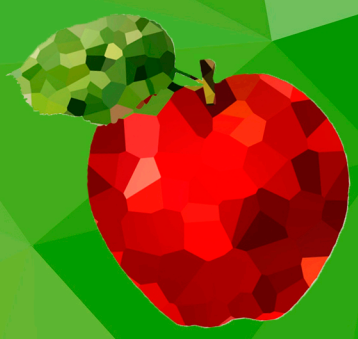
30 years IPBB

2024 ICPBB

Proceedings of

THE INTERNATIONAL CONFERENCE ON PLANT BIOLOGY AND BIOTECHNOLOGY (ICPBB 2024)

Best Western Plus Atakent Park Hotel
June 3-6, 2024
Almaty, Kazakhstan



ҚАЗАҚСТАН РЕСПУБЛИКАСЫ ҒЫЛЫМ ЖӘНЕ ЖОҒАРЫ БІЛІМ МИНИСТРЛІГІ
ҒЫЛЫМ КОМИТЕТІ
БИОЛОГИЯ ЖӘНЕ ӨСІМДІКТЕР БИОТЕХНОЛОГИЯСЫ ИНСТИТУТЫ

МИНИСТЕРСТВО НАУКИ И ВЫСШЕГО ОБРАЗОВАНИЯ РЕСПУБЛИКИ КАЗАХСТАН
КОМИТЕТ НАУКИ
ИНСТИТУТ БИОЛОГИИ И БИОТЕХНОЛОГИИ РАСТЕНИЙ

MINISTRY OF SCIENCE AND HIGHER EDUCATION OF THE REPUBLIC OF KAZAKHSTAN
SCIENCE COMMITTEE
INSTITUTE OF PLANT BIOLOGY AND BIOTECHNOLOGY

«INTERNATIONAL CONFERENCE ON PLANT BIOLOGY AND BIOTECHNOLOGY (ICPBB 2024)»

Халықаралық конференцияның материалдары
3-6 маусым 2024 ж.

«INTERNATIONAL CONFERENCE ON PLANT BIOLOGY AND BIOTECHNOLOGY (ICPBB 2024)»

Материалы международной конференции
3-6 июня 2024 г.

«INTERNATIONAL CONFERENCE ON PLANT BIOLOGY AND BIOTECHNOLOGY (ICPBB 2024)»

Materials of the international conference
June 3-6, 2024

АЛМАТЫ 2024

УДК 581; 574; 575; 631.52

ББК 28.5

Р71

«International Conference on Plant Biology and Biotechnology (ICPBB 2024)»: Материалы международной конференции / под общей редакцией Е.К. Туруспекова, С.И. Абугалиевой. – Алматы: ИББР, 2024 – 247 с.

ISBN 978-601-08-4104-8

В сборнике представлены материалы международной конференции «International Conference on Plant Biology and Biotechnology (ICPBB 2024)», проведенной в г. Алматы 3 – 6 июня 2024 г. В публикациях изложены результаты оригинальных исследований в области изучения, сохранения и использования генетических ресурсов, генетики, селекции, биоинформатики и биотехнологии растений.

Сборник рассчитан на биологов, генетиков, биотехнологов, селекционеров, специалистов, занимающихся генетическими ресурсами растений, и студентов биологического и сельскохозяйственного профилей.

Тезисы докладов представлены в авторской редакции.

Рекомендовано к изданию Ученым советом РГП на ПХВ «Институт биологии и биотехнологии растений» Комитета науки Министерства науки и высшего образования Республики Казахстан (Протокол №3 от 25.04.2024 г.)

Proceedings of the «INTERNATIONAL CONFERENCE ON PLANT BIOLOGY AND BIOTECHNOLOGY (ICPBB 2024) »

June 3-6, 2024 - Almaty, Kazakhstan

Editors
Yerlan Turuspekov, Saule Abugalieva

Editorial Board: Doctor of Biological Sciences, Prof. Abugalieva S.I.; Doctor of Biological Sciences, Prof. Kokhmetova A.M.; Candidate Biological Sciences, Prof. Turuspekov Y.K.; Candidate Biological Sciences, Prof. Kushnarenko S.V.; PhD Gritsenko D.A.; PhD Almerekova S.S.; PhD Anuarbek S.N.; PhD Sapakhova Z.; PhD Zatybekov A.K.

Publisher
Institute of Plant Biology and Biotechnology

Responsibility for the text content of each abstract is with the respective authors.

Venue: Best Western Plus Atakent Park Hotel, 42 Timiryazev str., 050040
Almaty, Kazakhstan

Conference webpage: https://primerdigital.com/ICPBB2024/

Hosted by: Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan

Correct citation: Turuspekov Ye., Abugalieva S. (editors) (2024) Proceedings of the «International Conference on Plant Biology and Biotechnology» (ICPBB 2024), Almaty, Kazakhstan, June 3-6, 2024, IPBB, Almaty, Kazakhstan; ISBN

ISBN 978-601-08-4104-8

Welcome Greetings from Organizers

Dear Colleagues,

On behalf of the Organizing Committee of the ICPBB 2024, I am cordially inviting you to this event in Almaty, Kazakhstan.

Approximately 200 participants from 17 different countries of the World are attending this international conference. We will witness 14 plenary talks from leading scientists in Plant Biology, 84 oral presentations in parallel sections, and 92 poster presentations.

We often say that Kazakhstan is the land where the East meets the West, and it is truly a multicultural country where over 130 ethnic groups live in peace and friendship.

Therefore, it is very symbolic that we have large groups of colleagues from many former USSR countries, Europe, the Far East, and West Asia attending this forum. We are happy to see our old friends and looking forward to finding new friends and partners!

Using this opportunity, I would like to thank the Local Organizing Committee led by Prof. Saule Abugalieva and her entire group at the IPBB for their outstanding job in managing all aspects of the conference preparation.

I want to thank Dr. Ruslan Kalendar (Nazarbayev University, Astana, Kazakhstan) for his constant support of the conference and administration of the web page of the ICPBB 2024.

This event could not have been accomplished without the support of sponsors. Therefore, I appreciate the group of main sponsors of the conference, led by Zalma Ltd (General Sponsor), Veld Ltd, Juggernaut Ltd, TechPrime Ltd, and Sesana Ltd (Golden sponsors), and others for their valuable help in hosting this conference in Almaty City.

Finally, and most importantly, I am grateful to all participants of the ICPBB 2024 for your interest in this conference, and I hope you will enjoy the forum and have a wonderful time in our city!

Yerlan Turuspekov
Chairman of the International
Organizing Committee ICPBB 2024,
IPBB, Almaty, Kazakhstan

Session 1.

Genetic Resources and Biodiversity

PLANT GENETIC RESOURCES FOR BREEDING AND RESEARCH

Andreas Börner

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

E-mail: boerner@ipk-gatersleben.de

Plant genetic resources for food and agriculture (PGRFA) play a major role for global food security. The most significant and widespread mean of conserving PGRFA is *ex situ* conservation. World-wide 7.4 million accessions are stored in about 1,750 *ex situ* genebanks. Plant *ex situ* genebank collections comprise seed genebanks, field genebanks as well as *in vitro* and cryo collections. Species whose seed can be dried, without damage, down to low moisture contents can be conserved in specially designed cold stores. Such "orthodox" seeds can be expected to maintain a high level of vigour and viability for decades. Field genebanks, *in vitro* and cryo storage are used primarily for species which are either vegetatively propagated or which have non-orthodox seeds that cannot be dried and stored for long periods. With a total inventory of 150,000 accessions from 3,212 plant species and 776 genera, the 'Federal *ex situ* Genebank of Germany' in Gatersleben holds one of the most comprehensive collections worldwide. It comprises wild and primitive forms, landraces as well as old and more recent cultivars of mainly cereals but also other crops.

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

Furthermore, in cereals, mainly wheat and barley, a number of bi-parental mapping populations and association mapping panels have been established to allow for the genetic analysis of various traits. The current focus covers resistance/tolerance to a number of biotic and abiotic stresses, in particular drought and cold.

PLANT GENETIC RESOURCES IN THE CONTEXT OF GENETIC TECHNOLOGIES

Khlestkina E.K. [1*], *Ukhatova Yu.V.* [1], *Agakhanov M.M.* [1], *Antonova E.V.* [1,2], *Baymukhametova E.A.* [3], *Börner A.* [4], *Dodueva I.E.* [1,5], *Egorova A.A.*[1,6], *Erastenkova M.V.* [1], *Evlash A.Ya.* [1,7], *Gancheva M.S.* [1,5], *Gerasimova S.V.* [1,6], *Goncharova E.E.* [1,7], *Gordeeva E.I.* [1,6], *Hertig C.W.* [4], *Inozemtseva A.V.* [1], *Khatefov E.B.* [1], *Kolosovskaya E.V.* [1,4], *Korotkova A.M.* [1,6], *Kukoeva T.V.* [1,7], *Krylova E.A.* [1], *Kuluev B.R.* [1,3], *Kumlehn J.* [4], *Lebedeva M.A.* [1,5], *Loskutov I.G.* [1], *Lutova L.A.* [1,5], *Mikhailova A.S.* [1], *Mikhailova E.V.* [1,3], *Musin K.G.* [3], *Popov V.S.* [1], *Putina O.V.* [1], *Rakhmangulov R.S.* [1], *Rozanova I.V.* [1], *Semilet T.V.* [1], *Sokolova D.V.* [1], *Solovieva A.V.* [1], *Tikhonova N.G.* [1], *Tvorogova V.E.* [1,5], *Ul'yanov A.V.* [1], *Shvachko N.A.* [1], *Shimalina N.S.* [1,2], *Zavarzin A.A.* [1], *Zykova T.I.* [1], *Shoeva O.Yu.* [1,6]

[1]*N.I. Vavilov All-Russian Institute of Plant Genetic Resources, St. Petersburg, Russia*
[2] *Institute of Plant and Animal Ecology UB RAS, Yekaterinburg, Russia*
[3] *Ufa Federal Research Center RAS, Institute of Biochemistry and Genetics, Ufa, Russia*
[4]*IPK-Gatersleben, Gatersleben, Germany*
[5] *Saint Petersburg State University, Saint Petersburg, Russia*
[6] *Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia*
[7]*Sirius University, Sirius, Russia*

**E-mail:* director@vir.nw.ru

The conservation and utilisation of plant genetic resources (PGR) is the base for breeding and plant production. At the same time, basic research on PGR collections is a way for development of breakthrough technologies for crop improvement. VIR as a key holder of one of the largest world's PGR collections, collaborates closely in the field of genome editing, providing research teams with proper material to be edited, with new target genes and the improved laboratory protocols. We report on genotype improvement for different crops in our joint projects as well as complex studies of modified genotypes and development of protocols for edited material documentation, conservation and management in Genebank. Over 10 crops and 20 target genes are involved into joint studies. The target genes related to traits with mono- and oligogenic control mostly represent the genes to be knocked out (such as *Ant2*, *Nud* and *Win1* in barley, *Lpx1*, *Cer9* or *CKX1* in wheat, *TFL1* in cowpea, *E4* in soybean or the *PsSBE* and *PsCle* genes in pea) by break and further NHEJ resulting in frameshift. Along with loss-of-function we aimed at gain-of-function mutations using the same mechanism (NHEJ) but resulting in excision of 1bp (*Myc2* in barley) or the longer insertion (*Rg-B1a* in wheat or *MybA1* in grapes) to restore either frameshift in cds or cis regulatory region in noncoding gene part. We applied editing to both, widely used genotypes, like barley Golden Promise, or elite cultivars like wheat Sigma, Taya and Fisht. Besides expected phenotype changes, we observed both positive and negative pleiotropic effects (certain examples are reported). Thus, the lines obtained (currently, over 40 edited lines are under documentation to be conserved in Genebank) represent both, the models for reverse genetics studies as well as valuable material for plant breeding.

The research is supported by the Ministry of Science and Higher Education of the Russian Federation research programmes 075-15- 2021-1066 (editing wheat and triticale), 075-15- 2021-1050 (protocols for edited PGR management) and Russian Science Foundation (project No 21-66-00012 editing other crops, besides wheat and triticale).

A LOOK INTO TURKEY'S CEREAL GERMPLASM RESOURCES: DIVERSITY AND APPLICATION

Hakan Özkan

Çukurova University, Agriculture Faculty, Department of Field Crops, Adana, Türkiye

E-mail: hozkan@cu.edu.tr

Wild cereal relatives have been used in plant breeding as a crucial practice that increases cultivated cereal varieties' genetic diversity and resilience. In Turkey, wild cereal relatives are found in different regions, providing a diverse gene pool with valuable traits such as resistance to abiotic and biotic stress and adaptability to various climatic conditions. It is crucial to preserve the genetic integrity of these wild relatives in their natural habitats through conservation efforts and ensure their availability for future breeding programs. Genetic studies focusing on these wild cereal relatives aim to uncover the genetic mechanisms for beneficial traits that can be exploited in breeding programs to increase cultivated cereal crops' yield, quality, and resilience. The exploration and utilization of the genetic diversity of wild cereal species in Turkey offer significant opportunities for sustainable cereal breeding initiatives and agricultural advances. During the meeting, I will discuss the diversity of the Turkish cereal’s gene pool and its use in plant breeding.

GENETIC FEATURES IN PLANT DOMESTICATION

Takao Komatsuda

Shandong Academy of Agricultural Sciences (SAAS), Crop Research Institute, Jinan, Shandong, China

Plant domestication is the process of accumulation of genetic modifications associated with morphological and physiological changes towards human merit. Barley (*Hordeum vulgare* L.) is one of the earliest domesticated crops in the Fertile Crescent as shown by archaeological studies. Six-rowed spikes and non-brittle rachis are diagnostic morphological features of domesticated barley observed in archaeological sites, whereas reduced seed dormancy is a physiological one absent from sites. The genes responsible for these domestication traits are encoded in several parts of the plant's enormous genome, highlighting a rather prominent event in the domestication and development of this plant as a staple food crop in the early civilization.

EXAMINATION OF PLANT RESOURCES OF CENTRAL ASIA BY VIR EXPEDITIONS: HISTORY OF TRAVELS AND COOPERATION

***Ozerski P.V.*[1], Ozerskaya T.M.*[2]**

[1] *Institute of Zoology Republic of Kazakhstan, Almaty, Kazakhstan*
[2] *Federal Research Center N.I. Vavilov All-Russian Institute of Plant Genetic Resources (VIR), St. Petersburg, Russia*

**E-mail:* ozerski@list.ru

The study and preservation of the plant gene pool is very important. Expeditionary surveys of territories are part of fundamental scientific research; they also make it possible to replenish the gene pool of the collection with samples of wild relatives of cultivated plants, local cultivars of agricultural crops. To preserve the entire diversity of plant genetic material, there are gene banks, one of the largest of which is VIR.

The first expeditions in Central Asia were carried out in 1912 by V.M. Benzin (in the Semirechye province) and A.K. Golbeck (in Turkestan, Bukhara and the Trans-Caspian province). In 1916 N.I. Vavilov undertook an expedition to the Pamirs.

In total, from 1912 to the present, VIR has conducted more than 400 expeditions to Central Asia (Kazakhstan – 119; Kyrgyzstan – 62; Tajikistan – 103; Turkmenistan – 148; Uzbekistan – 113). Often these expeditions were attended also by employees of local scientific institutions, scientists from various countries, and specialists from international organizations. The first comprehensive Soviet-American expedition to Central Asia took place in 1929. Since 1992, almost all expeditions in Central Asia were tripartite. The expeditions were attended by researchers from universities and research centers, as well as representatives of farmers and seed breeders organizations from different countries.

CURRENT STATE OF FLORA OF THE MANGISTAU REGION

Imanbyaeva A.A., Belozerov I.F.

Mangyshlak Experimental Botanical Garden, Aktau, Kazakhstan

E-mail: imangarden@mail.ru; bif17@mail.ru

In 2023-2024 within the framework of the implementation of the scientific and technological progress program "Study of the current state of species diversity of vascular plants in Kazakhstan using modern methods of botany, molecular genetics and bioinformatics in the Mangistau and Atyrau regions", the formation of preliminary lists of flowering and higher spore plants, including rare, endemic, alien, weeds, ruderal and alien taxa in Microsoft Excel spreadsheet format. Information about the ecological group, life form, status and economic value, distribution throughout the territory of Kazakhstan according to floristic zoning, and morphological description of taxa was also collected and entered.

When compiling the lists, an analysis was carried out of literary sources, materials from existing field surveys and collections, as well as the composition of the local and server versions of the floristic databases developed by the MEBS computer program "BD-PLANT-KZ".

At this time, the preliminary list of plants of the flora of the Mangistau region includes 668 taxa from 4 divisions, 4 classes, 12 subclasses, 25 superorders, 53 orders, 10 suborders, 70 families and 295 genera.

More than half (64.1%) of plants (428) with information available in the database are representatives of the 8 most numerous families: Asteraceae Dumort. (88), Boraginaceae Juss. (27), Brassicaceae Burnett (50), Caryophyllaceae Juss. (28), Chenopodiaceae Vent. (97), Fabaceae Lindl. (55), Poaceae Barnh. (64) and Polygonaceae Juss. (19). Among the genera, Artemisia L. (18 - 2.7%), Astragalus L. (26 - 3.9%), Atriplex L. (10 - 1.5%), Galium L. (8 - 1.2%) significantly prevail, Salsola L. (15 - 2.2%) and Tamarix L. (11 - 1.6%).

In total, the flora of the region contains 3 herbaceous and 6 woody life forms of plants. Moreover, the dry conditions of Mangistau contributed to a significant predominance of perennial (266 species, 39.8%) and annual (256 - 38.3%) herbaceous plants. Also, due to the aridity of the climate and, primarily, the lack of precipitation, tree taxa are quite rare in the flora. Trees are represented by only 10 species, shrubs - 53, subshrubs - 39, shrubs - 10, subshrubs - 6 and vines - only 1 species.

A comparative analysis of the ecological properties of plants showed the presence of 8 groups in the flora in relation to moisture conditions: ultraxerophytes, xerophytes, xeromesophytes, mesophytes, mesohygrophytes, hygrophytes, hydrohygrophytes and hydrophytes. It was expected that in the desert zone of Mangistau the flora would be dominated by taxa of the xerophytic series: xerophytes proper (298 species - 44.6%) and xeromesophytes (193 - 28.9%). Mesophytes account for 18.1% of the composition (121 species). There are very few mesohygrophytes (37 - 5.5%), hygrophytes (6 - 0.9%), hydrohygrophytes (2 - 0.3%) and hydrophytes (5 - 0.7%). At the same time, especially on sandy massifs, even ultraxerophytes grow in a total of 15 taxa (2.2%).

In general, the flora of the Mangystau region contains 194 ecological groups of plants growing in 476 ecotopes. According to status, there are 3 alien, 4 relict and 40 endemic species.

14 plant species are included in the Red Book of the Republic of Kazakhstan (2014), 40 species are included in the Catalog of Rare and Endangered Plant Species of the Mangystau Region (Red Book) (2006). To preserve their populations, it is necessary to carry out a number of activities, the most important of which are: inclusion in the list of protected species, creation or expansion of the territory of a protected object, introduction to culture, as well as monitoring and control of the state of populations.

Currently, MEBS is intensively working on preparing a list of flora for placement on the GBIF platform and developing a web application for the BD-PLANT-KZ computer program, which allows online entry of information about plants of natural flora from any computer in botanical gardens, connected to the Internet.

ASSESSMENT OF SPECIES COMPOSITION OF FRUIT AND BERRY PLANTS OF CENTRAL KAZAKHSTAN FLORA

Ishmuratova M.Yu., Madieva A.N., Zhanayeva M.B., Tleukenova S.U.

Karaganda Buketov University, Karaganda, Kazakhstan

E-mail: Margarita.ishmur@mail.ru

The problem of preservation of genetic diversity of fruit and berry plants, its practical introduction into culture, and use in modern breeding is one of the basic bases for creation of new varieties, forms and hybrids. The necessity of work on the study of genetic potential of wild fruit and berry plants and creation of gene pool of new assortment is dictated by the fact that due to climate change, anthropogenic impact on biocenoses their habitats are sharply decreasing, up to the threat of complete extinction [1]. The research is conditioned by the need of Kazakhstan to assess the current state of wild fruit and berry plants for solving the problem of food security, in monitoring for scientifically based conservation measures.

For selection of promising species and nursery establishment, the necessary stage of the research is the analysis of the full species composition of fruit and berry plants of the local flora.

The complexity of natural reliefs, significant amplitude of temperatures, precipitation and humidity determined the diversity of vegetation of Karaganda and Ulytau regions (Central Kazakhstan). Thus, in Central Kazakhstan there are more than 1250 species of vascular plants from 434 genera and 99 families [2]. As the preliminary analysis showed, the studied flora contains a significant number of species of economic value, including wild fruit plants. This group is represented by 31 species belonging to 14 genera and 7 families.

Dominant number of species belongs to the family *Rosaceae*: 14 species from 7 genera; the second place is occupied by the family *Grossulariaceae* - 4 species from 2 genera; on the third place is the family *Caprifoliaceae*: 2 species from 1 genus. The other families are represented by 1 genus and species. Woody-shrubby plants (21 species) prevail among life forms; and herbaceous plants are represented by only 3 species (*Fragaria vesca, Fragaria viridis* and *Rubus saxatilis*). In relation to moisture conditions, species were divided into mesophytes (21 species: *Rubus idaeus, Ribes nigrum, Rubus saxatilis, Berberis sibirica, Rosa laxa, Lonicera tatarica*, etc.) and xerophytes (3 species: *Elaeagnus oxycarpa, Nitraria schoberi, Rosa spinosissima*, etc.).

A review of species distribution over the territory shows their unevenness. Most of the species are confined to the northern, north-western and central parts characterized by higher annual precipitation, moderate summer temperatures and the presence of coniferous, mixed coniferous forests and numerous shrub thickets.

Southern, south-western territories are characterized by extremely arid conditions, poor soils and high summer temperatures. Fruit crops in these habitats are mainly concentrated along river valleys, in the vicinity of springs. All described species are well adapted to the conditions of Central Kazakhstan and can be used for introduction into culture as fruit crops.

Based on the analyzed material, areal maps were drawn up and promising localities for the selection of source material were identified.

The research was carried out within the framework of the program BR21882166 "Scientific and practical bases of reproduction WILD RELATIVE CULTURAL PLANTS FLORA OF UZBEKISTAN

, conservation, use of fruit and berry plants of natural flora of western, eastern, central and northern Kazakhstan to ensure food security" (2023-2025).

References

1 Del Rio Celestino M., Font R. (2020). The health benefits of fruits and vegetables. *Foods, 9(3*); 369. https://doi.org/10.3390/foods9030369

2 Ishmuratova M.Yu., Tleukenova S.U. (2009). About vascular plants of Central Kazakhstan flora. *Bulletin of the Karaganda University, 4(56)*; 9-20.

WILD RELATIVE CULTURAL PLANTS FLORA OF UZBEKISTAN

Abduraimov O.S., Shomurodov H.F.

Institute of Botany of the Academy of Sciences of the Republic of Uzbekistan

E-mail: ozodbek88@bk.ru

Growing research interest in wild relative cultural plants (WRCP) has highlighted their value for crop improvement, particularly to mitigate the impact of climate change and contribute to global food security. As most conservation activities are implemented at national level there is a requirement for each country to develop and implement a national WRCP conservation strategy.

The Central Asiatisc Region is commonly known as one of the primary centers of origin of cultivated plants, especially for apricots, cherries, apples, pears, pistachios, almonds, walnuts, and some vegetables. However, it lacks exact data and information about cultivated plants in this region.

Central Asia is famous as a center of diversity of apples, pears, onion, spinach, carrot, and other crops. Therefore, Vavilov defined Central Asia as one of the centers of origin of cultivated plants in different stages.

Uzbekistan is a landlocked, largely mountainous country of Central Asia. Its territory totals 447,400 km², with the mountains covering ca. 15% of the country. The territory lies between 37°11′ and 45°36′ of northern latitude and 56° and 73°10′ of eastern longitude, stretching for ca. 1,400 km from west to east and 925 km from north to south. Uzbekistan shares borders with Kazakhstan, Kyrgyzstan, Tajikistan, Turkmenistan and Afghanistan.

In spite of all the achievements, an updated checklist of vascular plants of Uzbekistan is still lacking. Summarizing the published data, we estimate that the number of native species of vascular plants in the country is no less than 4,300.

In the flora of Uzbekistan, it is very important to study the cultural plant and their current state. As a result of a literary review and analysis of previous studies, 224 species of WRCP belonging to 106 genera and 28 families were identified in the flora of Uzbekistan.

That the largest number of species falls on the Poaceae family – 63 species, Fabaceae – 32, Rosaceae – 24. These three families include about 55% of the species of the WRCP of Uzbekistan.

We have analyzed economically valuable groups of plants. Thus, it was determined that among the WRCP, the largest number refers to forage plants - 130 species, the second position is occupied by food plants - 59 species, in the third-place honey plants - 34 species. Medicinal plants are represented by 25 species, technical - 11, vitamin - 7, decorative - 6 species.

Thus, 224 species of WRCP from 106 genera and 28 families grow in the flora of Uzbekistan. The Rosaceae, Poaceae and Fabaceae families are the richest. The genera *Poa, Aegilops, Hordeum, Vicia, Medicago, Prunus, Lathyrus, Allium* are characterized by a high species diversity of the WRCP. It should be noted that the figures given for the composition of wild relatives of cultivated plants of the flora of Uzbekistan are not yet final.

Further detailed study of the flora of certain regions of the republic should undoubtedly lead to clarification of the number of genera and species of flora of the republic that have economic value. Currently, the demand for natural reserves of plants of this species is growing.

The preliminary results show the wide biological diversity of the WRCP flora of Uzbekistan and the prospects for their widespread use and introduction into culture. In turn, there is no doubt that comprehensive research on WRCP, an analysis of the current state of natural populations, and the development of a system of protection and rational use are necessary.

The research was carried out within the framework of the scientific research program "Assessment of the current state of populations and creation of a living collection of economically valuable species of wild relatives of cultivated plants of the flora of Uzbekistan" of the laboratory "Population Biology and Plant Ecology" of the Institute of Botany of the Academy of Sciences of the Republic of Uzbekistan.

RESEARCH OF PROMISING SPECIES OF ESSENTIAL OIL PLANTS OF THE ISSYK-KUL BASIN

Sazykulova G.J., Sodombekov I.S., Ashymbaeva B.A.

Kyrgyz State University named after I. Arabaev, Bishkek, Kyrgyzstan

E-mail: Gulbaira.dj@rambler.ru

The vegetation of the Issyk-Kul depression contains the richest genetic resources of raw materials of wild essential oil plants, therefore the conservation and sustainable use of promising species is of extremely important ecological, economic, social and aesthetic importance.

The purpose of our research is to identify and study the most common local wild-growing promising species of essential oil plants containing essential oils growing in the mountainous areas of the Issyk-Kul depression.

Hundreds of species of medicinal and essential oil plants are considered promising, of which not all species have been studied, and the species indicated in the work, found in the natural conditions of the Issyk-Kul depression, have already been included in the State Pharmacopoeia. Based on an analysis of literary sources and data from our studies of essential oil plants, the essential oil content was identified and the place where this species grows was given.

Currently, due to the return to natural medicines, interest in medicinal plants in general and those containing essential oils (EOs) in particular has increased. In addition to the traditional use of essential oil plants in perfume production and the food industry, they are increasingly used as medicines.

Of the total number of species of flora of Kyrgyzstan, essential oil plants make up (9.9%, by the number of genera - 20.6%, by the number of families - 41.6%).

The largest number of genera is represented in the families: Apiaceae - 22.2% (of the total number of genera), Lamiaceae and Asteraceae, 12.9 and 13.4%, respectively, Rosaceae - 8.8%. The following families are distinguished by the number of species: Apiaceae and Liliaceae - 20.1% each, Asteraceae - 13.9%, Lamiaceae - 9.8%.

Wild essential oil plants are distributed unevenly across the biogeographical regions of Kyrgyzstan. There are about 130-132 species in the Issyk-Kul basin.

As a result of the research, innovative technologies for propagation and cultivation of valuable medicinal and essential oil plants will be proposed for introduction into production and sale to the population. Work will be carried out to determine the bactericidal properties of essential oils and determine the category of pharmacopoeial, traditional and promising essential oil plants of this region.

THE GRID MAPPING OF THE SPECIES OF POACEAE IN KUHITANG BOTANICAL-GEOGRAPHICAL REGION

Dilarom Tajetdinova

Institute of Botany, Academy of Sciences of the Republic of Uzbekistan, Tashkent, Uzbekistan

E-mail: t-dilyia@mail.ru

Since 2021, the work program in the laboratory of the "Flora Uzbekistan" in the Botany institute of the Academy of Sciences of the Republic of Uzbekistan has included grid mapping of the Western Hissar, Hissar-Darvaz and Panj districts in Mountainous Central Asian province.

The Kuhitang botanical-geographical region includes the Kuhitang ridge and its northeastern spur – the Susyztau mountain, as well as the southern slope of the Tyubere-Oland mountain. It borders the Surkhan-Sherabad and Tarkapchigay region of the Western Hissar district, the western part of the district is located on the territory of the Republic of Turkmenistan.

The territory of the Kuhitang botanical-geographical region was divided in the GIS environment into 130 indexes with dimensions 5x5 km.

According to the results obtained, 1162 herbarium specimens belonging to 101 species of the family of Poaceae were collected in 113 indexes, mainly in the North-East of the Uzbekistan part of the Kuhitang ridge.

Mostly, on the territory of the Kuhitang botanical-geographical region, the species richness of representatives of the Poaceae family is low (1–9 species) in eighty-seven indixes. There are only twenty indexes with average abundance of species (10–19), and six indexes with high abundance (23–29 species). Basically, the indexes with high and medium species richness correspond to the desert part of the area.

The maximum collection density of Poaceae was 43 collections for index W193, which corresponds to the index with maximum species richness.

Analysis of the georeferencing of herbarium specimens shows that most of the field research was carried out in the piedmont plain and foothill zone, therefore the maximum number of species and herbarium collections per index falls on these plain zones. The attention to the composition of the flora of the piedmont plain and foothills, as well as to the flora of anthropogenic landscapes, was very low.

Available specimens of Poaceae, mainly belong to polymorphic genera or rare species of the flora of the region. In this regard, the grid mapping of the flora of the Kupitang botanical-geographical region has important scientific and practical significance in identifying the features of the spatial distribution of the flora species of Uzbekistan.

THE RESULTS OF THE INTRODUCTION OF FLORAL AND DECORATIVE PERENNIALS OF NON-DISTRICT AND CULTURAL FLORA IN THE ALTAI BOTANICAL GARDEN

Aituganova B.Zh, Satekov E.Y.

Altai Botanical Garden, Ridder, Kazakhstan

E-mail: botagoz89ast.mail.ru

The collection fund of floral and ornamental plants of the cultural flora includes 915 taxa - species, subspecies, variety, form, variety. The introduced material came in the form of live plants, bulbs, tubers and seeds from botanical institutions of the former USSR and other countries, and was also imported during expedition trips. Individual taxa entered the collection as a gift from private collections and were purchased at garden centers. The seeds were received through the international exchange fund and collected in nature.

When reconciling the names of varieties and matching the names of taxa, the following sources were used: Ornamental herbaceous plants for the open ground of the USSR, Vascular plants of Russia and neighboring countries

Catalog of floral and decorative herbaceous plants of the botanical gardens of the CIS and Baltic countries, Varieties of hybrid garden iris of foreign selection grown in the USSR, as well as Online resources: http://www.daffseek.org , http://www.daylilies.org , http://www.flower-iris.ru and others.

To review the results of the introduction tests in East Kazakhstan, an analysis of the assortment of floral and ornamental plants recommended for green construction in the East Kazakhstan region was carried out. The assortment under consideration is based on the results of direct introduction tests.

The seasonal rhythms of the development of introducents were studied according to the generally accepted Methodology of phenological observations in botanical gardens, the success of intoreduction was according to the methodology of V.V. Bakanova, the decorative effect of introducents was evaluated on a scale given by V.N. Bylov and R.A. Karpisonova.

Based on a number of indicators (winter hardiness, generative development, vegetative reproduction, resistance to diseases and pests, preservation of habitus), an integral assessment of the success of the introduction of floral and decorative perennials is given. There are 6 classes of prospects: the most promising, promising, less promising, unpromising, unpromising, unsuitable. A comprehensive assessment of perennials is carried out on a three-point scale proposed by Bylov, Karpisonova

The collection of floral and decorative perennials of the informational and cultural flora of the Altai Botanical Garden includes 915 taxa from 102 genera, which belong to 38 families.

The article was written within the framework of the scientific and technical program IRN BR 21882166 "Scientific and practical foundations of reproduction, conservation, use of fruit and berry plants of the natural flora of Western, Eastern, Central and Northern Kazakhstan to ensure food security" with the financial support of the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan for 2023-2025.

DEVELOPMENT OF A HERBARIUM DATABASE

Shevtsov V.A., Nazarec N.A.

National Center of Biotechnology Republic of Kazakhstan, Astana, Kazakhstan

E-mail: shevtsovvladislav111@gmail.com

The importance of developing an electronic herbarium for rare and endangered plant species in the light of preserving the ecological balance and biodiversity is indisputable. In today's context, where plants are threatened by human actions, climate change and other factors, information on these species is often unavailable or incomplete, making it difficult to effectively manage their conservation.

The development of an electronic herbarium will systematize and centralize information on rare and endangered plant species, providing easy access for the scientific community, conservationists and decision-makers. Herbarium records, which are an important source of data on the distribution and condition of plants, will be available in electronic format, which will greatly facilitate their use in research, monitoring and conservation planning.

The advantages of an electronic herbarium include easy access to information, the ability to quickly update and disseminate data. This will make information about rare and endangered plant species more relevant and useful for nature conservation, as well as for the development of systematic approaches to their conservation.

Thus, the creation of an electronic herbarium represents an important step in ensuring the effective management of rare and endangered plant species, providing the necessary information for the development and implementation of nature conservation and biodiversity conservation programs.

As part of our research, an extensive database of rare and endangered plant species was developed. The database contains information on the distribution, characteristics and conservation status of various plants, including information on habitats, threat levels, population sizes and other relevant data.

To create this database, we used herbarium records, literature sources, field research results, and other available data sources. An important aspect of the development of the database was its structuring and organization to provide convenient access and analysis of information for researchers, conservationists and other stakeholders.

PROTECTED AREAS OF UZBEKISTAN AND CONSERVATION OF PLANT BIODIVERSITY

Beshko N.Yu.

Institute of Botany, Academy of Sciences of the Republic of Uzbekistan

E-mail: natalia_beshko@mail.ru

The Republic of Uzbekistan is a home to a rich plant biodiversity with a large number of endangered species, endemics, relicts and crop wild relatives. Currently, more than 4380 species of vascular plants are recorded in the wild. Globally threatened (CR, EN and VU categories of the IUCN Red List) are 27 representatives of the flora of Uzbekistan; 314 species (7.1% of flora) are listed in the national Red Data Book, among them, 15 species are assessed as probably extinct, 98 critically endangered, 130 endangered, and 71 vulnerable. The leading families and genera are Asteraceae (*Cousinia* s.l., *Jurinea*, *Artemisia*, *Taraxacum*), Fabaceae (*Astragalus*, *Oxytropis*, *Hedysarum*), Poaceae (*Bromus*, *Elymus*, *Poa*, *Stipa*), Brassicaceae (*Draba*, *Parrya*, *Strigosella*), Apiaceae (*Ferula*, *Seseli*), Lamiaceae (*Nepeta*, *Phlomoides*, *Salvia*, *Scutellaria*), Rosaceae (*Potentilla*, *Rosa*), Caryophyllaceae (*Silene*), Boraginaceae (*Lappula*), Ranunculaceae (*Ranunculus*), Amaranthaceae (*Salsola* s.l., *Climacoptera*, *Suaeda*), Amaryllidaceae (*Allium*), Liliaceae (*Gagea*, *Tulipa*), Iridaceae (*Iris*), Asphodelaceae (*Eremurus*), Polygonaceae (*Calligonum*, *Polygonum*), Plumbaginaceae (*Acantholimon*), etc.. In terms of biogeography, Uzbekistan belongs to the Mountain Central Asian and Turan floristic provinces of Iran-Turanian region of Ancient Mediterranean subkingdom of the Holarctic Kingdom; the mountains of Uzbekistan are divided into 8 floristic districts, and the deserts are divided into 8 floristic districts. There are five main types of natural ecosystems: deserts and semi-deserts; foothills and lowlands; mountains; river and coastal ecosystems; wetlands. Modified habitats occupy about 20% of territory. Uzbekistan.

The first nature reserve in Uzbekistan and one of the oldest protected areas in Central Asia, Zaamin State Nature Reserve, was established in 1928 under the name "Guralash Reserve" in the western part of the Turkestan Range for the conservation of mountain juniper forests and initially covered 8000 hectares (its current area is 26 840 ha). The next protected area, Chatkal State Reserve, was created in 1947 in the western part of the Chatkal Range under the name “Mountain-Forest Reserve”, and it was designated a UNESCO biosphere reserve in 1986. This nature reserve was established to protect the unique landscapes, flora and fauna of the Western Tien Shan. At the present, ecosystems and outstanding biodiversity of Uzbekistan are protected in 8 state nature reserves (protected areas of IUCN category Ia), 1 landscape wildlife sanctuary (category Ib), 13 national parks (IUCN category II), 11 state nature monuments (category III), 12 wildlife sanctuaries and 1 wildlife nursery (category IV), and in 2 state biosphere reserves (a special category of protected areas). In total, protected areas of IUCN categories I–IV occupy almost 6 mln. hectares (13.3% of the country) and cover all types of ecosystems and landscapes of Uzbekistan. Nature reserves, national parks and biosphere reserves provide in-situ protection for 195 plant species listed in the Red Data Book of Uzbekistan (61.2 %).

The flora of mountain reserves and national parks of Uzbekistan is significantly richest than the flora of protected areas situated in the desert zone. The Ugam-Chatkal National Park (506 941 hectares) situated in the mountainous part of Tashkent Region ranks first in the number of flora species (1724 species, 54 of them are red-listed at the national level). The second position occupy the flora of Hissar Nature Reserve (78 986 ha) situated in highlands of the Hissar Range, which counts 1298 species (34 red-listed). Actually, the flora of Zaamin Nature Reserve includes 1192 species, 1118 species are reported for the Ugam-Chatkal biosphere reserve established in 2018, 877 plant species grow in the Kitab National Park, 848 species of vascular plants are found in Nuratau Nature Reserve, 774 in Chatkal Nature Reserve and 718 in Surkhan Nature Reserve. Following numbers of plant species are recorded for protected areas of the desert zone of Uzbekistan: 378 species in Khorezm National Park, 235 species in Kyzylkum Nature Reserve. The flora of some protected areas is still poorly studied, especially recently established nature reserves and national parks, as Tupalang, Babatag, Pap, Central Kyzylkum and Southern Ustyurt national parks or Aktau-Tamdy nature reserve. In this connection, the revised National Strategy and Action Plan on the Biodiversity targeted to complete inventory of biodiversity of all protected areas of Uzbekistan.

GENETIC DIVESITY OF WILD PLANT SPECIES OF KAZAKHSTAN

Abugalieva S., Almerekova Sh., Yermagambetova M., Turuspekov Y.

Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan

E-mail: absaule@yahoo.com

Kazakhstan is the ninth-largest country in the world and it is home to more than 6,000 of vascular plant species. The country's territory was divided into 29 main floristic regions, each having specific natural conditions with own composition of species and natural populations. Floristic regions with a high number of endemic species are located in mountainous regions of the south, south-east, and east of Kazakhstan, Karatau, West Tian Shan, Zailiskiy and Dhungar Alatau. Every mountain chain is characterizing by a specific representation of endemic species from different floristic families and genus of vascular plants. Flora of Kazakhstan is specific and unique in its own way, including by composition and area of distribution of wildly growing populations.

In the framework of the Program 0237/PTF «Genetic diversity and preservation of genetic resources of endemic, rare and industrially important plants in the Republic of Kazakhstan», 841 populations of 502 endemic, rare, endangered and wildly valuable plant species were collected in 6 State National Reserves and 9 State National Nature Parks in the Eastern, Central, Northern, Western, Southeast, and Southern Kazakhstan. The program combined the efforts of botanists, geneticists, biotechnologists from Botanical gardens, universities, specially protected areas (reserves and parks). The main goal was to study genetic diversity of endemic, rare, and economically important plant species from different regions of the country, with the focus on National State Reserves and National Nature Parks of Kazakhstan, and other territories in different floristic regions.

Samples from 818 populations of 502 species (214 genus, 75 family) were collected. For each collected species, a reference herbarium was compiled in duplicate. Plant samples of 841 populations of 502 species were used to isolate and purify DNA. Three DNA markers of nuclear and chloroplast genomes were selected for DNA barcoding of flora species - ITS, *mat*K and *rbc*L. The nucleotide sequences were deposited into the NCBI database.

DNA barcoding markers can be successfully used (1) in taxonomy of plant species and (2) correct identification of medicinal plants.

The first steps have been taken to digitalize data on molecular genetic and botanical documentation of the wild flora of Kazakhstan.

Several studies on genetic diversity of wild plant species from different genera were conducted.

The research was conducted in the framework of the grants AP14870612, AP14869593 (2022-2024), AP09259027 (2021-2023), AP05131621 (2018-2020), Program 0237/PTF-14 (2015-2017) supported by the Ministry of Sciences and Higher Education of the Republic of Kazakhstan.

THE COMPARATIVE ASSESSMENT OF COMPLETE PLASTID SEQUENCES OF *TULIPA* L. (LILIACEAE JUSS.) SPECIES FROM KAZAKHSTAN

***Almerekova S.*[1], *Yermagambetova M.*[1], *Ivaschenko A.A.*[2], *Turuspekov Y.*[1], *Abugalieva S.**[1]**

[1] *Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan*
[2] *Institute of Zoology, Almaty, Kazakhstan*

* *E-mail:* absaule@yahoo.com

Tulipa L. known as economically important genus in the family Liliaceae Juss. and comprises ca. 150 wild species all over the world (Veldkamp and Zonneveld, 2012). The Tian Shan and Pamir-Alay Mountain ranges in Central Asia are recognized as principal centers for *Tulipa* species diversity (Botschantzeva, 1962), hosting around 80 species (Tojibaev and Beshko, 2014). Specifically, Kazakhstan hosts 42 *Tulipa* species (Ivashchenko, 2019), with 18 among them listed in the Red Book of Kazakhstan (2014). Tulips pose taxonomic challenges that cannot be sufficiently resolved solely through morphological analysis or by relying on a limited set of genetic markers.

This study focuses on evaluating the complete plastid sequences of *Tulipa* species collected in Kazakhstan. Previously published plastomes were retrieved from GenBank for comparison and phylogenetic analysis. Within the *Tulipa* plastomes, a total of 136 genes were annotated, with 113 being unique. Among these unique genes, 79 were protein-coding, 30 were transfer RNA, and four were ribosomal RNA genes. Simple sequence repeats, tandem, forward, palindromic, reverse, and complementary repeats were identified in the studied *Tulipa* plastomes. Regions exhibiting relatively high polymorphism were identified, which may potentially serve as DNA barcoding markers for the genus. The data obtained from *Tulipa* plastome sequences could important for future phylogenetic studies of the *Tulipa* genus based on plastid genomes.

This research has been funded by the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan (Grant No. AP14870612).

References:

Veldkamp J.F., Zonneveld B.J.M., The infrageneric nomenclature of *Tulipa* (Liliaceae), Plant Syst. Evol. 268 (2012) 87–92.

Botschantzeva Z.P., Tulips: taxonomy, morphology, cytology, phytogeography, and physiology, Rotterdam: Balkema, Crc Press (1962).

Tojibaev K., Beshko N., Reassessment of diversity and analysis of distribution in *Tulipa* (Liliaceae) in Uzbekistan, Nord. J. Bot. 33(3) (2014) 324–334. doi:10.1111/njb.00616

Ivashchenko A.A., O.V. Belyalov, Kazakhstan is the birthplace of tulips, Almaty: Atamura (2019) 368.

The Red Book of Kazakhstan. Plants. Re-edition, completed and revised, Astana 2 (1) (2014) 446.

ENDEMIC SPECIES OF FLORA OF UZBEKISTAN

Turginov O.T.

Institute of Botany, Academy of Sciences of the Republic of Uzbekistan, Tashkent, Uzbekistan, National University of Uzbekistan named after Mirzo Ulugbek, Tashkent, Uzbekistan

E-mail: orzimat@mail.ru

Uzbekistan shares borders with Kazakhstan, Kyrgyzstan, Tajikistan, Turkmenistan and Afghanistan. The country's altitudes vary between 12 and 4643 m above sea level. Lowlands occupy northern, western, and central parts of the country and are largely deserted, except for the depressions of Ferghana, Zeravshan, and Surkhon-Sherobod with mild climatic conditions, which are mostly turned into arable lands. The main mountain systems in Uzbekistan include the Western Tien Shan and the Pamir-Aloy, which are small parts of their territory, and most of the larger mountain ranges they share with neighboring countries. The region of the plain corresponds to the desert Kyzyl-Kum.

The flora of Uzbekistan has a long history of studies, perhaps the strongest in Central Asia. After a period of the first plant descriptions from the area (1840–1920), published mainly by botanists affiliated with the Russian Academy of Sciences in St. Petersburg based on materials collected in the course of the Russian colonization of Central Asia, and culminated in the first synopsis of the flora of Central Asia, the first university in Central Asia was established in Tashkent in 1920.

The old Flora of Uzbekistan (Kudryashev 1941, Vvedensky 1953–1962) provided the first detailed treatment of vascular plants of Uzbekistan, largely following but sometimes (as for part of the Asteraceae) being ahead of the Flora of the USSR. When completed, this Flora included treatments of 3,663 native species. Despite all the progress, there is still no updated checklist of vascular plants in Uzbekistan. Summarizing the published data, we estimate that the number of local species of vascular plants in the country is more than 4400.

Flora of Uzbekistan has many endemic, threatened, and globally important species. In the endemic species flora of Uzbekistan, 32 families belonging to 101 genera have the status of 313 endemics (these numbers are not free from changes, there are *ined* species). Endemics make up 7.25% of the entire flora of Uzbekistan. Among them, dicots (Eudicotyledons) consist of 251species belonging to 25 families and 91 genera (80.65%), and monocots (Monocotyledons) consist of 62 species (19.35%) belonging to 7 families and 10 genera. The overall ratio of monocots to dicots is 1:4.16. Endemics of Uzbekistan have 1 to 60 species in families, an average of 9.75 species per family. The total ratio of endemics is 1:3.18:9.75. The taxonomic structure of endemic species was analyzed and it was found that they are predominantly represented by Asteraceae, Fabaceae, Lamiaceae, Apiaceae, Liliaceae, Amaryllidaceae, and genera such as *Astragalus* L., *Cousinia* Cass., *Allium* L., *Gagea* Salisb., *Oxytropis* DC., *Phlomoides* Moench, *Silene* L., *Iris* L., and *Hedysarum* L. These genera are considered polymorphic for the mountainous regions of Central Asia, which explains the high diversity of species in these families. This diversity is due to the process of species formation in mountainous Central Asia, particularly in the mountain and foothills regions of Uzbekistan.

Life form was based on the classification developed by S.Raunkiaer (1934). Accordingly, the endemics of Uzbekistan consist of 41 therophytes, 73 cryptophytes, 155 hemicryptophytes, 41 chamaephytes, and 6 phanerophytes. Among endemic species, hemicryptophytes (155 species) dominate in number, which is recognized as one of the features characteristic of mountainous Central Asia. Extensive research is ongoing.

GENETIC DIVERSITY AND POPULATION STRUCTURE OF *JUNIPERUS SERAVSCHANICA* KOM. COLLECTED IN CENTRAL ASIA

Yermagambetova M. [1], ***Almerekova S.***[1], ***Abugalieva S.*** [1], ***Turginov O.***[2], ***Sultangaziev O.***[3], ***Turuspekov Y.***[1*]

[1]*Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan*
[2]*Institute of Botany, Academy of Sciences of the Republic of Uzbekistan, Tashkent, Uzbekistan*
[3]*Fauna and Flora International, Bishkek, Kyrgyzstan*

**E-mail:* yerlant@yahoo.com

Juniperus seravschanica Kom., a species widespread in the mountainous regions from Central Asia to Oman, plays a crucial role in developing shrub-forest formations and stabilizing and draining soils at various elevations. Understanding the genetic variability and the structure of its populations is fundamental for evaluating the current condition of *J. seravschanica*'s resources, which is vital for devising future preservation strategies. This study involved collecting samples from 15 different populations of *J. seravschanica* across the mountainous terrains of Uzbekistan, Kyrgyzstan, and Kazakhstan. An assessment of these populations' genetic diversity and structure was conducted using 11 polymorphic simple sequence repeat (SSR) markers. Several genetic diversity indicators were measured, such as the total number of alleles, the effective number of alleles, Shannon's information index, the proportion of polymorphic sites, Nei's genetic diversity index, and principal coordinate analysis. From the study of the 15 populations using these 11 SSR markers, 35 alleles were identified. The average polymorphic information content (PIC) value was 0.432, with the highest marker (*JT_40*) showing a value of 0.662. Nei's genetic diversity index across the populations was 0.450, with a range from 0.407 (in population 14) to 0.566 (in population 4). The analysis of molecular variance (AMOVA) indicated that 90.3% of the genetic variation exists within populations. The gene flow among all populations was calculated to be 4.654. The analysis of population structure showed limited clustering, corroborating the AMOVA findings. The results from this research are instrumental in supporting the conservation efforts for *J. seravschanica* throughout Central Asia.

This research was funded by the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan (Grant No. AP09259027).

DNA BARCODING OF KAZAKHSTANI *BETULA* SPECIES

Turzhanova A.S., Magzumova S.M., Danilova A.N.

National Center for Biotechnology, Astana, Kazakhstan

E-mail: turzhanova-ainur@mail.ru

The problem of studying, conserving, and sustainably utilizing biodiversity remains relevant amid anthropogenic stresses and global environmental changes. The genus *Betula*, or birch, plays a significant role in the ecosystem of the Kazakh Altai, exerting a notable influence on the natural environment and human activities in the region. Birches are essential components of forest ecosystems, contributing to biodiversity conservation and soil enrichment with organic substances. One of the methods for studying biodiversity and genetic identification is DNA barcoding. Recently, this method has been considered one of the most useful and objective "tools" for species identification based on the diversity of sequences of nuclear and chloroplast genome marker genes. Numerous studies highlight the high efficiency of using large subunits of RuBisCo (rbcL) combined with the intron matK as markers, as well as nuclear genome markers - ribosomal internal transcribed spacers (ITS). These are the most extensively characterized and rapidly evolving genes, with their resolving power being sufficiently high when used together.

This study was conducted to determine the genetic diversity and establish relationships between different birch species found in the territory of the Kazakh Altai.

The study focused on herbarium specimens of 8 Betula species: *Betula*: *B. glandulosa, B. humilis, B. pendula, B. pubescens, B. rotundifolia, B. rezniczenkoana, B. tianschanica* и *B. microphylla*, collected in the territory of the Kazakh Altai. Botanical identification of the species was conducted by specialists from the RSE "Altai Botanical Garden".

After analyzing the GenBank data using the BLAST algorithm, it was found that the ITS markers were the most effective: in all cases, the consensus marker sequences of the species matched those in the NCBI database with 98–100% identity. However, for other markers, such as rbcL for species *B. rezniczenkoana* and *B. tianschanica*, as well as matK for *B. microphylla*, the identity scores were lower. It is worth noting that there are no relevant marker sequences *for B. rezniczenkoana* in the international NCBI database, and only ITS sequences are available *for B. humilis*.

The comparative analysis of sequenced marker gene sequences revealed different frequencies of nucleotide occurrence, emphasizing the genetic variability among *Betula* species. The observed differences in nucleotide frequencies between species indicate their genetic diversity and adaptive strategies. For example, species such as *B. pendula* and *B. pubescens* are characterized by a high adenine (A) content, while other species, such as *B. humilis* and *B. microphylla*, demonstrate a predominance of thymine (T) and cytosine (C). These differences may be associated with the characteristics of their ecological niche and historical factors.

It is interesting to note that the average (G+C) content for all studied species was 43.7%, which corresponds to expected values for this taxonomic group of plants and indicates the preservation of a certain degree of genetic conservatism among birch species in this region.

The obtained results expand our understanding of the genetic architecture and evolutionary relationships within *Betula* L. species. Such efforts are crucial for effective conservation strategies and sustainable management of *Betula* species in the face of environmental challenges.

DIGITAL PHENOTYPING OF DISEASES IN FRUIT GENETIC RESOURCES

Reim S. [1]***, Maß V.*** [2]***, Richter S.*** [1]***, Alirezazadeh P.*** [1]***, Seidl-Schulz J.*** [3]***, Leipnitz M.*** [3]***, Fritzsche E.*** [1]***, Geyer M.*** [2]***, Wöhner T.*** [1]***, Pflanz M.*** [2]

[1] *Julius Kühn-Institute, Federal Research Centre for Cultivated Plants, Institute for Breeding Research on Fruit Crops, Dresden, Germany*
[2] *Leibniz Institute for Agricultural Engineering and Bioeconomy, Potsdam, Germany*
[3] *Geo-konzept, Gesellschaft für Umweltplanungssysteme mbH, Adelschlag, Germany*

The phenotyping of pathogens is an important prerequisite for the evaluation of genetic resources and the provision of resistant genotypes for subsequent fruit breeding. However, phenotyping is still mainly done manually and therefore the bottleneck in fruit breeding.

To increase the efficiency of phenotyping, two high-throughput digital phenotyping methods, one for use in the laboratory and the other for use in the field. Both methods are based on an object recognition approach that recognizes disease symptoms in RGB images using apple blotch (*Diplocarpon coronariae*) and European pear rust (*Gymnosporangium sabinae*) as model pathogens.

The apple blotch resistance test is carried out in the laboratory and is based on the appearance of black spots on detached leaves after artificial inoculation with *D. coronariae*. Resistance to pear rust is assessed directly in the field by observing the conspicuous yellow-orange symptoms on the tree.

For model training, an image dataset with apple blotch symptoms was recorded in the laboratory using a handheld camera. For pear rust symptoms an image dataset was recorded in the field using a UAV camera.

After annotating the respective symptoms with the Computer Vision Annotation Tool (CVAT), annotated image datasets were used to train a YOLOv5 algorithm. As a result, we created a model for digital detection with a symptom prediction accuracy of 95% for apple blotch and 81 % for pear rust. The precise localization of pear rust symptoms within the orchard is made possible by a novel photogrammetry approach on georeferenced image data.

In the future, these two approaches can be used for high-throughput digital phenotyping to evaluate genetic resources in the laboratory and in the field.

DEVELOPMENT OF CRYOBIOTECHNOLOGIES FOR PRESERVATION OF PLANT GERMPLASM IN KAZAKHSTAN

Kushnarenko S.V.**, Romadanova N.V., Rymkhanova N.K., Aralbayeva M., Manapkanova U.A., Rakhimbaev I.R.

Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan

* *E-mail:* sv.kushnarenko.bio@gmail.com

In recent decades, cryobiotechnologies such as cryopreservation and cryotherapy have found wide practical application in agriculture, crop production and conservation of biological diversity. Cryopreservation has proven effective in long-term preservation of plant genetic resources at ultra-low temperatures. Cryotherapy is implemented to eliminate phytopathogens (viruses, viroids and phytoplasma) and produce healthy plant material.

In Kazakhstan, research on plant cryopreservation began in 2002 at the Institute of Plant Biology and Biotechnology. To date, the Laboratory of Germplasm Cryopreservation has developed cryobiotechnologies for use in the following areas:

- to preserve the biodiversity of rare and endangered species of Kazakhstan flora in *in vitro* culture and in a cryogenic bank;
- to preserve germplasm of valuable agricultural crops, including foreign and local varieties and hybrids;
- for eliminating viruses and obtaining virus-free plant material for various clonally propagated crops.

Micropropagation and cryopreservation protocols have been developed for a wide range of valuable food crops such as apple, pear, apricot, raspberry, blackcurrant, barberry, honeysuckle, cherry, potato, hazelnut, and walnut. Plant material from fruit and berry native populations have been cryopreserved using seeds, from nut populations using excised embryonic axes. Cryopreservation of shoot tip isolated from *in vitro*-grown plants has been used as another option for clonal germplasm conservation (selected wild forms, varieties, and hybrids). Cryotherapy protocols in combination with chemotherapy and thermotherapy for eradication of viruses from apple, raspberry and potato *in vitro* plants have been developed. The cryogenic bank at -196°C for preservation of valuable plant germplasm has been established in Kazakhstan. It consists of 1240 accessions of wild forms and varieties of *Malus, Pyrus, Rubus, Ribes, Lonicera, and Berberis*. Some of the most valuable accessions in the cryogenic bank are rare wild species listed in the Red Book of Kazakhstan: relict endemic species *Malus sieversii*, whose populations are decreasing; endemic threatened species *Berberis iliensis* and *Lonicera iliensis*, and rare threatened species *Coryllus avellana*.

Cryobiotechnologies, in addition to conventional methods of preserving biodiversity in botanical gardens and field gene banks, have great potential for *ex situ* conservation of plant germplasm.

This research was funded by the Science Committee of the Ministry of Science and Higher Education of the Kazakhstan Republic, Grant # AP19676481.

ANALYSIS OF POST-CRYOGENIC POLEN REGENERATION OF PEACH (*PERSICA VULGARIS* MILL.) AND NECTARINE (*PERSICA VULGARIS VAR.NECTARINA* (MAX) HOLUB.) FROM THE VIR GENETIC RESOURCES COLLECTION

Khokhlenko A.A. [1], *Verzhuk V.G.* [1], *Eremina O.V.* [1,2], *Eremin V.G.* [1,2]

[1]*N.I. Vavilov All-Russian Institute of Plant Genetic Resources (VIR) St. Petersburg, Russia;*
E-mail: annhohlenko@yandex.ru

[2] *Krymsk Experimental Breeding Station of VIR, Krymsk, Krasnodar Region, Russia*
E-mail: kross67@mail.ru

The instability of climatic conditions and ecological situation in the world indicates the need to create a reliable doublet for preservation of genetic resources of vegetatively propagated crop collections in a viable state by cryopreservation in liquid nitrogen or its vapors. Studies carried out at the turn of XX-XXI centuries on cryopreservation of fruit and berry plants showed the possibility of preserving plant material in the form of separate parts - vegetative cuttings, buds, pollen and apices of microshoots (Sakai, Noshiro, 1975; Tumanov, 1979; Forsline et al, 1998; Barbara B.M. Reed,2008; Pavlov et al., 2019; Tikhonova, 2020; Verzhuk, Erastenkova, Khokhlenko, Agakhanov, Kislin, Ukhatova, 2022; Verzhuk, Eremin et al., 2023). Cryopreservation of pollen viability has practical application in breeding and biotechnological programs according to the following criteria: 1. year-round provision and exchange of genetic material inside and outside the country; 2. minimizing the loss of valuable specimens; 3. reducing material costs of maintaining plant resources.

The study and evaluation of pollen viability of peach and nectarine pollen after exposure to ultra-low temperatures of liquid nitrogen (-196°C) were carried out on seven peach varieties: Red PF Big George, Golden Jubilee, Peach of the Peace, Vesna, Lel`, Cio-Cio-San, Mao-Tha-Or and two nectarine varieties: Orion and Obilny. Pollen collection was carried out in 2022, during the flowering period of the varieties in the collection garden of the branch of the Crimean Experimental Breeding Station of VIR. Pollen was extracted from unopened buds, dried, placed in cryotubes and the initial viability of the samples was determined by germination. Pollen of the samples was germinated in Petri dishes on nutrient medium containing 10% sucrose and 0.8% agar-agar. Dry pollen was frozen by vitrification – direct immersion of cryotubes with pollen in liquid nitrogen. Incubation in nitrogen was 1 year. After extraction from cryotanks, pollen was thawed at room temperature +18 – +20°C, germinated and post-cryogenic assessment of its viability was performed.

At the end of the research the following results were obtained: the initial pollen viability of the studied varieties ranged from 10.79% to 75.56%, after a year of storage in nitrogen - from 5.08% to 56.3%. Mao-Tha-Or peach variety showed the highest pollen viability at ultralow temperatures (56.3%). The lowest viability was found in peach variety Lel (5.08%). After storage in nitrogen, most peach and nectarine accessions showed a slight decrease in viability, on average by 8.0%. However, an increase in pollen viability by 24.64% was observed in the variety Cio-Cio-San. Assessment of the adaptive potential of peach and nectarine pollen allows us to conclude that pollen of the studied stone fruit crops tolerates well the impact of ultralow temperatures of liquid nitrogen and its vapors (-196-185°C).

MOLECULAR IDENTIFICATION AND OPTIMIZATION OF MICROPROPAGATION TECHNOLOGY OF HAWTHORN

Zhanybekova Zh., Magzumova G., Nurtaza A., Kakimzhanova A.

National center for biotechnology, Astana, Kazakhstan

E-mail: zhanargul.zhanybekova0210@gmail.com

Hawthorn (*Crataegus spp.*), a popular plant species belonging to the *Rosaceae* family and Maloideae sub-family, is found worldwide, comprising approximately 280 species.

The studies on hawthorn development, which clarify the evolution of its nutritional content and beneficial properties, align with the broader interest in exploring wild plant species for their potential pharmacological effects.

Understanding the biochemical processes of hawthorn species not only offers insights into their nutritional value but also illuminates their potential therapeutic benefits against diseases. The specific compounds and metabolites identified in connection with fruit maturation highlight the complex nature of hawthorn's bioactive profile.

A series of studies effectively validated the anti-cancer properties of Crataegus species extract through multiple approaches. This comprehensive investigation strengthens the evidence confirming the plant's effectiveness as a natural anti-cancer agent. Furthermore, it highlights the importance of conserving high biodiversity due to its role in preserving the genetic diversity of plant species, which may harbor novel bioactive compounds. Thus, the conservation of diverse ecosystems becomes not only an ecological but also a crucial aspect of pharmacology.

Assessing genetic diversity and identifying plant species is crucial for promptly conserving endangered valuable plant genera. DNA barcoding serves as an efficient tool for species identification. Numerous studies have demonstrated that the ITS region shows genetic variations, making it valuable for classification. Additionally, *matK* and *rbcL*, have been recognized for their ability to differentiate genera.

The objective of this study was the molecular identification of valuable plant species and optimization of micropropagation protocol for the conservation and maintenance of the genetic diversity of hawthorn.

Scientific literature is specifically lacking on the micropropagation of *Crataegus sanguinea* even the plant has a wide specter of applications. The choice of nutrient medium and hormone concentration for proliferation is genotype-specific. This process might be influenced by secondary metabolites that are produced by plants with pharmaceutical properties. It is important to customize the micropropagation protocols, including the selection of nutrient medium and hormone concentrations, based on the specific genotype to achieve optimal results. In the experiment, we identified an effective hormone concentration for promoting shoot proliferation and growth in tissue culture. In conclusion, the identified and evaluated genetic diversity of plants using molecular markers supports the conservation of genetic resources of valuable species in Kazakhstan. Uniquely identified species used as medicines help prevent their misuse. Micropropagation of wild plants has potential perspectives in ecosystem restoration and biodiversity conservation, discovering the diverse benefits that these plants offer to society.

The research is conducted in the framework of the program BR21882166 with financial support from the Ministry of Science and Higher Education of the Republic of Kazakhstan (duration: 2023-2025).

MALUS ORIENTALIS FROM THE COLLECTION MISSION IN THE CAUCASUS TO THE APPLE BREEDING

Höfer M. [*]***, Peil A., Reim S., Wöhner T., Flachowsky H.***

Julius Kühn Institute, Federal Research Centre for Cultivated Plants, Institute for Breeding Research on Fruit Crops, Pillnitzer Platz 3a, D-01326 Dresden, Germany

**E-mail*: monika.hoefer@julius-kuehn.de

Malus orientalis (Uglitz.) is the predominant *Malus* species of the Caucasian forests, distributed in the north of Anatolia, Armenia, Russia as well as in Iran. It is considered as one of the probable minor ancestors of domestic apples. Although *Malus orientalis* has a lower diversity of fruit quality, other valuable traits such as later blooming, adaptation to a wider array of habitats, and capacity for longer storage of the apples should be taken into account for improving the genetic makeup of the domestic apple.

Joint expeditions of scientists of the Julius Kühn-Institute (JKI) from Germany, the Nikolaj I. Vavilov Research Institute of Plant Industry from Russia, the Department at Scientific-Research Center of Agriculture from Georgia, and the Azerbaijan National Academy of Sciences, Genetic Resources Institute from Azerbaijan were conducted in the North and South Caucasus regions during August/ September 2011, 2012 and 2014. Altogether, the collection material included seed samples from 249 mother trees of *Malus orientalis*, as well as seed samples from 26 mother trees of *Pyrus caucasica* and stones from 10 trees of *Prunus ceracifera*.

Currently, 1,165 seedlings of *Malus orientalis*, 55 *Pyrus caucasica* and 47 seedlings of *Prunus ceracifera* are available for characterisation and evaluation in the JKI orchard. The aim of the research project is the comprehensive characterization and evaluation of fruit genetic resources collected during three Caucasus expeditions. The assessment of morphological and fruit-growing relevant traits, as well as the evaluation of susceptibility to diseases occurring in the field on leaves and fruits, will be carried out with the seedling material. After field evaluation, testing of the material evaluated as robust will be conducted using artificial tests in the laboratory and greenhouse. Additionally, since the trees are not sprayed with pesticides, the material will be used to establish a digital phenotyping by unmanned aerial vehicle to determine apple scab symptoms. Based on the phenotypic and genetic data obtained, a core collection will be derived, especially for *Malus orientalis*. After project completion, the selected genotypes will be transferred to the permanent collections of the fruit gene bank to be available for future work in breeding research and breeding. The first results will be presented in the presentation.

THE STUDY OF THE CURRENT STATUS OF VASCULAR PLANTS DIVERSITY IN THE KOSTANAY REGION

Kakimzhanova A. [1], ***Nurtaza A.*** [1], ***Zhanybekova Zh.*** [1], ***Perezhogin Yu.V.*** [2], ***Borodulina O.V.*** [2], ***Mukhtubayeva S.K.*** [3], ***Koblanova S.A.*** [1], ***Abileva G.A.*** [1], ***Kurlov S.I.*** [2]

[1] *National Center for Biotechnology, Astana, Kazakhstan*
[2] *Akhmet Baitursynuly Kostanay Regional University, Kostanay, Kazakhstan*
[3] *Astana Botanical Garden, Astana, Kazakhstan*

E-mail: kakimzhanova@biocenter.kz

Plant identification traditionally relied on morphology that could be observed visually. However, over the past decade, DNA barcoding of plants has emerged as a cutting-edge scientific tool, commonly employed for species identification and taxonomic purposes. This approach has demonstrated high efficacy in plant species identification through the analysis of short DNA sequences from particular genome regions. DNA barcoding typically involves the utilization of both plastid DNA, which includes regions such as *rbcL, matK, trnL,* and *trnH-psbA*, as well as nuclear DNA, comprising regions ITS and ITS2. The Consortium for the Barcode of Life (CBOL) advocates for the use of *rbcL* and *matK* regions as the standard two-locus barcode for global plant databases due to their ability to differentiate species. DNA material for barcoding purposes can be extracted from fresh plant material as well as herbarium specimens.

By employing a combination of modern and classical botanical methods, molecular genetics, and bioinformatics, we analyzed the species diversity of vascular plants in the Kostanay Region. Subsequently, routes were carefully developed to ensure comprehensive coverage of the study areas, facilitating field expeditions aimed at studying the species diversity of the regional flora and collecting samples across various vegetative stages.

We utilized both herbarium specimens and fresh plant material to extract genomic DNA using various DNA extraction protocols. The DNA collection contains 250 plant samples. We employed commonly accepted gene regions, including *matK, rbcL,* and ITS, as markers for DNA barcoding to identify species of higher vascular and spore-bearing plants. In total, 70 species were sequenced and 190 sequences were deposited to NCBI across the three markers.

Therefore, utilizing three distinct DNA barcoding regions (ITS, *matK* and *rbcL)* facilitated the identification of species for studying the current status of plant diversity in the Kostanay region.

The research is conducted in the framework of the program BR18574125 with financial support from the Ministry of Science and Higher Education of the Republic of Kazakhstan (duration: 2023-2024).

DEVELOPMENT OF BIOTECHNOLOGY FOR *EX SITU* CONSERVATION OF RARE ENDANGERED *ROSACEAE* SPECIES

Romadanova N.V. ***[*1]*, *Zemtsova A.S.* [1], *Aralbayeva M.M.* [1], *Altayeva N.A.* [1], *Artimovich N.A.* [1], *Aleksandrova A.M.* [2], *Kushnarenko S.V.* [1]

[1] *Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan*
[2] *M.A. Aitkhozhin Institute of Molecular Biology and Biochemistry, Almaty, Kazakhstan*

E-mail: nata_romadanova@mail.ru

The purpose of this research is to develop a biotechnology for preserving *in vitro* and in a cryogenic bank germplasm of rare, endangered plant of the *Rosaceae* species, listed in the Red Book of Kazakhstan. The objects of the study were seeds of *Crataegus ambigua* C.A. Mey. ex A. Beck, *Louiseania ulmifolia* (Franch.) Pachom., *Malus sieversii* (Ledeb.) M. Roem., *Prunus tenella* Batsch, *Sibiraea altaiensis* (Laxm.) Schneid., and *Spiraeanthus schrenckianus* Maxim.

The seeds were surface sterilized with a solution of "Belizna" bleach diluted 1:1 for 5 minutes, washed with distilled water and placed: 1) for stratification in moist perlite at 4°C for 8 weeks with a light intensity of 10 μE $m^{-2}s^{-1}$, 16-hour photoperiod; 2) for stratification in plastic containers at 4°C for 8 weeks with a light intensity of 10 μE $m^{-2}s^{-1}$, 16-hour photoperiod; 3) germinated in perlite under standard conditions (25°C, light intensity 40 μE $m^{-2}s^{-1}$, 16-hour photoperiod); 4) germinated seeds or embryonic axes under standard conditions on Knop medium of the following composition: 1 g/L $Ca(NO_3)_2$, 0.25 g/L $MgSO_4*7H_2O$, 0.25 g/L KH_2PO_4, 0.125 g/L KCI, 27.8 mg/L $FeSO_4*7H_2O$, 37.3 mg/L $Na_2EDTA*2H_2O$, 1.75 g/L Gelrite™, 4 g/L agar, pH 5.7; 5) seeds or embryonic axes were germinated under standard conditions on Murashige and Skoog (MS) medium; with 30 g/L sucrose, 1 mg/L 6-benzylaminopurine (BAP), 0.1 mg/L indolyl-3-butyric acid (IBA), 1.75 g/L Gelrite™, 4 g/L agar, pH 5.7.

For *C. ambigua*, the percentage of germination was in the following variants: 1) 63.6%; 2) 54.3%; 3) 32.1%; 4) 28.0%. For *L. ulmifolia*: 2) 24.3%; 4) 8.0%. For *M. sieversii*: 1) 66.6%; 2) 64.3%; 3) 62.1%; 4) 63.1%; 5) 13.2%. For *P. tenella*: 2) 40.5%; 4) 26.4%. For *S. altaiensis*: 1) 52.2%; 2) 54.3%; 4) 28.3%. For *S. schrenckianus*: 1) 26.6%; 2) 24.3%; 4) 26.2%; 5) 0%. It should be noted that in all accessions, stratification at 4°C either increased or did not affect the percentage of seed germination; *in vitro* germination of seeds on MS medium gave consistently low germination results in the all variants.

Non-sterile shoots 1-2 cm in size obtained from seeds were cut and disinfected in a laminar air flow chamber in 0.1% solution of $HgCl_2$ for 3-5 minutes. After disinfection, the tips of the shoots were placed in the tubes with MS medium with various concentrations of phytohormones. Currently, the composition of the nutrient media for *in vitro Rosaceae* plants have been optimized. The most optimal for *C. ambigua*, *L. ulmifolia*, *M. sieversii* and *P. tenella* was MS medium with 0.5 mg/L BAP, 0.01 mg/L IBA. For *S. altaiensis*: MS with 1.0 mg/L BAP, 0.01 mg/L IBA. For *S. schrenckianus*, MS medium without the addition of growth regulators is optimal.

The creation of a cryogenic bank of seeds and DNA at -196°C has begun. Seeds from 12 *S. schrenckianus* accessions were placed in liquid nitrogen for long-term storage. Total DNA was isolated from leaves of *M. sieversii*, *S. persica* and *L. ulmifolia*, and DNA quality was tested using electropherograms. As a result, 20 DNA accessions of *S. persica*, 16 accessions of *M. sieversii*, and 6 accessions of *L. ulmifolia* were placed in a cryogenic bank for long-term storage.

Keywords: *Rosaceae*, seeds, embryonic axes, *in vitro* culture, cryogenic bank.

This research was funded by the Science Committee of the Ministry of Science and Higher Education of the Kazakhstan Republic AP19676010.

PROPAGATION AND CONSERVATION BY TISSUE CULTURE TECHNIQUE OF THE RARE SPECIES OF *RIBES JANCZEWSKII*

Nurtaza A.S. [1], ***Islamova S.S.*** [1,2], ***Samatova I.N.*** [1,2], ***Kakimzhanova A.A.*** [1]

[1] *National Center for Biotechnology, Astana, Kazakhstan*
[2] *L.N. Gumilyov Eurasian National University, Astana, Kazakhstan*

E-mail: nurtazaaidana6@gmail.com

Ribes janczewskii is an important and valuable species listed in the Red Book of Kazakhstan and the International Red List. The species holds significance for selection purposes, as it exhibits resistance to many negative biotic factors. The fruits are rich in high content of ascorbic acid, polyphenols, and anthocyanins. This currant species is an endemic, growing in limited ecosystems and facing the threat of extinction due to various anthropogenic and natural factors. Therefore, the conservation and propagation of *Ribes janczewskii* become a relevant task in the context of conserving the biodiversity of Kazakhstan.

In this study, young leaves and one-year-old shoots of *Ribes janczewskii* from natural populations growing within the territory of the "Sayram-Ugam" National Park were used as the research objects. Species identification of the selected samples was conducted using molecular-genetic markers *matK, rbcL* and *ITS*. For each sample, the consensus sequence was compared with nucleotide sequences in the NCBI, and inventory numbers were obtained for novel sequence data. To investigate intraspecific polymorphism among populations, genetic diversity was studied using the iPBS amplification profiling method.

To conserve the species under *ex vitro* conditions, a protocol for micropropagation has been developed. The stages of establishment of *in vitro* culture and micropropagation have been optimized. The WPM nutrient medium was selected with the addition of 0.25 mg/L 6-benzylaminopurine, 0.5 mg/L gibberellic acid, and 0.5 mg/L indole-3-butric acid for the propagation of additional shoots of *Ribes janczewskii*. The obtained microshoots were used to create an *in vitro* collection. For this purpose, a protocol for medium-term storage of shoots was optimized. Mannitol was chosen as the osmotic agent, allowing the microshoots to be stored for four months without intermediate culturing. Thus, the comprehensive research conducted enabled the study, propagation, and preservation of the rare and valuable *Ribes janczewskii* species.

The research is conducted in the framework of the project AR 14869409 with financial support from the Ministry of Science and Higher Education of the Republic of Kazakhstan (duration: 2022-2024).

ESTABLISHING AN *IN VITRO* COLLECTION OF KAZAKHSTAN WILD CHERRY SPECIES

Manapkanova U.A., Aralbayeva M.M., Rymkhanova N.K., Kushnarenko S.V.

Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan

* *E-mail:* ylzhanchikm@gmail.com

Cherry (*Rosaceae* family) is one of the most popular stone fruits in the world. Currently, 150 species of cherry are known, four species grow in Kazakhstan: *Prunus fruticosa* Pall., *P. erythrocarpa* (Nevski) Gilli, *P. griffithii* var. *tianshanica* (Pojark.) Ingram, *P. verrucosa* Franch.

Expedition trips were carried out to Zhambyl, Turkestan, Kostanay and Almaty regions and 87 accessions of cherry were collected.

Morphoanatomical study showed that seeds of wild cherry consist of three parts: the seed coat, the embryo (embryo axis and cotyledons) and residual endosperm. *In vitro* initiation of four wild cherry species has begun, surface disinfection was carried out using 0.1% mercuric chloride for 5 minutes, then material was washed with sterile distilled water 3 times for 1 minute. For *in vitro* culture initiation the embryo and embryo axis were used. Further observation showed that the most effective explant for initiation was embryo, due to fast, stable development. Six different media were tested for *in vitro* initiation and further micropropagation: Murashige-Skoog (MS) or Woody Plant Medium (WPM) with/without hormones (0.5 mg/L 6-benzylaminopurine (BAP) and 0.01 mg/L indolyl-3-butyric acid (IBA), 0.75 mg/L gibberellic acid (GA)). The optimal media for micropropagation was MS with 0.5 mg/L BAP, 0.01 mg/L IBA and 30 g/L sucrose, pH 5.7, the multiplication rate ranged from 3.6 to 4.8 depending on species.

Twenty-two accessions of four wild cherry species were initiated into *in vitro* culture, average of 29.8% tissue necrosis, fungal and bacterial contamination was found in 13.5% explants, the green plants percentage was 56.7%. The *in vitro* shoots were tested for endophytic contamination on a specialized medium 523, the samples were 100% aseptically clean. As a result, *in vitro* culture initiation and micropropagation was carried out, a collection of Kazakhstan wild cherry species was established. These wild cherry accessions have never been cultured before, so this study contributes to the preservation of valuable *Prunus* genetic resources.

Key words: cherry, *Prunus sp., in vitro* culture, micropropagation

This research was funded by the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan, Project No. AP19676481.

PLANT BIODIVERSITY AT THE ENBEKSHI MONITORING SITE IN THE ALMATY REGION

Aitzhan M.*, Inelova Z., Zaparina Ye.

al-Farabi Kazakh National University, Almaty, Kazakhstan

* *Email:* Aitzhan.mengtay@med-kaznu.com

Flora is not merely a random assortment of plant species in a given area; rather, it constitutes a complex assembly with its own internal structural patterns, geographical and genetic connections, all of which are influenced by various environmental factors. Kazakhstan, as a participant in the Convention on Biological Diversity, is obligated to preserve plant biological diversity. According to the UN Convention on Biodiversity, the initial step towards conservation is conducting an inventory. In the contemporary context, conducting an inventory of flora and natural plant resources, both at regional and national levels, and augmenting it with new information about beneficial properties, serves as the foundation for developing a scientifically based algorithm for the rational use of plant resources.

Despite numerous measures aimed at preserving biological diversity, plant biodiversity continues to face threats associated with rapidly advancing scientific and technological progress, increasing anthropogenic load, and the development of industry and transport communications. These factors contribute to the deterioration of the natural environment and disruption of the normal functioning of natural communities, ultimately leading to a reduction in biodiversity.

In this context, the objective of this study was to assess the species diversity of wild and forage plants in the village of Enbekshi, a location with a history of pesticide warehouses.

In the study area of the village of Enbekshi, we identified 121 species from 94 genera and 30 families, with the dominant families being *Asteraceae* (25 species or 20.66%, 19 genera), *Rosaceae* (15 species or 12.40%, 11 genera), *Brassicaceae* (12 species or 9.92%, 10 genera) among Dicotyledons, and *Poaceae* (13 species or 10.74%, 11 genera) among Monocots. The dominant families constitute 53.72% of the total number of plant species in this area. Leading genera include *Artemisia*, *Potentilla*, *Rumex*, and *Geranium*. No endemic species were identified.

The natural vegetation cover around the villages is degraded and is primarily represented by weed species such as cocklebur (*Xanthium strumarium*), brunette (*Sophora alopecuroides*), hemp (*Cannabis ruderalis* Janisch.), *Bassia scoparia* (L.) A.J.Scott, among others.

These areas with severe disturbances of phytocenoses are localized and do not cover large areas. The number of weed species identified is 78.

At the Enbekshi monitoring point, 33 forage plant species were identified. Representatives of the food species include *Bromus inermis* (Leyss.) Holub, *Rumex confertus* Willd., *Trifolium pratense* L., *Artemisia scoparia* Waldst. & Kit., *Stipa capillata* L., *Zea mays* L., *Chenopodium album* L., *Carduus nutans* L., *Carex physodes* Bieb., *Medicago sativa* L., etc.

In some areas, the replacement of forage species (cereals, wormwood) with weeds, plants of low nutritional value (*Xanthium strumarium*), and poisonous species (*Sophora alopecuroides*) was observed.

This research was funded by the Science Committee of the Ministry of Education and Science of the Republic of Kazakhstan (Grant No. BR05236379) for 2018-2020.

COMPARATIVE CHARACTERIZATION OF THE PLASTID GENOME SEQUENCES OF FOUR *CAROXYLON* SPECIES FROM KAZAKHSTAN

Almerekova S.[1], Yermagambetova M.[1], Osmanali B.[2], Vesselova P.[2], Abugalieva S.[1], Turuspekov Y.*[1]

[1] Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan
[2] Institute of Botany and Phytointroduction, Almaty, Kazakhstan

* *Email:* yerlant@yahoo.com

The Chenopodiaceae Vent. is one of the largest and oldest plant families found in desert and semi-desert regions across the globe (Kadereit, 2005; Müller & Borsch, 2005). With an approximate count of 1700 species spread across approximately 110 genera (Kadereit et al., 2003), the Chenopodiaceae family holds significant ecological importance in desert ecosystems. These plants serve as essential food sources for herbivores and play a vital role in soil stabilization (Osmonali et al., 2022). Despite numerous studies attempting to delineate the taxonomy of this family, utilizing both morphological traits and molecular genetic methods, a precise taxonomy remains elusive (Akhani et al., 2007).

In this study, we compared various genomic features, nucleotide diversity, and repeat sequences, alongside conducting a phylogenetic analysis of Salsoleae s.l. species. Each analyzed plastid genome contained 133 genes, comprising 114 unique genes, including 80 protein-coding genes, 30 tRNA genes, and 4 rRNA genes. Within the Salsoleae s.l. plastid genomes, eight distinct regions (accD, atpF, matK, ndhF-ndhG, petB, rpl20-rpl22, rpoC2, and ycf3) displaying significant divergence were identified, which may serve as DNA barcoding markers. Additionally, various repeat elements were detected, encompassing simple sequence repeats, tandem repeats, forward repeats, palindromic repeats, and reverse repeats. The phylogenetic analysis provided robust support for the relationships among Caroxylon species. This data constitutes a valuable resource for conducting future phylogenetic studies within the genus.

This research is funded by the Science Committee of the Ministry of Education and Science of the Republic of Kazakhstan (Grant No. AP14869593).

References:

Kadereit, G. (2005). Origin and age of Australian Chenopodiaceae. Organisms Diversity & Evolution, 5(1), 59–80. doi:10.1016/j.ode.2004.07.002

Müller, K., & Borsch, T. (2005). Phylogenetics of Amaranthaceae Based on matK/trnK Sequence Data: Evidence from Parsimony, Likelihood, and Bayesian Analyses. Annals of the Missouri Botanical Garden, 92(1), 66–102. http://www.jstor.org/stable/3298649

Kadereit, G., Borsch, T., Weising, K., & Freitag, H. (2003). Phylogeny of Amaranthaceae and Chenopodiaceae and the evolution of C4 photosynthesis. International journal of plant sciences, 164(6), 959-986.

Osmonali B. B., Vesselova P. V., Kudabayeva G. M., Akhtayeva N. Z. Phytocenotic features of species of the genus *Salsola* L. (Chenopodiaceae Vent. / Amaranthaceae Juss.) in the desert part of the Syrdarya river valley // Bulletin of the Karaganda university. Biology. Medicine. Geography series, 2022. – № 1(105). P. 78–85. DOI: 10.31489/2022BMG1/78-85

Akhani, H., Edwards, G., & Roalson, E. H. (2007). Diversification of the old world Salsoleae sl (Chenopodiaceae): molecular phylogenetic analysis of nuclear and chloroplast data sets and a revised classification. International Journal of Plant Sciences, 168(6), 931-956.

STUDY OF BIODIVERSITY OF THE RARE ENDANGERED SPECIES *PRUNUS ARMENIACA* L. AND *EX SITU* CONSERVATION OF GENOTYPES WITH VALUABLE ECONOMIC AND BIOLOGICAL TRAITS

Altayeva N.A., Aralbayeva M.M., Zemtsova A.S., Kushnarenko S.V., Romadanova N.V.

Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan

* *E-mail*: altnazira@gmail.com

The mountains of southeast Kazakhstan are unique in their richness of wild fruit plants. About 130 species grow here, including *Prunus armeniaca* L. Common apricot is the only representative of the apricot genus in Kazakhstan; it is a rare species with a sharply shrinking range, which is listed in the Red Book of Kazakhstan. Academician V.L. Komarov points out that the ancestor of the cultivated apricot should be considered precisely this Tien Shan wild apricot, which, together with the apple, forms forests in the mountains and foothills. Wild apricots are characterized by increased winter hardiness, have exceptional polymorphism in ripening time, fruit quality, long dormant period, high winter hardiness of flower buds and wood, and disease resistance. In connection with the above, apricots are the most valuable material for breeding. Purpose of the study was creation of an *in vitro* collection of *P. armeniaca* to obtain planting material that will be used in restoring the ecology of natural habitats.

Embryonic axes isolated from apricot seeds after stratification for 8 weeks at 4°C were used as explants for *in vitro* initiation. The seeds, peeled from the hard shell, were sterilized with a solution of commercial bleach ¼ "Belizna" for 4 min, followed by rinsing in running water for 5 min. Then, in a laminar flow hood, sterilization was carried out in a 0.1% $HgCl_2$ solution for 3 min, followed by three rinses with sterile bidistilled water. The isolated embryonic axes were placed on two media: 1) Knop (1 g/L $Ca(NO_3)_2$, 0.25 g/L $MgSO_4*7H_2O$, 0.25 g/L KH_2PO_4, 0.125 g/L KCI, 27.8 mg/L $FeSO_4*7H_2O$, 37.3 mg/L $Na_2EDTA*2H_2O$, 1.75 g/L Gelrite™, 4 g/L agar, pH 5.7) and 2) Murashige-Skoog (MS) with 30 g/L sucrose, 1 mg/L 6-benzylaminopurine (BAP), 0.1 mg/L indolyl-3-butyric acid (IBA), 1.75 g/L Gelrite™, 4 g/L agar, pH 5.7. A total of 143 embryonic axes (10 apricot accessions) were *in vitro* initiated. The first sprouts appeared on Knop medium on the 3rd day, on MS medium on the 6th day. The percentage of laboratory germination varied on Knop medium from 75.0% to 91.2%, and on MS medium from 53.3% to 82.4%. Obtained *in vitro* plants were tested for the presence of endophytic contamination on a specialized medium 523 for the detection of fungi and bacteria: 10 g/L sucrose, 8 g/L casein hydrolysate, 4 g/L yeast extract, 2 g/L KH_2PO_4, 0.15 g/L $MgSO_4*7H_2O$, 6 g/L Gelrite™, pH 6.9. As a result, endophytic contamination was detected only in accession No. 42. For micropropagation, MS medium with different composition and concentration of growth regulators was used: 1) 0.5 mg/L BAP, 0.1 mg/L IBA; 2) 1 mg/L BAP, 0.1 mg/L IBA, 0.1 mg/L gibberellic acid. Vigorous plant growth was noted on both variants of the medium, the multiplication rate on the 2nd variant was slightly higher – 4.0; on the 1st variant – 3.4. Further optimization of the medium is planned.

Keywords: *Prunus armeniaca* L., *in vitro* initiation, embryonic axes, micropropagation, *in vitro* collection.

The work was carried out within the framework of the project: BR21882024 "Study of biodiversity and development of methods for *ex situ* conservation of genetic resources of fruit and nut plants", project 0123PK01118 "Study of biodiversity of the rare endangered species *Prunus armeniaca* L. and *ex situ* conservation of genotypes with valuable economic and biological traits".

DEVELOPMENT OF MICROPRPAGATION AND CRYOPRESERVATION TECHNIQUES FOR CONSERVATION OF RARE ENDANGERED SPECIES *CORYLUS AVELLANA* L.

***Aralbayeva M.M.*[1], Rymkhanova N.K.[1], Manapkanova U.A.[1], Amirova A.K.[2], Kushnarenko S.V[1]**

[1] *Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan*
[2] *al-Farabi Kazakh National University, Almaty, Kazakhstan*

E-mail: berim.moldir@mail.ru

European hazelnut (*Corylus avellana* L.) is one of the most economically important nut crops. In Kazakhstan, *C. avellana* wild population has been registered in the west region and protected in the "Dubrava" State Botanical Reserve along the Zhaiyk River (Ural River). A survey of this population was carried out in 2018-2023 and the unsatisfactory condition of the plants was revealed. In 2018, only 30% of plants had fruits that were collected for *in vitro* culture initiation using isolated embryonic axes as explants. No fruiting plants were found during the survey in 2023 and annual shoots were collected to initiate *in vitro* culture. *In vitro C. avellana* shoots were propagated on modified Driver and Kuniyki walnut medium (DKW) with 1 mg/L 6-benzylaminopurine (BAP), 0.01 mg/L indolbutyric acid (IBA), 4.0 g/L agar, 1.75 g/L gerlite, pH 5.7. Shoot cultures were maintained in a growth room at 24±1°C with light intensity of 40 μmol•m^{-2}•s^{-1}, photoperiod 8/16 hours.

After successful micropropagation, cryopreservation technique for shoot tips isolated from *in vitro*-grown *C. avellana* shoots was developed. The main purpose of the study was to determine the effect of cold acclimation duration (0-5 weeks) with alternating temperatures (8 h at 22°C, light intensity 10 μmol $m^{-2}s^{-1}$ / 16 h at -1°C, in the dark) on shoot tip regrowth after cryopreservation by PVS vitrification. Shoot tips (1.8-2.0 mm) were dissected from *in vitro*-grown shoots of *C. avellana* wild accessions. Regrowth of cryopreserved shoot tips increased and was significantly higher ($P < 0.05$) after 4-5 weeks cold acclimation. For three accessions tested, the highest regrowth ranged between 50-55% after 4 weeks cold acclimation and 80 min of PVS2 exposure. Micropropagation and cryopreservation techniques will allow for the propagation and preservation of rare endangered species *C. avellana* L. valuable material, which will make it possible to restore the only degraded population in Kazakhstan.

Key words: *Corylus avellana* L., micropropagation, *in vitro* culture, cold acclimation, shoot tips, PVS2 vitrification, cryopreservation

This research was funded by the Science Committee of the Ministry of Science and Higher Education of the Kazakhstan Republic (Scientific and technical program BR21882024).

MONITORING OF VIRAL DISEASES OF POTATO IN KAZAKHSTAN

Argynbayeva A. [1,2]***, Daurov D.***[2]***, Daurova A.***[2]***, Sapakhova Z.***[2]***, Shamekova M.***[2]

[1] *Kazakh National Agrarian Research University, Almaty, Kazakhstan*
[2] *Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan*

E-mail: asselargynbayeva@gmail.com

Potato (*Solanum tuberosum* L.) is one of the main food crops worldwide, including in Kazakhstan. According to the Bureau of National Statistics, the average per capita consumption of potatoes in Kazakhstan is 44.975 kg per year per capita, i.e. potatoes are still the second bread for Kazakhstanis.

The sown area of potatoes in the Republic of Kazakhstan for 2023 amounted to: 187.8 thousand hectares, with gross yield: 3788.1 thousand tons, and potato yield: 20.5 tons/ha.

The volume of annual potato production in the world market is increasing every year, this shows that the importance of potato production for food security makes more sense than ever.

The study is devoted to identification of phytosanitary status of potato virus diseases in Kazakhstan and creation of potato virus distribution map.

Viral diseases are a major constraint to sustainable potato production, as they cause large losses in crop quantity and quality. To determine the current status of potato production in Kazakhstan, we studied tuber and leaf samples in large seed and commercial farms of the Republic. Samples of tuber and leaf samples randomly sampled according to international potato field inspection methods as well as the international EPPO protocol were tested for five main viruses: potato virus Y (PVY), potato virus X (PVX), potato virus M (PVM), potato virus S (PVS), and potato leafroll virus (PLRV). A multiplex reverse transcription polymerase chain reaction (mpRT-PCR) was used to monitor viral infection. During the monitoring of tuber samples, it was found that the most common virus in almost all regions was the PVS virus at 64.5%. Moreover, most of the viruses originated in commercial farms. As a result of the analysis of leaves selected in the fields, it was found that the most common viruses in the regions were PVM at 46% and PVS at 35.3%. The work performed to monitor viral diseases in various regions of Kazakhstan will enable direct actions to maintain and improve the phytosanitary status of potatoes in Kazakhstan in the future.

MONITORING THE SPREAD OF *JUGLANS REGIA* L. IN THE SOUTHERN AND SOUTHEASTERN REGIONS OF KAZAKHSTAN AND MORPHOLOGICAL STUDY OF WALNUT FRUITS

Bakhytuly K., Kokhmetova A., Kumarbayeva M., Keishilov Zh., Kokhmetova As., Mukhametzhanov K.

Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan

Email: kanat1499@gmail.com

Walnut (*Juglans regia L.*) is one of the main nut crops of world importance. The conservation and effective use of walnut genetic resources is one of the fundamental principles of breeding work. Today, China, the United States, and Iran are the largest producers of walnuts, accounting for more than 74.7% of global production. In general, the global production of walnuts has grown by almost 250% over the past 20 years. According to FAO statistics, the annual production of walnuts in the world is approximately 3.74 million tons. In Kazakhstan in 2016, according to the Statistics Committee, nuts were grown in an area of 414.9 hectares. This, of course, is not enough.

Morphological studies have an important role in plant breeding. Plant breeding has led to increased uniformity of crops in the world, contributing to increased genetic vulnerability to biotic and abiotic stresses. For these reasons, it is important to better understand the impact of modern plant breeding on genetic diversity. Similarly, prudent management of this diversity can provide valuable assistance to breeders. The diversity of germplasm is usually assessed using morphological descriptors. This is usually the first step in the classification and description of germplasm and in the study of the heritability of traits for a new breeding program and the selection of superior genotypes. Thus, morphological studies provide a direction for choosing from varieties suitable for specific growing conditions. The distribution of *Juglans regia L.* in the southern and southeastern regions of Kazakhstan was monitored; phenotyping and nut fruit quality indicators were studied. As a result of the expedition work, a collection of 60 walnut samples was formed. The collection of wild specimens was carried out on the territory of the Ugam branch of the Sayram-Ugam State National Natural Park. 30 walnut trees of various age groups have been described by international descriptors. 7 trees were described on the territory of Mashat village, Tulkubassky district of Turkestan region. Ten trees were found near the village of Sarkyrama in the Saryagash district of Turkestan region. Seven samples were examined in the Kyrgyz Republic. Six walnut trees have been described on the territory of the Almaty region. Herbarium material and fruits of the *Juglans regia L.* walnut (60 genotypes) were collected from all trees, indicating the geographical coordinates of the collection site based on GPS. Walnuts were collected from 57 fruit-bearing trees (95% of the collection) to study the morphological characteristics of the fruits. The diversity of the collection in shape, size, and color of fruits was noted. The quality of walnut fruits was studied according to the main characteristics and criteria of the quality and productivity of the walnut kernel; six of the most productive by weight and yield of the kernel were selected. Based on the obtained data from the collection phenotyping, a dendrogram was constructed using the Ward method. In assessing the diversity, the studied walnut samples were grouped into five clusters according to the phenotypic characteristics of the walnut collection. In the future, thanks to this research work, it will be possible to study the genetic diversity of the walnut, which will help determine different varieties, disease resistance, adaptation to different climatic conditions, and other valuable genetic characteristics of the walnut.

This research has been funded by the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan (Grant No. BR21882024).

INVENTORY AND MAPPING OF THE FLORA OF UZBEKISTAN AND MAINTAINING THE STATE CADASTER

Beshko N.Yu., Turginov O.T.

Institute of Botany, Tashkent, Uzbekistan

E-mail: natalia_beshko@mail.ru

A total of 4,148 species is given in the six-volume first edition of the "Flora of Uzbekistan" (1941–1962), including 3,663 native and 485 non-native species (aliens together with cultivated crops and ornamentals). Since the publication of this fundamental treatment, a lot of botanical findings have been made and many new plant species and even genera have been described. In this connection, the Institute of Botany of the Academy of Sciences of the Republic of Uzbekistan launched a large-scale international project dedicated to the publication of a new edition of the national flora. The first six volumes of the new edition of Flora of Uzbekistan containing treatments of 20 families with 184 genera and 820 species (about 19% of flora) have been published in 2016–2023; herbarium specimens are cited and distribution maps based on their georeferencing are given for each species.

At the same time with the fundamental taxonomical revision of the flora, the Institute of Botany performed several scientific projects targeted to the step-by-step inventory and mapping of flora of the administrative regions of Uzbekistan and compilation of the state cadaster of threatened plants. At the present, the inventory of the flora of Bukhara, Dzhizak, Kashkadarya, Navoi, Samarkand and Tashkent regions was completed. The flora of Bukhara Region includes 764 species of vascular plants, 25 species of them are listed in the Red Data Book of Uzbekistan. The check-list of the flora of Dzhizak Region includes 1991 species (50 nationally red-listed); 2022 plant species are reported for Kashkadarya Region (88 species are red-listed at the national level); the check-list of the flora of Samarkand Region includes 1687 species (53 nationally red-listed). The richest is the flora of Tashkent Region that consists of 2344 species of vascular plants, or more than 53% of the flora of Uzbekistan and 25% of the flora of Central Asia, including 71 species listed in the Red Data Book of Uzbekistan. The inventory of flora of Surkhandarya Region is still in progress, 2152 species are recorded in total. A new project devoted to the flora of Syrdarya Region started recently. To date, only 515 species are revealed for this administrative region almost entirely occupied by anthropogenic landscapes. The following information for each species is provided in these floristic checklists: life form, habitat, distribution, conservation status, and economic use.

A new area of botanical research in Uzbekistan is the grid mapping of plant species distibution based on georeferenced herbarium specimens and field data. Thus, 62,204 occurrence records of 2152 species were georeferenced for Surkhandarya Region divided into 884 grid cells (5x5 km). Another example is a recently completed project focused on an inventory and grid mapping of the urban flora of Tashkent and Bukhara. As a result of this project, 620 plant species were recorded in Tashkent city and mapped using 1x1 km cells (591 cells in total), and 208 species were identified for the urban flora of Bukhara city divided into 85 cells. The species richness and collection density patterns were analyzed.

Some studies focused on the inventory of alien plants also have been conducted in Uzbekistan, and the results have been summarized in the national check-list of 228 naturalized and invasive alien species published in 2018 in GBIF. During the last five years, a number of new adventive species was recorded as a result of researches devoted to the inventory of the flora of administrative regions of Uzbekistan and publication of a new national "Flora". Some native weedy species were mistakenly considered adventive in the first version of the above mentioned check-list, and their status should be corrected. In this regard, the national check-list of naturalized and invasive alien species is currently being revised and updated.

ASSESSMENT OF THE GENETIC DIVERSITY OF LYMANTRIA DISPAR USING RAPD MARKERS

***Dairbekova Z.*[1,2], *Kolchenko M.*[1], *Taskuzhina A.*[1,2], *Kostyukova V.*[1], *Gritsenko D.*[1]**

[1] *Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan*
[2] *al-Farabi Kazakh National University, Almaty, Kazakhstan*

**E-mail*: dairbekovaz2001@gmail.com

The gypsy moth (*Lymantria dispar*) is a hazardous forest pest, listed among the "100 worst invasive species in the world." This species poses a significant threat as it can consume over 400 species of trees, potentially leading to the depletion of vast forest resources. The most well-known subspecies include *Lymantria dispar dispar*, *Lymantria dispar asiatica*, and *Lymantria dispar japonica*. Females of the latter two subspecies possess the ability for long-distance flight, thereby elevating the risk of their global dissemination.

Identifying the subspecies at the early stages of moth development is a crucial objective in managing the distribution of this pest. Evaluating genetic diversity will facilitate the assessment of subspecies hybridization levels and determine the genetic potential for evolution. To understand the genetic diversity of moths distributed in Kazakhstan, we employed randomly amplified polymorphic DNA (RAPD) markers, which revealed a high level of polymorphism. Five universal RAPD markers AB1-4, AB2-2, AB6-15, AB9-3, and UBC278 were chosen.

A total of 83 samples were collected from the territory of the Almaty region. The results of the study using markers AB1-4, AB2-2, AB6-15, and UBC278 demonstrated substantial genetic diversity. The number of amplified fragments ranged from 1 to 12, with sizes varying between 410 and 2200 bp. However, the AB9-3 marker did not exhibit genetic diversity, as all samples displayed only one amplified fragment. In this study we for first time evaluated AB1-4, AB2-2, AB6-15, and UBC278 markers for population genetics of *Lymantria dispar*.

CONSERVATION OF WILD POPULATIONS OF VALUABLE *PYRUS* SPECIES RESISTANT TO PATHOGENS USING *IN VITRO* CULTURE

Dyussembekova D., Kakimzhanova A.

National Center for Biotechnology, Astana, Kazakhstan

E-mail: dussembekova.damira@gmail.com

Pear, one of Central Asia's oldest fruit crops and second only to apple among pome crops, boasts a diverse array of wild species and cultivated varieties. Central Asia serves as a hotspot for the speciation of the *Pyrus* L. genus, with wild pear species offering valuable allelic diversity for breeding programs, providing resistance and tolerance to various stresses.

Notable varieties include the *Pyrus regelii* from Kazakhstan, prized for its economic value and exceptional drought resistance, ideal for afforestation in arid regions with poor soil conditions. The *Pyrus ussuriensis*, native to the Russian Far East, Manchuria, and Japan, stands out for its remarkable winter hardiness, making it a favored choice for breeding programs.

While pears naturally reproduce via seeds and cuttings, biotechnological methods offer efficient means to produce virus-free planting material identical to the parent plant. Preservation techniques such as in vitro culture and cryopreservation in liquid nitrogen ensure long-term storage of germplasm, safeguarding valuable genetic resources against loss.

To preserve biodiversity and create new pear varieties that are resistant to disease, wild genotypes of the *P. regelii* were selected in the Sayram-Ugam State National Natural Park and the *P. ussuriensis* in the Botanical Garden of Astana. Selection of pathogen-resistant genotypes was carried out using molecular markers RAPD and SSR. 3 resistant populations of *P. regelii* and 4 resistant populations of *P. ussuriensis* were selected. These populations were used for further studies.

To preserve wild pear genotypes *in vitro,* the method of micropropagation was used. The first step is sterilization and establishment *in vitro* culture. To effectively sterilize the *P. regelii*, 12% H_2O_2 was used for 5 minutes; with this sterilization, the viability of the explants was 70%. For *P. ussuriensis*, sterilization with 10% “Belizna” for 15 minutes was effective - 60% of explants proved to be viable.

For the establishment *in vitro* culture of *P. regelii*, the optimal composition of the nutrient medium was shown by DKW (Juglans medium) with the addition of BAP (6-Benzylaminopurine) - 1.5 mg/l. For *P. ussuriensis* WPM (Woody Plant Medium) and DKW with BAP – 1.0 mg/l. With these options, a formed main shoot was formed, without callus and vitrification of leaves.

Thus, a collection of pathogen-resistant wild genotypes of *P. regelii* in the amount of 500 microshoots and *P. ussuriensis* in the amount of 150 microshoots was created.

The research is conducted in the framework of the program BR21882024 with financial support from the Ministry of Science and Higher Education of the Republic of Kazakhstan (duration: 2023-2025).

BRACHYPODIUM DISTACHYON AS A MODEL PLANT FOR ASSAY THE PATHOGENICITY OF *FUSARIUM* FUNGI PRODUCING T-2/HT-2 TOXINS TO SMALL GRAIN CEREALS

Gavrilova O.P., Gagkaeva T.Yu.

All-Russian Institute of Plant Protection (VIZR), St. Petersburg, Russia

E-mail: olgavrilova1@yandex.ru

In recent years, the grass *Brachypodium dystachion* (Bd) has been actively used as a model to assess the interaction between host plant and pathogenic fungi, including *Fusarium* (Peraldi et al., 2011; Tancic, 2017; Dinolfo et al., 2021). The process of small grain cereals infection with weakly aggressive *F. langsethiae* and *F. sibiricum* fungi, producing the T-2/HT-2 toxins (T-2/HT-2), still remains poorly studied. Inoculation with these fungi of plants does not lead to the appearance of visually noticeable disease symptoms (Martin et al., 2018; Aamot et al., 2022; Somma et al., 2022), but results in the mycotoxins accumulation in the grain.

The aim of study was to evaluate the response of two lines Bd 21 and Bd 3-1 to infection with *F. langsethiae* or *F. sibiricum* strains in laboratory conditions. Plants were sprayed with the fungal conidial suspensions, and quantitative infection parameters were analyzed in the obtained grain. The amounts of fungal DNA and T-2/HT-2 in grain were estimated using real-time PCR and ELISA, respectively.

In the grain of all inoculated plants, *F. langsethiae* DNA (0.4–13.3 ng/ng) or *F. sibiricum* DNA (0.5–56.9 ng/ng), as well as T-2/HT-2 (124–3797 μg/kg) were detected. At Bd inoculation with *F. langsethiae* strains the amount of T-2/HT-2 in grain was significantly lower (on average 729 μg/kg) than in case of the plant inoculation with *F. sibiricum* strains (2081 μg/kg). The Bd 21 line was more susceptible to infection by fungi, especially *F. sibiricum*, than the Bd 3-1 line. However, the average amount of T-2/HT-2 in the Bd 21 grain was 3 times lower than in the Bd 3-1 grain.

Thus, *B. distachion* is a promising model plant for studying the interaction of *Fusarium* species with cereals, especially due to a short generation time (2 months) and prolific seed production through self-pollination.

The study was supported by the Russian Science Foundation (project № 19-76-30005).

PRESERVATION POTENTIAL: EXPLORING CRYOPRESERVATION TECHNIQUES FOR *EUONYMUS KOOPMANNII*

Gubaidullin N., Manabayeva S*

National Center of Biotechnology, Astana, Kazakhstan

* *E-mail:* manabayeva@biocenter.kz

Cryopreservation is a crucial strategy for preserving the genetic diversity of endangered plant species, safeguarding them against the threats posed by climate change and human activities. This study focuses on *Euonymus koopmannii* Lauche, a protected botanical species found in various regions globally, particularly in Aksu-Zhabagly nature reserve in Kazakhstan, and listed in the Red Book of the country. *E.koopmannii* is at risk of extinction despite its ecological significance and ornamental value. This research aims to aid conservation efforts by developing an effective cryopreservation protocol for its meristematic tissues.

The optimized cryopreservation procedure for *E. koopmannii* meristems was determined through experiments involving sucrose concentration and treatment duration. A sucrose concentration of 0.3M resulted in the highest survival rate (56.7%). A 30-minute treatment with PVS2 cryoprotectant yielded the most effective post-thaw viability (93.02%). Furthermore, a recovery medium containing MS with 20 g/L sucrose demonstrated superior efficacy with a survival rate of 54.7±2.4%. Cryopreservation influenced cellular regeneration, requiring multiple passages for complete recovery of plant components. Although the height was reduced, the cryopreserved regenerants showed an increase in shoot number and root development compared to the control group. However, cryopreserved specimens showed a discernible trade-off between vegetative growth and root development.

This study's refined cryopreservation protocol provides valuable insights into the preservation and regeneration of *E.koopmannii* meristems. The text highlights the importance of precise treatment modalities and nutrient medium composition in facilitating successful cryopreservation and subsequent tissue culture-based regeneration. This research contributes foundational knowledge essential for the conservation of *E.koopmannii* by elucidating these intricacies.

RECOVERY OF REPRESENTATIVES OF THE GENUS *AEGILOPS* L.

***Imirsinova A.*[1], *Kurbanova M.*[2], *Rustamov A.*[1]**

[1] *National University of Uzbekistan. Tashkent, Uzbekistan*
[2] *Andijan State University. Andijan, Uzbekistan*

In the course of the research, the geographical distribution of representatives of the *Aegilops* L. genus throughout the Fergana Valley, the seed reserve in the cenopopulations, and the regeneration from the seed were determined. A GIS map and species composition were determined based on the data obtained throughout the Fergana Valley. Among the species studied is *Aegilops crassa* Boiss. We observed that the ecological range of Fergana Valley is somewhat limited. This species was found only in the Khojabad district of Andijan region, Imam ota hillsides (940032'47.66"N, 72036'21.8"E, at an altitude of 807 m above sea level, at a latitude of 2010 south-west). The number of bushes was small, 19 per 1 m^2.

In recent years, the genus *Aegilops* L. has been the most intensively studied group of grasses, especially since its close relationship with wheat cultivars was discovered. In particular, it helps to improve complex traits such as abiotic tolerance for drought and heat, in increasing the productivity of wheat varieties. Therefore, studying the influence of climatic conditions on the change of the biological characteristics of the species of the genus, their geographical distribution in the Ferghana Valley is of great scientific and practical importance.

In recent years, many countries of the world have created National programs for the conservation of plant genetic resources. The basis of these programs is the preservation of species in situ. To date, the importance of the problem of preserving wild relatives of cultivated plants "in situ" in Uzbekistan is very great, and their comprehensive systematic analysis has not been fully covered. Human activities in agriculture and urbanization processes lead to the genetic erosion of wild relatives of cultivated plants. *Aegilops* L. family *Poaceae* Barnh. is considered one of the important categories of the family. The representatives of this group deserve attention because they are of great importance in creating useful genes in wheat varieties and in animal husbandry. In recent years, the genus *Aegilops* L. has been the most intensively studied group of grasses, especially since its close relationship with wheat cultivars was discovered. In particular, it helps to improve complex traits such as abiotic tolerance for drought and heat, in increasing the productivity of wheat varieties. Therefore, the study of the biological characteristics of the species of the series, and their geographical distribution is of great scientific and practical value. Such studies allow determining ways to preserve various ecological and biological diversity of plants.

At the same time, by studying the modern cenopopulation status and geographical distribution of these plants in different natural areas of the Fergana Valley, it is possible to assess the current status of representatives of the genus (*Aegilops* L.) throughout the valley and develop strategies for restoring cenopopulations.

Today, biomorphological and population studies are widely used in the world's leading scientific research centers to solve the issues of plant biodiversity conservation.

Among the studied regions, in Andijan and Fergana regions of the Fergana Valley, due to the increase of anthropogenic influence, the soil seed reserve of the representatives of the genus and the self-regeneration of species from it to the generative stage gives a somewhat low indicator. Therefore, it is important to preserve the representatives of this group in natural ecotopes, where the representatives of this group have acquired specific adaptations over the years.

Aegilops crassa Boiss. distribution in the Fergana Valley is somewhat limited, this species was found only in the Khojabad District of Andijan Region, Imam Ota hillside (940032'47.66"N, 72036'21.8"E, at an altitude of h-807 m above sea level, at a latitude of 2010 in the southwest).

FIRES AS A FACTOR AFFECTING FLORA AND ITS BIODIVERSITY

Issayeva D.A.

Kostanay Regional University named after Akhmet Baitursynuly, Kostanay, Kazakhstan

E-mail: dinar.issayeva@gmail.com

The impact of fires on plants is determined by various factors including fire intensity, plant species and their stage of development. Negative consequences of fires include the destruction of vegetation, damage to root systems, stems, leaves, and seeds, as well as alteration of soil cover, which can lead to biodiversity loss, soil degradation, and reduced fertility hindering ecosystem recovery. However, some plants possess adaptive mechanisms, such as sprouting from dormant buds, seed dispersal from specialized structures, or regeneration from residual root systems, enabling them to survive or recover after a fire. Fires can also contribute to competitor removal, reduction of vegetation density and creation of conditions for ecosystem renewal, promoting species diversity enrichment and improvement of vegetation condition.

In early studies on the impact of fires on plants including the works of N. Sushkina (1931), it is noted that fires contribute to the natural regeneration of coniferous trees (*Pinus sylvestris*), emphasizing their importance in the regeneration of forest ecosystems. In recent research, such as that by A. Geraskina (2021) the positive influence of fires on the biodiversity of forest ecosystems is underscored, along with their role in the formation and evolution of forest biota. According to a study by Santacruz-García et al. (2021) it was found that shrub species like *Acacia emarginata, Sargassum johnstonii* and *Celtis ehrenbergiana* exhibited a higher capacity for germination after the occurrence of fires, whereas woody species like *Sarcomphalus mistol*, *Schinopsis Lorentzii* and *Aspidosperma quebracho-blanco* showed reduced germination ability. These results may be associated with the size and height of shoots. Additionally, the research showed that the physical stress induced by fires stimulates plants to increase the production of secondary metabolites such as terpenoids and phenolic compounds, which play an important role in regulating germination capacity after fires. As a result of the studies, it was determined that tannins play a key role in detoxification mechanisms, contributing to increased plant survival in the post-fire period.

For a deeper understanding of the mechanisms of fires' impact on plants, soil microbiome and biodiversity research, utilizing modern molecular biology methods is necessary. This will help improve understanding of the impact of fires on forest ecosystems which is important in the context of a changing climate and the impact of human activity.

Scientific supervisors: G.Zh. Sultanagazina, Candidate of Biological Sciences, Professor of the Department of Biology, Ecology, and Chemistry at Kostanay Regional University named after Akhmet Baitursynuly, T.M. Yergaliev, PhD

ASSESSING THE RESPONSE OF WILD TREES IN THE TIAN SHAN REGION TO CLIMATE CHANGE OVER THE PAST TWO DECADES

***Khusnitdinova M.*[1], *Taskuzhina A.*[1,2], *Kerimbek N.*[1,2], *Pozharskiy A.*[1], *Nizamdinova G.*[1], *Gritsenko D.*[1]**

[1] *Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan*
[2] *al-Farabi Kazakh National University, Almaty, Kazakhstan*

* *E-mail*: germironame@gmail.com

The variations in the normalized difference vegetation index (NDVI) primarily depend on changes in climatic factors such as precipitation and temperature. In this study, our focus was on assessing the inter-annual variation in the normalized difference vegetation index (NDVI) of wild trees in the Tian Shan region, particularly within the Ile Alatau State National Natural Park (SNNP), spanning from 2006 to 2023, with a specific emphasis on data collected in August. NDVI values and their classification were derived from Landsat images, specifically Landsat 4-5 and Landsat 8-9. The Landsat images were processed using the QGIS software. Temperature and precipitation data were obtained from the gridded monthly time series provided by the Kazakhstan Meteorological Database, specifically from weather stations located in the study area, including Assy, Almaty (Kamenskoe plato), Esik, Shelek, BAL, and Mynzhylky. In the results, we developed maps depicting NDVI values for the SNNP, as well as diagrams illustrating the inter-annual variation of NDVI, precipitation, and temperature. Furthermore, we conducted analyses to investigate the variations and trends in NDVI response to climate factors using regression models. On average, NDVI values of wild trees in the study area ranged from 0.29 to 0.47, with maximum values approaching 0.50-0.55. The relationship between climatic factors and NDVI values was analyzed using simple linear regression and correlation coefficient analysis.

The results reveal that NDVI is positively correlated with precipitation and shows little correlation with temperature. The trends observed in NDVI time series are crucial indicators of the risk of declining growth in wild tree forests. In the years 2006, 2008, 2012, 2014, 2016, 2021, and 2022, low NDVI values were observed, which were closely correlated with precipitation levels. The brief intervals between unfavorable years may lead to genetic erosion within wild tree populations. These results underscore the importance of preserving biodiversity among wild trees, particularly by considering the trends in vegetation responses to climate change.

DETECTION OF ACLSV AND ASPV IN SEEDS OF POME FRUIT CROPS AND ASSESSMENT OF THE LIKELIHOOD OF VIRUS TRANSMISSION BY SEEDS

Kukharchyk N., Kolbanova E., Bazhydai T.

Institute for Fruit Growing, Minsk Region, Belarus

E-mail: kychnataly@rambler.ru

The analysis of scientific literature shows that the data on the transmission of viruses by seeds is ambiguous. It was previously believed that in pome crops viruses are not transmitted by seeds. Therefore, in the production system of healthy planting material, seedling rootstocks of apple and pear trees were classified as virus-free without additional tests.

The current study was conducted to evaluate whether some viruses of pome fruit crops (ACLSV, ASPV) are seed transmitted.

The research was carried out from 2021 to 2023 as part of the State Scientific Research Program «Agricultural Technologies and Food Security» for 2021–2025, R&D 1.6.4 «Identification of the features of accumulation and main ways of vertical transmission of the most pathogenic viruses of fruit plants (apple, pear, plum, cherry)».

Seeds were extracted from fruits collected from pear trees infected with ASPV and from apple trees infected with ACLSV and ASPV.

ELISA assay revealed the presence of viruses in fruits and seeds. More detailed research was carried out using the real-time PCR method.

A total of 500 seeds were tested for viruses. ASPV was detected in 100% (197 out of 197) of tested apple seeds and in 89.6% (172 out of 192) of tested pear seeds. ACLSV was detected in 100% (111 out of 111) of tested apple seeds.

In order to analyze the seed transmission of ACLSV, ASPV to seedlings, seeds harvested from these virus-positive apple trees were stratified and sowed in pots. One-, three-, and six-month-old seedlings were tested for ACLSV and ASPV using ELISA and real-time PCR to assess the occurrence of seed transmission. Of 27 progeny of virus-infected apple trees, none was found to be positive for virus. These results showed that seed transmission did not occur in this study, but further study of this issue, retesting of these seedlings, and assessment of virus accumulation during plant growth are necessary.

METAGENOMIC ANALYSIS OF APPLE AND HAWTHORN POPULATIONS

Makhambetov A., Mendybayeva A., Nizamdinova G., Gritsenko D.

Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan

The wide variety of apple and hawthorn populations make up a significant portion of the Kazakhstan's natural biodiversity. The apple tree is an endemic to the Almaty region and is highly valued to Kazhakhstan's agricultural industry. One of the problems that affects the hawthorn and apple tree wild populations of the Almaty region is the wide spread of bacterial and fungi pathogens, such as *Erwinia amylovora*.

Nowadays there is a reliable method of analyzing the spread of pathogen infection and its impact on plant's natural habitat. The main object of this research was to perform metagenomic analysis of apple and hawthorn trees growing in wild populations. In order to compel the study following analyzing methods were utilized: Bacterial DNA extraction, amplification using 16S and ITS primers, and Nanopore sequencing.

In this research 210 apple tree and hawthorn tree samples were collected and studied. The samples were collected from 4 populations of Almaty region: Dzungarian Alatau, Ile-Alatau, Ketpentau and Sumbe. The branches of trees were used to prepare plant extract by following plating it onto Bacteria screening medium 523. The bacteria cultured on the Petri dish were carefully washed off using TE buffer to remove any contaminants or residual media. Subsequently, genomic DNA extraction was performed for further analysis. The isolated DNA was amplified using universal 16s and ITS1-ITS2 primers by following ligation of barcodes for sequencing. Before sequencing, the PCR products were combined in sets of 5 samples from the same population.

Predominantly, pathogenic microflora included bacteria of the genus *Erwinia*, while the endophytic microflora comprised *Pseudomonas, Klebsiella*, and *Pantoea*. Associated microflora mainly consisted of bacteria of the genus *Pseudomonas*. In wild populations of apple trees, hawthorn, and rowan, *Erwinia* was not detected, only in orchards with cultivated apple trees. Among plants in wild populations, the endophytic microflora predominantly featured *Pseudomonas fluorescens*. Pathogenic fungi of the genus *Alternaria*, predominantly *Alternaria mali*, causing apple alternariosis, were detected in more than 60% of the samples from wild populations. In cultivated orchards, this pathogen was found in only 5% of the samples. Among hawthorn and rowan trees, pathogenic fungi including *Diplocarpon mespili*, *Alternaria*, and *Monilinia johnsonii* were identified, with a 13.9% prevalence of infected plants. Endophytic fungi species identified included *Alternaria infectoria*, *Alternaria sclerotigenum*, *Aspergillus terreus*, *Penicillium chrysogenum*, and *Fusarium lateritium*. All of these endophytic fungal species were detected in wild populations, while in cultivated orchards, only *Alternaria infectoria* was found (20% of the samples).

The composition of pathogenic and endophytic microflora varied depending on the plant organ studied. In leaves *Pseudomonas, Klebsiella, Pantoea, Alternaria sclerotigenum, Aspergillus terreus,* and *Alternaria mali* were detected. Meanwhile, in branches, *Erwinia, Pseudomonas fluorescens, Alternaria infectoria, Alternaria sclerotigenum, Aspergillus terreus, Penicillium chrysogenum,* and *Fusarium lateritium* were identified.

Presently, our assessments reveal that the majority of the surveyed regions harbor dangerous pathogens, underscoring the need for management strategies to mitigate potential threats to biodiversity and ecosystem integrity.

SEED POTATO QUALITY CONTROL – INSPECTION AND CERTIFICATION

Raissova N., Shamekova M., Sapakhova Z., Zhambakin K.

Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan

E-mail: n.raissova@ipbb.kz

The market of potato seeds and planting material of fruit crops in the country needs increased regulation both in the domestic market and in imports. Cases of low-quality seed material from both domestic sources and illegal imports are often detected, resulting in lower yields, and the spread of diseases. Protection of the rights of farmers purchasing seeds and planting material is a prerequisite to ensure the production of high-quality products suitable for both domestic consumption and export to international markets.

Industrialized countries possess their quality assurance frameworks for seeds and planting materials (such as ESCAA, EPPO, NAPPO, etc.), which are not standardized with the system in Kazakhstan. Current seed quality control in Kazakhstan is carried out according to an outdated Soviet system, where the manufacturer himself issues a certificate of seed quality and the demand for modernizing Kazakhstan's seed and nursery production system is incredibly pressing. This modernization aims to generate top-quality domestic seeds and planting materials for both domestic consumption and export, as well as to allure investments from both local and international investors.

By the order of the Ministry of Agriculture of the Republic of Kazakhstan, during 2021-2023, researchers of the Institute of Plant Biology and Biotechnology developed a scientific program and implemented a scientifically based system of certification and inspection of seed potatoes and planting material of fruit crops in the Republic of Kazakhstan.

The program was aimed at solving the problem of quality control of seed and planting material produced in Kazakhstan, as well as imported into Kazakhstan. In terms of program implementation, the following work has been done:

- analysis of the inspection and certification systems of leading countries producing seed potatoes, fruit and berry crops was carried out and the optimal model was determined - the inspection system of the Kingdom of the Netherlands for transfer to Kazakhstan.
- inspectors were trained at the Inspection Services of the Kingdom of the Netherlands for seed potatoes and planting material of fruit crops, 9 inspectors for seed potatoes, and 9 inspectors for planting material of fruit crops.
- work algorithm of the authorized body on inspection and certification of seed potatoes and planting material of fruit crops in the Republic of Kazakhstan and its interaction with other organizations was developed.
- system for certification and traceability of seeds after micropropagation has been defined.
- a national standard for seed potatoes based on UNECE Standard S1, developed for harmonization with European standards.
- after assessing the industry's status and the legal landscape, a preliminary draft of the Law of the Republic of Kazakhstan, aimed on the implementation of a new inspection system and titled "On Amendments and Supplements to Certain Legislative Acts of the Republic of Kazakhstan Regarding Support for Seed Production" was formulated.
- draft rules for accreditation by the authorized body (MoA) of professional organizations have been developed.
- five detection systems for identifying the most perilous pathogens affecting potatoes, walnuts, apples, raspberries, and plums were devised and put into practical use.
- genetic bank of detected phytopathogens created.
- pilot inspections of seed potatoes and fruit crop planting materials were carried out in alignment with the established inspection and certification system, utilizing a developed database.
- a database for tracking seed potatoes in Kazakhstan and fruit crop planting material was developed and tested in pilot inspections conducted in seed farms throughout Kazakhstan.

FEATURES OF *IN VITRO* PROPAGATION OF RARE AND ENDANGERED TULIP SPECIES IN KAZAKHSTAN

Rakhimzhanova A.O.,* *Manabayeva S.A.

National Center for Biotechnology, Astana, Kazakhstan

E-mail: r.aizhann@mail.ru

Kazakhstan is the homeland of tulips. Currently, there are 35 species of wild tulips in Kazakhstan, 18 of which are listed in the Red Book. They are distributed across the entire territory of the country. Conservation of tulip species is a significant global challenge, and relying solely on in situ conservation methods does not guarantee their complete preservation. To solve this issue, biotechnological methods associated with in vitro conservation and propagation are proposed, allowing for the reproduction of valuable genotypes in natural populations.

The aim of our research was to study the features of in vitro propagation of rare and endangered tulip species in Kazakhstan. Rare and endangered tulip species in Kazakhstan, namely *Tulipa greigii*, *Tulipa bifloriformis*, and *Tulipa patens*, collected from their natural habitats in the Aksu-Zhabagly State Nature Reserve, were selected as research objects.

The first and obligatory stage of biotechnological research related to in vitro culture is the introduction of plant material into a sterile culture. For the normal development of explants in in vitro culture, complete sterilization of the initial material is necessary. Tulip bulbs have been used as primary explants. The sterilization of bulb scales presents certain challenges, requiring healthy scales without mechanical damage. To overcome these challenges, the bulbs were prewashed with tap water and a commercial bleach product (Domestos). Further sterilization of the prepared bulbs was performed under sterile conditions in a laminar flow hood. We tested the effectiveness of several disinfectants, including sodium hypochlorite, hydrogen peroxide, ethanol, and a 0.1% solution of corrosive sublimate. The most optimal disinfectant was a solution of corrosive sublimate solution, which resulted in both sterile and viable explants. The lowest number of sterile explants was obtained with sodium hypochlorite. The sterile bulbs were sliced into cross-sections and placed on agarized Murashige and Skoog (MS) medium containing zeatin (3.0 mg/l) and NAA (1.0 mg/l). Cultivation was carried out in the dark at 25-26°C, and direct regeneration of microshoots was observed after 7-8 weeks. On average, 2 to 5 microshoots were formed on one cross-section. For further growth and development of microshoots, media with different growth regulators (BA, NAA, thidiazuron, kinetin) and their combinations were used. The best growth was observed on a medium containing BA and NAA at concentrations of 2.0 and 1.0 mg/l, respectively. The selected sterilization scheme and cultivation conditions for bulb scales allowed obtaining a sufficiently high percentage of viable explants for subsequent in vitro propagation and the formation of microbulbs. Complete maturation of microbulbs was achieved on MS medium containing 0.1% methyl jasmonate.

Thus, the cultivation conditions for rare and endangered tulip species in Kazakhstan have been optimized *in vitro* culture. The achieved results contribute to the conservation of these species using biotechnological methods and enable the application of genetic engineering methods for improvement of these genotypes.

DNA BARCODING AND PHYLOGENETIC ANALYSIS OF *BRASSICACEAE BURNETT* SPECIES USING *RBCL* AND *MATK* MARKER GENES

Ramazanova M., Tussipkan D., Manabayeva S.A.

National Center for Biotechnology, Astana, Kazakhstan

E-mail: malikaramazan.7@mail.com

Precise identification of taxa or species of living organisms is crucial for various areas of research including biodiversity studies and conservation, molecular biology and genetics, expansion of biological prospecting and biotechnological applications. DNA barcoding is one of the effective methods for species identification. This is a modern method of molecular genetics that allows to distinguish an organism by certain genetic markers to classify within biological systematics at the species level.

The *Brassicaceae Burnet* species are widely spread across the world. This family includes various species that are essential for agriculture and horticulture. In the territory of Kazakhstan occur approximately 298 species including 15 species recorded in IUCN Red List. The aim of this work is to study biodiversity and phylogenetic relationships of the *Brassicaceae* family in Kazakhstan using suitable marker genes.

Research material consisted of herbarium specimens from 12 different species of *Brassicaceae* including *Capsella bursa-pastoris, Erysimum diffusum, Isatis tinctoria, Rorippa palustris, Clausia aprica, Odontarrhena tortuosa, Erysimum quadrangulum, Cardamine repens, Erysimum cheiranthoides, Isatis gymnocarpa, Sisymbrium polymorphum* and *Lepidium latifolium*. Two gene regions *rbcL* and *matK* were used as candidate barcodes to identify an effective interspecific variation in the mustard family. The obtained sequences were identified by BLAST in the NCBI Nucleotide database. Phylogenetic analyses were conducted using MEGA11.

The average evolutionary divergence across all species using *rbcL* was estimated to be 0.83. This allowed to divide the species into two main groups with a distance of 2.55. Using *matK* this value was estimated 0.12, resulting formation of three main groups among species. Based on the *rbcL* definite differentiation was observed at the species level with a maximum distance of 0,03274 between the species *Erysimum diffusum* and *Odontarrhena tortuosa*. Furthermore, the most prominent divergence according to *matK* with distance of 0,10775 was exhibited between species *Erysimum cheiranthoides* and *Odontarrhena tortuosa.* While a minimum distances of 0, 00000 for *rbcL* were exhibited between similar species *Erysimum diffusum* and *Erysimum quadrangulum*, and between *Rorippa* palustris and *Clausia aprica.* In addition, a minimum distances of 0, 00229 and 0,01864 were exhibited between similar species *Erysimum diffusum* and *Erysimum quadrangulum*, followed by *Isatis tinctoria* and *Isatis gymnocarpa* respectively.

Research has established that DNA barcoding is a practical and efficient method for identifying and tracking phylogenetic relationships among species. Two candidate barcoding loci, *rbcL* and *matK*, were shown to be the most appropriate candidate barcodes with the highest interspecific divergence among the different species of the *Brassicaceae Burnet* family.

STUDY OF TAL-EFFECTORS IN *XANTHOMONAS CAMPESTRIS PV. CAMPESTRIS* AS VIRULENT FACTORS FOR *BRÁSSICA OLERÁCEA*

***Razhina O.L.*[1], *Chernyaev K.A.*[1], *Zlobin N.E.*[1], *Jalilov F.S.U.*[2], *Ignatov A.N.*[3], *Taranov V.V.*[1]**

[1] *All-Russia Research Institute of Agricultural Biotechnology, Moscow, Russia*

[2] *Russian State Agrarian University - Moscow Timiryazev Agricultural Academy, Moscow, Russia*

[3] *Peoples' Friendship University of Russia named after Patrice Lumumba, Moscow, Russia*

E-mail: oksana-razhina@yandex.ru

Xanthomonas campestris pv. campestris (Xcc) causes a black rot disease on various cultivated plants of the *Brassicaceae* family and especially damages cabbage crops. It was previously shown that some *Xcc* strains use TAL-effectors to bind promoter regions of some plant genes and change its expression in order to promote infection rates. The unique feature of the TAL-effectors is that the target DNA sequence can be determined according to the TAL-effector aminoacide sequence. Establishing the amino acid sequence of TAL-effectors makes it possible to reveal target plant genes, which can be considered as S-genes. Further modification of these genes will increase resistance to the cabbage black rot disease.

In this work, an examination of TALE genes biodiversity among a set of *Xcc* isolates belong to different races was performed. The *Xcc* isolates were collected from various regions of Russia and from different countries such as Belarus, Moldova, USA, China, Brazil, etc. More than 100 *Xcc* isolates were analyzed.

The work was financially supported by the Ministry of Science and Higher Education, project No. 13.2251.21.0205.

GENETIC ADAPTATION STRATEGIES OF RHODIOLA *LINEARIFOLIA* PLANTS FROM VARIOUS ECOLOGICAL AND GEOGRAPHICAL POPULATIONS

***Terletskaya N.V.*, *Khapilina O.N.*[2], *Erbay M.*[1], *Turzhanova A.S.*[2]**

[1] *Institute of Genetics and Physiology, Almaty, Kazakhstan*
[2] *National Center for Biotechnology, Astana, Kazakhstan*

E-mail: teni02@mail.ru

Representatives of the Crassulaceae family's genus Rhodiola are succulents and have a great capacity for adaptation to unfavorable environmental influences. We studied the individual specimens from from *R. linearifolia* Boriss. from three different natural populations of nature reserves in various mountainous regions of Kazakhstan.

One of the most significant tools for analyzing plant resources, including numerous genetic processes in wild populations, is the analysis of molecular genetic polymorphism. This work aimed to look at the polymorphisms of allelic variations of the superoxide dismutase (SOD) and auxin response factor (ARF) gene families, as well as the genetic diversity of from three different natural populations of *R. linearifolia*, using the retrotransposons-based fingerprinting approach. The multi-locus exon-primed intron-crossing (EPIC-PCR) profiling approach was used to examine allelic variations in the SOD and ARF gene families. We implemented the inter-primer binding site (iPBS) PCR amplification technique for genome profiling, which demonstrated a significant level of polymorphism in the Rhodiola samples studied. The results obtained in this study show a high level of molecular genetic polymorphism in the coding part of the genome in the studied samples.

Both SOD family genes and ARF genes had a great variety of EPIC-PCR amplicons in populations studied. Yes, the analyzed populations of *R. linearifolia*, respond mainly similarly to stress. But the results indicate the presence of genetic differences or structural features between these populations, which may be associated with adaptation to different environmental conditions or allelic drift.

The iPBS profiling analysis for the studied samples of analyzed populations also revealed the level of genetic differentiation of the studied populations and demonstrated Genetic profiles contained both common amplicons and unique one's characteristic of each specific population of *R. linearifolia*. Based on the results of genetic analysis of populations based on DNA profiling data, we can conclude that about 64% of genetic diversity is due to intrapopulation variability.

The variability in the regulatory regions of the ARFs and SOD genes may be associated with different plant responses to stress factors, while PBS polymorphism may be due to the geographic remoteness of populations and the influence of environmental conditions.

So, the genetic variety of wild populations of *R. linearifolia* leads to their improved tolerance of opposing environmental circumstances and evolutionary divergence.

GENE POOL OF WILD FRUIT AND BERRY PLANTS IN THE ALTAI BOTANICAL GARDEN

Vdovina T.A.*, Lagus O.A., Danilova A.N., Isakova E.A.

Altai Botanical Garden, Ridder, Kazakhstan

**E-mail:* lelik_ridder1994@mail.ru

The mobilization of genetic resources of fruit and berry crops is relevant in connection with the ever-increasing scale of extinction of valuable species and forms. In order to implement modern breeding programs and rational use of the world gene pool of horticultural crops, collections of adaptively significant and economically valuable qualitative and quantitative traits have been created in the Altai Botanical Garden (ABG) for *Hippophae* L., *Viburnum* L., *Lonicera* L., *Berberis* L., *Fragaria* L., *Rosa* L., *Ribes* L.

The genetic collection of fruit and berry crops in the ABG is represented by 11 genera: *Berberis* L. (one species – *Berberis heteropoda* Schrenk, 24 forms), *Crataegus* L. (one species – *Crataegus chlorocarpa* Lenne et c. Koch, 2 samples), *Fragaria* L. (two species – *Fragaria vesca* L., *Fragaria viridis* (Duch.) Mill., 15 specimens), *Hippophae* L. (one species – *Hippophae rhamnoides* L., 46 forms, one variety '*Yubileinaya Kotukhova*'), *Lonicera* L. (one species – *Lonicera altaica* Pall., 17 specimens, one form '*Blue Wave*'), *Rubus* L. (one species – *Rubus idaeus* L., 5 specimens), *Prunus* L. (one species – *Prunus padus* L., 13 specimens), *Ribes* L. (two species – *Ribes petraeum* Wulfen, *Ribes nigrum* L., 6 ecotypes), *Rosa* L. (two species – *Rosa acicularis* Lindl., *Rosa spinosissima* L., 4 samples), *Sorbus* L. (one species – *Sorbus aucuparia* subsp. *Glabrata* (Wimm. & Grab.) Hedl., 4 specimens), *Viburnum* L. (one species – *Viburnum opulus* L., 18 forms), from 6 families. Total 13 species, 89 forms, 6 ecotypes, 60 varieties, 1 variety.

Extensive breeding work has been carried out since 1968 on five species: *Ribes nigrum* L., *Hippophae rhamnoides* L., *Viburnum opulus* L., *Lonicera altaica* Pall., *Berberis heteropoda* Schrenk, the reserves of which are limited in nature. The main goal of the research is to study the biological characteristics, adaptive capabilities, biochemical composition of fruits, as well as their preservation in the collection.

As a result of the research, highly productive, adaptive species of fruit and berry crops were identified, with good consumer qualities of the fruits, with high vitamin value and antioxidant activity for their effective use in industrial and amateur gardening. For sea buckthorn, the following forms have been prepared for variety testing: '*Dolgozhdannaja*', '*Podarok Bajtulinu*', '*Solnyshko*', '*Nesravnennaja*', '*Shetlastinka*', '*Fakel*', '*Fejerverk*', '*Krasnoplodnaja*', '*Ljubimec*', '*Gustoj Tuman*', *Lonicera* form – '*Golubaja Volna*', *Viburnum* form: '*Shtambovaja*', '*Blestjashhaja*', '*Botanicheskaja*'. The selection fund of the above-mentioned species includes more than a thousand forms and seedlings: *Hippophae rhamnoides* - 374, *Berberis heteropoda* – more than 400, *Viburnum opulus* about 20, *Lonicera altaica* – 25.

In their natural form, in the fruit growing area (the southwestern slope of Mount Belkin) grow: *Prunus padus* Mill., two species of *Rosa*: *Rosa spinosissima* on an area of 67 – 120 m^2 and beyond on the total territory of the Altai Botanical Garden – 3.8 hectares. *R. acicularis* grows singly. Recently, there has been an intensive development of free sites by *Fragaria viridis*. Strawberries grow in small, sparse clumps from 15.0 to 60.0 m^2. The total projective coverage is 4–6%, previously it was 3–4%.

This research has been funded by the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan (BR21882166 «Scientific and practical basis of reproduction, conservation, use of fruit-berry plants of natural flora of Western, Eastern, Central and Northern Kazakhstan to ensure food security»).

GENETIC DIVERSITY OF VIRUSES INFECTING STRAWBERRIES IN THE SOUTHEAST OF KAZAKHSTAN

Yefremova Yu.,* *Malakhova N., Khanseitova A., Urazayeva M.

M. Aitkhozhin Institute of Molecular Biology and Biochemistry, Almaty, Kazakhstan

E-mail: ydyo@inbox.ru

Cultivation of strawberries in southeast Kazakhstan is an important part of industrial fruit growing, characterized by constant demand and high profitability. However, new approaches to the technology of cultivating and selling the products of this crop require improving the cycle of work on its cultivation, including control over viral infections characteristic of the agro-ecological conditions of the south-eastern region.

Modern conditions of agricultural market relations require a quick return on investment and subsequent receipt of regular, high profits. That is why potential productivity, depending in particular on susceptibility to certain viral diseases and the specific use of protective equipment, have a significant impact on the cost of finished berry products.

Since garden strawberries are perennial plants with a lifespan of 7-8 years and an active fruiting period of 2-3 years, they occupy an intermediate position between herbaceous and shrub forms, are characterized by compactness and high productivity - they are successfully grown throughout the south-east of Kazakhstan, in particular Almaty and Zhetysu regions.

This work includes the selection of biological tissue samples of stems, roots, leaves and fruits of garden strawberries of the four most industrially valuable varieties cultivated in the Almaty and Zhetysu regions for the purpose of screening for the presence of viral diseases, as well as analysis of their prevalence, molecular genetic analysis samples, purification of PCR amplification products, subsequent sequencing and establishment of phylogeny, further purification of viral particles for conducting a pathogenetic virulence test.

Thus, this work will contribute to a deeper understanding of the extent of the spread of viruses affecting strawberries in the south-eastern region of Kazakhstan, the severity of the infectious load, the phylogenetic specificity of viral agents, as well as their virulence. Since currently all garden strawberry planting material is imported from abroad, this work will help update information about the current infectious situation in the specified region, and consequently, increase the level of food security of produced berry products.

These studies are carried out as part of the implementation of a scientific and technical program with individual registration number BR21881942 “Development of biotechnological approaches for the control of phytopathogens in order to increase the productivity of agricultural crops”.

ESTABLISHMENT OF PLANT BACTERIA AND FUNGI COLLECTION

Yelchaninov M.I., Nizamdinova G., Gritsenko D.

Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan

E-mail: yelchaninov.mikhail@gmail.com

This study represents a crucial step in exploring and understanding the plant microbiome in the context of agriculture in Kazakhstan. Considering the growing need to increase crop productivity and resilience of agricultural crops to extreme climatic conditions, the creation of a collection of plant bacteria and fungi becomes particularly significant.

The research involved sampling the apple, walnut, and hawthorn tree material from various ecosystems in the regions of Zhongar Alatau, Ketpen, and Ile-Alatau, as well as targeted sampling from apple orchards, where apple bacteria were of particular interest. This allowed us to obtain extensive data on the biodiversity of microorganisms existing in natural and anthropogenically modified ecosystems of Kazakhstan. After collecting the samples, we processed and isolated microorganisms using standard culture methods.

Subsequently, Nanopore sequencing was applied for the identification and classification of microorganisms. These methods enabled us to obtain detailed information about the genera and, in some cases, species of bacteria. Presently, our collection comprises 25 isolates of *Erwinia*, 57 isolates of *Pseudomonas*, 31 isolates of *Klebsiella*, and 42 isolates of *Pantoea*. These isolates were obtained from diverse samples and populations. Additionally, glycerol stocks of *Erwinia amylovora* were prepared for long-term preservation at low temperatures. The potential biological agents, such as *Pseudomonas fluorescens*, were also preserved for subsequent testing to evaluate their efficacy in promoting plant health and combating pathogens. *Pseudomonas fluorescens* stands out as a powerful biocontrol agent against plant pathogens. Through mechanisms such as antibiosis, competition for nutrients, and induction of plant defense responses, this bacterium suppresses the growth of harmful organisms, thereby reducing the need for chemical pesticides. Moreover, *Pseudomonas fluorescens* has been shown to promote plant growth by facilitating nutrient uptake, enhancing stress tolerance, and stimulating root development.

The collection of plant bacteria has the prominent potential for enhancing agricultural production. Plant microbiome analysis will help to identify biological agents capable of increasing crop yields, protecting plants from diseases and stressful conditions, and improving soil fertility.

EVALUATING PHYSIOLOGICAL TRAITS IN WHEAT GENETIC RESOURCES ASSOCIATED WITH HEAT TOLERANCE AND DROUGHT RESISTANCE

Yessimbekova M.A., Suleimenova M.Sh., Mukin K.B.

Kazakh Research Institute of Agriculture and Plant Growing, Almalybak, Kazakhstan

E-mail: minura.esimbekova@mail.ru

The predicted global climate changes in the world are of particular importance for Kazakhstan, the main areas of agricultural production of which are characterized by high variability of environmental factors. According monitoring climate change, drought conditions and wheat production in Eurasia: the case study of Kazakhstan (Karatayev M (2022) by 2030, the average annual temperature in Kazakhstan is expected to increase by 1-2°C (on average 1.5°C), by 2050 by 2-3°C, even 3.5°C. The highest growth rate of average surface air temperature was noted in the southern and western regions in winter, from 0.21oC to 0.51oC per decade.

High temperature can be one of the main factors limiting the productivity of all agricultural crops, including wheat. In this regard, understanding the physiological problems associated with stress caused by high temperature is of great importance. The aim of the studies was to phenotype wheat germplasm (*Triticum aestivum* L.) to assess the potential of using NDVI (normalized difference vegetation index) and CTD (canopy temperature depression) measurements to identify wheat genotypes that show a high correlation of productivity with heat tolerance (CTD) and drought resistance (NDVI) cultures in the foothill and dry steppe zone of the Trans-Ili Alatau.

As a result of studies CTD, calculated as the difference between the temperature of the canopy and the environment, the genotypes were divided into 3 groups. The trend of increasing productivity with increasing CTD (r=0.67) was revealed. The five winter wheat accessions were selected as sources of productivity and adaptability to high temperatures.

Monitoring of the wheat gene pool using the “Greenseeker” optical sensor showed a change in the plant biomass index (NDVI) value depending on the conditions of cultivation, the phase of development. A connection (r=0.64) between NDVI and the yield of winter wheat was established. For spring wheat, a significant relationship (r=0.51-0.54) of NDVI with spike length, number of spikelets, kernels and weight of kernels per spike was noted.

Key words: bread wheat, physiological indicators, heat tolerance, drought resistance, yield.

IDENTIFICATION OF PLANTS OF THE *RANUNCULACEAE* FAMILY BY DNA BARCODING

Zhumabay N.B., Bekkuzhina S.S., Sutula M.Y., Manabayeva S.A.

National Center for Biotechnology, Astana, Kazakhstan

E-mail: nurbek.zhumabay10@gmail.com

In the context of global environmental change and the extinction of many plant species, the importance of biodiversity research and conservation is increasing. The identification of economically important plant species has become not only an urgent task, but also a strategic priority. DNA barcoding is a powerful tool for solving this problem. The use of the DNA barcoding method provides a deeper understanding of the genetic and evolutionary aspects. This method allows for more accurate identification and classification of plants, thus improving taxonomic understanding.

The *Ranunculaceae* family is widely used for its medicinal and pharmacological properties. There are about 180 species of this family in Kazakhstan, 9 of which are endemic. Of all the species found on the territory of Kazakhstan, 90 species are alkaloid-bearing, which in the future could be used in pharmaceutical production. The aim of this work is to study the biodiversity of species of the *Ranunculaceae* family in Kazakhstan, as well as the identification and study of taxonomy using the DNA barcoding method.

The materials were herbarium specimens brought from the botanical gardens of the Akmola, Karaganda, and Eastern Kazakhstan regions. DNA was isolated using a modified CTAB protocol. PCR amplification was performed in a volume of 25 μl. The following primers were used for amplification: rbcLa_F 5'-ATGTCACCAACAAACAGAGACTAAAGC-3', rbcLa_R 5'-GTAAAATCAAGTCCACCRCG-3', ITS4 5'-TCCTCCGCTTATTGATGC-3', ITS5 5'-GGAAGTAAAAGTCGTAACAAG-3', 3F_KIMf 5'- CGTACAGTACTTTTGTGTTTACGAG-3', 1R_KIMr 5'-ACCCCATTCATCGGAAATCTTGGTTC-3'. Sequencing was performed by the Sanger method using the BigDye Terminator sequencing kit. Identification was carried out using BLAST, the search was carried out in the NCBI global database. The analysis of all datasets (rbcL, ITS, mark) was performed using the MEGA11 software.

As a result of the search, 27 nucleotide sequences from 10 plant species of the *Ranunculaceae* family were obtained. In addition, 30 nucleotide sequences from 13 species were obtained from the GenBank database. In general, the species of the *Ranunculaceae* family from five regions of Kazakhstan (Altai, Kostanay, Akmola, Karaganda, Mangystau) were analysed. The concentration of the isolated DNA was >100 ng/μl, the absorbance ratio at A260/A280 was about 1.8. The primary data showed that the highest amplification rate was recorded in the rbcL DNA barcode (100%), the lowest rate in the matK marker (60%). The average length of the nucleotide sequences obtained was 507 bp, 634 bp and 708 bp, in rbcL, ITS and matK, respectively. rbcL sites proved to be the most conservative (86%), the matK marker turned out to be less conservative (79%). High divergence was found in ITS, the number of variable sites was about 37%. Identification by BLAST search at the generic level was 93-100% for rbcL, 90-100% for matK and 83-94% for ITS. Chloroplast markers (matK, rbcL) contain more conservative sites compared to ITS, which allowed effective identification of species within each genus of the Ranunculaceae family. The ITS, on the other hand, has a higher information content due to the high level of divergence. All the nucleotide sequences obtained were uploaded to the international database NCBI. Phylogenetic analysis will be performed on the results obtained.

Session 2.

GENETICS AND BREEDING

GENOMIC TOOLS AND STRATEGIES FOR DURUM WHEAT BREEDING

Nicola Pecchioni

Council for Agricultural Research and Economics, Foggia, Italy

The genome sequence of durum wheat, thanks to the efforts of an International consortium, has turned into its second (platinum) version, by long-read sequencing, and it is ongoing the assembly of its pangenome. This genomic path will be described, with insights into the discovery or characterization of genes and QTLs relevant to durum wheat breeding.

Association of genomic loci with key phenotypic traits will be also presented, as the application of genomic selection for single and multiple traits.

Development for durum wheat breeding of high-throughput, image-based phenotyping will be presented, together with a comparison between genomic and phenomic selection in the species.

Current programmes and strategies for durum wheat breeding will be then reviewed, including the experiences done in gene editing and cisgenesis.

GENETIC STRATEGIES TO INCREASE THE NUTRITIONAL DENSITY OF WHEAT

Simon Griffiths

John Innes Centre, Norwich, UK

The humble wheat grain was central to the birth of civilisation and, together with rice and maize, continues as a global staple on which humanity depends. The statistics which support these statements are worth careful consideration. In the season 2023-24 global wheat production was almost 785 million tonnes. Production steadily increases, most years are a new record, perfectly tracking global population increase which is predicted to peak in 2050 with no new land available to expand production. Can wheat continue to deliver for us until then? This depends on the success of plant breeders who made possible the increases achieved so far. From the late nineteenth century a select and quite random group of unimproved landraces were sampled from limited geographical ranges and became the founders of modern breeding programmes. We rely on the genetic gains delivered by reshuffling their genomes to this day! By reading the genetic code of global wheat landrace collection, assembled by AE Watkins in the early twentieth century an international team of researchers has shown that the foundations of modern wheat are simply too narrow and that most of the genetic diversity present in landraces has been unused in systematic breeding. Taking into account the existential challenges of climate change, biodiversity loss, declining soil health, and dietary crisis on top of our absolute need for food security I argue we need to revisit the origins of breeding and start again, enabled by the revolutionary technologies that underpin precision breeding.

SPEED BREEDING A POWERFUL TOOL TO FAST TRACK WHEAT VARIETAL DEVELOPMENT PROCESS

***Mahmood Z.*[1*], *Qamar M.*[1], *Arshad M.*[2], *Hussain I.*[3], *Aziz A.*[4], *Rasheed A.*[5]**

[1] *Wheat Programme, Crop Sciences Institute, National Agricultural Research Center (NARC), Park Road, Islamabad, Pakistan*

[2] *Crop Sciences Institute, National Agricultural Research Center (NARC), Islamabad, Pakistan*

[3] *Plant Sciences Division, Pakistan Agricultural Research Council (PARC), Islamabad, Pakistan*

[4] *International Maize and Wheat Improvement Center (CIMMYT) Pakistan Office, Islamabad, Pakistan*

[5] *Department of Plant Sciences, Quaid-i-Azam University, Islamabad, Pakistan*

**E-mail:* zeearid@gmail.com

Plant breeding programs desire many crop plant generations to be produced and assessed prior to crop cultivar is certified. Newly established speed breeding technique is capable of fast generation advancement through prolonged photoperiod in controlled glasshouses. Experiments were conducted on rapid wheat hybridization and generation advancement in speed breeding facilities at The University of Queensland, Australia and National Agricultural Research Centre, Pakistan. We harvested matured wheat accessions (synthetic hexaploids, landraces and hexaploid wheats) in 56–64 days under speed breeding glasshouse. We attempted 236 crosses and produced healthy seeds in a short time. F1 plants produced a maximum 21 healthy spikes and maximum 768 healthy seeds from a single plant. Through this technique in one year, we have developed 5200 wheat lines, their generations were advanced from F1 to F5 and now they are under field trials at F8 generation. Speed breeding procedure enables to harvest 5 to 6 spring wheat generations per year. By acceleration of generation advancement, speed breeding can save 5-7 years in the wheat varietal development process.

IMPLEMENTATION OF GENETIC TECHNOLOGIES IN SOYBEAN AND WHEAT BREEDING

Salina E.A.

Institute Cytology and Genetics SB RAS, Novosibirsk, Russia

E-mail: salina@bionet.nsc.ru

Over the past few years, various genetic and biotechnological approaches have been used for development of improved and relevant crop varieties. Such approaches include marker-assisted (MAS) and genomic selection, genome editing and dihaploid technologies.

A genetic platform for accelerated development of new breeding lines of cultivated soybean and bread wheat has been developed. The platform is based on the fundamental knowledge of identification and marking of unique alleles of genes defining agricultural valuable traits using gene sequencing and genome-wide association studies of a panel of 150-190 breeding accessions.

The main focus of genetic studies conducted on cultivated soybean was directed to the study of genes affecting the duration of the main phases of soybean development, first pod insertion height, protein content and yield components. Thirty-nine genetic locus were found to be significantly associated with the studied soybean traits, allelic variation in maturity genes E1-E4 effected on soybean adaptation in different regions of Russia was studied.

Organization of a genetic platform for spring and winter bread wheat was based on studies of gene identification affecting the heading and maturation date, resistance to fungal diseases, grain protein content, and resistance to pre-harvest sprouting.

The created database on molecular markers was used for acceleration of breeding of grain crops by MAS and dihaploid technology. Implementation of genetic data into breeding allowed for a short period of time (2 years) to obtain high-yielding lines of spring bread wheat, adaptive to different ecological and geographical zones, carrying target genes providing resistance to powdery mildew, leaf and stem rust, high protein and gluten content. More than 600 lines of spring wheat are now being tested in breeding nurseries in the Ural and West Siberian regions.

This research was funded by the Russian Science Foundation (RSF project No. 21-76-30003).

NGS-enabled wheat genotyping platforms for breeding application

***Rasheed A.*[1,2], *Xia X.*[2], *He Z.*[2]**

[1]*Department of Plant Sciences, Quaid-i-Azam University, Islamabad 45320, Pakistan*
[2]*Chinese Academy of Agricultural Sciences (CAAS), and CIMMYT-China office, 12 Zhongguancun South Street, Beijing 100081, China*

Improving the crop productivity, resilience to climate extremes, resistance to biotic stress and improving the quality are the main breeding objectives. Different tools, resources and strategies are used to precisely select the desirable cultivars in crop breeding. One of such tools is the genomics-assisted breeding (GAB), which improves selection accuracy during breeding cycles. However, practicing GAB depends on the availability of molecular markers for selecting the desired phenotypes. Once a marker is available for use in breeding, the efforts are then made to make it cost-effective and high-throughput to integrate its use in applied breeding. However, different breeding scenario like gene tagging, marker-assisted recurrent selection (MARS), background selection, diversity estimates, and genomic selection require different genotyping platforms, and there is no 'one size fits all' solution. We provided an overview of the efforts around developing cost-effective, high-throughput and breeding-oriented genotyping platforms in wheat. A successful genotyping platform would have the features of high genome coverage, least ascertainment bias, high power in gene discovery studies, balance between throughput and flexibility, provide high prediction accuracy in genomic selection, and, above all, affordable for most of the crop breeding programs.

NOVEL QTL HOTSPOTS FOR BARLEY FLOWERING TIME, PLANT ARCHITECTURE, AND GRAIN YIELD IDENTIFIED IN KAZAKHSTAN

***Genievskaya Y.*[1], *Chudinov V.*[2], *Abugalieva S.*[1,3], *Turuspekov Y.*[1, 3*]**

[1]*Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan*
[2]*Karabalyk Agricultural Experimental Station, Nauchnoe, Kostanay region, Kazakhstan*
[3]*al-Farabi Kazakh National University, Almaty, Kazakhstan*

**E-mail:* yerlant@yahoo.com

Barley (*Hordeum vulgare* L.) is an important cereal crop with high genome plasticity that is cultivated in all climatic zones. Traditionally, barley grain is used for animal feed, malting, brewing, and food production ensuring food security worldwide and within the country. Genetic studies empower us to conserve existing cultivars and breed superior ones using marker-assisted selection (MAS) approach. Modern barley breeding science and the usage of new molecular genetic technologies together may increase the efficiency of new cultivars development. The current study evaluates a diverse world collection of 273 two-rowed spring barley accessions, comprising cultivars and breeding lines from the USA, Kazakhstan, Europe, Africa and Middle East. The collection was grown during 3 seasons – 2019/2020, 2020/2021, and 2021/2022 – in fields of Kazakh Research Institute of Agriculture Plant Growing (southeastern Kazakhstan) and Karabalyk Agricultural Experimental Station (northern Kazakhstan). The collection was assessed by 5 plant adaptation traits (heading time, heading-maturity time, vegetation period, plant height, and peduncle length) and by grain yield per m^2. All 272 accessions were also genotyped using Barley 50k iSelect SNP Array resulting in 26,529 polymorphic SNP markers (MAF < 0.1).

A genome-wide association study (GWAS) using a multiple-locus mixed linear model (MLMM) for a GAPIT package in R software environment allowed for the identification of 95 significant (P < 1.00E-04) quantitative trait loci (QTLs) for the 6 studied agronomic traits of barley. Among them, for 58 QTLs we identified candidate genes and/or QTLs with the most of them associated with flowering time. The remaining 37 QTLs were presumably novel. The analysis of QTLs identified three genomic regions as QTL hotspot on chromosomes 1H, 3H, and 6H, wherein several QTLs associated with flowering time, plant architecture and grain yield were found to be co-localized. These QTLs could be used for gene mining and breeding programs, including MAS approach to improve barley adaptation parameters and to increase general grain yield of barley in Kazakhstan.

The research was funded by the Committee of Science of the Ministry of Science and Higher Education of the Republic of Kazakhstan (Program No. BR18574149).

QUANTITATIVE TRAIT LOCI FOR AGRONOMIC TRAITS IN TETRAPLOID WHEAT FIELD-TESTED IN KAZAKHSTAN ENVIRONMENTS

***Anuarbek S.*[1*], *Pecchioni N.*[2], *Laidò G.*[2], *Maccaferri M.*[3], *Tuberosa R.*[3], *Abugalieva S.*[1], *Turuspekov Y.*[1]**

[1] *Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan*
[2] *Research Centre for Cereal and Industrial Crops, Foggia, Italy*
[3] *Bologna University, Bologna, Italy*

**E-mail*: shynar.anuarbek@yahoo.com

Durum wheat (*Triticum turgidum* L. ssp. *durum*) is one of the top crops in Kazakhstan, where it is cultivated in different ecological niches, mainly at higher latitudes, in the steppe zone of the northern region. As a result, local durum wheat breeding programs in Northern Kazakhstan primarily aim to select for high productivity by introducing promising foreign germplasms and utilizing marker-assisted selection. In this study, a world tetraploid wheat collection consisting of 184 primitive and domesticated accessions that were previously genotyped using 16,425 polymorphic SNP markers was field-tested in northern and southeastern Kazakhstan. Field tests have allowed the identification of promising durum wheat lines in Northern Kazakhstan compared with a local standard cultivar. A genome-wide association study (GWAS) has allowed the identification of 59 QTLs for five agronomic traits (heading time, plant length, spike length, number of productive spikes, and 100-grain weight). The co-localization of a large number of QTLs with those previously published confirmed the validity of the results of this study. The QTLs reported here will provide an opportunity to implement marker-assisted selection in ongoing durum wheat breeding projects targeting higher productivity in the region.

This research has been funded by the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan (Grants No. AP05131328, AP14871383).

IDENTIFICATION OF PROMISING WHEAT LINES RESISTANT TO TAN SPOT (*PYRENOPHORA TRITICI-REPENTIS*) USING BREEDING AND MOLECULAR METHODS

Kumarbayeva M*, Kokhmetova A., Keishilov Zh.

Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan

**E-mail:* madina_kumar90@mail.ru

Tan spot of wheat, the causative agent of which is *Pyrenophora tritici-repentis* (Ptr), is the most aggressive among leaf diseases of wheat both worldwide and in Kazakhstan. Under favorable conditions for the development of the disease, crop losses reach 50-65%. The increased importance of tan spot of wheat in recent years is due to an increase in the acreage of wheat with a combination of direct sowing (no-till) and monoculture; the absence of disease-resistant wheat cultivars and the emergence of new Ptr races; the use of ineffective fungicides, which ensured the geographical spread of the pathogen over large areas. Tan spot management is achieved through existing strategies, mainly genetic breeding approaches. The creation of wheat varieties resistant to *P. tritici-repentis* is the best solution to the problem. To identify promising lines, a comprehensive study was conducted, including modern breeding and molecular research methods.

Phytopathological assessments of tan spot resistance in adult plants (APR) in the field identified 23 promising lines with an immune type of reaction (IT-0), 29 promising lines with a resistance type of reaction (R), and 25 samples with a moderately stable type of reaction (MR). Based on the results of phytopathological screening, the area under the disease progress curve (AUDPC) was estimated. As a result of the assessment, the susceptibility index (φ) was determined: 61 promising lines (48.03%) were classified as high (φ – 0.1-0.4) and 58 promising lines (45.7%) with an average susceptibility index (φ – 0.4-0.7).

Using molecular markers, sources of wheat resistance to tan spot were identified. Molecular screening of wheat samples was carried out using markers *Xfcp623* and *XBE444541* to diagnose the *Tsn1* and *Tsc2* genes, which control the sensitivity of toxins of the pathogen *P. tritici-repentis*. Based on the results of molecular screening, 94 genotypes (65.2%) were identified as carriers of the recessive *tsn1* gene linked to resistance to race 1 and the Ptr ToxA toxin. While 100 genotypes (69.4%) were identified as carriers of the recessive gene *tsc2* combined with resistance to race 5 and Ptr ToxB.

Principal component analysis (PCA) was performed based on the AUDPC results and the structural productivity analysis results. This analysis showed that the first two principal components explained 51.83% of the variance. According to ANOVA analysis ($p < 0.001$), the degree of tan spot development varied significantly between genotypes in different growing seasons (2022-2023). There was a significant negative correlation between AUDPC and 1000 grain weight ($r = -0.42$; $p < 0.001$).

As a result of comprehensive research, 28 promising lines have been identified that combine resistance to tan spot and high productivity. The identified promising lines combining adult plant resistance (APR) and tan spot resistance genes will be used in breeding hybridization programs to increase tan spot resistance.

This research has been funded by the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan (Grant No. AP22787867), as well as by the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan (Grant No. BR18574149, the task 01).

INDUCED MUTAGENESIS IN THE CREATION OF BARLEY *(HORDEUM VULGARE L.)* SOURCE MATERIAL FOR PRACTICAL BREEDING

Tokhetova L.A.[1], Sultan N.Zh.[2]

[1]Kazakh Research Institute of Rice Growing named after I. Zhakhaev,
[2]Korkyt Ata Kyzylorda University, Kyzylorda city, Republic of Kazakhstan,

E-mail: lauramarat_777@mail.ru, nazgulsultan@gmail.com

In conditions of intense global warming, which significantly affects the climate of the Kyzylorda region, the importance of breeding in the breeding of stress-resistant varieties is increasing, with special emphasis on drought-resistant crops such as barley *(Hordeum vulgare L.).* Scientists highlight its significant economic importance in arid climate conditions. For practical selection, the Aral region represents a special interest as a natural ecological background for evaluating plant resistance to a complex of stress factors. Breeders often face the problem of narrow genetic variability, which has led to the loss of alleles present in wild relatives. This will lead to the disappearance of traditional local varieties and indigenous forms, ultimately threatening food security worldwide. Therefore, the original material requires constant updating through the introduction of new beneficial genes.

In achieving these goals, alongside the utilization of classical selection potential, induced mutagenesis stands as one of the effective methods considered worldwide as a source for creating fundamentally new parental forms. Furthermore, the application of experimental mutagenesis methods reduces the time for breeding new varieties by 3-4 years, as mutant forms are not subject to segregation, which is inherent in hybrid lines. In recent years, many countries have shown interest in the peaceful use of atomic energy, particularly in the treatment of agricultural products with ionizing radiation. It is worth noting that in the last decade, the International Atomic Energy Agency (IAEA) of Austria has widely disseminated mutation breeding methods in Asian and Latin American regions and achieved very good results. Examples include the high-protein hulless barley mutant variety Molina-5, grown in the Andean mountain regions, and the rice variety Zhefu-802, occupying over 11 million hectares in China.

In this study, we developed a new method of radiation mutagenesis using the linear electron accelerator ILU-10 of the Joint Stock Company "Nuclear Technology Park" (Kurchatov, East Kazakhstan). The results showed that the most productive were mutant lines whose original varieties were treated in the absorbed dose range from 100 to 150 Gy. Among them are mutant lines: M 1/15-3-2I; M 1/15-2-3I; M 1/15-5-3I; M 1/15-5-3SA; M1/15-3-3 SA. Yield increases over the standard Syr Aruy variety ranged from 6.1 to 11.6 t/ha. Noticeable elongation of spike length and increase in the number of grains per spike up to 28 were observed. Important distinguishing features were their tallness combined with dense, strong straw and resistance to lodging.

In addition to visible changes in the biological development of plants, the use of mutagenesis causes the appearance of quantitative changes in various varieties and lines, which are the main criteria for searching for a breeder. The results showed that the productivity of M1 populations was significantly lower than the initial varieties and also decreased proportionally with an increase in the dose of ionizing radiation. Thus, the grain weight per 1 m2 of Syr Aruy decreased by 125.0 g (50± 10%) and 186.8 g (250± 10%); in Inkar by 223.3 g (50 ±10%) and 283.1 g (250± 10%), compared with the original genotypes. It was revealed that the Inkar variety, in comparison with the Syr Aruy variety, significantly reduces productivity under the action of mutagens, which indicates a significant share of the contribution of the genotype itself or the dependence of the mutagen effect on the genetic nature of the genotype.

In general, a significant increase in yield was determined mainly by the weight of grain per ear, due to the better grain content of the ear and the weight of 1000 grains. The selected mutant lines from the control nursery were included in the final stage of the selection process - as part of the competitive nursery in 2024.

GENETIC INSIGHTS INTO WILD APPLE POPULATIONS: A COMPREHENSIVE SNP GENOTYPING STUDY IN NORTHERN TIAN SHAN

***Taskuzhina A.K*[1],[2] *Khusnitdinova M.*[1], *Pozharskiy A.*[1], *Nizamdinova G.*[1], *Gritsenko D.*[1]**

[1] *Institute of Plant Biology and Biotechnology, Almaty, 050040, Kazakhstan*
[2] *Al Farabi Kazakh National University, Almaty, 050040, Kazakhstan*

E-mail: ataskuzina@gmail.com

Central Asia is home to numerous wild shrubs and fruit-bearing plants that survive harsh climatic conditions and high mountain altitudes. The wild apple tree *Malus sieversii* growing in the Tien Shan is one of the most important plants with a broad ecological adaptation under the extreme conditions of this environment and at the same time bearing biological and ecological importance. A scientific study of the wild apple tree and other wild-growing fruit plants is an important step in understanding adaptation mechanisms, as well as genetic diversity and evolution.

In the present study, genotyping was performed on *M. sieversii* and *Malus niedzwekyana* samples collected from various mountain regions of Northern Tien Shan, including the Zhongar Alatau, Ile-Alatau, and Ketmen. Additionally, samples were collected from the Tarbagatay mountain. In total, 352 samples of wild apple were genotyped and analyzed using the Axiom JKI50kMd apple genotyping array, which comprises 48,139 SNPs. Subsequently, after quality control 22,888 markers were selected for further analyses.

This investigation uncovered the genetic diversity of *M. sieversii* in the Northern Tien Shan. The principle component analysis was used to evaluate genetic struture of 331 wild apple genotypes using genotyping data. The three principal components (PCs) collectively captured 55.38% of the variability, with PC1 accounting for 38.06%, PC2 for 9.91%, and PC3 for 7.41%. The analysis of PC1 and PC2 indicated a clear differentiation between *M. sieversii* and *M. niedzwekyana*. PC3 has shown supplementary insights into the genetic disparities between these species, potentially elucidating finer-scale distinctions in their genetic profiles. The analysis of the population structure using ADMIXTURE algorithm indicated that the wild apple populations from the Zhongar Alatau and Ile-Alatau exhibited variations in the range of *K* values, spanning from three to eight. In contrast, *M. niedzwekyana* exhibited consistently different genetic characteristics across all *K* values, highlighting its distinct genetic makeup compared to *M. sieversii* populations. Cross validation of ADMUXTURE analysis with 10 repetitions was not able to reveal potential true *K* value.

The study findings revealed extensive genetic diversity within the wild apple populations of *Malus sieversii,* with notable genetic differentiation among populations inhabiting the Ile-Alatau and Zhongar Alatau mountains, indicative of their adaptation to varied ecological settings. Moreover, the analysis identified distinct genetic markers associated with crucial traits such as disease resistance, fruit quality, and environmental adaptability within these wild apple populations.

This study provides valuable information regarding conservation and sustainable management strategies that identify the significance of wild apple gene pools in breeding programs for cultivated varieties. This research is an important step forward in understanding the genetics and dynamics of evolution in *M.sieversii* within Central Asian mountain ranges; it is a foundation stone for future studies on important traits and breeding programs that are interested in this species.

THE STORY OF THE BREAD WHEAT ROOT: FROM AN INTROGRESSION CASE TO THE BREEDING EFFECT

Pshenichnikova T.A., Smirnova O.G., Simonov A.V., Bulatov I.O.

Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

Roots are an essential part of the plant organism. This is a primary organ that captures a state of the soil water status and transmits signals to the shoot. The architecture of the root system determines a solid plant rooting and effective absorption of nutrients and water from the soil. Among cultivated cereal plants, the genetic control of root system formation has been best studied in barley, corn, and rice. A number of genes involved in the gene networks of root system development were identified and cloned. In wheat, the second most important crop in the world, QTL associated with different parameters of the root system have been identified in many chromosomes. It was found that *Vrn-1* locus is involved in the genetic control of root growth and determines phenotypic features such as root angle, root length and weight, and root-to-shoot ratio. *Ae. tauschii* is currently intensively involved in the creation of synthetic wheats—genomic analogues of modern wheat cultivars. It was shown that the wheat genotypes obtained with the use of synthetic wheats have a larger root system. One of the first winter habit AABBDD synthetic hexaploid wheat called Synthetic 6x (Syn 6x), was obtained by crossing wild relatives of wheat *T. dicoccoides* and *Ae. tauschii*. Single chromosomes of Sen 6x were introduced into the genome of a spring variety Chinese Spring (CS), resulting in a complete set of single chromosome substitution lines CS (Syn 6x). Subsequently, on the base of the substitution lines, D-genome introgression lines were obtained including the lines for 5D chromosome. They carry *Ae. tauschii* chromosome 5D fragments of various lengths and some of them have large roots. In our work, we found that the size of the root system depends on the timing of vernalization (30, 45 or 60 days) and the water regime. The longer the vernalization and the shorter the period until flowering, the less were the length and weight of the roots. The QTL cluster for root lengths, root weights, and flowering time was localized on chromosome 5D in the region of the microsatellite marker *Xgwm292* and *Vrn-D1* gene. The lines with the introgression in this region had a significantly larger root length and weight compared with the recipient and donor under all conditions of irrigation and drought. We showed that among the three genes of *Vrn-1* locus, the gene *Vrn-A1* showed the greatest reducing effect on the size of roots. The further breeding aim of our investigation was to transfer this valuable trait to a spring cultivar Saratovskaya 29 (S29) with a small root system – the carrier of *Vrn-A1a* allele. During a series of successive selections of the hybrids between S29 and a line carrying introgression from *Ae. tauschii* in 5D chromosome, early ripening families were created with a large root system. The plants showed root length and weight comparable to the winter donor. Their average root length was 1.4 times longer than that of S29, and their root weight was more than three times heavier. The wide range of variation in stem length was found among the families, with the number of tillers exceeding that of S29 by 1.5 to 2.8 times. Grain weight per plant was two to five times higher than that of S29, while thousand kernel weight was essentially the same as that of the parent cultivar. In addition, most families inherited such an important economic trait as high protein and gluten content in grain. The presence of such a gene near *Vrn-D1* gene was predicted by Law et al. (1978). One of the families along with the strong root system and high gluten content demonstrated excellent physical properties of flour and dough, making it possible to classify the genotype as f strong wheat.

The Russian Science Foundation (project #23-26-10046) and the Ministry of Science and Innovation policy of Novosibirsk Region (project №р-59) supported this work.

DEVELOPMENT AND IMPLEMENTATION OF A BREEDING SCHEME FOR THE CREATION OF DOMESTIC WHITE CABBAGE HYBRIDS WITH INCREASED RESISTANCE TO BLACK ROT, FUSARIUM WILT AND ALTERNARIOSIS BASED ON MAS TECHNOLOGIES

Dubina E.V.*, *Makukha Yu.A.*, *Simonenko D.S.

Federal Scientific Rice Centre, Krasnodar, Russia

E-mail: lenakrug1@rambler.ru

One of the main reasons that significantly reduce the yield of white cabbage is diseases and pests. Among them the most harmful to white cabbage are *Xanthomonas campestris* pv. *campestris* (Pammel) Dowson, bacterium that causes black rot, *Fusarium oxysporum* f.sp. *conglutinans* (Wollenweb.), the fungus that causes fusarium wilt, and *Alternaria brassicicola*, the fungus that causes alternariosis [1, 2, 3]. The most reliable and modern method of combating these diseases is breeding resistant white cabbage hybrids using SSR markers.

The purpose of the work is to study the polymorphism of SSR markers that identify resistance genes to black rot, fusarium wilt and alternariosis, and to establish their linkage with the trait of white cabbage resistance to these diseases.

At the beginning of the study, contrasting plant forms of white cabbage in terms of resistance to black rot (resistant isogenic line 269-Yas12p-2 and susceptible isogenic line Pi714), to fusarium wilt (resistant isogenic line DT-46 and susceptible isogenic line Kb1P) and to alternariosis (resistant isogenic line Ten and the susceptible isogenic line 270-488), taken from the department of vegetable and potato growing of the Federal State Budgetary Scientific Research Center of Rice, were analyzed using PCR analysis with SSR markers taken from VegMarks database. Then the most polymorphic markers of them were tested on F2 and BC_1F_1 plants of segregating populations of the hybrid combinations 269-Yas12p-2 x Pi714, DT-46 x Kb1P and Ten x 270-488. At the same time, phytopathological testing of these plants was carried out to study the linkage of the selected markers with the trait of resistance to vascular black rot, fusarium wilt and alternariosis, according to the methodology of the All-Russian Rice Research Institute [4].

On the basis of the results of PCR analysis and phytopathological testing, the ratios of plants of segregating populations by genotype and phenotype were determined to establish the linkage of tested markers with resistance to black rot, fusarium wilt and alternariosis by statistical methods (chi-square). By means of scoring the recombination frequency the informative DNA marker systems have been identified: Ol10-C01 - for the resistance gene to black rot, Ol10-D01 - for the resistance gene to fusarium wilt, Ol11-B05 - for the resistance gene to alternariosis. They can be used for the accelerated breeding of resistant genotypes of white cabbage. It will significantly contribute to increasing the competitiveness of domestic hybrids and import substitution in the context of constantly changing conditions of vegetable crops market.

The research is carried out with the financial support of the Kuban Science Foundation and the Federal Scientific Rice Centre in the framework of the scientific project Num. MFI-P-20.1/41.

References

1. Williams P.H. / Black rot: a continuing threat to world crucifers // Plant disease. – 1980. – №64 (8). – P. 736-742.

2. Pu Z., Shimizu M., Zhang Yanju, Nagaoka T., Hayashi Takeshi, Hori H., Matsumoto S., Fujimoto R., Okazaki K. / Genetic mapping of a fusarium wilt resistance gene in Brassica oleracea // Molecular breeding. – 2012. – №30. – P. 809-818.

3. Doullah M.A.U., Meah M.B., Okazaki K. Development of an effective screening method for partial resistance to Alternaria brassicicola (dark leaf spot) in Brassica rapa // Eur. J. Plant. Pathol. – 2006. – 116(1). – P. 33-43.

4. Koroleva S.V., Dyakunchak S.A., Sitnikov S.V. Immunological assessment of breeding material when developing F_1 hybrids of white cabbage with group resistance to fusarium wilt and black rot (methodological recommendations). – M., 2012. – 16 p.

OPTIMIZING PRE-BREEDING: INTEGRATIVE WEIGHTING OF PHENOTYPES AND GENOTYPES IN CORE COLLECTIONS FOR ENHANCED NAM AND MAGIC PARENTAL IDENTIFICATION

Habib Y.[1*], Zamalutdinov A.[1], Boldyrev S.[1], Schegolkov A.[2], Ben C.[1], Gentzbittel L.[1]

[1]Skolkovo Institute of Science and Technology, Moscow, Russia
[2]SOKO, Krasnodar, Russia

**E-mail* : Yawar.habib@skoltech.ru

The progression of genetic mapping from biparental to multiparental populations signifies a substantial advancement in plant breeding, facilitating a more thorough comprehension of genetic diversity and trait heritability. Nested Association Mapping (NAM) and Multi-parent Advanced Generation Inter-Cross (MAGIC) populations, as examples of multiparental approaches, provide exceptional opportunities to dissect complex traits and accelerate the development of superior crop varieties. The careful selection of parental lines is a crucial aspect of utilizing the capabilities of these new type of mapping populations. This study aims to optimize the selection of pre-breeding resources by allocating different weights to phenotypic and genotypic data to compute core collections. By employing a weighted integration technique on a dataset consisting of 309 soybean lines, we delineated a core collection of 15 individuals that encompasses a large range of genetic diversity and phenotypic variation within the entire set. This core collection highlighted a significant retention of representativeness and genetic diversity, maintaining all 11 subpopulations that exist in the whole collection. Comparative pairwise phenotypic correlations using BLUPs confirmed that the core collection accurately mirrors the full set's trait interrelationships. Positive association between productivity and oil content (whole: r = 0.697, core: r = 0.842), a negative correlation with protein (whole: -0.443, core: -0.608), and a weaker negative one with the growing season (whole: -0.073, core: -0.390) are reflected in the whole and core collection. These findings suggest a methodology for the precise selection of parental lines, streamlining pre-breeding efforts for NAM and MAGIC populations. This method, which thoroughly accounts for both phenotypic and genotypic diversity, also holds significant promise for gene banks focused on conserving the breadth of diversity in their germplasm collection.

GENOME-WIDE ASSOCIATION STUDY OF AGRONOMIC TRAITS IN WINTER WHEAT COLLECTION GROWN IN KAZAKHSTAN

***Amalova A.*[1], *Yessimbekova M.*[2], *Ortaev A.*[3], *Griffiths S.*[4], *Burakhoja A.*[1], *Turuspekov Y.*[1*], *Abugalieva S.*[1]**

[1] *Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan;*
[2] *Kazakh Research Institute of Agriculture and Plant Industry, Almalybak, Almaty region, Kazakhstan;*
[3] *Krasnovodopad Breeding Station, Sarkyrama, Turkestan region, Kazakhstan;*
[4] *John Innes Centre, Norwich, United Kingdom;*

**E-mail*: yerlant@yahoo.com

Central Asia is an important region for the growth of winter wheat, with a cultivation area of more than 15 million hectares (ha). Despite this, the average yield remains notably lower, around 3 tons per ha, compared to that of developed countries. Consequently, there's a pressing need to prioritize the development of new, competitive, high-yielding cultivars in winter wheat breeding projects. Among these tools is the outcome of identifying novel genes and quantitative trait loci (QTLs) for agronomic traits through diverse germplasm panels and genome-wide association studies (GWAS). In this study, a panel of winter wheat accessions was curated, comprising 115 accessions from Central Asia and 162 from other regions of the world. The GWAS, based on a two-year field evaluation of the collection in Kazakhstan southern and southeastern regions and 10,481 polymorphic SNP (single-nucleotide polymorphism) markers, allowed for the detection of 173 stable QTLs in nine studied agronomic traits.

An analysis of existing scientific literature revealed that 23 out of these 173 stable QTLs align with previously reported QTLs, underlining the robustness of the findings. Furthermore, at Kazakhstan's southern and southeastern stations, 221 and 162 accessions, respectively, exceeded local standards cultivars for grain yield. Consequently, this study additional contribution to the identification of new QTLs key agronomic traits and identifies promising genetic lines for winter wheat breeding projects.

This research was funded by the Ministry of Science and Higher Education of the Republic of Kazakhstan (grant AP14871383).

BREAKING THE FOUNDER EFFECT CONTROLLING PLANT HEIGHT IN KAZAKH WHEAT GENE POOL

Yermekbayev K.[1,2,4]*, Turuspekov Y.[2], Wingen L.[1], Abugalieva S.[2], Hall A.[3], Orford S.[1], Griffiths S.[1]

[1]John Innes Centre, Norwich Research Park, Norwich, UK
[2]Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan
[3]Earlham Institute, Norwich Research Park, Norwich, UK
[4]Zhetysu University, Institute of Biotechnology and Ecology, Taldykorgan, Kazakhstan

**E-mail*: kanat.yermekbayev@gmail.com

Among agricultural crops, wheat cultivation and productivity is a matter of great importance to fight against global food insecurity. Kazakhstan annually produces 15-20 M tonnes of wheat grain a half of which is exported allowing the country to earn ~$1.2B per season and at the same time contributing to the regional and global food security significantly. Despite these significant economic and social impacts, the wheat growing area shrank from 14 to 11M h in the last decade due to the land code on diversification (https://adilet.zan.kz/).

This definitely poses a great threat to the local and global food security as most of the local dietary commodities consisted of wheat flour and Kazakhstan's share in global wheat exports accounts for ~2.35% (8 to 10 M/t) (www.oec.world). Moreover, the distraction in the global wheat grain supply chain caused by a recent unprecedented geopolitical turbulence has again proven wheat as a main source of nutrients in many parts of the world, including Kazakhstan itself when the cost of the 1 kg wheat flour tripled.

In addition to above mentioned challenges, the crossing scheme widely used by Kazakh wheat breeders resulted in the founder effect. This automatically diminished the chance of identifying exotic alleles and then use them in wheat improvement plans effectively through MAB (Marker Assisted Breeding).

Our recent study showed that this is the case as we were only able to identify and isolate the genetic factors that control plant height through crossing KZ wheat variety with the UK, not with KZ or genetically close RUS varieties. Importantly, these fixed alleles provided no yield and quality benefit in Kazakh wheat gene pool. Using the same sophisticated molecular breeding approaches that aimed at breaking the founder and genetic effects, we can strive to manipulate the final grain quality and yield via improving the genetic potential and resilience to stress.

FOUR MAPPING POPULATIONS AND THEIR GENETIC MAPS PROVIDED INSIGHTS INTO THE GENETICS OF ADAPTATION FOR KAZAKHSTANI WHEAT GERMPLASM

***Khamitova A.*[1], *Griffiths S.*[2], *Turuspekov Y.*[3], *Shoken M.*[1], *Yermekbayev K.*[1]**

[1]*Zhetysu University, Institute of Biotechnology and Ecology, Taldylorgan, Kazakhstan*
[2]*John Innes Centre, Norwich Research Park, Norwich, UK*
[3]*Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan*

E-mail: kanat.yermekbayev@gmail.com

Wheat is a vital cash crop in Kazakhstan. Since the reclamation of virgin land campaign in 1950's, the country remained as a main grain provider mitigating food insecurity comprehensively in Central Asia the home for several developing and underdeveloped nations. In spite of these significances, wheat growing area shrunken by more than 3M hectares (~ 30% of total land) giving a way to legumes which promoted by the recent land code. So, consideing the massive land under wheat (currently ~11M ha), a minor increase in grain yield could compensate the loss in total production. However, wheat breeding activities in many breeding stations rely on conventional style of plant breeding. With the aim of taking advantage of modern plant breeding approaches, we developed four mapping populations and their high density genetic maps simultaneously and we report that genetic mapping successfully combined with tranditional plant breeding methodologies stands as a cornerstone in unraveling the intricate genetic and phenotypic architecture of Kazakh wheat germplasm, paramount for enhancing crop breeding, identification of exotic allelic variants and agricultural productivity in the country.

FINE-TUNING WHEAT HEADING TIME THROUGH GENOME EDITING: INVESTIGATING THE IMPACT OF TRANSCRIPTION FACTOR BINDING SITES IN *PPD-1* GENE PROMOTER REGION

Kiseleva A.A.*[1,2], *Timonova E.M.*[1,2], *Berezhnaya A.A.*[1], *Kolozhvari A.E.*[1], *Kelbin V.N.*[1,2], *Salina E.A.*[2]

[1]*Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia*
[2]*Kurchatov Genomic Center, Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia*

**E-mail*: antkiseleva@bionet.nsc.ru

Wheat heading time stands as a crucial trait, significantly impacting plant yield and adaptability to environmental conditions. In our pursuit to engineer common wheat lines with tailored heading times and to dissect the genetic mechanisms governing this trait, we focused on the *PPD-1* genes responsible for wheat's photoperiod sensitivity. *PPD-1* genes are pivotal in determining heading time, with long deletions in their promoter regions leading to misexpression and accelerated flowering.

Employing CRISPR/Cas9 genome editing techniques, we engineered a series of wheat plants harboring diverse mutations within the promoter regions of *PPD-1* genes. These mutations encompassed nucleotide substitutions and indels of varying lengths, up to 500 base pairs, targeting regions housing binding sites for various transcriptional regulators. To elucidate the effects of these mutations, we conducted analyses of diurnal expression patterns of *PPD-1* under short-day conditions across 15 wheat lines. Our findings revealed that deletions spanning different lengths (ranging from 4 to 266 base pairs), which encompassed binding sites for the transcriptional repressor CHE, resulted in significant alterations in expression patterns compared to wild-type plants. These results substantiate the hypothesis positing these cis-elements as pivotal regulators of *PPD-1* expression. Furthermore, *PPD-1* variants harboring distinct mutations exhibited divergent expression patterns, suggesting the potential involvement of additional transcription factors in their regulation. Subsequently, we evaluated the phenotypes of T1 generation plants carrying various mutations, identifying individuals with accelerated heading times.

These findings collectively underscore the significant potential of genome editing in fine-tuning wheat heading time and shed light on the intricate regulatory networks governing this critical trait.

This work was done within the framework of State Assignment Kurchatov Genomic Center of ICG SB RAS (№075-15-2019-1662).

MAPPING OF QTL ASSOCIATED WITH RESISTANCE TO LEAF AND YELLOW RUST IN POPULATIONS OF RECOMBINANT INBRED WHEAT LINES

***Kokhmetova A.*[1], *Rathan N.D.*[2], *Sehgal D.*[3], *Kumarbayeva M.*[1], *Bolatbekova A.*[1], *Krishnappa G.*[4], *Gultyaeva E.* [5], *Kokhmetova As.*[1], *Keishilov Zh.*[1], *Bakhytuly K.*[1]**

[1]*Institute of Plant Biology and Biotechnology (IPBB), Almaty, Kazakhstan,*
[2]*Coverta Agriscience, India,*
[3]*Syngenta, Jealott's Hill International Research Centre, Berkshire, United Kingdom,*
[4]*ICAR-Sugarcane Breeding Institute, Coimbatore, India,*
[5]*All Russian Institute of Plant Protection, St. Petersburg-Pushkin, Russia*

E-mail: akokhmetova@gmail.com

Wheat stripe or yellow rust (YR) and leaf rust (LR) caused by *Puccinia striiformis* f. sp. *tritici* (Pst) and *Puccinia triticina* (Pt), respectively, are two important fungal diseases of common wheat (*Triticum aestivum*) across the globe. Stripe rust is a significant threat, it causes regular crop losses in the range of 0.1 to 5.0%, however, crop losses may shoot up to 5–25% based on varietal reaction and prevailing environmental conditions and in severe conditions, yield losses may reach up to 100%. The objective of the present study was to identify the novel genomic region(s) associated with the expression of yellow rust adult plant resistance (APR), leaf rust APR, yellow rust seedling resistance, or all-stage resistance (ASR), and leaf rust ASR two winter wheat recombinant inbred line (RIL) populations derived from a cross between Almaly × Avocet S (206 RILs) and Almaly × Anza (162 RILs). The RIL population was genotyped using DArTseqTM technology and phenotyped for APR in three environments (Almaly × Anza), APR in two environments (Almaly × Avocet S), and one environment for both leaf and yellow rust ASR. A linkage map was constructed, and QTLs and closely linked molecular markers associated with stripe and leaf rust resistance were identified. There are 51 QTLs including 22 for yellow rust APR, 11 for leaf rust ASR, and nine each for leaf rust APR and yellow rust ASR. Also, a set of 13 consistent QTLs including nine QTLs (*QYR-APR-2A.1, QYR-APR-2A.2, QYR-APR-4D.2, QYR-APR-1B, QYR-APR-2B.1, QYR-APR-2B.2, QYR-APR-3D, QYR-APR-4D.1, and QYR-APR-4D.2*) for yellow rust APR and four QTLs (*QLR-APR-4A, QLR-APR-2B, QLR-APR-3B,* and *QLR-APR-5A.2*) for leaf rust APR were identified. In the present study, only a few significant positive associations were reported between the races of the same rust or between the rusts or APR and ASR, these associations can be exploited in a breeding program for simultaneous improvement. Several putative candidate genes with important functions in the resistance mechanism of leaf and yellow rust were identified. Further validation and functional characterization of the candidate genes to elucidate the role of these genes in wheat is envisaged. The identified novel QTLs, particularly stable QTLs are useful for further validation and subsequent use in marker-assisted selection (MAS).

This research has been funded by the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan (Grant No. AP09258991), as well as by the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan (Grant No. BR18574099, the task 02).

EXPLORING THE RELATIONSHIP BETWEEN WHEAT TRAITS AND TOLERANCE TO RUST SPECIES AND TAN SPOT

Maulenbay A., Kurymbaeva N., Moldazhanova R., Rsaliyev A.

Research Institute for Biological Safety Problems, Guardeyskiy, Kazakhstan

E-mail: a.maulenbay@biosafety.kz

It is now widely recognized that plants employ two primary defense mechanisms against pathogens: resistance, which refers to the host's capacity to restrict pathogen multiplication, and tolerance, which denotes the host's ability to mitigate the negative impacts of infection. Despite extensive literature on wheat resistance to pathogens, tolerance has been relatively understudied.

Here, we examine the influence of morphological and immunological traits of wheat on tolerance to rust species and tan spot under an artificial infectious background. A total of 220 varieties of spring soft wheat and 80 varieties of winter wheat were investigated, with the experiments conducted using fungicides authorized for use in the territory of the Republic of Kazakhstan. In field conditions, the study examined the impact of wheat morphological parameters, as well as influence of the plant development phases such on tolerance to the rust species and tan spot. Additionally, the study investigated the effect of the infection type and severity on tolerance to fungal diseases.

The analysis of variance revealed a statistically significant difference in yield parameters among plots of the same samples affected by pathogens and those protected by fungicide in the experiment ($p<0.0001$). On average, the infected wheat cultivars exhibited a 6% increase in stem height and a 19% increase in flag leaf area, resulting in a 28.5% increase in yield parameters compared to fungicide-protected samples.The application of the principal component method unveiled a statistically significant effect of flag leaf area and plant height on the main factors (PC1), explaining 39.19% of the total variance. Immunological parameters also influenced the main factors (PC1), explaining 32.10% of the variability. Here, we explore traits that have the potential to measure various forms of tolerance.

Research funding: «Determination and conservation of wheat accessions with tolerance mechanisms to major fungal diseases» AP14870987.

FIRST REPORT OF ALTERNARIA ALTERNATA CAUSING EARLY BLIGHT OF TOMATO (*SOLANUM LYCOPERSICUM* L.) IN KAZAKHSTAN

***Yessimseitova A.*[1,2]., *Abdrakhmanova A.*[1,3]., *Kakimzhanova A.*[1]**

[1]*National center for biotechnology, Astana, Kazakhstan;*
[2]*S. Seifullin Kazakh Agrotechnical Research University, Astana, Kazakhstan;*
[3]*L.N. Gumilyov Eurasian National University, Astana, Kazakhstan;*

E-mail: asel_1388@bk.ru

Tomato (*Solanum lycopersicum* L.) is one of the most widespread vegetable crops in the world. Tomato fruit is a source of vitamins A and C and also contains lycopene, an antioxidant that protects the body from cancer and heart disease. However, widespread tomato production is hampered by biotic and abiotic stresses. Among the biotic stresses, early blight is one of the most damaging diseases of tomatoes in the world, and yield losses can reach from 35 to 80%. Plant material was collected in the fall of 2023 in the fields of the Kazakh Research Institute of Fruit and Vegetable Growing (FVRI), Almaty; a total of 200 samples of infected tomato leaves were collected. Small spots of gray and brown color increased in size as the disease progressed, and leaves defoliated. To isolate a pure culture of the fungus, pieces of the deseased tissues were transferred to petri dishes with potato carrot agar (PCA) and incubated at 25ºC.

The colonies initially appeared grayish-white and then turned dark green. The conidia (n = 50) were ovoid, measuring 9 to 42.9 µm x 4.3 to 13.6 µm with 2 to 7 transverse septa. The morphological characters corresponded to those of Alternaria spp. (Simmons 2007). For molecular identification, DNA was extracted from the mycelium of a purified single colony, amplified with universal primers ITS4/5, and sequenced. As a result, the analysis of the ITS segment of nucleotides 597 bp in length. showed 100% homology with the A. alternata accession MK972909.1 registered in the GenBank. To confirm the pathogenicity of A. alternata isolates, conidia were collected from a culture on PCA medium. The resulting spore suspensions were brought to a concentration of 10^6 per ml, with which healthy individual leaves of the Surpriz tomato variety were inoculated. Inoculated tomato leaves were placed in sterile plastic containers and incubated for 14 days at 25ºC. After 7 days, round or oval brown spots of disease were visible. The pathogen A. alternata was isolated to fulfill Koch's postulates. Morphological identification and sequencing confirmed the presence of A. alternata. These data form the basis for diagnosing and managing this disease.

The research is conducted in the framework of the project AR19679502 with financial support from the Ministry of Science and Higher Education of the Republic of Kazakhstan (duration: 2023-2025).

GWAS OF SOYBEAN BREEDING COLLECTION FOR YIELD AND SEED QUALITY GROWN IN SOUTH-EAST OF KAZAKHSTAN

Zatybekov A.[1], Abugalieva S.[1], Didorenko S.[2], Fang Ch.[3], Turuspekov Y.[1]

[1]Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan
[2]Kazakh Research Institute of Agriculture and Plant Production, Almalybak, Almaty region, Kazakhstan
[3]School of Life Sciences, Guangzhou University, Guangzhou, China

Soybean stands as the globe's primary oilseed crop, comprising approximately 60% of worldwide production. The vegetable oil derived from soybeans serves as a crucial protein source suitable for both human and animal consumption. Rich in heart-healthy lipids, it also offers soymeal, a protein-rich feed for livestock, poultry, and aquaculture. Augmenting soybean yield and seed quality remains a central challenge in its breeding and cultivation. Contemporary genomic research methods offer promise in enhancing breeding efforts aimed at improving soybean productivity and seed quality traits. Thus, this genome-wide association study (GWAS) aimed to scrutinize a soybean collection comprising 252 accessions concerning yield and seed quality traits. The collection underwent field evaluation in Kazakhstan's South-eastern region, a key area for soybean production. The study primarily sought to pinpoint quantitative trait loci (QTL) linked to yield components and seed quality. Leveraging resequencing data from 2,019,772 SNP markers via the Illumina HiSeq X Ten System, GWAS identified 145 marker-trait associations (MTAs) pertaining to yield components and seed quality. Among these, 91 exhibited associations with both yield components and seed quality, showcasing a pleiotropic effect. Notably, comparison with previously documented QTLs associated with these traits revealed that 49 of the identified associations were likely novel. These findings offer valuable insights for enhancing local breeding initiatives, particularly through marker-assisted selection approaches.

The authors would like to acknowledge the funding from the Ministry of Science and Higher Education of the Republic of Kazakhstan for the grant AP13068118.

INTRODUCTION, STUDY OF NEW FOREIGN AND DOMESTIC COTTON VARIETIES

Makhmadjanov S.P., Tohetova L.A., Daurenbek N.M., Tagaev A.M., Kostakov A.K., Aliev A.I.

LLP "Agricultural Experimental Station for Cotton and Melon Growing", Atakent village, Turkestan region

E-mail: kazcotton1150@mail.ru

The purpose of the research is to form, replenish, preserve, study, document and use genetic resources in cotton breeding and seed production.

Main areas of research: Collection, study, storage, documentation, use in breeding and seed programs.

The object of research is the culture of medium-fiber and fine-fiber cotton varieties.

The scientific significance lies in replenishing and preserving the gene pool of this crop, maintaining a collection of gene resources, studying economically valuable, biological characteristics and identifying donors for further breeding programs.

In 2021-2023, according to the planned calendar plan, a nursery was founded to study the collected material from local 127 samples of the Republic of Kazakhstan and 73 foreign samples of cotton genetic resources. In the process of studying the number of days from sowing to 50% ripening, when compared with the standard variety M-4005, it was revealed that 15 samples with a ripening period of 118-119 days were classified in the ultra-early ripening group. The early ripening group included 134 samples with a ripening period of 120-129 days. The mid-ripening group included 43 samples with a ripening period of 130-143 days, the late-ripening group included 8 samples with a ripening period of 143-153 days. The fiber yield showed that 119 samples exceeded the standard grade by 0.2-3.6%. In terms of fiber length, 157 samples exceeded the M-4005 standard by 0.1-1.4 mm. From the studied collection of genetic resources of 200 samples, 20 samples were selected based on high economically valuable traits. The yield of all 20 selected samples was very high, 46.5-74.9 c/ha, the excess over the standard variety M-4005 was high, the excess was 131.4-240.8%. 10 donor varieties M-4011, Myrzashol-80, M-4017, M-5027, Atakent-2010, M-4007, PA-3044 PA-3031, Bereke-07, M-5030 were selected based on basic economic and biological characteristics . The selected donor varieties for 3 years in the amount of 10 pieces in terms of early ripening, the ultra-early ripening group includes 8 samples with a ripening period of 115-119 days, 1 sample in the early ripening group with a ripening period of 125 days, 1 sample in the mid-ripening group with a ripening period of 135 days. 50 samples were transferred for use in the breeding process to the scientific divisions of LLP " Agricultural Experiment Station Cotton and Melon Growing" to the selection department.

300 samples of them are documented: 236 samples of Kazakhstan selection, 46 samples of Uzbek selection, 10 samples of Turkish selection, 3 samples of Chinese selection, 1 sample of Pakistan selection, 1 sample of Argentina selection, 1 sample of Brazilian selection, 1 sample of South African selection, 1 sample of USA selection .

100 samples were transferred to the genetic resources of Kazakh Scientific Research Institute of Agriculture and Plant Growing LLP with a description of economically valuable traits. Of the 100 samples deposited, 54 samples were identified for technological qualities, 47 samples for productivity, of which 43 samples showed themselves to be resistant to diseases during long-term testing.

The total number of cotton samples is 650. The structure of the gene pool includes 491 samples of national selection, including 31 ancient (15-20 years old) varieties of local selection, material from other countries - 159 samples.

The research is carried out with the financial support of the Ministry of Science and Higher Education of the Republic of Kazakhstan within the framework of grant funding for scientific and (or) scientific and technical projects for 2023-2025, grant No. AP19676175.

IDENTIFICATION OF ALLELIC DIVERSITY OF VERNALIZATION GENES (*VRN*) IN SAMPLES OF THE WORKING COLLECTION AND VARIETY BREEDING NURSERY OF WINTER AND SPRING BARLEY

Yerzhebayeva R.S., Bazylova T.A., Maykotov B.N., Baymuratov A.Zh., Sariev B.S.

LLP "Kazakh Research Institute of Agriculture and Plant Growing"

Barley (*Hordeum vulgare* L.) is an important multi-purpose food and feed crop. As an early ripening, drought- and salt-tolerant crop, barley is cultivated in almost all regions of the country. The area under barley cultivation in Kazakhstan is 2,175.7 thousand hectares (https://stat.gov.kz/). For each climatic zone of the Republic of Kazakhstan, varieties with a certain duration of the growing season are required. In barley, control of the duration of the germination–earing period is mainly carried out by the genetic systems of the Vrn (vernalization response) and Ppd (photoperiod response) genes. The variety of combinations of alleles of the Ppd and Vrn genes found in barley determines the adaptation of plants to different environmental conditions. To date, molecular markers have been developed for barley that allow the identification of Vrn and Ppd alleles in large samples of varieties and breeding lines using PCR and restriction analysis. The purpose of this study is to introduce DNA markers into practical breeding of barley for adaptability genes (Vrn and Ppd).

At the first stage, the allelic diversity of VRN genes was identified in samples of the working collection and senior breeding nurseries of winter and spring barley of the «Kazakh Research Institute of Agriculture and Plant Growing» LLP. Allelic polymorphism of vernalization genes of 196 accessions of the spring and winter barley collection was represented by the following combinations: VrnH1 vrnH2 vrnH3, vrnH1 VRNH2 vrnH3, VRNH1 vrnH2 VRNH3. It was established that the entire working collection of spring barley (100 samples) was represented by one combination VrnH1vrnH2vrn-H3. Identification of allelic variation of vernalization genes in collection samples makes it possible to draw up crossing schemes to obtain the desired combinations.

In 45 samples of the competitive variety testing nursery of spring barley, the following allelic variations of vernalization genes were identified - VrnH1 vrnH2 vrnH3, VrnH1 VRNH2 vrnH3, VrnH1 vrnH2 VRNH3. In 19 samples of the competitive variety testing nursery winter barley nursery, the following allelic variations of vernalization genes were identified: vrnH1 vrnH2 vrnH3, vrnH1 VRNH2 vrnH3. Identification in variety breeding nurseries makes it possible to predict the length of the growing season and carry out selection and differentiation for different regions of Kazakhstan.

The second stage is planned to use DNA markers in segregating hybrid populations and the KP nursery (control nursery).

This research has been funded by the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan Grant AP19678544 (2023-2025 y.)

EVALUATION OF POTATO GERMPLASM FOR RESISTANCE AGAINST PATHOGENS AND PESTS: TOWARDS SUSTAINABLE AGRICULTURE

Adilbayeva K.[1], Moisseyev R.[1], Nizamdinova G.[1], Khassanov V.[2], Azhimakhan M.[2], Gritsenko D.[1]

[1]Institute of Plant Biology and Biotechnology
[2] S. Seifullin Kazakh Agro Technical University

**E-mail*: kamila.adilbayeva@gmail.com

Potato (*Solanum tuberosum ssp. tuberosum L.)* is the fourth most important human food crop in the world after rice, wheat and maize, and the first non–grain among them. In Kazakhstan, potato is considered to be a staple food and is second only to wheat. However, infectious diseases caused by a number of pathogens and pests, including viruses, nematodes, oomycetes, and fungi lead to significant damage to crops, and the yield losses caused by them range from 20% to 80% worldwide. Furthermore, approximately 90% of the potato seeds utilized in Kazakhstan's agricultural sector are imported from Europe. This substantial reliance on foreign seed sources leads to the accidental introduction and exchange of various pathogens, including novel strains, isolates, and even new species, posing risks to local crop health and biosecurity, and requiring stringent monitoring and management practices. One of the prospective schemes aimed at pathogens and pests is cultivation and implementation of resistant varieties in mass breeding programs by DNA markers tightly linked to resistance genes.

In this study 352 potato genotypes from different origins grown in Kazakhstan were screened for the presence of resistance genes to the most harmful and economically important viral and fungal pathogens as well as nematodes using 30 DNA markers. These markers are tightly linked to *R*-genes that determine natural resistance to pathogens and pests. Resistance to PVY was evaluated by resistance genes: *Radg* (markers ADG1, ADG2, RYSC3), *Rysto (*STM003, SCARysto4), *Ry-fsto* ($GP122_{718}$) and *Rychc* (RY186). CAPS markers, SPUD237 and CP60, associated with *Nb* and *Rx*, respectively, were used to determine an extreme resistance response to PVX. For the detection of *Rladg*, conferring resistance to PLRV, RGA-derived SCAR marker RGASC850 was applied. Two CAPS markers, SC811 and CP16 were used to confirm genetic resistance to PVS. The presence of *Globodera rostochiensis* resistance genes was assessed by TG689, 239E4left, N146 N195 (*H1*), Gro1-4 (*Gro1*), U14, SCAR-X02 (*GroV1*) markers. C237 and GP34 were selected for determining $GpalV^{s}_{adg}$ and Gpa2 *Globodera pallida* resistance genes, respectively. Resistance to potato late blight was conducted by the following markers: GP76, BA47f2 *(R1),* $R1_{1400}$ *(R1),* GP179 *(R1),* 45/XI *(Rpi-Smira1),* CT214 *(Rpi-ber 1),* GP94 *(Rpi-ber 1).* N125 was used as the only marker for the evaluation of resistance to potato wart.

In the present study, two cultivars from Russian breeding programs, namely ‘Rucheek’ and ‘Spiridon’, have emerged as the most prominent for bearing resistant loci to different pathogens and pests, with 17 and 15 markers tested positively out of 30 analyzed, respectively. They are followed by the top cultivars: ‘Jigulevskii’, ‘Kolobok’, and ‘Resurs’ (Russia); ‘Fedor’ and ‘Janaisan’ (Kazakhstan); ‘Fioretta’ (Germany); ‘Escort’ and ‘Kondor’ (Netherlands); ‘Montana’ (USA); ‘Jivica’ and ‘Dina’ (Belarus). All these specimens were positive at least for 14 markers. Six potatoes viz., ‘Berkut’, ‘Janaisan’, ‘Maksim’, ‘Fedor’ cultivars and ‘42-16-03’, ‘12-15-03’ hybrids were superior within Kazakhstani selection, while no positive results were obtained with ‘21-16-03’, ‘04-08-02’ kazakhstani hybrids. Most of the specimens analyzed in the study exhibited resistance loci to potato viruses Y and X, rather than to other viruses. Dutch cultivar ‘Kondor’ was the only one that was characterized by the presence of simultaneous two resistance alleles to *G.pallida.* 57 out of 356 occasions were positive for single marker NL25, linked to the wart-resistance gene.

Identified potatoes with the highest resistance loci could have a great potential for further MAS and gene pyramiding strategy to develop new extreme resistance potato varieties. Further investigations include virus inoculation tests to ensure their 100% reliability and integration in breeding selection.

GENETIC DIVERSITY AND ASSOCIATION ANALYSIS OF SALT TOLERANCE IN ASIATIC COTTON (*GOSSYPIUM ARBOREUM*) WITH SSR AND SNP MARKERS

***Tussipkan D.,* Manabayeva S.A*.**

National Center for Biotechnology, 13/5, Qorghalzhyn Hwy., Astana, 010000, Kazakhstan

**E-mail:* manabayeva@biocenter.kz

Soil is a vital resource for feeding the growing global population. Excess soil salinity poses a significant threat to agricultural production and environmental health. Increased salt tolerance of perennial species used for fodder or fuel production is an important and natural method for controlling the spread of secondary salinity. However, different crop species have different threshold tolerance. Cotton is one of the advantageous salt-tolerant crop with a threshold salinity level of 7.7 dS·m−1.

This study was carried out to identify marker-trait association analysis using 7 traits and one comprehensive index of salt tolerance (CIST) and SSR and SNP markers for 215 accessions of Asiatic cotton (*G. arboretum*). The traits related to salt tolerance like germination rate (GR), fresh weight (FW), stem length (SL), water content (WC), chlorophyll content (ChlC), electric conduct (EC) and methylene dioxyamphetamine (MDA), of 215 cotton accessions were screened out using 150mM NaCl concentration after 7 days of seed growth. According to a comprehensive index of salt tolerance (CIST), 215 accessions were mainly categorized into four groups, and 11 accessions (top 5%) with high salinity tolerance were selected for breeding. Group 1 contained 12 accessions that were sensitive to high salt treatment (<0.6), group 2 contained 26 accessions that were moderate tolerant to salt treatment (0.6～1.5), group 3 includes 153 accession that were tolerant (1.5～2.5), and group 4 had 24 accessions that were highly tolerant to salt treatment (>2.5).

The natural population of 215 accessions of *G. arboretum* was first classified into 3 main groups by phylogenic analysis, in which Group 2 (G2) and Group 3 (G3) represented the Yellow River and Yangtze River accessions respectively, while Group 1 (G1) contained mixed cotton accessions which belongs to different cotton growing areas in China. The grouped accessions results were largely congruent with the breeding history and ecological region, which indicates the extensive genetic diversity of *G. arboretum* accessions both in phenotype and genotype.

The relative value (R) of the traits was used for marker-trait association analysis. Twenty-two strong SSR marker-trait associations were obtained with strict significant P value i.e. P< 0.01 and four makers including NAU1023, NAU1099, JESPR222, and NAU2783 were significantly related to salt tolerance. The marker NAU2783 was highest associated (P= 1.98E-12) with REC, and with the highest phenotype variation of 20.87%. Some markers are significantly associated with more than two traits. MUSS020 was significantly (P<0.01) related with RFW, and RMDA, NAU1375 was associated with RFW and RSL, while NAU3468 was significantly associated with RFW, RGR, and RWC.

By applying the threshold of $-\log_{10} P \geq 4.0$, the 2062 SNP markers covered all 13 chromosomes and 100 SNP markers locations that were unknown. Among these 2062 marker-trait associations, 61 markers were associated with RGR, 187 markers were associated with RFW, 255 markers were associated with RSL, 370 markers were associated with RWC, 190 markers were associated with RChlC, 583 markers were associated with REC, 335 markers were associated with RMDA and 81 markers were associated with CIST. The nine SNP rich regions analysis revealed 143 polymorphisms that distributed 40 candidate genes and significantly associated with salt tolerance. Notably, two SNP rich regions on chromosome 7 were found to be significantly associated with two salinity related traits, RFW and RSL, by the threshold of $-\log10P \geq 6.0$, and two candidate genes (Cotton_A_37775 and Cotton_A_35901) related to two key SNPs (Ca7_33607751 and Ca7_77004962) were possibly associated with salt tolerance in *G. arboreum*. The classification information derived from these studies may be used to facilitate the development of salt tolerant cotton accessions that could give economic yield in salinity prone areas. The strong marker-trait association results might provide insights for marker-assistant selecting salt-tolerant varieties and will be useful for future cotton breeding programs.

ESTABLISHMENT OF THE FIRST "SPEED BREEDING" FACILITY FOR THE USE OF WHEAT BREEDING IN KAZAKHSTAN: PERSPECTIVES AND PROSPECTIVES

Abduakassov A.*[1], *Mahmood Z.*[2], *Baimyrzayev K.*[1], *Yermekbayev K.*[1]

[1] *Zhetysu University, Institute of Biotechnology and Ecology, Taldykorgan, Kazakhstan*
[2] *National Agricultural Research Centre, Islamabad, Pakistan*

**E-mail:* kanat.yermekbayev@gmail.com

The major limiting factor of the current plant breeding is a prolonged timeline required for the new crop variety development with outstanding adaptive characteristics. Currently, a challenge of significantly shortening the breeding cycle is being addressed through the "speed breeding" technique which is developed to accelerate the breeding of crops, particularly for the purpose of creating new varieties or improving existing ones. The method is based on optimized growth conditions, such as light, temperature, and nutrients, to promote rapid growth and reproduction in plants. The technique has already been adapted to many economic agricultural crops such as wheat, barley and rice. Thus, the establishment of speed breeding platform is particularly valuable in Kazakhstan facing challenges such as stagnated grain yield, climate change, pests and diseases in wheat breeding. Despite the fact that Kazakhstani wheat is a vital contributor of regional and global food security, the entire sector is in danger due to economic inefficiencies and governmental regulations aimed at reducing its growing area. These challenges could potentially be addressed through the rapid creation of wheat varieties with traits such as drought tolerance, disease resistance, and/or improved yield and quality. Here, we discuss the challenges that we faced while establishing the first speed breeding facility in Kazakhstan for wheat breeding and its potential prospects.

EVALUATION OF PROSO MILLET (*PANICUM MILIACEUM* L.) GERMPLASM ON AGRONOMIC TRAITS UNDER CONDITIONS OF DRY-STEPPE ZONE OF KAZAKHSTAN

Abylkairova M., Dyussibayeva E., Rysbekova A.

S. Seifullin Kazakh Agrotechnical Research University, Astana, Kazakhstan

E-mail: margarita.abkv@gmail.com

Proso millet is a short season crop with low water requirement and high resistance to heat, salt and drought. It is valued for its extreme soil and climatic conditions tolerance as it yields reasonable harvest even in degraded soils under unfavorable weather conditions. In Kazakhstan, Russia and India, the breeding of proso millet is mainly aimed at high yield, large grain size, yellow seed coloring; so, the breeding process is mainly based on morphological and biological traits (Kotlyar at al., 2016; Dyusibayeva at al., 2016; Sidorenko at al., 2006).

The objective of this study was to evaluate and give an agronomic characterization of proso millet germplasm under conditions of dry steppe zone of Kazakhstan for identification of the most important accessions. A total of 90 proso millet accessions were used as materials, originating from 19 countries. The field experiments of the nursery collection were laid in the conditions of Akmola and Aktobe regions. During the study of the worldwide collection of proso millet, which contained 61 foreign varieties and 29 local varieties, phenotypic variability was recorded with a focus on the most important seven agronomic traits and the climatic conditions of the place of growth. As a result, it was revealed that in soil-climatic conditions of A.I. Baraev SPC GF (Akmola region) the average value of plant height ranged from 63.1 to 95.6 cm. In the conditions of Aktobe Agronomical Experimentation Station (Aktobe region), the same trait varied from 67.4 to 99.2 cm. The number and the weight of grains from the main panicle had the most significant association to growing conditions. Observations in the experimental areas showed that there was a fluctuation in the number of panicle grains in the conditions of A.I. Baraev SPC GF: 460±10.9 pieces in average, 706±16.6 pieces for the western region, the weight of panicle seeds: 2.6±0.09 and 2.55±0.08, respectively. Productive bushiness was 1.0-1.5 piece per plant in average in the conditions of Akmola region; on the contrary, this trait differed significantly in the conditions of Aktobe region: 0.8-3.8 piece per plant plant. The obtained field data show that though the plants were grown in the different regions of Kazakhstan and were formed in contrasting soil and climatic conditions, they do not differ in their yield traits, such as seed weight per panicle and weight of 1000 seeds. Average indicators affecting productivity of proso millet genotypes in the terms of the mass of 1000 seeds amounted to 5.7 g in the conditions of A.I. Baraev SPC GF, and to 6.45 g in Aktobe Agronomical Experimentation Station, respectively. Evaluation of the average grain yield of proso millet varieties revealed that the yield of the northern region (225-1248 g/m^2) was almost twice higher than the one of the western region (49.0-668.0 g/m^2). The difference in productivity between the two regions was 209 g/m^2. The study of seed productivity of proso millet plants per square meter allowed to identify the most productive genotypes, such as: Saratovskoye 3 (608.5 g/m^2), PI 209790 (635.3 g/m^2), K-2241 (636.0 g/m^2), Shortanda 7 (713 g/m^2), PI 177481(720.3 g/m^2), PI 211058 (738.5 g/m^2), K-2468 (1206.2 g/m^2); they managed to give a stable yield regardless of climatic conditions prevailing the year of research. According to the vegetation period, the collection can be divided into three groups: fast-ripening (67-70 days); mid-ripening (71-99); late-ripening forms (100 and more). In the current year, the vegetation period of three samples was shorter by 3.3% compared to the standard. In the Aktobe region, 18 varieties of the domestic collection had a growing season 20% shorter than the local standard Pamyati Bersieva. The studies conducted in this region showed that the vegetation periods of 27 foreign genotypes were shorter than Pamyati Bersiyeva local standard variety. According to the results of phenological observations the vegetation period averaged 90.4±2.1 days in the conditions of A.I. Baraev SPC GF. In the conditions of Aktobe Agronomical Experimentation Station it was shorter by 13.8 days and averaged 75.8±2.3 days.

As a result of research, the evaluation of proso millet initial material on traits was carried out and the varieties featuring high indices of growth, development and resistance to stress were selected. Promising permanent lines were selected for the conditions of dry-steppe zones of Kazakhstan according to structural analysis.

GENOME-WIDE ASSOCIATION STUDY OF PLANT ADAPTATION TRAITS IN NESTED ASSOCIATION MAPPING POPULATION GROWN IN KAZAKHSTAN

***Amalova A.*[1], *Babkenov A.* [2], *Philp C.* [3], *Griffiths S.*[3], *Abugalieva S.*[1], *TuruspekovY**[1]**

[1] *Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan*
[2] *A.I. Barayev Research and Production Centre of Grain Farming, Shortandy, Akmola Region, Kazakhstan*
[3] *John Innes Centre, Norwich, United Kingdom*

**E-mail:* yerlant@yahoo.com

In this study, we evaluated 290 recombinant inbred lines (RILs) of Nested Association Mapping (NAM) population of spring wheat from the UK. The population derived from 24 families, where the common reference parent was "Paragon" which is a spring elite cultivar from UK. All lines were tested in 2019-2022 in two regions of Kazakhstan: at the Kazakh Research Institute of Agriculture and Plant Industry (KRIAPI, Almaty region, Southeast Kazakhstan) and A.I. Barayev Research and Production Center for Grain Farming (SPCGF, Shortandy, Akmola region, Northern Kazakhstan).

The NAM population was evaluated on plant adaptation-related traits, including heading date (HD, days), seed maturation date (SMD, days), plant height (PH, cm), and peduncle length (PL, cm). In addition, the yield per m^2 (YM2, g/m2) was analyzed in both regions. GWAS was performed based on the population field-testing in five conditions and genotyping data of 10,448 polymorphic SNP (single-nucleotide polymorphism) markers, allowed for the detection of 81 QTLs for four studied agronomic traits. The Pearson correlation index showed a positive correlation between HD and PH and between PH and PL for both regions. The principal component analysis divided 290 RILs using PC1 (36.6%) and PC2 (21.6%). It appears that HD and SMD in the graph were forwarded in alternative directions. The assessment of the average YM2 values suggested that 11 and 60 RILs showed higher values than local check cultivars at KRIAPI and SPCGF, respectively. The results of research will be used for further studies related to adaptation and productivity of wheat in the breeding program.

This research was funded by the Ministry of Science and Higher Education of the Republic of Kazakhstan (grant AP14871383).

GENOME-WIDE ASSOCIATION STUDY OF LEAF RUST AND STEM RUST SEEDLING AND ADULT RESISTANCES IN TETRAPLOID WHEAT ACCESSIONS HARVESTED IN KAZAKHSTAN

***Anuarbek Sh.*[1], *Genievskaya Y.*[1], *Zatybekov A.*[1], *Pecchioni N.*[2], *Laidò G.*[2], *Rsaliyev A.* [3], *Chudinov V.* [4], *Turuspekov Y.*[1], *Abugalieva S.*[1]**

[1] *Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan*
[2] *Research Centre for Cereal and Industrial Crops, Foggia, Italy*
[3] *Research Institute of Biological Safety Problems, Gvardeisky, Zhambyl Region, Kazakhstan*
[4] *Karabalyk Agricultural Experimental Station, Nauchnoe, Kostanai Region, Kazakhstan*

E-mail: shynar.anuarbek@yahoo.com

Leaf rust (LR) and stem rust (SR) are diseases that increasingly affect wheat production worldwide. Fungal pathogens that cause rust diseases in wheat can cause yield losses of up to 50–60%. One of the most effective ways to prevent such losses is to create resistant cultivars with high-yield potential. Achieving this goal necessitates extensive breeding research, including the identification of key genetic factors that control rust resistance. The purpose of this study was to identify the sources of tetraploid wheat resistance to LR and SR races at both the seedling growth stage in the greenhouse and the adult plant stage in field experiments conducted in the North Kazakhstan region. In a genome-wide association study (GWAS), we utilized a panel of 193 tetraploid wheat accessions to investigate plant development in both seedling and adult stages. With 16,425 polymorphic SNP markers, we aimed to identify QTLs associated with LR and SR resistance. The panel under investigation comprised seven tetraploid subspecies (*Triticum turgidum* ssp. *durum*, ssp. *turanicum*, ssp. *turgidum*, ssp. *polonicum*, ssp. *carthlicum*, ssp. *dicoccum*, and ssp. *dicoccoides*). A GWAS analysis of the tetraploid collection identified 38 QTLs ($p < 0.001$) related to response to two rust species at seedling and adult stages: 17 for LR resistance and 21 for SR resistance. Ten QTLs were associated with the reaction to LR at the seedling stage; six QTLs were at the adult plant stage; and one QTL was at both the seedling and adult stages. Eleven QTLs were linked to SR response at the seedling stage, nine at the adult plant stage, and one at both stages. When these findings were compared to previous LR and SR studies, 11 of the 38 QTLs were identified as potentially novel loci. The identification of these QTLs in this study opens up the possibility of using them for marker-assisted selection of tetraploid and hexaploid wheat in breeding new LR- and SR-resistant cultivars.

This research has been funded by the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan (AP14871383).

NEW FAD OF THE KAZAKH UNIVERSITY BEAN COLLECTION: INTRODUCTION OF SNAPS

Aytasheva Z., Zhumabayeva B., Smekenov I., Lebedeva L., Dauletbayeva S., Chunetova Z.

al-Farabi Kazakh National University, Almaty, Kazakhstan

E-mail: zaure.aitasheva@kaznu.kz

The aim of this study was to ascertain the introduction potential of the three snap common bean cultivars from Great Britain in the mountain site of Almaty Region in 2023.

Previously, since 1972, the bean collection has been generated for many years by graduates of different years of the Kazakh National University, founders and associates of the Institute of Plant Biology and Biotechnology celebrating its 30-th anniversary (F.A. Polimbetova, L.K. Mamonov, O.N. Taranov, and one of the authors of this abstract). Between 2006 and 2022, the collection enlisted more than forty cultivars and accessions, and more than half of it was studied including bean batches from the Russian Federation, EU, USA, and Kazakhstan. Besides, the adzuki cultivars from stocks of the Japanese Genetic Foundation were examined. This became possible thanks to the implemented project 0213PK01168 "The establishment and comprehensive assessment of bush high-protein bean specimens and lines" (2012-2014). Propagation of domestic bean forms, and maintenance of the existing collection takes place these days in the mountainous zone of the Almaty Region, owing to exceptional enthusiasm of the staff of the Department of Molecular Biology and Genetics of the Kazakh National University.

Seeds of common bean, *Phaseolus vulgaris* L. (lines "Aktatti", "Karakoz", "Dzhungarskaya" (Kazakhstan), and snap bean cultivars "Amethyst", "Impero bianco", "Seline" from Great Britain, etc.) were planted on plots in the mountainous site of the Almaty Region. Each specimen was trialed on an area of 0.04 ha by applying the own computer program "Planting Manager" to plan the sown areas. Cultivars and lines were sown as 20-28 seeds in rows, at a half-meter distance in three replicas.

Plant structural analysis comprised of productivity, the dynamics of the stem elongation and the upper leaf parameters, bean (pod) size, number of pods and seeds per plant, and seed weight per pod. Wax leaf imprints were sampled in the end of July, at 68-74 days after planting from the adaxial surface with the following microphotography with the Axioscop FL-40 at X10 magnification.

Harvest time, plant growth dynamics, leaf expansion, its trichomes completed by the snaps productivity at technical maturity were identified. Cultivars "Amethyst" and "Seline" proved to be suitable snap breeding donors for local bush bean forms owing to their seed germination, plant leaf size and trichome parameters, alike to the domestic forms under trial.

Harvesting as investigating beans should be promoted in Kazakhstan for the following mainstream reasons: I, Supporting the food and superfood supply; II, The ancient human history and precious cultural values; III, Soil enrichment enabled by the beans and nitrogen fixers; IV, Water export in kinds of the beans delivery by the most prosperous countries; V, Ornamental worth of beans; VI, Use of bean collections for educational, commercial, agricultural skill development and promotional aims; VII, Application of bean collections in bringing up future breeders, geneticists, agronomists, gardeners and landscape designers.

The ongoing study is supposed to lead to the introduction of useful genetic traits of the snap bean cultivars into the specimens of local breeding.

GENETIC AND PHYTOPATHOLOGICAL STUDY OF THE RESISTANCE OF WINTER WHEAT VARIETIES TO LEAF RUST *PUCCINIA TRITICINA*

Bakhytuly K., Mukhametzhanov K.

Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan

E-mail: kanat1499@gmail.com

Wheat is one of the economically important crops of our country. Kazakhstan is among the leading countries in the production and export of wheat. Leaf rust disease of wheat is one of the diseases that directly affect its yield. Leaf rust disease appears on wheat leaves. The causative agent of the disease is the fungus *Puccinia triticina*. Since leaf rust disease is a fungal disease, rust disease can also damage varieties that were once resistant to this disease, due to the ability to form new races. Even a little rain is enough to infect wheat. Before the flowering period of wheat, leaf rust causes significant damage to the plant. The affected fungi use nutrients that are formed in wheat leaves, necessary for grain formation, which leads to premature fall of wheat leaves and improper grain formation due to a lack of nutrients in the grain, which reduces wheat yield. For these reasons, it is economically important to identify varieties resistant to leaf rust. The research was carried out in the Almaty region, the village of Almalybak, at the Kazakh Research Institute of Agriculture and Plant Growing and in the Laboratory of Genetics and Selection of the Institute of Plant Biology and Biotechnology. Thirty varieties of winter wheat were taken as the object of research. NDVI (Normalized Difference Vegetation Index) was used to predict plant health and performance in winter wheat varieties grown under natural conditions. It was measured with the GreenSeeker device. The resistance of samples to leaf rust was assessed according to McIntosh et. al., 1995. In addition, the area under disease progress (AUDP - Area under disease progress) was also assessed in the field. After harvesting, an analysis of yield components was carried out for each wheat variety. This analysis was carried out by determining the following parameters: spike length, number of spikelets per spike, number of grains per spike, grain weight per spike, and weight of 1000 grains. As a result of a phytopathological study of the resistance of 30 wheat varieties to *Puccinia triticina*, the immune level of resistance was determined in varieties Alikhan, Keremet, Naz, Rasad, Taza, Tyngysh. As a result of the yield component analysis, the highest level of traits was shown by winter wheat varieties Alatau, Kyzylbiday, Mayra, Mereke 70, Naz, Raminal, Rasad, and Sapaly. Among the 30 varieties of winter wheat, according to the results of a general study, the varieties Alatau, Alikhan, Almaly, Kyzylbiday, Mayra, Mereke 70, Naz, Raminal, Rasad, Sapaly, and Tyngysh were distinguished by resistance to leaf rust and valuable yield traits of the farm.

This research has been funded by the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan (Grant No. BR18574149).

SEARCH FOR CARRIERS OF RESISTANCE TO SEPTORIA IN THE COLLECTION OF WHEAT VARIETIES AND PROMISING LINES

Bolatbekova A., Kokhmetova A., Kumarbayeva M., Keishilov Zh., Kokhmetova As.

Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan

E-mail: ardashka1984@mail.ru

Wheat is the main food crop for the world's population. In Kazakhstan, the 2021 wheat harvest was 11.8 million tons, significantly below the five-year average. The decrease in yield is due to a combination of abiotic (droughts, high temperatures) and biotic (diseases, pests) stresses. Septoria blight is one of the most destructive leaf spot diseases of wheat. Of the five fungi of the genus Septoria registered in Kazakhstan, the main species of the disease are *Stagonospora (Septoria) nodorum* Berk. and *Septoria tritici*, caused by the ascomycete *Zymoseptoria tritici* (anamorph of *S. tritici* and *Mycosphaerella graminicola*). Septoria blight is a serious problem for wheat in Kazakhstan, where yield losses amount to 15-30%, and during epiphytotic periods they can reach 40-50%. The development of Septoria causes premature death of leaves and glumes, which interferes with photosynthesis and reduces yield. Rainfall and temperature will influence the spread of the disease, and high CO2 levels will favor the development of the disease. Treatment with fungicides becomes ineffective due to the emergence of resistance alleles and the growth of pathogen strains that are insensitive to fungicides. Using fungicides requires large financial and environmental costs that are not available to developing countries. In this regard, selection for host plant resistance is the most economical, effective, and environmentally friendly strategy for combating septoria. The objects of the study were 220 varieties and lines of hexaploid wheat from Kazakhstan (58 pcs.), Russia (57 pcs.), Belarus (22 pcs.), as well as samples from international nurseries CIMMYT-SEPTMON (31 pcs.) and KASIB (Kazakhstan-Siberian wheat improvement network) (52 pcs.) and disease differentiator varieties. A contrast in the manifestation of traits of productivity and disease resistance characterized the objects. As a result of molecular screening, 70 genotypes with Stb resistance genes were identified from 220 varieties and promising lines of wheat. The following genotypes contained a larger number of genes: Omskaya 18 contains 2 genes – *Stb2, Stb8;* Samgay 2 genes – *Stb4, Stb7*; JAC161/TEMU51.80 2 genes – *Stb2, Stb8*; KR12-5035 also contains 2 genes – *Stb2, Stb7*. The remaining genotypes that showed resistance to Septoria contained one gene each. Based on these data, we recommend using these genotypes for crossing and breeding programs to improve resistance to Septoria.

This research has been funded by the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan (Grant No. AP14869967).

STUDY OF BREEDING-VALUABLE TRAITS AND SNP DISCOVERY IN RAPESEED MUTANT LINES

Daurova A[1]., Oshergina I.[2], Daurov D.[1], Sapakhova Z.[1], Zhapar K.[1], Shamekova M.[1], Zhambakin K.[1]

[1] Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan
[2] A.I. Barayev Research and Production Centre for Grain Farming, Shortandy, Kazakhstan

E-mail: a.daurova@ipbb.kz

Rapeseed (*Brassica napus*) is an important oil crop distributed worldwide with a broad adaptation to different climate zones, and is widely used as food, an animal feedstock, and biodiesel. The cultivation of rapeseed is one of the most commercially viable areas in crop production. In Kazakhstan, the northern regions are the most suitable for rapeseed cultivation. However, the rapeseed varieties grown at an industrial scale in Kazakhstan largely originate from foreign breeding programs. Consequently, the primary objective of country-specific selection programs is to establish a diverse genetic reservoir to develop new, high-yielding cultivars that suit Kazakhstan's climate condition.

We evaluated 46 doubled haploid mutant lines using ethyl methanesulfonate (EMS) from plant material of 'Galant' and 'Kris' cultivars to enhance the diversity of rapeseed in Kazakhstan. The development of mutant lines was performed via embryo callusogenesis or embryo secondary callusogenesis. The fatty acid composition of seed oil, the agronomic characteristics forming the yield, and the investigation of mutation load using SNP were considered. The analyses showed highly significant differences between the mutants and original cultivars in all the studied characteristics. Mutant lines DHK12-3, DHK12-4, DHK12-8, DHG12-16, DHG12-18, and DHG12-10 combined improved indicators of fatty acid composition with high yield. The obtained lines were homozygous since they were doubled haploids, and the stability of agronomic and qualitative traits was observed in two generations. The results obtained confirm the higher productivity of doubled haploid mutant lines, as well as their availability to variable environmental conditions. Using the Brassica90k SNP array, we analyzed these mutants and identified 24,657 SNPs out of 26,256 SNPs after quality control on the Bra_napus_v2.0 genome assembly. Among these, 18,831 SNPs were linked to annotated genomic features. Most loci with predicted variants contained single SNPs with significant predicted effects, which are subject to further evaluation concerning the genotypes and phenotypes of the obtained mutant doubled haploid plants.

In summary, the mutation load and rate in the prospective lines according to agronomic traits were investigated. Subsequently, an attempt to derive homozygous plants from most perspectives' lines by self-pollinating and via the isolated microspore culture will be carried out. Our results may improve molecular breeding for suitable SNPs among rapeseed mutants and could be useful for the development of novel cultivars for mutation breeding programs.

Moreover, in the results of two-year field experiments at the final stages of the breeding process these doubled haploid mutant lines in northern Kazakhstan were identified as perspective genotypes. One of them has been served for variety registration.

EFFECT OF NO IRRIGATION ON YIELD OF DOMESTIC SOYBEAN VARIETIES UNDER CONDITIONS OF SOUTHEAST KAZAKHSTAN

Didorenko S.V., Yerzhebayeva R.S., Amangeldiyeva A., Kassenov R.Zh.

Kazakh Research Institute of Agriculture and Plant Growing, Almalybak, Kazakhstan

E-mail: svetl_did@mail.ru

Soybean is the leading oilseed and legume crop in world agriculture. In Kazakhstan in 2022, sown areas amounted to 128.0 thousand hectares, and gross yield – 250.4 thousand tons (www.fao.org/faostat). The leader in sown areas of soybean are irrigated arable lands in Almaty and Zhetysu regions, where 83.6% of soybean crops are concentrated.

Growth and development of all agricultural crops are affected by abiotic and biotic stress factors. Water is still the main limiting abiotic factor that dramatically affects crop yields, especially for such a monsoon crop as soybean. According to our research, lack of moisture reduces soybean yield by 30-80% depending on the variety.

Depending on the genotype, soybean plants use about 450-700 mm of water during the growing season. According to FAO statistics for Kazakhstan, there is a trend of increasing temperature and decreasing precipitation over the last 10-15 years (https://www.fao.org/faostat/ru/#data/ET). In 2021-2023, the level of precipitation during the growing season of soybean in Almaty region was 210-250 mm. Increase in temperature background, decrease in precipitation, shallowing of rivers cause risks of timely and sufficient supply of soybean regions of southeast Kazakhstan with irrigation water.

There is a need to screen the available varietal diversity of soybean for the effect of lack of irrigation on yield.

In the conditions of Almaty region studied 33 varieties of domestic selection of 5 groups of ripeness on two backgrounds – with drip irrigation and without irrigation. In 00, 00 and 0 groups of ripeness, the minimum yield loss of varieties under conditions without irrigation was 62.5%, 60.3%, and 60.0%, and the maximum was 73.4%, 76.2%, and 69.1%, respectively. Cultivation of varieties of these maturity groups without irrigation in southeastern Kazakhstan is inexpedient. In late maturing varieties of II and III ripeness groups, the minimum yield loss was 29.2–48.9% and maximum 63.9–66.4%, respectively. Among the medium-late varieties of soybean of domestic selection were identified – Zhansaya, Akku, Danaya, Milka, Aisaule reaching yield at drip irrigation 40.8–58.1 c/ha, without irrigation at the level of 1.93–2.25 t/ha. Yield reduction in these varieties without irrigation in the conditions of southeastern Kazakhstan is at the level of 52.7–56.4 %.

The work was carried out under the grant project (2023-2025) of the Ministry of Science and Higher Education of the Republic of Kazakhstan, AP19677163.

GENOTYPING SOYBEAN COLLECTION FOR RESISTANCE TO *HETERODERA GLYCINES* ICHINOHE

Doszhanova B.N.*[1,2], *Suzuki T.* [3], *Zatybekov A.K.*[2], *Turuspekov Y.K.*[2]

[1] *Al-Farabi Kazakh National University, Almaty, Kazakhstan*
[2] *Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan*
[3] *Hokkaido research Organization, Sapporo, Japan*

**E-mail:* sybanbaeva_bota@mail.ru

Soybean cyst nematode (SCN), *Heterodera glycines* Ichinohe, has been one of the most devastating pathogens affecting soybean production worldwide. Infection of SCN can impact growth and yield by removing plant nutrients, disrupting water uptake, and preventing root growth. It can also reduce the number of root nodules and therefore inhibit nitrogen fixation. SCN-infected plants may also be more susceptible to the development of root rot and seedling diseases, due to openings in the root created by cysts. Once above-ground symptoms are noticed, up to 30% yield loss can already be expected.

Heterodera glycines Ichinohe is included in the list of quarantine objects of the Euroasian Economic Union, where Kazakhstan is from the beginning. For Kazakhstan soybean relatively new culture and grows mainly in southeastern regions, but every year sowing territories broaden to the east and northern parts of the country. One of the most effective methods for regulating soybean nematode infestation is proper crop rotation systems and the usage of resistant soybean cultivars. So, for that reason, it is very important to identify genetical resources of soybeans resistant to SCN.

According to the literature search, several QTLs associated with soybean cyst nematode (SCN) resistance genes, such as *Rhg4*, *rhg1*, and *rhg2* (resistance to *Heterodera glycines* 1, 2, and 4 races), were discovered and their mapping information has been used in different breeding projects. Among them, the *Rhg1* gene provides the strongest protection and is commonly used to deploy SCN resistance in soybean germplasm.

In our research, we analyzed 288 soybean accessions from different origins, including Kazakhstan, Eastern and Western Europe, East Asia, and Northern America countries. DNA was extracted from the young soybean leaves by the CTAB method. The genotyping analysis was performed by PCR methods with genetic markers to genes *rhg1*, *rgh2*, and *Rhg4* developed in Hokkaido research Organization (Sapporo, Japan).

The results of genotyping by the *rhg1* gene of the studied collection identified a resistant R allele on 13 accessions. Those were soybean cultivars from Eastern Europe (11 accessions), Kazakhstan (2 accessions, lines “308/1” and “350/1”) and East Asia (2 accessions, cultivars “Kan Nun 8”, “Kan Fen 20”). Two accessions which have resistant allele on the *rhg2* gene were from Kazakhstan (cultivar “Nadezhda”) and East Asia (cultivar “Kan Nun 8”). The resistant allele according to the *Rhg4* gene were found on the two accessions from East Asia (cultivar “Xinjiang D10-135” and line “1065”), and one from North America (cultivar “Cobb 266”). Eastern Europe genotype, line “R121427”, had resistant allele for two genes *rhg1* and *Rhg4*, Chinese cultivar “Ken Nun 8” had resistant allele for two genes *rhg1* and *rhg2*. All identified soybean genotypes are important genetic resources and can be recommended for future breeding programs in developing SCN resistant soybean cultivars.

STUDY OF THE GENETIC DIVERSITY OF COLLECTION FORMS OF WILD SOYBEANS (*GLYCINE SOJA*) BASED ON AGRONOMIC CHARACTERS

Galichenko A.P.

Federal State Budget Scientific Institution Federal Research Center «All-Russian Scientific Research Institute of Soybean», Blagoveshchensk, Russia

E-mail: gap@vniisoi.ru

Soybean (*Glycine max (L.) Merr.*) is one of the economically important crops worldwide used as food for both humans and livestock. Although soybean yields have increased over the past century, soybean production still cannot meet the needs of the growing world population. The narrow genetic base impedes soybean improvement and significantly limits the development of new generation soybean varieties with high yields and stress resistance to changing environmental conditions. The research goal is to study the gene pool of *Glycine soja* of the Federal Research Center of the All-Russian Scientific Research Institute of Soybean and to identify sources of the main agronomic characters for their further use in breeding. The research objects were 46 collection forms of wild soybeans selected in various regions of Amur Region (Zeysky, Tambovsky, Belogorsky, Mikhaylovsky, Arkharinsky, Blagoveshchensky), 2 forms from the People's Republic of China, 1 – from Primorsky Territory, and 1 – from Khabarovsk Territory. Two samples were used as reference standards: the Lydia soybean variety – a cultivated type and KT-156 – a form of wild soybeans. The duration of the growing season for wild forms of soybeans ranged from 88 to 115 days. The study revealed an ultra-early-ripening sample selected from Zeysky District of Amur Region – KZ-642 (88 days). Most collection samples of *Glycine soja* (55%) were represented by early-ripening samples with a growing season of 90...99 days selected from different areas of the region. The weight of seeds per plant for the best samples of the wild soybean collection nursery ranged from 13.0 g for No. 20 – KBel-30 to 105.5 g for No. 37 – KBl-93, the wild soybean standard was exceeded by 16 forms (+ 14.2... 28.4 g to st). The weight of 1,000 seeds ranged from 9.2 g for No. 33 – KA-455 to 35.2 g for No. 27 – KA-346, 7 samples demonstrated the highest values (+ 0.3...5.7 g to st). The number of seeds per plant for the best forms of the wild soybean collection nursery ranged from 755 pcs for No. 20 – KBel-30 to 8,725 pcs for No. 33 – KA-455, the wild soybean standard was exceeded by 77.5% of the samples. The protein content was from 43.8% to 53.8%. An increased level of protein in seeds (> 50%) was found in 17 samples (42.5%). Of them, form No. 20, KBel-30, demonstrated the highest value in this character, however, in terms of weight and number of seeds per plant, this sample had the low values (13.0 g and 755 pcs, respectively).

An analysis of correlations established a direct pronounced relationship (on the Chaddock scale) between the weight of seeds per plant and the weight of 1,000 seeds (r = 0.59), an inverse pronounced relationship between the weight of seeds per plant and the protein content in seeds (r = –0.67), and between the growing season and the weight of 1,000 seeds (r = –0.64). The studies of the *Glycine soja* collection forms identified the following: 22 sources of early ripening (88...99 days), 8 – high seed weight per plant (91.3...105.5 g), 7 – high weight of 1,000 seeds (30.7...35.2 g), 6 – the largest number of seeds per plant (4,092...8,725 pcs) and 17 – high protein content in seeds (50.0...53.8%). The study also helped find sources combining two or more agronomic characters. These forms of wild soybeans are recommended for use in the breeding process as initial parent forms for hybridization.

The study was supported with Russian Science Foundation Grant No. 23-26-00076, https://rscf.ru/project/23-26-00076/

SSR-BASED ASSESSMENT OF GENETIC DIVERSITY IN TOMATO CULTIVARS AND LINES GROWN IN KAZAKHSTAN

***Genievskaya Yu.*[1], *Jantasov S.*[2], *Nurbayeva E.*[3], *Turuspekov Y.*[1*]**

[1] *Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan*
[2] *Kazakh National Agrarian Research University, Almaty, Kazakhstan*
[3] *Kazakh Research Institute of Fruit and Vegetable Growing, Almaty, Kazakhstan*

**E-mail:* yerlant@yahoo.com

Tomato (*Solanum lycopersicum* L.) is a versatile crop known for its nutritional value and health benefits, thriving in diverse climates worldwide. Nevertheless, regional variations persist in tomato yield, with Kazakhstan serving as an example of lower productivity in contrast to global averages. Closing this disparity requires comprehensive genetic studies and focused breeding efforts. This study is focused on the genetic diversity of 49 tomato cultivars and hybrids sourced from Kazakh Research Institute of Fruit and Vegetable Growing (Almaty), employing 10 SSR markers associated with important agronomic traits. SSR genotyping unveiled polymorphisms across 6 markers with variable allele numbers. Genetic diversity metrics highlighted significant genetic diversity within both outdoor and greenhouse tomato cultivars and lines. Bayesian clustering, Neighbor-joining (NJ) clustering, and principal coordinate analysis (PCoA) delineated genetic differentiation between outdoor and greenhouse tomatoes with small admixture, indicating distinct breeding directions for these two types. Highly polymorphic SSRs (PIC > 0.5) associated with essential fruit traits emerge as promising targets for marker-assisted selection (MAS) that can be used to enhance tomato breeding efficiency in Kazakhstan. According to 8 SSRs, 22 out of 30 outdoor accessions and 8 greenhouse tomato accessions were genetically uniform. The presence of genetic uniformity within cultivars provides a valuable information for the pedigree selection in refining breeding strategies. This study offers comprehensive insights into the genetic diversity and population structure of tomato cultivars and lines in Kazakhstan, laying the foundation for informed breeding endeavors aimed at bolstering yield and resilience in tomato crops.

PHYTOSANITARY MONITORING OF WHEAT YELLOW RUST DISEASE (*PUCCINIA STRIIFORMIS*) IN ZHAMBYL AND TURKESTAN REGIONS

Keishilov Zh., Kumarbayeva M., Kokhmetova A.

Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan

E-mail: Jeka-Sayko@mail.ru

Yellow rust of wheat (caused by *P. striiformis f. sp. tritici*) is one of the most common and serious fungal diseases that can lead to significant production and economic losses in wheat if not controlled. Yellow rust poses a serious threat to food security in many countries around the world. It is distributed throughout most of North and South America, Europe, East, Central and South Asia, North Africa, and Australia. This disease is known to occur in more than 60 countries and is the most common wheat disease in Kazakhstan. In extreme situations of very susceptible varieties and under favorable weather conditions, yellow rust can reduce yields by up to 100%. Monitoring the spread and harmfulness of yellow rust included phytopathological examinations of wheat crops in the Kordai, Shu, Ryskulov, Zhambyl, and Merke districts. In 2022, surveys in Zhambyl region included the production of wheat crops (20–150 ha). In the Zhambyl region, Kordai district, in the rural district of Sarybulak, the peasant farm of Nur Al LLP, the Steklovidnaya 24 and Bogarnaya 56 wheat varieties showed an average susceptibility to the disease with damage of 28-18%, the degree of disease development of these varieties was 1.60% and 0.90%. In the same area, in the rural districts of Kakpatas, Nogaybay, and Sharbakty, the Steklovidnaya 24 and Bogarnaya 56 varieties showed susceptibility to yellow rust, the damage rate was 0.60% and 0.80%, and the prevalence rate was 12% and 16%, respectively. In the Shu and Ryskulov districts, and the rural districts of Belbasar and Algabas, no symptoms of the pathogen were observed. All studied varieties showed an immune type of reaction (IT – 0).

In the Merke district, in the rural district of Surat, in the peasant farm of Sypatai Batyr LLP, the winter wheat varieties Euclid and Steklovidnaya 24 did not show symptoms of yellow rust (IT - 0). In the same area, in the rural districts of Tatti and Aspara, symptoms of *P. striiformis* were found on the Naz and Kazakhstanskaya 10 varieties; the prevalence of the disease was 26% and 32%, and the development rate was 1.30% and 1.60%, respectively. Zhambyl region, in the Besagash rural district, the peasant farm of the Zhambyl branch of KazNIIZR LLP, the variety Steklovidnaya 24, showed susceptibility to yellow rust, the infection rate was 1.20%, and the spread level was 24% and higher.

As a result of route research in the fields of Karabau and Zhibekzholinsky rural districts, Kazygurt and Saryagash districts, Turkestan region in the peasant farm of LLP "Karabau" and LLP "Krasnovodopadskaya SHOS" it was established that the development of yellow rust (*P. striiformis*) in the varieties Steklovidnaya 24 (super-elite) and Pamyat 47, was significant - 0.80% and 1.30%, and the prevalence index was - 16% and 18%, respectively. In the same area, in the peasant farm of Krasnovodopadskaya SHOS LLP, the level of damage to Steklovidnaya 24 in various fields (field 2, super-elite) and (field 3, super-elite) wheat showed susceptibility to the disease in the range of - 0.80% and 1.10 %, respectively. The disease prevalence was 14% and 16%. In the Sharbulak and Darbazinsky rural districts of the peasant farm of Sapa 2002 LLP, the wheat varieties Steklovidnaya 24 (super-elite), Shol (super-elite), Krasnovodopadskaya 210 and Shol (super-elite) did not show symptoms of yellow rust (IT – 0). As a result of monitoring work carried out in Zhambyl and Turkestan regions, it was established that most wheat varieties are not resistant to yellow rust and it is necessary to continue monitoring work to identify new varieties of wheat resistant to yellow rust disease.

This research has been funded by the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan (Grant No. BR18574099)

MASRUSPLANTS V2.0: AN UPDATED COMPREHENSIVE WEB RESOURCE OF DNA MARKERS ASSOCIATED WITH RUST RESISTANCE GENES VALIDATED IN RUSSIAN BREAD WHEAT

***Kelbin V.N.*[1,2], *Laprina Yu.V.*[1], *Skolotneva E.S.*[1], *Salina E.A.*[2]**

[1]*Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia*
[2]*Kurchatov Genomic Center, Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia*

E-mail: kelbin@bionet.nsc.ru

Bread wheat (*Triticum aestivum* L.), a valuable agricultural crop, is well-suited for cultivation across diverse ecological and climatic conditions. Throughout its life cycle, wheat faces numerous stresses that can diminish both yield and grain quality. Among these biotic stresses are rust fungi, the primary causal agents of cereal plant diseases. Under favorable climatic conditions, rust fungi can spread rapidly and cause widespread crop losses. It is considered an epiphytotic disease, meaning it has the potential to cause a large-scale outbreak.

Genetic protection is the most effective and environmentally friendly strategy to combat the causative agent of rust. To successfully implement this approach, advanced breeding methods are employed to develop new wheat varieties with diverse resistance types and genes. A supply of genetically characterized sources with rust resistance genes is crucial for timely variety changes.

The precise identification of wheat resistance genes stands as a main and expedited procedure within modern breeding, particularly through the employment of marker-assisted selection (MAS) techniques. To catalog information about DNA markers associated with rust resistance genes validated in Russian bread wheat, we have updated the online database MASRUSplants to v2.0, accessible at https://masrusplants.ru.

The primary goal of the MASRUSplants database v2.0 is to promote the utilization of wheat's genetic potential for resistance against fungal diseases and to make the MAS technique extensively accessible.

The MASRUSplants v2.0 carefully provides detailed information about DNA markers and their associated resistance genes, such as *Sr* genes (stem rust resistance), *Lr* genes (leaf rust resistance) and *Yr* genes (stripe rust resistance). Comprehensive information including marker type, genetic locus, primer sequence, PCR protocols, and bibliographic references accompanies each DNA marker record. In addition, the DNA markers presented in the database, tested in the Laboratory of Plant Molecular Genetics and Cytogenetics at the Institute of cytology and genetics SB RAS, are illustrated with original electropherograms. Notably, the MASRUSplants houses data of Russian and global wheat germplasm: name, pedigree, geographical origin, identified gene alleles and reaction to biotic stressors – rust fungi. On the main page, the database contains the following main objects: protocols, chromosomes, markers, plants, photographs of pathogens. We built simple relationships between objects aimed at information on DNA markers and resistance genes.

MASRUSplants is a comprehensive and user-friendly database that promotes the use of DNA markers in wheat breeding programs. By furnishing an abundance of information pertaining to resistance genes and their corresponding DNA markers, the database plays a pivotal role in advancing the creation of more robust wheat cultivars, ensuring sustainable agricultural practices and fortifying food security measures.

This work was done within the framework of State Assignment Kurchatov Genomic Center of ICG SB RAS (№075-15-2019-1662).

ASSESSMENT OF THE GENETIC DIVERSITY OF RICE USING SSR-MARKERS

Amalova A.[1], Kongyr B.[1], Tokhetova L.[2], Abugalieva S.[1], Turuspekov Y.[1*]

[1] Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan;
[2] Kazakh Rice Research Institute, Kyzylorda, Kazakhstan

**E-mail:* yerlant@yahoo.com

Rice stands as one of the world's most crucial cereal crops. In the 2022/2023 crop year, China produced about 146 million metric tons of milled rice, a higher volume than any other country. India came in second place with over 135 million metric tons of milled rice in that crop year. Understanding the genetic diversity within germplasm collections is pivotal for crop enhancement efforts. Molecular markers, particularly Simple Sequence Repeats (SSRs), play a vital role in characterizing germplasm and delineating genetic differences at the molecular level. SSR markers are known for their reliability, reproducibility, high polymorphism, and resolution.

In a study conducted at the Kazakh Rice Research Institute (Kyzylorda, Kazakhstan.), 60 rice samples analyzed microsatellite analysis utilizing 10 polymorphic SSR markers (*RM1*, *RM5*, *RM44*, *RM124*, *RM152*, *RM144*, *RM162*, *RM171*, *RM212*, and *RM215*). These markers are associated with different traits crucial for plant adaptability, yield components, stress resistance, and grain quality. For instance, markers *RM171* and *RM215* are linked to grain thickness and width, while *RM212* is associated with drought resistance, and *RM5* is closely tied to rice yield genes. The genetic analysis revealed varying numbers of alleles per locus, ranging from 2 to 7 across the markers, with an average of 3.30. Number of effective alleles ranged from 1.1 to 5.8, with an average of 2.2. The Shannon's information index and Nei's genetic diversity index, indicated a high level of genetic diversity among the analyzed rice accessions for the 10 polymorphic microsatellite markers. Through genotyping, the allelic statuses of 60 rice cultivars and lines were determined for the 10 SSR markers, directly linked to important agronomic traits of rice. These findings provide valuable information of rice varieties and lines, aiding in future breeding and improvement programs.

This research was funded by the Ministry of Science and Higher Education of the Republic of Kazakhstan (grant BR18574099; BR10765056).

GENOME EDITING-BASED CONTROL OF PLANTS PIGMENTS SYNTHESIS FOR PRACTICAL BREEDING PURPOSES

Mikhailova A.S.*[1], Smirnova N.V.[1], Sokolova D.V.[1], Popov V.S.[1], Kuluev B.R.[1,2], Baymukhametova E.A.[2], Musin K.G.[2], Mikhailova E.V.[1,2], Gerasimova S.V.[1,3], Shoeva O.Yu.[1,3], Shvachko N.A.[1], Khlestkina E.K.[1]

[1] *Federal Research Center the N.I. Vavilov All-Russian Institute of Plant Genetic Resources, Russian Federation, St. Petersburg, Russia*
[2] *Ufa Federal Research Center RAS, Institute of biochemistry and genetics, Ufa, Russia,*
[3] *Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia*

E-mail: a.mikhailova@vir.nw.ru

Beta vulgaris L. is a valuable raw material in the production of betalain pigments used in the food industry. The creation of high-betaine forms is an important practical problem that can be solved by genome editing. In our work, we identified suitable candidate genes (*CYP76AD5.1*, *CYP76AD5.2*, *CYP76AD5.3*, *CYP76AD6*) for knockout by NHEJ-based editing in order to increase the level of betanins. The gain-of-function effect of knockout is assumed to be due to avoiding competition for substrate. Another mechanism of using NHEJ to restore function (pigment synthesis) was previously demonstrated for the synthesis of anthocyanins in barley aleurone, restored by gain-of-function mutation (by reading frame restoration in target gene *Myc2*). The next example for using NHEJ to restore function is expected restoring of phlobaphene synthesis in wheat glumes by converting the recessive allele into the dominant via excision of insertion in 47 bp from intron (this insertion suppressed the gene necessary for pigment synthesis activation). Further target gene was its homoeologue with low expressivity and penetrance, which prevent the correct assessment of wheat varieties for uniformity, thus this gene should be knocked-out in order to solve this problem. In conclusion, when working with key crops, we diversified the use of the same editing mechanism - NHEJ - to control the synthesis of pigments by either enhancing, restoring or suppressing synthesis of different pigments, depending on the particulate breeding task. In the report, the details of target genes selection and analysis as well as construction of vectors for target gene modification and delivering of the constructs to the plants are presented.

The research is supported by Russian Science Foundation (project No 21-66-00012).

FIELD EVALUATION OF DOMESTIC BARLEY ACCESSIONS FOR RESISTANCE TO NET BLOTCH

Moldazhanova R., Maulenbay A., Kurymbaeva N., Rsaliyev A.

Research Institute for Biological Safety Problems, Laboratory for Phytosanitary Safety, Guardeyskiy, Kazakhstan

E-mail: rmoldazhan@bk.ru

Barley holds significant importance as a cereal crop, ranking as the fourth most essential grain globally. In Kazakhstan, barley harvests reached approximately 3.3 million tones, marking a notable 39% increase compared to previous years. However, challenges threaten both the quality and yield of these cultivated crops. Among the prevalent fungal diseases affecting barley, net blotch poses a significant threat. Developing resistant cultivars stands as a primary strategy in combating net blotch disease.

In this study, we conducted a phenotypic evaluation of infected barley by assessing the response to *Pyrenophora teres* f. *teres* resistance at the adult growth stage. Our research drew upon 106 spring barley accessions obtained from six different breeding stations in Kazakhstan. The evaluation of net form in barley accessions took place at RIBSP (Gvardeisky, Zhambyl region, southern Kazakhstan) in 2022. Disease severity scores were determined using a 0-100% scale based on the percentage of necrotic and chlorotic areas: ≤ 10% for resistant (R), 11-20% for moderately resistant (MR), 21-30% for moderately susceptible (MS), and 31-100% for susceptible (S) lines. Disease intensity over time was quantified by calculating the area under the disease progress curve (AUDPC).

Out of the 106 barley samples analyzed, the maximum disease severity reached 40%, with 47 lines and cultivars demonstrating resistance (R, 0-10%), 45 showing moderate resistance (MR, 20%), 11 displaying moderate susceptibility (MS, 30%), and 2 exhibiting susceptible symptoms (S, 40%). The AUDPC values varied, spanning from 0 to 490. Pearson's correlation coefficient between AUDPC and disease severity score indicated a positive correlation ($r = 0.885$). Collectively, our findings suggest the presence of potential sources of resistance within the examined barley accessions, which could be valuable in breeding efforts.

Research was done in the framework of the Program «Creation of highly productive varieties and hybrids of grain crops based on the achievements of biotechnology, genetics, physiology, biochemistry of plants for their sustainable production in different soil and climatic zones of Kazakhstan» (BR10765056).

BREEDING OF LOW- WATER-REQUIREMENT RICE VARIETIES: RELEVANCE FOR KAZAKHSTAN

Mukhambetzhanov S.K. [1, 2], *Usenbekov B.N.* [1,2], *Amirova A.K.* [1,2], *Mynbayeva D.* [1,2], *Berkimbay Kh.*[1]

[1]*Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan*
[2]*Al-Farabi Kazakh National University, Almaty, Kazakhstan*

E-mail: serik_m65@list.ru

In Kazakhstan, rice is an important crop that ensures food security and has export potential, so 45% of the rice produced in the country is used in the domestic market, and 55% is exported.

Rice production in Kazakhstan is localized mainly in the Kyzylorda, Almaty, Turkestan and Zhetysu regions, where 99.6% of the cultivated area is located. Since 2022, according to the Ministry of Ecology of the Republic of Kazakhstan, in these areas, water resources in the areas of the Syrdarya, Shu, Ili and Talas rivers used for irrigation are practically exhausted and there is an acute shortage of irrigation water. These problems, as a result of climate change and cross-border disputes, will only get worse. According to World Bank forecasts, the volume of water resources in Kazakhstan will decrease from 90 to 76 km³ per year by 2030, i.e. in six to seven years it will be about 15% per year. So, already now, in terms of water scarcity, Kazakhstan ranks 8-th among Asian countries and is included in the red zone, where the issue of water resource scarcity is a critical problem, and the level of water stress in the country's agricultural sector is already more than 80%.

Increasing trends in water scarcity due to climate change make the development of domestic low-water-requirement rice varieties an extremely important task for breeding programs.

In the last decade, there has been a growing number of studies in the world related to the creation of low-water-demanding varieties, which show that "low-water-requirement" rice can be defined as the ability to survive and maintain productivity under water deficit conditions. This is a complex trait that manifests itself at the morphological, physiological, biochemical and molecular genetic levels. Screening of thousands of rice genotypes for this trait led to the creation of a limited number of low-water-requiring varieties, which is due to the lack of truly low-water-requiring genotypes and the lack of suitable screening methods.

To solve this problem in Kazakhstan, it is proposed to use a modified method that combines physiological, biochemical methods and marker-associated selection. This will make it possible to select the best genotypes and reduce the time required for breeding low-water-requirement rice varieties that are resistant to water stress. The obtained samples will be used to provide the initial forms for breeding programs to create new varieties, conduct fundamental and applied research in breeding, physiology, genetics and biotechnology, as well as replenish the rice gene pool with new samples adapted to the changing climatic conditions of the rice-growing regions of Kazakhstan.

RICE BREEDING FOR RESISTANCE TO *MAGNAPORTHE ORYZAE* USING MAS ANALYSIS

***Mynbayeva D.*[1], *Amirova A.*[2], *Usenbekov B.*[1], *Berkimbay Kh.*[1], *Zhunusbayeva Zh.*[2]**

[1] *Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan*
[2]*Al-Farabi Kazakh National University, Almaty, Kazakhstan*

Rice is the most important food crop in terms of production in the world, ranking second among cereal crops. For most countries that grow rice, this crop serves as the main source of food products. There are many known diseases that affect different parts of the plant, and the most dangerous of them is considered to be rice blast. Blast is a rice disease caused by the fungus *Magnaporthe oryzae*, causing many lesions. There are three forms of blast disease - leaf, paniculate and nodular. Damage to the leaves and panicle indicates that it causes damage to both the vegetative and reproductive organs of rice plants. During epiphytotic years, blast disease can have a devastating impact on world rice production. The outbreak of the disease depends on the climatic conditions of different regions. The occurrence of the disease and symptoms vary from country to country. Also, the cause of the outbreak of the disease may be seed material imported from other countries. According to the Food and Agriculture Organization (FAO), rice production and consumption are steadily increasing every year, which indicates the need to grow healthy, non-infected material. Due to global climate change and the high variability of pathogen virulence, the study of rice blast and the development of new rice varieties resistant to blast is an urgent and promising direction.

In order to obtain a line of rice resistant to rice blast, in this study used domestic highly productive zoned rice varieties – Bakanas, Fatima, Aisaule and Aru. As donors of blast resistance genes, were used varieties provided by colleagues from the Federal State Budgetary Institution "Federal Scientific Centre of Rice" (Krasnodar, Russia). To obtain the initial hybrid material, the methods of pneumocastration and the "TVELL" method of pollination were used. The widely used marker-mediated selection (MAS) technology used to screen the initial genotypes and hybrid lines. To control gene transfer, the polymerase chain reaction (PCR) method were used using SSR markers that are closely linked to the resistance genes *Pi1, Pi2, Pi-ta* and *Pi33*. This feature guarantees the detection of a highly specific site in order to avoid false data.

As a result of crossing, 50 hybrid lines were obtained. Molecular screening of these hybrids was carried out for the presence of resistance genes to *Magnaporthe oryzae*. Based on the screening results, hybrids containing resistance genes were identified: for the *Pi1* gene – 14 dominant homozygous and one heterozygous lines; for the *Pi2* gene – 4 heterozygous hybrid lines; for the *Pi33* gene – two dominant homozygous and one heterozygous lines; for the *Pi-ta* gene – one dominant homozygous and 13 heterozygous lines. The studied hybrids studied do not contain these resistance genes. Selected hybrid lines containing genes for resistance to *Magnaporthe oryzae* are promising lines and will be used in further research.

This research has been funded by the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan Grant AP14869300.

DIVERSITY IN HIGH-MOLECULAR-WEIGHT GLUTENIN SUBUNIT LOCI IN DIFFERENT VARIETIES OF SPRING WHEAT (*TRITICUM AESTIVUM* L.)

***Najodov B.B.*[1,2], *Pylnev V.V.*[1], *Rubets V.S.*[2], *Moskalev E.A*[2], *Polkhovskaya E.S*[2], *Gruzdev I.V*[2]**

[1] *Russian State Agrarian University – Moscow Timiryazev Agricultural Academy, Moscow, Russia*
[2]*All-Russia Research Institute of Agricultural Biotechnology, Moscow, Russia*

E-mail: boburnajodov@gmail.com

Wheat (*Triticum aestivum* L.) is fundamental to global food security, with its flour quality largely attributed to high molecular weight glutenin subunits (HMW-GS). These proteins significantly affect the dough's viscoelastic properties, impacting critical baking quality traits such as dough strength, elasticity, extensibility, and water absorption. This study explores the allelic diversity of HMW-GS across 43 spring wheat cultivars through sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) and nanopore sequencing, targeting the allelic variants at the *Glu-1A*, *Glu-1B*, and *Glu-1D* loci.

One example of such a technique is sequencing the complete gene sequence by reading its amplicons on the ONT platform (Oxford Nanopore Technologies), which allows for comprehensive information on the polymorphism of loci encoding HMW-GS, information that is impossible or difficult to obtain using the standard SDS-PAGE method. In this study, SDS-PAGE identified the following allelic variants: in the *Glu-Ay1* locus – a (subunit 1), b (2*), c (null); in the *Glu-1B* locus - b (7+8), c (7+9), f (13+16), h (14+15), i (17+18); in the *Glu-1D* locus - a (2+12), d (5+10). Subsequently, the amplicons of genes encoding HMW-GS were sequenced on the ONT platform in 22 of the studied samples. Based on the nanopore sequencing data, the *Glu-1* locus alleles identified earlier by SDS-PAGE were detected in the studied samples; however, a detailed analysis of reads from amplified sequences in some samples revealed deletions in the gene encoding the Bx7 subunit and SNPs in the gene encoding the Ay1 subunit. These could potentially be associated with effects on baking properties different from those of the conventional Bx7 and Ay1 subunits.

Our findings underscore the critical role of HMW-GS allelic diversity in wheat breeding strategies aimed at enhancing flour quality. By identifying unique alleles and genetic variations, the study provides new insights into the genetic determinants of wheat flour's baking characteristics, offering avenues for targeted genetic improvements in wheat breeding programs.

QUANTITATIVE PCR AS A TOOL OF ASSAYING THE RESISTANCE OF WINTER WHEAT VARIETIES TO FUSARIUM HEAD BLIGHT

Orina A.S., Gavrilova O.P., Gagkaeva T.Yu.

All-Russian Institute of Plant Protection (VIZR), St-Petersburg-Pushkin, Russia

E-mail: orina-alex@yandex.ru

Fusarium fungi is common in grain and produce mycotoxins, that negatively effect on seed quality and health of grain consumers. The breeding of wheat varieties with high resistant to Fusarium head blight and other fungal diseases using molecular methods is of current concern.

In this study 17 winter wheat varieties created in National Center of Grain named after P.P. Lukyanenko were grown in Krasnodar region under the natural infections. Real-time PCR was used for quantification of DNA trichothecene producing *Fusarium* fungi (Tri-*Fusarium*) (Halstensen et al. 2006) and the most aggressive pathogen *F. graminearum* (Yli-Mattila et al., 2008) in the harvested grain. The fungal DNA content was represented as a proportion of the wheat DNA content (pg/ng).

A high amount of Tri-*Fusarium* DNA was found in the grain in range 0.14–0.42 pg/ng. The *F. graminearum* DNA content varied significantly from 0.01 to 0.43 pg/ng. The proportion of *F. graminearum* DNA as a percentage of the Tri-*Fusarium* DNA ranged from 6.1% to 100.9%. According to our observations, the value of this parameter above 30% means the susceptibility of varieties to *Fusarium* infection, and the smaller one is inherent in relatively resistant. The Adel, Tanya, Lebed', Kurs, Gurt and Yuka varieties in grain of which a low ratio of *F. graminearum* DNA in Tri-*Fusarium* fungi (no more than 10%) contained were the most promising.

The investigation was supported by the Russian Science Foundation (No. 19-76-30005).

SOWING SEEDS OF KNOWLEDGE: GENETIC EDUCATION FOR AGRICULTURAL ADVANCEMENT

***Sartbayeva Zh.*[1], *Özkan H.* [2], *Yermekbayev K.*[1]**

[1] *Zhetysu University, Institute of Biotechnology and Ecology, Taldykorgan, Kazakhstan*
[2] *Çukurova University, Ziraat Fakültesi, Tarla Bitkileri, Turkiye*

E-mail: sartbaeva98@list.ru

The discovery of the molecular structure of DNA was a turning point in the history of science and brought genetics to the forefront of biotechnological research studies. In agricultural sciences, this breakthrough catalyzed profound changes in plant/animal breeding, food production, land management and the promotion of sustainable development practices. Realizing these advances, however, depends largely on the collaborative efforts of scientists and the nurturing of new scientific talents.

Thus, our study examines the intersection of genetics education and agriculture, emphasizing the critical role of genetic knowledge in addressing current and future agricultural challenges. We examined the factors that influence student's engagement in science, identifying barriers such as lack of motivation, limited hands-on experience and difficulties in understanding the genetics as a subject. Consequenctly, we propose incorporating genetic knowledge into the curriculum: develop courses that include the basics of plant genetics and its extensive applications across various agricultural fields, showcasing its versatility and effectiveness to help students better understand the link between genetics and agriculture; increase student information literacy; attract qualified, most importantly experinced, teachers and researchers to help enrich instruction and bring new knowledge and techniques into the classroom; ignite a passion for science by immersing the students in laboratory experiments and incorporating them into their research; and encourage students to become more involved in science.

Educating future scientists and fostering a culture of scientific inquiry will enable agricultural communities to effectively navigate the complexities of a rapidly changing world. Ultimately, the trajectory of agricultural innovation and scientific discourse depends on the quality of education that today's budding scientists receive.

Key words: Genetic education, agriculture, future scientists, biotechnological research, sustainable development

RED-FLOWERED MUTANT OF WHITE CLOVER (*TRIFOLIUM REPENS* L.)

Shamustakimova A.O.*, *Ivanova A.A.*, *Klimenko I.A.

Federal Williams Research Center of Forage Production & Agroecology, Lobnya, Russia

E-mail: nastja_sham@mail.ru

White clover (*Trifolium repens* L.) is perennial, allotetraploid (2n=4x=32) legume species. The are 232 varieties of white clover in the global agricultural production. *T. repens* can be grown in the wide soil type and temperature range under the sufficient moisture and sunlight conditions.

As seen from the name white clover normally has white petals. However, there are two ornamental cultivars “Dragon’s blood” that have “blush” flower color. In 1950 and 1980 a red-flowered mutant of white clover also was found.

The most detailed analysis on red-flowered mutant was conducted by the group of scientists from China in 2018. The studied plant was found in a *T. repens* cv. “Regal” experimental field. Using transcriptome sequencing and subsequent quantitative real-time PCR (qRT-PCR) they identified eight key genes (CHS, F3’H, F3’5’H, UFGT, FLS, LAR, ANS and DFR) that might be responsible for certain type of flower pigmentation.

In 2021 we have found two plants with the same phenotype in our field. The part of obtained F1 generation seedlings has strong anthocyanin pigmentation and red flowers. Thus, the aim of our study was to compare promoter regions of eight genes from flavonoid biological synthesis pathway of red-flowered (RF) and white-flowered (WF) *T. repens* plants.

For experimental procedure ten plants (Five RW and five WF) were selected from greenhouse. DNA was extracted from young leaves of the mature plant using modified SDS method. To identify the certain region that is responsible for the observed biological appearance we design primers to amplify promoter regions (about 800 bp) of each 8 key genes from all ten plants. For PCR amplification, each 20 μL PCR reaction mixture consisted of 30 ng of genomic DNA, 10x Taq Turbo buffer, 50x dNTP mix, 2 units of Taq polymerase, 0,2 μmol of each primer. Amplification was carried out on “Bio-Rad iCycler, USA” as follows: 3 min at 94 ℃; 35 cycles are run at 94 ℃, 30 sec, 56/59/62 ℃, 1 min, and 72 ℃, 5 min, for denaturing, annealing and extension, respectively.

The analyzed PCR-product sizes for seven of eight promoter regions from all ten plants were as expected from NCBI data. The amplified fragments of F3’5’H gene promoter regions from WF and RW was 775 and 865 bp, respectively. Flavonoid 3’5’- hydroxylase (F3’5’H, CYP75A) is cytochrome P450-dependent monooxygenase. F3’5’H is responsible for blue delphinidin production. Comparison of two F3’5’H promoter regions from contrasted plants revealed the number of red-flowered plants and different cis-acting elements landscape.

MARKER-ASSISTED SELECTION FOR CULTIVAR UNIFORMITY CONTROL OF HEXAPLOID WHEAT (*TRITICUM AESTIVUM* L.): A CASE STUDY

***Smirnova N.V.*[1], *Mikhailova A.S.*[1], *Shvachko N.A.*[1], *Bespalova L.A.*[2], *Khlestkina E.K.*[1]**

[1] *Federal Research Center the N.I. Vavilov All-Russian Institute of Plant Genetic Resources, Russian Federation, St. Petersburg, Russia*

[2] *«National Grain Center named after. P.P. Lukyanenko», Central Estate of KNIISKH, Krasnodar, Russia*

E-mail: n.smirnova@vir.nw.ru

Glume color is one of the descriptors for bread wheat cultivars uniformity test. The trait is controlled by homoeologous loci *Rg-A1*, *Rg-B1* and *Rg-D1* (in chromosomes 1A, 1B and 1D, respectively), which are suggested to encode R2R3-MYB transcriptional factor. Some winter wheat cultivars bred as white-glumed may later express pseudoheterogenety by glume color, which prevents successful release of such cultivars. We assumed that they may carry the *Rg-A1b* allele responsible for the weak red color, well-known for old spring bread wheat varieties, but less studied in winter wheat. We hypothesized low penetrance and low expressivity of *Rg-A1b* in winter wheat to be a reason for pseudoheterogenety. In spring wheat diagnostic marker *Xgwm0136-264bp* was described for *Rg-A1b*. To exclude effect of homoeologs we developed ILP-marker to distinguish *Rg-B1b*. *Rg-D1b* was not considered, since cultivars studied had no synthetic allohexaploids developed using *Aegilops tauschii* (the donor of *Rg-D1b*) in their pedigree. Using *Xgwm0136* and ILP-marker developed we showed genotypes of winter cultivars Kupava and Fedor having pseudoheterogenety: *Rg-A1bRg-A1bRg-B1aRg-B1aRg-D1aRg-D1a*. Thus, these homogeneous cultivars are mistakenly assessed as heterogeneous due to low penetrance and low expressivity of *Rg-A1b*. Since these cultivars are used as parental genotypes in ongoing breeding programs, we use now diagnostic marker *Xgwm0136-264bp* to select offspring against *Rg-A1b* and the both *Xgwm0136* and the developed ILP-marker to control selection of white-glumed homozygous *Rg-A1aRg-A1aRg-B1aRg-B1aRg-D1aRg-D1a* genotypes.

THE GENETIC ASSESSMENT OF CUCUMBER (*CUCUMIS SATIVUS* L.) ACCESSIONS OF KAZAKHSTAN USING SSR MARKERS

***Yermagambetova M.*[1], *Nusupova A.O.* [2], *Abugalieva S.I.* [1], *Turuspekov Y.K.*[1*]**

[1] *Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan;*

[2] *Kazakh Scientific Research Institute of Fruit Growing and Viticulture, Almaty, Kazakhstan*

**E-mail:* yerlant@yahoo.com

Cucumber (*Cucumis sativus* L.) is an important agricultural crop in Kazakhstan, contributing significantly to both local consumption and the economy. Cultivated across various regions of Kazakhstan due to its adaptability to diverse climatic conditions, cucumbers are integral to local diets and agricultural practices. The country's unique geographical and climatic features allow for the cultivation of a wide array of cucumber varieties, each characterized by distinct qualities such as flavor, texture, and resistance to environmental stresses. Recent genetic studies in Kazakhstan focus on enhancing these traits through selective breeding and molecular genetics, particularly aimed at improving yield, disease resistance, and stress tolerance.

This study presents a comprehensive genetic analysis of cucumber (*Cucumis sativus*) accessions in Kazakhstan employing Simple Sequence Repeat (SSR) markers, aiming to explore the genetic diversity and structure within this important crop. We used 180 samples from various 60-cucumber accessions in 3 repeats and analyzed them using 15 SSR markers, 10 of which were highly polymorphic. This method facilitated the assessment of genetic diversity, the identification of unique and shared alleles, and the evaluation of genetic relationships among the accessions. The genetic diversity indices, including the number of alleles per locus, observed and expected heterozygosity, and Shannon's Information Index, were calculated to provide a detailed picture of the genetic landscape of cucumbers in Kazakhstan. Additionally, population structure analysis highlighted distinct genetic clusters within the accessions, suggesting the presence of different genetic lineages. This research contributes to the genetic conservation and breeding programs of cucumbers in Kazakhstan. It serves as a model for genetically assessing vegetable crops in other regions using SSR markers.

POPULATION STRUCTURE OF SOYBEAN WORLD COLLECTION BASED ON RESEQUENCING DATA

Zatybekov A. [1], ***Turuspekov Y**[1], Fang C.*** [2], ***Abugalieva S.*** [1]

[1] *Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan*
[2] *School of Life Sciences, Guangzhou University, Guangzhou, China*

**E-mail:* yerlant@yahoo.com

Soybean (*Glycine max* (L.) Merr) is an essential food, feed, and technical culture. In Kazakhstan the area under soybean is increasing every year, helping to solve the problem of protein deficiency in human nutrition and animal feeding. Analysis of population structure is an integral part of soybean breeding to assess genetic diversity of studied collection. The purpose of this study was to analysis the population structure and assess the genetic diversity in a collection of modern soybean cultivars from Kazakhstan, as well as accessions obtained from various geographical regions of the world, including wild species and landraces. This included studying both local and global population structures, as well as identifying important genes involved in soybean adaptation mechanisms. The genetic relatedness and population structure of soybean world collection consisted from 694 accessions, including local genotypes were examined using resequencing data for 80 972 single-nucleotide polymorphism (SNP) markers obtained from Illumina HiSeq x Ten System. In the initial approach, the construction of a neighbor-joining tree revealed ten subclusters and identified 10 subclusters in which wild forms and landraces were separated into a separate subcluster. Genotypes for Kazakhstan formed two large clusters together with modern cultivars from Europe and North America. These results offer promising potential for effective utilization in studies concerning soybean adaptation and can be integrated into breeding programs to develop novel, high-performing cultivars.

The authors would like to acknowledge the funding from the Ministry of Science and Higher Education of the Republic of Kazakhstan for the grant AP13068118.

VARIABILITY OF AGRONOMIC TRAITS IN CHICKPEA COLLECTION GROWN IN IRRIGATED AND NON-IRRIGATED CONDITIONS

***Zatybekov A.K.*[1], *Burakhoja A.K.*[1], *Kudaybergenov M.S.*[2], *Varshney R.*[3], *Krempa A.*[1], *Anuarbek Sh.*[1], *Turuspekov Y.K.*[1*]**

[1] *Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan*
[2] *Kazakh Research Institute of Agriculture and Plant Growing, Almalybak, Kazakhstan*
[3] *Murdoch University, State Agricultural Biotechnology Centre, Perth, Australia*

**E-mail:* yerlant@yahoo.com

Chickpea (*Cicer arietinum* L.) is a vital leguminous crop renowned for its nutritional value and adaptability to diverse environmental conditions. In Kazakhstan, due to crop diversification program, special attention is focused on pulse crops, including chickpea, as strategic crop for food security and fodder production. In this study, we investigate and compare the growth performance of world collection of chickpea (238 accessions) cultivated in irrigated and rainfed conditions of South-East of Kazakhstan.

Experiments in the field carried out using the generally accepted methodology of B.A. Dospekhov. The field experiments performed in 1 m lines with two randomized replications, the distance between rows will be 45 cm, the depth of seed sowing will be 4-5 cm. During plant growing were observed main vegetation periods (flowering time, pod fill, full maturity). After harvesting was conducted structural analysis of seven agronomic traits (plant height (PH), height of lower pods (HLP), number of lateral branches (NLB), number of fertile nods (NFN), number of seeds per plant (NSP), yield per plant (YP), thousand seeds weight (TSW)).

Our findings reveal significant disparities in chickpea growth dynamics between the two conditions. On irrigated soils, chickpea plants exhibited enhanced vegetative growth, increased leaf area, and more vigorous root development. Comparative analysis of morphological traits showed PH of accessions from irrigated soil (38.86 ± 8.33 cm) were higher than rainfed (36.47 ± 5.99 cm). The HLP on the contrary, showed the opposite effect, under irrigated conditions was 16.47 ± 4.68 cm and 19.28 ± 4.46 cm on rainfed. Moreover, plants in irrigated soils demonstrated superior reproductive performance, manifesting in higher pod counts, larger pod size, and elevated seed yield. Accessions under irrigation showed higher YP (5.95 ± 1.13 g) and TSW (160.71 ± 32.56 g) compared to rainfed YP (4.79 ± 1.76 g) and TSW (147.21 ± 23.05 g).

Our study underscores the crucial role of irrigation in shaping plant development and yield potential. Overall, this study sheds light on the contrasting growth responses of chickpeas cultivated on irrigated soils versus hard gypsum soils. The findings emphasize the importance of soil management practices and underscore the potential for targeted interventions to optimize chickpea production in diverse agroecological contexts.

This research was funded by the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan (Grant AP19677444).

MOLECULAR SCREENING OF SPRING WHEAT COLLECTION FOR THE PRESENCE OF YELLOW RUST RESISTANCE GENES

Zhanuzak D., Kokhmetova A., Bolatbekova A., Nurzhuma M.

Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan

E-mail: dolphin_969@mail.ru

Yellow rust of wheat caused by *Puccinia striiformis f.sp. tritici* is one of the most important diseases of cereal crops worldwide. Yellow rust causes large crop losses every year. In Kazakhstan, the main habitat of yellow rust is the southern and southeastern regions. The pathogen reduces yield, and seed quality, and can cause 100% yield loss when availability of optimal weather conditions. Yellow rust reduces the plant's ability to photosynthesize and increases evaporation. As a result, the pathogen leads to the drying of wheat grain and a decrease in its quality. Using resistant wheat varieties is an economically and environmentally sound method of disease control, thereby reducing the use of fungicides. Creating wheat varieties resistant to yellow rust and ensuring long-term preservation of their resistance remains the main task of breeding. Therefore, in this regard, a constant search for new donors of sustainability is always necessary.

The most effective resistant genes against stripe rust in Kazakhstan are *Yr2+*, *Yr4+*, *Yr5, Yr10* and *Yr15*. Additionally, there are a few *Yr* genes that confer non-race-specific resistance, acting at the adult plant stage such as *Yr18,* which is a multi-pathogen resistance gene and confers part field resistance against stripe rust, leaf rust, stem rust, and powdery mildew have been used in breeding programs for a century and so far, no pathogen adaptability has been found.

The objects of the study were 50 spring wheat varieties cultivated or used in breeding in Kazakhstan. The thesis presents the results of a study of a wheat collection of 50 samples; 15 varieties of spring wheat were identified that were carriers of the *Yr9* gene, 15 carriers of the *Yr10* gene, 17 carriers of the *Yr15* gene, one carrier of the *Yr17* gene, 4 carriers of the *Yr18* gene and 8 carriers of the *Yr29* gene. The highest frequency of occurrence among spring wheat samples was observed in the *Yr15* gene (34%), followed by the *Yr9* (30%), *Yr10* (30%), *Yr29* (16%), and *Yr18* (8%) genes. The *Yr17* gene was detected in only one (2%) wheat genotype.

This research has been funded by the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan (Grant No. *BR 18574099*, the task 02).

THE INFLUENCE OF THE DWARFING GENES *RHT* AND THE PRODUCTIVITY GENES *TAGW, TAGS* ON THE YIELD OF SPRING WHEAT VARIETIES IN THE CONDITIONS OF NORTHERN KAZAKHSTAN

Zotova L., Serikbay D., Gajimuradova A.

S. Seifullin Kazakh Agrotechnical Research University, Astana, Kazakhstan

E-mail: l.zotova@kazatu.edu.kz

When selecting parental and hybrid forms in the conditions of Northern Kazakhstan, it is important to choose samples with optimal height and coleoptile length, as well as high productivity indicators. Moreover, to expedite and optimize the selection process, it is crucial to take into account the genetic parameters of the samples. To identify effective productivity genes, an analysis of the *Rht* genes (*RhtB1a, RhtD1a, RhtB1b, RhtD1b*) and *GS/GW* genes (*TaGS 5-3A-T, TaGW8-B1a*) and their interactions was conducted. The study employed Spearman's correlation analysis, regression analysis, and analysis of quadratic values using OLS.

A significant positive correlation by Spearman (R=0.328, p=0.010) indicates that in the presence of the *TaGS5-3A-T* gene, the 1000 grain weight (TGW) also tends to increase. The *Rht* genes *(Rht-B1a, Rht-D1a, Rht-B1b, Rht-D1b*) more often show insignificant correlations with productivity traits. Even in the case where *Rht-B1a* exhibits moderate positive correlation with grain length (GL), this value is statistically insignificant (p=0.063). The *TaGS-3A-T* gene also demonstrates moderate positive correlation, but with grain weight (GW) (R=0.249, p=0.055), approaching statistical significance. The correlation of productivity with the *TaGW8-B1a* gene, compared to *TaGS5-3A-T*, is generally weaker and statistically insignificant, indicating that this gene has indirect or weak influence on the studied productivity traits. Ordinary Least Squares (OLS) regression analysis of TGW shows that 17.5% of its variability is explained by the studied genes. Additionally, the *TaGS5-3A-T* gene shows significant positive association with TGW ($p<0.05$). The parameter Grain size (GS) has about 8.8% of its variance explained by the influence of the studied genes. Regarding GS, the *TaGS5-3A-T* gene also shows a significant positive effect ($p<0.05$), while *Rht-B1b* has an almost significant negative effect (p=0.053). Analysis of R-squared values in the OLS regression analysis indicates an increase in TGW to 0.328 compared to the previous analysis. This suggests that around 32.8% of TGW variability is explained by both individual genes and their interactions. For example, according to this analysis, the interaction of *Rht-D1a_TaGS5-3A-T* ($p<0.1$) influences GS, indicating a potential effect when these genes are present together. The interaction of genes *RhtB1a_TaGS_3A, RhtD1a_TaGS_3A,* and *RhtB1b_TaGS_3A* at $p<0.05$ suggests significant interaction between these genes.

The studied correlation between genes and their interactions influencing grain productivity and optimal plant height under drought conditions indicates that the presented *Rht* genes should provide plant height ranging from 53 to 62 cm to ensure optimal productivity. This height ensures coleoptile length of more than 4 cm and resistance to lodging. The genetic basis of productivity, along with optimal wheat height, demonstrates the influence of the interaction of the *TAGS5-3A-T* gene on TGW and GS. In this context, the *TaGW8-B1a* gene does not exert a statistically significant influence on these indicators, or it may have an indirect effect.

Thus, the presented genes and their combinations contribute up to 32.8% of the influence on TGW, leading to an increase in total yield by 13-92% for individual samples.

Session 3.

PHYSIOLOGY, BIOCHEMISTRY AND BIOTECHNOLOGY

FURTHER IMPROVING SPIKE FERTILITY TRAITS IN WHEAT TO KEEP INCREASING YIELD POTENTIAL

Slafer G.A. [1,2]***, Savin R.***[1]*

[1]*Department of Agricultural and Forest Sciences and Engineering, University of Lleida – AGROTECNIO-CERCA Center, Av. Rovira Roure 191, 25198 Lleida, Spain*
[2]*ICREA, Catalonian Institution for Research and Advanced Studies, Barcelona, Spain*

**E-mail:* gustavo.slafer@udl.cat

When improving complex traits, such as crop yield, understanding the CROP-physiological basis is instrumental to identify underlying traits controlling yield (and eventually identifying genes responsible for these traits). Identifying such traits is critical in order to design strategic crosses and/or to generate selection criteria.

A comprehensive view of all physiological bases of yield determination identifying promising traits for designing alternative management practices or breeding strategies to increase yield would be impossible in the framework of this presentation. Although wheat yield is built up from sowing to maturity, there are phases of the crop that are more critical for yield determination. Considering yield as the balance between sources and sinks having in mind that the processes determining yield change during developmental progress would help in identifying most critical traits that could then be physiologically analysed and genetically determined.

The two most popular approaches to understand the crop-physiological determination of yield are the dry matter approach (considering growth and partitioning) and the yield components approach. The former is conceptually source driven, the latter basically sink driven. But in reality crop yield is limited by both source- and sink-strength, but not implying co-limitations. It seems more or less clear that yield is dominantly sink-limited during post-flowering (when grain weight is being realized) and source-limited during pre-flowering (when grain number is being determined); which could explain the huge difference in plasticity between these two main yield components and why yield is most frequently related to grain number. Thus, critical traits to improve yield would be those determining the level of sink-limitation during the effective period of grain filling, basically those determining the number of grains per unit land area (and to some degree the potential size of the grains).

Spike fertility is, in this context, a critical trait determining yield. The final determination of the number of grain number per spike is strongly dependent on the availability of resources allowing more floret primordia initiated to become fertile florets at anthesis and most of them filled grains at harvest. Thus, it depends upon both the availability of resources allocated to the juvenile spikes where florets are developing, and the efficiency in their use at the time the number of grains is being determined (fruiting efficiency). Indeed, the physiological bases for the step change produced by the Green Revolution is a proof of concept for the relevance of spike growth and development immediately before anthesis have. Fruiting efficiency reflects the fate of floret development and grain abortion: more efficient genotypes would show a higher survival of floret primordia, and/or a reduced level of grain abortion. As abortion is low (most fertile florets set grains) and failure of floret primordia to become fertile florets is large, differences in fruiting efficiency in elite material maybe more related to survival of floret primordia. This may be achieved through increased allocation of resources for the developing florets and/or through an intrinsic improved rate of floret development. Fruiting efficiency can be used as criterion for selecting parents for strategic crosses, as it showed substantial transgressive segregation and trade-offs with spike growth can be avoided. Although it has been shown that the trait responds to selection, its real application would depend on counting with molecular markers.

THE MUTANT POPULATION OF WILD BARLEY ACCELERATES GENE CLONING

Shun Sakuma

Faculty of Agriculture, Tottori University

Wild barley (*Hordeum vulgare* ssp. *spontaneum*) is the sole member of the primary gene pool of cultivated barley (*H. vulgare* ssp. *vulgare*) and hence a valuable genetic resource. Several wild barleys were used as genetic material for map-based cloning due to the presence of wild ancestral traits such as brittle rachis, strong seed dormancy, and two-rowed spike. These traits were controlled mainly by dominant functional alleles in the wild and recessive non-functional alleles in cultivated barley, respectively, suggesting that wild barley leaves many intact genes for lesions. Here we have developed a large-scale mutant population from wild barley accession OUH602 to accelerate forward genetics mainly focusing on inflorescence structure. From sowing to harvest, plants were exposed to weak irradiation by cobalt 60 in the gamma field from the time of sowing to harvesting. This system is called chronic irradiation as opposed to acute irradiation commonly in plant mutagenesis. M2 seeds were harvested manually and through the phenotypic screening of about 50,000 M3 plants, we found domestication-related mutants like six-rowed spikes and several novel plant architecture mutants. Causal genes were identified through a combination of traditional mapping approaches and rapid identification of the causal mutations using next-generation sequencing technology together with the OUH602 chromosome-scale assembly. This wild barley mutant population is instrumental in improving barley and the discovery of novel genes and their mode of action.

ADDRESSING QUANTITATIVE DISEASE RESISTANCE IN LEGUMES VIA WHOLE-GENOME ANALYSIS AND BIOTECHNOLOGY

Ben C.*[1,2], Sidorov L.[1], Boldyrev S.[1], Baik A.[1], Mazurier M.[2], Sbeiti A.[2], Djouider I.[2], Fartash A.[2], Koteletsev I.[1], Martynova E.[1], Samad S.[1], Bondarenko E.[3], Volkova P.[4], Rickauer M.[2], Gentzbittel L.[1]

[1]Skolkovo Institute of Science and Technology, Project Center for Agro Technologies, Moscow, Russia
[2]CRBE, Université de Toulouse, CNRS, 31062 Toulouse, France
[3]Department Molecular and cellular biology, Russian Institute of Radiology and Agroecology, 249032 Obninsk, Russia
[4]Independent Researcher, Geel, Belgium

**E-mail:* C.Ben@skoltech.ru

Controlling legume diseases is pivotal for sustainable agriculture and global food security. Leveraging advanced technologies in genome analysis and biotechnology, we aim to enhance legume quantitative disease resistance, offering increased durability and broad-spectrum effectiveness. Our research spans various legume species, including lupine, alfalfa, vetch, and *Medicago truncatula*, investigating their response to fungal pathogens like *Verticillium* sp. and *Colletotrichum lupini*, exploring intricate genetic mechanisms among host genetics, pathogen variability, and environmental factors. Primary objectives involve elucidating genomic regions linked to disease resistance, uncovering molecular pathways in plant-pathogen interactions, and utilizing biotechnological tools for breeding resilient legume varieties.

White lupine (*Lupinus albus* L.), a promising protein source, faces threats from anthracnose. Analysing the whole genomes of six *C. lupini* strains from the same field yet exhibiting differing fitness and aggressiveness levels, we uncovered varying genetic relationships and genomic characteristics within putative virulence factors. Variant calling unveiled missense mutations occurring in the coding sequences of 35 genes, potentially associated with the virulence and fitness of the two most aggressive strains. Using LC-MS/MS-based proteomic analysis, we investigated the response of three lupine cultivars with distinct tolerance levels when infected with these two *C. lupini* strains. This approach led to the identification of candidate genes and pathways linked to either tolerance or susceptibility. Notably, changes in glutamate and proline metabolism were shown as essential in the response of the more tolerant Muchirinskij cultivar. Aspartate aminotransferase (AspAT) and nodulin 19 (Nod19) proteins were identified as potential modulators of the response to infection. sgRNAs were devised for targeted knockdown of these candidate genes utilizing the CRISPR-Cas system.

To better understand the interplay between biotic and abiotic stresses in legumes, we assessed resistance to Verticillium wilt amidst rising temperatures and salinity levels in *Medicago* sp. The experimental adaptation of *V. alfalfae* to elevated temperatures in *M. truncatula* resulted in increased aggressiveness, even towards alfalfa, a closely related crop. This indicates that root pathogen interactions are affected by global warming, with heat-adapted pathogens posing potential threats due to their broader host range and increased aggressiveness. Genome-Wide Association Studies (GWAS) unveiled a shift towards heightened susceptibility and distinct genetic control when exposed to a "warm" Iranian strain compared to a "temperate" French strain at two different temperature levels. Salinity also impacted the plant's response to *V. alfalfae*. GWAS revealed distinct genetic architecture governing the response to infection alone *versus* when combined with salt stress, with no overlap between these conditions. The exploration of ecologically relevant genetic material, along with monitoring the emergence of newly adapted pathogens, are crucial for identifying resistance sources and guiding future breeding endeavors.

INVASIVE PLANT-ENVIRONMENT INTERACTIONS: CASE STUDY OF *IMPATIENS PARVIFLORA* DC.

***Kupcinskiene E.,* Marozas V., Jociene L., Krokaite E., Rekasius T., Janulioniene R., Stravinskaite K., Paulauskas A.**

Vytautas Magnus University, K. Donelaicio str. 58, LT-44248 Kaunas, Lithuania

The world is facing multiple environmental challenges simultaneously, including chemical and biological pollution, climate change, degradation, and loss of biological diversity. Overcoming these challenges has become increasingly complicated due to the raise of temporal and spatial human-environment interactions. Phenomenon of species invasion is considered among the most harmful processes, creating threats to agriculture and forestry, health and the global economy. To date, an unusually large amount of time and money has been spent controlling invaders. The regulation of invasive alien species has become a top priority for conservation policy at the national and European levels. Information about steps and vitality of populations of alien herbs in North-East parts of Europe still remains very fragmental.

Small balsam (*Impatiens parviflora* DC. from *Balsaminaceae*) could be classified in this category as alien species that is extremely penetrative into various natural, semi-natural ecosystems. *Impatiens parviflora* is an exceptionally successful invader of forest vegetation and is presently the most common alien plant in European woodlands. According to the biotope *I. parviflora* sites might be divided into urban forests, riparian forests and agrarian shrublands. Extensive investigations of *I. parviflora* have started long before the dawn of molecular methods for population studies. Till now, *I. parviflora* remains among the least genetically examined invasive alien plant species world-wise. The aim of this study was to assess the genetic diversity of Lithuanian *I. parviflora* populations using a set of molecular markers and to correlate the genetic parameters with the species' abiotic and biotic environments.

Twenty-one populations (315 individuals) of small balsam (*Impatiens parviflora* DC.) were selected in the way to cover all the territory of Lithuania. The coverage of each species was calculated using Braun-Blanquet methodology and transformed into mean-percentage values for each degree (0.1%, 0.5%, 3%, 15%, 38%, 63%, 88%). For evaluation of environmental preferences of *I. parviflora* in each site, Ellenberg indicator values, i.e. – light, temperature, continentality, soil moisture, soil reaction and soil nutrients, were quantified. To assess the similarity of assemblages of herbaceous plant species in the sites, a cluster analysis was performed, applying program PC-ORD.

For genetic analyses six inter-simple sequence repeat primers (GGCC(AG)8, GGCC(AC)8, CCGG(AG)8, CCGG(AC)8, GCGC(AG)8, and GCGC(AC)8), six simple sequence repeat (SSR) primer pairs (IGNSSR101-EF025990, IGNSSR104-EF025992, IGNSSR106-EF025993, IGNSSR203-EF025994, IGNSSR210-EF025995, and IGNSSR240-EF025997), eight randomly amplified polymorphic DNA (RAPD) markers (OPA-20, OPD-20, 222, 250, 269, 340, 474, and 516) and eight amplified fragment length polymorphism (AFLP) markers were used. For identification of gene clusters of *I. parviflora* populations, Bayesian analysis was performed using STRUCTURE. To explain were the most important parameters for the variability of *I. parviflora* populations, principal component (PC) analysis was performed.

The number of herbaceous species at one site ranged from 13 to 32. A total of 138 herbaceous plant species or (after elimination of the species that grew at single sites only) of 76 herbs growing along with *I. parviflora* were grouped by two-way cluster analysis into species dendrogram. *Urtica dioica* was found at all sites. The polymorphism extent at ISSR and AFLP loci was significantly positively correlated with the total coverage of herbaceous plant species. Bayesian Structure analyses of molecular data demonstrated existence of many genetic clusters and this finding is in support to multiple introduction of the species. Defined by principal component analysis, the variability of study sites was most related to the coverage of herbaceous plants and least related to the molecular features of *I. parviflora* populations.

RHIZOSPHERE MICROBIOME OF THE BIOENERGETIC PLANT *MISCANTHUS* × *GIGANTEUS* AND ITS REMEDIATION POTENTIAL

***Muratova A.*[1], *Nurzhanova A.*[2]**

[1]*Institute of Biochemistry and Physiology of Plants and Microorganisms RAS, Saratov, Russia*
[2]*Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan*

Giant miscanthus (*Miscanthus* × *giganteus* Greef et Deu) is a promising bioenergy species that can grow on marginal and abandoned fallow lands, maintaining its high productivity and showing the ability to clean soils from organic and inorganic pollutants. Studying the formation of the rhizosphere microbial community, which ensures plant growth in unfavorable conditions and remediation of contaminated soil, is an important aspect of assessing the possibility of growing *Miscanthus* on contaminated soil.

The objective of the research was to characterize the influence of organic (oil sludge) and inorganic (heavy metals) pollutants on the physiological and biochemical characteristics of the plant *Miscanthus* × *giganteus* and the formation of its rhizosphere microbial community.

Plants were grown for 6 months under laboratory conditions in soil (leached chernozem) contaminated with zinc (1650 mg/kg), oil sludge (15 mL/kg), or both, after which the taxonomic structure of the rhizosphere microbial communities was examined by metagenomic 16S rRNA gene analysis. Oil sludge caused more pronounced changes in the taxonomic structure of the *Miscanthus* rhizobiome than did zinc, largely determining the nature of the effect of mixed pollution on this parameter. Under the influence of zinc, the proportion of Actinobacteria in the rhizosphere microflora increased, and oil sludge promoted the growth of Proteobacteria. Oil sludge and zinc, both individually and in combination, contributed to an increase in the proportion of Sphingomonadaceae. We, therefore, speculated that members of this family can participate in the cleansing of soil from oil sludge, be resistant to zinc as an accompanying pollutant, and effectively survive in the *Miscanthus* rhizosphere. In addition, the *Miscanthus* rhizosphere community contained taxa with plant-growth-promoting potential. From polluted rhizosphere samples, microbial strains were isolated and examined for their resistance to heavy metals and for plant-growth-promoting potential, manifested through nitrogen fixation, phosphorous mobilization, and synthesis of siderophores and phytohormones. Isolation of pure cultures and detailed studies on the microorganisms associated with the *Miscanthus* rhizosphere may be promising in the making of biological agents to promote plant growth and remediation of contaminated soils. Some rhizobacterial strains were examined to improve the performance of *Miscanthus* plants growing on polluted soils.

This research was funded by the Ministry of Education and Science of the Republic of Kazakhstan (project no. AP 19679273).

PLANT GROWTH PROMOTING (PGPR) RHIZOBACTERIA IN PHYTOREMEDIATION OF SOIL POLLUTED WITH TRACE ELEMENTS AND FUTURE PROSPECTS

Nurzhanova A.[1*], Mamirova A.[2], Muratova A.[3], Berzhanova R.[2], Nurmagambetova A.[1], Zhumasheva Zh.[1], Pidlisnyuk V.[4]

[1] Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan
[2] Al-Farabi Kazakh National University, Al-Farabi, Almaty, Kazakhstan
[3] Institute of Biochemistry and Physiology of Plants and Microorganisms, Saratov, Russia
[4] Jan Evangelista Purkyně University, Usti nad Labem, Czech Republic

Phytoremediation strategies using rhizobacteria adapted to heavy metals are attracting more and more attention, as soil contamination with toxic elements is a serious environmental problem that negatively affects human health and agriculture. Phytoremediation is a promising method for the remediation of environments contaminated with heavy metals. However, there are limitations: long remediation time, low biomass, inhibition of growth and development, and slow and limited bioavailability of some elements. Various agricultural practices, growth regulators, and microbial organisms are used to improve biomass production and increase phytoremediation efficiency. Of particular interest is the study of rhizospheric bacteria, which belong to the PGPRs, as they are resistant to metals in the composition of engineered plant-microbial complexes while having a growth-promoting effect on phytosanitizing.

Goal: to develop an effective technology for phytoremediation of soils contaminated with heavy metals by increasing the productivity of the bioenergetic phyto plant *M. x giganteus* using rhizobacteria (PGPR).

M×g inoculation with PGPR strains (*Rhizobium sp., Pseudomonas sp., Agrobacterium sp., Shinella sp., yeast Trichosporon sp.*) which were isolated from the rhizosphere of miscanthus has an ambiguous effect on HMs mobility and bioavailability in the soil, depending on the strain used. The rhizobacteria *p* growing on technogenically contaminated soil. When *M×g* inoculated with PGPRs, Sr and Mn accumulated in the aboveground in all experimental variants. Among the studied microorganisms, *Rhizobium* sp. and *Shinella* sp. translocated almost all elements (excluding V, Mn) from the root system into aboveground biomass relative to non-inoculated plants (TLF ≥1). Inoculation of *M×g* with *Trichosporon* sp., *Pseudomonas* sp., and consortium *Trichosporon sp. + Rhizobium sp.* increased the immobilization of Pb, V, Cr, Co, Ni, Cu, Cd, As, and Ba not only in the soil but also in plants - TLF values ≤ 1 relative to non-inoculated plants. In relation to the toxic elements Cd, Pb, and As, which are not involved in biological systems, *M×g* inoculation with PGPR strains reduced their bioavailability, and prevented their migration to terrestrial organs, thereby reducing the likelihood of metals entering the food chain.

The comprehensive bio-concentration index of inoculated *M×g* for 14 studied elements (As, Pb, Zn, Co, Ni, Cr, Cu, Sr, Cd, Mn, Ba, V, U and Fe) showed that *Trichosporon* sp. and *Rhizobium* sp. improved phytostabilization potential; consortium *Trichosporon sp. + Rhizobium sp*. and *Pseudomonas* sp. induced HMs mobility within plants; *Shinella* sp. – enhanced phytoextraction. Inoculants *Trichosporon* sp., *Pseudomonas* sp., and consortium *Trichosporon sp. + Rhizobium sp*. can be used in phytostabilization of Pb, V, Cr, Co, Ni, Cu, Cd, As, and Ba; *Shinella* sp. and *Pseudomonas* sp. for phytoextraction of Zn.

Utilization of PGPR strains to increase the phytoremediation efficiency of HM-contaminated soil can be considered promising from an economic perspective compared to physical and chemical approaches. Furthermore, PGPR utilization is beneficial to increase productivity and phytostabilise HMs in the soil for further cultivation of *M×g* as an energy crop.

Acknowledgements. This research was funded by the SC of the MSHE RK (Grant AP 19679273)

THE INFLUENCE OF IONIZING RADIATION IN LOW DOSES ON THE MECHANISMS OF FORMATION OF RESISTANCE TO ENVIRONMENTAL STRESS FACTORS IN PLANTS

Grinberg M.A.**, Nemtsova Y.A., Ivanova A.V., Vodeneev V.A.

Lobachevsky State University of Nizhny Novgorod, Nizhny Novgorod, Russia

* *E-mail:* mag1355@yandex.ru

Due to natural and anthropogenic reasons, there are areas on Earth with increased background radiation. It is known that the state of living organisms, including plants, in such areas may differ somewhat from that under normal radiation background. There is reason to believe that the most pronounced differences appear under the influence of additional unfavorable conditions. In our work, we investigated the ability of plants to develop resistance to short-term (heat stress) and long-term (drought) unfavorable conditions against the background of low-intensity chronic ionizing radiation (IR) in laboratory conditions. We considered the effect of IR on signaling systems as a mechanism for modifying resistance.

Experiments were performed on 2-week-old wheat (*Triticum aestivum* L.) and 6-week-old tobacco plants (*Nicotiana tabacum* L.) expressing the pH-sensitive genetically encoded sensor Pt-GFP. Irradiation (30 μGy/hour, 90Sr-90Y β-emitter) lasted throughout the growing period. Short-term heat stress was set by heating in a thermostat. Drought was simulated by stopping irrigation. The activity of photosynthesis (PAM fluorimetry) and transpiration (thermal imaging) were measured to assess plant status. Electrical signals were considered as significant stress signals for the formation of resistance. Their parameters were recorded using macroelectrode technology. The pH shifts accompanying the electrical signals were recorded by the fluorescence of the Pt-GFP sensor.

It was shown that IR has virtually no effect on the morphometric parameters and photosynthetic activity in plants in the absence of additional stress factors. However, IR significantly modifies plant resistance to short-term (heat stress) and long-term (drought) unfavorable conditions. This effect may be based on changes in the parameters of stress-induced electrical signals: their amplitude increases in irradiated plants. The key element sensitive to IR and involved in changing the activity of physiological processes that contribute to the formation of resistance appears to be pH shifts.

The work was supported by the Russian Science Foundation (project no. 23-24-00340).

WHEAT CELL CULTURE AS A SOURCE OF POLYSACCHARIDES WITH ANTICANCEROUS POTENTIAL

Murtazina A.[2,3], Marchal J.A.[3], Tarabayeva A.S.[2], Bitanova E.Zh.[2], McDougall G.[4], Boulaiz H.[3], Bishimbayeva N.K.[1]

[1]Research Institute of Biology and Biotechnology, Al-Farabi Kazakh National University, Almaty, Kazakhstan
[2]Department of General Immunology, Faculty of Medicine, Asfendiyarov Kazakh National Medical University, Almaty, Kazakhstan
[3]Biopathology and Regenerative Medicine Institute (IBIMER), Centre for Biomedical Research, University of Granada, Granada E-18100, Spain
[4]Plant Biochemistry and Food Quality Group, Environmental and Biochemical Sciences Department, The James Hutton Institute, Invergowrie, Dundee

**E-mail:* hboulaiz@ugr.es, nbishimbayeva@gmail.com

There is a global need to discover effective anti-cancerous compounds from natural sources. Cultivated wheat cells can be a valuable source of non-toxic or low toxic plant-derived polysaccharides. In this study we evaluated the antitumor ability of seven fractions of wheat cell culture polysaccharides (WCCPSs) in the HCT-116 colon cancer cell line. Almost all (6/7) fractions had an inhibitory effect on the proliferation of colon cancer cells, and two fractions (A-b and A-f) had considerable therapeutic indexes. The WCCPS fractions induced cell cycle arrest in the G1 phase and induced different rates of apoptosis (≤48%). Transmission and scanning electron microscopy revealed that WCCPS fractions caused apoptotic changes in the nucleus and cytoplasm, including damage to mitochondria and external morphological signs of apoptosis. In addition, the WCCPSs induced an increase in the levels of Bax, cytochrome c, caspases 8 and 3, indicating that cell death was assessed through intrinsic and extrinsic pathways of apoptosis. Furthermore, some fractions caused a significant decrease of c-Myc, b-catenin, NFkB2 and HCAM (CD 44) levels, indicating enhanced cell differentiation. Thus, for the first time, our results provide a proof of concept of the anti-cancer capacity of WCCPS fractions in colorectal cancer.

This research was supported by the FEDER Operational Program 2020/Junta de Andalucía-Consejería de Economía y Conocimiento/ Project (B-CTS-562-UGR20) and the Chair “Doctors Galera-Requena in cancer stem cell research” (CMC-CTS963); Erasmus+ Mobility Program; “Bolashak” Presidential Scholarship of the Republic of Kazakhstan for scientific work abroad; Scottish Government’s Rural and Environment Science and Analytical Services (RESAS) division.

UNDERSTANDING THE CONTROL OF STARCH GRANULE SIZE IN WHEAT AND ITS IMPACT ON STARCH DIGESTIBILITY

Makhamadjonov F.

John Innes Centre, Norwich, Unigted Kingdom

Starch is a ubiquitous polysaccharide in plants and an important source of carbohydrates in the human diet. In most plants including modern staple crops like wheat (*Triticum aestivum*), it is synthesized and stored in semicrystalline granules. In wheat endosperm, there are two types of starch granules – larger lenticular A-type granules and smaller spherical B-type granules. The properties of these granules affect the nutritional quality of starch, however, the mechanisms that control those properties are not well understood. B-GRANULE CONTENT 1 (BGC1) – a carbohydrate-binding protein with no enzymatic activity has been implicated in B-type granule initiation and morphology in wheat. It is known to interact with many other starch biosynthesis proteins, but its function and mechanism of action is not clear. In this project, we aim to further our understanding of the role of BGC1 in the control of wheat B-type starch granule formation and morphology and its implications on human health. We have discovered that BGC1 strongly interacts with itself and forms dimers. We will investigate the functional importance of this oligomerization, along with the structure and function of native BGC1, with *in vitro* mutagenesis and mutant wheat populations, crystallography, and substrate binding assays. Mutant wheat populations with varying starch granule phenotypes will be used to make pasta and analyze its nutritional properties, such as digestibility and effects on the gut microbiome. These investigations will help understand how starch granule morphology is controlled in wheat and its impact on human health.

BIOTECHNOLOGICAL APPROACHES TO *IN VITRO* CULTURE INTRODUCTION OF *RHAPONTICUM CARTHAMOIDES*

Raizer O.B.*, Akinfeeva E.V.

National Center of Biotechnology, Astana, Kazakhstan

**E-mail:* 2008olesya @mail.ru

Biological diversity is a necessary condition and factor in increasing the viability and vital activity of all biological objects. Consequently, the conservation of biodiversity is not only an important ecological, botanical task, but a problem that generally solves our well-being.

A solution to the problem of preserving the biological diversity of flora can be found through the use of biotechnological methods. The need to use tissue culture of rare, medicinal and endangered plant species is dictated by the biological characteristics of their development, namely the slow restoration of population numbers in natural growing conditions.

Rhaponticum carthamoides - one of the valuable medicinal plants used in official and folk medicine, is the most important large herb species of the world flora, with the ability to synthesize ultra-high levels of ecdysteroids, the potential for productive longevity and significant productivity. Due to the high medicinal and resource significance, *R. carthamoides* is listed in the Red Book of Kazakhstan.

To obtain a sterile culture of *R. carthamoides*, 6 options for seed sterilization were optimized using various sterilizing agents and exposure times. A multi-stage method of seed sterilization was most effective when *R. carthamoides* was introduced into *in vitro* culture.

At the first stage, pre-sterilization was carried out using a 0.1% solution of potassium permanganate and soaking the seeds for two days in sterile distilled water to remove lightweight seeds. Actually, the sterilization stage consisted of sequential treatment of seeds in a 10% sodium hypochlorite solution and a 0.1% mercuric chloride solution. The sterility of explants using this sterilization scheme reached 85%.

Surface-sterilized seeds were placed on MS and MS media containing ½ mineral salts with different hormonal compositions. Signs of germination in *R. carthamoides* seeds appeared on days 3-5 of cultivation; seed viability depended on both the sterilization scheme and the hormonal composition of the medium and ranged from 42.9 to 85.5%. Thus, the lowest percentage of germination was noted on the B0 medium option (½ MS) - 42.9%. The highest percentage of germination was in seeds on the B3 medium option (MS + 3 mg/l BAP + 3 mg/l kinetin), in this option the germination percentage was 85.8%. The combination of various phytohormones in all environments did not affect the morphological characteristics (growth and development) of *R. carthamoides* seedlings.

As a result of the research, individual stages of *in vitro* cultivation of *R. carthamoides* were optimized - sterilization of seeds, obtaining sterile seedlings.

BIOTECHNOLOGY AND GENOMIC STUDY OF FAR EASTERN *ACTINIDIA* SPECIES, CULTIVARS AND FORMS

***Mitrofanova I.*[1], *Krakhmaleva I.*[1], *Molkanova O.*[1], *Gladysheva-Azgari M.*[1,2], *Slobodova N.*[1,2], *Sharko F.*[2], *Tsygankova S.*[1,2]**

[1]*N.V. Tsitsin Main Botanical Garden, Russian Academy of Sciences, Moscow, Russia*
[2] *National Research Center "Kurchatov Institute", Moscow, Russia*

**E-mail:* irimitrofanova@yandex.ru

Actinidia (*Actinidia* Lindl.) is a large genus (about 70 species), the center of diversity is in East Asia. Most of the *Actinidia* species have edible fruits containing a large amount of laxative, antidiabetic, anti-oxidant, anti-inflammatory, and other health-promoting compounds. Fruits are widely used in various branches of food industry. Flowers and fruits are promising raw material for the cosmetic industry.

Three frost resistant species can be cultivated in places with cold winters: *A. arguta* (Sieb. et Zucc.) Planch. ex Miq., *A. kolomikta* (Maxim. et Rupr.) Maxim., and *A. polygama* (Sieb. et Zucc.) Maxim. *A. arguta* и *A. polygama* withstand temperatures up to -31°C without damages, while *A. kolomikta* – up to -40°C). The most representative *Actinidia* collection in Russia about 200 samples was placed at Federal Horticultural Center for Breeding, Agrotechnology and Nursery and now is placed at N.V. Tsitsin Main Botanical Garden (MBG RAS) in Moscow.

The objective of the study was to investigate biotechnology approaches of three Far Eastern *Actinidia* species propagation: *A. arguta*, *A. kolomikta*, *A. polygama*, and some genomic aspects of four Far Eastern Actinidia species, included *A. purpurea*.

The *in vitro* collection was created at the MBG and have a unique assemblage of Far Eastern *Actinidia* species: more 60 cultivars of 3 species: *A. arguta*, *A. kolomikta*, and *A. polygama*. It was found that the genus traits affected the multiplication rate of the genus *Actinidia* representatives more than cultivar traits. The explants of different *Actinidia* species vary significantly by the regeneration capacity. Microshoots of *A. arguta* and *A. polygama* developed faster (multiplication rate from 6.3 to 8.4 and from 6.0 to 7.7) than explants of *A. kolomikta* (from 4.6 to 5.5) at the initiation and micropropagation stages. The regeneration capacity of explants and the number of *Actinidia* microshoot formed depended on the genotype and on the composition of the culture medium. It was demonstrated that meta-topolin induced the formation of a large number of adventitious shoots at the base of cultured explants and the induction of axillary and adventitious buds on microshoots, compared to other cytokinins, such as 6-BAP and 2-ip. The cultivation on QL culture media with mT contributed to significant increase of multiplication rate of *A. arguta* (by 1.3 and 1.7 times) and *A. kolomikta* (by 1.5 and 1.7 times).

Draft nuclear genomes of *A. arguta* and *A. kolomikta* were collected for the first time. Mitochondrial genome of *A. purpurea* is not represented in international databases and is assembled completely for the first time. Over 90 thousand SNPs were obtained characterizing each cultivar group during of genotype 113 samples of *Actinidia* by modified RADseq protocol. The genetic structure of the Russian *Actinidia* collection was determined. The cultivars and forms of *A. kolomikta* are characterized by a homogeneous genome structure, in contrast to the cultivars of *A. arguta* and *A. polygama*, between which a high degree of hybridization was found.

Thus, first time the complete biotechnology and genomic investigation of Far Eastern *Actinidia* collection in Russia was done as a base on new modern breeding and mass propagation of valuable healthy plant material.

This study was funded by a research grant № 22-16-00074 of the Russian Science Foundation.

Keywords: *Actinidia arguta*, *A. kolomikta*, and *A. polygama*, regeneration capacity, multiplication rate, chloroplast and mitochondrial genome, SNP, genome structure

THE IMPACT OF CHITOSAN-CAFFEIC ACID CONJUGATE WITH BACILLUS SUBTILIS 47 ON PLANT DEFENSE AGAINST PVY UNDER SOIL WATER DEFICIT

***Yalouskaya N.A.*[1], *Kalatskaja J.N.*[1], *Rybinskaya K.I.*[1], *Ivanov O.A.*[1], *Hileuskaya K.S.*[2], *Nikalaichuk V.V.*[2], *Yarullina L.G.*[3], *Burkhanova G.F.*[3], *Zaikina E.A.*[3]**

[1]*V.F. Kuprevich Institute of Experimental Botany of the National Academy of Sciences of Belarus, Minsk, Republic of Belarus*
[2]*Institute of Chemistry of New Materials of the National Academy of Sciences of Belarus, Minsk, Republic of Belarus*
[3]*Institute of Biochemistry and genetics-separate structural subdivision of the Ufa Federal Research Centre of the Russian Academy of Sciences, Ufa, Russia*

*****_E-mail:_ yalouskaya92@mail.ru

Plant Growth Promoting Bacteria is an eco-friendly method for achieving sustainable agriculture. *Bacillus* species are commonly studied as biocontrol agents to suppress plant pathogens, but are sensitive to environmental factors. Biopesticides can be combined with bioactive compounds based on chitosan. The aim of our work was to investigate the potential of chitosan-caffeic acid conjugate (Ch-CA) with a mixture of *Bacillus subtilis* strain 47 to protect potato plants against PVY under water deficient stress.

The conjugates exhibit a significant antibacterial effect against *Pectobacterium carotovorum* and *Pseudomonas syringae*. The antibacterial activity of the conjugates Ch-CA against *B. subtilis* 47, used in a mixture with conjugates against PVY, showed that the strains of *B. subtilis* 47 resistant to the conjugate.

It was found that the application of Ch-CA significantly reduced the infection rate of PVY in potato plants grown under optimal and stress conditions. The production of hydrogen peroxide and changes in antioxidant levels due to Ch-CA may play a crucial role in maintaining potato resistance to PVY. The combination of *B. subtilis* 47 and Ch-CA reduced infection levels only in plants under soil water deficit. Lower antioxidant activity and hydrogen peroxide content are correlated with susceptibility to PVY infections when applying the mixture of *B. subtilis* 47 + Ch-CA under optimal conditions. Ch-CA and *B. subtilis* 47 + Ch-CA induced the expression of several PR genes were involved in the development of induced systemic resistance in potato plants.

This work was supported by the Russian Scientific Foundation, grant number 23-16-00139.

AIR HUMIDITY EFFECT ON PLANT ARCHITECTONICS AND GENE EXPRESSION: DEEP STUDY INTO UNINVESTIGATED MOLECULAR MECHANISMS

Krylova E.A.*, Burlyaeva M.O., Khlestkina E.K.

N.I. Vavilov All-Russian Institute of Plant Genetic Resources, Saint-Petersburg, Russia

**E-mail:* e.krylova@vir.nw.ru

The introduction of some demanded plant species from arid and semi-arid areas into crop production in countries with a humid climate is a difficult task. The molecular mechanisms for tolerance to high air humidity remain the least studied in comparison with those for other biotic stress factors (drought, heat, cold, flooding, etc.). The purpose of the work is to study the molecular mechanisms of resistance to excessive air humidity. We studied cowpea (*Vigna unguiculata* (L.) Walp) to improve finally its breeding programs for sowing areas in Northeast Asia, where typical cowpea accessions from arid and semi-arid zones are not suitable.

Analysis under contrasting natural and controlled moisture conditions revealed different responses of different cowpea genotypes. The architecture (and therefore the suitability for mechanized harvesting) of some genotypes changed significantly in response to high air humidity, while other genotypes were tolerant. Such contrasting genotypes were taken for comparative transcriptomic analysis. In total we identified 657 upregulated and 630 downregulated DEGs. Fine differences between RNA-seq results for different genotypes are discussed in the report. DEGs associated with jasmonic acid metabolism are proposed to be key contributors into maintenance of compact architecture under humid conditions. In addition, we create isogenic lines by the *TFL1* gene editing. This gene controls plant architecture by determining where and when flowers are made by delaying the switch from vegetative phase to flowering, so finally it controls determinate/indeterminate type of stem growth. Having such isogenic lines one can distinguish the mechanisms of plant architecture formation depending on and independent of humidity. The results of genome editing aimed on *TFL1* knockout are also presented in the report.

The work was supported by the Russian Science Foundation (project no. 21-66-00012).

PROSPECTS FOR THE PRACTICAL APPLICATION OF RNA INTERFERENCE FOR THE INDUCTION OF PLANT DEFENSE MECHANISMS

Sutula M.Y.**, Manabayeva S.A.

National Center for Biotechnology, Astana, Kazakhstan

**E-mail*: m.sutula@biocenter.kz

Plant viruses pose significant challenges to the economy and agriculture of the Republic of Kazakhstan, with current control methods often insufficient due to the emergence of new viral strains each season. When viral RNA enters a plant cell, it generates dsRNAs, initiating an intracellular mechanism through the DICER enzyme, that produces short RNAs. Short interfering RNAs (siRNAs) activate viral resistance by programming the effector RNA-induced silencing complex (RISC).

However, evolutionary viruses exploit cellular machinery to synthesize suppressor proteins, such as PVY-HC-Pro, which blocks protective RNA interference by trapping and retaining short RNAs on the protein subunits surfaces. RNA-mediated gene knockout technology presents a promising avenue in enhancing plant resistance to viruses. This technology utilizes double-stranded RNA (dsRNA) to initiate RNA interference (RNAi), producing short interfering RNAs that specifically target and degrade viral RNA molecules.

Our research demonstrates a novel methodological approach utilizing preprogrammed siRNAs to confer resistance to viruses in *S. tuberosum* plants infected with Potato virus Y (PVY). From 2020 to 2023, on model plants *N. benthamiana* and three varieties of potatoes from Kazakhstan, we observed that siRNA-treated plants exhibited minimal disease symptoms in the early stage of PVY infection completely disappearing by days 21-27 after PVY inoculation. The development of aboveground parts and tuber material proceeded normally until the end of the growing season. Furthermore, siRNA treatment led to an 80% reduction in viral particle accumulation in plant cells and tissues after inoculation, as confirmed by ELISA and PCR analyses. Laboratory and field trial results indicated that the viability of second-generation plants derived from immunized siRNA-treated plants after PVY infection exceeded 90%, with symptoms of PVY observed in only 60% of immunized plants. Notably, potato tubers were unaffected by viral infections, including various types of necrosis. Second-generation plants treated with CP-PVY siRNA displayed mild PVY symptoms, primarily in the early stages of development. By the end of the growing season, all plants exhibited a recovery phenotype, with no tuber necrosis symptoms, indicating a high resistance level to PVY. These findings are consistent with those of foreign researchers investigating RNA interference and the suppression of plant defense mechanisms by viral proteins.

The potential of RNA interference extends to a broad spectrum of viruses encoding suppressor proteins similar to HC-Pro, including Barley stripe mosaic virus (BSMV), Cucumber vein yellowing virus (CVYV), Turnip mosaic virus (TuMV), Potato virus S (PVS), Tomato aspermy virus (TAV), and Cucumber mosaic virus (CMV). Understanding the interaction between these viruses and RNAi components provides avenues for developing tailored approaches to effectively combat viral infections.

Discovery of antimicrobial proteins and peptides from dandelion (*Taraxacum officinale* Wigg.) as a new tool FOR development of biopesticides

***Rogozhin E.A.*[1,2]**

[1]*Institute of Bioorganic Chemistry Russian Academy of Sciences, Moscow, Russia*
[2]*All-Russian Institute for Plant Protection, Saint-Petersburg-Pushkin, Russia*

**E-mail:* rea21@list.ru

In order to develop a direction for a fundamentally oriented study of a group of protein-peptide extracts of wild plants that showed pronounced antimicrobial activity against a group of filamentous fungi and bacteria (including phytopathogenic species), fractionation of individual samples was carried out using liquid chromatography methods, followed by structural and functional analysis of individual peptides. As one of the objects, we selected a cosmopolitan weed species - dandelion (*Taraxacum officinale* Wigg.), which earlier in a series of our previous studies showed potential in terms of containing a complex of polypeptides with antimicrobial action (AMP), and their presence was supposedly completely contrasting in flowers and seeds. Thus, representatives of three unique structural motifs (with 6-8 cysteine residues, forming 3-4 disulfide bridges) from the ToAMP1-4 group were isolated from a water-acid extract of flowers of this plant, as well as two linear proline/hydroxyproline-rich peptides modified with pentose residues through glycosidic bonds (ToHyp1-2); from seeds - a complex of isoforms of storage proteins, 2S-albumins (ToA1-3), which also have protective functions, apparently ensuring safety from biotic factors of seeds in the soil, as well as at the stage of initiation of germination. The functional characterization of proline-hydroxyproline-rich glycopeptides of the ToHyps group of the dandelion flowers (*T. officinale*) was also carried out in the aspect of a more detailed study of the manifestation of possible signaling properties, which can classify these molecules as bifunctional. The first block of experiments concerned the testing of total protein-peptide extracts of a number of wild plants for the manifestation of a reactivating effect on pre-stressed (UV irradiated) yeast cells (*S. cerevisiae*). As a result, it can be observed that at a final effective concentration of 3 mg/mL, the dandelion flower concentrate increased the survival rate of the yeast test culture CFU by more than 1.5 times, while the dandelion seed extract was inactive. In addition to the previously obtained data on the specific antifungal activity of the complex of protective peptides of dandelion flowers from the ToHyps and ToAMP groups, their effect on the inhibition of collection opportunistic micellyal and yeast cultures was studied. The antimicrobial activity of dandelion defense peptides was studied against pathogenic fungi: *A. niger*, *A. fumigatus*, *P. chrysogenum*, *F. oxysporum*, *C. albicans* using the disk diffusion method at 0.1 mg/mL. According to the results of the study, none of the peptides had activity against *A. niger*. Also, the peptides ToAMP1, ToAMP2, ToHyp1 demonstrated a lack of antimicrobial activity against these pathogens. Only ToAMP3, ToHyp2, ToHyp3 showed antimicrobial activity against *A. fumigatus* and *P. chryzogenum*. At the same time, ToHyp1 has an average, and ToHyp3 a weak activity in relation to both test microorganisms. ToAMP3 exhibited a moderate antifungal action against *P. chryzogenum* and a weak one against *A. fumigatus*. The purpose of this block of research was determined by the formulation of fundamental and potentially applied problems. The first was to clarify the method of antifungal action of one of the groups of AMPs of dandelion flowers, which may expand the existing understanding of the peptide actions to pathogens, while the solution of the second will provide an actual understanding of the so-called "suitability" of whole protein-peptide concentrate of dandelion as a prototype of a "new generation" biofungicide through an introduction to peptidomic analysis.

This work was supported by the Russian Science Foundation (grant № 19-76-30005-P).

FEATURES OF SEED GERMINATION OF ENDEMIC SPECIES TULIPA SP. NORTH AND CENTRAL KAZAKHSTAN

Tagimanova D.*, Raizer O., Nagmetova G.

National Center for Biotechnology, Astana, Kazakhstan

* *E-mail*: tagds@mail.ru

Kazakhstan is located in the centre of Eurasia with an area ranking ninth in the world and has almost all types of landscapes existing on the globe. In the republic 14 % of the flora (about 700 species) belong to endemic species. A significant number of endemics (about 20%) are represented in the genus *Tulip* Kazakhstan is one of the key centres of tulip distribution in the world, on the territory of which more than 30 species of tulips grow, the habitats of 9 species are located in Northern and Central Kazakhstan, of which 2 species are endemics: *Tulipa auliekolica, Tulipa turgaica*.

Conservation of these species is a serious problem worldwide, and the use of *in situ* conservation methods alone does not guarantee their full conservation. To solve this problem, the use of biotechnological methods related to conservation and propagation in in vitro culture is proposed, allowing the reproduction of valuable genotypes in natural populations. Despite the fact that work on the study and conservation of rare endemic species of *Tulipa sp*. is actively carried out, the development of in vitro conservation technologies is required for new endemic species in need of conservation.

Tulips are propagated *in situ* mainly by seeds, but a period of seed dormancy results in low germination rates. Dormancy is a biological adaptation of seeds regulated by many factors. Temperature is the major environmental factor responsible for various changes in seed dormancy, and the dormancy period can be disturbed by temperature fluctuations or warm/cold stratification. Hormones also influence the process of seed dormancy and germination.

The aim of our research is to study the effect of temperature and growth regulators on seed germination of *T. auliekolica, T. turgaica.*

Seeds of *T. auliekolica* and *T. turgaica* were used as research material. Seeds were sterilized in 0.1% thiabendazole solution for 20 minutes, washed three times in distilled water. Seeds were considered germinated when a seedling petiole 1-2 mm long appeared. The seeds were cultured with constant temperature and temperature fluctuations in the dark. The constant temperatures were 4, 10 and 20°C. The temperature fluctuations were carried out as follows: 4/10°C, 10/20°C, 20/4°C. The effect of gibberellin 13 and 52 mg/L (GA3), potassium nitrate 100 mg/L (KNO3), thiourea 100 mg/L (CH4N2S) was investigated to improve seed germination.

Analysis of the effect of temperature factor on seed germination rate showed species differences. The highest germination rate of 72% was for *T. auliecolica* at a constant temperature of 4°C, while the optimal temperature for *T. turgaika* was 10°C, with a germination rate of 43%. At 20°C the seeds did not germinate. Temperature fluctuations had a positive effect on germination, which was increased from 72% (4°C) to 78% (4/10°C) in *T. auliecolica* species and from 53% (10°C) to 57% (10/20°C) in *T. turgaika* species. The effect of exogenous growth regulators was also studied to improve seed germination. Gibberellic acid (GAZ) significantly improved seed germination of *T. auliecolica* species, the highest germination percentage was obtained on medium with 52 mg/l GAZ - 93%, in *T. turgaika* species this indicator was - 53%. KNO3 also had a positive effect on seed germination of both species: *T. auliecolica* - 85%, *T. turgaika* - 50%. The germination of the studied species on media with thiourea addition was low. It was revealed that gibberellin plays a key role in seed dormancy disruption and increases germination. The nitrogenous compound KNO3 also had a positive effect on reducing dormancy and promoted seed germination, increasing overall germination. Thus, analysis of the data obtained showed that the germination of *Tulipa* seeds under different temperature regimes was species dependent. For *T. auliecolica* species, the optimum is cultivation at 4°C, and for *T. turgaika* species, cultivation at 10°C on ½ MS medium supplemented with 52 mg/l GAZ.

PHYSIOLOGICAL BASES FOR THE TRADE-OFF BETWEEN GRAIN WEIGHT AND GRAIN NUMBER ACROSS MODERN WHEAT UNDER CONTRASTING SOIL NITROGEN CONDITIONS

Kim J.W.[1], Slafer G.A.[1,2], Savin R.[1]*

[1]Department of Agricultural and Forest Sciences and Engineering, University of Lleida – AGROTECNIO-CERCA Center, Av. Rovira Roure 191, 25198 Lleida, Spain
[2]ICREA, Catalonian Institution for Research and Advanced Studies, Barcelona, Spain

* *E-mail*: roxana.savin@udl.cat

The concept that yield is most frequently sink-limited during grain filling, does not get along well with the fact that a negative relationship between average grain weight (AGW) and grain number (GN) is commonly found when genotypic or management factors increase GN. As the critical period to determine GN and AGW is minimally overlapping during wheat growth, this negative relationship might not be involved in feedback process. Generally, this negative relationship has been interpreted as reflecting a competitive mechanism (i.e. a true trade-off between GN and AGW), though non-competitive alternatives, representing only an apparent trade-off are possible. Ascertaining whether the negative relationship driven by genotypic factors is due to competition or not would be critical to justify that further increasing GN might be still a good strategy for yield improvement. Possibly, whether or not grain growth of particular wheats are mainly sink-limited during grain filling may depend on the background environmental condition. If so, in regions with lower chances of successfully exploiting increases in GN, attempting to increase AGW might be a better breeding strategy. In this context, it would be a key point to quantify the magnitude of source or sink limitation in modern elite wheat cultivars, and plasticity of wheat yield components in response to environmental conditions to understand the putative traits related to GN and AGW in modern, elite genotypes of wheat. Therefore, the main objective of this research was to elucidate whether the reduction in AGW in response to genetic increases in GN represents a case of source-limitation under low or high soil fertility conditions. GN and AGW showed a noticeable difference in phenotypic plasticity (in response to the contrasting nitrogen condition). Across three field studies, GN and yield showed to be very plastic, while AGW was extremely conservative. But the relevance of particular components in determining yield is not independent from the source of variation. Whilst GN was much more strongly affected by two contrasting soil nitrogen availability levels, the genotypic effect was quite relevant for AGW. The reduction in AGW was not due to an increased proportion of small grains as when GN increased, discarding the most plausible explanation for such negative relationship not involving competition among grains: in general, all grain size classes were smaller in genotypes with more GN than in those with less GN.

STUDY OF THE MECHANISMS OF PHOTOSYNTHETIC CONTROL - A KEY REGULATORY PROCESS ADJUSTING THE RATE OF PHOTOSYNTHETIC ELECTRON TRANSPORT IN CHLOROPLASTS UNDER CHANGING ENVIRONMENTAL CONDITIONS

Kozuleva M., Vilyanen D.

Institute of Basic Biological Problems, Pushchino Scientific Center for Biological Research, Pushchino, Russia

Photosynthesis is the basis of plant bioenergetics and biochemistry. Changing environmental conditions affect the rate of photosynthesis, which is realized at different levels. The rate of light reactions is largely controlled by the pH value of the thylakoid lumen. When protons accumulate in the lumen, a protective mechanism, named photosynthetic control, is triggered by the slowing of electron transport during the step of oxidation of plastoquinol (PQH2) to plastoquinone (PQ) in the quinol-oxidizing (Qo)-site of the cytochrome b6f complex. This slowdown is due to the fact that electron transfer from PQH2 to the cytochrome b6f complex involves deprotonation of PQH2 followed by proton diffusion into the lumen. The diffusion of protons from the Qo-site to lumen is accomplished through two channels in the cytochrome b6f complex. Little research attention has been paid to the functioning of these channels and their role in the regulation of photosynthesis.

In our work, we have developed an approach to investigate the mechanism by which lumen pH affects proton diffusion through these channels during PQH2 oxidation in the Qo-site of the cytochrome b6f complex and the development of photosynthetic control. In experiments with isolated thylakoids from higher plants (*Pisum sativum* and *Arabidopsis thaliana*), we found that lumen pH differentially affects the affinity of the Qo-site for two competitive inhibitors of PQH2 oxidation, 2,4-dinitrophenyl ether of 2-iodo-4-nitrothymol (DNP-INT) and 2,5-dibromo-3-methyl-6-isopropylbenzoquinone (DBMIB), leading to different level of inhibition of electron transport under given conditions and allowing us to assess the effect of lumen pH on the functioning of the cytochrome b6f complex. The experimental data obtained suggest that the effect of lumen pH on the binding of these inhibitors in the Qo-site is realized through different proton channels. The developed approach makes possible to selectively investigate the two channels for proton diffusion in the cytochrome b6f complex under different stress conditions and in plants of different genotypes.

This work was supported by the Russian Scientific Foundation (RSF) grant No. 23-14-00396.

THE LONG WAY TO PVY-RESISTANT POTATO PLANTS DEVELOPMENT

***Karlov V.D.*[1], *Nezhdanova A.V.*[2], *Razhina O.L.*[1], *Kolesnikova V.V.*[1,2], *Nikonova E.Y.*[2], *Lebedeva M.V.*[1], *Zlobin N.E.*[1], *Babakov O.V.*[1], *Kamionskaya A.M.*[2], *Nikonov O.S.*[3], *Taranov V.V.*[1]**

[1] *All-Russia Research Institute of Agricultural Biotechnology, RAS, Moscow, Russia*
[2] *Federal Research Centre "Fundamentals of Biotechnology", RAS, Moscow, Russia*
[3] *Institute of Protein Research, RAS, Puschino, Russia*

Potato virus Y (PVY) belongs to a large family of plant RNA-viruses *Potyviridae* and is considered as one of the most harmful pathogens affecting potato farming. Viral genome is composed of 10kb single-stranded (+)RNA with polyadenylated 3'-end and covalently linked VPg protein at the 5'-end. Successful development of PVY infection results from availability of susceptibility factors, namely eukaryotic translation initiation factors 4E (eIF4E). It's considered that VPg recognises specific eIF4E after the disassembly of the capsid. This interaction reorganizes plant translational machinery to synthesize viral polypeptide. Although there are several PVY-resistant *Solanaceae* species carrying mutant form of *eif4e* genes: with substitutions in coding sequence in pepper and tomato and with deleterious mutation in tobacco. Unfortunately, there is still no potato *S. tuberosum L.* plants possessing strong resistance to PVY. So, the main purpose of our work become the pursuit and implementation of such modification of potato *eif4e* gene, which could help to achieve a strong resistance to PVY infection.

As the other *Solanaceae* plants, potato contains a small family of eIF4E, which is consisted of eIF4E-1 and its paralog eIF4E-2, eIF(iso)4E, nCBP. Initially, we've determined that both eIF4E-1 and eIF4E-2 are able to bind VPg of PVY using yeast two-hybrid assay. However, the interaction between VPg with eIF4E-2 was weaker than with eIF4E-1. The main fork in the road was to decide, which modification should be introduced in certain *eif4ie* gene: knock-out or amino acid substitution? To further deepen our understanding of main features of PVY infection development, especially VPg partner *in planta*, we obtained *eif4e-1* and *eif4e-2* knock-out potato plants by CRISPR/Cas9 technology. Also, we've found a few point mutations for both eIF4E-1 and eIF4E-2 that disrupted their interaction with the variety of the most common VPg by analysing a set of different mutant eIF4E. Chosen mutations of eIF4E were tested for their functionality in yeast model system.

This work was funded by the Comprehensive Research Program "Development of Potato Breeding and Seed Production".

THE ROLE OF ROS SCAVENGING ENZYMES IN RESPONSE TO HIGH TEMPERATURE STRESS IN CROPS

Samat A.**, Kurmanbayeva A.

L.N. Gumilyov Eurasian National University, Astana, Kazakhstan

* *E-mail:* abay.samatuli07@gmail.com

Heat stress is the most impactful factor affecting agriculture and the economy, reducing crop yields by up to 40% worldwide. According to modern concepts, high temperatures induce oxidative stress in plant cells due to the accumulation of Reactive Oxygen Species (ROS), leading to irreparable cellular damage. To mitigate the adverse effects of heat stress, plants activate defensive mechanisms, including enzymatic and non-enzymatic pathways. ROS-scavenging enzymes function by converting reactive oxygen species into less harmful alternatives, thus reducing their toxic effects on cells. Our findings in *Hordeum vulgare* demonstrate that under stress conditions (40°C) with low humidity, barley activates ROS-scavenging enzymes such as Catalase and Superoxide Dismutase. However, their activity depends on the duration of stress; SOD activity peaks on the 3rd day of stress but decreases gradually thereafter. Similarly, Catalase activity follows this trend, albeit less actively than SOD. Aldehyde oxidase activity mirrors that of Catalase. Correspondingly, the levels of MDA and proline content in stressed plants are higher than those in control plants, peaking on the 3rd day and gradually decreasing thereafter.

Acknowledgements: The study has been supported by the Budget project: AP19676731.

OBTAINING ASEPTIC PLANTS OF *HIPPOPHAE RHAMNOIDES L. IN VITRO* CULTURE

Tumenbayeva A.R., Vdovina T.A., Khapilina O.N.

National Center for Biotechnology, Astana, Kazakhstan

**E-mail:* asem.tumenbaeva2016@mail.ru

Sea buckthorn (*Hippophae rhamnoides L.*) is an ancient crop traditionally used as a medicinal plant, a health tonic, and a food supplement. The fruits of *H. rhamnoides L.*, as a source of carotenoids, have been harvested since ancient times, but it was only introduced into cultivation in the early 20th century. Currently, sea buckthorn berries are harvested on an industrial scale due to the high content of bioactive substances, which has significantly increased consumer interest in sea buckthorn products, leading to their expanded use in the food industry and medicine. Thanks to its bioactive compounds, high content of vitamin C, flavonoids, carotenoids, and tocopherols, sea buckthorn berries are excellent raw material for functional food products.

The aim of this work was to obtain aseptic plants of *H. rhamnoides L. in vitro* culture from seeds collected at different times, develop effective sterilization regimes, and study the effects of various antioxidants and phytohormones to develop an effective reproducible protocol for multiple regeneration of sea buckthorn plants.

Seeds of *H. rhamnoides* collected from natural populations in the territory of the Kazakh Altai served as material for initiating a sterile culture. Solutions of 0.1% Mercury (II) chloride, 34% hydrogen peroxide, and a 10% solution of "Domestos" were used for seed sterilization, with an exposure period of 20 minutes. The seeds were then sown on the surface of WPM nutrient medium supplemented with 1 mg/l BA and 1 mg/l GA. Activated charcoal, ascorbic acid, silver nitrate, and polyvinylpyrrolidone were used as antioxidants and inhibitors to reduce the accumulation of phenolics in the medium. The control consisted of a medium without added hormones and antioxidants.

Germination began on the 7th day depending on the genotype of sea buckthorn. The minimum number of infected seeds was observed when using 0.1% Mercury (II) chloride. When using hydrogen peroxide, seed infection rates with fungal and bacterial infections ranged from 40.8% to 45.5%.

The evaluation of the influence of various antioxidants on sea buckthorn seedlings *in vitro* conditions showed that maximum growth and development were observed on media supplemented with activated charcoal. Sterile seedlings were characterized by intense green coloration and well-developed cotyledon leaves. Intensive growth and the appearance of the second node were observed in individual genotypes. For seedlings cultivated on media supplemented with polyvinylpyrrolidone, hypocotyl growth and the formation of callus-like structures were noted.

Thus, it was established that activated charcoal is a highly active antioxidant capable of inhibiting the negative effects of phenolics *in vitro* culture. The optimized conditions for obtaining sterile seedlings of *H. rhamnoides L. in vitro* culture will allow obtaining shoots for subsequent microclonal propagation.

ADVENTITIOUS ROOTS CULTURE OF *ALLOCHRUSA GYPSOPHILOIDES*: SAPONINS-BEARING RARE SPECIES

Mursaliyeva V.K.*, Mukhanov T.M.

Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan

* *E-mail:* gen_mursal@mail.ru

Allochrusa gypsophiloides (Regel) Schischk (fam. Caryophyllaceae Juss.), Turkestan soap root (TSR) is a rare species of the natural flora of Central Asia and Kazakhstan with a limited habitat in the Western Tien Shan and Pamir-Alai is a valuable saponin-bearing plant. The rare TSR has pharmacological value and technical application as an effective foaming agent and emulsifier. For further scientific and practical utilization of the unique potential of this valuable crop, it is relevant to develop an alternative approach based on *in vitro* system to replace wild TSR raw material. Adventitious roots (AR) cultures are characterized by genetic and biosynthetic stability, optimization of the main factors of the nutrient medium allows to achieve intensive growth of root biomass and stable level of biologically active metabolite in culture. The aim of the research was comparative evaluation of AR culture and natural roots of wild plants from Kazakhstan for total saponins, phenols and flavonoids content, antioxidant (AOA) and antimicrobial activity in model test systems. In AR culture, growth index and secondary metabolites were evaluated on days 25 -, 45-, 60- of cultivation on ½ MS medium without (control) and with auxin application. The conducted studies revealed differences in the content of secondary metabolites in AR culture material and in wild plants, as well as in their AOA and antimicrobial activity in model test systems. The levels of saponins and flavonoids were higher in AR culture at optimal timing and medium of cultivation compared to native roots. High antimicrobial activity was detected in control extracts of in vitro AR culture with increased levels of saponins. The hormonal composition of the medium determined the nature of the relationship between AR culture growth and the accumulation of secondary metabolites in it. The content of saponins and flavonoids positively correlated with the growth of the culture on the control medium and on the NAA medium. *In vitro* AR culture is promising for obtaining triterpene saponins TSR with high antibacterial and antifungal activity.

DEVELOPMENT OF CHEMOTHERAPY TECHNIQUE FOR VIRUS ERADICATION IN FRUIT AND BERRY *IN VITRO* PLANTS

***Tolegen A.B.*[1,2*], *Romadanova N.V.*[1,2], *Kushnarenko S.V.*[1]**

[1] *Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan*
[2] *Al-Farabi Kazakh National University, Almaty, Kazakhstan*

***E-mail:* tolegenarman7@gmail.com**

Virus-free planting material is one of the significant factors in obtaining high yields of fruit and berry crops. As is known, clonally propagated fruit and berry crops are severely affected by various infections, including intracellular pathogens such as viruses, which negatively affects the yield and quality of fruit and berry products. The purpose of the work was to study the state of infection of commercial varieties of fruit and berry crops with viral diseases and to develop technique for virus eradication from *in vitro* plants.

The objects of the study were *in vitro* plants of 39 *Malus* accessions including varieties and clonal rootstocks (*Malus domestica* Borkh.) and wild accessions (*Malus sieversii* (Ledeb.) M. Roem., and 3 blackberry varieties: Natchez, Cacanska Bestrna and Chester. *In vitro* collection was established and maintained in the Laboratory of Germplasm Cryopreservation at the Institute of Plant Biology and Biotechnology. *In vitro* plants were tested using RT-PCR method. *Malus* plants were tested for four viruses: *Apple chlorotic leaf spot virus* (ACLSV), *Apple stem pitting virus* (ASPV), *Apple stem grooving virus* (ASGV), and *Apple* mosaic virus (ApMV). Blackberry plants were tested for five viruses: *Raspberry bushy dwarf virus* (RBDV), *Strawberry necrotic shock virus* (SNSV), ApMV, *Black raspberry necrosis virus* (BRNV), and *Blackberry yellow vein virus* (BYVV).

The various combinations of viruses were detected in 19 *Malus* accessions. No viruses have been identified in blackberry plants. For chemotherapy, infected *Malus* accessions were used: Aport Alexander (ACLSV, ApMV, ASPV), Gold Rush (ACLSV, ASPV), Red Free (ACLSV), Landsberger Renette (ACLSV, ASPV), Suislepper (ACLSV, ASPV), and clonal rootstock: B 7-35 (ASGV). *In vitro* shoots were cultured on MS medium containing 0.5 mg/L BAP, 0.01 mg/L IBA, with addition 50, 75 or 100 mg/L ribavirin. *In vitro* shoots were cultured in plant growth room at 23-25°C, light intensity of 40 μE m².s', 16-hour photoperiod. The duration of culturing (1 passage) was 45 days, the number of passages was from 1 to 3. It was revealed that 75 and 100 mg/L ribavirin had detrimental effect on *in vitro* plants whereas 50 mg/L ribavirin resulted only 5% shoot necrosis. As a result of the experiment, three subcultures on 50 mg/L ribavirin resulted 100% shoots free of ACLSV, ApMV, ASPV, and ASGV. A virus-free *in vitro* collection of apple and blackberry was established, which will be used for create a cryobank of shoot tips at -196°C and to obtain virus-free planting stocks.

The work was carried out with the support of the Ministry of Science and Higher Education of the Republic of Kazakhstan within the framework of the scientific and technical program BR18574099.

OPTIMIZATION OF *IN VITRO* CULTURE KAZAKHSTAN SPECIES *RHODIOLA*

Yessenbekova N.A., Khapilina O.N.

National Center of Biotechnology, Astana, Kazakhstan

**E-mail:* yessenbekova@biocenter.kz

Plants of the genus *Rhodiola* sp. (*Crassulaceae*) are common in Eastern Siberia, Scandinavia, Alaska and Northern Europe and are widely used in folk and traditional medicine, they have antioxidant, anti-inflammatory and regenerative activity, which is due to the presence of various biol ogically active substances. More than 100 species of *Rhodiola* sp. are known in the world, the most studied are the species *R. rosea* and *R. crenulata*. The most valuable representative is *R.rosea* L., global demand for it contributes to the fact that this species has become rare and endangered, as the raw material is harvested from natural populations. In Kazakhstan and other countries, this species is listed in the Red Book. Uncontrolled destruction of natural populations negatively affects its conservation and availability for use in medicine. This encourages the search for other alternative sources of biologically active substances (BAS) in plant materials, similar in biological value to *R. rosea*. There are 11 species of *Rhodiola* growing in Kazakhstan, the most promising of which are *R. quadrifida, R. algida, R. linearifolia, R. semenovii.*

The use of biotechnology methods, based on the cultivation of isolated plant cells, tissues, and organs of plants on artificial nutrient media, is one of the solutions to the problems of providing high-quality and renewable plant raw materials for medical needs in accordance with GMP standards. In addition, plant tissue culture allows us to preserve the diversity of natural populations of rare and endangered plant species.

The purpose of the research was to optimize the production of callus cultures of various species of *Rhodiola* sp. Seeds, shoot apexes, leaf fragments, and rhizoid buds were used as explants. The introduction of plants into *in vitro* culture was carried out in laboratory conditions, after preliminary sterilization with various types of antiseptics, the concentrations and exposure time of which were selected empirically. Cultivation was carried out on Murashige and Skoog nutrient media, supplemented with various growth regulators.

In our research, a certain dependence of the type of explants on the sterilization protocol used. Thus, leaf explants of *R. semenovii*, unlike other species, were most sensitive to the use of chlorine-containing agents, which caused necrosis even during short-term sterilization.

The analysis of the results revealed that the callus induction occurs most actively when using shoot apexes and leaf explants in all studied *Rhodiola* species. The frequency of callus formation when using these types of explants was higher on media supplemented with thidiazuron (TDZ) and naphthaleneacetic acid (NAA) in a 1:2 ratio. For *R. quadrifida*, cultivation on a medium supplemented with 2,4-D, NAA and kinetin in a ratio of 1:2:0.5 was effective. When using rhizome buds as explants for all species, the MS medium enriched with casein hydrolyzate with the addition of zeatin was optimal. Additionally, it was shown that the callus induction occurs very slowly when using stem explants; the frequency of callus formation was less than 10% of explants.

As a result of the conducted research, the features of introducing various species of *Rhodiola* sp. into *in vitro* conditions were studied, and aseptic, stably growing callus cultures were obtained in all studied species.

PHYTOREMEDIATION OF CONTAMINATED SOILS BY INDUSTRIAL EMISSIONS IN ALMATY CITY

***Akhmetzhanova D.*[*1], *Khamitova K.*[2]**

[1]*Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan*
[2]*Al-Farabi Kazakh National University, Almaty, Kazakhstan*

**E-mail:* adana128128@gmail.com

Plants known to play an important role in establishing ecological balance and stopping the further pollution migration due to their dust-collecting properties. Phytoremediation, which uses the combined metabolic potential of microorganisms and plants, plays a special role in freeing the arable soil layer from toxicants.

The choice of plant objects for research is based on Almaty region characteristic flora. Features of the species were that plants have a short ripening period and do not require special care conditions, they are distinguished by a high stem and wide large leaves, as well as a fibrous root system, which allows you to fully assess the impact of pollutants on all organs. Dandelion (*Taraxacum* L.) is a genus of perennial herbaceous plants of the Asteraceae family. Dandelion officinalis reacts to the increased content of heavy metals in soils by intensifying the processes of lipid peroxidation. Field sow thistle (*Sonchus arvensis* L.) is a species of herbaceous plants of the genus Sow thistle resistant to the effects of oil pollution, which is associated with a developed root system that allows it to receive nutrition outside of oil pollution. Bonfire (*Bromus* L.) is a genus of perennial herbaceous plants of the Poaceae family accumulates oil products from the soil and getting stimulating effect on germination compared to background indicators.

Plant samples were taken on the territory of Almaty CHPP-1, located in the central part of the city and being one of the large operating enterprises in Almaty. Environmental control of the territory of CHPP-1 over the condition of soils is carried out at 5 points of the monitoring network at the ash dump site and at 5 points at the industrial site, located both on the border of sanitary protection zones and inside them. According to the results of laboratory tests, the soils are contaminated with lead, cadmium, nitrates, fluorides and petroleum products.

Results of the dried plant samples elemental analysis and soil atomic absorption analysis showed accumulation of the heavy metals by the plants, which explains the low content of lead and the almost complete absence of cadmium in the soil, despite the high concentration in solutions. The concentration of lead in the soil decreased from 7 mg/kg to 0.62, cadmium from 5 to 0.57 mg/kg.

According to the elemental analysis results samples accumulated higher levels of other elements, such as potassium (5.66 mg/kg), magnesium (1.07 mg/kg), chlorine (1.06 mg.kg) and calcium (3.58 mg.kg).

It can be assumed that carbon in the composition of soot can act as a factor that increases the absorption of nutrients by plants. Most likely the rapid withering in both experiments is caused by the toxic effects of benzene. However, it should be taken into account that not all control samples continued to grow after the sixth week, so it becomes possible to study carbon black as growth enhancers in small quantities within the framework of zero-waste production.

A comparative analysis of the research results showed that the ability of plants to accumulate heavy metals at an industrial facility was lower than during laboratory studies. The reason is the additional influence of external factors, such as: ventilation, temperature changes, light conditions, humidity, frequency of precipitation, atmospheric pressure, zoocenosis and others.

TECHNOLOGY FOR PROCESSING BAST FIBERS ON WOOLEN EQUIPMENT

***Otynshiyev M.*[*1,2], *Assanova A.*[2], *Niyazbekov B.*[2], *Abilda Zh.*[1], *Toishimanov M.*[1], *Shamekova M.*[1]**

[1]*Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan*
[2]*Almaty Technological University, Almaty, Kazakhstan*

**E-mail:* asutormo@mail.ru

Kazakhstan is producing bast plants like oil flax, fiber flax, and industrial hemp. There is no special equipment for processing bast fibers. But at the same time, there are factories for processing wool into yarn and non-woven materials which stopped now.

According to classical technology, bast fibers are used to produce yarn intended for producing fabrics and knitwear for clothing, using the so-called wet spinning technology. Kazakhstan occupies a leading position in the cultivation and export of oilseed flax and hemp; however, enterprises cannot provide a full cycle of processing of these crops. The need for rational use of oilseed flax stem mass, which is simply burned, is especially acute. The main problem of processing bast fibers in Kazakhstan is the lack of processing technology.

A distinctive feature of bast fibers is that the coefficient of friction of the fibers strongly depends on the force of normal pressure on the fiber. Therefore, to obtain high-account yarn from bast fibers using a dry spinning system, it is necessary to change the friction properties of these fibers. In this case, the optimal values of the static friction coefficient should be a maximum of 0.2, and dynamic - 0.15. This can be achieved by mixing wool, cotton, or chemical fibers or using special lubricants.

In this work, acrylic fiber (20%) was used to mix with oilseed flax fibers. This mixture was processed using the worsted wool spinning system to produce NM 10 yarn.

The linear density of the fibers after decortication is 87-91 tex. During the processing process, it decreased by 25 tex. The average fiber length during processing decreased from 96-107 mm to 52.7-60.6 mm. This length is sufficient for processing flax fibers on worsted wool equipment.

The lignin content in the feedstock of oilseed flax was 14.7%, in the sliver after carding - 2.2%.

Thus, from Kazakhstan linen material it is possible to produce various textile materials, including non-woven fabric for technical purposes, yarn, and then fabrics from it for both technical and household purposes.

The main problem in the textile processing of oil flax material is the presence of a large number of stalks in the technical fiber when using modern high-speed combines to harvest oil flax seeds by tearing them off the stems. In this case, the stalks remain on the stem and are not removed during primary processing. To remove the stalks, you can use a combing process, which allows you to get rid of them almost completely.

The physical and mechanical properties of oilseed flax fiber practically do not differ from the parameters of short fiber and tow obtained by processing long flax fiber.

To process bast fibers, you can use worsted equipment. But the equipment needs to be partially modernized.

The properties of the resulting yarn meet the requirements of yarn standards for technical textiles and furniture fabrics.

ECOLOGICAL ASSESSMENT OF HEAVY METAL ACCUMULATION BY SWEET POTATO ON THE TERRITORY OF AN ABANDONED LEAD PLANT

Abilda Z*, Toishimanov M., Daurov D., Daurova A., Zhapar K., Sapakhova Z., Kanat R., Stamgaliyeva Z., Zhambakin K., Shamekova M.

Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan

**Email:* zemaletta@gmail.com

Accumulation of heavy metals in the soil to a certain extent not only leads to its degradation but also suppresses plant growth and development.

The territories adjacent to Shymkent city are characterized by ordinary gray soil, xerosol type. Since these are alkaline soils, the pH of which is 7.5-8, with absolute dominance of oxidative processes, they do not have a high ability to accumulate lead, zinc, or cadmium directly, but lead processing wastes have been polluting this territory for more than 70 years. High heavy metal concentrations of 1354, 226 and 61 mg/kg for Pb, Zn and Cd, respectively, were determined in the ash dumps. At point № 1 (50 m from the epicenter of the ash dump) in the top layer (5 cm) of soils near the ash dump the highest heavy metal concentrations were 551, 245, and 14 mg/kg. Thus, the amount of lead at point 1 in the adjacent plant area exceeds from 11.5 to 17 times the MPC. The geoaccumulation index proposed by Muller indicated high levels for all metals at all sampling points. The highest index was 11.32 units for Zn in Field 3 at a depth of 5 cm and was characterized as extreme Zn contamination. Analyzing the overall ecological risk level for each metal, it is worth noting the high values of lead and cadmium. The 1st and 3rd sampling points are characterized by significant environmental risk.

The HM concentrations were significantly higher in the sweet potato samples than in the control samples. The highest HM concentrations were found in Field 3, in which the Pb, Zn, and Cd concentrations in tubers were 34.0 ± 0.03, 94.2 ± 0.07, and 1.19 ± 0.03 mg/kg and in leaves were 32.5 ± 0.09, 59.4 ± 0.01, and 2.75 ± 0.01, respectively. Furthermore, in the experimental sites Field 1 and Field 2, the Pb, Zn, and Cd concentrations in tubers varied from 28.7 ± 0.07 to 45.1 ± 0.09, 70.0 ± 0.05 to 94.1 ± 0.09, and 0 to 1.80 ± 0.02 mg/kg, respectively.

The bioconcentration factor is one of the main indicators of the phytoremediation efficiency of a plant. The sweet potato tuber BCFs for Zn in Fields 1, 2, and 3 were 18.08, 35.77, and 0.85, respectively. This correlated with the results for the leaf BCF, which were 12.18, 17.72, and 1.34, respectively. HM accumulation. Pb values for Fields 1, 2, and 3 were 10.5, 9.12, and 6.36, and for leaves 1.7, 4.22, and 6.01, respectively. The ability of sweet potato to accumulate metals was as follows: Zn > Pb > Cd. Except for Cd with BCF < 1, this indicator was >1 for Zn and Pb, from which we can conclude that sweet potato has great potential for use in phytoremediation. It was found that sweet potato plants accumulated HMs in their aerial and root parts. According to the data obtained, concentrations in the roots (tubers) were higher than those in the aerial parts (leaves). In addition, Pb and Zn concentrations in plants were high, whereas Cd was found only in tubers from Field 3.

According to the contamination coefficients obtained for HM concentrations, the soil in the experimental plots was moderately contaminated. It was found that sweet potato is a hyperaccumulative plant for two heavy metals, Pb and Zn.

SELECTION OF RICE LINES FOR RESISTANCE TO MULTIPLE STRESS FACTORS

Amirova A.[1], Usenbekov B.[2], Mynbayeva D.[2], Berkimbay Kh.[2]

[1]Al-Farabi Kazakh National University, 050040, Kazakhstan, Almaty
[2]Institute of plant biology and biotechnology, Almaty, 050040, Kazakhstan

* *E-mail:* aigul_amir@mail.ru

Rice is an important grain crop that is grown in many countries around the world with different climatic conditions and can be subject to a huge number of environmental stresses, both biotic (fungi, bacteria, viruses, insects) and abiotic (cold, drought, salinity, etc.), which limit rice productivity. Due to climate change in the world the improvement of rice to multiple stresses is the best decision in increasing of the efficiency of selection processes. Breeders and scientists are trying to find effective measures to combat stress factors to ensure global food security. The development of high-yielding, stress-resistant and good-quality new rice varieties is relevant to meet the needs of a growing population in the context of a simultaneous reduction in arable land as a result of global climate change.

As research objects 13 parent varieties and 28 rice breeding lines from the collection of the Institute of Plant Biology and Biotechnology (IPBB) were used. Molecular screening of studied rice genotypes to cold tolerance was carried out using markers RM24545, RM1377, RM231 and RM569 associated with QTLs (*qPSST-3*, *qPSST-7* and *qPSST-9*). When studying the presence of the blast resistance gene in genotypes, pre-selected for cold 7 parental varieties and 21 rice line were used as research objects. Molecular markers Pi-ta, Pita3, RM224, RM1233, Z56592, MSM6, 9871.T7E2b, 195R-1, NMSMPi9-1, TRS26 and Pikh MAS, associated with blast resistance genes *Pi-ta*, *Pita*, *Pi-1*, *Pi-40*, *Pi-9* and *Pi-54*, were used for PCR.

Molecular screening of rice lines and parental varieties to cold tolerance was identified the presence of three QTLs characterizes the cold resistance of studied genotypes, and the absence of one of them leads to cold sensitivity. As a result, 21 cold-resistant out of the 28 studied rice lines were identified. These selected cold-resistant rice varieties and rice lines were screened for presence of blast resistance genes *Pi-ta*, *Pita*, *Pi-1*, *Pi-40*, *Pi-9* and *Pi-54*. It was revealed that 17 rice lines from 21 studied cold-resistant lines contain 5-6 genes of blast resistance. It should be noted that according to the blast resistance strategy, the presence of 5 or more genes ensures the formation of stable resistance to *Magnaporthe oryzae*. Thus, molecular screening allows to identify lines resistant to multiple stress factors. 17 rice lines resistant to multiple stresses such as cold and blast disease were developed. It should be noted that 5 of the selected lines are high-yielding, which is very important in rice breeding program. These selected rice lines can be used in breeding process as starting lines, germplasm exchange as a source of resistant genes for the creation of new rice varieties that are resistant to different stress factors. It seems that in connection with global climate change, in the process of creating new rice varieties, it is very important to screen promising lines for the presence of resistance genes not only to one stress factor, but also to other stresses, which reduces the time in rice breeding to multiple stresses.

This research has funded by the Science Committee of the Ministry of Education and Science of the Republic of Kazakhstan Grant AP14869300.

INDUCED MUTAGENESIS AND HAPLID BIOTECHNOLOGY IN THE SELECTION OF *TRITICUM AESTIVUM* L.

Anapiyaev B.B.*[*1], Iskakova K.M.[2], Beysenbek E.B.[1], Nurpeisov I.A.[3]

[1] Satbayev University, Almaty, Kazakhstan
[2] Kazakh National Agrarian Research University, Almaty, Kazakhstan
[3] Kazakh Research Institute of Agriculture and Plant growing, Almalybak, Kazakhstan

* *E-mail:* bak_anapiyayev@mail.ru

Haploids are unique objects for cell selection and genetic engineering. Our work presents the results of the use of induced mutation selection and haploid biotechnology in the practical selection of *Triticum aestivum* L. for resistance to rust diseases. In the first series of experiments, the field resistance of the original wheat varieties and hybrids under conditions of an infectious nursery was determined. The greatest resistance to rust was shown by the isogenic line *Lr 24:* to yellow rust - 2/20, to brown - 2/10, and was immune to stem rust. Similar values of resistance to yellow and brown rust showed isogenic lines *Lr 19, Lr 25*. By resistance to stem rust, the isogenic line *Lr 25* was weakly susceptible - 2/20, and *Lr 19* showed an average susceptibility - 3/30, respectively. In the second series of experiments, the varieties of common wheat were crossed with donors of effective resistance genes - isogenic lines *Lr 19, Lr 24, Lr 25*. Valuable wheat hybrids were genetically stabilized by haploid biotechnology based on in vitro culture of isolated microspores. As a result of studies on the use of haploid biotechnology based on in vitro culture of isolated microspores in the selection of wheat Triticum aestivum L. for resistance to rust diseases, we obtained embryoids, morphogenic calli and regenerant plants from which dihaploid lines were created. To determine the resistance of dihaploid lines to rust diseases, they were studied in the conditions of an infectious nursery of South-East Kazakhstan. As a result of the studies conducted in an infectious nursery, dihaploid wheat lines were selected, which showed a high level of resistance to rust diseases. Thus, it was shown that haploid biotechnology is an effective method for accelerating the selection process and rapid genetic stabilization of promising mutants. In the early stages of the selection process, wheat ADH lines carrying the genes for resistance to rust diseases were selected.

THE CORRELATION OF THE RESISTANCE OF PLANTS OF THE WILD POTATO SPECIES *S. CHACOENSE* TO THE POTATO VIRUS Y WITH THE PRESENCE OF DNA MARKERS FOR THE *RYCHC* RESISTANCE GENE

***Antipov A.D.*[1], *Gurina A.A.*[2]. *Rogozina E.V.*[2], *Zlobin N.E.*[1]**

[1] *All-Russia Research Institute of Agricultural Biotechnology.*
[2] *All-Russian Institute of Plant Genetic Resources named after N.I. Vavilov*

For the Solanaceae family, and, in particular, for potatoes, the most dangerous viral disease today can be considered potato virus Y (PVY), infection with which leads to large yield losses. One of the main mechanisms for protecting potato plants from viral diseases can be considered a mechanism based on resistance genes. Thus, the *Rychc* gene, found in the wild potato *S.chacoense*, is a valuable gene for potato breeding programs because it confers extreme resistance to PVY. *Rychc* was first introduced into the commercial variety "Konafubuki" from the doubled *S.chacoense* "w84" and was mapped to the distal end of the long arm of chromosome nine. In 2022, a group of Chinese scientists reported cloning the *Rychc* gene into bacterial artificial chromosomes and, by screening clones, determined the sequence of the *Rychc* gene and its belonging to the group of LRR proteins, and also proposed their own DNA marker, which is aimed at the sequence of the gene itself [1]. Then a group of Japanese scientists also obtained the *Rychc* sequence and presented their DNA marker, confirming previously obtained data on the sequence and location of the gene [2]. It is noteworthy that in both studies there was a 100% correlation between the phenotype and the presence of a marker for the *Rychc* gene. We examined the correlation between the presence of published DNA markers and PVY resistance in a large sample of *S.chacoense* genotypes. In our work, we assessed the resistance of wild potato plants *S.chacoense* (43 individuals) to PVY by artificial inoculation with the sap of *Nicotiana tabacum* infected and their further identification by ELISA. The same plants were analyzed for the presence of markers for the *Rychc* gene using PCR. As a result, it was found that in 6 plants there was no correlation between the presence of a marker for the resistance gene and resistance to the PVY itself. Thus, it was shown that the presence of DNA markers for the *Rychc* gene in plants does not provide a 100% chance that the plant will be resistant to PVY. The lack of resistance in the presence of the *Rychc* gene gives reason to believe that unstable genotypes may contain non-functional allelic variants of the *Rychc* gene. To test this assumption, the complete sequences of the *Ry* genes were sequenced on the OxfordNanopore platform, which revealed the presence of polymorphisms.

The study was supported by the RSF project № 21-76-10050.

References:

1. Li G. et al. *Rychc* confers extreme resistance to potato virus Y in potato //Cells. – 2022. –T. 11. – №. 16. – C. 2577.

2. Akai K. et al. De novo genome assembly of the partial homozygous dihaploid potato identified PVY resistance gene (*Rychc*) derived from *Solanum chacoense* //Breeding Science. – 2023. – T. 73. – №. 2. – C. 168-179.Science. – 2023. – vol. 73. – No. 2. – pp. 168-179.

BIOTECHNOLOGICAL APPROACH TO THE CONSERVATION OF ENDEMIC CENTRAL ASIA – *ALLIUM PSKEMENSE* B. FEDTSCH.

Bashylau A.V., Spirydovich E.V., Tarasevich A.Y.

Central Botanical Garden of the National Academy of Sciences of Belarus

Solving the global problem of plant biodiversity conservation at the current stage is impossible without searching for new strategies and approaches. Therefore, today's promising direction biology is the biotechnology of plant conservation. The main aim of this direction is to complement existing traditional methods of ex situ biodiversity conservation with modern biotechnological tools that allow mass reproduction of valuable genotypes without causing damage to natural populations.

Research on the culture of plant cells and tissues in the Department of Plant Biochemistry and Biotechnology of the Central Botanical Garden of the NAS of Belarus began in the late 70s. In 1986 under the leadership of Academician of the NAS of Belarus V.N. Reshetnikov was written the first dissertation in Belarus on the culture of plant tissue. In 1998 the researches on creating and expanding the *in vitro* collection began.

Allium pskemense B. Fedtsch. – an endemic of Central Asia, listed in the Red Book of Kazakhstan, Uzbekistan and Kyrgyzstan, it is one of the plants on the verge of extinction. A big problem of cultivation *A. pskemense* is reproduction from seed material: in natural conditions, seeds undergo multi-stage stratification, which negatively affects their germination.

To introduce *A. pskemense* seeds into *in vitro* culture, a stratification technique was used (60 days of exposure at +4 °C), after which Petri dishes with seeds were placed in initial conditions (16/8 photoperiod, +25 °C, illumination 3000 Lux). On the 4th day after changing the cultivation conditions, seed germination was observed. The seedlings were cultivated after 15 days on a modified nutrient medium containing mineral salts according to the Murashige & Skoog prescription with the addition of 0.5 mg/l 6-benzylaminopurine and 15 g/l sucrose. In this way, a stable in vitro culture of *A. pskemense* was obtained. It has been established that microseedlings in *in vitro* culture have a low growth rate. Seedlings of *A. pskemense* were first planted on an artificial ion-exchange substrate under LED lighting (for 3 months) (DSL 26-01-RC-01, 1800 Lm), and then, after the end of frost, in open ground, where they produced healthy plants.

To obtain a callus culture, leaf blades and roots were used as primary explants, which were transferred into callusogenic media containing mineral salts according to the Murashige & Skoog recipe, with the addition of 1.0 mg/l 2,4-dichlorophenoxyacetic acid, 0.2 mg/l 6-benzylaminopurine and 30 g/l sugar. Cultivation conditions: thermostat, darkness, +25 °C. After 3 months, callusogenesis was observed in only 15% of the total first-hand explants. In explants from the leaf blade at the 3rd month of cultivation there was no initiation of callusogenesis. The resulting callus tissue was of a loose type and had a low growth rate.

To obtain a suspension culture of *A. pskemense*, callus was used. It was macerated before being added to a liquid nutrient medium of the following composition: mineral salts according to Murashige & Skoog with the addition of 1.5 mg/l 2,4-dichlorophenoxyacetic acid, 0.2 mg/l 6-benzylaminopurine, 30 g/l sucrose. Cultivation of suspensions of *A. pskemense* plant cells was carried out using a laboratory shaker (US-1350O) at a speed of 110 rpm in room conditions of +23 °C. A resistant culture of *A. pskemense* has been obtained which requires further study.

We have obtained data on the biotechnological reproduction and conservation of the Central Asian endemic *A. pskemense*. Additionally, callus and suspension culture were obtained, which require further study not only in the field of preserving the gene pool of *A. pskemense*.

COLLECTIONS *IN VITRO* - A WAY OF PLANT BIODIVERSITY CONSERVATION AND RATIONAL USE

Spirydovich E.V., Chizhik O.V., Bashylau A.V., Reshetnikov V.N.

Department of plant biochemistry and biotechnology/The Central Botanical Garden / National Academy of Sciences of Belarus/ Belarus

Plant biotechnology use collections *in vitro* to produce sterile test-tube plants, culture organs, tissues or plant cells, and to isolate protoplasts. Based on the final products, the biotechnologies are divided into two groups: first produces intact economically-useful plants, in the second group the end products are biomass cell cultures and/or phytochemicals. Thus, the aim of this work is to review *in vitro* collections from Central Botanical Garden NAN of Belarus in its broadest sense and to explore its use across many fields of application: from the conservation of endangered species to the storage of economically important crop plants and industrial plant cell culture collections.

A wide range of biotechnological methods were utilized including: 1) tissue culture; 2) cell culture techniques; 3) molecular genome analysis; 4) cryopreservation for the collection long-term storage 5) documentation, 6) microclonal propagation, 7) patenting, 8) storage, 9) techniques to deposit of rare and endemic plants species, including medicine; 10) exchange of plant genetic resources

Plant *in vitro* collections of wild flora of Russia and Belarus on the basis of natural sources and existing collections in EurAsEC countries and the experience of their creation were analyzed. The Central Botanical Gardens of NAS of Belarus was awarded with a Certificate of the Ministry of Natural Resources and Environmental Protection RB for the collection of aseptic cultures of economically useful plants in 2005. Currently, it contains 242 taxa from more than 20 families of angiosperms. Aseptic collection of were established for the purpose of conservation, reintroduction and development of industrial use. Plant biotechnologies (from plants in the test-tube to protoplasts) are directed toward creating new plant forms, simplifying selection processes, and effectively reproducing and improving valuable genotypes. Optimization of nutrient media for the tissue culture propagation and the deposit of rare and endemic plants species, including medicinal were carried out. Many medicinal plants are rare and endangered species that are important not only for environmental aims (species conservation), but also, they have considerable economic significance. To preserve unique genotypes, it is important to stop formation of cell populations *in vitro* in the beginning of the plant cell cultures. Otherwise due to somaclonal variation it's possible to lose the valuable properties of the varieties. In this case the test tube individuals, plant organs or tissue can be used as the storage objects. Seeds and meristem of several rare species from Belarus were deposited to cryobank of the Timiryazev Institute of Plant Physiology of Russian Academy of Sciences for the long-term storage.

Common platform concerning creating, maintaining, and utilizing of biotechnological collections was developed: protocols of preservation of genetic resources and deposition at low temperatures of *in vitro* plant banks; protocols for plant clonal micropropagation to obtain high quality planting material; protocols of plant cell and tissue culture using for BAS production: protocols for production of natural herbal remedies for various purposes; protocols for assessing the genetic diversity (GD) parameters of natural populations of protected natural flora for including in the collection. Genotyping and genetic certification are carried out in the CBG to assess the genetic diversity of populations, samples, and varieties of collections. It means that each individual or form is checked on the presence or character of the display of the set of molecular genetic markers.

The work is supported by the SPSI "Biotechnology", "Natural Resources and the Environment" 2020 - 2025 and the biotechnology commission of the Scientific Council of Botanical Gardens of the CIS countries at the IAAS.

THE PROLIFERATIVE CAPACITY OF *CISTANCHE DESERTICOLA* IN CELL CULTURE AND THE ANALYSIS OF THE QUANTITATIVE CONTENT OF BIOLOGICALLY ACTIVE SUBSTANCES

Bekkuzhina S.S.*, Rakhimzhanova A.O. Manabayeva S.A.

Plant Genetic Engineering Laboratory, National Center for Biotechnology, Astana, Kazakhstan

In vitro technology offers the potential to produce environmentally friendly raw materials all year round, regardless of climatic conditions and difficulties in collecting raw materials, to increase the yield of biologically active substances and to regulate their accumulation in the culture. Unfortunately, like most parasitic plants, the *Cistanche deserticola* has been relatively poorly studied in Kazakhstan and around the world, although it has significant scientific and practical interest. Research is particularly important to study both the theoretical and applied aspects of the cell culture of this specific parasitic plant, with a focus on its pharmaceutical applications.

While suspension culture presents advantages for the production of active ingredients, there are cases where the synthesis of desired secondary metabolites may be lower than in intact plants. In some cases, entirely new substances have been synthesized in cell cultures. Sustainable proliferation depends on genetic, physiological, and environmental factorsin addition to balance between media volume and cellular biomass. Therefore, investigating the impact of initial inoculum mass on biomass growth in suspension cultures of three different lines - light (white), dark grey and brown – is of great interest.

The growth dynamics of *Cistanche* suspension cell cultures were assessed by monitoring dry matter accumulation during growth cycles. Optimal suspension concentrations of 20-30 ml were identified to achieve notable growth rates, with deviations resulting in diminished growth activity, likely due to medium depletion and waste product accumulation. Notably, light and dark gray cell suspension cultures exhibited higher growth activity compared to dark cells.

Quantitative analysis of biologically active substances in *Cistanche* suspension cell cultures was conducted via HPLC chromatography, referencing external standards like apigenin, rutin, and quercetin. Flavonoid content ranged from 0.01% to 0.52%, with the highest levels observed in extracts from light callus cells (Line I). Flavonoid content demonstrated a declining trend from light to brown cultures. Rutin concentration peaked in *Cistanche* seed extracts, while quercetin was exclusively identified in Line I suspension culture cell extracts.

SELECTION OF PROMISING RICE LINES OF THE LATE GENERATION WITH COLORED PERICARP BASED ON TECHNOLOGICAL GRAIN QUALITY

***Berkimbay Kh.*[1], *Usenbekov B.N.*[1,2], *Amirova A.K.*[1,2], *Mynbayeva D.O.*[1], *Mukhametzhanov S.*[1,2], *Zhanbyrbaev E.*[3].**

[1]*Institute of Plant Biology and Biotechnology, Almaty, 050040, Kazakhstan*
[2]*Kazakh National Agrarian Research University, Almaty,050010, Republic of Kazakhstan*
[3]*Kazakh National Agrarian Research University, Almaty, 050040, Republic of Kazakhstan*

Black and red rice (*Oryza sativa* L.) are a set of forms that appeared as a result of centuries-old introduction into the culture of wild rice, which has a colored pericarp of the grain. Unlike white rice, rice with colored pericarp is characterized by higher antioxidant activity.

Depending on the biochemical composition of rice grains, including the content of amylose, protein, vitamins, microelements and antioxidants, as well as the morphological characteristics of the varieties of this crop can be used in functional or traditional nutrition. The antioxidant properties of rice with colored pericarp are due to the presence of anthocyanin pigment, phenolic acids, vitamin E and phytic acid in the pericarp. For example, glutinous rice has a beneficial effect on indigestion and heartburn. Brown rice extracts are used to treat breast and stomach cancer, as well as warts. They have also been used to treat nausea and diarrhea. Some pigmented varieties of rice are still used to treat skin diseases, blood pressure, fever, paralysis, rheumatism and leucorrhoea, and even as the basis of general tonics.

Seed quality is an important characteristic in the initial stages of the plant life cycle, and special attention should be paid to this characteristic, since seed quality is necessary for the preservation and reproducibility of the genome of a variety or hybrid from generation to generation [6]. Technological indicators depend on the degree of crystallinity or amorphism of the starch grains that form the basis of the endosperm of the rice grain, and its productivity. The total yield of cereals depends on filminess; the best varieties have less filminess. The filminess of unhusked rice ranges from 14 to 35%; The average structure of rice when cut is glassy.

As research objects were used rice lines with colored pericarp of the late generation and the red grain variety Almavita. The hybrid lines were assessed for some important technological indicators, such as filminess, glassiness, cracking and grain shape. Filminess was determined according to GOST 10843-73, glassiness and fracturing according to GOST 10986-76 using a diaphanoscope DSZ-2M.

As a result of the research, several genotypes with different grain shapes, filminess and fissuring of the endosperm were identified. A high grain shape index was observed in genotype F_8 Mavr/Pak-Li var. Bansmatica Koern (3.02 mm), and in other varieties it ranged from 2.02 to 2.89 (mm), including genotypes F_7 Yir 5815/Bakanas var.pyrocarpa Alef. and F_8 Black Rice/Viola var.desvauxii Koern showed the same values (2.13 mm). Filminess indicates the percentage of shells (films) around the grain relative to its total mass. The filminess index varied from 16.42% to 21.95% (F_8 Mavr/Pak-Li var.bansmatica Koern and F_7 Yir 5815/Bakanas var.pyrocarpa Alef), respectively.

Cracking indicates the percentage of cracks or breaks within the endosperm (the main nutritional part of the grain). A zero indicator is observed in the hybrid combinations: F_7 Yir 5815/Bakanassky var. sundensis Koern, F_7 Yir 5815/Pak-Li *var.subpyrocarpa Gust*, several hybrid combinations of Black rice with Yantar, Marzhan, Bakanas and Viola, dihaploid DH2 F_2 Black rice/Bakanas and Almavita variety. Cracking in the combination of Mavr and Kurchanka varied from 0% to 10% (F_8 Mavr/Kurchanka *var.pyrocarpa Alef*, F_8 Mavr/Kurchanka *var.sundensis Koern*), respectively. For other genotypes, this trait ranges from 10-20%.

Thus, damaged grains respire more intensively, which increases biological losses during post-harvest ripening and disruption of the integumentary tissue creates favorable conditions for the development of microorganisms and pests. All this reduces the safety of grain and deteriorates its quality, so it is necessary to select genotypes that are most resistant to kernel crushing.

This research has funded by the Science Committee of the Ministry of Education and Science of the Republic of Kazakhstan Program-targeted financing BR 18574149.

DEVELOPMENT AND USE OF MARKERS IN SOYBEAN (*GLYCINE MAX* (L.) MERR.) AND SUNFLOWER (*HELIANTHUS ANNUUS* L.) BREEDING AND GENETIC PROGRAMS BASED ON KOMPETITIVE ALLELE SPECIFIC PCR (KASP)

Boldyrev S.V., Habib Y., Baik A.S., Ben C., Gentzbittel L.

Skolkovo Institute of Science and Technology (Skoltech)

Kompetitive allele-specific PCR is increasingly used in plant and animal breeding and genetic programs, as well as in medicine. The advantage of this system is recognized as codominant, good scalability, robustness, low cost, and the possibility of setting up the experiment both on instruments for quantitative PCR and in combination of a classical amplifier with a microplate reader with the ability to read fluorescent signals from FAM and HEX/VIC.[1]

For sunflower collection, markers were developed and tested for traits of broomrape resistance (*Or7*), fertility restoration (*Rf1*), branching (*B*), and herbicide resistance (*Ahasl*).[2,3]

For soybean collection, markers linked to the seed protein content trait and flowering time were tested (*E1, E2, E3, E4*, qSPC_20-1, qSPC_20-2, qSPC_20-3, qSPC_15-1, qSPC_15-2, qSPC_08-1, qSPC_08-2, qFirstflower, qFlower_number_1-2, QDTF).[4–7]

Most of the combinations of the selected primers successfully determined both homozygous and heterozygous states for the listed markers. However, for some of the primer combinations, it was not possible to get success results.

1. Semagn K. et al. Single nucleotide polymorphism genotyping using Kompetitive Allele Specific PCR (KASP): overview of the technology and its application in crop improvement // Mol. Breed. 2014. Vol. 33, № 1. P. 1–14.

2. Goryunov D.V. et al. Association mapping of fertility restorer gene for CMS PET1 in sunflower // Agronomy. MDPI, 2019. Vol. 9, № 2. P. 49.

3. Sivolapova A.B. et al. Refinement of Rf1-gene localization and development of the new molecular markers for fertility restoration in sunflower // Mol. Biol. Rep. 2023. Vol. 50, № 9. P. 7919–7926.

4. Hwang E.-Y. et al. A genome-wide association study of seed protein and oil content in soybean // BMC Genomics. 2014. Vol. 15, № 1. P. 1.

5. Kim W.J. et al. Quantitative Trait Loci (QTL) Analysis of Seed Protein and Oil Content in Wild Soybean (Glycine soja) // Int. J. Mol. Sci. MDPI, 2023. Vol. 24, № 4. P. 4077.

6. Mao T. et al. Association mapping of loci controlling genetic and environmental interaction of soybean flowering time under various photo-thermal conditions // BMC Genomics. 2017. Vol. 18, № 1. P. 415.

7. Wang J. et al. Genetic mapping high protein content QTL from soybean ‘Nanxiadou 25’ and candidate gene analysis // BMC Plant Biol. 2021. Vol. 21, № 1. P. 388.

CLEAN-UP OF HEAVY METALS FROM CONTAMINATED SOIL BY PHYTOREMEDIATION

***Daurov D.*[1,2*], *Daurova A.*[1], *Sapakhova Z.*[1], *Zhapar K.*[1], *Abilda Z.*[1], *Toishimanov M.*[1,2], *Shamekova M.*[1], *Zhambakin K.*[1]**

[1]*Institute of Plant Biology and Biotechnology, 050040 Almaty, Kazakhstan*
[2]*Kazakh National Agrarian Research University, 050010 Almaty, Kazakhstan*

[*]*E-mail:* d.daurov@ipbb.kz

One of the most serious problems worldwide is heavy metal (HM) pollution. HMs can have a toxic effect on human health and thus cause serious diseases. To date, various mechanical or physicochemical methods have been developed, which are crucially needed for the remediation of technogenically polluted areas. The use of physical and chemical methods of soil cleaning, namely, leaching, chemical oxidation, and reduction, often leads to the accumulation of secondary pollutants and requires additional manipulations related to the removal of contaminated soil cover and subsequent waste collection. In addition, physicochemical cleaning methods are based on the use of special reagents that are not always safe for the environment. Unfortunately, there are limitations to such approaches: high cost, inefficiency at low metal concentrations, and irreversible changes in the physicochemical and biological properties of soils, which lead to deterioration of the soil ecosystem. Thus, for effective soil remediation, additional efficient and environmentally friendly soil restoration technologies are required for soils contaminated with heavy metals. Phytoremediation technology, which, unlike traditional methods, is inexpensive, environmentally friendly, and generally available, is one of the most promising new methods for restoring the environment. Hyperaccumulator plants represent a valuable resource for the remediation of metal-contaminated sites as they can carry, absorb, and translocate high levels of HMs that would be toxic to most organisms.

Sweetpotato [*Ipomoea batatas* (L.) Lam], the sixth most important food crop in the world, is tolerant to various environmental stresses, owing to its high antioxidant capacity. Sweetpotato has a high biomass ratio of both stem and tuber necessary for remediation.

In this study, we selected sweetpotato cultivars showing high tolerance to lead (Pb) for phytoremediation-related applications. These cultivars were kindly provided by Sang-Soo Kwak from Korea Research Institute of Bioscience and Biotechnology (KRIBB). Young seedlings of 20 sweetpotato cultivars were treated with 30 mM Pb. Daeyumi (KO-12) and Dahomi (KO-5) were selected as Pb-tolerant and -sensitive cultivars, respectively, based on their photosynthetic activity and growth inhibition index (I_{50}). In the Pb treatment, hydrogen peroxide and malondialdehyde contents of KO-12 were 1.5-fold less than those of KO-5. In addition, KO-12 showed higher ability to accumulate Pb in roots and leaves than KO-5. Expression levels of four Pb-responsive genes, including the metallothionein gene *IbMT1*, were higher in the roots and leaves of KO-12 than in those of KO-5. Interestingly, KO-12 showed greater tolerance to high Pb concentrations than sunflower and rapeseed, which have been well-studied for phytoremediation.

Our results suggest that sweetpotato is a suitable biomaterial for the phytoremediation of soils contaminated with HMs, including Pb, for sustainable agriculture. Futher, tolerance cultivars of sweetpotatoes will be studied for their ability to accumulate HMs from the lead plant, located in Shymkent city. Additionally, cultivation of sweetpotato for the phytoremediation of lead-contaminated soils is possible with the subsequent production of biofuel.

EFFICACY OF A NUMBER OF FUNGICIDES AGAINST THE WALNUT PATHOGEN *ALTERNARIA ALTERNATA* IN THE SOUTHERN ZONE OF FRUIT GROWING IN KAZAKHSTAN

***Ismagulova E.S.**, Kairova G.N.**

Kazakh National Agrarian Research University, Almaty, Republic of Kazakhstan

E-mail: elya_ismagulova@mail.ru

Since ancient times walnut has been considered a miracle of nature, which by the number of useful properties has no analogues in the plant world. Walnut (*Juglans regia L.*) is valued as a food, technical, tannin, medicinal, ornamental plant. The yield of walnut depends on many factors, one of them are diseases. To tackle this problem, it is necessary to precisely identify the pathogens and protective measures against them.

It was revealed that in the southern fruit-growing zone of Kazakhstan the most widespread disease of walnut is *Alternaria alternata*, found on leaves in the form of spotting. The aim of the study was to determine the biological efficacy of a number of fungicides against the causative agent of the disease, caused by the fungal pathogen *Alternaria alternata*.

Field studies were carried out in 2022-2023 in LLP "Integration - Turgen" of Almaty region, and laboratory studies were carried out in the laboratory of LLP "Kazakh Research Institute for Fruit and Vegetable Growing". In laboratory and field experiments we tested four types of fungicides of different mechanism of action: Scor 250, c.e. (difenoconazole, 250 g/l), Horus 750, v.d.g. (cyprodinil, 750 g/kg), Stroby 50%, v.d.g. (kresoxim - methyl, 500 g/kg), Luna Tranquility, c.s. (fluopyram,125 g/l + pyrimethanil, 375 g/l).

Alternaria alternata pathogen was initially isolated from infected leaves and fruits of walnut and identified on the basis of microbiological and molecular-genetic methods. Further, in laboratory studies, the efficacy of 4 fungicides were tested against the pathogen under aseptic conditions using agar block methoдин. In field studies, fungicides were applied three times during the season - at full leaf opening, at the end of flowering and 30 days after the second treatment. The rate of working fluid consumption was 1000 litres/ha. Control plants were sprayed with water for objective comparison. Three repetitions of each treatment were carried out during the experiment. During the season 4 surveys were conducted: before fungicide treatment and 25, 50 and 80 days after the first survey. The presence and degree of disease development were visually determined on four labelled branches on each tree, located on four sides of each tree, on which all leaves were examined.

The studies allowed to establish the following: in vitro studies showed high efficacy of fungicide Scor (difenoconazole) against the pathogen of walnut disease caused by *Alternaria alternata* fungus. The fungicide had a high inhibitory effect against the pathogen, inhibiting the growth of mycelium isolates relative to the control from 68.68 to 92.42% on the 7th day of cultivation, and from 59.25 to 91.71% on the 14th day of growth. The in vivo studies showed that, Fungicides Scor and Stroby successfully protected walnut plants against *Alternaria alternata* pathogen with biological efficacy of more than 90% and 80%, respectively.

STUDY OF *SORGHUM BICOLOR* L. FOR SYRUP PRODUCTION IN THE CONDITIONS OF THE SOUTH-EAST OF KAZAKHSTAN

Iskakova K.M.*[*1], Anapiyayev B.B.[2], Beissenbek Y.B.[2], Omarova A.Sh.[3], Sagimbaeva A.M.[2]

[1]Kazakh National Agrarian Research University, Almaty, Kazakhstan
[2]Satbayev University, Almaty, Kazakhstan
[3]Kazakh Research Institute of Agriculture and Plant growing, Almalybak, Kazakhstan

**E-mail:* konirsha_b@mail.ru

The *Sorghum bicolor* L. is the fifth most important cereal crop after wheat, corn, rice, and barley. Food sorghum is used as food in 30 countries for more than 500 million people living in tropical Africa and South Asia. Forage sorghum is the main ingredient for the preparation of feed for divorce. Sugar sorghum is grown on an industrial scale for the production of syrup, malt, starch, and protein is also a promising raw material for the production of bioethanol.

We have conducted studies on the factors affecting the frequency of formation of morphogenic calluses in a culture of somatic sorghum cells grown in the conditions of the South-East of Kazakhstan.

During the cultivation of somatic sorghum cells, it was noted that the frequency of callus cell formation and their morphology was significantly influenced by the original genotype of the donor plant.

It should be noted that during the cultivation of somatic sorghum cells, the main problem for most genotypes is the phenolic compounds, which are secreted by somatic cells on the seventh to the tenth day of in vitro cultivation. Phenolic compounds are substances of an aromatic nature containing one or more hydroxyl groups of an aromatic ring.

In the process of the research it was found that the frequency of callus formation during the cultivation of somatic sorghum cells in vitro grown in the conditions of the South-East of Kazakhstan depends on the original genotype. Also, sorghum genotypes have been found that are capable of forming morphogenic calli that can be used in cell selection for resistance to biotic and abiotic environmental stress factors and production of syrup on an industrial scale.

SANITATION OF PLUM AND APRICOT GENOTYPES FROM PLUM POX VIRUS USING COMBINATION OF THERMOTHERAPY AND TISSUE CULTURE

***Kabylbekova B.*[1*], *Nurseitova T.*[1,2], *Yusupova Z.*[1], *Turdiev T.*[3], *Madenova A.*[3], *Soltanbekov S.*[1], *Dolgikh S.*[1], *Kovalchuk I.*[1]**

[1] *Kazakh Fruit and Vegetable Research Institute, Almaty, Kazakhstan*
[2] *Abai Kazakh National Pedagogical University, Almaty, Kazakhstan*
[3] *Kazakh National Agrarian Research University, Almaty, Kazakhstan*

[*]*E-mail:* k_b_zh@mail.ru

Viral diseases of stone fruits, especially "Sharka", lead to species and varietal degeneration, and also decrease a yield and quality of fruits and, as a result, to large economic losses. Recovery of plants from viral infection and planting elite and super-elite basic plantings with healthy planting material will significantly increase productivity. The south-east of the country is origin of the endemic apricot species of *Prunus armeniaca, vulgaris* Lam and two species of plum *Prunus Sogdiana* Vass. (cherry plum) and *Prunus spinosa* (thorn). Commercial and home gardens of domestic and foreign varieties are also grown. Using a real-time RT-PCR test, the Plum pox potyvirus (PPV) was detected on plum cultivars Ayana, Ansar, Stanley, apricot cultivar Monitoba and *P. armeniaca*.

Virus clearance was performed in a stepwise manner under in vitro conditions. The apical tips of the plants were introduced into aseptic culture. Precultivation and adaptation were carried out on MS N75% medium, BAP-0.5 mg/l, GA-1.0 mg/l, IBA-0.1 mg/l, at 24°C±0.5 in variable light mode - 16 hours illumination (25 μmol m-2s-1) and 8 hours without illumination (n = 15). Combinations of sanitation methods were tested on 'Stanley', 'Ansar' and P.armeniaca: 1) Thermotherapy + Shoot apical meristem (SAM); 2) Thermotherapy + Chemotherapy (treatment with Ribavirin) + SAM. Thermotherapy of microshoots in vitro was carried out for 12 days at 36°C, humidity 70%, light mode – 16 hours of illumination (25 μmol m-2s-1) and 8 hours without lighting. During chemotherapy, 15 or 25 mg/l Ribavirin was added to the MS N75% nutrient medium. From the microplants grown under such conditions, the shoot tips with apical meristems measuring 1.5-3 mm was isolated and transplanted onto a nutrient medium of MS N75%, BAP-0.2 mg/l, GA-1, 0 mg/l, IBA-0.1 mg/l for the regeneration. After completing all stages of therapy, a control diagnosis was carried out on day 30.

In the Thermotherapy + SAM option, growth and reproduction were observed in three microshoots of 'Stanley' and three of 'Ansar', and *P.armeniaca* plants died. Control diagnostics for the presence of PPV showed that 'Stanley' and 'Ansar' are free from the virus.

During the course of recovery with the combination of Thermotherapy + Chemotherapy + SAM, the influence of the concentrations of the antiviral drug Ribavirin on the survival of plants at the stage of thermotherapy was noted. After treatment at a concentration of 15 mg/l, 5 viable microshoots of 'Stanley' were noted; all shoots of 'Ansar' and *P. Armeniaca* died. Treatment with Ribavirin at a concentration of 25 mg/l was more successful: 7 shoots of the 'Stanley' survived, 5 of *P. armeniaca* survived, and all shoots of 'Ansar' also died. After reproduction on the nutrient medium, control diagnostics showed that the use of the methods Thermotherapy + Chemotherapy + SAM (treatment with ribavirin at a concentration of both 15 and 25 mg/l) was successful for the plum 'Stanley', the shoots were free from the PPV virus; the presence of the PPV virus in the tissues of P. *Armeniaca* plants could not be eliminated.

Based on the results of our experiments, the combination of thermo- and chemotherapy with Shoot apical meristem appears to be a promising approach for obtaining virus-free stone fruit plants. Work on recovery from viruses will continue using a combination of thermotherapy, chemotherapy and cryotherapy.

CHARACTERIZATION OF FUNCTIONAL ACTIVITY OF RECOMBINANT PROTEINS EIF4E FAMILY FROM SOLANUM TUBEROSUM IN VITRO

***Kolesnikova V.V.*[1,2*], *Nikonova E.Yu.*[1], *Balobanov V.A.*[1], *Korchinskaya V.Yu.*[2], *Andreytsev V.V.*[1] *Nikonov O.S.*[1]**

[1] *Institute of protein research, Pushchino, Russia*
[2] *All-Russia Research Institute of Agricultural Biotechnology, Moscow, Russia*

**E-mail:* kolesnikovavicto@yandex.ru

Potato virus Y is phytopathogens and a major limited factor potato yield. For a realized life cycle viruses need to recruit a cell translation apparatus to translate viral RNA. Viral protein VPg mimics the cellular mRNA cap structure and interacts with eukaryotic initiation translation factor 4E (eIF4E), which allows for the initiation of biosynthesis of viral proteins. We have combined genetic, biochemical, and bioinformatic methods to study the formation of resistance in *Solanum tuberosum* against potyviruses. Previously, using molecular modeling and dynamics, we have obtained a structural interpretation of the biochemistry results. In this project, we characterized functional activity recombinant proteins family eIF4E from *Solanum tuberosum*. Recombinant proteins of the eIF4E family were obtained in the bacterial system and purification using chromatography. The ability of each purified protein to bind cap-analog and VPg was checked using fluorescence spectroscopy. Isoforms of eIF4E show different affinity to the cap analog and VPg.

IDENTIFICATION OF EIF4E ISOFORMS INTERACTING WITH THE VIRAL PROTEIN VPG OF POTATO VIRUS Y

***Korchinskaya V.Yu.*[1,2*], *Karlov V.D.*[1], *Klychnikov O.I.*[2]**

[1]*All-Russia Research Institute of Agricultural Biotechnology, Moscow, Russia*
[2]*Lomonosov Moscow State University, Moscow, Russia*

**E-mail:* KorchinskayaV@yandex.ru

Virus Y is an economically important pathogen of the *Solanaceae* family, including potato. A key role in the reproduction of this virus is played by the viral protein VPg, the interaction of which with translation initiation factor 4E (eIF4E) of the host plant is necessary for the translation of viral mRNA. Determining which eIF4E isoforms VPg uses and their quantification in potato plants will facilitate understanding of the mechanisms of infection and resistance to virus Y. This goal can be achieved using proteomics methods based on mass-spectrometry, which have recently become powerful a high-throughput approach to characterize entire viral interactomes.

In our study, we decided to use a tandem mass-spectrometry approach in combination with the pull-down method, which will allow us to characterize the eIF4E isoforms that directly interact with viral VPg. We created a genetic construct for the expression of recombinant VPg in *E. coli* cells; induction of protein synthesis was carried out under a wide range of conditions. As a result of a pull-down using purified recombinant VPg and subsequent mass-spectrometric analysis, we identified the binding of VPg to the eIF4E-1, eIF4E-2 and eIF(iso)4E isoforms and didn't detect interaction with the nCBP isoform. To determine whether the interaction of VPg and the three eIF4E isoforms is due to their high content in cells or to the high affinity of VPg even for small amounts of certain eIF4Es, we further performed quantitative mass-spectrometric assessment of the content of all eIF4E isoforms in potato plants. It has been shown that nCBP is indeed the least represented isoform.

In total, these results indicate the high adaptive ability of the virus to use several isoforms at once to carry out its own life cycle, and confirm the low importance of nCBP for translation initiation, shown previously in the literature.

The work was supported by the Russian Science Foundation (Grant No. 21-76-10050).

PLANT TISSUE CULTURE-MEDIATED BIOTECHNOLOGICAL APPROACHES OF SOME REPRESENTATIVES OF THE GENUS *LYCIUM*

***Lapchanka K.A.*[1], *Stralkouski V.V.*[1], *Barysevich K.G.*[1], *Allaberdiev R.Kh.*[2], *Spirydovich E.V.*[1]**

[1]*Central Botanical Garden of the National Academy of Sciences of Belarus*
[2]*National University of Uzbekistan named after Mirzo Ulugbek*

The following biotechnological directions are well-developed at the Central Botanical Garden of the National Academy of Sciences of Belarus: conservation and propagation of endemics, rare species, elite plant varieties; plants that have lost the ability to produce seeds; obtaining a large number of healthy, uniform plant material; creation of varieties by methods of cell selection; and exchange of sterile material for research purposes.

The purpose of our study was to investigate the growth and development under *in vitro* conditions of three economically valuable species, medicinal species of the *Lycium* genus (*L. barbarum, L. ruthenicum, L. chinence*) of the *Solanaceae* family, widespread in the territory of the Southern Aral and the Priaralye, for preservation in the collection of aseptic cultures of the CBG and successful introduction in the conditions of Belarus.

Seeds were used for introduction into *in vitro* culture. Dried fruits were soaked for 12 hours in distilled water and rubbed through a fine sieve to remove fruit pulp from the seeds, which were then sterilized. For this, a 2% solution of 72% household soap (5 minutes), 0.05% solution of difenoconazole - a systemic fungicide (brand name *Score*) - (5 minutes), 0.1% solution of $AgNO_3$ (5 minutes) were used. At the end of exposure in each sterilizing agent, the seeds were washed twice for 3 minutes with sterile distilled water and transferred directly to the nutrient medium.

The selection of nutrient medium options was based on the composition of soils in the natural habitats of the *Lycium* L. genus in the territory of Uzbekistan. Nutrient – mineral base DKW, 15 g/l sucrose, 0.2 mg/l kinetin (6-furfurylaminopurine); variants differ in pH (5.6–7.8) before autoclaving, as well as NaCl concentration (1–1.5 g/l). 25 seeds were placed on each nutrient medium. Cultivation conditions: 16-hour photoperiod and temperature 25±2 °C.

On the 8th day after introduction into aseptic culture, the first seedlings suitable for subsequent subculturing appeared. The presence of NaCl in the nutrient medium inhibited seed germination, as did high pH values. When the seedlings were 1.0±0.5 cm in length, they were transferred to cultural vessels (180 ml) on the nutrient medium different from the introduction medium – Woody Plant Medium (WPM) – with the addition of 15 g/l sucrose, pH 5.6–5.8 before autoclaving. After 7 days, the transferred seedlings looked as follows: active growth and development of plants in *in vitro* conditions were noted, with the formation of an extensive root system, and there were no developmental anomalies such as vitrification, callus formation, etc.

As a result of the experiment, peculiarities of seed germination of plants of the *Lycium* genus (*L. barbarum, L. ruthenicum, L. chinence*) under *in vitro* conditions were revealed. The obtained data indicates the suitability for cultivation of the proposed nutrient medium and the successful introduction of the studied plants into *in vitro* culture.

CALLUS INDUCTION AND PLANT REGENERATION FROM EMBRYOGENIC CALLUS OF PAULOWNIA 9501 HYBRID (*PAULOWNIA TOMENTOSA×PAULOWNIA FORTUNEI*)

Gubarevich A.V., Lapchanka E.A., Spirydovich E.V.

Central Botanical Garden of the National Academy of Sciences of Belarus

Paulownia is a valuable woody plant belonging to the family *Paulowniaceae*. It is native to Southeast Asia. *Paulownia* is a 10–30 m tall tree with a wide crown and large (about 70 cm in diameter) heart-shaped leaves with long petioles. The flowers are pale purple in erect pyramidal inflorescences up to 30 cm long.

All parts of *Paulownia* are used for different purposes: leaves and flowers used for medicine, leaves – rich proteins and nitrogen, a trunk – a source of timber. *Paulownia* is not only a decorative tree, it's also a multi-purpose plant and a source of renewable energy.

The use of biotechnological methods of microclonal propagation and plant regeneration *in vitro* increase plant production. The use of modern biotechnological methods of *in vitro* plant propagation can overcome main disadvantages the traditional method of propagation (genetic diversity of the resulting planting material and the duration of the juvenile period) and increase the production of plants. Biotechnology at the Central Botanical Garden of the National Academy of Sciences of Belarus in its broadest sense explores its use across many fields of application from the conservation of endangered species to the storage of economically important crop plants and to the industrial plant cell culture collections. Higher plant cell culture can be an alternative method of raw plant material production for medicine, veterinary science, perfumery, and in food industry. The main point is to obtain biomass in large volume bioreactors in sterile conditions.

The purpose of this paper was to study the effect of plant growth regulators on callus induction and *in vitro* morphogenesis using various explants of hybrid 9501 *(Paulownia tomentosa×Paulownia fortunei).*

Testing of the various nutrient media for callus induction and plant regeneration capacities of hybrid 9501 used MS nutrient media supplemented with 6.0 g/L agar, 30g/L sucrose and plant growth regulators. Nutrient mediums: MS1 – MS+8 mg/L BAP+1 mg/L NAA, MS2 – MS+5 mg/L BAP+ 1 mg/L NAA, MS3 – MS+6 mg/L BAP+0.1 mg/L NAA. Types of explants were used for callus induction: leaf laminae, petioles, stem part with and without bud. Cultivation conditions: thermostat, darkness, +24.6±0.5°C and light, fotoperiod 16/8, 25±2°C.

A high percentage of callus formation was observed in all types of explants. The frequency of callus induction from leaves and stem with bud was higher than others.

The optimal medium for obtaining nonmorphogenic callus is MS medium containing 5 mg/L 6-BAP and 1 mg/L NAA (callus induction darkness – 88,85%, light – 61,43%). MS medium with 6mg/L BAP and 0.1 mg/L NAA (darkness – 65,68%, light – 31,46%) and MS medium with 8 mg/L BAP and 1 mg/L NAA (darkness – 66,65%, light – 65,48%) can also be used for callus induction, but with lower efficiency. MS medium with 6 mg/L BAP and 0.1 mg/L NAA (plant regeneration darkness – 16,26%, light – 25,91%) can be used to induce morphogenic callus and regeneration of new plants by forming several shoots from a single bud. MS medium with 5 mg/L BAP and 1mg/L NAA (darkness – 4,00%, light – 22,28 %) and MS medium with 8 mg/L BAP and 1 mg/L NAA (darkness – 18,00%, light – 21,81%) can also be used for plant regeneration, but with lower efficiency.

All of the selected media can be used for regeneration of shoots from callus. Shoot formation from an explant with a bud was observed on all media, best under lighting conditions with a photoperiod of 16/8 at 25±2°C. The most favourable cultivation conditions for obtaining a nonmorphogenic callus is cultivation under unlit thermostat conditions at 24.6±0.5°C.

The work was supported by SCSTI "Biotechnology", "Natural Resources and Ecology" 2020 - 2025 and carried out as part of the Master's thesis.

CLONAL MICROPROPAGATION IN THE RECOVERY OF REGRESSING TURANGA POPULATIONS

Mikhailenko N.V.[1], Turdiyev T.T.[1,2], Kovalchuk I.Yu.[1], Kuan A.A.[2], Yemesheva K.B.[2], Baizhumanova S.S.[2], Tuigunov Z.T.[1,] Rakhimbayev I.R.[1]

[1]Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan
[2]Kazakh National Agrarian Research University, Almaty, Kazakhstan

E-mail: georgi-nata@mail.ru; turdievtt@mail.ru

In Kazakhstan, forests cover only about 5 per cent of the territory. The main reasons restraining the spread of forests are the aridity of the climate, and desertification of a large part of the territory (about 60%). One way to combat desertification is through the use of drought-resistant and salinity-tolerant woody plant species. These include *Populus diversifolia* Schrenk and *Populus pruinosa* Schrenk, which can grow on sandy, saline and depleted soils. In the natural environment they reproduce by seeds, but for a number of reasons they do not take root well in harsh environmental conditions, which leads to population regression. They are also capable of vegetative propagation, which makes it possible to use clonal micropropagation, selecting the best trees with high growth and development rates.

In winter, after the rest phase was completed, trees in the floodplain of the Ili River were used to cut 20-25 cm long annual tree cuttings. *In vitro* inoculation was carried out in two ways: 1) lignofied cuttings were cut into segments 6-7 cm long with 2-3 buds, sterilized and planted on the nutrient medium; 2) shoots from lignified cuttings were germinated, divided into segments with one bud, sterilized and planted on a nutrient medium. In both versions, the saprophytic microflora was sterilized by using bleach «Whiteness (Belizna)» (1:1) 10 min and 0.1% HgCl2 solution 5 min, washed 3 times with sterile distilled water. The second method of *in vitro* inoculation was the most effective. In this case, the number of aseptic plants produced was 57%.

Aseptic mini cuttings were placed in Murashige and Skoog (MS) medium with growth regulators: 6-benzylaminopurine (BAP) in concentrations of 0.3 mg/l and R-indole-3-oil acid (IMA) – 0.01 mg/l. After the leaves are formed for growth and propagation, they are transplanted to nutrient media of different composition: 1) MS, BAP – 0.1 mg/l, GA – 0.01 mg/l, sucrose – 30 g/l, pH 5.7. 2) MS, BAP – 0.1 mg/l; GA – 0.01mg/l; sucrose – 20 g/l; pH 5.7. 3) MS, B_1 – 0.5 mg/l; BAP – 0.2 mg/l; GA – 0.02 mg/l; sucrose – 20 g/l; pH 5.7. 4) MS, B_1 – 0.5 mg/l; BAP – 0.1 mg/l; GA – 0.02 mg/l; sucrose – 20 g/l; pH 5.7. 5) MS, B_1 – 0.5 mg/l; BAP – 0.1 mg/l; GA – 0.02 mg/l; glucose – 20 g/l; pH 5.7. The medium containing glucose was the best, the propagation rate over 3-4, depending on the species. The use of sucrose ranged from 1.5 to 2, and plants were in poor condition.

For rhizogenesis, propagated plants were transplanted to nutrient media MS, IBA – 0.5 mg/l or MS½ + IBA – 0.5 mg/l. The best was the second variant of medium, after 2 weeks plants began to appear and develop a root system. After 4-5 weeks, the root system amounted 80-91.1% depending on the species.

The rooted turanga plants were transplanted into containers, 10 cm in height and 10 cm in diameter, filled with layers: 6 cm peat and 4 cm perlite, poured with a solution of fungicide (fludioxonil – 25 g/l) in a concentration of 4 ml/2 l of water and covered with transparent caps with a lid. After 6-7 days, the lids were opened. As soon as there were signs of active growth in transplanted plants, gradually opened caps until the plants fully adapt to ex vitro conditions. This usually took three to four weeks.

ADVENTITIOUS ROOTS CULTURE OF *ALLOCHRUSA GYPSOPHILOIDES*: SAPONINS-BEARING RARE SPECIES

Mursaliyeva V.K.*, Mukhanov T.M.

Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan

**E-mail:* gen_mursal@mail.ru

Allochrusa gypsophiloides (Regel) Schischk (fam. Caryophyllaceae Juss.), Turkestan soap root (TSR) is a rare species of the natural flora of Central Asia and Kazakhstan with a limited habitat in the Western Tien Shan and Pamir-Alai is a valuable saponin-bearing plant. The rare TSR has pharmacological value and technical application as an effective foaming agent and emulsifier. For further scientific and practical utilization of the unique potential of this valuable crop, it is relevant to develop an alternative approach based on *in vitro* system to replace wild TSR raw material. Adventitious roots (AR) cultures are characterized by genetic and biosynthetic stability, optimization of the main factors of the nutrient medium allows to achieve intensive growth of root biomass and stable level of biologically active metabolite in culture. The aim of the research was comparative evaluation of AR culture and natural roots of wild plants from Kazakhstan for total saponins, phenols and flavonoids content, antioxidant (AOA) and antimicrobial activity in model test systems. In AR culture, growth index and secondary metabolites were evaluated on days 25 -, 45-, 60- of cultivation on ½ MS medium without (control) and with auxin application. The conducted studies revealed differences in the content of secondary metabolites in AR culture material and in wild plants, as well as in their AOA and antimicrobial activity in model test systems. The levels of saponins and flavonoids were higher in AR culture at optimal timing and medium of cultivation compared to native roots. High antimicrobial activity was detected in control extracts of in vitro AR culture with increased levels of saponins. The hormonal composition of the medium determined the nature of the relationship between AR culture growth and the accumulation of secondary metabolites in it. The content of saponins and flavonoids positively correlated with the growth of the culture on the control medium and on the NAA medium. *In vitro* AR culture is promising for obtaining triterpene saponins TSR with high antibacterial and antifungal activity.

GROWTH OF BARLEY SEEDLINGS WITH TREATMENT SEEDS OF CHITOSAN AND HYDROXYCINNAMIC ACIDS CONJUGATES UNDER SALINITY STRESS

***Ovchinnikov I.A.*[1*], *Kalatskaja J.N.*[1], *Rybinskaya K.I.*[1], *Herasimovich K.M.*[1], *Nikalaichuk V.V.*[2], *Hileuskaya K.S.*[2]**

[1]*V.F. Kuprevich Institute of Experimental Botany, the National Academy of Sciences of Belarus, Minsk, Republic of Belarus*

[2]*Institute of Chemistry of New Materials, the National Academy of Sciences of Belarus, Minsk, Republic of Belarus*

**E-mail:* igor-1606@mail.ru

The challenge of maintaining plant productivity in water scarcity conditions is of paramount importance worldwide. Phenolic acids, including hydroxycinnamic acids and their derivatives, are rapidly induced by various stressors, such as salinity (NaCl) stress. Applying hydroxycinnamic acids exogenously to plants can enhance their sustainability to stress. One way to alter the bioavailability of hydroxycinnamic acids is to bind them to a carrier polymer matrix. Chitosan is one of the promising biopolymers in this regard. The modification of chitosan chemically enables the production of derivatives with improved solubility, growth-promoting properties, and antioxidant activities.

The purpose of this study is to investigate the impact of treating barley seeds with conjugate chitosan and either caffeic acid (Ch-CA) or ferulic acid (Ch-FA) on growth and antioxidant components during short-term salinity (NaCI) stress and in the post-stress period.

The growth of seedlings was inhibited by the Ch-CA conjugate under stressful salinity conditions. The slowdown in growth was more pronounced in the root system, where the MDA content increased by 18%. Additionally, the SOD and POX activities increased by 2 and 2.5 times, respectively. The adaptation in the post-stress period was more active with Ch-CA conjugate treatment, as reflected in an increase in root length and dry biomass, and a decrease in antioxidant activity. The dry biomass and proline accumulation were noted in the leaves, along with an increase in SOD and POX activities, but a decrease in APX and GR activities.

The application of the Ch-FA conjugate did not significantly affect the growth of the seedlings. However, it did contribute to the accumulation of proline content in the roots and induced the activities of SOD and POX in both the roots and leaves of the seedlings. No activation of growth and development of the seedlings was detected during the repair period, and the indicators of the antioxidant status were lower than those in the control.

The Ch-CA conjugate exerted a low stressful effect on barley seedlings induced of resistance to salt stress, activated antioxidant components to minimize oxidative damage and maintain cellular homeostasis.

EARLY CHANGES IN PHOTOSYNTHESIS ACTIVITY ARE MODULATED BY DISTANT SIGNALS DURING SALINITY IN POTATO PLANTS

Pecherina A.A.*, Mudrilov M.A., Brilkina A.A., Vodeneev V.A.

Lobachevsky State University of Nizhny Novgorod, Nizhny Novgorod, Russia

**E-mail:* pechyorinaa@gmail.com

Salinity is one of the most important abiotic stressors that reduce crop yield. The roots of plant come into direct contact with high concentrations of Na^+ and Cl^- in soil or water, but salinity affects the plant as a whole. A change in the osmolarity of the solution due to an excess of Na^+ and Cl^- (osmotic stress) and the entry of these ions into cells (ionic stress) activate various signaling systems, and modulated distant signals can change physiological processes. In this work, we studied the salt-induced signals in the root, and their effect on photosynthesis activity in potato plants.

There were used five-week-old potato plants of the Nevsky variety grown under hydroponic conditions. The plants were treated with 100 mM NaCl, 200 mM sorbitol (simulate the osmotic component of salinity) or 100 mM KCl (test the role of Na^+ in salt stress). Photosynthesis activity was measured using PAM fluorimetry. The effect of salinity on transpiration was determined using the Crop Water Stress Index. Cytosolic pH was determined using a genetically encoded sensor Pt-GFP, and Ca^{2+} was visualized using a probe Fluo4.

The decrease in photosynthesis activity began 15 minutes after salt treatment. However, transpiration decreased only 40 minutes after NaCl addition. The Na^+ accumulation in the leaves occurred 6 hours after NaCl treatment. Also, several types of signals were detected in roots: Ca^{2+} signal and hyperpolarization. However, only the Ca^{2+} signal propagated through the shoot. This signal was Na^+-induced, and this NaCl-induced Ca^{2+} signal caused cytosolic alkalization of root cells. In addition, the propagation of a hydraulic wave was recorded in the shoot, which was caused by the osmotic component of salinity. Osmotic stress could modulate transpiration and late decrease in photosynthesis activity. Early changes in photosynthesis activity were modulated by Ca^{2+}, which was confirmed by inhibitory analysis.

The work was supported by the Russian Science Foundation (project no. 22-14-00388).

DEVELOPMENT OF MICROPROPAGATION TECHNIQUE FOR PRODUCTION OF ELITE BLUEBERRY PLANTING MATERIAL IN KAZAKHSTAN

Rymkhanova N.K.*, ***Manapkanova U.A., Kushnarenko S.V.***

Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan

**E-mail:* n.rymkhanova@gmail.com

Blueberry (*Vaccinium corymbosum* L.) is a valuable berry crop, both economically and biologically. Blueberry is most often planted for their nutritional and beneficial properties, but high yields and quality fruits require proper planting material.

During *in vitro* culture initiation of blueberry varieties, it was found that the apices of blueberry shoots are sensitive to mercuric chloride. Disinfection in 0.1% mercuric $HgCl_2$ for 10 minutes led to necrosis of all initiated blueberry explants; treatment for 7 minutes caused necrosis in 40-50% of the initiated apices. Reducing the disinfection duration with mercuric chloride to 4 minutes had a positive effect on the formation of green blueberry plants. With this treatment, bacterial and fungal contamination was observed only in 3.2-10.3% of explants; necrosis varied from 0 to 34.2%, and green plants were formed in 39.4-93.7% of explants, depending on the variety. The highest percentage of green plants (93.7%) was obtained in Meader variety. *In vitro* plants with detected endophytic bacterial contamination were removed. As a result of detection endophytic contamination 26.3 to 75% aseptic blueberry plants were obtained. Aseptic blueberry plants were further used for micropropagation.

An important step of micropropagation is optimizing the medium composition for blueberry. Seven variants of media were used based on WPM medium with various phytohormones: zeatin, 6-benzylaminopurine (BAP), indolyl-3-butyric acid (IBA) and gibberellic acid (GA). It was found that during blueberry micropropagation, the main problem was high callus formation on leaves and shoots. This was especially evident in the WPM medium with BAP, even at a low concentration (0.1 mg/L). Replacing the cytokinin BAP with zeatin gave a positive result: the condition of the shoots was better, the multiplication rate Kr exceeded 3.6, and no callus formation was observed.

Key words: Blueberry, aseptic plants, micropropagation

This research was funded by the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan, Scientific and Technical Program BR18574099

TECHNICAL REGULATIONS AND PRACTICAL RECOMMENDATIONS OF TECHNOLOGIES FOR GRANULATION OF MULTICOMPONENT FERTILIZER "AGROBIONOV"

***Salikhov T.K.*[1,2*], *Elubaev S.Z.*[1], *Sarsenova A.A.*[1], *Salikhova T.S.*[1,2], *Soloviev D.A.*[3], *Smirnova Yu.D.*[3]**

[1]*Abay Myrzakhmetov Kokshetau University, Kokshetau, Kazakhstan*
[2]*L.N. Gumilyov Eurasian National University, Astana, Kazakhstan*
[3]*All-Russian Scientific Research Institute of Reclaimed Lands branch of the Federal Research Center "Dokuchaev Soil Science Institute", Moscow, Russia*

**E-mail:* tuatai_76@mail.ru

In Kazakhstan, the annual yield of ash and ash-slag mixtures during coal combustion is about 19 million tons, and more than 300 million tons of waste have been accumulated in ash dumps to date. The stock of accumulated ash and slag waste in the Akmola region alone is about 599.2 thousand tons, 423.4 thousand tons of ash and slag waste is generated by industrial centers, the rest by suburban and residential sectors. These wastes are stored in the vicinity of the city in special ash dumps, occupying huge territories and having a negative impact on the environmental situation.

Due to the rise in the cost of traditional fertilizers, their use is decreasing, which leads to the consideration of alternative drugs and ameliorants that allow reducing the doses of basic fertilizers.

The research work is based on the research results on the use of a powdery form of granulated fertilizer "Agrobionov". Experimental data have shown a positive effect of the drug "Agrobionov" on increasing soil fertility, yields of the studied crops on reducing doses of basic fertilizers with the complex use of an ash-carbon preparation, environmental safety, and high economic efficiency of its use.

However, the powdered form of the drug "Agrobionov" is very non-technological with mechanized application. Thus, the research results will help solve the issues of creating granulation technologies and a method for applying new multicomponent fertilizers, recycling production waste and reducing environmental pollution.

The purpose of the research is to develop technologies for granulating multicomponent carbon fertilizer "Agrobionov" in the grain crop rotation of Northern Kazakhstan.

The research work was carried out within the framework of scientific projects grant financing of the Ministry of Internal Affairs of the Republic of Kazakhstan IRN AP19677557 "Development of the optimal granulation technology and effective methods for applying the Agrobionov polycomponent fertilizer in the grain crop rotation of Northern Kazakhstan".

Studies have been conducted to determine the optimal modes of the granulation technological process and the strength of granules to fracture of the fractional composition, their shapes, and uniformity. The type of binder component of the granulated mixture and the optimal modes of the technological process are determined. Recommendations are given for the preparation of technical regulations for granulation and packing of "Agrobionov" fertilizer.

Thus, gypsum has been considered as an effective binding component in terms of availability, low cost, improved reclamation properties, the ability to pass into the soil solution, and the standard strength of granules to destruction (abrasion) has been achieved. The optimal amount of gypsum binder in a mixture with the "Agrobionov" fertilizer has been determined, which ultimately is a cost-effective and environmentally friendly complex granular fertilizer.

In granular form, "Agrobionov" multicomponent fertilizer has great potential for commercialization and scaling up of the project in production.

STUDY OF THE EFFICIENCY OF SWEET POTATO GROWING IN KAZAKHSTAN BY DIFFERENT METHODS OF MULCHING

***Sapakhova Z.*[1*], *Islam K.R.*[2], *Toishimanov M.*[1,3], *Zhapar K.*[1], *Daurov D.*[1,3], *Daurova A.*[1], *Raissova N.*[1], *Kanat R.*[1], *Shamekova M.*[1], *Zhambakin K.*[1]**

[1]*Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan*
[2]*The Ohio State University South Centers, Piketon, OH, United States of America*
[3]*Kazakh National Agrarian Research University, Almaty, Kazakhstan*

**E-mail:* z.sapakhova@ipbb.kz

Sweet potato (*Ipomoea batatas* L.) is a high-yielding nutritious specialty crop. There is a growing need for proactive information on the sustainable production of sweet potatoes under short growing seasons. The objective of our study was to evaluate the effects of crop residue and synthetic mulches on the growth, yield, and quality parameters of three varieties of sweet potatoes. Three types of mulch, wheat straw (straw), white polyethylene film (white mulch), and black plastic film (black mulch), and a control (no mulch) were evaluated during the 2021 and 2022 growing seasons in the south-eastern region of Kazakhstan.

The application of mulch increased the yield components of sweet potato compared to the results with no mulch application. The studied varieties behaved differently according to the quality of the tubers, depending on the climatic conditions, variety, and mulch applications. The Fv/Fm value for the control ranged from 0.598 to 0.748 in the three sweet potato genotypes, whereas the three mulch treatments had Fv/Fm values higher than those of the control in 2021 and 2022. The application of white and black mulch significantly increased the length of the vine and meristem number in all three genotypes at levels of $p < 0.05$ and $p < 0.05$, while the use of straw increased the vine length and meristem number of Rizi 0603 and the meristem number of Xushu 25. The tuber number per plant and tuber weight were significant under polyethylene mulches. Organic straw mulch significantly increased the tuber number per plant in Xushu 25 and Rizi 0603. As a result of this technological approach, the total average production yield for the three sweet potato varieties was 11.0 t/ha in straw, 28.3 t/ha in white mulch, and 38.8 t/ha in black mulch compared with 9.8 t/ha for the non-mulched plots. The largest difference between the mulch and mulch-free crop system was observed in Xushu 25 (+25.2 t/ha) followed by the Beauregard variety (+13.2 t/ha) and Rizi 0603 (+10.3 t/ha).

In this study, Beauregard showed an increase in fructose, glucose, and maltose, while Xushu 25 showed a consistent increase in sucrose. The application of organic mulch as straw and polyethylene mulch significantly increased monosaccharides and disaccharides in the tuber of sweet potato.

The PCA provided a multidimensional statistical analysis of the possible mulching effects of sweet potatoes on the dependent variables. The group consisting of straw and control for each sweet potato genotype presented similar results due to their similar qualities, including morphological and carbohydrate contents. The other group of sweet potatoes included white and black mulch treatments.

The results of the LCA assessment showed that total carbon emission was 128.2 kg; 219.8 kg; and 221.2 kg CO2eq ha^{-1} in organic, white, and black polyethylene mulches, respectively.

The results of the present study will be used to develop other technological sequences for the cultivation of sweet potatoes in the southeastern region of Kazakhstan. Plastic mulch will help to increase our knowledge about climate change's effects on various plant species in the world, including in developing countries.

DECIPHERING THE GENETIC CONTROL AND MOLECULAR REGULATORY NETWORKS UNDERLYING QUANTITATIVE RESISTANCE TO DISEASES IN LEGUMES

Stepanova A[1*]., Merkushkin D.[1], Gentzbittel L.[1], Ben C.[1]

[1]Skolkovo Institute of Science and Technology, Moscow, Russia

**E-mail:* anastasiia.stepanova@skoltech.ru

Legumes includes valuable crops for world food production, being protein-rich nutrition for humans and animals, as well as productive forage crops. Soybean is a particularly important oilseed crop for Russian agriculture. However, the yield of most legume species is severely affected by root diseases, causing losses to the global economy (FAO, 2019).

Quantitative Disease Resistant (QDR) conditioned by multiple genes of partial effect is the most common form of plant disease resistance. Breeding for root QDR is proposed to be efficient in epidemic control of soil-borne root diseases, because chemical control of these pathogenic species is nearly imposible. We propose to reveal the genetic control and molecular regulation of some networks underlying root resistance in legumes.

Previous GWAS studies combined with transcriptomic analysis have identified two candidate genes involved in the response to *Verticillium* infection in *Medicago truncatula*: Medtr7g070480 encoding a SEC14 cytosolic PITP (phosphatidylinositol transfer protein) required for the transport of secretory proteins from the Golgi complex and Medtr1g042160.1 encoding a MATH1 protein (meprin and tumor necrosis factor receptor-associated factors (TRAF-C) homology).

To validate the role of *Sec14* & *Math1* genes in the QDR against *Verticillium* wilt in *M. truncatula* we generated overexpressing *ovx-Sec14*, *ovx-Math1 M. truncatula* mutant hairy roots (HaRo) and CRISPR/Cas9-mediated knock-outed *ko-sec14* and *ko-math1* HaRo.

An *Agrobacterium rhizogenes*-mediated transformation protocol was used to deliver the vectors of interest into roots of resistant (A17, 2HA) and susceptible (R108, F83005.5) *M. truncatula* ecotypes towards *Verticillium* wilt. Resistant A17 and susceptible R108 ecotypes exhibited better transformation efficiency as compared to 2HA and F83005.5 ecotypes.

Ovx-Sec14 HaRo and HaRo with empty vector (negative control) of R108 were inoculated with *Verticillium alfalfae* strain V31.2 to assess the disease phenotype. *Ovx-Sec14* samples displayed higher infection rate as compared to the negative control. Therefore, *Sec14* is likely a gene of susceptibility.

The development of CRISPR-edited HaRo includes: i) gRNA design; ii) gRNA testing; iii) vector construction; iv) optimization of vector delivery method.

Two gRNAs were designed for each of the target genes using CRISPR-P http://crispr.hzau.edu.cn/CRISPR2/ and CRISPOR http://crispor.tefor.net/ online platforms. To test the efficiency of the selected gRNAs, an *in vitro* assay was performed using synthetic RNPs. The corresponding gRNA sequences were then inserted into binary CRISPR/Cas9 vectors resulting in pCas9-*math1* and pCas9-*sec14* binary plasmids.

To test the *in vivo* efficiency of selected gRNAs, *M. truncatula* leaf protoplasts were transformed with the RNP complexes or pCas9-*math1* and -*sec14* vectors. Edition events of the target genes were confirmed by genomic DNA sequencing.

Agrobacterium rhizogenes-mediated transformation was used to deliver CRISPR/Cas9 vectors into *M. truncatula* roots in order to generate mutant *ko-math1* and -*sec14 M. truncatula* HaRo culture.

THE EFFECT OF WATER DEFICIT ON THE GROWTH AND DEVELOPMENT TO BARLEY PLANTS

Sushkova D.V.*, Murgan O.K., Danilova E. D., Kolomeichuk L.V., Efimova M.V.

National Research Tomsk State University, Tomsk, Russia

**E-mail:* dary.108@mail.ru

Climate aridity is a serious environmental problem that greatly affects plant life. Water deficiency causes a number of changes in the morphological and physiological parameters of plants. Thus, under the action of drought there is a decrease in water potential of tissues and, as a consequence, disruption of photosynthetic apparatus functioning, formation of reactive oxygen species, increase of lipid peroxidation intensity. In order to increase the sustainability of crops important for agriculture, it is necessary to better understand the mechanisms action of water deficiency on plants.

Barley seedlings of Biom variety were used to study the resistance of monocotyledonous plants to water deficit conditions. The seeds were sterilized with 70% ethanol, washed with distilled water and stratified at a temperature of 4 ° C for three days. Then the seeds were germinated in the light. Seeds were then sown in soil substrate weighing approx. 600 grams in darkened 1-liter vessels. Vegetation was carried out in white light (fluorescent lamps L36W/77 Fluora with a flux density of 200-250 μmol/$m^2 \cdot s^{-1}$, photoperiod 16/8 hh, air temperature 20±3 ° C).

Plants were divided into three variants: (1) control, in which irrigation was carried out until the soil was completely saturated, (2) 20% irrigation (the amount of water was calculated according to soil moisture capacity from the amount of irrigation in the control variant) and (3) no irrigation at all. During the second week, 100% watering was restored for half of the plants subjected to the stress (20% irrigation and drought) were restored 100% irrigation. At the end of the second week, growth parameters (biomass of aboveground plant parts and relative water content (RWC)) were recorded for five variants (control, 20% irrigation, drought, 20% irrigation + recovery, drought + recovery), as well as material to determination of osmotic potential value, proline content.

The results showed that the biomass of the above-ground part of plants was lower after the action of two-week drought by 5 times, and at 20% irrigation - by 2 times, relative to the control (0.99±0.04 grams). The RWC values were 40 and 90%, respectively, of the control variant. Restoration of irrigation contributed to the increase of biomass index to 0.64±0.03 (no irrigation) and 0.72±0.02 (partial irrigation), and RWC to the values of control plants.

It is known that stress factors promote the synthesis of the imino acid proline, which in turn exhibits antioxidant and osmoprotective properties. Barley plants subjected to complete or partial drought accumulated 7.5 and 1.6 times more proline, while the value of osmotic potential decreased 2 and 1.3 times, respectively. Soil rehydration leads to a decrease in proline content up to 56 and 80% relative to the control, and restoration of osmotic potential values.

So, we have shown that barley plants demonstrated physiological response to both partial and complete cessation of irrigation. As regulatory mechanisms in response to water deficit barley plants accumulate osmoprotectants (proline), which leads to a decrease in the value of water potential and moisture retention. At the same time, resumption of irrigation after one-week stress promoted the recovery of all studied physiological parameters.

This study was supported by the Russian Science Foundation, project no. 23-44-10019.

Key words: *barley, water deficiency, RWC, osmotic potential, proline.*

DETECTION AND IDENTIFICATION OF OIL'S MAJOR VOLATILE COMPOUNDS IN RAPESEED HYBRIDS BY GC-MS

***Toishimanov M.*[1,2], *Sapakhova Z.*[*1], *Daurov D.*[1,2], *Daurova A.*[1], *Abilda Zh.*[1], *Kanat R.*[1], *Shamekova M.*[1], *Zhambakin K.*[1]**

[1]*Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan*
[2]*Kazakh National Agrarian Research University, Almaty, Kazakhstan*

**E-mail:* m.toishimanov@ipbb.kz

Canola oil is a vegetable oil derived from rapeseed cultivars specifically bred for low erucic acid content. Canola oil can provide consumers with many health benefits that others cannot. For example, canola oil is low in saturated fat and high in polyunsaturated fat with a good ratio of omega-6 to omega-3, making it very suitable for cooking. Since canola oil has its specific function for the human body, it has become one of the most susceptible food materials adulterated with other lower quality vegetable oils, posing a serious threat to consumer health. Therefore, reliable tools and methods for analyzing the purity of edible vegetable oil are needed. Modern methods of gas chromatography combined with tandem mass spectrometry (GC-MS) are effective in obtaining the most comprehensive information on metabolites of potential nutritional sources. Using a N,O-bis (trimethylsilyl) trifluoroacetamide (BSTFA)-pyridine method and identified by their electron ionization (EI) and positive chemical ionization (PCI) spectra. Compounds were identified using XCalibur software (National Institute of Standards and Technology, USA). All obtained compounds compared with mass spectra libraries, which used in the process of analysis: NIST 2010 (National Institute of Standards and Technology, USA). A semi-quantitative assay of the metabolite profiles was performed by calculation of the total ion peak areas. About more 200 compounds were identified.

Determination of canola oil compounds in interspecific hybrid lines rapeseed (*Br.napus x Br.campestris*) revealed the content of most amino acid and fatty acid components compared to the results with a rapeseed (*Br.napus*) oil sample. In both sample Phenylpropanolamine, 1-(Trimethylsilyl)-3-[(trimethylsilyl)oxy]urea, L-Valine, Palmitic Acid, 9-Octadecenoic acid, (E), 1-Monomyristin, 2,3-Dihydroxypropyl 12-methyltridecanoate, 1-Monopalmitin, Octadecanoic acid, Glycerol monostearate were main components, which contained more than 25% of whole components. On the other hand, after hybridization Kris&Zolotoy canola oil sample amino acid contents increased, such as proline (13%), serine (2%), threonine (2%), oxoproline (7%). Also, significantly increased carbohydrates, such as D-Fructose (47%), D-(-)-Tagatose – (37,3%), d-Glucose (79,3%). Nevertheless, total fatty acid contents mostly decreased, such as Palmitic Acid (19%), 9,12-Octadecadienoic acid (Z,Z) (13%) 1-Monopalmitin (28%), Glycerol monostearate (34%)

In summary, the determination and identification of compounds in oil of interspecific rape hybrids by gas chromatography coupled with tandem mass spectrometry was investigated, where changes in carbohydrates and amino acids, and fatty acids in interspecific rape hybrids were detected.

Subsequently, an attempt will be made to derive perspective homozygous hybrid rapeseed plants via the isolated microspores culture. The results of this research will be used to further study changes in fatty acids and differential metabolites of rape hybrids and to identify stress response mechanisms in rapeseed hybrids.

DEVELOPMENT OF COLORED PERICARP RICE WITH DIFFERENT AMYLOSE CONTENTS FOR BREEDING

Usenbekov B.[1], Amirova A.[2], Baiseitova G.[3], Mynbayeva D.[1], Berkimbay Kh.[1]

[1]Institute of Plant Biology and Biotechnology, Almaty, 050040, Kazakhstan
[2]Al-Farabi Kazakh National University, 050040, Kazakhstan, Almaty
[3]Kazakh National Agrarian Research University, Kazakhstan, Almaty

E-mail: bakdaulet7@yandex.kz

Colored pericarp rice is an important dietary crop that is more beneficial to the human body than white rice. Regardless of the type of rice, the amount of amylose in a rice grain is a decisive indicator that determines the quality of rice. Evaluation of breeding material based on a protein marker makes it possible to quickly and efficiently select and control the transfer of desired traits from parental forms to hybrid populations. The advantage of protein as a genetic marker is conditioned by the fact that protein is the primary and direct product of the genetic system. Proteins are least susceptible to phenotypic variability and, accordingly, have a well-expressed biological specificity. Among the protein markers in plants, seed proteins occupy a special position. These highly polymorphic proteins make it possible to identify the gene pool of varieties with sufficient completeness, distinguish and register their biotypes and hybrid lines, and analyze varietal, hybrid, and natural populations. Rice proteins consist of four traditionally classified fractions depending on solubility: albumin (water-soluble), globulin (salt-soluble), glutelin (alkali-soluble), and prolamine (alcohol-soluble). Globulin (about 12%) and glutelin (about 80%) are the main components of rice protein.

As the objects of study were late-generation hybrids obtained by hybridizing Kazakhstani white rice varieties with foreign-bred rice varieties with colored pericarp (Black Rice (China), Mavr (Russia), Yir 5815 (Ukraine)) and doubled haploids from hybrids. The presence of a protein with a molecular weight of 60 kDa was identified on electrophoregram by visual evaluation of the gel. The intensity of this protein band is associated with a high or low amylose content. The quantitative content of amylose was determined by the Giuliano method: 1 ml of 96% ethanol (C2H5OH) and 9 ml of 1N NaOH were added to 100 mg of a rice sample ground into flour.

The results of the study of the protein spectrum showed the presence of a protein with a molecular weight of 60 kDa in the following hybrids: F_7 Yir 5815/Bakanassky *var. sundensis* Koern.; F_8 Mavr/Pak Li *var. bansmatica* Koern; F_8 Mavr/Bakanassky *var. Desvauxii* Koern; F_7 Yir 5815/Marjan *var. pyrocarpa* Alef.; and DH_2 F_2 Yir 5815/Marjan *var. pyrocarpa* Alef. This protein is a product of the Wx gene that controls the amylose content. Analyzing the results of electrophoresis and the amount of amylose, it was found that hybrid lines differed in amylose content. The studied hybrids were divided into five groups based on their amylose content: one of the studied hybrids was high in amylose, four had a medium amylose content, ten had a low amylose content, three had a very low amylose content, and six were glutinous. The results show that the hybrids obtained as a result of hybridization are true hybrids and as a result of long-term selection, the amylose content in the F7-F8 hybrids stabilized. The hybrids can be used in further breeding of rice with colored pericarp. It is planned to derive rice varieties with colored pericarp with different amylose content from these hybrids.

This research has funded by the Science Committee of the Ministry of Education and Science of the Republic of Kazakhstan Program-targeted financing BR18574149.

IN SITU FIELD GENEBANK OF KOK-SAGHYZ DANDELION (TARAXACUM KOK-SAGHYZ L.E. RODIN) - SOURCE OF HIGH RUBBER

***Kairat Uteulin*[1,*], *Gabit Bari*[2], *Bulat Kuluev*[3*]**

[1*]*Institute of Plant Biology and Biotechnology, St. Timiryazev 45, 050040 Almaty, Kazakhstan. E-mail: gen_uteulink@mail.ru (KU)*

[2*]*Laboratory of Microclonal Propagation of Plants, Kazakh National Agrarian Research University, St. Valikhanov 137, 050000 Almaty, Kazakhstan. E-mail: baracuda.co@mail.ru*

[3*]*Institute of Biochemistry and Genetics of UFRC RAS, 71 Pr. Oktyabrya, 450054 Ufa, Russia. E-mail: kuluev@bk.ru (BK)*

Dandelion kok-saghyz (*Taraxacum kok-saghyz* L.E. Rodin, TKS), as a source of high-quality natural rubber (NR), is recognized as a promising agricultural crop for cultivation in the temperate climate zone of the USA, Canada, Germany, the Russian Federation, Kazakhstan and other countries where the traditional source NK tropical tree Hevea (*Hevea brasiliensis* (Willd. ex A. Juss.) Muell. Arg.) does not acclimatize.

For the first time, in the center of origin of TKS - in the intermountain valleys of the Tien Shan, an *in situ* field gene bank of this rare species has been organized specifically for the long-term storage of its genetic resources, as well as for the collection and transfer of seeds to ex situ seed collections (Kazakh and foreign), to research, breeding programs. An *in situ* field genebank provides access to TKS genetic resources, while the removal of derivatives from Kazakhstan in situ TKS coenopopulations is significantly limited or prohibited. The in situ field gene bank of TKS ensures the protection of this rare species included in the Red Book of Kazakhstan. The in situ TKS field genebank was cleared of other low-rubber dandelion species.

The transfer of TKS seeds to Kazakh and foreign research centers ensures progress in fundamental research: biosynthesis of the biopolymer cis-1,4-polyisoprene (NC), genome sequencing, search for molecular markers, genetic transformation technologies, TKS genome editing.

This research was funded by the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan (grant no. AP 14870355).

CREATION OF A HIGHLY PRODUCTIVE TABLE GRAPE VARIETY BASED ON *IN VITRO* BIOTECHNOLOGY AND MOLECULAR LABELING

Zemtsova A.S.[1*], Aralbayeva M.M.[1], Aleksandrova A.M.[2], Kazybaeva S.Zh.[3], Tauyrbaeva Zh.T.[3], Kushnarenko S.V.[1], Romadanova N.V.[1]

[1] Institute of Plant Biology and Biotechnology, Almaty 050040, Kazakhstan
[2] M.A. Aitkhozhin Institute of Molecular Biology and Biochemistry, Almaty 050012, Kazakhstan
[3] Kazakh Scientific Research Institute of Fruit Growing and Viticulture, Almaty 050060, Kazakhstan

**E-mail:* zemtsovaaalina@gmail.com

Grapes (*Vitis vinifera* L.) is a fruit crop widely grown throughout the world and has high economic importance. The grapevine mainly suffers from diseases of a fungal nature: *Venturia pirina* Adern. and *Plasmopara viticola* (Berk. & Curt.) Berl. & de Toni. These pathogens harm the leaves, shoots, inflorescences and berries of grapes. Using the latest DNA technologies, it is possible to effectively develop the selection process in viticulture, which focuses on creating highly resistant varieties with the best adaptive characteristics to environmental factors, including pathogens of various diseases.

The objects of the study were cuttings of 17 selected grape hybrids obtained from the Kazakh Scientific Research Institute of Fruit Growing and Viticulture, in Almaty and Turkestan regions: 1) KV-2/9, 2) DV-10/11, 3) IV-6/9, 4) KII-1/29, 5) KVI-1/10, 6) XII-17/2, 7) VII-6/72, 8) VII-3/15, 9) XII-9/3, 10) XI-14/9, 11) III-7/15 , 12) III-02/22, 13) V-7/9, 14) XI-13/90, 15) KIY-1/64, 16) KV-2/35, 17) IV-4/74.

Based on the results of the selection work and molecular genetic analysis for the presence of resistance genes Rpv3 and Rpv12 using primers UDV-737, it was established that the Rpv3 gene is present in accessions 2, 4, 5, 9, 11, 12, 13, 14 and 17 , as well as in minor quantities in accession 6; the use of UDV-305 primers made it possible to determine the Rpv3 gene only in accession 12; the resistance gene Rpv12 was detected during PCR analysis using primers UDV-343 accessions 1, 2, 3, 4, 5, 6, 7, 8, 10, 12, 13, 14, 15.

Disease-resistant hybrids were initiated and propagated in *in vitro* culture on a modified medium Murashige and Skoog with 30 g/L sucrose, 1 mg/L 6-benzylaminopurine, 0.1 mg/L indolylbutyric acid, 0.1 ml/L gibberellic acid, 1.5 g/L Gelrite™, 4 g/L agar, pH 5.7. The highest multiplication rate was achieved in hybrids: III 02/22 (3.6), DV 10/11 (3.2), and KV 2/9 (3.0).

Further observations of the growth and development of plants during cultivation showed that in accessions III 02/22, DV 10/11 and KV 2/9 the average leaf size was 18 mm, the average leaf width was 13.5 mm, the average shoot length was 38 mm, which is 1.2 times higher than the values obtained on another studied medium. All shoots initiated into *in vitro* culture were tested for the presence of endophytic infection on specialized medium 523 with 8 g/L casein hydrolysate, 10 g/L sucrose, 4 g/L yeast extract, 2 g/L KH_2PO_4, 0.15 g/L $MgSO_4 \cdot 7H_2O$, 6 g/L Gelrite™, pH 6.9. As a result, after 1-2 weeks, contamination was detected in 45,2% of the shoots. Study will be continued with aseptic accessions.

The hybrid DV-10/11 showed high resistance to fungal diseases, and was also superior to other hybrids in a number of valuable economic characteristics (yield, sugar content, bunch weight, etc.). As a result, it was submitted for state variety testing as the ‘Nazerke’ variety.

Keywords: grape; *in vitro* culture; grapes diseases; grape breeding.

The work was carried out with financial support from the Ministry of Science and Higher Education of the Republic of Kazakhstan within the framework of the Scientific and Technical Program BR18574149, project IRN: 0123RK00028.

USE OF BIOREACTOR FOR EFFICIENT POTATO CULTIVATION

Volkov D.[1,2*], Daurov D.[1,2], Daurova A.[1], Sapakhova Z.[1], Shamekova M.[1], Zhambakin K.[1]

[1]Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan
[2]Kazakh National Agrarian Research University, Almaty, Kazakhstan

**E-mail:* volkovdmitriykz@gmail.com

Potato production is one of the key crop production sectors determining the food security of Kazakhstan. The Republic needs up to 700,000 tonnes of seed potatoes per year. In addition to seed potatoes grown in Kazakhstan, about 30,000 tonnes of seed potatoes are imported annually, with about 80% of this volume imported from the Netherlands through private companies. It is known that one of the main reasons for low potato yields is poor quality seed. The main requirement for quality seed is the absence of pathogenic and quarantine diseases. There are about 40 species of viruses and 2 viroids to which potatoes are susceptible. Viral disease infections have a strong effect on yield. Healthy and good quality potato seed is the basis of potato seed production. First of all, the seed must be free of pathogens. After obtaining virus-free plants in vitro through meristem culture, mini tubers are produced in most technological processes. The production of mini tubers is the final stage in the production of virus-free material. Recently, the production of micro tubers from which mini tubers are obtained as in vitro meristem plants has been frequently used. Microtubers are the result of in vitro cultivation of plants in an artificial nutrient medium.

Existing technologies for virus-free planting material production are not efficient enough. They require large premises where sterile conditions must be maintained, are energy intensive, and require bulky facilities. Cultivation in liquid culture results in better growth because a larger area of explants is in contact with the medium. The most efficient method for microtuber production in bioreactors is the temporary tidal immersion method in a liquid nutrient medium. Currently, several prototypes of simple and productive bioreactors have been developed such as T. I. S.

Production of virus-free potato seed material in Kazakhstan is mainly carried out through the isolation of apical meristems with subsequent production of in vitro plants on agarose nutrient medium and further formation of mini tubers from them in closed soil. Obtaining mini tubers from meristem plants is not carried out in the production of potato seed material in *vitro*, although this method is one of the successful methods of increasing potato material under *in vitro* conditions. Based on the above-mentioned problem, we set the aim to optimize liquid nutrient medium MS for *in vitro* potato micro tuber production from meristem plants with the prospect of introducing this procedure in the process of seed material production in seed farms. The obtained data are applicable at the initial stages of potato seed production, during the production of the first tuber generation of healthy material, in particular, during *in vitro* plant replication and microtuber production.

It was found that when four therapies were used, the most effective was chemotherapy with a ribavirin concentration of 40 mg/litre. The most optimal medium for *in vitro* production of plants from apical meristems was MS medium containing 2 mg/L kinetin. Monitoring was carried out for the major viruses PVM, PVS, PVX, and PVY, where 40 mg/l chemotherapy was the most effective. A sucrose concentration of 3% with the addition of the phytohormone kinetin and GA at concentrations of 2 and 0.5 mg/l was found to increase shoot and root length and number of internodes. As a result of optimizing the conditions for microtuber production in the bioreactor, the addition of sucrose 9% and kinetin at a concentration of 2 mg/l was the best option. Monitoring was carried out 6 months after micro tubers were obtained, the results of the analysis showed the absence of viral diseases. The results of the study may become a basis for the cultivation of plants in a bioreactor for mass production of virus-free potato micro tubers.

Session 4. Cellular and Genetic Engineering

Session 5. Genomics, Proteomics, and Bioinformatics

THE REGULATORY LANDSCAPE OF GENOME EDITING PLANTS WITH FOCUS ON REGULATORY POLICIES: WHERE WE ARE HEADING

Allah Bakhsh

Centre of Excellence in Molecular Biology, University of the Punjab, Lahore, Pakistan

**E-mail:* allahbakhsh@cemb.edu.pk

Modern day techniques have enabled scientists to break the conventional barriers and combat insect pests and diseases of crop plants by adopting novel molecular approaches. The crops plants are exposed to insect pests and diseases from emergence to harvesting. The scientific literature suggests that 35-40 % yield losses are incurred to crop yield because of insect pests and diseases. The researchers are exploiting new crop protection technologies (especially genome editing) for crop improvement against pests and diseases. Recently, we have witnessed the advent of genetically engineered crops in the market. Overall, genome editing technology has proven robust against insect pests and diseases worldwide. The advanced and developing countries are adopting different strategies to regulate the genome edited crops based on the type of mutation induced. The regulation of genome-edited crops aims to ensure that these products are safe, environmentally sustainable, and contribute to food security while also addressing public concerns and fostering innovation in agriculture. I will present data on recent genome editing approaches and will also talk about how these techniques can efficiently be used as modern crop protection tools. The regulatory landscape of the genome edited crops and future perspective will also be discussed during the talk.

Keywords: Genome editing, CRISPR-Cas systems, site directed nucleases, crops

SITE-DIRECTED GENOME MODIFICATION OF GRAIN DORMANCY GENES IN BARLEY

Hiroshi Hisano

Institute of Plant Science and Resources, Okayama University, Kurashiki, Japan

E-mail: hiroshi.hisano@okayama-u.ac.jp

Site-directed mutagenesis is a promising new breeding technique for efficiently producing desired mutants. Barley requires longer grain dormancy to increase tolerance to pre-harvest sprouting, while too long grain dormancy is unsuitable for malt production. In this study, our research group employed CRISPR/Cas9-based site-directed genome modification to generate mutants of the *Qsd1* (*QTL seed dormancy 1*) and *Qsd2* genes for fine-tuning grain dormancy in barley. Two guide-RNAs (gRNAs) were designed for each exon of *Qsd1* and *Qsd2*, and barley transformation was performed by the *Agrobacterium*-mediated method. As a result, 19 and 24 mutation events were obtained for each gene, respectively. Molecular analysis of the T_1 generation confirmed that the mutations were inherited. These progenies included individuals in which the mutation was fixed as homozygous and the transgene was removed by segregation. After six weeks of after-ripening treatment of grains at 25°C, germination tests showed that all control lines, including the non-transgenic lines, had a germination rate of over 90%. However, the *Qsd1* and *Qsd2* mutants showed 0% for seven days after imbibition. As well, grains that did not germinate for seven days finally germinated when germination was hastened with 3% hydrogen peroxide. This suggested that the mutant grains were not lethal and had an extremely long dormancy period. These results indicate that induced mutations in *Qsd1* and *Qsd2* inhibit rapid grain germination and may contribute to breeding for pre-harvest sprouting tolerance in barley.

A FABA BEAN PAN-GENOME FOR ADVANCING SUSTAINABLE PROTEIN SECURITY

Auvinen P.[1], Chang W.[1,2], Holm L.[1], Jääskeläinen M.[1,2], Khazaei H.[3], Laine P.K.[1], Paulin L.[1], Salgado M.[1], Stoddard F.[2,4], Tanskanen J.[2,3], Törönen P.[1], Schulman A.H.[1,2,3*]

[1]Institute of Biotechnology, University of Helsinki, Helsinki, Finland,
[2] Viikki Plant Science Centre (ViPS), University of Helsinki, Helsinki, Finland
[3]Natural Resources Institute Finland (LUKE), Helsinki, Finland
[4]Department of Agricultural Sciences, Faculty of Agriculture and Forestry, University of Helsinki, Helsinki, Finland

Many parts of the world suffer from a deficit in local plant protein production, relying on imports subject to trade disruption and to the environmental consequences of rainforest clearance for fields in the countries of export. Having an average protein content of 29%, faba bean (*Vicia faba* L.) is a widely adapted protein crop that could substantially improve protein sovereignty and security, both for food and for feed. It is well suited to regions worldwide where it is a traditional, staple food. Moreover, its range of climatic adaptation is complementary to soy, which is adapted to warm regions and does poorly where faba bean does well. Faba bean like other crops, however, faces unprecedented challenges from the biotic and abiotic stresses made worse by climate change. Breeders need new tools to develop sustainable, secure crops more efficiently, which have the properties processers need [1]. The large size of the faba bean genome (13 Gbp diploid) has until recently hindered a high-quality assembly, but new advances have enabled production of a highly contiguous reference genome [2]. In the PanFaba project, we are now producing a pan-genome spanning the diversity space of the species to deliver the insight and tools needed for rapid improvement of faba bean. We have assembled the genomes of five accessions; these will be complemented by at least 15 others in an international effort. The assemblies are complemented by transcriptomics and gene annotation. The PanFaba project will enable the high-resolution linkage of genotype to phenotype that is needed to improve faba bean as a protein crop and adapt it to likely future climatic conditions in various regions worldwide.

1. Khazaei H, O'Sullivan DM, Stoddard FL, Adhikari KN, Paull JG, Schulman AH, Andersen SU, Vandenberg A. 2021. Recent advances in faba bean genetic and genomic tools for crop improvement. Legum Sci. 3:e75. doi: 10.1002/leg3.75.

2. Jayakodi M, Golicz AA, Kreplak J, Fechete LI, Angra D, Bednář P, Bornhofen E, Zhang H, Boussageon R, Kaur S, Cheung K, Čížková J, Gundlach H, Hallab A, Imbert B, Keeble-Gagnère G, Koblížková A, Kobrlová L, Krejčí P, Mouritzen TW, Neumann P, Nadzieja M, Nielsen LK, Novák P, Orabi J, Padmarasu S, Robertson-Shersby-Harvie T, Robledillo LÁ, Schiemann A, Tanskanen J, Törönen P, Warsame AO, Wittenberg AHJ, Himmelbach A, Aubert G, Courty PE, Doležel J, Holm LU, Janss LL, Khazaei H, Macas J, Mascher M, Smýkal P, Snowdon RJ, Stein N, Stoddard FL, Stougaard J, Tayeh N, Torres AM, Usadel B, Schubert I, O'Sullivan DM, Schulman AH, Andersen SU. 2023. The giant diploid faba genome unlocks variation in a global protein crop. Nature. 615: 652-659. doi: 10.1038/s41586-023-05791-5.

THE ROLE OF VIRUSES IN GENOME EVOLUTION AND ADAPTATION

Ruslan Kalendar

National Laboratory Astana, Centre for Life Sciences, Nazarbayev University, 53 Kabanbay batyr Ave., 010000, Astana, Kazakhstan

E-mail: ruslan.kalendar@nu.edu.kz

The question of the living has always been a central scientific question and will occupy more and more of science in the future. It also includes biocommunication research that deals with sign-mediated interactions between cells, cellular elements, organs, and organisms, in which molecular biological, sociological, linguistic, and, finally, epistemological and philosophical aspects complement each other. One milliliter of seawater contains 1 million bacteria, 10 to 100 times as many viruses, and countless viral particles and RNA fragments, about the functions of which we know almost nothing in a systemic context. Although viruses can spread through the air, water, and soil, they remain functionally linked to their host organisms. They are part of the organism but not directly related to it spatially. As the phylogenetic analysis shows, practically all organisms of all kingdoms of organisms are infected with viruses or are densely populated by them from the very beginning of life. A better understanding of the genomes of viruses has shown that most of their genes are not found in animals, plants, or bacteria. 90% of virus genomes did not detect any relationship with known gene sequences, i.e., these are new viruses with their properties. This means that viruses can create complex genes. Mostly, they are assembled from pieces that mostly come from other viruses. The oceans are full of such viruses. Thus, viruses are a super genome with a high degree of variability. The recently discovered giant viruses represent a revolution in modern virology: these organisms are a transitional form between viruses and bacteria and, therefore, beneficial for our understanding of evolution. They are larger than many bacteria and have up to 2500 genes (Pandoravirus). The Pandoravirus genome contains a strange mixture of largely unknown nucleotide sequences; for 93% of pandora genes, there are no homologs in gene databases, which is a puzzle to explore. Horizontal gene transfer is widespread in animals and humans and gives rise to tens or hundreds of active genes. Surprisingly, horizontal gene transfer is uncommon and has contributed to the evolution of many, perhaps all, animals. New genetic combinations always reveal the basis for the "new" for innovative, adaptive, modification, and developmental processes. Human health also critically depends on the diversity of bacteria in our gut. Adaptation, evolution, and health are driven by genetic variation. All gene physiology, genetic recombination, translation, transcription, and transposition, as conserved within the eukaryotic cell, were originally external viral processes. Thus, viruses are, genetically, one of the decisive factors in evolutionary innovation and species diversity. Diversity is always an indicator of vital and healthy ecosystems.

ADVANCEMENTS IN COMPUTATIONAL PIPELINES FOR GENETIC DIVERSITY ANALYSES AND GENOMIC PREDICTIONS: IMPLICATIONS FOR LEGUME CROP RESEARCH

Gentzbittel L.*[*1], Boldyrev S.[1], Zamalutdinov A.[1], Habib Y.[1], Balapanov I.[1], Ben C.[1]

[1]*Skolkovo Institute of Science and Technology, Project Center for Agro Technologies, Moscow, Russia*

**E-mail*: l.gentzbittel@skoltech.ru

Computational pipelines revolutionize genetic diversity analyses and genomic predictions, noyably in legume crop research. Three types of technologies and pipelines streamline genome-based approaches.

The first set of methods involve computational pipelines essential for managing and storing Single Nucleotide Polymorphism (SNP) data from diverse platforms such as whole genome sequencing, Genotyping-by-Sequencing (GBS), or chip arrays. These pipelines encompass procedures like population structure analysis, haplotype inference, and imputation, forming a robust foundation for genetic analyses.

The second set of pipelines implements sophisticated multivariate statistical machine learning methods, often utilizing R. These methods identify genetic variants associated with crucial traits and predict breeding values. Success depends on high-quality phenotypic data. Genomic predictions expedite breeding cycles by accurately forecasting complex traits like yield, disease resistance, and nutrient content, aiding in the development of resilient crop cultivars suitable for diverse environmental conditions and empowering breeders to make informed decisions.

The third set of tools comprises tailored software solutions to manage the diverse data from breeding programs. Handling vast amounts of phenotypic data from greenhouse and field experiments is crucial for reproducible research. Digital data recording tools, plant breeding data management platforms, and crop ontology provide essential infrastructure for organizing and analyzing phenotypic data. This involves developing relational databases and intuitive interfaces to catalog phenotypic information efficiently, track varieties or entries, and store data from field experiments. Robust statistical analyses are pivotal in extracting meaningful insights from complex datasets to target breeding strategies. Additionally, platform-facilitated data interoperability ensures seamless integration and utilization of genetic variation data across different breeding programs, enhancing collaboration and knowledge sharing within the scientific community.

In conclusion, computational pipelines are crucial in advancing genetic diversity analyses and genomic predictions in crop breeding. By providing scientists and plant breeders with tools to navigate genetic landscapes, these pipelines facilitate the development of improved crop varieties, meeting evolving agricultural demands and ensuring food security.

UTILIZATION OF NEW TECHNOLOGIES IN ENHANCING CROP QUALITY, PLANT MOLECULAR FARMING, AND SAFEGUARDING BIODIVERSITY

Manabayeva S.A.

National Center for Biotechnology, Astana, Kazakhstan

E-mail: manabayeva@biocenter.kz

Breakthroughs in genome engineering began with the development of nucleases capable of precisely recognizing and cleaving target DNA. Zinc finger nucleases (ZFNs) and transcription activator-like effector nucleases (TALENs) were early endonucleases used for genome editing. While effective, there is a need for robust, affordable, and easily engineered technologies. CRISPR offers an alternative strategy, utilizing the unique CRISPR-Cas9 technology. This system uses Cas9 as "molecular scissors" and guide RNA for targeted genome editing by creating double-stranded DNA breaks that are subsequently repaired by cellular mechanisms. We have successfully used CRISPR/Cas9 technology to edit the potato genome, achieving changes in starch quality by completely disrupting the GBSS gene.

The development of plant biotechnology allows plants to serve as viable alternatives for expressing proteins with post-translational modifications. *The Tomato bushy stunt virus* (TBSV) genome-based viral vector is valuable for the rapid production of recombinant proteins. The TBSV vector system, in which the p19 protein inhibits post-transcriptional silencing and enhances gene expression, is used to produce the envelope glycoprotein gp51 of *Bovine leukemia virus* in *Nicotiana benthamiana* plants for diagnostic purposes.

The flora of Kazakhstan includes more than 13 thousand species. About 500 species are endemic. Several strategies are used to protect biodiversity. One of them is *in-situ* conservation, which allows plants to be preserved in their natural habitat. In Kazakhstan, the established natural habitats include state nature reserves, state national nature parks, state botanical gardens and state protected areas. To halt the continuing loss of plant biodiversity, the Global Strategy for Plant Conservation promotes the development of both *in situ* and *ex situ* conservation methods for rare and endangered species. *Ex situ* conservation preserves plants them away from their natural habitats. *In vitro* technology for plant conservation is an important technology. In our study, the main objective was to introduce rare and endangered *Tulipa* and other species *in vitro* for ex *situ* conservation. Protocols for sterilization, micropropagation, slow-growth *in vitro* conservation and cryopreservation have been optimized.

DNA barcoding is a widely used and efficient tool for the rapid and inexpensive identification of plants. Its application to the identification of endangered wildlife allows enable researchers and consumers to make informed biodiversity management. The internal transcribed spacer (ITS) of nuclear ribosomal DNA and the plastid sequences rpoB, rpoC1, rbcL, matK, psbK-psbI, trnH-psbA, atpF-atpH are the most commonly used DNA markers in plant phylogenetic and DNA barcoding analyses, and they have been recommended as the core DNA barcode. DNA barcoding can be used to combat illegal wildlife trade. In our research we have DNA markers to analyze endemic and endangered species and unravel phylogenetic relationships within the species.

SOLANUM TUBEROSUM L. GENOME EDITING AS AN INSTRUMENT FOR THE CROP IMPROVEMENT

Lebedeva M.[1], Karlov V.[1], Komakhin R.[1], Konovalova L.[1], Ivanova L.[1], Volkov M. [1], Monakhova, Y.[1], Zlobin N.[1], Klepikova A.[2], Babakov A.[1], Taranov V.[1] *

[1]All-Russia Research Institute of Agricultural Biotechnology, Moscow, Russia
[2]Institute for Information Transmission Problems of the RAS, Moscow, Russia

Solanum tuberosum L. is an important agricultural crop. Complex tetraploid genome and difficult crossing strongly hinder potato breeding. Modern instruments for genomic manipulations, such as CRISPR/Cas9, enable to speed up this process. However, editing efficiency should be very high in order to affect all alleles of the polyploid genome.

In our research we successfully applied CRISPR/Cas9 genome editing system to inactivate few genes, which influence on valuable potato traits: *StLFY, StDRM6-1* and *StVLNV.*

StLFY in potato is a key regulator of the transition to flowering and tuberization. *StLFY* knockout led to phenotypic alterations both in inflorescences and stolons. These lines can be used as a model for tuberization regulation studies.

Second part of work included a multiplex potato genome editing in order to knockout *StDRM6-1* and *StVLNV* genes simultaneously. It is believed, that DMR6 protein involved in a suppression of plant immune response based on the salicylic acid pathway. Enormous increase of the *StDRM6-1* expression is taken place by *Phytophthora infestans* likely in order to promote infection. *StVLNV* encodes a vacuolar invertase — a key ferment in cold-induced sweetening in potato tubers. High-temperature processing of these tubers results in dark-colored products with high amount of acrylamide, a neurotoxin and potential carcinogen. Knockout of the both genes should led to significantly improvement of the selected potato lines.

This work was partially funded by the Comprehensive Research Program “Development of Potato Breeding and Seed Production”.

TOOLBOX OF PLANT PROTEOMICS – CURRENT STATE AND PERSPECTIVES

Frolov A.A.

K.A. Timiryazev Institute of Plant Physiology, Russian Academy of Sciences, Moscow, Russia

Email: afrolov0375@yandex.ru

Proteomics is one of the powerful methodological platforms of post-genomic research and represents a versatile tool in the current plant biology. In comparison to other biological objects, plants demonstrate impressing chemical diversity of their tissues, representing thereby much more complex matrices for proteome characterization. This complexity and diversity, as well as far incomplete coverage of plant objects with sequencing programs, represent the major challenge of plant proteomics today. Therefore, in our work we focus on implementation of the state-of-the-art sample preparation techniques and digestion protocols and optimization them for the specific tasks of current research. For this, we implement detergent-assisted digestion and filter-aided sample preparation in the plant proteomics workflow. At the next step, we optimized these techniques for different plant tissues, including such difficult matrices as seeds or root nodules. Finally, we adjusted our data processing workflows to the work with incompletely characterized organisms. Having these powerful tools in hand we could make an as essential step forward in understanding of plant response to various stresses and plant microbial interactions, such as legume-rhizobial symbiosis and arbuscular micorriza.

HAIRY ROOTS INDUCTION AND REGENERATION OF TRANSGENIC NON-MODEL PLANTS *FAGOPYRUM ESCULENTUM*

Omelchenko D.O. [†1] ****, Glagoleva E.S.*** [†1,2]***, Omelchenko L.V.*** [1,3]***, Abdulkina L.R.*** [1]***, Logacheva M.D.*** [1,3]

[1] *Laboratory of Plant Genomics, Institute for Information Transmission Problems, Moscow, Russia*
[2] *Department of Plant Physiology, Faculty of Biology, Lomonosov Moscow State University, Moscow, Russia*
[3] *Center for Molecular and Cellular Biology, Skolkovo Institute of Science and Technology, Moscow, Russia*

† - equal contribution

Buckwheat (*Fagopyrum esculentum* Moench) is a pseudo-cereal crop that belongs to the Polygonaceae family. Due to its high nutritional value and bioactive compounds, it is widely used in the food and pharmaceutical industries. Gene editing offers opportunities to introduce desirable traits and remove undesired ones to generate new, improved buckwheat varieties faster than classical breeding. One of the approaches to obtain genetically modified buckwheat is through transformation and gene editing, followed by regeneration of transgenic plants through hairy root culture.

Two self-compatible buckwheat varieties KK8 и Shinano-SC were used in this study. Agrobacterium rhizogenes strains A4 and R1000 were tested for induction of hairy roots and transfer of T-DNA. The binary vectors used in this work included GFP and BAR expression cassettes for selection of transformed plants, as well as CRISPR/Cas9 expression cassettes for knockout of DFR and LFY genes. All vectors and expression cassettes were created using the modules of the MoClo Toolkit and CRISRP Plants kits (Addgene) cloning system.

Both *A. rhizogenes* strains efficiently induced hairy root growth in buckwheat explants, but only hairy roots induced by R1000 strain had green fluorescence, i.e., successfully transferred the T-DNA from the binary vectors into the plant genome. Callus cultures from hairy roots of *F. esculentum* can be obtained with a different set of hormones, but we found the classical composition of MS3 medium with 2 mg/L 2,4-Dichlorophenoxyacetic acid and 2 mg/L Kinetin for callus induction to be optimal. For regeneration from callus culture, the MS3 medium composition including 6-Benzylaminopurine (2 mg/L), Kinetin (0.2 mg/L), and Indole-3-acetic acid (0.2 mg/L) was optimal. It is also noteworthy that the fluorescence of the GFP marker gradually disappeared as the regenerants grew, even though the morphogenic callus from which they were derived was fully fluorescent and the regenerated plants still contained T-DNA based on PCR test. Regenerated plants of the KK8 и Shinano-SC varieties were successfully acclimated to non-sterile soil conditions.

SEQUENCE VARIATION OF SLMLO GENES IN TOMATO

***Pozharskiy A.S.*[1, 2], *Kostyukova V. S.*[1], *Gritsenko D.A.*[1]**

[1]*Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan*
[2]*Al Farabi Kazakh National University, Almaty, Kazakhstan*

E-mail: aspozharsky@gmail.com

MLO (mildew resistance locus *o*) is the family of transmembrane proteins involved into various signal transduction processes in plants as receptor molecules. Particularly, some MLO homologs are known to be a crucial part of interaction between plants and Erysiphaceae fungi, the causal agents of powdery mildew. Natural and induced loss-of function mutations in the corresponding genes were shown to be responsible for high levels of resistance against powdery mildew in various mono- and dicotyledon plant species. In tomato, 16 *SlMlo* genes were described, of which *SlMlo1, SlMlo5,* and *SlMlo8* have been identified as associated with susceptibility agains powdery mildew caused by *Oidium neolycopersici. SlMlo1* is considered the most promising target for selection and genetic engineering as it is the primary susceptibility factor, whereas *SlMlo5* and *SlMlo8* confer minor effects. In the present work, we have used the publicly available data on genomic variation of tomato based on the Varitome project by Solanum Genomics Consortium, to identify polymorphic sites within *SlMlo* genes, in respect to their coding sequences. Reference tomato genome assembly SL2.5 and Bsftools and Samtools command line software were used to obtain gene sequences by applying the variants of the respective regions to the reference. As a result, 166 sequences from various tomato accessions were obtained for each of 16 genes of *SlMlo* family. *SlMlo5* gene (Solyc03g095650) was found to be the most variable, with up to 56 used variation per individual sequence, with total sequence length 8145 bp. The number of variants in *SlMlo1* gene (Solyc04g049090) has not exceeded 12 per sequence, with total sequence length 6526 bp. The number of variants in *SlMlo8* gene (Solyc11g069220) was up to 34 per sequence, with total sequence length 7194 bp. In the observed sequences, only small amount of variation was to found in coding sequences, predominantly at the end part of the predicted transcript. This implies only limited effect of gene variations of MLO protein functions, which are to be further evaluated in relation to available tomato phenotypes.

WHOLE GENOME-BASED EVALUATION OF *VICIA SP* GENETIC DIVERSITY

***Zamalutdinov A.V.*[1], *Boldyrev S.V.*[1], *Maalouf F.*[2], *Rubiales D.*[3], *Vaz Patto M.C.*[4], *Fustec J.*[5], *Gentzbittel L.*[1], *Ben C.*[1]**

[1]*Skolkovo Institute of Science and Technology, Moscow, Russia*
[2]*International Center for Agricultural Research in the Dry Areas (ICARDA), Beirut, Lebanon*
[3]*Institute for Sustainable Agriculture, CSIC, Avda. Menéndez Pidal s/n, Córdoba, Spain*
[4]*Instituto de Tecnologia Química e Biológica António Xavier, Universidade Nova de Lisboa, Oeiras, Portugal*
[5]*USC 1432 LEVA, Ecole Supérieure des Agricultures, INRAE, Angers, France*

E-mail: Alexey.Zamalutdinov@skoltech.ru

Legumes are an important source of protein and are known for their root nodules with symbiotic nitrogen-fixing bacteria. They play a multifunctional role in agroecosystems, improving the coupling of nitrogen, carbon and phosphorus cycles, limiting erosion, and helping to cope with resource scarcity and sudden stress. Inter- and mix- cropping with legumes leads to a better use of natural abiotic resources such as water and nitrogen, especially in low-input cropping systems. However, the use of such systems is limited by the lack of suitable varieties. Here we focused on two *Vicia* species: *Vicia sativa*, which is mainly used as green manure and fodder and *Vicia faba*, which is used as a crop and a valuable component of ecosystems due to its high nitrogen fixation rate and nectar-rich flowers. Studying their genetic diversity is a crucial step in designing a breeding programme.

We genotyped a collection of 281 *V. sativa* and 300 of *V. faba* accessions using the GBS approach. We tested several enzyme combinations commonly used for the GBS in different plant species (HindIII-FaeI, PstI-MspI, ApeKI). We chose HindIII-FaeI because it produces more SNPs and a wider coverage of the genome.

For the *V. sativa* collection, we obtained 272 643 high quality SNPs for 277 accessions as a result of an extensive SNP filtering process. Based on this set, the estimated number of subpopulations within the diversity panel is 9, according to Admixture and k-means clustering. In *V. faba* collection 309 379 high-quality SNPs were obtained for 294 accessions. Using this set we estimated that the number of subpopulations within the diversity panel is equal to 3. In both collections, the accessions are well clustered according to DAPC.

The results obtained can be used for further studies to define breeding targets, such as GWAS and genomic selection, as well as for the creation of core collections.

Project is supported by DiVicia project, PRIMA (Partnership for Research and Innovation in the Mediterranean Area), N°2019-section2-9.

HIGH-THROUGHPUT SEQUENCING AS SENSITIVE APPROACH FOR THE DETECTION VIRUSES AND VIROIDS IN POTATOES

Kapytina A.*, Mendybayeva A., Kenzhebekova R., Gritsenko D.A

Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan

Potatoes, a vital agricultural crop cultivated worldwide, encounter substantial challenges due to viral diseases. Standard diagnostic methods like ELISA, PCR, or targeted sequencing provide promising levels of sensitivity and specificity. However, their effectiveness relies on the availability of specific primers or sera, which in turn requires prior knowledge about the pathogen being diagnosed. However, accurate diagnosis faces challenges due to the emergence of genetic mutations and varying concentrations of viral components in co-infections. High throughput sequencing (HTS) is a powerful technology capable of identifying all viruses present in a sample without prior knowledge of the targeted pathogens. This approach offers significant advantages in diagnosing viral infections, particularly in cases where multiple pathogens may be present or when dealing with emerging infectious diseases. Oxford Nanopore Technologies (ONT) offers a solution through direct, real-time sequencing. This advancement enhances virus detection, surveillance, identification of new viruses, and research on virus evolution.

In this study, we used the HTS technique to perform viral metagenomics analysis of the potato fields in Kazakhstan. Before, only *Potato leafroll virus* (PLRV), *Potato virus X* (PVX), *Potato virus Y* (PVY), *Potato virus S* (PVS), and *Potato virus M* (PVM) had been studied in the country. In the present research, 370 samples of potato samples were analyzed from both north and south fields, which are the most important potato-producing regions in Kazakhstan. rRNA-depleted total RNA was utilized as the starting material to construct cDNA libraries, aiming to detect even the less abundant viruses. The obtained sequences were compared with NCBI Virus database, including 249,328 genome sequences of plant viruses. In addition to the well-known viruses *PLRV, PVY, PVX, PVS,* and *PVM*, this study unveiled the presence of Potato rough dwarf virus (PRDV), Tobacco vein clearing virus (TVCV), and Potato spindle tuber viroid (PSTVd) for the first time. PLRV and PVM was detected less frequently, while *TVCV, PVX*, and *PVY* were predominant in the fields. *TVCV* was detected in every field, with the sequencing depth ranging from 5 to 315X according to different fields. Additionally, *PSTVd* was also detected in the northern region of Kazakhstan. During detection, ONT enabled the sequencing of the whole genome of *PVX*, with sequencing depth exceeding 250X and genome coverage of 150X.

Our results demonstrate that high-throughput sequencing technology supplies a valuable diagnostic tool for identifying various virus species. The technology offers rapid insight into the spectrum of plant viruses previously undetected in Kazakhstan. Implementing HTS for virus detection will enhance current diagnostic methods for identifying fast-evolving pathogens or newly emerged ones.

METAGENOMIC ANALYSIS OF FRUIT TREES IN KAZAKHSTAN

***Gritsenko D.*[1]., *Taskuzhina A.*[1,2]., *Kerimbek N.*[1,2]., *Nizamdinova G.*[1]., *Pozharskiy A.*[1,2]**

[1]*Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan*
[2]*al-Farabi Kazakh National University, Almaty, Kazakhstan*

E-mail: d.kopytina@gmail.com

Plant diversity represents a valuable resource that safeguards the national security of any country by serving as the primary source of agricultural products. Losses in biodiversity can lead to the disruption of crucial ecological processes, ultimately resulting in significant changes to habitats that are conducive to sustaining life on a global scale. Wild trees and their hybrids hold significant value as a reservoir of genetic resistance against both biotic and abiotic stressors, playing the pivotal role in breeding programs worldwide. Natural fruit tree forests are esteemed as the most valuable plant communities in terms of their uniqueness, genetic potential, ecological, scientific, and practical significance. The safety of wild populations is closely linked to the management of pests and pathogens distribution among crops.

In the present research, the metagenomic analysis was performed for large populations of wild apples, hawthorn, mountain ash, cultivated apples and pears. More than 1000 samples were analyzed. Viral metagenomics analysis was performed by RNA sequencing using Oxford Nanopore technology on MinION platform. Apple stem pitting virus, Apple stem grooving virus, Tomato ringspot virus, and Apple chlorotic leaf spot virus were identified in cultivated apples, while wild apples were infected predominantly by Apple chlorotic leaf spot virus. Additionally, in wild and cultivated apple trees, Apple rubbery wood virus 1 and 2, Apple necrotic mosaic virus and Apple latent spherical virus were identified in Kazakhstan for first time. The number of reads did not exceed 10.

DNA barcoding on bacteria by whole 16S sequences revealed the pathogenetic and endophytic microflora of every population. Pathogenic and endophytic microflora included bacteria of the genus *Pseudomonas* (310,449 reads), *Pantoea* (157,984 reads), *Curtobacterium* (51,842 reads), *Stenotrophomonas* (11,789 reads), *Serratia* (8,289 reads), *Achromobacter* (2,958 reads) and *Erwinia* (1,713 reads). *Erwinia amylovora* accounted for 39 reads out of 1,716. Among plants in wild populations, the endophytic microflora predominantly consists of *Pseudomonas fluorescens*. It is worth mentioning that the composition of pathogenic and endophytic microflora varied depending on the plant organ studied.

ADDRESSING S-NITROSYLATION IN WHEAT ROOTS: BOTTOM-UP PROTEOMIC APPROACH

Lukasheva E.*[*1], Mazina A.[2], Gorbach D.[3], Frolova N.[3], Shumilina J.[3], Minibaeva F.[2] and Frolov A.[3]

[1]Saint-Petersburg State University, Saint-Petersburg, Russia
[2]Kazan Institute of Biochemistry and Biophysics, Kazan, Russia
[3]K.A. Timiryazev Institute of Plant Physiology, Russian Academy of Sciences, Moscow, Russia

Proteomic, as well as transcriptomic and metabolomic, represent powerful tools of post-genomic researches. It gives a direct access to the molecular mechanisms underlying plant response to environmental and developmental signals and protein post-translation modifications (PTMs) are one of the most wide-spread regulatory networks involved in these responses. Such PTM as protein S-nitrosylation of sulfhydryl (thiol) groups by nitric oxide is a protein activity regulator. Protein S-nitrosylation involves in a multivarious processes such as seed germination, phytohormones, including auxin, cytokinin and abscisic acid, leaf senescence, flowering time and root development (*J Integr Plant Biol.* 2019 Dec;61(12):1206-1223. doi: 10.1111/jipb.12780).

Therefore, here we address S-nitrosylated proteome bread wheat roots (*Triticum aestivum L.* variety Kazanskaya Yubileinay) (*Life* 2023, *13*(10), 2024; doi:10.3390/life13102024). Intact roots of 4 days old seedlings were incubated in distilled water (control), 1 μM antimycin A (AA)-a mitochondrial inhibitor, 1 mM KNO_2, a NO donor, and in 5 mM S-nitrosoglutathione (GSNO), a biological source of NO as positive control and harvested. Water-soluble proteins were isolated from the root tips and we applied a complex approach including polyacrylamide gel electrophoresis (PAGE) and immunoblotting with monoclonal antibodies, which specifically recognize bound forms of S-nitroso-L-cysteine, followed by protein identification in visualized electrophoretic zones (bands) using the bottom-up proteomics approach, i.e., tryptic digestion of individual bands with subsequent UHPLCQqTOF-MS/MS analysis relied on data-dependent acquisition experiments. With analysis of tryptic protein hydrolysates were identified a total of 298 proteins. More than half of these proteins (177 entries) were present in all experimental groups. An analysis of the group-specific changes in the root proteome revealed 35 unique proteins in the roots treated with antimycin A, 14 proteins in the roots treated with KNO2, and 44 proteins in the roots treated with GSNO. Functional annotation of identified proteins is discussed.

PLANT METABOLOME STUDY: RECENT ANALYTICAL TOOLS AND TECHNIQUES

***Frolova N.V.*[1], *Orlova A.A.*[1], *Erofeeva N.O.*[2], *Bilova T.E.*[1,2] *and Frolov A.A.*[1]**

[1]*K.A. Timiryazev Institute of Plant Physiology, Russian Academy of Sciences, Moscow, Russia*
[2]*St. Petersburg State University, St. Petersburg, Russia*

E-mail: frolovanadja@yandex.ru

Metabolomics is now widely regarded as a large-scale and sensitive approach to provide information on the composition and dynamics of the plant metabolome. This information has even more applications for both phenotyping and chemotyping of plants, for understanding the mechanisms behind the plant response to various environmental stresses. Therefore, metabolomics essentially impacts on breeding the next-generation crops with improved stress tolerance traits. The plant metabolome is featured with a complex pattern of primary and secondary metabolites, including ionic inorganic compounds, hydrophilic carbohydrates, amino acids, organic acids, and compounds bound to hydrophobic lipids. The high complexity of the plant metabolome imposes essential challenges in development of the analytical tools for efficient separation and identification of individual metabolites. The huge volume of data generated by these comprehensive analytical techniques requires powerful statistical and bioinformatics tools, as well as representative databases for their efficient processing and post-processing. To date, an integrated approach to characterize the dynamics of primary and secondary metabolome is established in the Laboratory of Analytical Biochemistry and Biotechnology in the K.A. Timiryazev Institute of Plant Physiology of the Russian Academy of Sciences. Our analytical strategy assumes analysis of primary thermostable and thermolabile metabolites by gas chromatography coupled on-line to the electron ionisation quadrupole mass spectrometry (GC-EI-Q-MS) and ion-pair reversed phase high-performance liquid chromatography, coupled online to tandem mass spectrometry accomplished with a triple-quadrupole mass analyser (RP-IP-HPLC-QqQ-MS/MS). Secondary metabolites are analysed by RP-HPLC coupled on-line to tandem mass spectrometry in a hybrid mass analyzer based on a combination of electrodynamic and orbitrap ion traps (RP-UHPLC-ESI-LIT-Orbitrap-MS/MS). Identification of the primary thermally stable metabolites relies on the spectral similarity search with consideration of the characteristic retention times (t_{RS}), and retention indeci (RIs) of analytes in experimental samples and standard substances of known mass spectrometric libraries of NIST (National Institute of Standards and Technology), GMD (Golm Metabolome Database) and in-house library based on defined mixtures of authentic standards. Analysis of the primary thermally labile metabolites relies on multiple reaction monitoring (MRM) experiments and representative panel of relevant authentic standards using MultiQuant™ 3.0.3 software. Processing of the secondary metabolite data was accomplished with the MS-DIAL software. The result matrices constructed for primary and secondary metabolites are processed with the online tool MetaboAnalyst 6.0. While analysis of the dynamics of primary and secondary metabolome (including detailed deciphering the impact of individual metabolic reactions) might give access to the key regulatory pathways and possible mechanisms behind the metabolic shifts accompanying plant development, ageing and stress response, the involvement of genomics, proteomics, and physiology data essentially contributes to the understanding the ontogenetic and ecological plasticity of the plant metabolome.

PIPELINE FOR PROCESSING GENOTYPING DATA FOR BACTERIAL STRAINS

Shevtsov V.A., Ismailova A.A.

Kazakh Agrotechnical University named after S. Seifullin, Astana, Kazakhstan

E-mail: shevtsovvladislav111@gmail.com

The integration of pregenomic era microorganism genotyping data with modern genomic data presents a significant challenge stemming from variations in DNA study protocols over the evolution of genotyping technologies. Early genotyping methods, such as DNA fragmentation followed by fragment separation using pulsed-field gel electrophoresis (PFGE), Random Amplified Polymorphic DNA (RAPD), and Restriction Fragment Length Polymorphism (RFLP), have been supplanted by simpler, more accurate, and easily replicable techniques like Multilocus Variable Tandem Repeat Analysis (MLVA) and Multilocus Sequence Typing (MLST).

Currently, a transitional phase requires the amalgamation of data obtained globally through various genotyping methodologies and retrospective analysis of previously acquired genotyping results of circulating strains for comprehensive epidemiological studies. During this transition, many laboratories are compelled to employ whole genome sequencing, PFGE, and MLVA simultaneously for certain pathogens to conduct thorough epidemiological surveillance.

Therefore, the development of in silico genotyping methods based on genome-wide data is imperative, particularly for pathogens where MLVA and MLST have been established as the gold standard for genotyping, such as Brucella spp., Bacillus anthracis, Yersenia pestis, Francisella tularensis, and Neisseria meningitides.

In this study, we present a Python3 script designed to identify Variable Number Tandem Repeat (VNTR) sequences by utilizing primers flanking the region of interest within sequencing reads. Our method offers the advantage of utilizing raw data, thus significantly reducing the likelihood of errors associated with assembly-based approaches. Assembler programs often generate chimeric sequences during assembly, leading to the exclusion of tandem repeat sequences due to breaks or disruption of K-mer size or homoplasy in the region. Additionally, our script enables quantification of different repeat sizes within the sample, facilitating the identification of contaminated samples.

This work was supported by the Science Committee of the Ministry of Education and Science of the Republic of Kazakhstan in the framework of program funding for research (AP19678041).

LARGE-SCALE WHOLE-GENOME SEQUENCING OF POTATO VIRUSES

***Kenzhebekova R.T.*[1, 2], *Mendybayeva A.S.*[1], *Gritsenko D.A.*[1]**

[1]*Institute of Plant Biology and Biotechnology, Almaty, 050040, Kazakhstan*
[2]*al-Farabi Kazakh National University, Almaty, Kazakhstan*

E-mail: rozakenzhebekova344@gmail.com

Potato virus Y (PVY), Potato virus X (PVX), Potato virus S (PVS), Potato leafroll virus (PLRV), and Potato virus M (PVM) are the most distributed viruses of potato in Kazakhstan. One of the most prevalent and extensively dispersed in the fields is PVX. It is a member of the *Alphaflexiviridae* family and *Potexvirus* genus. PVX mostly affects potato plants (*Solanum tuberosum*), but it can also infect tomatoes and peppers, as well as other plants in the *Solanaceae* family. This virus can propagate mechanically by handling during cultivation procedures, contact between plants, and infected seed potatoes.

Nanopore sequencing was employed to analyze the genetic diversity and mutation activity of potato viruses found in the fields of the country. Contigs covering more than 90% of the viral genomes, based on the reference genomes, and with sequencing depth exceeding 150X were selected for analysis. The reference genomes were obtained from NCBI Virus database.

Complete genomic contigs were acquired for PVX isolates. The number of contigs reached 37 out of 2,272 reads. The reference genome, NC_011620.1, was retrieved from the NCBI database to assess coverage and diversity. Mapping to reference genome revealed that sequencing depth and genome coverage exceeding 250X and 150X, respectively. The percentage of pairwise residues was 81.2%. Eleven polymorphic nucleotides were observed in the replicase region, including nine transitions, one transversion, and one substitution.

The PVS genome was sequenced with a maximum depth of 29X, covering 100% of the reference sequence NC_007289.1. The only single reads covering partially genomes of PVY, PVM, and PLRV were obtained by sequencing potato samples without concentrating viruses. The data acquisition was performed on the MinION platform for a duration of 18 hours, yielding 2.7 Gb of data. This is the first report about the detection and whole genome sequencing of potato viruses in Kazakhstan using Oxford Nanopore technology.

Nanopore sequencing holds significant potential in agricultural virus control and research by providing rapid and accurate identification of pathogens within diseased plants.

THE PRELIMINARY ASSESSMENT OF SUGAR BEET FIELDS FOR THE PRESENCE OF VIRUSES USING OXFORD NANOPORE TECHNOLOGY

Kostyukova V*., ***Moisseyev R., Pozharskiy A., Mendybayeva A., Gritsenko D.***

Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan

* *Email:* valera.kostykova.15@gmail.com

The viral infections pose significant challenges to sugar beet cultivation, impacting crop yield and quality. Therefore, thorough monitoring and management of these pathogens are essential to ensure sustainable production. *Beet Necrotic Yellow Vein Virus* (BNYVV) is a highly destructive pathogen that can cause severe damage to sugar beet crops, resulting in substantial yield losses. Its ability to infect and spread rapidly makes it a significant concern for sugar beet growers worldwide. Real-time PCR and next-generation sequencing have been employed to evaluate viral diseases in sugar beet fields in Kazakhstan. Samples of beetroot have also been found to contain the *Beet Cryptic Virus* (BCV).

60 samples of beetroot of the Viorika KWS variety (Germany) and 63 samples of the Ardan variety (France) were analyzed. In addition, random soil samples were taken from the same area where the beet plants were grown. The presence of BNYVV in beetroots and *Polymixia betae* in the soil was confirmed using real-time PCR. Subsequent high-throughput sequencing using Oxford Nanopore technology also confirmed the presence of BNYVV and revealed the presence of a new Beet cryptic virus in the tested plant samples.

The presence of the BNYVV virus of pathotype B was confirmed in two samples from both varieties. 49 of the 60 samples of Viorika KWS and 57 of the 63 samples of Ardan tested positive for pathotype A. Only one sample of Viorika KWS and three samples of Ardan tested positive for pathotype P. Simultaneous infection with several pathotypes was not observed. *Polymyxa betae*, the main vector of the BNYVV virus, was identified in 91 out of 106 soil samples studied from two fields.

Using sequencing on the Oxford Nanopore platform, we confirmed the infection of plants with new virus BCV which had not previously been detected in Kazakhstan.

The scarcity of research on BCV in Kazakhstan and its relatively low study level worldwide, combined with the high incidence of infection with various pathotypes of the BNYVV virus in beet plants, underscores the importance of understanding and managing infection prevention.

UNVEILING THE VIROME OF APPLE TREES IN SOUTH KAZAKHSTAN

Kerimbek N.[1,2], Mendybayeva A.[1], Nizamdinova G.[1], Taskuzhina A.[1,2], Khusnitdinova M.[1], Gritsenko D[1]

[1]Institute of Plant Biology and Biotechnology, Timiryazev street 45, Almaty, Kazakhstan
[2]Al-Farabi Kazakh National University, al-Farabi 71, Almaty, Kazakhstan

Apples (Malus spp.) are among the most valuable fruits in the world. Wild apple trees and cultivars face significant threats from various viruses and virus-like diseases. These include well-known ones such as *Apple mosaic virus* (ApMV), *Apple necrotic mosaic virus* (ApNMV), *Apple stem pitting virus* (ASPV), *Apple stem grooving virus* (ASGV), and *Apple chlorotic leaf spot virus* (ACLSV). ApMV and ApNMV are members of the genus *Ilarvirus* (family *Bromoviridae*) and can cause apple mosaic disease. The disease stands as a significant economic threat, with global prevalence in apple cultivation, posing a severe risk to the industry. The researched viruses are known to infect a wide range of apple cultivars, leading to various symptoms such as stem grooving, chlorotic leaf spots, stem pitting, and mosaic patterns on the fruits and leaves. In addition, some of these viruses can cause graft-transmissible disorders, phloem necrosis, and decline of commercial cultivars, ultimately affecting the quality and yield of the fruits. The objective of this study was to assess the incidence of the apple viruses in apple-growing regions of southern Kazakhstan specifically in five sites, including Chundja, Ketpentau, Sumbe, Chilik and Taraz with a total number of 221 leaf and branch samples. We have utilized PCR-based and Nanopore sequencing detection methods. The average positive rates of ACLSV, ASPV and ASGV were 42.1%, 57% and 12.6% respectively. ApMV and ApNMV were not detected. The study revealed a high incidence of mixed infections of the three apple viruses in Kazakhstan, with 60.6% of the infected apple plants harboring more than one species of virus. The most frequent virus combination was ACLSV+ASPV, with an incidence of 31.7%, followed by ACLSV+ASGV (10.9%), ASPV+ASGV (10%) and ACLSV+ASPV+ASGV (8.2%). Additionally, Tomato Ringspot Virus and Apple rubbery wood virus were identified only by Nanopore sequencing. The number of reads did not exceed 10.

The high prevalence of single and mixed infections in surveyed regions underscores the need for comprehensive and integrated approaches to disease management. Continuous research on the prevalence of viruses in both cultivated and wild apple populations, along with monitoring the dynamics of virus transmission, will help in developing effective preventive strategies.

EDITING THE *VINV* GENE OF POTATOES USING CRISPR/CAS9 TECHNOLOGY

Akhmetollayeva A.S., Kali B.R., Manabayeva S.A*

National Center for Biotechnology, Astana, Kazakhstan

**E-mail*: manabayeva@biocenter.kz

Potato *(Solanum tuberosum* L.*)* is one of the most important food and industrial crop worldwide, including in Kazakhstan. To preserve potato quality for an extended period, low temperature conditions (2-4°C) are necessary. However, prolonged storage can cause physiological changes, such as tuber saccharification or the accumulation of reducing sugars. The Maillard reaction occurs when preparing potatoes for making chips or french fries. Reducing sugars react with free amino acids, particularly asparagine, resulting in the browning of the product. Unfortunately, acrylamide, a carcinogenic compound, is also formed during this process. Acrylamide is a suspected carcinogen that may cause several typed of cancer.

Therefore, it is highly relevant to obtain new potato plant lines that are resistant to cold-induced saccharification. It is a well-established fact that the gene encoding vacuolar invertase (*VInv*) hydrolyzes sucrose, which is formed during starch breakdown, into glucose and fructose. These reducing sugars tend to accumulate in tuber cells. Therefore, we have selected the *VInv* gene from the NCBI database (ID HQ110080.1), which encodes acidic vacuolar invertase. This gene has a length of 6097 bp and consists of 7 exons and 6 introns.

To reduce the sugar level in potatoes, CRISPR/Cas9 technology was used to edit the *VInv* gene. RNA was extracted from domestic potato varieties and analyzed for potential changes in exons 1 and 3 of the *VInv* gene and target sequences with minimal nonspecific binding cite in the genome were selected. Binary expression vectors were created, encoding *Cas9* gene and the suppressor gene *p19* (TBSV), as along with chimeric guide RNAs. Monthly microclonal propagation was conducted for the *Agrobacterium*-mediated transformation of potato variety Aksor. A total of 1327 stem explants and 1123 callus of the potato variety Aksor were transformed. Successful regeneration was achieved from mutated and genome-edited cells at a frequency of 21.2% from stem explants and 5.8% from callus. The presence of *Cas9* and *p19* genes in regenerated plants was confirmed through DNA monitoring. Sequencing revealed numerous mutations, such as substitutions, insertions, and deletions. The analysis of reducing sugars and acrylamide content in the tubers of genome-edited potatoes confirmed the successful use of CRISPR/Cas9 technology to improve potato production.

DEVELOPMENT OF A SET OF VECTORS WITH AN UNIFIED CLONING SITE FOR PLANT MOLECULAR BIOLOGY

Chernyaev K.A., Karlov V.D., Lebedeva M.V., Taranov V.V.

All-Russia Research Institute of Agricultural Biotechnology (ARRIAB), Moscow, Russia

E-mail: skdw12345@gmail.com

Current challenges in agriculture, require an intensification and acceleration of breeding process, especially breeding of important crops, such as potato (*Solanum tuberosum* L.) – one of the most significant worldwide culture. However it is impossible without solid knowledge about molecular basis of valuable traits and characteristics of individual plant proteins. The first step of protein examination is cloning its DNA coding sequence in a genetic vector. The main problem of the gene cloning by consequent restriction and ligation in a number of vectors with different polylinkers is the necessary of obtain few PCR fragments with recognition sites of different restriction enzymes for each vector. Therefore a fragment cloning in different plasmids turns to time-consuming and expensive procedure.

In this work a set of vectors suitable for plant proteins investigation with unified cloning site was created. The set including the vector for yeast-two assays for protein-protein interaction analysis; the vector for yeast complementation for a protein functional analysis; the vector for gene overexpression in dicotyledonous plants and the vector for protein production in bacteria cells and further isolation. The vector kit is based on Golden Gate assembly technology, which allows to carry on restriction and ligation in one reaction mix simultaneously and number of restriction enzymes is not necessary – only BsaI restriction enzyme is used. In order to simplify a verification of cloning success a RFP expression cassette was added inside the unified cloning site. RFP expression in bacteria turns the colonies in magenta colour, so that white colonies indicate about successfully cloning, during which RFP cassette was eliminated. As a result, using the one-4-all set for plant proteins investigation can significantly speed up and simplify the gene engineering part of the work.

The work was somehow financially supported by the Comprehensive Research Program “Development of Potato Breeding and Seed Production”.

VIRUS-MEDIATED DELIVERY OF CAS9 CONSTRUCT USING TBSV AS A VECTOR

Kanat R.,* *Sapakhova Z., Shamekova M., Zhambakin K., Daurov D., Daurova A.

Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan

E-mail: udinjate.tt0ey@8shield.net

The delivery of the Cas9 protein construct is an important step for the efficient editing of the genome in plants. Its efficiency depends on many factors one of the influential ones is the plant RNA silencing pathway.

RNA silencing is an evolutionarily conserved post-transcriptional gene silencing (PTGS) mechanism in eukaryotes that is used to regulate gene expression and combat invading nucleic acids such as viruses. To counter this antiviral host defense response, plant viruses have evolved viral suppressors of RNA silencing. For example, the Tomato bushy stunt virus has a p19 protein that inhibits the host's RNA interference system.

SgRNA guides Cas9 protein to the genomic sequence where the cut will be performed using nickase domain of Cas9 protein. In particular, the RNA interference system, which is well developed in plants as an immune system against viral RNA invasion, acts against the sgRNA of the Cas9 structure. Therefore, direct injection of plasmids containing Cas9 and sgRNA is less effective in plant transformation than injection together with viral particles containing inhibitory proteins.

We developed constructs for viral delivery from 3 mutants of the TBSV virus: wild type, RMJ-1, and RMJ-2. Both RMJ-1 and RMJ-2 are TBSV strains with defective p19 protein and lack of the capsid protein. Wild type strain has highly expressive p19 protein which has negative side effects to plant health, while both mutant strains have partially or fully inactive p19 suppressor protein, to find the best construct to simultaneously suppress RNA interference system that inhibits expression of sgRNA and lower damage to the plant. In addition, the lack of the CP gene allows the virus to move from cell to cell through the plasmodesmata but cannot systemically spread to other parts of the plant. Instead, high levels of recombinant proteins accumulate in the infiltrated and adjacent tissues. In addition, because of the lack of a CP gene, the virus can move between cells, but cannot systematically spread to other parts of the plant. Instead, large amounts of recombinant protein accumulate in infected and neighboring tissues.

We used TBSV to carry sgRNA and expressed Cas9 protein in plant using agrobacterial infiltration with pKSE401 plasmid, which led to multiple fold to Cas9 higher expression. To prepare our constructs, we used molecular cloning methods combination of Gibson and NEBuilder® HiFi DNA Assembly with the use of pKSE401, pFH14, TBSV-wt, TBSV-rmj-1 and TBSV-rmj-2 plasmids. gRNAs that target MLO-1-like protein and PDS genes were used to test constructs in model plant *Nicotiana benthamiana*.

DETECTION OF POTATO VIRUSES USING NEXT-GENERATION SEQUENCING IN RUSSIA

Antipov A.D.[1], Porotikova E.V.[2], Vinogradova S.V.[2], Lebedeva M.V.[1*]

[1]All-Russia Research Institute of Agricultural Biotechnology, Moscow, Russia
[2]Federal Research Centre of Biotechnology RAS, Moscow, Russia

**E-mail:* marilistik@mail.ru

Potato (*Solanum tuberosum* L.) is one of the most significant agricultural crops. Due to vegetative propagation potato is strongly affected by viral diseases, which lead to yield decrease. There are a few dozen different viruses was found on the potato plants all around the world. In Russia seed potato in industry are tested only for 7 viruses and 1 viroid via PCR or ELISA. However, these approaches can reveal only limited number of species and strains, while veritable viral biodiversity can be notably different. Moreover, many viruses generate recombination forms between different strains and actual strain landscape is still sparse.

In this work potato plantings of different cultivars and generations were explored in the Central region of Russia. Some selected potato plants were used for RNA extraction, cDNA library preparation and sequencing on the Illumina platform.

The work was supported by Russian Science Foundation, project № 23-76-01066.

THE GOLD-OF-PLEASURE AGROBACTERIUM-MEDIATED TRANSFORMATION

***Razhina P.L.*[1], *Veselkin A.A.*[1], *Lebedeva M.V.*[1], *Kozenkova P.I.*[2], *Taranov V.V.*[1]**

[1] *All-Russia Research Institute of Agricultural Biotechnology, Moscow, Russia*
[2] *Russian State Agrarian University - Moscow Timiryazev Agricultural Academy, Moscow, Russia*

Camelina sativa (L.) or gold-of-pleasure is an oilseed crop of the *Cruciferous* family, which has begun to gain popularity in recent years. Gold-of-pleasure oil applies in the industry for biofuel production, varnishes and paints, and animal forage. Also, gold-of-pleasure adapts for food as a valuable source of Omega-6 and Omega-9, linolenic fatty acids, and beta-carotene. In fatty acids composition gold-of-pleasure oil is similar to flaxseed oil, however, gold-of-pleasure oil costs cheaper, retains its properties longer, and contains more vitamin E.

Currently, new varieties of gold-of-pleasure are being actively developed around the world, including using the CRISPR-Cas9 genome editing system to improve the oil composition, herbicide resistance and increasing the oil content in the seeds. However, genome editing requires an efficient plant transformation in order to deliver editing system components. In this study, we used camelina cultivars Omich, Isilkulets, and Crystal (kindly provided by L. A. Gorlova, VNIIMK, Krasnodar) in order to optimize transformation protocol and compare two different approaches – a floral dip transformation as *in planta* and a callus-mediated as *in vitro*.

BASE EDITING TECHNOLOGY FOR THE *NICOTIANA TABACUM* GENOME MODIFICATION

Sushchenko A.S. [1, 2], ***Lebedeva M.V.*** [1], ***Razhina O.L.*** [1], ***Nikanorkina V.V.*** [1], ***Taranov V.V.*** [1]

[1] *All-Russia Research Institute of Agricultural Biotechnology, Moscow, Russia*
[2] *Moscow Institute of Physics and Technology, Dolgoprudny, Russia*

E-mail: andreysusch2000@mail.ru

Nowadays CRISPR-Cas9 technology is the most widely used approach for genome editing. It allows to introduce double-strand breaks in a target DNA and cause a gene knockout by indel mutation. However, the approach is unsuitable when not gene knockout, but gene modification and protein properties alteration are needed. Therefore, if an amino acid replacement in a protein is required, a more advanced CRISPR/Cas9 technology - base editing with deaminases - will be more applicable. This approach allows to replace a single nucleobase inside a deaminase editing window.

Nicotiana tabacum L. is a plant from the *Solanaceae* family, the same as potato, tomato and pepper. All these plants are strongly affected by potato virus Y (PVY). It is known that PVY recruits host translation initiation factor eIF4E by the viral protein VPg in order to start synthesis its proteins. If eIF4E can't interact with VPg, plant will be resistant.

Previously, several mutations in the tobacco eIF4E, which disrupt its interaction with VPg and don't affect factor functions, were established using model yeast systems. In this study, two sgRNAs were designed in order to modify the eIF4E gene in tobacco using a cytidine-deaminase base editing approach. Vectors with cloned sgRNAs were used for the tobacco agrobacterium transformation. The *N. tabacum* PDS (phytoene desaturase) gene editing with specific sgRNAs was used as a transformation control and for the effectiveness evaluation of nucleotide substitutions. The gRNAs were targeted in three different exons and should lead to stop-codon appearance in order to PDS gene knockout. Regenerated plants lacking chlorophyll confirmed the success of the transformation and genome editing.

This work is supported by State Task No. 0431-2022-0004.

ESTABLISHMENT OF PLANT BACTERIA AND FUNGI COLLECTION

Yelchaninov M.I., Nizamdinova G., Gritsenko D.

Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan

E-mail: yelchaninov.mikhail@gmail.com

This study represents a crucial step in exploring and understanding the plant microbiome in the context of agriculture in Kazakhstan. Considering the growing need to increase crop productivity and resilience of agricultural crops to extreme climatic conditions, the creation of a collection of plant bacteria and fungi becomes particularly significant.

The research involved sampling the apple, walnut, and hawthorn tree material from various ecosystems in the regions of Zhongar Alatau, Ketpen, and Ile-Alatau, as well as targeted sampling from apple orchards, where apple bacteria were of particular interest. This allowed us to obtain extensive data on the biodiversity of microorganisms existing in natural and anthropogenically modified ecosystems of Kazakhstan. After collecting the samples, we processed and isolated microorganisms using standard culture methods.

Subsequently, Nanopore sequencing was applied for the identification and classification of microorganisms. These methods enabled us to obtain detailed information about the genera and, in some cases, species of bacteria. Presently, our collection comprises 25 isolates of *Erwinia*, 57 isolates of *Pseudomonas*, 31 isolates of *Klebsiella*, and 42 isolates of *Pantoea*. These isolates were obtained from diverse samples and populations. Additionally, glycerol stocks of *Erwinia amylovora* were prepared for long-term preservation at low temperatures. The potential biological agents, such as *Pseudomonas fluorescens*, were also preserved for subsequent testing to evaluate their efficacy in promoting plant health and combating pathogens. *Pseudomonas fluorescens* stands out as a powerful biocontrol agent against plant pathogens. Through mechanisms such as antibiosis, competition for nutrients, and induction of plant defense responses, this bacterium suppresses the growth of harmful organisms, thereby reducing the need for chemical pesticides. Moreover, *Pseudomonas fluorescens* has been shown to promote plant growth by facilitating nutrient uptake, enhancing stress tolerance, and stimulating root development.

The collection of plant bacteria has the prominent potential for enhancing agricultural production. Plant microbiome analysis will help to identify biological agents capable of increasing crop yields, protecting plants from diseases and stressful conditions, and improving soil fertility.

INCREASING THE REGENERATION POTENTIAL OF PROSO MILLET (*PANICUM MILIACEUM* L.) *IN VITRO* CULTURE

Zhumabek A.T.*, Manabayeva S.A.

Plant Genetic Engineering Laboratory, National Center for Biotechnology, Astana, Kazakhstan

**E-mail:* manabayeva@biocenter.kz

Panicum miliaceum L. is an important drought-tolerant crop that has recently become a research focus due to its significance in healthcare and nutrition. Proso millet's resilience to harsh climates and its gluten-free nature make it an attractive option for researchers, farmers, and consumers, especially in regions susceptible to climate change and food insecurity.

Furthermore, the use of proso millet as a gluten-free alternative highlights the significance of traditional knowledge and biodiversity in addressing modern challenges in food production and nutrition. No protein has gotten more attention in recent years than gluten. Gluten, the main storage protein found in many grains, such as wheat, rye, and barley, has received significant attention in recent years. It is a complex mixture of hundreds of related but distinct proteins, primarily gliadin and glutenin. Similar storage proteins exist in rye as secalin, in barley as hordein, and in oats as avenins. These proteins are collectively referred to as "gluten". Gliadin contains peptide sequences that are highly resistant to gastric, pancreatic, and intestinal proteolytic digestion in the gastrointestinal tract. The average daily intake of gluten in a human's diet is estimated to be 5-20 g/day and has been linked to several disorders. Given these facts, the study of the introducing of proso millet into *in vitro* culture is highly relevant and it is necessary to improve its genome in order to change quantitative and qualitative characteristics. To achieve this, understanding the regenerative potential of proso millet is essential.

A study was carried out to investigate the regeneration potential of proso millet (*Panicum miliaceum* L.) *in vitro* culture. The proso millet seeds from Kazakhstan breeding: Kormovoe-14 and Yarkoe-6 used in this study. An optimization of various exogenous hormones was conducted in the *in vitro* culture for callus induction and differentiation, as well as plant regeneration, and rhizogenesis of these two varieties.

To induce callusogenesis in cell culture, sterile proso millet seeds were cultured on Murashige and Skoog (MS) medium with a pH = 5.8 and 30 g/l maltose, containing 2 mg/l 2.4-D and 0.5 mg/l BAP. L-Proline (500 mg/l) and casein hydrolysate (300 mg/l) were added as an additional nitrogen sources. The seeds produced friable calli with a white and yellow-cream color. The frequency of callus induction was 95% for Kormovoe-14 and Yarkoe-6. All cultivars showed 100 % embryogenic callus induction when using MS medium supplemented with 2 g/l L-Proline, 30 g/l maltose, 5 mg/l 2.4-D and 1 mg/l BAP. The greatest number of plantlets was obtained on auxin-free MS medium containing 4 mg/l BAP. Regenerated plantlets showed significant rooting, when transferred to full-strength MS medium supplemented with 0.2 mg/l IBA + 0.1 mg/l BAP and 2% sucrose. The rooted plantlets were hardened and transferred to soil.

COMPARATIVE ANALYSIS OF THE EFFICACY OF LIMITED PROTEOLYSIS STRATEGIES FOR PROTEOME INVESTIGATION OF PLANT-DERIVED BIOLOGICAL MATRICES

***Danko K.V.*[1,2*], *Lukasheva E.M.*[2], *Zgoda V.G.*[3], *Frolov A.A.*[1]**

[1]*Laboratory of Analytical Biochemistry and Biotechnology, K.A. Timiryazev Institute of Plant Physiology RAS, Moscow, Russia*

[2]*Department of Plant Physiology and Biochemistry, Saint Petersburg State University, Saint Petersburg, Russia.*

[3]*Institute of Biomedical Chemistry, Moscow, Russia.*

**E-mail:* danko_katerina@mail.ru

Bottom-up shotgun proteomics encompasses a variety of robust and high-throughput techniques, both gel-based and gel-free, that enable the accurate protein identification by analysis of their peptides generated by proteolytic digestion. However, although detergents and chaotropic agents are essential for efficient proteolysis during sample preparation in terms of gel-free proteomics strategies, their supplementation to protein solubilization buffers negatively affects the chromatographic separation and ionization of peptides. Although this methodological conflict can be resolved by various proteolysis strategies and commercially available products, the relative efficiency of these approaches against plant-derived matrices remains unexplored. Therefore, we addressed the efficiency of three digestion strategies, including in-solution and filter-aided digestion methods, for proteomics analysis of the rosette leaf of *Arabidopsis thaliana* and seeds of *Pisum sativum*. In-solution digestion strategies involved application of MS-compatible detergent, namely anionic acid-labile surfactant AALS II. Filter-based approach was represented with the filter-aided sample preparation (FASP) protocol. Supplementation of the samples with urea was used as a reference protocol. Nano-flow liquid chromatography-(tandem) mass spectrometry (nanoLC-MS and MS/MS) analysis revealed slight differences in the numbers of identified proteins observed between the different strategies of limited proteolysis in both biological matrices. Significant differences in the recoveries of individual proteins were observed between the FASP method and AALS II in plant samples. While the FASP protocol yielded the highest efficiency of proteolysis, it was accompanied by the formation of short peptides that could potentially result in their poor retention the reverse-phase column. Overall, the FASP strategy demonstrated the highest potential for detection of membrane and high-molecular-weight proteins in both *Arabidopsis thaliana* leaves and *Pisum sativum* seeds.

PROTEOMICS APPROACH IN UNDERSTANDING THE ROLE OF GROWTH-STIMULATING RHIZOBACTERIA IN DROUGHT TOLERANCE OF TOMATO PLANTS

***Gurina A.*[1], *Frolova N,*[2] *Lukasheva E.*[1], *Kuznetsova A.*[1], *Shumilina J.*[2], *Alhajje K.*[2], *Bilova T.*[1,2], *Orlova A.*[2], *Silinskaya S.*[2], *Cherevatskaya M.*[1], *Leonova T.*[2], *Shaposhnikov A.I.*[3], *Belimov A.A,*[3] *Frolov A.*[2]**

[1]*Department of Plant Physiology and Biochemistry, Saint Petersburg State University, Universitetskaya emb., 7/9, St. Petersburg, Russia;*
[2]*Laboratory of Analytical Biochemistry and Biotechnology, K.A. Timiryazev Institute of Plant Physiology, Russian Academy of Sciences, 35 Botanicheskaya str., Moscow, Russia;*
[3]*Laboratory of rhizosphere microflora, All-Russia Research Institute for Agricultural Microbiology, Pushkin 8, hwy. Podbelsky, 3, St. Petersburg, Russia*

E-mail: gnastyak0@gmail.com

Practical application of the symbiosis between plants and growth-promoting microorganisms (in particular, rhizobacteria from the PGPR group) is a promising biotechnological approach in suppression of the negative effects of abiotic stressors like drought on the quality of highly valuable crops. It is assumed that the observed positive effects of rhizobacteria on plant growth under water deficit are underlied by their high potential for the consumption of 1-amino-1-cyclopropane carboxylate (ACC) exuding from roots - the precursor in ethylene biosynthesis. It is known that this effect is mediated by natural expression of the bacterial gene for the ACC deaminase enzyme, where the gene product breaks down ACC to ammonium and 2-ketobutyrate. It was shown earlier, that inoculation with *P. brassicacearum* strain Am3, but not with T8-1 (the genotype with a decreased ACC deaminase activity), is able to reduce the negative effects of drought on plant biomass gain. However, the specific signaling and metabolic pathways involved in reducing the effects of ethylene on the inoculated plants remain unknown. To fill this gap, here we address the drought-related dynamics of the tomato shoot proteome in the presence and absence of the above mentioned rhizobacterial inoculants. After isolation of the total protein fraction and limited enzymatic protelysis, the resulting proteolytic peptides were analyzed by nano-flow reverse-phase chromatography coupled on-line to an Orbitrap Fusion Tribrid mass spectrometer (nanoRP-HPLC-LIT/Q-Orbitrap-MS). Statistical analysis relied on specific proteomics software and R packages, the following bioinformatics allowed deep understanding of the functional plant proteome response to drought in the presence and absence of symbiotic bacteria.

This work was supported by the Russian Ministry of Education and Science (agreement No. 075-15-2922-320 of 20.04.2022).

GENETIC DATABASES FOR BREEDING CEREAL CROPS FOR RESISTANCE TO FUNGAL DISEASES

Karimova A.*, Serikbayeva G., Urazaliyev K., Bayadilova G.

Kazakh National Agrarian Research University, Almaty, Kazakhstan

Fungal diseases remain a serious threat to cereal crops, reducing yield and quality. In recent decades, bioinformatics has played a key role in disease resistance research, providing valuable tools for analyzing genetic databases. In this regard, the identification and utilization of genetic mechanisms conferring resistance to fungal diseases becomes critical in the breeding of new varieties.

This article discusses various genetic databases, their role in breeding of resistant cereal varieties and prospects for further research.

Bioinformatics plays a key role in plant breeding for disease resistance by providing powerful tools for analyzing genetic databases and identifying candidate genes associated with fungal disease resistance. There are several large genetic databases containing information on cereal crop genomes and associated phenotypic data on fungal disease resistance. These databases, such as GenBank, Ensembl and others, provide valuable resources for researchers and breeders to identify genes and molecular markers that may be associated with disease resistance.

The application of bioinformatics techniques, such as next-generation sequencing, association analysis and functional genome annotation, allows us to efficiently identify potential candidate genes and understand their role in resistance mechanisms. This provides the basis for the development of new cereal crop varieties that are more resistant to fungal diseases, which in turn can significantly improve yields and sustainability of agricultural production.

We have conducted preliminary studies on collection and analysis of genomic information from various databases to create a generalized local database of resistance genes to fungal diseases of cereal crops in order to create the most resistant genotypes to these models. For this purpose, we studied and searched for barley rust and wheat blight resistance genes in the NCBI database.

As a result of this research, 20 resistance genes to barley dwarf rust, 8 resistance genes to brown rust and 5 resistance genes to stem rust, 10 resistance genes to hard bunt, 10 resistance genes to dusty bunt and 5 resistance genes to dwarf bunt were found.

Rust is a serious disease that can lead to crop loss. The Rph1 gene plays an important role in protecting wheat against rust.

The Rph1 (Resistance to *Puccinia herminis*) gene encodes a protein responsible for wheat resistance to rust caused by the fungus *Puccinia graminis f. sp. tritici*.

The protein encoded by Rph1 recognizes specific molecules present on the surface of the fungus *Puccinia graminis f. sp. tritici*. It detects pathogens and triggers a cascade of defense reactions, including the production of antimicrobial compounds and cell wall reinforcement. The defense reactions activated by Rph1 lead to the death of *Puccinia graminis f. sp. tritici*, preventing its spread and damage to the plant.

Durum bunt (*Tilletia caries*) is a fungal disease affecting wheat and other cereals. The disease results in the formation of heads instead of grains, which significantly reduces yields and grain quality.

Gt1 is a group of genes for durum bunt resistance localized on chromosome 1B of wheat. To date, 15 Gt1 genes are known to provide varying degrees of resistance to the pathogen.

Gt1 genes encode receptor proteins that are found on the surface of plant cells. These receptors recognize specific molecules called effectors that are secreted by the pathogen. When a receptor protein binds to an effector, it triggers a cascade of signaling reactions that leads to the activation of the plant's defense responses. These reactions prevent the pathogen from entering the cell and the molecules are toxic to the pathogen and the proteins kill the pathogen. As a result of activation of defense reactions, the pathogen is killed, and the plant is not infected.

The development and application of genetic databases and bioinformatic methods in breeding cereal crops for resistance to fungal diseases represents an important area of research that can significantly contribute to improving agricultural productivity and sustainability in the future.

EVALUATION OF SELECTION DIRECTION IN PLASTID GENES OF SOME REPRESENTATIVES OF THE *POOIDEAE* SUBFAMILY

***Kusakin A.V.*[1], *Rodionov A.V.*[2], *Loskutov I.G.*[1]**

[1] *Federal Research Center the N.I. Vavilov All-Russian Institute of Plant Genetic Resources (VIR), St. Petersburg, Russia*

[2] *Komarov Botanical Institute, Russian Academy of Sciences, St. Petersburg, Russia*

The subfamily *Pooideae* includes numerous cultivated species that are extensively used in agriculture. During domestication and dispersal to new habitats across continents, cereals have undergone significant genetic changes. Plastid genomes are commonly used to study such changes because they are well characterized and therefore useful for comparative purposes in phylogenetics and evolutionary biology.

This study evaluates the direction of selection of 73 plastid genes common among the genera *Avena*, *Hordeum*, *Triticum*, and *Secale*. Understanding the adaptive evolution of these cereals in response to changing environmental conditions requires studying the direction of selection. Additionally, this study establishes the foundation for further investigation of the complex evolutionary dynamics of not only plastid but also nuclear genes in the subfamily *Pooideae*.

The plastid genomes used in this study were obtained from the public NCBI GeneBank database. A total of 17 species were included, namely: 4 species from the *Triticum* genus (*T. aestivum*, *T. monococcum*, *T. turgidum*, and *T. urartu*); 3 species from the *Hordeum* genus (*H. jubatum*, *H. vulgare*, and *H. brevisubulatum*); 5 species from the *Avena* genus (*A. abyssinica*, *A. barbata*, *A. fatua*, *A. sativa*, and *A. sterilis*); and 3 species from the *Secale* genus (*S. cereale*, *S. strictum*, and *S. sylvestre*). Additionally, 2 members of the PACMAD clade, *Zea mays* and *Panicum miliaceum*, were used for tree rooting. Nucleotide sequence alignment was performed using the MACSE 2 program. Dendrogram construction was carried out using IQ-TREE 2. The direction of selection was evaluated using the PAML program, with both the M0 (one-ratio) model and Site model being tested.

The M0 model was tested first, which assumes a homogeneous ratio of nonsynonymous to synonymous substitutions (ω) along the entire length of the gene. This model allowed the identification of 15 genes with positive selection ($\omega > 1$). These genes include those involved in ATP synthesis (atpB, atpE), components of photosystem II (psbA, psbE, psbF, psbJ), a small subunit of the ribosome (rps3, rps8, rps11, rps16), and others with various functions (ndhA, ndhF, clpP1, pafI, rpl14).

The Site model was tested to allow different values of ω for different codons, enabling the identification of amino acids that underwent positive selection. The results indicate the presence of such sites in the genes atpB (489 V), ndhA (243 T, 244 Y, 247 I), ndhF (557 S, 629 H, 631 P, 635 F, 670 L), rbcL (14 K, 94 D, 142 P, 145 S, 270 L, 471 E), and rps11 (137 A). Notably, the M0 model failed to detect the rbcL gene, suggesting that strong purifying selection ($\omega < 1$) may be affecting all other codons in this gene. Considering the role of the rbcL gene product in forming large subunits of the RuBisCO protein, these mutations may have altered the activity of this enzyme and possibly provided advantages in settling new territories. However, additional research is required to test this hypothesis.

Future research aims to identify the impact of amino acid substitutions at these sites. Other models of evolution will also be tested, along with nuclear genes associated with useful agricultural traits.

Our research was supported by the Russian Science Foundation (No. 23-76-00005 (AVK, IGL)) and by the Ministry of Science and Higher Education of the Russian Federation (No. 124020100136-0 (AVR)).

DEVELOPMENT OF A GBS PROTOCOL FOR COMMON HOPS (HUMULUS LUPULUS) TO STUDY THE GENETIC DIVERSITY OF THE HOP WITHIN RUSSIA

***Martynova E.*[1], *Chernyaeva E.*[2], *Zamalutdinov A.*[1], *Baik A.*[1]**

[1] *Skolkovo Institute of Science and Technology, Bol'shoi Bulevard, 30, build. 1, Moscow, 121205 Russia*

[2] *Russian State Agrarian University - Moscow Timiryazev Agricultural Academy, Timiryazevskaya Str., 49, Moscow, 127434 Russia*

Hop (*Humulus lupulus* L.) is a perennial dioecious plant in the Cannabaceae family. Hops are an important agricultural crop with the cones produced by female plants being an indispensable material for the beer brewing industry.

Being a component which imparts special aroma to beer owing to the secondary metabolites contained in cones hops are essential to adapt beer to consumers changing demands. For this reason, the hop cultivars with varying properties should be available and hop breeders should be highly responsive to existing demands. Understanding genetic diversity can make it possible to use the available hop germplasm more effectively thus accelerating the breeding process. To study genetic diversity, high density SNP markers are needed. Genotyping-by-sequencing (GBS) is currently gaining its position as a "gold standard" for producing thousands of SNPs for large populations. However, there is no effective GBS protocol for hop. Thus, the goal of this work was to design a GBS protocol for hops to study the genetic diversity of the largest hop genetic collection in Russia (Chuvash Agricultural Research Institute).

At the first stage of protocol design, an in silico search for best performing restriction enzymes was carried out, which allowed choosing a number of restriction enzymes as a basis for the future protocol. Restriction enzymes were further tested empirically through whole genome restriction and two enzymes were selected: *Ape*KI and *Hind*III. Two different GBS protocols were devised and used to produce hop genome libraries for NGS. *Hind*III-based protocol made it possible to obtain better quality library based on first electrophoretic assessment and QC. NGS results also showed more generated reads, sequencing tags, and SNPs for the *Hind*III library, although the sequencing coverage was higher for *Ape*KI. SNP quality was comparable for both libraries. In such a way, *Hind*III restriction enzyme could be recommended as restriction enzyme of choice for hop.

Hop plant material was kindly provided by I.Yu. Ivanova, PhD, deputy director (Chuvash Agricultural Research Institute, Cheboksary). The work was supported by the Russian Scientific Foundation (grant no. 24-26-00165, https://rscf.ru/project/24-26-00165/).

EXPLORING THE GENETIC DIVERSITY OF POTATO SPINDLE TUBER VIROID IN THE NORTHERN FIELDS OF KAZAKHSTAN

Mendybayeva A., Kapytina A., Kerimbek N., Gritsenko D.

Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan

Potato spindle tuber viroid (PSTVd) is a small non-coding RNA pathogen that, due to its adaptability and virulence, has significant genetic plasticity manifested through sequence heterogeneity and structural polymorphism. Intrinsic variability of PSTVd highlights its pivotal role in plant pathology and requires careful investigation using advanced technologies such as next generation sequencing (NGS). Thus, this study characterizes the genetic diversity and distribution of PSTVd variants in different regions of Northern Kazakhstan.

During the sample collection, material showing pronounced signs of infection as well as visually healthy specimens were gathered. In total, 477 potato samples were collected from 7 fields across various regions of Pavlodar, Kokshetau, and Astana. Viroid detection was carried out utilizing the conventional yet highly reliable RT-PCR method, allowing for accurate identification of PSTVd presence within the collected samples using specific primers.

Sequencing was carried out on a MinION device from Oxford Nanopore Technologies, renowned for its capacity for rapid, real-time nucleic acid sequencing. Up to 50 samples were selected from each field, followed by the addition of the corresponding barcode. The library preparation was carried out on the basis of the latest V14 chemistry, which enables highly accurate and tuneable sequencing. The sequencing process took 18 hours, resulting in 2.7 GB of accumulated information. The data collected was sufficient for subsequent analysis using bioinformatics platforms such as Epi2Me and Geneious Prime. The resulting reads were aligned to a reference sequence NC_002030.1 of PSTVd using the NCBI database. The coverage resulted 100%. Alignment in the Geneious Prime program resulted in two reads of lengths 1117 bp and 710 bp. Both reads were collected from a field in the Astana region. In addition, BLAST analysis showed that all matches belong to the target viroid with an E-value not exceeding 1e-78 out of 100 rendition matches. The highest % identity of 86,2% belongs to the PSTVd Fujian isolate (KM588065.1). However, the query coverage does not exceed 29% since the length of the retrieved reads was longer than the existing sequences in the database.

Epi2me analysis also showed the presence of Tobacco vein clearing virus (TVCV), Potato leafroll virus (PLRV), Potato virus X (PVX), Potato virus Y (PVY), Potato virus S (PVS), and Potato virus M (PVM) by sequencing on the nanopore platform.

PSTVd stands out as a major plant affliction, causing substantial economic harm to crop within the *Solanaceae* family, notably potatoes. Understanding the genetic diversity of PSTVd is essential for deciphering its evolutionary vector, predicting disease outbreaks, and subsequently developing resistant potato varieties.

INOCULATION TEST OF A, B, AND P- STRAINS OF BEET NECROTIC YELLOW VEIN VIRUS

Moisseyev R., Pozharskiy A., Khusnitdinova M., Nizamdinova G., Gritsenko D.

[1]*Institute of Plant Biology and Biotechnology, Timiryazev street 45, Almaty, Kazakhstan*

Rhizomania is a devastating disease affecting sugar beet crops, characterized by the formation of root swellings, necrosis, and yellowing of veins. Its primary vector is the single-celled parasitic organism *Polymyxa betae*, belonging to the order Plasmodiophorales. The disease exhibits heightened virulence under conditions of high temperature and soil moisture, with relatively dry soil mitigating its impact. The detrimental effects of rhizomania manifest in significant reductions in root mass, with infected roots weighing 10–15 times less than healthy ones. Additionally, rhizomania-infected roots experience decreased sugar content and diminished sugar yield, thereby compromising the technological quality of the raw material. To prevent disease spread, stringent quarantine measures must be observed during the import, export, transportation, and storage of planting material containing soil. Furthermore, the adoption of rhizomania-resistant sugar beet hybrids is imperative for disease management. Thus, understanding the interplay between viral strains and host resistance mechanisms is crucial for developing effective control strategies and preserving sugar beet yields in the face of this formidable disease.

In the present study, we confirmed the presence of *Beet Necrotic Yellow Vein Virus* (BNYVV) in beet plants (Viorika cultivar) sampled in the fields of Zhetysu region. The Zhetysu region is recognized as the largest center for sugar beet cultivation in Kazakhstan. The virus was detected using a qPCR commercial kit (Letgen), which identified A, B, and P pathotypes. All three pathotypes were present in the region. To recover all pathotypes in laboratory conditions, Viorka plants in three replicates were inoculated with sap obtained from infected samples. Before inoculation, the sap was subjected to metagenomic analysis using MinION technology. The presence of only A pathotype was confirmed. The consistent results were obtained following testing of inoculated plants using both nanopore sequencing and PCR analysis at the third and seventh days after inoculation. The presence of P and B pathotypes could be detected in primary samples due to false positive amplification and/or inaccurate primer design. Nevertheless, we confirmed the biological activity of the BNYVV preserved in the primary samples for a year at -80°C.

CONTENT

Session 1. GENETIC RESOURCES AND BIODIVERSITY

Session 2. GENETICS AND BREEDING

Session 3. PHYSIOLOGY, BIOCHEMISTRY AND BIOTECHNOLOGY

Session 4. CELLULAR AND GENETIC ENGINEERING

PLENARY SESSION

Session 5. GENOMICS, PROTEOMICS, AND BIOINFORMATICS

PLENARY SESSION

AUTHOR INDEX

INTERNATIONAL CONFERENCE ON PLANT BIOLOGY AND BIOTECHNOLOGY (ICPBB 2024)

Best Western Plus Atakent Park Hotel

Almaty, Kazakhstan, June 3-6, 2024

SPONSORS СПОНСОРЫ СПОНСОРЛАР

ZALMA

SEVANA

Veld Ltd
Deliveries of labware and medical equipment over Kazakhstan

JUGGERNAUT

TECHPRIME
Top-notch technologies now

LAB Instruments

adrena

30 MEDILAND ANNIVERSARY

PARTNERS ПАРТНЕРЫ СЕРІКТЕСТЕР

ЛаборфармА

АЛЬГИМЕД

НАЦИОНАЛЬНАЯ АКАДЕМИЯ НАУК
ПРИ ПРЕЗИДЕНТЕ РЕСПУБЛИКИ КАЗАХСТАН

Primer Digital

General Sponsor

ТОО «ZALMA Ltd.» (ЦАЛМА Лтд.),
г. Алматы, ул. Богенбай батыра 305А
info@zalma.org
+7 (727) 374 35 70

ZALMA

АФ ТОО «ZALMA Ltd.» (ЦАЛМА Лтд.),
г. Астана, ул. 23-15, дом 11, блок А, кв. 132
info.astana@zalma.org
+7 (717) 225 99 75

CALL-CENTER +7 701 031 27 29

Компания ТОО Zalma Ltd. - одна из самых быстро развивающихся и надежных компаний на казахстанском рынке лабораторной техники. Основным направлением нашей деятельности является внедрение передовых лабораторных технологий, подготовка и реализация системных решений для отечественных лабораторий.

Наши системные решения включают полное оснащение лабораторий специализированным оборудованием и расходными материалами. Мы также предлагаем методическую и сервисную поддержку, гарантийное и послегарантийное обслуживание, обучение персонала лаборатории, как на базе заказчика, так и на базе производителя оборудования.

Несомненным конкурентным преимуществом нашей команды является понимание основных задач, стоящих перед нашими заказчиками, и применение максимально эффективного и конструктивного подхода к их успешному решению. Это достигается, с одной стороны, благодаря высокому профессионализму наших сотрудников, с другой стороны, благодаря нашим надежным поставщикам, ведущим зарубежным производителям лабораторного оборудования и материалов, среди которых такие известные во всем мире бренды, как **Applied Biosystems™, Invitrogen™, OneLambda™, Gibco™** и многие другие. Наш главный поставщик - **Thermo Fisher Scientific** - предлагает широкий спектр продукции и услуг, от оборудования до повседневных лабораторных материалов, гарантирует качество и производительность для каждой лаборатории, каждого приложения.

Мы плодотворно сотрудничаем с различными лабораториями медицинской, аграрной, пищевой отраслей, а также с научно-исследовательскими институтами, органами контроля качества и стандартизации, международными организациями и фондами. Специалистами нашей компании реализован целый ряд масштабных проектов, которые получили высокую оценку многих государственных структур и корпоративных клиентов.

Сотрудники сервисного отдела **Компании ТОО Zalma Ltd.** проходят регулярное обучение на тренингах компаний-производителей. Наши сервисные инженеры сертифицированы на проведение IQ OQ/PQ, ремонта и регулярного сервисного обслуживания.

Мы знаем и понимаем задачи, стоящие перед нашими заказчиками, и внимательно следим за развитием рынка передовых лабораторных технологий, старясь максимально быстро внедрять новейшие технологии в практику работы отечественных лабораторий; всегда готовы оказать максимальное содействие и поддержку в системном и комплексном решении задач, стоящих перед нашими партнерами и заказчиками.

Обратитесь к нам, чтобы узнать больше о том, как мы можем помочь вашей лаборатории достичь новых высот.

General Sponsor

«ZALMA Ltd.» LTD.
Almaty, st. Bogenbai Batyr 305A
info@zalma.org
+7 (727) 374 35 70

ZALMA

«ZALMA Ltd.» LTD.
Astana, st. 23-15, building 11, block A, apt. 132
info.astana@zalma.org
+7 (717) 225 99 75

CALL-CENTER +7 701 031 27 29

Zalma Ltd. is one of the fastest-growing and most reliable companies in the Kazakhstan laboratory equipment market. Our main focus is on implementing advanced laboratory technologies and providing comprehensive solutions for domestic laboratories.

Our solutions include the complete outfitting of laboratories with specialized equipment and consumables. We also offer methodological and service support, warranty and post-warranty services, and training for laboratory personnel both at the client's site and at the equipment manufacturer's facilities.

ThermoFisher SCIENTIFIC applied biosystems gibco by Thermo Fisher Scientific ONE LAMBDA A Thermo Fisher Scientific Brand

Our team's undeniable competitive advantage lies in our deep understanding of our clients' primary tasks and our highly effective and constructive approach to solving them. This is achieved through the high professionalism of our staff and our reliable suppliers, including leading international manufacturers of laboratory equipment and materials such as Applied Biosystems™, Invitrogen™, OneLambda™, Gibco™, and many others. Our main supplier, Thermo Fisher Scientific, offers a wide range of products and services, from equipment to everyday laboratory materials, ensuring quality and performance for every laboratory and application.

We collaborate productively with various laboratories in the medical, agricultural, and food industries, as well as research institutes, quality control and standardization bodies, international organizations, and foundations. Our specialists have implemented a number of large-scale projects that have been highly praised by numerous government agencies and corporate clients.

The service department staff at Zalma Ltd. undergo regular training with manufacturer companies. Our service engineers are certified to conduct IQ OQ/PQ, repairs, and regular maintenance.

We understand the challenges our clients face and closely monitor the development of advanced laboratory technologies, striving to implement the latest technologies in the practice of domestic laboratories as quickly as possible. We are always ready to provide maximum assistance and support in systematically and comprehensively solving the tasks faced by our partners and clients.

Contact us to learn more about how we can help your laboratory reach new heights.

Golden Sponsor

Компания “Вельд”

Компания «Вельд» находится в авангарде научных инноваций и с гордостью выступает вашим преданным партнером в предоставлении передового лабораторного оборудования, реагентов и расходных материалов. Благодаря неизменной приверженности качеству, надежности и удовлетворенности клиентов мы остаемся высококвалифицированным дистрибьютором в динамично развивающемся мире лабораторного оборудования. Мы предлагаем широкий ассортимент продукции от ведущих мировых производителей, начиная с самых необходимых вещей в любой лаборатории до уникальных современных аналитических приборов и точнейших лабораторных инструментов. Наше стремление оставаться в лидерах технологических достижений гарантирует вам доступ к новейшим инновациям, которые способны поднять вашу работу на новые, ранее невиданные вам высоты.

Помимо нашего стремления предоставлять первоклассные лабораторные решения, мы гордимся созданием долгосрочных партнерских отношений. Наша компания — не просто поставщик, а соавтор в вашем лабораторном путешествии. Сконцентрировавшись на наших клиентах, мы стремимся понять ваши уникальные требования и предоставить индивидуальные решения, которые будут соответствовать вашим ожиданиям и превосходить их.

Наши сервисные инженеры проходят ежегодные курсы повышения квалификации и имеют действующие сертификаты множества мировых производителей. Установка, калибровка, монтаж, сертификация, гарантийный и пост гарантийный ремонт, а также тренинг по использованию оборудования, все это входит в слуги наших инженеров. Наш ремонтный центр в городе Алматы имеет возможность на ремонтные работы широкого спектра оборудования. Выезд инженера возможен в любую точку Казахстана.

Наш склад, это наша гордость. Компания «Вельд» имеет самые большие складские площади и самые крупные товарные запасы лабораторного оборудования и расходных материалов в центральной Азии. Наличие продукта на складе сокращает доставку товаров и удовлетворяет ваши потребности в самые короткие сроки. Наш склад в городе Алматы обустроен по Европейским стандартам и обеспечивает надежность хранения любого товара.

Добро пожаловать в ТОО «Вельд», где ваш успех в лаборатории является нашим приоритетом!

Golden Sponsor

JUGGERNAUT

НАША КОМПАНИЯ БЫЛА ОСНОВАНА В 2018 ГОДУ И ЗАНИМАЕТСЯ КОМПЛЕКСНЫМ ОСНАЩЕНИЕМ НАУЧНО-ИССЛЕДОВАТЕЛЬСКИХ ЛАБОРАТОРИЙ. МЫ ГОТОВЫ СТАТЬ ЛУЧШИМ ПАРТНЕРОМ ДЛЯ НАШИХ КЛИЕНТОВ, СВОЕВРЕМЕННО ПОСТАВЛЯЮЩИМ НЕОБХОДИМЫЕ ХИМИЧЕСКИЕ РЕАКТИВЫ, РАСХОДНЫЕ МАТЕРИАЛЫ И ЛАБОРАТОРНОЕ ОБОРУДОВАНИЕ, НЕЗАВИСИМО ОТ ТОГО, В КАКОМ ГОРОДЕ КАЗАХСТАНА ОНИ НАХОДЯТСЯ.

МЫ ПРЕДЛАГАЕМ

БОЛЬШОЙ АССОРТИМЕНТ ХИМИЧЕСКИХ РЕАКТИВОВ, РАСХОДНЫХ МАТЕРИАЛОВ И ЛАБОРАТОРНОГО ОБОРУДОВАНИЯ ДЛЯ ЛАБОРАТОРИЙ ВСЕХ ОТРАСЛЕЙ

- МИКРОБИОЛОГИЯ
- МОЛЕКУЛЯРНАЯ БИОЛОГИЯ
- ГЕНЕТИКА И ЦИТОГЕНЕТИКА
- ЛАБОРАТОРНОЕ И МЕДИЦИНСКОЕ ОБОРУДОВАНИЕ
- ГЕННАЯ ИНЖЕНЕРИЯ
- КЛЕТОЧНАЯ БИОТЕХНОЛОГИЯ
- КУЛЬТИВИРОВАНИЕ МИКРООРГАНИЗМОВ
- ИММУНОХИМИЯ И ИММУНОБИОТЕХНОЛОГИЯ

ПОРТФОЛИО НАШЕЙ КОМПАНИИ ВКЛЮЧАЕТ В СЕБЯ ВЕДУЩИХ МИРОВЫХ ПРОИЗВОДИТЕЛЕЙ

- ПРОИЗВОДСТВО РЕАГЕНТОВ, ПИТАТЕЛЬНЫХ СРЕД, АНТИБИОТИКОВ, СЫВОРОТОК КРОВИ ЖИВОТНЫХ ДЛЯ КЛЕТОЧНЫХ КУЛЬТУР
- ОБЩЕЛАБОРАТОРНЫЕ И АНАЛИТИЧЕСКИЕ ХИМИЧЕСКИЕ РЕАКТИВЫ
- ЛИГАНДЫ, СЕЛЕКТИВНЫЕ АНТИБИОТИКИ, АНТИМИКРОБНЫЕ РЕАГЕНТЫ, АДЪЮВАНТЫ ДЛЯ ВАКЦИН И ДР.
- РЕАГЕНТЫ ДЛЯ ФЛУОРЕСЦЕНТНОЙ МИКРОСКОПИИ, АНТИТЕЛА, КОНЪЮГАТЫ, КРАСИТЕЛИ
- НАБОРЫ ДЛЯ ВЫДЕЛЕНИЯ И ОЧИСТКИ ДНК/РНК
- ИФА И ПЦР НАБОРЫ ДЛЯ ВЫЯВЛЕНИЯ БОЛЕЗНЕЙ ЖИВОТНЫХ
- РЕАГЕНТЫ ДЛЯ МОЛЕКУЛЯРНОЙ БИОЛОГИИ, ВКЛЮЧАЮЩИЕ ДНК-ПОЛИМЕРАЗЫ, ГОТОВЫЕ СМЕСИ И РЕАГЕНТЫ ДЛЯ ПЦР/ОТ-ПЦР/РЕАЛ-ТАЙМ ПЦР, КЛОНИРОВАНИЯ, NGS-ПРОБОПОДГОТОВКИ
- РАСХОДНЫЕ МАТЕРИАЛЫ ИЗ ПЛАСТИКА
- НАСТОЛЬНОЕ ЛАБОРАТОРНОЕ ОБОРУДОВАНИЕ, ВЕСЫ, ДОЗАТОРЫ, СИСТЕМЫ ОЧИСТКИ ВОДЫ

НАШИ ПРЕИМУЩЕСТВА

- НАЛИЧИЕ ПРОДУКЦИИ НА НАШЕМ СКЛАДЕ
- ПРЯМЫЕ ПОСТАВКИ ОТ НАШИХ ПАРТНЕРОВ, ЧТО ГАРАНТИРУЕТ ПОЛУЧЕНИЕ ТОВАРА В ОПТИМАЛЬНЫЕ СРОКИ И ОПТИМАЛЬНОЕ ЦЕНООБРАЗОВАНИЕ
- ВЫСОКОКВАЛИФИЦИРОВАННЫЕ СПЕЦИАЛИСТЫ, КОТОРЫЕ МОГУТ ОКАЗАТЬ ПОМОЩЬ В ПОДБОРЕ ТОВАРА
- ОТЛАЖЕННАЯ ЛОГИСТИКА ПО ДОСТАВКАМ В РЕГИОНЫ

050000, РЕСПУБЛИКА КАЗАХСТАН, ГОРОД АЛМАТЫ, ТУРКСИБСКИЙ РАЙОН, ПРОСПЕКТ СУЙІНБАЙ, ДОМ 211
E-MAIL: SELLING1346@GMAIL.COM, SALEJUGGER@GMAIL.COM
ТЕЛ.: 8 (727) 367-17-37; 8 (708) 198-31-93

КОМПАНИЯ JUGGERNAUT ЯВЛЯЕТСЯ ОФИЦИАЛЬНЫМ ДИСТРИБЬЮТОРОМ:

biotium
CAPP
ratiolab disposables for sciences
InvivoGen
SARTORIUS
CAPRICORN SCIENTIFIC
abbexa
BI Biological Industries
NEST
neoFroxx For a greener laboratory
PRIMER DESIGN
Oxford NANOPORE Technologies
iST Innuscreen GmbH
PCRBIOSYSTEMS simplifying research
TPP

Golden Sponsor

TechPrime is a trusted supplier of laboratory equipment, reagents, and chemicals for clinical and research laboratories. We help customers to choose appropriate instruments and reagents for experiments in the field of molecular biology and more since 2017. The expert team consists of molecular biologists, biotechnologists, and bioengineers, who understand laboratory diagnostics and fundamental research from the inside out and know which products are suitable in each case. We cooperate directly with research institutes, genomic centers, and laboratories in tailoring solutions individually for each customer. Every day we are ready to find new solutions for your diagnostic target or life science experiment.

TechPrime offers expertise in the following areas: Clinical Research, Human genomics, Population genomics, Microbiology, Animals, Microbiome, Cancer, Transcriptome, Environmental research & conservation, COVID-19/SARS-COV-2, Infectious diseases, Bioinformatics.

We offer comprehensive solutions for NGS research from sample preparation to sequencing and data analysis. We work with market leaders such as Oxford Nanopore Technologies, New England Biolabs, Thermo Scientific, Nimagen, and Diagenode.

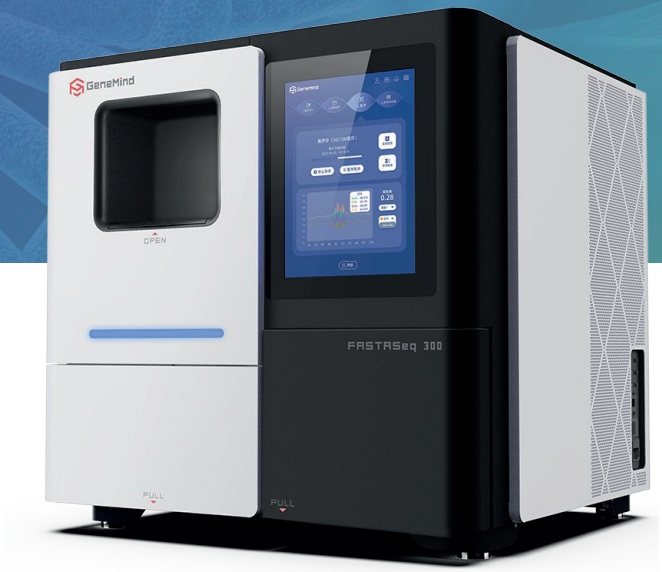
Golden Sponsor

SESANA

GeneMind

FASTASEQ 300

- Совместим с TruSeq/NexteraTM
- 100 - 250 M прочтений
- 4 независимые дорожки в 1 ячейке



НОВЫЙ СТАНДАРТ СКОРОСТИ В NGS

Благодаря усовершенствованной химии, а также параллельному проведению реакции, регистрации и обработки сигнала, FASTASeq 300 позволяет проводить секвенирование PE150 всего за 21 час, выдавая при этом 30 Гб данных.

sales@sesana.ru www.sesana.ru +7(495)128-82-74

Golden Sponsor

SESANA

GeneMind

Ячейка	Прочтений	Тип	Выход, Gb	Q30	Время,часов
FCM	100 M	SE75	7,5	85	7
		PE75	15	85	13
		PE150	30	80	21
FCH	250 M	SE75	18,5	85	8
		PE75	37,5	85	14
		PE150	75	80	24

	Количество информации на образец	Количество образцов за запуск
Экзом человека	12 Gb	6
Транскриптом*	30M прочтений SE75	8
НИПТ / ПГТ	5M прочтений SE75	50
Малая онко-панель	2 Mb	до 384
Малые геномы	6 Mb	до 384
Метагеномное секвенирование (mNGS)	20M прочтений PE150	12

*FASTASeq 300 подходит для секвенирования единичных клеток (scRNAseq)

sales@sesana.ru www.sesana.ru +7(495)128-82-74

Bronze Sponsor

LAB Instruments

Компания «ЛАБИНСТРУМЕНТЫ» предлагает комплексные решения в оснащении научных и исследовательских лабораторий, а также в поставке лабораторного оборудования и приборов, расходных материалов для науки и производства.

Основные поставщики компании «ЛАБИНСТРУМЕНТЫ» — хорошо зарекомендовавшие себя Китайские производители: **Innova, Labwit, Midea Biomedical, Yocell, CytoNiche, Pri-Eco, Li-Ca, Farcitech, Healthy Photon, Laboao, Jiupo** и многие другие. Это обеспечивает высокое качество поставляемой продукции и надежность предлагаемых технических решений.

Коллектив нашей компании обладает большим опытом комплексного оснащения лабораторий научных учреждений, биотехнологических и фармацевтических производств. Ориентируясь на индивидуальный подход к покупателям, сотрудники компании по Вашей заявке помогут приобрести, доставить и ввести в эксплуатацию редкое и уникальное оборудование от производителей, не представленных на рынке.

Цель компании «ЛАБИНСТРУМЕНТЫ» — предложить Вам, нашему покупателю, разнообразный ассортимент качественных товаров и профессиональный сервис. А накопленный нами опыт, знания и желание развиваться дальше сделают наше предложение максимально выгодным для Вас.

Сфера деятельности

Компания «ЛАБИНСТРУМЕНТЫ» обеспечивает полный комплекс услуг для решения задач, поставленных покупателем:

- сотрудники компании, имеющие большой опыт работы в научно-исследовательских учреждениях, помогут выбрать оборудование для решения конкретной задачи и подберут оптимальный вариант по соотношению цена-качество;
- мы осуществляем доставку оборудования от производителя до заказчика, используя отлаженную систему логистики;
- высококвалифицированные инженеры сервисной службы выполняют ввод в эксплуатацию, гарантийное и послегарантийное обслуживание приобретенного оборудования;
- сервисная служба компании «ЛАБИНСТРУМЕНТЫ» предлагает услуги по ремонту и дальнейшему обслуживанию приборов производства независимо от источника покупки, а также морозильного оборудования любых марок и года выпуска, возможен выезд инженера в регионы.
- связавшись с нашими специалистами, Вы можете сделать заявку на интересующие Вас каталоги производителей, представленных на нашем сайте.

+7(499)213-2652

sales@labinstruments.ru

INNOVA The passion for science

Midea | Biomedical

Bronze Sponsor

LAB Instruments

Midea | Biomedical

LABWIT®

Фармацевтические холодильники

Шейкеры лабораторные

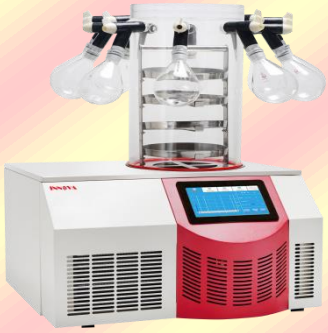
INNOVA

The passion for science

Лабораторные посудомоечные машины

Спектрофотометры

Лиофильные сушилки



Bronze Sponsor

ЛАБ Инструменты

ООО «ЛАБИНСТРУМЕНТЫ»
+7(903)762-0296
+7(499)213-2652, доб. 901
sa@labinstruments.ru
www.labinstruments.ru

ЛАБОРАТОРНОЕ ОБОРУДОВАНИЕ ДЛЯ ИЗУЧЕНИЯ И ВЫРАЩИВАНИЯ РАСТЕНИЙ

Оборудование для анализа фотосинтеза, для анализа физиологических и морфологических параметров растений, системы измерения газообмена растений, климатические камеры для выращивания растений, фотобиореакторы для культивирования водорослей и многое другое!

ВСЕГДА САМЫЕ НИЗКИЕ ЦЕНЫ ДЛЯ ВАС!

В нашем ассортименте самое современное научное оборудование от ведущих мировых производителей!

Анализаторы параметров растений
Анализаторы площади листьев RC-70, RC-80, RC-90, Rinch
Анализатор листового индекса RC-100, Rinch
Анализатор транспирации растений RC-TRM01, Rinch
Анализатор зерна FG1030-C, LICA
Измерители уровня хлорофилла RC-SPAD01, RC-SPAD02, Rinch
Имаджер корней растений RhizoScan In Situ, PRI-ECO

Анализаторы газообмена (дыхания) растений
Система измерения газообмена растений RC-P60, Rinch
Изотопная система измерения газообмена растений IPS-1000, PRI-ECO

Фотобиореакторы для культивирования водорослей и др.
Фотобиореактор с рабочим объёмом 5 литров LBR-5GJG, LABOAO
Фотобиореактор с рабочим объёмом 200 литров LBR-200SJAG, LABOAO

Камеры климатические для выращивания растений
Камеры серии Smart and Simple, объем 50-200 литров, JIUPO
Камеры серии Plant Growth, объем 300-2000 литров, JIUPO
Камеры серии Seed Preservation, объем 300-2000 литров, JIUPO
Камеры серии Tissue Culture, объем 300-2000 литров, JIUPO

ЛАБ Инструменты

ООО «ЛАБИНСТРУМЕНТЫ»
+7(903)762-0296
+7(499)213-2652 (доб. 901)
sa@labinstruments.ru
www.labinstruments.ru

ЛАБ Инструменты

ООО «ЛАБИНСТРУМЕНТЫ»
+7(903)762-0296
+7(499)213-2652, доб. 901
sa@labinstruments.ru
www.labinstruments.ru

ЛАБОРАТОРНОЕ ОБОРУДОВАНИЕ ДЛЯ ИЗУЧЕНИЯ ОКРУЖАЮЩЕЙ СРЕДЫ

Системы измерения газообмена почв, анализаторы параметров почв, газоанализаторы парниковых газов, станции eddy covariance и другое!

ВСЕГДА САМЫЕ НИЗКИЕ ЦЕНЫ ДЛЯ ВАС!

Анализаторы параметров почв

Система измерения влажности и температуры почвы Plover TDR, PRI-ECO

Портативные однокамерные системы измерения газообмена почв

Система PS-9000 (CO_2/H_2O), LICA
Система PRI-8610 (CO_2/H_2O), PRI-ECO
Система PRI-8610U (CO_2/H_2O) ультракомпактная, PRI-ECO
Система PRI-8620 ($CO_2/H_2O/CH_4$), PRI-ECO
Система PRI-8630 ($CO_2/H_2O/N_2O$), PRI-ECO
Система PRI-8640 ($CO_2/H_2O/CH_4/N_2O$), PRI-ECO

Стационарные многокамерные системы измерения газообмена почв

Система SF-9000 (до 18 камер), LICA
Система PRI-8600D/Long-Term (до 32 камер), PRI-ECO

Газоанализаторы парниковых газов портативные

Портативный газоанализатор (CO_2, H_2O) PS-9000, LICA
Портативный газоанализатор (CO_2, H_2O) HT8810, Healthy Photon
Портативный газоанализатор (CO_2, H_2O) PRI-8610, PRI-ECO
Портативный газоанализатор (CH_4, N_2O, H_2O) HT8820, Healthy Photon
Портативный газоанализатор (CO_2, N_2O, H_2O) HT8830, Healthy Photon
Портативный газоанализатор (CO_2, N_2O, H_2O) PRI-8630, PRI-ECO
Портативный газоанализатор (CO_2, CH_4, H_2O) HT8840, Healthy Photon
Портативный газоанализатор (CO_2, CH_4, H_2O) PRI-8620, PRI-ECO
Портативный газоанализатор (CO_2, CH_4, N_2O, H_2O) HT8850, Healthy Photon
Портативный газоанализатор (CO_2, CH_4, N_2O, H_2O) PRI-8640, PRI-ECO

Газоанализаторы парниковых газов для станций eddy covariance

Газоанализатор H_2O открытого типа HT1800, Healthy Photon
Газоанализатор N_2O открытого типа HT8500, Healthy Photon
Газоанализатор CH_4 открытого типа HT8600, Healthy Photon
Газоанализатор NH_3 открытого типа HT8700, Healthy Photon
Газоанализатор CO_2, H_2O закрытого типа PRI-5251e, PRI-ECO

ЛАБ Инструменты

ООО «ЛАБИНСТРУМЕНТЫ»
+7(903)762-0296
+7(499)213-2652 (доб. 901)
sa@labinstruments.ru
www.labinstruments.ru

Bronze Sponsor

Location: Astana
Region: CIS countries +
(Kazakhstan, Uzbekistan, Azerbajan,
Armenia, Georgia, Kyrgyztan, Tadjikistan)
Market area: Biopharma, Life Sciences
E-mail: info@advena-bio.com
Phone: +7 705 182 11 07

advena

Cell Biology

Flow Cytometry,
Cell Sorting, Digital Imaging,
Cell culture Media, FBS,
Real-time Cytotoxicity,
FC Antibodies,
Immunotherapeutic assays,
Cell culture plastic & reagents

Base Equipment

Freezers,
Deep-Freezers,
Centrifuges,
Biosafety Cabinets,
Cryo Storage,
CO2-incubator,
Shakers

Molecular Biology

dPCR, qPCR,
classic PCR, dNTPs,
NA Purification Station
& Kits, research PCR-tests,
Ferments, Plastic & Reagents,
NGS reagents,
Sanger sequensing

Protein Analysis & Biotechnology

FPLC, Resins, Gel-documentation,
Up-stream,
Filtration solutions, TFF,
Down-stream, Microbiology
Counters, Oligosynthes,
R&D platforms, SFM

advena-bio.com

Bronze Sponsor

Location: Astana
Region: CIS countries +
(Kazakhstan, Uzbekistan, Azerbajan,
Armenia, Georgia, Kyrgyztan, Tadjikistan)
Market area: Biopharma, Life Sciences
E-mail: info@advena-bio.com
Phone: +7 705 182 11 07

logos biosystems

NimaGen.

sePax Sepax Technologies

SERVA Electrophoresis

MERCK

R&D SYSTEMS

SONY Sony Biotechnology Inc.

QIAGEN

SARSTEDT

KLAB Keen Innovative Solutions

Cell Signaling TECHNOLOGY®

hanil

汉邦科技 Hanbon Sci.& Tech

centrion BIO SCIENTIFIC TECHNOLOGY

iCLUEBIO

MABTECH

*Not all the brands are available
for all the countries*

@ADVENA_LSG

advena-bio.com

Bronze Sponsor

ТОО Научно-производственная фирма «Медилэнд» организованная в 1993 году, специализируется в области поставок медицинской техники, оборудования и расходных материалов для медицинских и научных лабораторий и является официальным дистрибьютором на территории Казахстана ведущих мировых производителей, таких как Apacor (Великобритания), Arctiko (Дания), Bandelin (Германия), BD Biosciences (США), BioMerieux (Франция), BioSan (Латвия), BioSystems S.A (Испания), Boditech Med Inc. (Южная Корея), Brand (Германия), CHROMagar (Франция), Evoqua (Германия), EXIAS Medical GmbH (Австрия), QINGDAO HAIER BIOMEDICAL (Китай), Eppendorf (Германия), Instrumentation Laboratory (США), Kojair (Финляндия), Lauda (Германия), Martin Christ (Германия), Memmert (Германия), Nabertherm (Германия), Snibe Co. Ltd (Китай), Sartorius (Германия), Sebia (Франция), Sigma Laborzentrifugen (Германия), Sysmex Corporation» (Япония), Systec (Германия), YD Diagnostics Corporation (Республика Корея). Компания обеспечивает сервисное и постгарантийное обслуживание поставленного оборудования, проводит обучение специалистов организаций-заказчиков методикам работы на приборах и оказывает консультационную поддержку по поставляемому оборудованию в различных областях применения. Все специалисты компании регулярно проходят обучение и повышают свою квалификацию на заводах компаний-производителей и имеют соответствующие сертификаты.

ТОО «НПФ Медилэнд» ставит перед собой цели по внедрению инновационных технологий в области медицины и исследовательского оборудования, предоставляя в распоряжение клиентов последние технические разработки наряду с приборами, уже зарекомендовавшими себя и проверенными обширной практикой пользователей. Компания осуществляет консультирование клиента от этапа выбора оборудования с максимальным учетом его целей, задач и запросов, до послепродажной информационной поддержки в виде:

- организации и проведения учебных семинаров и научно-практических конференций;
- поддержке участия пользователей в международных программах фирм-производителей предлагаемого оборудования;
- оказания консультативно-методической и практической помощи пользователям оборудования;
- регулярного информирования о новинках в методиках, технологиях и оборудовании для клинической диагностики.

ТОО «ЛаборФарма»

Входит в Группу компаний «Алтей» и работает на лабораторном рынке Казахстана с 1992 года. В Группу компаний «Алтей» входят ТОО «ЛаборФарма» и ПК ТОО «Lezart».

ТОО «ЛаборФарма» поставляет:

- различное лабораторное, аналитическое и медицинское оборудование и приборы,
- лабораторную мебель,
- реагенты,
- стеклянную, пластиковую, фарфоровую посуду,
- расходные материалы,
- средства защиты и т.п.

Мы поставляем товары 200+ брендов со всего мира.

ТОО «ЛаборФарма» является официальным дистрибьютором таких известных компаний как: SHIMADZU Europa GmbH, Velp Scientifica Srl, Memmert GmbH, Preekem, ASEM srl, TOP AIR Systems, ColeParmer (бренды BibbyScientific, Electrothermal andTechne, Stuart, Specs). WESTMEDICA mbH, Astori Technica, Isolab GmbH, LGC Standards, Reagecon Diagnostic, Vitlab GmbH, Duran DWK Group и других.

По поставке реагентов, лабораторной посуды, систем водоподготовки, фильтрации и расходных материалов мы являемся авторизированным дистрибьютором всемирно известных брендов входящих в MERCK GROUP: MERCK, Millipore, Sigma-Aldrich GmbH.

Ассортимент поставляемой продукции насчитывает свыше 100 000 наименований товаров, и он постоянно растет.

Мы имеем собственный оборудованный склад площадью более 1200 м2, на котором в наличие всегда большой выбор стеклянной и пластиковой лабораторной посуды общего назначения, мерной посуды, различных приборов и установок из стекла, аналитических приборов, химических реактивов общего назначения, индикаторов, органических растворителей, стандартных образцов, прекурсоров и ядов, расходных материалов.

У нас имеется собственное казахстанское производство мебели под торговой маркой Лезарт. А также производство аттестованных смесей пестицидов и микотоксинов.

Мы имеем 3 торгово-выставочных зала для удобства наших клиентов: 2 в г. Алматы и 1 в г. Астана. В ближайшем будущем для наших заказчиков откроет двери также новый демонстрационно-учебный центр.

В штате нашей компании более 50 высококвалифицированных специалистов, среди которых опытные химики, микробиологи, сервис-инженеры, метрологи, логисты, работники склада.

У нас более 7000 заказчиков по всему Казахстану. Нашими постоянными покупателями являются Национальные Центры экспертизы и сертификации, Национальный центр экспертизы лекарственных средств, центры судебной экспертизы, все фармацевтические компании Казахстана, производители пищевых продуктов, большинство ведущих университетов, институтов и НИИ, ветеринарные лаборатории, больницы и медицинские центры, военные организации, школы и другие предприятия.

Мы оказываем нашим заказчикам всестороннее сервисное обслуживание и техническую поддержку:

Сертифицированные сервис-инженеры

Инсталляция и постпродажное обслуживание поставляемого оборудования

Обучение специалистов заказчика

Сервисное обслуживание и ремонт

Методическая и Метрологическая поддержка

АЛЬГИМЕД

Комплексное оснащение лабораторий в Казахстане

Компания Альгимед - один из ведущих поставщиков реагентов и химических реактивов, оборудования и мебели для лабораторий различной направленности.

Обратившись в нашу компанию вы получаете:

Помощь опытных специалистов в подборе оптимального решения в соответствии с потребностями вашей лаборатории;
Персональный подход и индивидуальное предложение, учитывающее все аспекты: актуальность продукции, специальные предложения и бонусы компании и наших партнеров;
Послепродажное сопровождение и поддержка с выездом на инсталляцию, запуск оборудования, обслуживание и ремонт, проведение обучения по использованию оборудования для ваших сотрудников.

Наши направления
Мы имеем большой опыт поставок лабораторного оборудования, химических реактивов, наборов реагентов и различных расходных материалов для лабораторий в таких областях как фармацевтика, медицина и здравоохранение, пищевая безопасность, микроскопия, судебная экспертиза, оборудование и реагенты для NGS, цитологии и патоморфологии и др.

Все оборудование поставляется с необходимыми для эксплуатации лицензиями, сертификатами, регистрационными удостоверениями, инструкциями и прочими разрешительными документами.

Партнеры
На сегодняшний день компания ТОО «Альгимед» является официальным партнером многих мировых компаний и имеет возможность поставлять оборудование и расходные материалы на более выгодных для конечного потребителя условиях. Список наших партнёров постоянно увеличивается.