and hybrid variety breeding studies. As a result of these studies, Halep 18, Kemer, Topan, Aydın Siyahı 55, Fener F1, Karun F1, Karya F1 and Hisar F1 eggplant varieties registered by AARI.

Keywords: Local variety, morphological, variety, resistance

Evaluation of Plant Genetic Resources: Beşirli 77 Onion Variety

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Abstract: Red onion populations are widely grown as domestic variety in Bursa and Balikesir, southern provinces of the Marmara Region. In 1990-1993, locally grown genotypes were collected in these regions and their morphological characterizations were made using UPOV criteria and breeding program was started. Variety candidates were developed from the populations between 1993-2009 with the Phenotypic Repetitive Single Selection Method. Since onion is a biennial plant species, breeding step progress could be achieved every two years. The variety candidate was registered in 2011 under the name Beşirli 77 for Atatürk Horticultural Central Research Institute. The skin and flesh color are red, the number of skin layers are 2-3, head shape; wide inverted egg, dominant growth point is 1-2, cross-section is symmetrical, head firmness is medium, water soluble dry matter 10-11%, average head weight is 120-150 g and the top view of the head is round. It is a variety that can be produced directly from seeds. It is a variety that can be produced directly from seeds and average yield is 7 tons/da. The commercial production rights of the variety, which is in demand by producers and consumers in the Marmara Region and throughout Turkey, have been transferred to the private sector for 10 years in 2024.

Keywords: Domestic variety, red onion, selection

Regeneration and Some Preliminary Improvement Assessment Activities in Wheat Genetic Resources

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Abstract: Türkiye is a very rich country in terms of plant diversity and genetic resources and is the gene center of many plant species. Village populations which are considered local varieties, wild relatives, old varieties that are no longer used today and lines with clearly defined genetic characteristics, constitute the country's wheat genetic resources. Rapid population growth, urbanization, unconscious use of plant resources, and replacement of local varieties with yield-oriented improved varieties cause genetic resources to decrease or even disappear. To increase agricultural production, the development of new variety that high-yielding, high-quality, disease resistant varieties will be possible by using genetic resources with a wide range of variation. Therefore, preserving and protecting existing plant diversity and ensuring it is passed on to future generations without erosion is crucial, wheat seed samples obtained from various collection programs conducted in different regions over many years, or imported from abroad, are preserved in the Aegean Agricultural Research Institute (AARI) Seed Gene Bank.

This study was conducted at the Aegean Agricultural Research Institute's experimental field in the Menemen district of Izmir province for a period of five years, between 2020 and 2024. In addition to production renewal studies, preliminary evaluation of wheat genetic resources obtained from the AARI. National Seed Gene Bank was conducted for breeding purposes. Heading date, plant height, and rust disease reaction observations were made from 160, 150, 150, 154, and 218 materials planted in 2 m-long plots consisting of 4-6 rows, respectively, according to the years. Production renewal studies were completed and 149, 131, 99, 186, and 138 were submitted to the seed gene bank. Eight of these materials were selected in 2020 and 28 in 2021 for use in different projects and breeding.

Keywords: Wheat, genetic resources, landraces, Seed Gene Bank.

The Rebirth of Flax Fıber Efe: 35 & Cemre 35

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Abstract: Flax (***Linum ussitatissimum* L**.), is one of the oldest and most common crop plants in the world and provides valuable raw materials for various industries such as; flaxseed oil for food and industrial paint, flax fibers for textile and composite, flaxseed pulp for feed and animal husbandry, woody parts for paper and construction industry. The importance of flax farming increases day by day, especially in Europe, America and Canada; whereas, flax cultivation in Turkey unfortunately has come to an at 1990s end even Turkey was known as one of the main homeland for flax during 1950 - 1980s. Türkiye is one of the geographies suitable for flax agriculture in terms of climatic conditions and is home to a large number of flax populations in terms of genetic diversity. However, there are not enough registered varieties for flax fibre production. This study covers the registration process of prominent candidates as a fibrous flax variety as a result of studies conducted with flax genotypes stored in the National Seed Gene Bank of the Aegean Agricultural Research Institute. Morphometric characterization data of 169 genotypes stored in the National Seed Gene Bank were examined and trials were established in 2020-2021 with the selected genotypes. 2 fiber flax variety candidates were determined from the trials in which 4 candidates and 3 standards were evaluated in terms of fiber properties. As a result of the study, KTN-03 and KTN-04, which stood out in terms of plant height, technical stalk length, fiber yield, and stalk yield, were registered in 2024 by the Variety Registration and Seed Certification Center under the names EFE 35 and CEMRE 35 as the first fiber flax varieties in the Aegean Region.

Keywords: ***Linum ussitatissimum***, Flax, National Seed Gene Bank

Analysis of Local Tobacco Varieties in Türkiye

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Abstract: This study provides an in-depth examination of local tobacco varieties traditionally cultivated in Turkey, specifically focusing on those classified as "self-smokable" due to their ability to be consumed without blending. These varieties are primarily grown in the Eastern and Southeastern Anatolia regions, including provinces such as Adıyaman, Bitlis, Mardin, Hakkari, Hatay and Muş, where tobacco cultivation has long been embedded in rural agricultural systems. Over time, local ecotypes have emerged, adapted to specific microclimates and soils and developed unique morphological and chemical characteristics. Among these, the balance of nicotine, total reducing substances and nitrogen plays a critical role in providing smoking quality without the need for additives or mixing with other tobacco types. The research analyzes not only the agronomic and biochemical traits of these varieties but also evaluates their position within the Turkish tobacco industry. The sector is dominated by multinational companies, creating an oligopolistic market structure. Small-scale local farmers, particularly those growing self-smokable varieties, are often excluded from formal contract farming models and lack access to organized marketing channels such as auctions. Despite these challenges, production of these tobaccos has reached approximately 20 million kilograms annually, indicating their significant but underrecognized contribution to the national market. Current legislation offers limited support for cooperative development, resulting in weak producer organization and restricted market influence. The study emphasizes the need for targeted policies to protect and promote these unique genetic resources. It advocates for the development of producer cooperatives, improved legal frameworks and increased local value-added through sustainable production and marketing models. Ultimately, self-smokable local tobacco varieties are not only a vital part of Türkiye's agricultural heritage but also represent a strategic asset for rural economic development.

Keywords: Local tobacco varieties, self-smokable tobacco, non-contract farming, tobacco policy, producer cooperatives, Turkish tobacco industry

Investigation of Fungal Disease Susceptibility in Wheat (Triticum spp.) Genotypes Under Field Conditions

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Abstract: Fungal diseases like yellow rust, brown rust, and powdery mildew remain major threats to wheat (***Triticum spp***.) crops globally. These diseases reduce yields and degrade wheat grain quality, making them less viable for consumption and trade. Recent research over the past decade has underscored the growing impact of these pathogens in field settings, emphasizing the need for improved management practices to counteract their harmful effects. The goal of this study is to assess the vulnerability of various wheat genotypes to these fungal diseases under field conditions and to investigate potential strategies for effective disease control. In this study, 16 bread wheat (***Triticum aestivum* L.**) and 14 durum wheat (***Triticum durum***) genotypes were planted based on specific agronomic standards and a custom-designed sowing method, with their resistance to fungal diseases evaluated. The infection rate of yellow rust (***Puccinia striiformis f.* sp. *tritici***) was assessed approximately two weeks after the flowering phenological stage, under sunny weather conditions, between 10:00 AM and 2:00 PM, using a modified Cobb methodology. The brown rust disease caused by Puccinia graminis spreads rapidly in conditions of 19-26°C and high humidity, with the assessment carried out on sunny days between 10:00 AM and 2:00 PM, following the modified Cobb method. The development of powdery mildew (***Blumeria graminis f.* sp. *tritici)*** is most intense under 60-100% relative humidity and a temperature range of 0-20°C. The severity of the disease was evaluated using the Geschele scale (0-9 point nomenclature). Based on the results of the assessments, the reactions to the diseases varied among the genotypes studied. Some were classified as susceptible (S), while others were categorized as moderately susceptible (MS), moderately resistant (MR), and resistant (R). Among the bread wheat genotypes Renovatum, and among the durum wheat genotypes Alexandrinum, Africanum, Erythromelan and Leucomelan demonstrated resistance to the assessed fungal diseases.

Keywords: ***Triticum spp., Puccinia striiformis, Puccinia graminis, Blumeria garminis***

Reducing Pesticide Loads by Altitude

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Abstract: Our research revealed that vertical zonality has a significant impact on the bioecological characteristics of these pests. Specifically, as altitude above sea level increases, the number of pest generations decreases. This creates an opportunity to reduce additional costs in organizing control measures, ensures the cultivation of safe products and creates the basis for environmental protection. The scientific research was carried out on farms located in the Ganja-Dashkesan economic region. This region lies between 40°82' and 41°43' north latitude and 44°95' and 46°82' east longitude. The sum of effective temperatures reaches 3800–4400 °C. The length of the vegetation period is 210–213 days. Dark gray-brown, gray-brown, light gray-brown, and meadow soils are the most widespread. Annual precipitation varies between 250–410 mm. According to moisture conditions, the region belongs to the semi-humid and arid zones. The abstract reflects the results of studies on the effect of ecological factors, including soil temperature, on the development and generational dynamics of the Colorado potato beetle (***Leptinotarsa desemlenata Say***). Generally accepted methods were used to conduct the study. Ecological factors limiting the reproductive capacity of the colorado beetle:

-In areas of the Ganja-Dashkesan economic region above 1000 meters above sea level, freezing of the upper layer of the soil and low temperatures (0,5-0,6 °C) in relatively lower layers (up to 100 meters) were detected during the winter months.

-Since the soil layer gradually warms up in the summer, the temperature in the soil layer where the Colorado potato beetle hibernates reaches 14-15 C in late May and early June, which creates the basis for the pest to emerge from hibernation in the first and second decades of June. Therefore, in areas higher than 1000 meters above sea level, there are conditions for the development of only two generations of the Colorado potato beetle.

Keywords: Potato, soil environment, Colorado potato beetle, altitude above sea level

Creation of New Corn Varieties and Hybrids Adapted to Climate Conditions

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Abstract: Considering that flint corn samples impart early maturity, good germination and strong seedlings to hybrids, and dent corn samples impart productivity, lodging resistance, absence of bushiness, resistance to smut and other diseases, in order to create early-maturing corn hybrids, local varieties and variety samples selected from the National Gene Bank collection for positive economic and biological indicators were crossed with dent corn samples due to their breeding significance, and simple interlinear and varietal-linear hybrids were obtained. Fifteen F_6 hybrid lines, derived from inbred crossings of selected corn accessions from the GenBank collection, were planted in the Parzivan field with supply rainfed conditions (Zagatala RES) to study their suitability for this condition at all stages of development. The hybrid corn's habit was visually assessed at both the early (3-7 leaves) and late stages of development, yield, protein, and fat content were determined. Among the studied hybrids, the maximum protein content (13.8%) was observed in the Emil x Za-420/2017 line, and the minimum (8.5%) was observed in the Fakhri x Gurur /2017, Populyatsiya 2008 x Zak-68/2017 and Sp 85 x 31/UGSh 43 4 x UGSh145/2017 lines. In general, the protein content in the grain of the studied hybrids varied within 8.5–13.8%. The average protein content was found in the lines Gurur x Fakhri/2017 and Populyatsiya 2008 x Gurur/2017 (11.4%), Emil x Zak-68/2017 and Zak 68 x Fakhri/2017 (11.8%), which is 17.4% and 14.5% less than the maximum value and 25.4% and 28.0% more than the minimum value, respectively. The grain oil content of the corn hybrids varied within the range of 9.0–13.9%. The hybrids Zak-420 × Fakhri/2017 (13.9%), Gurur × Populyatsiya 2008/2017 (13.4%), Fakhri × Gurur /2017, and Zak-420 × Emil/2017 (12.0%) had higher grain oil content. A general pattern was observed: low protein content in samples with high oil content.

Keywords: Corn, hybrid generation, grain, quality indicators

Evaluation of Drought Tolerance Chickpea (Cicer arietinum L.) Genotypes

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Abstract: In this study, 56 chickpea (***Cicer arietinum*** **L**.) genotypes introduced by the ICARDA were evaluated for drought tolerance and genetic diversity under field conditions. Trials were conducted under both irrigated conditions at the GEI Research Station and non-irrigated conditions at the Gobustan Research Station of the Experimental Training and Agricultural Innovation Institute, following international chickpea descriptor standards. Mean yield, Stress Tolerance Index, Drought Tolerance Index, and genetic variation values were calculated for each genotype. Under normal irrigation, the genotypes exhibited a vegetation period ranging from 183 to 196 days, plant height from 65 to 85 cm, seed weight per plant from 5.8 to 9.6 g, number of seeds per plant from 55 to 100, and number of pods per plant from 38 to 96. In contrast, under drought conditions, these values were reduced to 125–145 days of vegetation, 45–60 cm in plant height, 4.5–6.0 g seed weight per plant, 40.5–46.5 g 100-seed weight, 44–60 seeds per plant, and 15–36 pods per plant. The drought tolerance Index ranged from 8.24 to 30.8, while the stress susceptibility index varied between 0.48 and 1.28. Based on these indices, the genotypes Flip 13-154, Flip 13-151, Flip 11-364, Flip 11-05, Flip 11-214, Flip 11-208, Flip 82-150, Flip 07-305, and Flip 11-66 were identified as drought-tolerant. Cluster analysis based on the drought tolerance Index calculated from seed weight per plant grouped the genotypes into three major clusters, each containing two sub-clusters, indicating significant genetic diversity among the tested lines.

Keywords: Chickpea, drought stress, genetic diversity, stress tolerance index, cluster

Eco-geographical Distribution Features of Wild Species of the Sainfoin Genus (Onobrychis Mill.) in Azerbaijan

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Abstract: Within the framework of this study, based on descriptor data of ***Onobrychis*** species collected from different regions of Azerbaijan, some of their ecological-geographical indicators were evaluated. For the research, criteria such as species diversity, landscape structure, floristic analysis, distribution by altitude zones, and ecological factors (temperature, anthropogenic impact, etc.) were selected.

According to the results obtained, the highest species diversity was observed in Goygol, Gadabay, and Nakhchivan regions, while only a single species was recorded in Absheron, Ujar, Gobustan, and Guba districts.

Based on the geographical distribution of the species, ***O. cornuta, O. buhseana, O. komarovii, O. nemecii, O. kachetica, O. hajastana, O. bobrovii, O. bungei, O. arenaria*** subsp. ***cana***, and ***O. arenaria*** were found only in one location, whereas ***O. cyri*** and ***O. altissima*** were collected from at least 10 different districts.

In terms of grazing impact, strong anthropogenic pressure was observed in Agdash, Ujar, Goychay, Nakhchivan, Guba, and Lerik. These mainly covered the lower and middle mountain belts.

According to climatic parameters, species collected from Fuzuli and Nakhchivan, where the highest temperatures were observed, include ***O. cornuta, O. radiata, O. altissima, O. komarovii, O. iberica, O. cyri, O. hajastana***, and ***O. transcaucasica***. From Shusha, where the lowest temperatures were recorded, ***O. cyri*** and ***O. transcaucasica*** were collected.

The occurrence of ***O. iberica, O. kachetica,*** and ***O. altissima*** in various altitude belts demonstrates their level of ecological adaptation and plasticity.

The study revealed that the distribution of wild species of ***Onobrychis*** in Azerbaijan occurs across a wide ecological-geographical range, strongly associated with different landscape belts, altitude zones, and climatic factors. The highest species diversity was recorded in mountainous regions with complex relief such as Goygol, Gadabay, and Nakhchivan, highlighting the influence of ecological conditions on species richness.

Keywords: *Onobrychis* Mill., eco-geographic distribution, species diversity, flora of Azerbaijan

A Promising Wild Edible Mushroom with Commercial Potential: Pleurotus cystidiosus O.K. Miller

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Abstract: Fungal genetic resources constitute a vital component of global biodiversity, offering significant ecological, nutritional, and pharmaceutical benefits; however, they face increasing threats from habitat loss, pollution, climate change, and unsustainable harvesting practices. In response to concerns about genetic erosion, Republic of Türkiye Ministry of Agriculture and Forestry launched the "Researches on Mushroom Genetic Resources Project" in 2006 under Aegean Agricultural Research Institute (AARI), currently conducted in collaboration with the Atatürk Horticultural Central Research Institute, aiming to collect, identify, conserve, and sustainably utilize the country's macrofungal biodiversity. This study aims to present information regarding the conservation and sustainable use of ***Pleurotus cystidiosus*** **O.K. Miller**, which was isolated for the first time in Türkiye within the scope of this project. Known as the summer oyster mushroom, this species is valued for both its edible and medicinal properties and has attracted international scientific interest due to its potential applications in functional foods and pharmaceuticals. Native to the southeastern USA, Taiwan, and South Africa, and commercially marketed in several Asian countries, ***P. cystidiosus*** had not previously been recorded in Türkiye's national checklists. Molecular identification based on ITS1 and ITS2 region sequencing demonstrated 99.80% and 100% identity with reference sequences in the NCBI BLAST database. The isolates are preserved at +4 °C, where they are regularly subcultured on malt extract agar, and additionally at –80 °C for long-term conservation. Given its novelty and potential, integrating ***P. cystidiosus*** into Türkiye's mushroom cultivation systems promises to diversify the industry and support the sustainable use and conservation of fungal genetic resources, thereby contributing positively to economic development and biodiversity preservation.

Keywords: ***Pleurotus cystidiosus***, macrofungi, edible mushroom, genetic resources, conservation, Türkiye, molecular identification.

Morphological Diversity Assessment of Anacyclus pyrethrum (L.) Link: an Underutilized Medicinal Plant Genetic Resource

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Abstract: ***Anacyclus pyrethrum*** **(L.) Link**, commonly known as Mount Atlas daisy or Akarkara, represents a critically underutilized plant genetic resource with significant medicinal and economic potential endemic to North Africa. This neglected crop species faces conservation challenges due to habitat degradation and limited cultivation practices, making morphological characterization crucial for its preservation and utilization. The present study evaluated phenotypic diversity and morphological variations across different populations of ***A. pyrethrum*** to assess genetic variability and identify promising accessions for conservation and breeding programs. Morphological characterization was conducted using standardized descriptors covering vegetative and reproductive traits, including plant height, leaf morphology, flower characteristics, root system architecture, and biomass parameters. Significant morphological variations were observed among populations, particularly in flower shape, leaf shape & size, plant stature, flower head diameter, and root characteristics, indicating substantial phenotypic diversity within the species. The documented morphological variations suggest the presence of distinct ecotypes adapted to different environmental conditions, providing valuable genetic resources for crop improvement and conservation strategies. Root morphology showed considerable variation in length, diameter, and branching patterns, which is particularly important given the medicinal value of ***A. pyrethrum*** roots in traditional medicine systems. These findings provide essential baseline data for the conservation of this underutilized species and highlight the importance of preserving its genetic diversity through both in situ and ex-situ conservation approaches to prevent genetic erosion of this valuable plant genetic resource.

Keywords: Akarkara, ***Anacyclus pyrethrum***, morphology, variation

The Effect of Organic Fertilizers on the Biological Characteristics of the Avangard Rice Variety and its Strategic Role in Food Security

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Abstract: Food security is an important component of the national security strategy of each country and is closely related to agriculture, food production, import-export, market regulation and social welfare of the population. The main objective of the study is to evaluate the effect of various organic fertilizers on the productivity of the Avangard rice variety, to comparatively evaluate their impact on productivity indicators, as well as to determine an ecologically and economically correct fertilization system in rice production. To achieve this goal, the main tasks were to study the effect of various doses of cattle, sheep, poultry manure and mineral fertilizers on the Avangard rice variety, to conduct a comparative analysis of the productivity indicators of the rice plant in various fertilizer options, to identify the observed differences and signs, to select the most efficient fertilization option based on the results obtained and make recommendations for production, and to assess soil fertility, as well as ecological sustainability opportunities. The study was conducted on irrigated clayey-yellow soils of the Lankaran-Astara region. The yield of the Avangard rice variety per hectare was 5.2 tons in cattle manure, 5.7 tons in poultry manure, 5.9 tons in sheep manure, 7.6 tons in mineral fertilizer application, and 4.5 tons in the fertilizer-free variant. Based on the results, it can be noted that the application of sheep manure is effective among organic fertilizers. Thus, the height of plants, broom length, number of stems and the number of grains per plant were the highest in the variants where sheep manure was applied. This result is due to the improvement of the soil structure and increased activity of microorganisms.

Keywords: Avangard rice variety, food security, organic fertilizers, Lankaran, productivity

Antioxidant Activity of Anthocyanin-rich Corn Hybrids

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Abstract: Dark-grain corn (***Z. mays* L.**) accumulates valuable anthocyanin pigments, which are characterized as natural antioxidants. Anthocyanins in foods exhibit many beneficial properties for the human body, including antioxidant (antiradical), antidiabetic, anti-inflammatory, anticarcinogenic, and other properties. Dark-colored corn kernels are rich in anthocyanins and, in addition to their nutritional value, have preventative and therapeutic value. Therefore, breeding aimed at increasing the antioxidant activity of colored corn kernels for use as a functional food is relevant. The development of anthocyanin-rich corn varieties from local corn adapted to the soil and climatic conditions of Azerbaijan is important for their sustainable production. The aim of the study was to investigate the antioxidant activity of anthocyanin-rich corn hybrids obtained by crossing anthocyanin-rich inbred lines. Cobs of 22 hybrid accessions with red kernels were obtained and analyzed for five morphological traits: length, number of kernel rows, number of kernels per row, thousand-kernel weight, and kernel color spectrum. High values of the economically valuable trait-thousand-kernel weight-were observed in six accessions with homogeneous and intense kernel color. The total anthocyanin content (based on the molar extinction of cyanidin-3-glucoside) and antioxidant activity were determined spectrophotometrically in kernel extracts of these forms, obtained by maintaining the grain homogenate in a 0.1 M aqueous HCl solution and subsequent filtration. The antioxidant activity of anthocyanin extracts of these accessions was determined using a method based on the ability of antioxidant compounds to reduce the concentration of 2,2-diphenyl-1-picrylhydrazyl (DPPH) radicals. Anthocyanin extracts from the KF94r x EHM269r, KF28r x GSp-100r, and UgShl76r x KF94r hybrids at a concentration of 20 nL reduced DPPH radical scavenging by 50%, twice as effective as other forms tested. However, the anthocyanin content of these hybrids was significantly lower than that of other samples. Corn varieties with high antioxidant potential are considered promising for inclusion in biofortification schemes.

Keywords: Corn, cob traits, anthocyanins, antioxidant activity

Functional Potential of Traditional Oat (Avena sativa L.) Genetic Resources in Food Innovation

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Abstract: Oat (***Avena sativa*** **L.**) has emerged as a valuable crop in the development of functional foods, primarily due to its distinct composition that includes bioactive fibers, balanced protein content, and a spectrum of antioxidant molecules. Notably, β-glucan, a soluble fiber found abundantly in oats, is known for its positive effects on blood cholesterol and glycemic response. These properties, along with naturally occurring phenolics such as avenanthramides, make oats increasingly attractive in the context of health-focused food design. Traditional oat varieties—comprising landraces and regionally adapted genotypes—possess a wealth of genetic and biochemical diversity. These underutilized resources often exhibit unique combinations of agronomic and nutritional traits, such as high protein content, variable kernel hardness, and favorable functional properties for processing. Their potential lies in the opportunity to create specialized formulations, including high-fiber bakery products, dairy alternatives, and nutrient-enriched beverages, tailored to specific health or consumer demands. Furthermore, these local oat populations, having been shaped by long-term adaptation to distinct ecological zones, often demonstrate enhanced resilience to stress factors like drought, low temperatures, and poor soil fertility. Their cultivation supports sustainable food systems by reducing the reliance on high-input, genetically uniform commercial cultivars. At the same time, their utilization in food innovation helps preserve regional biodiversity and maintain agricultural heritage. This review aims to highlight the strategic value of traditional oat genetic resources in bridging nutritional science, crop diversity, and sustainable innovation. Harnessing their functional attributes within modern food systems may lead not only to improved public health outcomes but also to strengthened food security and environmental sustainability. Promoting the use of these resources aligns with global efforts toward circular bioeconomy models and could serve as a foundation for new product development grounded in authenticity and local identity.

Keywords: Oat, functional food, plant genetic resources, β-glucan, food innovation

Fatty Acid Profiles of Hulled Wheat Genotypes

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Abstract: This study aimed to compare the fatty acid compositions of 17 wheat samples collected from different regions of Türkiye, including hulled wheats such as einkorn (***Triticum monococcum***) and emmer (***Triticum dicoccum***). Fatty acids were identified using gas chromatography and analyzed with heatmap visualization, principal component analysis (PCA), and hierarchical clustering. Palmitic acid was the predominant saturated fatty acid, reaching 18.11% in B13 and 17.25% in B15. Oleic acid was the main monounsaturated fatty acid, with the highest levels found in B3 (35.72%) and B5 (34.51%). Polyunsaturated fatty acids such as linoleic acid and linolenic acid (C18:3n3) were abundant in B5 (43.78%) and B7 (43.43%), leading to ∑PUFA values as high as 44.66%. PCA clearly differentiated samples based on their lipid profiles, separating B13 and B15 for high ∑SFA, while B5 and B3 clustered based on high ∑MUFA and ∑PUFA. Dendrogram analysis grouped the genotypes into two major clusters reflecting similar fatty acid patterns. The heatmap effectively highlighted samples rich in linoleic and oleic acids, clearly distinguishing genotypes with superior fatty acid profiles. Overall, the results of the study indicated that hulled wheats are rich in unsaturated fatty acids and possess a valuable nutritional profile, offering significant potential for use in functional food development and health-oriented grain-based products.

Keywords: GC-MS, PCA, PUFA, ***Triticum monococcum***, ***Triticum dicoccum***

Kemerot (Ipomoea nil): A Multipurpose Medicinal Plant of Dhofar, Oman

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Abstract: Kemerot (***Ipomoea nil***), locally recognized by this name in Dhofar, is a fast-growing seasonal vine that thrives in the mountainous regions of southern Oman during the monsoon season (locally known as Khareef). Native to tropical America, this species has become naturalized in Dhofar's unique humid microclimate, where it is commonly observed climbing over shrubs, rocks, and walls. It's striking funnel-shaped blue flowers, which bloom in the early morning and fade by midday, make it easily identifiable and add significant aesthetic value to the natural landscape. Beyond its visual appeal, Kemerot holds considerable ecological, medicinal, and ethnobotanical importance. Ecologically, the plant contributes to slope stabilization by covering soil surfaces and reducing erosion caused by seasonal rainfall. It also provides supplementary fodder for grazing animals, especially during the green season. From a medicinal perspective, the seeds of Ipomoea nil are the primary component used in traditional healing practices across the Dhofar region. These seeds are ground into pastes or decoctions and used to treat various conditions including head lice, skin fungal infections, constipation, intestinal worms, joint inflammation, fever, and respiratory discomfort. In veterinary folk medicine, the plant is used to treat mastitis and eye infections in livestock, and its leaves are browsed by animals. Additionally, the seeds are valued for their cleansing properties and are used in washing and personal hygiene, including the ritual purification of deceased individuals before burial. The multifunctional nature of Kemerot reflects the deep interconnection between local biodiversity and traditional knowledge systems. Its diverse uses underscore its potential value for future pharmacological studies, ecological restoration projects, and cultural heritage preservation in Oman. As such, Ipomoea nil should be recognized as a vital species within the flora of Dhofar and promoted as part of sustainable land and health practices in arid regions.

Keywords: Kemerot, ***Ipomoea nil***, Dhofar, medicinal plant, traditional medicine

Some Geographical, Morphological and Quality Characteristics of Turkish Elderberry (Sambucus nigra L.) Populations

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Abstract: In this study, it was aimed to determine certain geographic, morphological, and quality characteristics of black elderberry (***Sambucus nigra***) populations distributed in Turkey. The soil structure, slope of the terrain, dominant vegetation of the areas where elderberry populations grow in the Aegean, Marmara, and Western Black Sea regions were identified. Additionally, characteristics such as tree height, age, trunk diameter, growth form, vigor, and fruit yield were also determined. Observations and measurements were made on a total of 84 trees belonging to 8 different populations in 3 different regions. According to the data obtained, it was determined that the ages of the trees ranged from 1 to 12, their heights ranged from 2 to 10, and their trunk diameters ranged from 20 to 70 cm. It was observed that the trees were dense and well developed within the populations. When the terrain was examined, it was found to be mostly flat and partially sloped, with no rocky areas, and featuring a soil structure with a stream bed and undulating surface. In the 84 populations from which fruit samples were taken, the anthocyanin content ranged from 0.27% to 1.49%. Cuttings were taken from 4 populations with an anthocyanin content of over 1.2% and rooted. The rooted seedlings were planted in the field and were observed to adapt well to the cultural conditions. They began to flower and produce fruit from the second year onwards.

Keywords: Elderberry, populations, geographical, morphology, quality

Determination of Fruit Quality Characteristics of Local Winter Pear (Pyrus communis L.) Genotypes Grown in Konya Province and Their Evaluation as Genetic Resources

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Abstract: This study was conducted to determine the fruit quality traits of local winter pear (***Pyrus communis*** **L**.) genotypes grown in Konya province and to conserve the superior genotypes as genetic resources. In the study, 17 local winter pear genotypes were identified throughout Konya and examined for fruit shape, external quality (attractiveness), eating quality, fruit size, crispness, juiciness, rustiness, grittiness and aroma. Fruit shape of the examined genotypes was evaluated as long in 11, oval in 5 and short in 1. In terms of external quality, 3 genotypes were determined as very good, 3 genotypes as good, 4 genotypes as average and 7 genotypes as poor. In terms of rustiness status, which is an important criterion in pears, 3 genotypes were evaluated as no rust, 1 genotype as slightly rusty, 4 genotypes as moderately rusty and 9 genotypes as very rusty. In the winter pear genotypes, fruit weight varied between 40.07 g and 180.40 g; fruit length varied between 39.58 mm and 88.61 mm; fruit width varied between 42.78 mm and 69.74 mm; soluble solids content varied between 12.27% (42.K.07) and 22.23% (42.K.14) and titratable acid content varied between 0.29% (42.K.12) and 1.38% (42.K.05). As a result of the weighted scoring evaluation, genotype numbered 42.K.13 was identified as a promising genotype with a total score of 809. The study findings revealed significant variation among the winter pear genotypes in Konya province. The genotypes obtained as a result of the study will be multiplied and protected to be used as breeding material.

Keywords: Fruit size, eating quality, russeting, fruit firmness, local pear

A Preliminary Study on Some Fruit Characteristics of Quince Genotypes Collected from Artvin Province

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Abstract: Quince (***Cydonia oblonga*** Mill.) is an important fruit species widely used both for fresh consumption and processed products. Türkiye holds a significant position in the world for quince production, especially Artvin province, which, with its unique microclimatic characteristics, has rich plant diversity and great potential for the conservation and evaluation of the genetic diversity of quince genotypes. Indeed, this diversity is very important for breeding studies. In recent years, the investigation of genetic and environmental factors determining fruit quality has gained importance in improving cultivation and developing marketing strategies. In this context, examining the fruit characteristics of different quince genotypes is valuable, particularly for revealing diversity in terms of taste, texture, aroma, and chemical composition. This study aims to contribute to the evaluation of genetic resources in the region by determining some important fruit characteristics of quince genotypes collected from Artvin province. The findings are intended to provide basic data for quince breeding programs and regional agricultural development projects. In this study conducted between 2022-2023, some fruit characteristics of 13 quince genotypes grown or naturally collected in Artvin were examined. Fruit weight, fruit length and width, shape index, soluble solid content, and titratable acidity were measured. The fruit weights of the examined quince genotypes ranged from 59.43 to 275.35 g, fruit length from 49.44 to 91.97 mm, and fruit width from 60.51 to 102.21 mm. The soluble solid content varied between 10.00% and 16.50%.

Keywords: Selection, fruit characteristics, local cultivar, ***Cydonia oblonga***

Determination of Some Leaf and Flower Characteristics of Morus alba Genotypes

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Abstract: Mulberry, a berry like fruit species, has been cultivated for many years both globally and in Türkiye. Due to its low selectivity regarding climatic and soil requirements, it can grow in almost every region of Türkiye. The genetic variations that form the basis of breeding studies are highly diverse, owing to the country's wide range of climatic and soil conditions. In this context, mulberry species also exhibit extensive genetic variation within the natural flora. This study was conducted to determine the leaf and flower characteristics of 13 selected white mulberry (***Morus alba***) genotypes as a result of selection studies carried out in the Eastern and Central Black Sea regions. In the white mulberry genotypes, leaf length ranged from 12.92 to 35.81 cm, and leaf width ranged from 9.67 to 17.57 cm. The shape of the leaf blade was oval, and the leaf apex shape was pointed to inverted V shaped. The shape of the leaf margin teeth was irregular and blunt; the leaf petiole sinus shape was slightly indented and M shaped, while the petiole color was yellowish light green. All white mulberry types exhibited monoecious flower structure. The number of flower clusters ranged from 2.33 to 6.00 per branch, and the number of flowers per cluster varied between 1.31 and 2.76.

Keywords: Flower characteristics, ***Morus alba***, morphological characterization, leaf morphology

Some Plant Characteristics of Pecan Nut (Carya illioinensis) Genetic Resources of the Batı Akdeniz Agricultural Research Institute

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Abstract: The first adaptation studies on pecans in Türkiye were initiated by the Antalya Citrus Research Institute in 1969, with the introduction of 14 varieties. In 1990, the number of varieties was increased to 26, and the country's first pecan genetic resources plot was established. Based on data obtained from the 14 varieties introduced in 1969 and subjected to adaptation studies, the Mahan, Choctaw, Wichita, and Western varieties were registered as pollinator varieties, while the Burkett variety was registered as a seed rootstock variety and introduced into production. The characteristics of the varieties in the Pecan Genetic Resource plot, established with 26 varieties at the Serik-Kayaburnu location of the Batı Akdeniz Agricultural Research Institute in 1990, were determined according to UPOV criteria. These varieties were added to the Turkish Land Gene Bank records. This study describes the phenological characteristics, as well as tree, leaf, flower, and fruit traits of the varieties that constitute the genetic resources of pecans in Türkiye. The optimal pollination time intervals for male and female flowers, which are critical for successful fertilization in pecan, were determined in this study. Detailed morphological and phenological characteristics of the 26 varieties are presented in this study.

Keywords: Pecan, genetic resource, phenological characteristics, pollination and fertilization

Pomegranate Sour Production in Some Pomegranate Varieties and Genotypes

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Abstract: Pomegranate (***Punica granatum* Linn**.) is a fruit rich in bioactive compounds. Thanks to its antioxidant properties, these bioactive compounds play a role in the prevention of many diseases, such as cardiovascular disease and cancer. Therefore, interest in pomegranates, their juice and concentrate, pomegranate jam, and pomegranate syrup is increasing every year. According to the Turkish Standards Institute's TS 12720 standard, pomegranate syrup is a product obtained by properly dividing and pressing the pomegranate fruit, clarifying the resulting pomegranate juice, and then concentrating it in the open or under vacuum, using the appropriate technique. In Turkey, pomegranate syrup is generally produced using traditional methods. However, research has revealed that the compound hydroxymethylfurfural (HMF) is harmful to human health. Indeed, according to the TS 12720 Pomegranate Syrup Standard, the maximum HMF content in the product is limited to 50 mg/kg. Many studies have reported that HMF levels exceed this limit in pomegranate syrups produced using traditional methods. This study utilized material from the Pomegranate Genetic Resources Parcel established at the Alata Horticultural Research Institute in Mersin province. Juices from two pomegranate varieties and two pomegranate genotypes were clarified, and the resulting juices were concentrated under vacuum to produce pomegranate syrup. The resulting pomegranate syrup samples were analyzed for turbidity, pH, water-soluble solids (SDS), and hydroxymethylfurfural (HMF). All analyses determined that all pomegranate syrup samples met the standards specified in the TS 12720 Pomegranate Syrup Standard.

Keywords: Pomegranate, pomegranate juice, clarification, pomegranate syrup, HMF

Determination of Molasses Properties of Species and Genotypes in Carob Genetic Resources

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Abstract: Carob is an evergreen plant that generally grows in regions with a Mediterranean climate, without being cultivated and without the need for any artificial additives during growth. While carob fruit can be used for table consumption, it is mostly used in the production of molasses, a traditional food product specific to our country. In Türkiye, the carob population is mostly found naturally as a single tree. Its distribution extends along a 1,750 km² coastline from Izmir-Urla to the Samandağ district of Hatay, with the highest density occurring 1-2 km inland. According to 2022 data from the Turkish Statistical Institute (TURKSTAT), approximately 43.5% of Turkey's production comes from Mersin. In recent years, as a result of increased awareness of its importance in the food industry and increased product diversity, cultivation has accelerated, and indoor gardens have begun to be established. It is anticipated that annual production will increase even further in the coming years. In this study, HMF and Sugar Component (Glucose, Fructose and Sucrose) values of carob molasses produced by hot and cold extraction methods from carob species and genotypes in the Carob Genetic Resources Parcel established in Alata Horticultural Research Institute (Mersin) were measured. 5 species and 2 carobs were used in the study. The HMF values were determined to be 0.12 ppm in molasses samples obtained by cold extraction and 0.28 ppm in those obtained by hot extraction. All HMF values were below 5 ppm, which is well within the legal limit of 50 ppm. The average amounts of glucose, fructose, and sucrose were found to be 14.19%, 9.08%, and 24.05%, respectively, in cold extraction, and 13.38%, 11.63%, and 32.23% in hot extraction.

Keywords: Carob, HMF, Sugar Content

Türkiye Grapevine Field Gene Bank

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Abstract: Türkiye has many kinds of grape genotypes due to its location, Asia Minor, which is among the homelands of grapes. To protect this richness, "The Determination, Conservation and Identification of Turkish Vine Genetic Resources" project was started in 1965. Therefore, 1459 varieties/genotypes have been preserved in the vineyard field gene bank of Tekirdağ Viticulture Research Institute until now. In the last 5 years, ampelographic characterizations of a total of 31 genotypes were made, including 11 genotypes in 2021 (Kıtkıt beyaz, Ağın beyazı, Kıtkıt siyah, Tahannebi, Karatevek, Ternebi, Kırmızı kışlık, unnamed1 (Mazgirt), unnamed2 (Mazgirt), unnamed3 (Ovacık), Tenturiye grape), 5 genotypes in 2022 (Çatalkarası (Çatal dimrit), Eksenez, Kınalı grape, Selvikarası, Sömbeki) and 15 unnamed Çanakkale genotypes in 2024. Çanakkale genotypes are coded with the letter Ç. In the observations of shoot tip and mature leaf hairiness and anthocyanin accumulation, especially Tenturiye grape and unnamed 2 genotypes attracted attention in terms of intensity. In young leaf upper surface colors, Karatevek and unnamed 2 genotypes differed from other cultivars with their copper-red color. Tahannebi, Ternebi, Selvikarası, Ç6, Ç12 and Ç14 genotypes have female-retrograde stamens and other cultivars have hermaphrodite flower structure. Cluster lengths (OIV 202) varied between 28.0 cm (Ağın beyazı, very long) and 9,5 cm (Ç12, very short), cluster weights (OIV 502) varied between 413 g (Sömbeki, medium) and 53 g (Ç12, very low). The berry lengths (OIV 220) varied between 24,9 mm (Ç14, long) and 10,1 mm (Ç12, very low) and the berry weights (OIV 503) varied between 4.17 g (Ağın beyazı, medium) and 0,71 g (Ç12, very low).

Keywords: ***Vitis vinifera* L.**, grapevine field gene bank, ampelography

Determination of the Suitability of Some Medicinal and Aromatic Plants for Mechanized Seeding and Optimization of Seeding Performance

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Abstract: The objective of this study was to determine the suitability of selected medicinal and aromatic plant seeds for mechanized seeding, to evaluate their seed flow characteristics and in-row seed distribution uniformity under different operational conditions, and to optimize the seeding performance. Weighing tests were conducted to determine the seed flow characteristics, while sticky-belt tests were employed to assess the in-row seed distribution uniformity of the seed metering unit. The experiments were designed based on Response Surface Methodology (RSM), and Central Composite Design (CCD) was applied as the experimental layout. A conveyor belt-type micro-granular applicator was used as the metering unit, and all performance evaluations were carried out based on the common drill method. Among medicinal and aromatic plant species, sage, black cumin, and coriander -which differ in their physical properties- were tested. For each seed, both weighing and sticky-belt tests were performed under five levels of seed rate (orifice size), five levels of forward speed, and five levels of seed release angle. Flow uniformity was evaluated based on the coefficient of variation (CV), whereas in-row seed distribution uniformity was assessed using the variation factor (V_f) and the goodness criterion (λ). Polynomial model equations were developed for each seed based on experimental data. Optimum operating conditions specific to each seed were determined from these model equations. The validity of the models was verified by sensitivity analysis, and the accuracy of the optimum conditions was confirmed by applying verification tests. The results demonstrated that all seeds are suitable for seeding by conveyor belt-type micro-granular applicator, and their seeding performances were successfully optimized.

Keywords: Micro-granular applicator, flow uniformity, in-row seed distribution uniformity, optimization

Economic Potential and Sustainable Use Strategies of Wild Rose Species in the Sheki Region

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Abstract: The rosehip is a widely distributed wild shrub species in the foothill and mountainous zones of the Sheki region, possessing high biological and economic importance. In the area, species such as the Field rose (***Rosa arvensis***), Multiflora rose (***Rosa multiflora***), and Austrian briar (***Rosa foetida***) are found. A comprehensive study has been conducted on the general characteristics of plants belonging to the Rosaceae family, the classification of the ***Rosa*** genus and its species, their biomorphological traits, as well as their associations with plant communities. The aim of the research was to investigate the biomorphological characteristics, distribution areas, and economic potential of these natural populations, and to substantiate strategies for their sustainable use and conservation. As research material, samples of rosehip distributed across different ecological zones of the Sheki region were examined. The methods applied included morphological analyses, field observations, and comparative analysis of literature data. The results indicate that wild forms of this species occur at forest edges, slopes, and river valleys, exhibiting various morphological forms and demonstrating a high adaptability. The fruits are rich in vitamin C and antioxidants, making the plant promising for the pharmaceutical, cosmetic, and food industries. Its genetic diversity and reproductive capacity further enhance its potential for breeding programs. At the same time, strategies such as controlled harvesting, semi-cultivation practices, and the involvement of local communities and institutions can ensure sustainable utilization and support regional economic development.

Keywords: ***Rosa*** genus, Sheki, natural resources, sustainable use, economic potential

The Impact of Drought on Tobacco Production

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Abstract: Drought is a significant natural disaster resulting from climate change, characterized by reductions in precipitation, increases in temperature, and disruptions in seasonal patterns. This environmental issue profoundly impacts the agricultural sector, which is highly dependent on climatic conditions. In Türkiye, many crops face considerable yield losses due to drought, adversely affecting the national agricultural economy. Tobacco, extensively cultivated in the Aegean Region, stands out as a particularly vulnerable crop to drought stress. Drought negatively affects the growth and development processes of tobacco plants, reducing both the quality and quantity of production and thereby complicating cultivation conditions. These adverse effects weaken farmers' resolve to continue agricultural activities and increase their tendency to abandon production. The widespread abandonment of tobacco farming poses a serious threat to the sustainability of tobacco production. Therefore, developing effective adaptation strategies and shaping agricultural policies accordingly is crucial to mitigate the impacts of climate change. Within the scope of this study, face-to-face surveys were conducted with tobacco farmers in Denizli province, and the collected data were analyzed using descriptive statistical methods. The analysis aims to reveal farmers' attitudes toward drought, the challenges they face, and the impacts on their production decisions. The findings are expected to contribute to the development of policy recommendations necessary to ensure the sustainability of tobacco farming in the region and facilitate climate change adaptation.

Keywords: Climate change, drought, tobacco cultivation, yield loss, production abandonment

Middle School Students' Perceptions of Biodiversity, Gene Banks, and Local Seeds

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Abstract: Biodiversity loss is rapidly increasing in the world, agricultural genetic resources and seeds are increasingly affected by the changes experienced. Gene banks play an important role in maintain the genetic diversity. In this study, it was attempted to determine the perceptions of middle school students who visit the Aegean Agricultural Research Institute, where the first gene bank of Türkiye, established in 1964, regarding the concepts of biodiversity, local seeds and gene banks. The study was conducted with the participation of 151 students between March and June 2025. Data were collected with a semi-structured questionnaire applied before and after the briefings. Students were asked to write down the concepts that the words biodiversity, local seeds and gene bank evoked in their minds. Content analysis method, one of the qualitative research methods, was used in the analysis and interpretation of the collected data. As a result of the content analysis, the frequency of use of the concepts in the students' comments was examined. The concepts were shaped by word cloud analysis. Before the technical visit and briefings, it was determined that the concept of biodiversity was mostly perceived as "diversity of living things" (39.7%); local seed as "seed produced in Türkiye" (23.8%) and the concept of gene bank as "place where genes are stored" (23.8%). After the technical visit and briefings, although there was no significant change in the perception of the concepts in question, proportional changes were determined in the concepts of diversity of living things (34.4%); seed produced in Türkiye (43.0%) and place where genes are stored (42.0%). As a result, it is emphasized that the effect of practical training given at an early age is important in order to increase the awareness of future generations on the protection and development of biodiversity and to shape their perceptions correctly.

Keywords: Biodiversity, local seed, gene bank, middle school students, Aegean Agricultural Research Institute

Technology for Extracting Medicinal Nanoparticles from Extracts of Certain Medicinal Plants in Azerbaijani Flora

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Abstract: The main goal of these studies was to develop optimal methods for preparing extracts and homogenates of medicinal plants to obtain drug nanoparticles. Metal-based nanoparticles Ag and Fe were prepared using a green synthesis method involving AgNO3 and FeCl3 salts, aqueous extract, and homogenate of medicinal plants ***Melissa officinalis*** **L.** and flowers ***Eleaegnus caspica*** **E**. The properties of the nanoparticles were characterized using SEM, UV-Vis, XRD, and FTIR methods. Medicinal plants contain terpenes, phenolic components, volatile compounds, phenols, etc. These components play an important role in the synthesis of nanoparticles as reducing and stabilizing agents, thus contributing to their transformation into drug nanoparticles. The size, shape, and quantity of drug nanoparticles were found to depend on the dosage, extraction time, and stabilization time. Drug nanoparticles obtained from the aqueous extract and homogenate were characterized as spherical particles with diameters between 10 and 80 nm, as well as other shapes. XRD analysis showed that nanoparticles formed as a result of the reduction of silver and iron ions using the aqueous extract had a crystalline nature. The functional groups of the aqueous extract involved in the synthesis and stabilization of nanoparticles were studied by FTIR. The functional groups OH and CO of plant extracts play a dual role as reducing and stabilizing agents of nanoparticles. Therefore, it can be inferred that drug nanoparticles obtained through optimal synthesis in the aqueous extract of medicinal plants hold promising medicinal properties. Consequently, experiments of this nature enable the synthesis of nanoparticles in medicinal plant extracts, leading to the production of medicinal preparations, or in other words, medicinal nanoparticles.

Keywords: Nanobiotechnology, medicinal plants, extracts, drug nanoparticles, iron nanoparticles

Expression of Haemagglutinin HA gene in Maize for Production of Edible Vaccine against Avian Influenza Virus

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Abstract: Avian Influenza Virus is a viral disease that causes Influenza , strenuous breathing, and ataxia in the majority of avian species. The available vaccines against Avian Influenza Virus (AIV) are limited, Temperature stable and multiple dosage requirements. Plant-based machinery provides an attractive and safe system for vaccine production. In the current study, we attempted to express hemagglutinin (HA) protein (the protective antigens against AIV) under constitutive 35S and seed-specific Zein promoters, respectively. Almost 2–7.1-fold higher expression of HA gene mRNA in transgenic corn seeds were observed, when the expression was analyzed by real-time PCR on a relative basis as compared to non-transgenic control plant material (seeds). Similarly, 1.66 µg/ml of HA protein in corn leaves, i.e., 0.5% of total soluble protein, and 2.4 µg/ml of HA protein in corn seed found when calculated through ELISA. Similar levels of immunological response were generated in chicks immunized through injection of E. coli-produced pET HA protein as in chickens orally fed seeds of maize with expressed immunogenic protein. Moreover, the detection of anti-AIV antibodies in the sera of chickens that were fed maize with immunogenic protein, and the absence of these antibodies in chickens fed a normal diet, confirmed the specificity of the antibodies generated through feeding, and demonstrated the potential of utilizing plants for producing more vaccine doses, vaccine generation at higher levels and against other infectious diseases.

Keywords: Expression, edible vaccine, AIV

Marker-Trait Association Analysis For Grain Traits Based on Microsatellite Markers Under Post-Anthesis Drought Stress in Wheat (Triticum spp.)

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Abstract: At the post-anthesis stage, a diverse set of wheat genotypes, consisting of eleven wheat genotypes with varying levels of drought tolerance, was assessed under drought stress. A series of 11 wheat microsatellite markers were used to establish the allele spectrum of quantitative trait loci (QTLs) linked to drought tolerance. Subsequently, the genotypes were genotyped based on grain traits. In total, 24 important marker-trait associations (Srm) defined QTLs for grain area (Gai), grain length (Gli), grain width (Gwi), grain circumference (Gci), grain roundness (Gri), and stem reserve mobilization. More QTLs were located on chromosomes 12, 7, and 5 of the B, D, and A genomes, respectively. SSR marker association analysis found four microsatellite markers (Xgwm389, Xgwm003, Xgwm513, and Xgwm46) on chromosomes 3B, 3D, 4B, and 7B to have a significant association with most grain characteristics. Detection of QTLs for grain traits on various chromosomes showed that certain characters are controlled by multiple loci. Higher R2 values in QGli.gebri.3B.1 and QSrm.gebri.3B.2 ranged from 0.327* to 0.736** for Gli and Srm, respectively, for most characteristics. Genetic analysis has established the best microsatellite markers attributed to post-anthesis drought tolerance in bread wheat. This information can be useful for marker-assisted selection to enhance drought tolerance in wheat genotypes. Breeders may use this knowledge to develop crosses that combine new, potentially stable combinations of drought tolerance genes to improve wheat genotypes.

Keywords: Wheat, grain traits, microsatellite allele size, QTLs, drought tolerance

Study of the Effect of Waxy Genes on Quality Indicators in Local and Introduced Soft Wheat Varieties

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Abstract: 60% of the Earth's population consumes dietary carbohydrates and protein precisely through the use of wheat grain. In wheat, the main component, which reflects many technological properties, is starch. For this purpose, 36 samples and one tetraploid wheat (“Pirinc”), selected for many years for their quality indicators and of indicators falling number, were determined using the following primers to evaluate the allelic variants of the Wx gene collection: AFC/AR2, Wx-A1b-F-MH/Wx-A1b-R-MH, Sun1F/Sun1R, BDFL/BRD, 4F/4R, BDFL/BRC1/BRC2/BFC, WxB1L/Wx-B1R, Wx-D1-2F/Wx-D1-2R, Wx-D1-1F/Wx-D1-1R, BDFL/DRSL. As a result, it turned out that, based on the analysis of 14 durum wheat samples, Wx-B1 - Wx-B1e genes (amplification of the e-allele type) were detected in four samples. The "Qarabagh" and "Shiraslan 23" samples are heterogeneous, with "e" and "a" alleles for Wx-B1. The "Parvin" and "Shafaq 2" samples (soft wheat) carry the "e" allele in Wx-B1 - Wx-B1e (amplification with the e-allele type). In the "Ekinchi 84" and "Ghonen" soft wheat samples, a probable "b" allele for Wx-B1 - Wx-B1b (null allele) was detected using molecular markers. Although the Ekinchi 84 variety, one of the local soft wheat varieties, is one of the samples with the lowest of falling number grains (6-year average of 127 seconds), it was found that, along with the “Gönen” variety (work of Turkish breeders) (6-year average of 214 seconds), it has the “b” allele (null allele). However, the 6-year average result of the baking quality indicator of both samples was 4.5 points for the Ekinchi 84 variety, and 4.8 points for the Gonen variety. It is known that the most significant reduction in amylose content is achieved by the null allele of the WxB1 gene, from this point of view, the Ekinchi 84 and Gonen varieties are considered very valuable as genetic material.

Keywords: Soft wheat, starch, falling grain number, Waxy genes

Studies on Propagation of Some Crocus L. Species in Western Anatolia by Tissue Culture Methods

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Abstract: The objective of this study is to cultivate some ***Crocus*** taxa that are naturally spreading in Western Anatolia and determine the potential of the taxa for use as ornamental plants. Field studies and propagation trials were carried out. The materials included four Crocus taxa that are spreading naturally in the flora of Türkiye and include two endemics. While one of them blossoms during autumn (***C. pallasii* ssp. *pallasii***), the other three blossom during spring (***C. olivieri* ssp. *balansae, C. chrysanthus, C. baytopiorum***). The taxa were collected around the regions where they spread, their soil requirements were determined and species were identified. Propagation studies of tissue culture were carried out with corms. The corms were planted into MS medium including plant growth regulators such as 4.0 mg/l BAP; 5.0 mg/l BAP; 6.0 mg/l BAP; 4.0 mg/l BAP+0.5 mg/l NAA; 1.0 mg/l BAP+10.0 mg/l NAA with Gamborg vitamins; 2.0 mg/l BAP+20.0 mg/l NAA with Gamborg vitamins; 1.0 mg/l BAP+0.5 mg/l NAA; 2.0 mg/l BAP+0.5 mg/l NAA and 2.0 mg/l BAP+1.0 mg/l NAA. Viability rate, in vitro cormlet rate and adaptation to the external conditions rates were determined for all taxa. For Crocus olivieri ssp. balansae the high viability (85.7), cormlet (114.3) and adaptation rates (42.9) were taken from the treatment of 4.0 mg/l BAP. Crocus chrysanthus had the highest viability (60), cormlet (60) and adaptation rates (40) at the treatment of 4.0 mg/l BAP+ 0.5 mg/l NAA. Crocus baytopiorum the high viability (50), cormlet (200) and adaptation (50) rates treated of 4.0 mg/l BAP medium. For Crocus pallasii ssp. pallasii, the treatments had the same viability rates (33.3), exception of 4.0 mg/l BAP and 6.0 mg/l BAP treatments. The cormlet formation was observed at 2.0 BAP+1.0 NAA and 2.0 BAP+20.0 NAA treatments

Keywords: ***Crocus ssp***., geophyte, endemic, propagation

Evaluation of Durum Wheat (T. durum Desf.) Samples for Grain Quality Indicators and Protein Genetic Markers

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Abstract: Since the basis of the endosperm of wheat grain is the storage proteins gliadin and glutenin, the identification of allelic genes encoding these proteins and the study of their relationship with grain quality traits are very important. A total of 38 samples of durum wheat, including the varieties Barakatli-95, Maya, Auradur and the standard variety Karabakh, were studied. Physical indicators, plant yield per 1 m2 area, quantity and quality of raw gluten, quantity of dry gluten, total nitrogen, electrophoretic analyses of gliadin and glutenin storage proteins were carried out in the grains of wheat genotypes. The Langdon durum wheat variety was taken as a marker for the identification of gliadin- and glutenincoding loci in durum wheat varieties and samples. The yield in the studied samples was between 45-65 s/ha (45-65 s/ha), and the results obtained for the vitreous trait were positive (84% - 100%). The indicators were also satisfactory in terms of the mass of 1000 grains, this indicator was between (50-60 gr.). According to the results of the conducted research, the amount of gluten in the samples had an indicator of 25.9-40.0%. The deformation coefficient of gluten varied between (85-110 c.g.). The amount of total protein was in the Karabakh durum wheat variety (13.2%), in other samples starting from 14% and higher (***v.obscurum*** 16.7%, ***v.murciense*** 17.0%). In the study, electrophoretic analysis of grains of 38 durum wheat samples was performed on polyacrylamide gel (A-PAGE). As a result of electrophoretic analysis, prolamin storage proteins were conventionally divided into four zones: ω-, γ-, β- and α-gliadins. Genetic identification of the studied samples was carried out based on standard catalogs for the gliadin-encoding loci Gli 1A, Gli 1B, Gli 6A and Gli 6B and gluten-encoding loci Glu 1A and Glu 1B.

Keywords: Variety, grain, protein, locus, allele

Study of Polymorphism of Bread Wheat (T. aestivum L.) Samples with Gliadin Protein Markers

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Abstract: In the study, 34 local and introduced bread wheat samples belonging to the ***T.aestivum* L.** species were used and electrophoretic analysis of gliadin storage proteins in their grains was performed by A-PAGE (acidic polyacrylamide gel electrophoresis) method. The aim was to determine the allelic component blocks of the gliadincoding loci of bread wheat samples and determine their polymorphism based on gliadin protein markers. 43 known and 1 new allelic component block were identified in the gliadincoding loci of bread wheat samples. Thus, the Gld 1B3 and Gld 1D1 allelic component blocks were identified in the Gld 1B locus and the Gld 1D1 allelic component blocks were identified in the Gld 1B locus of the 130/32-***T.aestivum* L**. bread wheat sample, respectively. During the analysis of gliadin electrophoresis, a total of 36 spectra and 76 patterns were observed in the samples and their frequencies were calculated. 17 spectra and 29 different patterns were studied in the ω-(omega) zone of the gliadin electrophoresis of the samples. The ω- 2, ω- 4 and ω- 17 patterns of this zone had a frequency of 6.0% in 34 samples, and the ω- 5 and ω- 11 patterns had a frequency of 5.8%. 6 spectra and 11 patterns were observed in the ϒ-(gamma) zone of the gliadin electrophoresis. 5 spectra and 9 patterns were determined in the β- (beta) zone. 8 spectra and 27 patterns were detected in the α- (alpha) zone. Genetic diversity coefficients were calculated for each of the 4 zones by applying the Nei formula. As a result of the calculations, a high genetic diversity index was determined in the ω- zone (H=0.960), a low one in the ϒ- zone (H=0.550) and β- zone (H=0.544) and an average one in the α- zone (H=0.770).

Keywords: Bread wheat, gliadin, allele, locus, identification.

Uncovering Genomic Diversity in Global Durum Wheat Germplasm Through SSR Marker Profiling

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Abstract: Understanding genetic diversity and effectively managing genetic resources are fundamental components of modern plant breeding programs. Genetic diversity serves as the foundation for all selection processes, and access to this variation is crucial for the development and selection of desirable genotypes and plant specimens. A range of methods is available for assessing genetic diversity in plant species, including morphological, agronomic, cytological, biochemical, and molecular approaches—particularly those based on DNA markers. Among these, plant breeders often favor DNA-based molecular markers due to their higher reliability and accuracy in evaluating genetic variation, especially when compared to morphological markers. The genetic diversity of durum wheat (***Triticum turgidum* ssp. *durum***) germplasm was evaluated using microsatellite (SSR) markers. A total of 41 durum wheat landraces originating from diverse geographic regions including Turkey, Lebanon, Morocco, Ethiopia, China, Kazakhstan, and Mongolia were analyzed using 27 carefully selected SSR markers with genome-wide coverage. Among these, 17 loci were found to be polymorphic, generating a total of 67 allelic variants. The number of alleles per locus ranged from two to seven, with an average of 3.94 alleles per locus. The polymorphic information content (PIC) values varied from 0.071 (Xgwm371) to 0.647 (Xgwm120), indicating a wide range of marker informativeness. Cluster analysis grouped the landraces into four distinct genetic clusters, revealing a clear correlation between genetic variation and geographic origin. Notably, landraces from Africa and Western Asia exhibited higher levels of genetic diversity compared to those from Central and East Asia. These findings suggest that Western Asia and Africa particularly southeastern Turkey may represent primary centers of genetic diversity for durum wheat. This highlights the significance of these regions in germplasm conservation and breeding programs aimed at enhancing genetic resilience and crop improvement.

Keywords: Durum wheat, genetic diversity, molecular markers, SSR profiling

Genetic Diversity and Population Structure of Bread Wheat Evaluated by GBS

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Abstract: Breeders need genetic diversity as a resource to enhance new cultivars with desired traits. In many crop species, including those with large genomes, genotyping-by-sequencing (GBS), a next-generation sequencing (NGS) technology that simplifies complex genomes, has recently been utilized as a high-throughput and cost-effective molecular tool for routine breeding and screening. The development of Next-Generation Sequencing technology has led to the widespread use of genotyping by sequencing (GBS), an effective molecular tool for examining the genetic diversity of wheat. In plant genomes, single-nucleotide polymorphisms (SNPs) are the most common type of sequence variation. Genetic variation analysis, population structure, marker-trait association, genomic selection, QTL mapping, map-based cloning, and other plant breeding applications that require a large number of markers to cover entire genomes can all benefit from their use.

In this study, GBS was used to characterize 924 bread wheat genotypes from different origins. A total of 55,520 high-quality single-nucleotide polymorphism (SNP) markers were used to assess genetic diversity and population structure. RefSeqv1.0 and RefSeqv2.0 references were used to analyze the results of the GBS analysis. The B genome has the most SNP markers (27,030-48%), followed by the A genome (20,755-38%), and the D genome (8,175-14%) has the fewest. There was an alignment between the centers of origin of the genotypes, and the results of the principal component and cluster analyses were comparable.

Keywords: Genotyping-by-sequencing (GBS), Single-nucleotide polymorphisms (SNPs), wheat, breeding, genetic diversity

Molecular Genetic Evaluation of Azerbaijani Grape Genotypes

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Abstract: The genepool of Azerbaijan's grapes is characterised by extensive polymorphism. Populations of genotypes, formed from various biotypes, clones, forms, and variations, carry valuable traits of economic and breeding significance. Therefore, every grape sample in the gene pool must be identified, collected, securely preserved, effectively used, and passed on to future generations. By maximising their potential, it is essential to meet the demand for viticulture and winemaking products while achieving sustainable development in the industry. The evaluation of the grape gene pool using modern molecular genetic methods, its effective use, preservation, and successful inclusion in breeding and commercial activities, remains relevant.

In 2009-2024, 366 variety accessions in the institute's collection, as well as those collected during scientific expeditions, were subjected to molecular genetic analysis (for 24 SSR microsatellite loci: VVS2, VVMD5, VVMD7, VVMD21, VVMD24, VVMD25, VVMD27, VVMD28, VVMD32, VrZAG62, VrZAG67, VrZAG79, VrZAG83, VMC4f3.1, VMC1b11, VVIb01, VVIh54, VVIn16, VVIn73, VVIp31, VVIp60, VVIq52, VVIv37, VVIv67); as a result, it was revealed that 137 varieties are unique profiles belonging to the local genetic pool. Based on the genetic profiles of varieties and forms of Azerbaijan, unique profiles, synonyms, and homonyms were identified, and as a result of the study of gene similarity, their "genetic relationship" was determined.

As a result of these studies, the Azerbaijani grape varieties, indicated in some sources as Armenian – Khindogny, Gyomushumeme (Apoi hagog), and Malayi (Areni), were accepted as Azerbaijani varieties in the International Catalogue of Grape Varieties (VIVC).

116 varietal samples and wild forms, discovered in various regions (Gabala, Ismailly, Shamakhy, Absheron, Salyan, Lerik, Fizuli, Khojavend, Aghdam, Jalilabad, Lankaran, Gakh, Zagatala, etc.), and not yet studied on a scientific basis, are molecularly genetically analysed in collaboration with the German Institute of Grape Breeding Geilweilerhoff, pure profiles are identified and studied to obtain biologically and genetically certified planting material in the future.

Keywords: Grape, molecular-genetic analysis, SSR marker

The Effect of Climate Change on Anatolian Flora and Beekeeping

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Abstract: Anatolia is a very florally rich geographical area hosting 12.000 plant species. Bees play a critical role in the continuity of plant diversity (pollination duty). There are five different honey bee races (***Apis mellifera anatolia, Apis mellifera caucasica, Apis mellifera carnica, Apis mellifera syrica, Api melifera meda***) in Turkey and there are also different ecotypes of the Anatolian bee. As a result of this richness, Turkey is among the top three in the world rankings with 9 million colonies and around 100 thousand tons of honey production. The effect of rapidly changing climate conditions on fauna and flora is increasing day by day. As a result, there are many observed and possible effects. For this reason, all actors in agricultural activities should work together and in a planned manner based on sustainability. When we consider that bees have lived for about 100 million years, we understand how good their adaptation ability is. It is understood that the biggest impact on colony deaths experienced today is created by producers. The best evaluation of genetic structure and floral resources according to changing climate conditions and regional modeling are necessary for the future of beekeeping. It should not be forgotten that sustainable beekeeping is a sustainable future.

Keywords: Climate change, honey bee, genetics, sustainability, productivity

Climate Change Adaptation: Effects on Plant Genetic Resources and Honey Bees

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Abstract: Climate change not only influences the adaptation process of plant species in agricultural ecosystems but also profoundly affects plant–pollinator interactions. Rising temperatures and irregular precipitation patterns cause shifts in flowering times, resulting in reduced nectar and pollen production. Consequently, phenological mismatches between plants and pollinators occur, limiting the availability of balanced nutrition for honeybees and negatively impacting colony health and honey production. Sustainable colony development requires continuous floral diversity and synchronized blooming of various plant species. However, climate-induced disruptions in flowering windows create “flora deficiencies,” leading to nutritional imbalance, reduced colony energy regulation, and weakened immune systems in honeybees. In this context, the evaluation and conservation of plant genetic resources, particularly those tolerant to stress conditions (e.g., drought and heat), are of critical importance for identifying resilient varieties. Such genotypes, by extending flowering duration and enriching nectar and pollen content, may contribute significantly to meeting pollinator nutritional requirements. For instance, a study published in *Nature* reported that extreme rainfall increased nectar energy content by 74–79%, yet prolonged drought reduced it by 34–98%. These fluctuations intensify nutritional stress in bees and increase colony vulnerability. Therefore, adaptation strategies within the scope of climate change should prioritize the preservation of genetic resources in gene banks, the utilization of locally adapted and wild species, the integration of stress-tolerant varieties into breeding programs, monitoring of phenological shifts, and the establishment of pollinator-friendly floral corridors. In conclusion, effective adaptation strategies against climate change must focus on ensuring the sustainable use of plant genetic resources while safeguarding the ecological and economic roles of pollinators.

Keywords: Plant genetics, climate adaptation, honeybee, flora deficiency, flowering mismatch, pollinator stress

Ecological Classification of Interactions Between Apis mellifera and Angiosperms: Mutualism or Protocooperation?

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Abstract: The honey bee (***Apis mellifera***) is one of the most critical pollinator species for the continuity of ecosystems. Its interactions with flowering plants (*Angiospermae*) are of great importance not only for the nutrition of honey bees and the sustainability of colonies but also for agricultural productivity and the conservation of biodiversity. These interactions can be classified ecologically under different categories. On one side lies facultative mutualism, characterized by regular and recurring reciprocal benefits; on the other, protocooperation, which refers to looser, opportunistic, and short-term interactions. In this study, the interactions between ***Apis mellifera*** and various angiosperm species were evaluated within the framework of an ecological classification based on literature. As examples of mutualism, honey bee pollination plays a vital role in agriculturally important species such as apple, almond, and sunflower. In contrast, protocooperation is illustrated by plants such as alfalfa (***Medicago sativa***), where sporadic or seasonal visits by bees provide mutual benefit but lack continuity and partner fidelity. This distinction highlights the need to assess pollinator–plant interactions not only from a biological perspective but also within ecological and agricultural contexts. In conclusion, the ecological classification of ***Apis mellifera***–angiosperm interactions offers important insights both for basic ecology and for the development of sustainable agricultural strategies. Stable interactions based on mutualism contribute to securing agricultural productivity, whereas more transient protocooperative interactions play a complementary role in maintaining plant diversity. This dual perspective provides a valuable framework for understanding the multifaceted ecological functions of honey bees.

Keywords: ***Apis mellifera***, angiosperms, mutualism, protocooperation, pollination ecology

Use of Medicinal and Aromatic Plants from Our Genetic Resources Against Bee Diseases and Sustainable Solutions

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Abstract: Honey bee health plays a critical role in maintaining ecosystem balance and ensuring agricultural productivity. However, bee diseases and parasites—especially ***Varroa destructor*** and ***Nosema* spp**.—cause significant losses in beekeeping. In addition to conventional treatment methods, medicinal and aromatic plants offer natural and sustainable alternatives for controlling these diseases. These plants, with their genetic diversity, hold potential for the treatment of various diseases. This presentation highlights not only the effects of medicinal and aromatic plants on bee diseases but also the importance of conserving plant genetic resources. Plants such as ***Thymus vulgaris*** (thyme) – thymol, ***Lavandula angustifolia*** (lavender) – linalool, linalyl acetate, ***Rosmarinus officinalis*** (rosemary) – carnosic acid, carnosol, rosmarinic acid, ***Mentha piperita*** (peppermint) – menthol, menthone, ***Salvia officinalis*** (sage) – thujone, cineole, camphor, and ***Eucalyptus*** spp. – eucalyptol (1,8-cineole), have shown remarkable efficacy against pathogens such as ***Varroa destructor*** and ***Nosema* spp**. Moreover, the genetic diversity of these plants ensures the preservation of traits that enhance their ability to combat diseases. The genetic resources of plants enhance the effectiveness of such treatments and enable the development of more efficient solutions under various environmental and climatic conditions. The genetic diversity of medicinal and aromatic plants plays a crucial role in the development of sustainable practices in apiculture. These plants possess properties that strengthen the immune system of honey bees and hold great potential for the conservation and improvement of plant genetic resources. Furthermore, preserving the biological diversity of these plants enhances the reliability and efficacy of natural treatment methods. This presentation highlights the potential strategies offered by conserving the genetic resources of medicinal and aromatic plants to improve bee health and reduce dependency on chemical acaricides. Moreover, the role of plant genetic resources in developing resistance to bee diseases represents a significant contribution to sustainable beekeeping.

Keywords: Medicinal and aromatic plant, bee diseases, ***Varroa destructor***, ***Nosema spp***., plant genetic resources, genetic diversity, natural treatment methods, bee health

POSTER PRESENTATIONS

Study of the Genetic Resources of Sweet Chestnut (Castanea sativa Mill.) in the Sheki-Zagatala Region

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Abstract: The aim of the study was to determine the distribution areas of genetic resources related to sweet chestnut (***Castanea sativa* Mill.)** in the Sheki-Zagatala region, to perform pomological descriptions, and to evaluate their biological and economic indicators. The material for the research consisted of local traditional selection varieties and forms of sweet chestnut grown by local farmers in the household plots of the Sheki-Zagatala region. The biomorphological description of the samples, their productivity, fruit quality indicators, resistance to diseases and pests, as well as the selection of promising forms, were carried out in accordance with modern methods. The Sheki-Zagatala region is the main area of sweet chestnut cultivation in our republic. As a result of the searches, 53 sweet chestnut samples were identified in the territories of Ismayilli, Gabala, Oghuz, Zagatala and Balakan districts. These cultivated varieties and forms of sweet chestnut were described in comparison to the origin of the plant, including geographic coordinates, height, trunk diameter, crown shape, approximate age, flowering period, fruit shape, color, length, width, height, ripening period, productivity following international descriptors. Initial selection was conducted on productive samples with large fruits, high taste quality, ripening at different times, and relative resistance to various biotic and abiotic stress factors in the environment. Their agronomic and biological indicators were evaluated, and pomological properties were described using modern methods. These varieties and forms are used by the local population for food and sale purposes. However, the number of such varieties and forms, which contain a rich genetic fund created over many centuries by local people, has sharply decreased in recent years. Collecting, studying, passporting, creating collections of the genetic diversity of sweet chestnut that are cultivated and naturally distributed in the Sheki-Zagatala region is one of the most pressing issues of our modern times.

Keywords: Sweet chestnut, variety, genetic resources

Using Modern Biotechnologies for Conservation of the Genepool of Commercial and Wild Grapes

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Abstract: Plant genetic resources represent a fundamental basis for biodiversity and the sustainable development of agriculture. Their conservation is critically important for breeding, adaptation to climate change, and ensuring food security. One of the most effective approaches for the preservation and regeneration of rare and endangered plant forms is the use of in vitro technologies. This study aimed to develop an in vitro initiation protocol for commercial grape cultivars «Rizamat» and «Taifi Rozoviy», as well as the wild subspecies Vitis vinifera ssp. silvestris. Thimerosal was used as a sterilizing agent at different concentrations. The most effective treatment was 0.1 mg/L for 5-7 minutes, which ensured complete sterility and 100.0% explant survival. Two hormone-free nutrient media, MS and WPM, were tested. The MS medium demonstrated superior performance, with 90.0% bud break and up to 80.0% shoot induction. Shoots developed strong morphology and normal structure. In contrast, the WPM medium resulted in slower development and thinner shoots. Rooting was performed on a modified MS medium supplemented with 0.2 mg/L NAA. Optimal rooting occurred in shoots measuring 2.5-3.0 cm in height and bearing 2-3 well-developed leaves. These shoots developed complete and functional root systems. The developed protocol enables efficient cultivation of both cultivated and wild grape forms. It provides a valuable foundation for the production of healthy planting material and for the long-term conservation of grapevine germplasm. The results are applicable in the practice of micropropagation, grapevine biotechnology, and breeding programs in Uzbekistan and other countries with similar agro-climatic conditions.

Keywords: Grape, micropropagation, *in vitro*, production of healthy mother plants

Researches on propagation of Sideritis tmolea P.H.Davis with tissue culture

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Abstract: Endemic plant species, which are more vulnerable to natural changes occurring on Earth, are at greater risk of extinction than other plant species. In addition, endemic plants are highly valuable in terms of biodiversity and are also unique breeding materials. Sideritis tmolea is a rare and endemic plant species native to Türkiye. The long-term conservation of this species, which is naturally distributed in certain regions of our country, will contribute to our country's biodiversity and serve many fields such as pharmacology, industry, and medicine. Biotechnological studies conducted on our natural biological resources will raise awareness on such rare plants and thus contribute to science. The aim of our study is to investigate the vegetative propagation potential of ***Sideritis tmolea***, which has limited distribution area in our country, under in vitro conditions. For this purpose, Murashige and Skoog's (MS) basal medium which was supplemented with either 6-Benzylaminopurine (BAP), Thidiazuron (TDZ), 2-Isopentenyladenine(2ip) at the following concentrations: 1.0, 2.0 and 3.0 mgl-1 plus 0.1 mgl-1 Indole-3-acetic acid (IAA). In this study, shoot tips were used as explant sources. Observations related to the experiment were evaluated at the end of two subcultures. In the study, the best results were obtained in MS medium containing 3.0 mgl-1 TDZ+0.1 mgl-1 IAA, with a 100% percentages of shoots rate and 10.1 number of shoots per explant. The lowest shoot number (1.0 shoots per explant) was attained in media containing 1.0 mgl-1 TDZ+ 0.1 mgl-1 IAA and control. The data obtained will shed light on studies related to the sustainability of biodiversity.

Keywords: Biodiversity, endemic plant, *in vitro* culture, multiplication

Development of a National Strategic Action Plan for British Crop Wild Relative Diversity

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Abstract: CWR (crop wild relatives) represent critical plant genetic resources essential for crop improvement programmes to enhance agricultural resilience and ensure global food security, especially in the context of climate change, biodiversity loss, and food inequality. Despite their importance, these taxa frequently face threats from habitat degradation, climate pressures, and inadequate conservation measures. This PhD research addresses this gap by developing a National Strategic Action Plan aimed at conserving Britain's CWR, safeguarding vital genetic diversity for the stability of British and international agriculture.

To date, this research has successfully established a comprehensive national checklist and prioritised inventory of British CWR taxa. A parallel prioritisation approach was used to appropriately identify species in most urgent need of conservation action. This resulted in 221 priority taxa from 31 plant families, showing that Britain hosts a wide range of CWR.

Current analyses involve detailed examination of occurrence data for these priority taxa to uncover significant gaps in existing conservation measures, both *ex situ* in gene banks and *in situ* within protected and unprotected areas. Upcoming research phases will further evaluate these priority species using CAPFITOGEN tools to assess predictive modelling of climate change impact, complementarity analyses and the generation of comprehensive ecogeographic land characterisation maps. Moreover, genetic analyses will be conducted to provide deeper insights into genetic diversity within and between populations, significantly enhancing the effectiveness of conservation management strategies and increasing the knowledge base of British CWR.

Ultimately, the integration of taxonomic, ecological, geographic, genetic, and climatic data will culminate in a detailed and actionable National Strategic Action Plan for Britain. The resulting recommendations will directly support policymakers and stakeholders, including Defra, Natural England, and the UK Plant Genetic Resources Group, to guide evidence-based decisions to secure the future of Britain's essential crop wild relatives.

Keywords: Crop wild relatives, National Strategic Action Plan, genetic diversity

Characterization of Tomato Starting Selection Materials According to the Main Economic Significant Indicators, Traits and Phenotypical Variability

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Abstract: The aim of this study was to investigate the phenotypic variability and the main economically important traits of initial parental forms to be used in open-field hybridization. The methodological guidelines developed by VASKHNIL for tomato breeding in open and protected fields were used in the research. As initial material, tomato varieties Sladkiy million, Sladkaya grozd, Senyorita, Ocharovaniye, Tigrich, Sammersan, Slivka krasnaya, as well as hybrid lines 16/3, 14/2, 15/1, 17/1, 14/4, 18/3, 13/2, 12/2 were used. It was established that depending on cultivation conditions, different changes occurred in the phenotypes of tomato samples. One of the main indicators for tomato samples is fruit set, which significantly affects yield. The study revealed that in the first cluster, higher fruit setting (94–100%) was recorded in varieties Sladkiy million, Tigrich, Ocharovaniye, Sammersan, Senyorita, and in lines 15/1, 16/3, 14/2, 12/2, 17/1, 18/3, 14/4, 13/2. In the second cluster, higher fruit setting (92–100%) was observed in varieties Sladkiy million, Sladkaya grozd, Ocharovaniye, Sammersan, Senyorita, and lines 15/1, 12/2, 17/1, 18/3. The varieties Sladkiy million, Sladkaya grozd, Ocharovaniye, Sammersan, Senyorita, and lines 15/1, 17/1, 18/3 were characterized by higher fruit setting (93–100%) in the third cluster. In the fourth cluster, higher fruit setting (80–96%) was recorded in varieties Sladkiy million, Sladkaya grozd, Sammersan, Senyorita, and line 17/1. Relative stability of fruit setting across clusters I–IV was observed in varieties Sladkiy million and Sammersan. Analysis of total yield showed that in 2021–2023, relatively high-yielding varieties (5.3–5.4 kg/m²) were Ocharovaniye, Slivka krasnaya, and lines 16/3, 13/2, 17/1. Based on high total sugar content (4.2–4.9%), the varieties Sladkiy million, Tigrich, Sammersan, and lines 14/2, 18/3, 14/4, 13/2 stood out. Considering complex traits, the varieties Sladkiy million, Sammersan, Ocharovaniye, Senyorita, and lines 14/4, 13/2 were distinguished. These initial samples can be used to develop heterotic F^1 hybrids belonging to cherry and cocktail groups.

Keywords: Tomato, variety, line, initial material, trait, variability

Biomorphological Assessment of Avena L. Populations Spreading in Azerbaijan

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Abstract: The main objective of the study is to investigate the biomorphological characteristics and distribution of wild oat (*Avena* L.) species under natural conditions in Azerbaijan. The expeditions covered 50 routes encompassing all botanical-geographical regions of Azerbaijan (Absheron, Greater Caucasus, Lesser Caucasus, Kura–Araz lowland, Lankaran–Astara, and Nakhchivan). The research of the collected wild oat species revealed that they are predominantly distributed in the Absheron and Kura–Araz lowland botanical-geographical regions. A collection of 230 herbarium and seed materials, was gathered following international descriptor guidelines. Geographic coordinates were recorded with a GPS device. Cluster analysis was performed using SPSS Win software. In 2019-2024, 10 species of the genus ***Avena* L.** (***A. eriantha, A. clauda, A. wiestii, A. barbata, A. hirtula, A. bruhnsiana, A. ventricosa, A. trichophylla, A. fatua, A. ludoviciana***) collected from various regions of Azerbaijan were biomorphologically assessed for 29 quantitative and 16 qualitative traits, and their ecogeographical and phytocenological characteristics were recorded. The research revealed that four species of the genus *Avena* L. distributed in Azerbaijan (***A. hirtula*, *A. wiestii*, *A. bruhnsiana*, *A. trichophylla***) are synonyms. Thus, the species ***A. wiestii*** and ***A. hirtula*** are synonyms of the species ***A. barbata***; ***A. bruhnsiana*** is a synonym of ***A. ventricosa***; ***A. trichophylla*** is a synonym of ***A. sterilis* subsp. *ludoviciana***. These synonymized species possess identical morphological traits, occur in the same botanical–geographical regions, and are found within the same phytocoenoses. Geobotanical and floristic research indicated that oat species are widely distributed in cereal-legume-mixed formations, xerophilous shrub associations, grasslands, and cultivated fields. They are particularly common along roadsides, in crops, meadows, and coastal sand dunes. The results of the study indicate that species of the genus *Avena* L. exhibit high ecological adaptability and highlight the importance of their conservation as genetic resources.

Keywords: ***Avena***, population, biomorphology, SPSS

Evaluation of a Lentil Collection for Biomorphological Traits, Yield and Quality

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Abstract: Lentil (***Lens culinaris*** **Medik**.) is an ancient and valuable legume crop. Its seeds are rich in vitamins, carbohydrates and essential amino acids — notably tryptophan, lysine, methionine, valine and leucine — which are important for normal development of humans and animals. To increase lentil production in our country, priority tasks include developing new high-yielding, quality and disease-resistant cultivars, organizing seed production, identifying optimal cultivation technologies, mechanizing harvest, and promoting adoption at the farm level. In breeding, traits such as vegetation period, plant height, disease resistance and yield receive special attention; therefore, comprehensive study of these characteristics is essential for pulse crops.The research was conducted in 2023–2024 at the GEI Absheron Experimental Station following ICARDA protocols. Field phenological observations, assessment of stand characteristics, and evaluations of drought, salinity and disease tolerance were performed. The tested lentil accessions had vegetation periods ranging from 163 to 175 days. Regarding plant height, 14.4% of accessions were shorter than 30 cm, 66.5% ranged between 30 and 40 cm, and 19.1% exceeded 40 cm. For 100-seed weight, 46.7% of accessions fell below 5 g while 53.3% exceeded 5 g.The diversity of edaphic and climatic conditions across the country necessitates the creation of intensive-type cultivars that are high-yielding and adaptive to environmental stresses and diseases. Alongside international germplasm received from ICARDA, local collection samples are being systematically evaluated. The National Genebank of the Institute of Genetic Resources currently conserves over 400 lentil forms; these resources are comprehensively studied and effectively used in breeding.

Keywords: Lentil, protein, vitamins

Evaluation of Eggplant (Solanum melongena L.) Genotypes in Absheron Varieties

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Abstract: Eggplant (***Solanum melongena* L.)** is one of the most important agricultural crops cultivated in tropical and subtropical regions around the world. Assessing the genetic diversity of available genotypes is a crucial step toward the development of improved cultivars with superior agronomic traits. Eggplant is widely appreciated for its high nutritional value, pleasant taste, and substantial caloric content. The species is believed to have originated in India and was primarily cultivated as an ornamental plant until the 17th–18th centuries. From the 18th century onward, it became an established crop in the Caucasus region. In Azerbaijan, several eggplant varieties have been registered, including early-, mid-, and late-maturing types. In this study, a total of 40 eggplant genotypes, including both varieties and breeding lines, were evaluated for their quantitative traits and interrelationships. The genotypes were cultivated in 2024 at the Saray experimental field of the Genetic Resources Institute using a randomized complete block design with three replications. Traits such as plant height, fruit weight, number of fruits per plant, days to 50% flowering, branch number, fruit length, fruit diameter, and total yield were assessed. Analysis revealed statistically significant differences ($P<0.01$) among genotypes for all traits. Correlation and stepwise regression analyses indicated strong associations between yield and several traits, especially fruit number and fruit weight, which were also included in the final regression model. Biplot analysis confirmed wide genetic diversity among the studied genotypes, highlighting their potential for use in future breeding programs.

Keywords: Eggplant, breeding, genotype, correlation, yield

Impact of Introgression of Alien Genetic Material on the Grain Quality of Common Wheat

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Abstract: In order to enrich and improve the gene pool of common wheat, we involved the species samples of the genus ***Triticum*** (***T. dicoccoides, T. dicoccum, T. durum, T. spelta*** and ***T. kiharae***) in crossing with ***Triticum aestivum*** varieties. Previously, in the introgressive wheat lines we developed, the chromosomal localization of the genetic material of species of the genus *Triticum* was established using C-banding and molecular analysis. The study aims to evaluate the impact of foreign genetic material on the main grain quality traits of introgressive wheat lines. The study material included 32 introgressive lines and their parental forms. The protein and gluten content in grain and the gluten quality (GDI – the gluten deformation index) were established using the infrared analyzer “Infra LUM FT-12”. Analysis of grain quality parameters over 5 years showed that wheat relatives significantly surpassed common wheat varieties in these characteristics. The highest values by grain protein content were found for wild and domesticated emmer samples ***T. dicoccoides*** (23.8%) and **T. dicoccum** k-45926 (23.54%); by gluten accumulation – ***T. kiharae*** (46.43%); by gluten quality –T. dicoccum k-45926 (75.6 cu, GDI) and ***T. kiharae*** (77.7 cu, GDI). On average, over 5 years, 1000 grain weight in the group of varieties was higher than in the group of wheat relatives (40.4g and 38.3g respectively). However, by this trait, the T. kiharae sample (44.8g) exceeded not only other related species but also varieties. In the group of introgressive lines, the protein and gluten content, GDI and 1000 grain weight for the entire observation period were on average 19.11%, 37.20%, 82.67 cu and 41.20g respectively, which is closer to variety values. Ten introgressive lines, surpassing parental varieties by a set of grain quality traits and not inferior to them in 1000 grain weight that are of interest for wheat breeding, were identified.

Keywords: Wheat relatives, introgressive lines of common wheat, grain quality

Study of Heterosis in Tomato Hybrids

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Abstract: The regularities of inheritance of valuable selection traits have been studied in our research on the selection of F1 hybrids with heterosis effect between local and introduced varieties of tomato. A number of economically important traits were used in the descriptor for tomato developed by the International Biodiversity Institute. The values of the average heterosis effects changed as follows: the parental heterosis effects ranged between 28.1 and 161%, the heterosis effect of the superior parents changed from 6.5 to 105%, and the values for the standard heterosis ranged between 8.9 and 181%. According to the average productivity of varieties with superior parental indicators, the hybrids of combinations Leyla × Utro (105%), Masalli v/f × Utro (81%), Masalli v/f × Volgograd-5/95 (19%), Garant × Ilkin (58%), Garant × Volgograd-5/95 (13%), Shahin × Ilkin (101%), Shahin × Utro (17%), Sahin × Volgograd-5/95 (33%), Sheker × Volgograd- 5/95 (-12%), Tamara × Ilkin (22%), Tamara × Volgograd-5/95 (-10%), and Zafar × Volgograd-5/95 (27%) were distinguished by their high performance. Hybrids with standard heterosis effect were related to the combinations Leyla × Utro (161.8%), Masalli v/f × Utro (95.7%), Masalli v/f × Volgograd-5/95 (54.4%), Garant × Ilkin (61.1%), Garant x Volgograd-5/95 (48.2%), Shahin × Ilkin (181.9%), Shahin × Utro (58.8%), Sahin × Volgograd-5/95 (80%), Sheker × Volgograd- 5/95 (62.9%), Tamara × Ilkin (44.3%), Tamara × Volgograd-5/95 (17.5%), Zafar × Utro (50.8%), and Zafar × Volgograd-5/95 (65.5%). In the future, breeders can use this information to increase the heterosis effect by obtaining hybrids with high productivity by influencing the environment.

Keywords: Heterosis effect, inheritance, local varieties, introduced varieties

Evaluation of Biomorphological and Biochemical Indicators of Tomato Genotypes Cultivated Under Greenhouse Conditions, Selection of Valuable Donors for Breeding

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Abstract: In 2023–2024, 42 tomato genotypes cultivated in cocopeat under greenhouse conditions at the "Vegetable Growing Research Institute" public legal entity were evaluated at the technical maturity stage based on certain morphological traits (fruit height, diameter, index, average fresh and dry weight per fruit) and biochemical parameters (dry matter, sugars, extractive substances, total acidity, sugar-to-acid ratio, nitrates). It was determined that in the studied tomato genotypes fruit height ranged from 32.97–64.29 mm, diameter 24.10–71.97 mm, index 0.76–1.50, average fresh and dry weight per fruit 7.41–135.67 g and 0.49–7.73 g, respectively; dry matter content 4.33–7.28%, sugars 1.0–4.28%, extractive substances (soluble in cell sap) 2.73–5.46%, total acidity 0.23–0.51%, sugar–acid ratio 1.96–13.38, nitrate content 56.0–201.9 mg/kg. The wide variation in these indicators among the studied tomato genotypes made it possible to select 10 samples differing in both appearance and biochemical composition, which can be used as valuable initial parental forms in future quality-oriented breeding. Such samples include genotypes 343, 394, 398, 401, 462, A-6 F1, A-8 F1, A-12 F1, A-15 F1, and A-17 F1. In these samples, dry matter content was 5.65–7.28%, sugars 2.68–4.28%, extractive substances 4.06–5.46%, total acidity 0.23–0.38%, sugar–acid ratio 7.38–13.38, and nitrate content 56.0–185.6 mg/kg. Four of the selected F1 hybrids also stood out for their lowest nitrate content (56.0–90.1 mg/kg), which is 3.33–5.36 times lower than the maximum permissible level (300 mg/kg) set by the Ministry of Health of the Republic of Azerbaijan for greenhouse-grown tomatoes. Therefore, these hybrids can undoubtedly serve as valuable initial donors in breeding programs aimed at producing environmentally safe products.

Keywords: Tomato genotypes, biomorphological indicators, biochemical indicators, breeding, greenhouse

Investigation of the Genetic Resources of Bread Wheat (Triticum aestivum L.) under the Conditions of Karabakh, Selection of Promising Forms, and Development of New Varieties

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Abstract: Enhancing the productivity and quality of bread wheat (***Triticum aestivum* L.**) plays a crucial role in ensuring national food security and reducing dependence on imports. In the context of global climate and environmental change, it is increasingly important to conduct pre-breeding studies on genotypes resistant to stress factors such as high temperatures, drought, salinity, and various diseases. Enriching wheat germplasm through hybridization, studying hybrid materials, and incorporating them into breeding programs are essential steps toward developing and introducing new varieties adaptable to diverse agroecological conditions. At the Genetic Resources Institute – National Genebank, approximately 1,500 bread wheat genotypes have been collected and involved in extensive breeding research over several decades at the Karabakh Experimental Research Station. Crosses were performed among accessions with valuable agronomic traits, and the resulting hybrid generations underwent multi-year evaluations for yield, quality parameters, lodging resistance, and disease tolerance. The best-performing lines were re-evaluated and selected as promising forms for regional trials.

In recent years, several newly developed bread wheat varieties characterized by high yield potential and grain quality — Start (TT 09214/3-5 lutescens [TB 0815/2-2 [(TB Axatsikhis Tsiteli Doli × 45319 Panonia) × 45319 Panonia] × AB 01090 (Sharbat sonora × Dwarf)]), Cənub ([Uluqbey × Mexican spring line] × Sanzor 6, erythrospermum), Xəmsə (v. erythrospermum × v. albidum), Almaz (TT 09214/3 lutescens × TB 0815/2-2 [(TB Axatsikhis Tsiteli Doli × 45319 Panonia) × 45319 Panonia] × AB 01090 [Sharbat sonora × Dwarf]), Viləş (TT 09214/3-7-2-1 lutescens 0815/2-2 [Axatsikhis Tsiteli Doli × 290612 Pov.ke.pet.rul] × 01090 [Sharbat sonora × Dwarf]), Şuşa (Lutescens × Graecum), and Yaşma (Pehlivan/4/Babax/Lr42//Babax2/3/Kuruku/4-1-4-2*) — have been officially registered, patented, and included in the State Register of the Republic of Azerbaijan. These varieties are currently cultivated on a large scale across the country.

Keywords: Bread wheat, hybridization, stress tolerance, variety development

Genetic Enhancement of Wheat using Genetic and Genomics Resources for Food Security

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Abstract: Wheat, a staple food for about 40% of the world's population, plays an important role in food security. The need to accelerate the development of wheat genotypes that are both resistant to and productive under stress conditions is heightened by the global population growth and the increasing demand for food by a growing world population. One promising option to address these challenges is the use of genomics tools to improve wheat for high yield, better quality, and enhanced resistance to environmental stress by exploring wheat genetic resources. Several decades of progress in genomics have tremendously advanced our understanding of the molecular and genetic mechanisms underlying complex traits in wheat. The availability of rich genetic resources in wheat, such as landraces and wild relatives, along with advanced genomics tools, has heralded what might be considered a "golden age" of wheat genetic improvement. Here, the importance of these genetic resources for breeding new wheat cultivars and their benefits in our wheat breeding program will be discussed. The pre-breeding, where genetic regions associated with desirable traits are identified and transferred into materials ready for use in breeding programs, will be outlined. Finally, the role of wheat landraces and wild relatives will be discussed in the development of perennial, BNI, and biofortified wheats.

Keywords: Genetic resources, genomic tools, pre-breeding, wheat

Determination of Resistance Markers for Venturia pyrina Pathogen in Pear Genotypes Cultivated in Azerbaijan

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Abstract: Scab disease (***Venturia pyrina* Aderh**.) is a fungal disease that occurs in the leaves, sprouts and fruits of the plant from the flowering period to harvest in pear (***Pyrus* L**.) cultivated areas in Azerbaijan. This disease also negatively affects productivity and fruit quality. For the Rvi2 gene resistant to Venturia pyrina pathogen, CH02b10 marker was selected in 175% of plants, CH05e03 marker in 125% of plants, OPL-19 marker in 83.3% of plants. However, the ratios of all 3 markers for resistance gene Rvi2 showed differences. This phenomenon is due to CH02b10 marker being closer to the gene than CH05e03 and OPL19 markers. Therefore, the percentage rate of the CH02b10 marker was estimated at 175%. The resistance marker CH03d10 for the Rvi4 gene was detected in 250% of the total plants. This allows us to think as a result of unwanted cross-pollination in those varieties. The results of molecular marker analysis showed that the ratios of CH05d08 and Hi07h02 markers for the Rvi5 gene were different. Thus, the CH05d08 marker was selected for the Rvi5 gene in 33.3% of the plants, and the Hi07h02 marker in 150% of the plants. This is due to the fact that the Hi07h02 marker is closer to the gene than the CH05d08 marker. Therefore, the percentage of the Hi07h02 marker was higher than that of the CH05d08 marker. The primers found in different pear genotypes cultivated in the republic during the conducted research can be used to identify new varieties resistant to Venturia pyrina pathogen.

Keywords: ***Pyrus, Venturia pyrina,*** pathogen, molecular marker, percentage indicators

Analysis of Wild Barley (Hordeum spontaneum L.) Specimens for Powdery Mildew

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Abstract: In this study, a comparative analysis of 59 wild barley (***Hordeum spontaneum*** **L.**) specimens cultivated in the field of the Absheron Scientific Experimental Farm under the Institute of Genetic Resources was carried out in the first decade of November 2022 with respect to powdery mildew (***Blumeria graminis*** **DC. f. sp.** ***hordei*** **Marchal**). Powdery mildew is one of the most widespread cereal diseases and can cause significant damage to plants. The disease affects all above-ground organs - leaves, leaf tissues, stems, and, during intense growth stages, even the spike leaves. The mentioned specimens were collected during expeditions conducted in various regions of the Republic of Azerbaijan in 2018 and have been preserved in the Genbank under the Institute of Genetic Resources. The selected specimens were planted in three replicates using a randomized method in accordance with the requirements of the international descriptor. From each genotype, 10 plant specimens were randomly selected from the central part of the rows, labeled, and the average of the measured disease severity in these 10 plants was included in the disease analyses. Observations were made on all plants, and the severity of powdery mildew was determined on a scale from 1 to 10 in accordance with the international descriptor. Phenological analyses revealed that 11 wild barley specimens were susceptible to powdery mildew, whereas 9 specimens showed high resistance to this disease. Among the resistant forms, GNOR-107, GNOR-126, and GNOR-312 should be particularly noted. Besides, these specimens also exhibited high tolerance to yellow rust (***Puccinia striiformis West***) and brown rust (***Puccinia recondita***). These specimens have been recommended for use as initial material in the development of new varieties based on disease resistance traits and for the establishment of new collections.

Keywords: ***Hordeum vulgare*** **L.**, powdery mildew, disease resistance, phenological analysis

Field Evaluation of Wheat-alien Interamphidiploid Hybrids for Susceptibility to Fungal Diseases in Absheron Peninsula

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Abstract: Wide hybridization in cereals plays a crucial role in enhancing resistance to fungal diseases by introducing novel alleles and resistance genes from wild relatives and alien species into cultivated genomes. 227 stable and partially stable hybrid plants (F_8 – F_9) obtained from crosses between wheat-alien amphidiploids (***T. turgidum* subsp. *durum* / *Dasypyrum villosum***, genome 2n=28 (AABB) + 2n=14 (VV); ***T. aestivum* cv. Zhong** 4 /***Th. Intermedium*, genome** 2n=42 (AABBDD)+ 2n=14 (Ai); ***T. aestivum* subsp. *aestivum*/*Agropyron distichum*, genome** 2n=42 (AABBDD) +2n=14 (***Ag. distichum***); *T. aestivum* / *Agropyron junceum*, 2n=42(AABBDD)+ 2n=14(JJ)) and hexaploid triticale ABDR (2n = 6x = 42, genome AABBRR) were monitored and scored according to modified Cobb scale (% infected tissue) and Saari & Prescott scale at the ZGS 60–80 and ZGS 30–70 growth stages for Stripe/Leaf/Stem Rust and Powdery Mildew, respectively. The research was conducted between 2023 and 2025 at the Absheron Experimental Station of the Genetic Resources Institute (Azerbaijan). Absheron peninsula has the moderately warm and humid climate during spring–early summer supports the development of foliar diseases, especially rusts and powdery mildew. Yellow rust and powdery mildew can cause *15–40% losses* in biomass under conducive weather (cool, high humidity) at critical development stages of wheats in Azerbaijan. Among the 227 monitored interamphidiploid hybrids, most plants exhibited resistance to one or two fungal diseases, while only 10 from the combination ABDR × ***T. aestivum* / *Agropyron junceum*** displayed complete resistance to all observed fungal pathogens. Hence, interamphiploid hybridization proved effective in introducing novel alleles and broadening the pool of disease-resistance traits in wheat.

Keywords: Field evaluation, fungal diseases, wheat – alien amphidiploids

The Role of Genetic Resources in Agricultural Breeding Studies: The Case of Walnut (Juglans regia L.)

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Abstract: Agriculture, as one of the most fundamental economic activities in human history, forms the basis of food security and sustainable development. However, global threats such as population growth, climate change, soil degradation, and biotic/abiotic stress factors are significantly affecting the future of agricultural production. In this context, the conservation and effective utilization of plant genetic resources play a strategic role in agricultural breeding programs. Genetic resources encompass the wild relatives of cultivated plants, landraces, materials preserved in gene banks, and genotypes maintained within traditional farming systems. These resources are indispensable for enhancing plants' tolerance to environmental stresses, developing disease-resistant varieties, and improving agronomic traits such as yield. Particularly, local genetic diversity is of great importance for identifying genotypes with high adaptive potential. This study examines the role of genetic resources in agricultural breeding through the example of the walnut (***Juglans regia*** **L**.). Walnut is a strategic fruit species with both high nutritional value and significant economic importance. Türkiye possesses a rich potential in terms of walnut genetic resources, hosting numerous local genotypes naturally distributed across diverse ecological regions. This diversity indicates the presence of valuable genetic material that can be utilized in walnut breeding. Evaluations based on the walnut example aim to provide a concrete framework for the conservation, characterization, and integration of genetic resources into breeding programs. In this way, it will be possible to enhance both yield and quality in walnut production while supporting the sustainability of agricultural biodiversity.

Keywords: Genetic resources, agricultural breeding, walnut, ***Juglans regia*** L., Turkish walnut genotypes

A Novel Disinfection Technique in Plant Aseptic Culture: Acid-Base Technique

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Abstract: Providing disinfected explants in plant tissue culture is an initial, crucial, and sensitive stage. Since the introduction of in-vitro culture, sterilizing some explants are troublesome. The goal of this research was to evaluate the effect of drastic swings in pH on removing microbial contamination in explants to make them germ-free. To reach this objective the effect of Acid-Base method and commercial bleach (containing 5% chorine) efficiency on surface sterilization of wheat, rice, and tomato seeds was compared. Results indicated a significant effect between these two types of surface sterilization methods in rice seeds but not on other plants' seeds. In rice, the average percentage of seed contamination was 4.16 and 20.83 in Acid-Base and commercial bleach techniques, respectively. Moreover, Acid-Base techniques did not reflect significant side effects on seed germination. Along with the disinfection properties of the Acid-Base technique, it can facilitate seed germination by breaking seed dormancy in plants that have recalcitrant seed germination processes. Overall, the Acid-Base method demonstrated great privilege compared to the common disinfectant (commercial bleach) in plant aseptic culture. In addition to its germicidal properties, this technique also has chemical scarification properties which can be used to break the dormancy of the seeds. Here, the Acid-Base method is introduced as a novel disinfection method in plant tissue culture that can be used alone or in along with other disinfection methods for providing germ-free explants. To use this new method for sterilizing other sorts of explants such as leaves and softer explants it is vital to optimize the concentration and exposure time of the Acid-Base method.

Keywords: Acid-Base method, commercial bleach, explant sterilizing, plant tissue culture.

Diagnostic Evaluation of Drought Stress Tolerance in Hordeum L. Samples Using Physiological Parameters

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Abstract: Plants grown under natural and field conditions are always subjected to stress factors. Among the most significant stress factors are drought and salinity. Recently, there has been growing interest in studying the physiological-biochemical processes occurring in plants under stress conditions, such as drought and salinity, and in determining the plants' resistance to unfavorable environmental factors. The water retention capacity of leaves was studied during the flowering phase of the plants. Leaf material was taken from each sample in triplicate and stored at a thermostat set to 22°C for 4 hours. The water retention capacity of the leaves is determined by the amount of water they lose after a certain period (4 hours) and is calculated based on the initial weight of the leaves and the amount of water lost after 4 hours. The water retention capacity of the leaves in the studied samples ranged from 23-56%. Ten samples that lost less water (***H. vulgare*** **L. subsp.** ***v. nutans***, ***H. vulgare*** **L. subsp.** ***v. pallidium***, ***H. vulgare*** **L. subsp.** ***v. pallidium***, ***H. vulgare*** **L. subsp.** ***v. pallidium***, ***H. vulgare*** **L. subsp.** ***v. pallidium***, ***H. vulgare*** **L. subsp.** ***v. pallidium***, ***H. vulgare*** **L. subsp.** ***v. pallidium***, ***H. vulgare*** **L. subsp.** ***v. nutans,*** ***H. vulgare*** **L. subsp.** ***v. nutans***, ***H. vulgare*** **L. subsp.** ***v. nutans***) were evaluated as drought-resistant. These samples lost 23-29% of their water after 4 hours. Twelve samples that lost 30-45% of their total water were considered moderately drought-resistant by us. Two samples with a water retention capacity of 51 and 56 percent (***H. vulgare*** **L. subsp.** ***v. pallidium***, ***H. vulgare*** **L. subsp.** ***v. pallidium***) were identified as sensitive. It is suggested that these drought-resistant barley samples, selected using this method, should undergo further research before being used as donors in the selection process.

Keywords: Drought, salinity, drought resistance

Drought and Salinity Stress Resistance in Lathyrus sativus Samples

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Abstract: Environmental factors such as drought, salinity, heat, cold, and other stress factors have a negative impact on plants in large areas.Successful resolution of these issues involves applying methods and techniques that study plant resilience during the course of research. Plant resilience refers to their ability to carry out their life functions fully in adverse environmental conditions. This research was conducted on 9 samples (5 cultivated, 4 wild) of the Lathyrus sativus species from the collection of the AR NAS Genetic Resources Institute, with the aim of assessing the degree of resistance to drought and salinity. Changes in the amount of chlorophyll a + b, which is a photosynthesis indicator, were determined, and samples with high, moderate, and low resistance to stress were selected. The cultivated forms of ***Lathyrus sativus*** (LASA 7-68, LASA 5-69, LASA 2-76, LASA 92-01, ZIRVƏ) showed resistance to both stresses. The chlorophyll content increased by 6% to 21% under drought, and by 9% to 26% under salinity. Among the 4 wild forms, two samples showed high resistance to both stresses: ***Lathyrus cyaneus***-LACU-62-01 and ***Lathyrus chlorantus***-LACI-32. In these samples, chlorophyll content increased by 23% under drought and 62% under salinity for ***Lathyrus cyaneus***-LACU-62-01, and by 24% under drought and 12% under salinity for ***Lathyrus chlorantus***-LACI-32. Two other wild forms, ***Lathyrus cyaneus***-LACU-38 and ***Lathyrus chlorantus***-LACI-37, showed moderate resistance to drought and high resistance to salinity. Specifically, ***Lathyrus cyaneus-***LACU-38 experienced a 3% decrease under drought and an 8% increase under salinity, while ***Lathyrus chlorantus***-LACI-37 had a 7% decrease under drought and a 22% increase under salinity. As a result of this study, 5 cultivated ***Lathyrus samples*** with high resistance to both drought and salinity stress were identified, and these samples are recommended for use as donors in future selection work.

Keywords: Drought, salinity, photosynthesis, abiotic stress

Evaluation and Selection of Durum Wheat (Triticum durum Desf.) Varieties for Resistance to Stress Factors

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Abstract: Research has been conducted to study the drought and salinity stress resistance characteristics of hard wheat varieties. Comprehensive studies were conducted on hard wheat samples taken from the Department of Cereal Crops to determine stress resistance indicators. Out of the studied samples, 6 are ancient varieties and 7 are new varieties. Changes in the amount of chlorophyll and carotenoids in the leaves of these samples, under the influence of drought and salinity stresses during the heading phase, were identified, and the stress-resistant samples were selected. Among them, 125-129 are ancient varieties, and 130-136 are new varieties. From the ancient varieties studied, two samples, 126-Qaraqılçıq var.*provinciale* and 128-Şirvan buğda var.*hordeiforme*, were evaluated as highly resistant to drought. Changes in the amount of chlorophyll due to drought ranged between (101% -102%). Among the studied ancient varieties, the following were identified as drought-resistant samples: Durum parents - Landras Sarı buğda var.***hordeiforme***; Ruset buğda var.***apulicum***; and Zoğal buğda var.***horanomelanopus*** (99%). Sensitive and moderately resistant samples were not detected. For salinity stress, the ancient varieties Durum parents – Landras Sarı buğda var.*hordeiforme* (116%); Qaraqılçıq var.*provinciale* (115%); Ruset buğda var.***apulicum*** (104%); and Şirvan buğda var.***hordeiforme*** (107%) were highly resistant. Zoğal buğda var.***horanomelanopus*** (98%) resistant to salinity. Based on the results obtained during the study, it can be stated that among the new varieties (130-136), Korifey-88 var.***leucurum***, Comərd-90 var ***leucomelan***, Ağdərə var.***leucurum***, Zəfər var.***leucurum***, and Qarqar var.***leucurum*** showed high resistance to both salinity and drought stress. Changes in chlorophyll content due to drought ranged between 109% and 148%, and changes in chlorophyll content due to salinity ranged between 103% and 142%. Two samples, Zəngəzur var.***provinciale*** and Salvartı var.***leucurum***, were selected as resistant to both drought (80%-82%) and salinity (88%). New varieties showed higher resistance to stress factors compared to ancient varieties. Results identified stress-resistant genotypes for breeding use.

Keywords: Hard wheat, chlorophyll, drought, salinity

Effect of Global Climate Change on Varieties and Forms of Sweet Cherry Cultivated in Azerbaijan

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Abstract: Due to increasing interest in sweet cherry cultivation, intensive breeding efforts are underway worldwide. Sweet cherry (***Prunus avium*** **L**.) is highly sensitive to changing climatic conditions, and its production faces serious risks from extreme weather caused by global warming. Therefore, in recent years, high temperatures and cold weather observed during the spring season have caused sweet cherry blossoms to wither during the flowering period, negatively affecting fruit formation. At the same time, heavy rains occurring before harvest lead to the cracking of sweet cherry fruits. Breeding efforts aimed at developing new sweet cherry varieties capable of adapting to these changing climate conditions are of great importance. This review examines the major sweet cherry breeding programs implemented worldwide and evaluates the current situation in our country. Thus, the main objective of the study is to identify sweet cherry varieties that are adapted to global climate change, resistant to diseases and pests, high-yielding, and meet market demands. On April 16, 2025, the amount of precipitation in the Guba region reached 75 mm (157% of the monthly norm), which directly disrupted the pollination and fertilization processes during the flowering stage of late-ripening sweet cherry varieties (Regina, Ziraat 0900, North Vander, and Napoleon). As a result, a sharp decrease in productivity occurred. In early-ripening varieties (Samba, Lapins, Ramon Oliva, Early Lory, Krim, Sari Denissema), flowering occurred in March, so the yield was not negatively affected. Besides, foreign varieties that have been cultivated in Azerbaijan for many years (Mayovka, Franz Joseph, Bigarreau Burlat) have adapted to the changing weather conditions and demonstrated greater tolerance, particularly to temperature fluctuations and irregular precipitation patterns. Breeding programs in Turkey, Greece, Hungary, and Italy, have produced high-yielding, large-fruited, and climate-resilient cultivars. Since 2019, several of these have been introduced in Azerbaijan, and the most promising were registered in 2025.

Keywords: Sweet cherry, global climate change, productivity

Evaluation of the Potential for Resistance to Winter Stress Factors Based on the Determination of Winter Hardiness Components of Hazelnuts and Walnuts

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Abstract: The aim of these studies was to assess the winter hardiness potential of the parent material of hazelnuts and walnuts under modelled conditions to identify adaptive genotypes for use in breeding. The objects of the research were 12 cultivars of hazelnuts of different geographical origin: ‘Akademik Yablokov’, ‘Ivanteevsky Krasny’, ‘Ispolin’, ‘Moskovsky Rubin’, ‘Tambovsky Ranniy’ (Russian selection), ‘Lal’, ‘Yashma’ (Belarusian selection), ‘Ata-Baba’ (Azerbaijani selection), ‘Red Lambert’, ‘White Lambert’, Katalonski, Tonda di Giffoni (European selection) and 12 walnuts samples of Belarusian selection: ‘Pinsky’, ‘Pamyat Minova’, ‘Samokhvalovichsky-1’, ‘Samokhvalovichsky-2’, S.5-78-P, PR-98, 1-121, 1-02-T, P-Kh-1, O-M-V, 2-203, 9-2-76-S. Modeling of stress factors for freezing of plant samples according to four components of winter hardiness was carried out based on the analysis of meteorological conditions of winter periods in Belarus over the last 18 years of observations. Component I – the resistance to low temperatures in the autumn-winter period; II – the resistance to critical frosts in the middle of winter (up to -30°C); III – the resistance to a rapid increase in frost (up to -30°C) after a thaw; IV – the ability to restore frost resistance during repeated hardening after a thaw. As a result of the evaluation of resistance to low temperatures in laboratory conditions carried out in 2024-2025, the differences between cultivars were established for components II, III, IV. In the group of winter-hardy (maximum damage to all types of tissues not more than 3 points) 5 cultivars of hazelnut and 6 hybrids of walnut of Belarusian selection were classified. It was determined that for hazelnut the most important components of winter hardiness were: the resistance to air temperature drop to -30°C in the middle of winter (the most susceptible tissues of an one-year-old shoot to damage are the bark and the cambium) and the resistance to a rapid increase in frost (up to -30°C) after a thaw in February (the most susceptible tissues are the conducting tubes of buds). For walnut, the limiting component was the component II of winter hardiness and the most susceptible tissues to cold stress were the conducting tubes of buds and the cambium.

Keywords: Hazelnut, walnut, winter hardiness, modeling conditions

Quality Indicators of Wheat Bread Baked with Additives from Barley Accessions Selected Based on Their Biochemical Characteristics

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Abstract: Barley (***Hordeum vulgare* L.)** plays a crucial role in ensuring the feed base for livestock and, consequently, in maintaining food security in our country. Barley grains are rich in protein, particularly in essential amino acids such as lysine, tryptophan, and others. Due to the grain's acidity, bread baked from barley flour or a mixture of barley and wheat flour is considered highly beneficial from a dietary perspective. This type of bread, often referred to as “black bread,” is absorbed more slowly by the body. In this study, the biochemical composition of the grain of 21 barley accessions collected from various regions of Azerbaijan and other countries and preserved in the National Genebank collection under the Genetic Resources Institute was investigated using standard methods. Results showed that protein content in the grain ranged from 13.6% to 17.3%, and starch content ranged from 49.4% to 69.7%. Based on the analyses, accessions belonging to the ***spontaneum*** subspecies accession numbers 84/86, SP 21, and 20/27 demonstrated high protein (15.0–17.0%) and starch (49.4–53.1%) levels. Considering other traits relevant for bread-making, such as grain hull smoothness in barley, the effect of adding 10%, 20%, and 30% barley flour to bread wheat flour from the “Gobustan” variety on bread quality was studied. In accession 84/86, the bread volume was 420, 400, and 390 units at 10%, 20%, and 30% substitution levels respectively; volume scores were 2.1, 1.9, and 1.7, with total scores of 3.6, 3.6, and 3.3. For SP 21, volumes were 440, 400, and 380; volume scores were 3.0, 1.9, and 1.2; total scores were 3.5, 3.6, and 3.4. For accession 20/27, the corresponding values were 480, 400, and 360 for volume; 2.4, 1.9, and 1.5 for volume scores; and 3.7, 3.6, and 3.6 for total scores, respectively. Overall, bread samples with 10% barley flour addition exhibited more uniform crumb porosity an important quality trait compared to higher substitution levels.

Keywords: Barley, protein, starch, bread, crumb porosity

Study and Evaluation of Biological and Agriculturally Important Characteristics of Tomato Collection Varieties

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Abstract: The article discusses the study of biomorphological characteristics and quality characteristics of tomato cultivars of different geographical origins. High-yielding, high-quality cultivars have been selected based on the indicated characteristics, and research on them is ongoing. The research work was conducted in the Scientific Research Institute of Vegetable Growing, in 2022-2024. 24 varieties were planted in the study. The main goal of the scientific research work is to select varieties of various geographical origins that are suitable for local conditions, have valuable and economically important traits, quality indicators, and are resistant to abiotic factors, and submit them to the Agricultural Services Agency under the MA. Varietal samples were studied in the collection area of the starting material pithomnik and promising varieties were selected. Varietal samples were placed in the collection area without repetition and Elim and Zarrabi varieties were used as controls. It was determined that the varietal samples were classified into early-maturing, medium-maturing and medium-late-maturing groups according to the length of the vegetation period. Thus, from the time of emergence to the last harvest, samples numbered 1, 9, 12, 122, 124, 125, 149, 150, 151 belonged to the early-maturing group and lasted 100-105 days, samples numbered 8, 14, 114, 116, 119, 132, 136, 136/A belonged to the medium-maturing group and lasted 110-113 days, and samples numbered 20, 21, 22, 23, 127, 137, 138 belonged to the medium-maturing group and lasted 118-121 days. The yield from one plant, according to valuable economic traits, was between 2.1-3.5 kg in the collection samples. The fruit weight was 10.0-194.0 g in the variety samples. From the three-year (2022-2024) research work conducted, it can be concluded that some of the variety samples tested in the collection area of the starting material pithomnik in Absheron conditions were distinguished and selected for their valuable and economic indicators.

Keywords: Selection, hybrid, origin, pithomnik

Variability of Biochemical Composition in Carrot Varieties Depending on Storage Conditions

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Abstract: The changes in biochemical composition of 6 carrot samples (No. 1, No. 2, No. 2/1, No. 3, No. 4, No. 5) cultivated in open field conditions were studied immediately after harvest and during 35 days of storage at 13°C and 75% relative humidity. It was determined that immediately after harvest the dry matter content of carrot samples ranged from 11.28–13.70%, sugars 7.60–9.63%, extractive substances 9.25–11.04%, total acidity 0.052–0.11%, sugar–acid ratio 70.46–185.19, and nitrate content 38.9–56.6 mg/kg. It was indicated that storage conditions had a positive effect on biochemical composition, and after 35 days of storage, the studied genotypes contained 12.88–14.20% dry matter (1.02–1.13-fold increase), 8.26–10.08% sugars (1.02–1.28-fold increase), and 9.72–11.60% extractive substances (1.04–1.20-fold increase). The increase in these indicators after storage may be explained by water loss in carrot roots (drying process). Although total acidity increased 1.29–1.73 times in all studied samples, the highest increase was recorded in hybrid No. 2 (1.73 times). Overall, due to increased acidity during storage, the sugar–acid ratio decreased (1.09–1.71 times), with the highest decrease observed in sample No. 3. Storage conditions did not significantly affect the nitrate content. It should be noted that the nitrate levels in carrot roots were much lower (4.42–6.70 times lower) than the maximum permissible limit set by the Ministry of Health of the Republic of Azerbaijan (250 mg/kg). The highest nitrate content was found immediately after harvest in hybrids No. 3 (51.4 mg/kg) and No. 4 (56.6 mg/kg), while the lowest levels were recorded after 35 days of storage in samples No. 2/1 (37.3 mg/kg) and No. 5 (38.3 mg/kg). The low accumulation of nitrates in carrot roots should be explained by the biological characteristics of this crop.

Keywords: Carrot, biochemical composition, storage conditions, hybrid

The Effect of Different Nanoparticles on the Development of Fruits in Various Fruit Trees

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Abstract: In recent years, various scientific studies have been conducted on the use of nanomaterials, particularly nanoparticles, as mineral fertilizers in agriculture. It has been observed that nanoparticles can enhance plant productivity and increase resistance to stress factors. Experiments show that nanoparticles influence the morphological, physiological, and biochemical structure of plants. This research investigates the effects of Fe_3O_4 (magnetite) and SiO_2 (silicon dioxide) nanoparticles on the pollination of flowers, accumulation in fruits, and potential toxicity in the Golden Delicious apple and Early Burlat cherry varieties. The experiments were conducted during the 2023–2024 seasons at the experimental site of the Fruit and Tea Research Institute in Zardabi settlement, Guba region. The results showed that nanoparticles positively influenced the number of fertilized fruits. They also significantly affected the chemical composition and yield of the fruits, with nanoparticles accumulating in both the peel and the flesh. Biochemical analyses were performed to assess food safety, and no pathological conditions were observed during laboratory testing. In plots treated with Fe_3O_4 nanoparticles, the number of mature apples increased 2.5 times compared to the control. For SiO_2-treated trees, the yield doubled. At the end of the experiment, 30 fruits were selected from each tree and weighed. Cherries treated with Fe_3O_4 were visibly larger than those in the control group, and overall yield increased by 1.2 times. These findings indicate that nanoparticles positively influence flower fertilization, resulting in a higher number of fertilized flowers.

Keywords: Nanoparticles, nanomaterials, Early Burlat cherry variety, yield, Golden Delicious apple varirty

Phenotipic and Transcriptomic Response of Durum Wheat to Drought Stress

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Abstract: Climate change is affecting crop productivity especially in some areas of the planet. The countries facing the Mediterranean Sea are particularly exposed to increasing heat and drought periods, and durum wheat, one of the most widely cultivated crops in these regions, is exposed to environmental variations. To find genetic material resilient to drought stress and to deepen our knowledge on the genes involved in this performance, a panel of traditional varieties were grown under different water regimes and phenotypic and transcriptomic studies were performed on the genotypes analysed. Flag leaves and immature seeds were collected from three replicates of each control and drought-stressed landrace at the late milk stage for RNA extraction and sequencing. Under drought conditions, we identified a few favorable genotypes, showing a higher green area and delayed senescence, while exhibiting a smaller reduction in kernel weight, compared to Svevo, our reference cultivar. Data from phenotyping and transcriptomics approaches will be integrated and will help recognize common and unique mechanisms adopted by the different varieties in response to drought, contributing to a better understanding of the biological processes underlying stress tolerance. This information will be critical for developing strategies to improve durum wheat resilience and support productivity under conditions of increasing water scarcity. This work was supported by: i) the Agritech National Research Center and received funding from the European Union Next-GenerationEU (PIANO NAZIONALE DI RIPRESA E RESILIENZA (PNRR)MISSIONE 4 COMPONENTE 2, INVESTIMENTO 1.4D.D. 1032 17/06/2022, CN00000022) - This contribution reflects only the authors' views and opinions; neither the European Union nor the European Commission can be considered responsible for them.

Keywords: Durum wheat, traditional varieties, drought stress

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