PROCEEDINGS

of the 4th International conference

"Plant Genetics, Genomics, Bioinformatics and Biotechnology"

(PlantGen2017)

Best Western Plus Atakent Park Hotel

May 29 – June 02, 2017,

Almaty, Kazakhstan

УДК 581 (063)

ББК 28.5

Р71

"Plant Genetics, Genomics, Bioinformatics and Biotechnology": Материалы Международной конференции 4th International conference PlantGen2017 / *под общей редакцией Е.К. Туруспекова, С.И. Абугалиевой.* – Алматы: ИББР, 2017 – 216 с.

ISBN 978-601-80631-2-1

В сборнике представлены материалы 4 Международной конференции по генетике, геномике, биоинформатике и биотехнологии растений (**PlantGen2017)**, проведенной в г. Алматы 29 мая -2 июня 2017 г. В публикациях изложены результаты оригинальных исследований в области изучения, сохранения и использования генетических ресурсов, генетики и селекции, биоинформатики и биотехнологии растений.

Сборник рассчитан на биологов, генетиков, биотехнологов, селекционеров, специалистов, занимающихся генетическими ресурсами растений, и студентов биологического и сельско-хозяйственного профиля.

Тезисы докладов представлены в авторской редакции.

***Рекомендовано к изданию Ученым советом РГП «Института** биологии и биотехнологии растений» Комитета науки Министерства образования и науки Республики Казахстан* (Протокол № 2 от 04.05.2017 г.).

УДК 581 (063)
ББК 285

ISBN 978-601-80631-2-1

Proceedings of the 4th International Conference "Plant Genetics, Genomics, Bioinformatics and Biotechnology" (PlantGen2017)

May 29 – June 02 2017 – Almaty, Kazakhstan

Editors

Yerlan Turuspekov, Saule Abugalieva

Publisher

Institute of Plant Biology and Biotechnology

Plant Molecular Genetics Lab

ISBN: 978-601-80631-2-1

Date: May 29 – June 02 2017

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

Conference webpage: http://primerdigital.com/PlantGen2017/en/

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

IPBB

Correct citation: Turuspekov Ye., Abugalieva S. (editors) (2017) Proceedings of the 4th International conference "Plant Genetics, Genomics, Bioinformatics and Biotechnology" (PlantGen2017), Almaty, Kazakhstan, May 29 – June 02 2017, IPBB, Almaty, Kazakhstan; ISBN 978-601-80631-2-1

ISBN 978-601-80631-2-1

Welcome Greetings from the organizers

With great privilege and pleasure my team and I took over responsibility to organize the 4th PlantGen 2017 international conference in Almaty, Kazakhstan. Approximately 200 participants from 15 different countries of the World are attending this event. We will witness 12 plenary talks from leading scientists in the field of Plant Genetics, 46 oral and 71 poster presentations, among them 38 presenters are students.

We often say that Kazakhstan is the land where East meets West, and it is truly multicultural country where over 130 ethnics groups living in peace and friendship. Therefore, it is very symbolic that we have large groups of colleagues attending this forum from almost all former USSR countries, from Europe, from Far East and West Asia. We are happy to see here old friends and looking forward to find new friends and partners!

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

I also thank my co-chair of the International Organizing Committee Dr. Elena Salina for her enthusiastic work in advertising this forum in Russian Federation, and we are very happy to have more than 60 attendees from the Russian Federation, and this is a largest group among foreign countries.

My special thanks to Dr. Ruslan Kalendar (NCB, Astana, Kazakhstan), who was in charge of our web page design and administration.

Without sponsors and industry support this conference could not be accomplished. Therefore, I appreciate all our supporters, including the administration of the Best Western Plus Atakent Park Hotel - the venue of this event, for their valuable help to host this conference in Almaty.

Finally, I am grateful to all participants of the PlantGen 2017 for your interest in this conference and trust that you will enjoy presentations, exchange ideas and knowledge, establish new contacts and cooperation, and appreciate your stay in Almaty, Kazakhstan.

Yerlan Turuspekov
Chairman of the International
Organizing Committee PlantGen 2017,
IPBB, Almaty, Kazakhstan

Session 1.

Genetic Resources and Evolution

TAXONOMY, ARCHITECTONIC OF PLANT AND MOLECULAR PHYLOGENY OF THE GENUS *Triticum* L.

N. P. Goncharov

Institute of Cytology and Genetics, Novosibirsk, Russia
e-mail: gonch@bionet.nsc.ru

Searching for ways of biodiversity increasing and preservation is the key point in biology of the 21st century, whereas increasing and preservation of cultivated wheat species biodiversity is a strategic task of food security. The first step of reasonable biodiversity preservation is drawing up a phenotypic identification and inventory and the second is its genetic and taxonomic analysis.

Distribution areas of wheat landraces, local endemic species and their related wheat species are continuously reducing. So collecting, replenishing, reproducing, studying and maintaining those species living, being a constant supply for breeding are important to preserve biodiversity resources and future food security. It is obviously not feasible to gather again Vavilov's or Kihara's wheat biodiversity collections, even after following the routes of their expeditions. Nature has not spared the biodiversity existing in their times, and this emphasizes the significance of reasonable maintenance of the maximally possible biodiversity presently stored in genebanks. The questions of how to preserve and of what to undertake so that biodiversity would not be subjected to erosion are more timely as ever. Reduction in the natural areas of wild endangered wheat species, as well as in their polymorphism due to their reproduction in small populations: in genebanks, decrease the potential biodiversity of cultivated wheat species. To knowledgeably preserve gene pools maintained as small size populations, accessions should be fuller genetically characterised. This would allow goal-oriented preservation of the natural gene pool of the accessions. Rearrangement of huge germplasm bank collections is the taxonomy task.

Traditionally, the taxonomy methods are based on revealing the affinity among organisms, determining the homology of their traits and common origin. At present, there is a tendency of juxtaposition of classical taxonomy, which had historically developed on the basis of comparative morphology, against modern taxonomy based on genetic and molecular-genetic investigations. The main goal of modern wheat taxonomy is to establish such a classification of whear genera and species which would reflect both their phylogenetic relationships and genetic structure. Good and rigorous taxomony is necessary for effective conservation and increasing cultivated plant biodiversity by introgressive hybridization. This is complicated by the lack of consensus concerning the taxonomy of wheat species and subspecies and by unresolved questions regarding the domestication and spread of naked wheats.

Poor classifications are not just less useful, they are positively harmful. In the absence of acceptable criteria for distinguishing individual taxa, genebank staff cannot be expected to monitor the purity of their accessions, and important accessions may be eliminated because their significance is not appreciated. Indeed, failure to provide formal taxonomic, and hence nomenclatural, recognition of distinct entities may lead to what Dr. Michael Windham has referred to as ''extinction by nomenclature.'' Clearly, a classification that requires expertise in cytogenetic and/or molecular genetics will not be practical for many of those who work with *Triticum*. What is needed is a classification system that takes account of phylogenetic, cytogenetic, and molecular information but is accompanied by detailed morphological descriptions, workable keys, and correct nomenclature. The place of some subspecies in the genera *Triticum* taxomony is discussed.

Swaminatan and Rao (1961) showed that differences in taxonomically important traits of hexaploid wheats are controlled by four pairs of nonallelic genes. The review examines the state of knowledge about those taxonomically important genes which control the architectonics of wheat plant (spike morphology). These knowledge gaps hinder crop diversity conservation efforts and allows to produce a modern wheat commercial cultivars.

The work was supported by the Russian Science Foundation (grant number: 16-16-10021).

THE EVOLUTION OF THE WHEAT GRASSES: CENOGENOME VS. TAXONOMIC DIVERSIFICATION

***Frank R. Blattner**, Nadine Bernhardt*

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

E-mail: blattner@ipk-gatersleben.de

The wheat grasses (Triticeae–Poaceae) are notorious for their complex patterns of evolutionary relationships. This is partly due to the high amount of allopolyploid taxa combining the genomes of two to four parental species/genera. But also on the level of diploid taxa phylogenetic inference did up to now not result in a convincing hypothesis of species relationships, although numerous molecular studies were conducted during the last 25 years. The partly contradictory results can be attributed to (*i*) differences in methodology (i.e. analysis methods) and also (*ii*) taxon sampling heavily influences the outcome of such analyses. In addition (*iii*) also the studied loci (i.e. chloroplast or different nuclear genomic regions) seems to have a certain impact on the results obtained in phylogenetic analyses.

To better understand this latter topic and to come up with a conclusive phylogenetic hypothesis for the diploid members of Triticeae we used next-generation sequencing to obtain gene trees from 250 genes evenly distributed over the seven chromosomes of the members of the tribe. In addition we assembled the chloroplast genomes of 183 individuals, representing 53 species. Phylogenetic analyses were conducted with Bayesian and maximum-likelihood algorithms, and species trees were deduced from gene trees in a coalescent framework.

Comparison of the phylogenies of single loci showed that the 250 analysed genes resulted all in different phylogenetic trees, partly deviating considerably from each other. Multispecies coalescent analysis showed that the *Psathyrostachys* and *Hordeum* lineages originated first within the tribe while the species of *Aegilops*, *Amblyopyrum* and *Triticum* constitute the youngest group of genera. The other Triticeae taxa (among them *Agropyron*, *Dasypyrum*, *Eremopyrum*, *Secale*, *Taeniatherum*) group in between.

Analysing hybridisation signal in the dataset we identified several diploid lineages, which seem to have originated via reticulate evolution, i.e. involving initial homoploid hybrid speciation. But also introgression of genomic regions, due to hybridisation and repeated backcrossing of the hybrid with one parent, is an important mechanism that, together with differential sorting of ancient polymorphisms (i.e. incomplete lineage sorting), contributes to a pan genome-like structure of the Triticeae gene pool that we term *cenogenome*. Recognition of this cenogenome provides a framework to better understand the evolution of the lineages within the tribe and the permeable and fluent nature of Triticeae genomes.

BARLEY GENETIC RESOURCES AND DEVELOPMENT OF GENOTYPING INFRASTUCTURE

T. Tanaka

Institute of Crop Science, NARO, Ibaraki, Japan

E-mail: tstanaka@affrc.go.jp

Barley (*Hordeum vulgare* L.) is the fourth most important cereal crop and used for many purposes including human food, malting and animal feed. After the publication of a draft genome sequences of the North American six-row spring malting barley cultivar "Morex" by the International Barley Sequencing Consortium (IBSC) in 2012, genome wide study has been accelerated even in barley. However, in Japanese barley breeding, genome wide study is still backward. To overcome this situation, we have developed the infrastructure for barley genome study using Japanese barley cultivars. We determined transcriptome and genome data of Haruna Nijo, a Japanese malting barley cultivar, and developed a database, named bex-db (http://barleyflc.dna.affrc.go.jp/bexdb/), to provide them comprehensively. We are consolidating genotypic diversity of Japanese barley cultivars on Haruna Nijo genome and RNA-Seq data from each cultivar. Since mapping of RNA-Seq data showed better mapping on Haruna Nijo genome than the latest version of Morex genome,we consider that genome-wide information from closer cultivars produces great effects to the domestic breeding. In this presentation, I will survey current infrastructure of barley genome data in Japan from the view point of bioinformatics.

COLLECTION AND EVALUATION OF ENDEMIC AND RARE SPECIES OF FLORA IN KAZAKHSTAN

***S. Abugalieva*[1], *A. Ivaschenko*[2], *M. Ishmuratova*[3], *Y. Kotukhov*[4], *A. Danilova*[4], *A. Myrzagalieva*[5], *P. Veselova*[6], *G. Kudabayeva*[6], *G. Sitpayeva*[6], *A. Imanbayeva*[7], *G. Sakauova*[8], *A. Kakimzhanova*[9], *Y. Turuspekov**[1]**

1 – Institute of Biology and Biotechnology, Almaty, Kazakhstan;
2 – Ile-Alatau National Nature Reserve, Almaty region, Kazakhstan;
3 – Karaganda State University, Karaganda, Kazakhstan;
4 – Altai Botanical Garden, Ridder, Kazakhstan;
5 – East Kazakhstan State University, Ust-Kamenogorsk, Kazakhstan;
6 – Institute of Botany and Phytointroduction, Almaty, Kazakhstan;
7 – Mangyshlak Experimental Botanical Garden, Aktau, Kazakhstan;
8 – Karatau National Nature Reserve, Kentau, Kazakhstan;
9 – National Biotechnology Centre, Astana, Kazakshatn

e-mail: yerlant@yahoo.com

Kazakhstan is the ninth-largest country in the world by territory, and it is home to more than 6,000 plant species. In 2015, a new project was launched with the main goal being to study genetic variation of endemic, rare, and economically important plant species in National State Reserves and National Nature Parks of Kazakhstan. Genetic diversity of plant populations will be studied by using different types of DNA markers, including universal markers of nuclear and chloroplast genomes. The project combines the efforts of botanists and geneticists from National State Reserves and State National Nature Parks, National Universities, Botanical Gardens, and two Biotechnology Research Institutes. Currently nearly 600 populations representing 439 species were collected in fifteen National Parks and Reservations across the country. Exact location of species growth was recorded per each sampling site by use of GPS. Herbarium samples were prepared for each species as well. DNA samples were extracted predominantly from fresh leaves of collected populations and purified DNA were kept at -80^{0}C freezer. Currently the entire collection of DNA samples under the genetic evaluation using DNA barcodes of ITS (internal transcribed spacers), matK and rbcL.

The research was conducted in the framework of the Program 0237/PTF-14 supported by the Ministry of Education and Sciences of the Republic of Kazakhstan (duration: 2015-2017).

MOLECULAR AND AGRO-MORPHOLOGIC CHARACTERIZATION OF EINKORN (*T. MONOCOCCUM*) AND EMMER (*T. DICOCCON*) HULLED WHEAT LANDRACES

Kahraman GURCAN[1], Fatih DEMIREL[2], Mehmet TEKIN[3], Taner AKAR[3*]

[1]Department of Agricultural Biotechnology, Faculty of Agriculture, Erciyes University, Kayseri, Turkey

[2]Department of Field Crops, Faculty of Agriculture, Igdır University, Iğdır, Turkey

[3]Department of Field Crops, Faculty of Agriculture, Akdeniz University, Antalya, Turkey

[*]e-mail: tanerakar@akdeniz.edu.tr

Hulled wheats were among the earliest domesticated plants and known to be benefited for many millennia in Near East including Turkey. Hulled wheat species are neglected in many countries. However its farming has been continued in some region of Turkey for many millennia and represents useful sources for broadening the genetic base of prominent wheat breeding germplasm due to increasing demands for diversity and quality of food. In this research, hulled wheats and registered wheat varieties were characterized at agro-morphological and molecular level. 65 hulled wheat populations were collected from Kastamonu (23), Kars (15), Konya (16) and Kayseri (11) provinces of Turkey. Quantitative traits such as plant height, grain per spike, single plant yield, heading time, maturity time, 1000 kernel weight, protein ratio and qualitative traits such as hairiness, glaucosity, growth habitus and grain hull were determined for each population. 23 hulled wheat population collected from Kastamonu province were distinguished into 9 emmer (*T. dicoccon*) and 14 einkorn (*T. monoccocum*) wheats at morphologic level. Kars, Konya and Kayseri populations were characterized as hexaploid wheat landraces, einkorn and emmer, respectively. Protein ratios of hulled wheats were higher than registered varieties. All the genotypes were distinguished by molecular characterization based on 11 polymorphic SSR primers analyzed through capillary system. The SSR loci analysis produced alleles ranging from 6 to 16 with a mean value 9. The lowest, mean and highest polymorphism information content (PIC) values of the populations were 0.5, 0.67 and 0.86, respectively. To sum up, these results illustrated a large genetic variation of these germplasm to be used as a progenitor for further wheat breeding program.

This research was financially supported by the Erciyes University Scientific Research Projects Coordination Unit, Turkey.

PHYLOGENETIC ANALYSIS OF ENDEMIC SPECIES *OXYTROPIS ALMAATENSIS* BAJT. FROM KAZAKHSTAN

Sh.S. Almerekova [1,2], ***N.M. Mukhitdinov*** [2], ***M.S. Kurmanbayeva*** [2]

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

Family *Fabaceae*, comprising 750 genera and over 18,000 species, is one of the largest family of dicotyledonous with the high economic value. *Oxytropis* is an important genus of the family *Fabaceae*. *Oxytropis* DC. represents comprehensive taxonomic genera, which includes about 450 species, with the greatest diversity in the mountains of Asia (Malyshev, 2008). In Kazakhstan, the genus is represented by 124 species, and 10 are listed as endangered (Red List of Kazakhstan, 2014). The loss of rare species of plants under the influence of any negative factors, regardless of their nature, is a global problem with serious consequences, the extinction of any species - is an irreparable loss. Conservation of rare species and prevent their extinction by Yu. Zlobin et al. (2013) has become one of the main scientific and organizational problems ecologists and botanists all over the world. The aim of present study was to examine the phylogenetic position of rare, narrowly endemic species with a threatened area of distribution *Oxytropis almaatensis* Bajt.

Plant materials were collected from 3 natural populations from Trans Ili Alatau Mountains in 2016. The plant leaves collected randomly and dried in silica gel. Total genomic DNA was extracted using a modified CTAB protocol (Doyle & Doyle 1987), which detailed in Sramko *et al.* (Sramkó *et al.* 2014). The phylogenetic position of *Oxytropis almaatensis* was investigated by DNA sequences of the *nr*ITS. The phylogenetic analysis was conducted by Neighbor Joining (NJ) in MEGA 5. And analysis involved 24 nucleotide sequences, including our object of study *Oxytropis almaatensis.* The size of the aligned nucleotide sequences of ITS 601 bp. The names of the sections and subgenus are given according to the Malyshev (2008).

The phylogenetic analysis of *Oxytropis* species generated 2 clades. The clade I represented by the subgenus: *Phacoxytropis* (*Mesogaea*), *Physoxytropis* (*Lycotriche*) and *Oxytropis* (*Chrysantha*). The section *Mesogaea* from subgenus *Phacoxytropis* represented by following species *O.deflaxa, O.kansuenesis, O.glabra.* The section *Janthina* of the same subgenus is together with the subgenus *Oxytropis* sections. *O.pallasii, O.pilosa* and *O.almaatensis* from section *Chrysantha* and subgenus *Oxytropis* are together with the *Phacoxytropis* sections in clade I. Our object of study *O.almaatensis* is closely related to the *O.glabra,* but both of them are belongs to different subgenus and section based on classification. Most species in clade II are belongs to the subgenus *Oxytropis*, except *O.caerulea, O.filiformis*, which are correspond to the section *Janthina* of subgenus *Phacoxytropis.* Sections of this clade are *Polyadena, Verticillares, Orobia, Xerobia, Gloeocephala, Arctobia*. The analysis of ITS region showed monophyly of *Oxytropis* genus, as it is confirmed by other scientists before. According to the ITS sequences *O.almaatensis* phylogenetically closely related to the species *O.glabra* from section *Mesogaea. O.almaatensis* and *O.glabra* species have the same nucleotide variation at positions 57, 201, 548, but different at the positions 67, 117, 422 which suggest that these mutation can be used in differentiation of these two species.

PLANT DEVELOPMENT TYPE AND ITS CORRELATION WITH OTHER TRAITS IN *LUNARIA* GENUS (*CRUCIFERAE*)

Olena Boika

Zaporizhzhya National University, Zaporizhzhia, Ukraine

*e-mail: olena.boika.ua@gmail.com

Lunaria is one of the new perspective crops from *Cruciferae (Brassicaceae)* family. This genus includes two species with different type of plant development. *Lunaria annua* is an annual species (in North regions it can be biennial) and *Lunaria rediviva* – perennial plant. At Zaporizhzhia National University the interspecific hybrids between this species were obtained. It was very interesting to investigate how hybrids will be inheriting the type of plant development. It was reviled that perennial type dominance over annual type. But reciprocal cross-combinations show differences in type of development in the second (F_2) generation. In case when as a mother plant was used annual species appear plants with intermediate type of plant development. Annual plants are germinating, blowing,and forming pods and seeds during one vegetation season. After seeds maturing they are died. Perennial species in the first year forming only leaves and this plants blowing next spring. But after maturing pods they don't die. Plants with intermediate type of development blows in the first year, but later than typical annual plants and after maturing of the pods they don't die. At the next spring they blow with the perennial plants and only after second pods formation they die.Initial species has several different morphological and physiological traits. And some of them interspecific hybrids inherited as intermediate type of inheritance, and some traits showed full dominance. It was estimate a correlation between all investigated traits and between this traits and type of plant development. Almost all investigated traits has a week correlation between each other. And this provides a good and wide facilities to the breeding process because its very easy to combine different traits at one line or variety. Only few traits show relationships with type of plant development (shape of leaf base, plant color and roots tubes). So, we can make a conclusion that *Lunaria* genus is a very interesting and perspective genus for the breeding.

Keynote

GENETIC RESOURCES FOR FOOD AND AGRICULTURE – CONSERVATION AND UTILISATION

A. Börner [*1], ***M. Nagel*** [1], ***M. Agacka-Mołdoch*** [1,2], ***M. Börner*** [1,3], ***U. Lohwasser*** [1], ***D. Riewe*** [1], ***J. Wiebach*** [1], ***T. Altmann*** [1], ***T.A. Pshenichnikova*** [4], ***E. Khlestkina*** [4]

[1] Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany
[2] Institute of Soil Science and Plant Cultivation, State Research Institute, Puławy, Poland
[3] Enza Zaden, Research and Development B.V., Enkhuizen, The Netherlands
[4] Institute of Cytology and Genetics, Siberian Branch, Russian Academy of Sciences,Novosibirsk, Russia

[*]boerner@ipk-gatersleben.de

Plant genetic resources play a major role for global food security. The most significant and widespread mean of preserving plant genetic resources is *ex situ* conservation. Today about 1,750*ex situ* genebanks world-wide maintain 7.4 million accessions. One of the ten largest *ex situ* collections of our globe is located at the Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) in Gatersleben, Germany, conserving 150,000 accessions from 3,200 plant species and 780 genera. Since the majority of genebank holdings globally is maintained as seed, seed storability is of exceptional importance for germplasm conservation.

At IPK research on seed longevity was initiated for a range of crops and wild relatives stored over decades. Historical germination data accumulated during 35 years of seed germination monitoring were analysed to predict species specific seed longevities. The study considered 75 species comprising 79,075 accessions and 157,402 observations. Beside interspecific differences variation was also detected within species and genetic analyses were initiated in barley, wheat, oilseed rape and tobacco.

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

Beside research on seed storability genebank accessions and genetic stocks have been extensively used for genetic and genomic studies. Data on mapping of loci/marker trait associations for a range of different traits will be presented.

A POTENTIAL FOOD CROP *AGRIOPHYLLUM SQUARROSUM*

Guoxiong Chen*, *Jiecai Zhao, Xin Zhao, Pengshan Zhao, Jiwei Zhang

Shapotou Desert Research & Experiment Station, Northwest Institute of Eco-Environment and Resources, Chinese Academy of Sciences,Lanzhou 730000, P.R. China

Agriophyllum squarrosum (L.) Moqis an annual psammophyte adapted to mobile sand dunes in aridand semi-arid regions of Central Asia. The species has evolved a range of physiological, morphological, and ecological adaptations to allow it to be a pioneer species of unstable, nutrient-poor, drought-prone and hot sand dunes. Local populations in the sandy desert regions of China consume the seed of the species during periods of food shortage, and refer to the plantas ‘‘shami’’ in Chinese, which translates as ‘‘sand rice’’. The sand rice seeds have high nutritional value, containing around 23 % protein, 9 % lipid, 45 % carbohydrates, 8 % crude fiber and 5 % ash. The protein fraction includes the full range of essential amino acids required in the human diet. The lipid fraction comprises mostly polyunsaturated fatty acid. The ash fraction is rich in iron. We generated a deep transcriptomic sequencing of sand rice, which uncovers 67,741 unigenes. A set of genes likely relevant for resistance to heat stress, was functionally annotated according to expression levels, sequence annotation, and comparisons corresponding transcriptome profiling results in Arabidopsis. Sand rice could be grown in farmer’s field and some chemical induced sand rice mutants have been identified, which reveal the possibility that sand rice can be domesticated. Thus, sand rice is a good candidate species for domestication to provide a food crop resilient to future climate change.

GENETIC VARIATION OF SAND RICE (*AGROPHILLIUM SQUAROSUM* L.) COLLECTED FROM TWO DIFFERENT REGIONS OF KAZAKHSTAN

S. Abugalieva [1], Y. Genievskaya [1], D. Shamshadin [1], F. Sagyntay[1], A. Zhubanysheva [2]., Y. Turuspekov [1]

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

[2] Aktobe breeding station, Aktobe region, Kazakhstan

Sand rice (*Agriophyllum squarrosum*) is an annual herb adapted to mobile sand dunes in arid and semi-arid regions of Central Asia. The sand rice seeds have excellent nutrition value and have been historically consumed by local populations in the desert regions of Central Asia and northwest China. It is also an important fodder crop (on young stages of growth) for domestic animals in Kazakhstan. Sand rice is a potential food crop resilient to ongoing climate change and has high nutrient content with concentration of protein and carbohydrates. The main purpose of this study was the assessment of the genetic diversity of sand rice samples collected from two different regions of Kazakhstan based on ITS and *matK* DNA markers. Samples were collected in Western and South-eastern parts of Kazakhstan and separated from each by large distances. The analysis of nucleotide sequences showed clear partition of *Agriophyllum squarrosum* from *Agriophyllum minus*, which is also grow in typical sandy dune environments. Also, the sequences of Agriophyllum squarrosumfrom Western and South-eastern regions of the country were different in ITS and matK. The research is suggesting that ITS and matK markers can be effectively used in discrimination of *Agriophyllum squarrosum* from other Agriophyllum species and also successfully used in partitioning of population within the species that grow far apart from each other geographically.

The research was conducted in the framework of the Program 0237/PTF-14 supported by the Ministry of Education and Sciences of the Republic of Kazakhstan (duration: 2015-2017).

GEOGRAPHICAL VARIATION AND EVALUATION OF IRANIAN LANDRACES OF *RICINUS COMMUNIS* L.

A.Hassanzadeh Ghorttapeh*[1*], M. Abasali[2], F. Ghanavati[2], N. Allahyari[3], G.R. Khakizad[4], A. Mirakhorli[5], R.A. Alitabar[6], A. Taheripor [7], R. Kanani[8], M.R. Kyani[9], H.R.Fanaei[10], S. Habibifar[10] H. Ghojig[11], A. Nakhaei[12], M.J.Karami[13], G.R.Abadoz[14], K.Abbasi[15], A. Hamzehnegad[16], S. Safari[17], SH Asgari [18], H.Azizi[19], H. Manochehri[20], A. Fathi[21], M. Asadi-Pour[22], A. Soltani[23], A.H. Asgari[24], N. Kazerani[25], N. Foromadi[26], M. Samani[27]

1 – Agricultural and Natural Resources Research and Education Center of West Azerbaijan province, Urmia, Iran. 2 – Seed and Plant Improvement Institute, Karaj, Iran. 3 – Agricultural and Natural Resources Research, and Education Center of Ardabil province, Ardabil, Iran. 4 – Agricultural and Natural Resources Research, and Education Center of Hamadan province, Hamadan, Iran.5 – Agricultural and Natural Resources Research, and Education Center of Kermanshah province, Kermanshah, Iran. 6 – Agricultural and Natural Resources Research, and Education Center of Mazandaran province, Sari, Iran. 7 – Agricultural and Natural Resources Research, and Education Center of Zanjan province, Zanjan, Iran. 8 – Agricultural and Natural Resources Research, and Education Center of East Azerbaijan province, Tabriz, Iran. 9 – Agricultural and Natural Resources Research, and Education Center of Khorasan Razavi province, Mashhad, Iran. 10 – Agricultural and Natural Resources Research, and Education Center of Sistan va Blochestan province, Iran. 11 – Agricultural and Natural Resources Research, and Education Center of Golestan province, Gorgan, Iran. 12 – Agricultural and Natural Resources Research, and Education Center of Khorasan Jenobi province, Birjand, Iran. 13 – Agricultural and Natural Resources Research, and Education Center of Fars province, Shiraz, Iran. 14 – Agricultural and Natural Resources Research, and Education Center of Khozestan province, Ahvaz, Iran.15 – Agricultural and Natural Resources Research, and Education Center of Kordestan province, Sanandaj, Iran. 16 – Agricultural and Natural Resources Research, and Education Center of Kerman province, Kerman, Iran.17 – Agricultural and Natural Resources Research, and Education Center of Charmahal va Bakhtyari povince, Shahrkord, Iran. 18 – Agricultural and Natural Resources Research, and Education Center of Ilam province, Ilam, Iran. 19 – Agricultural and Natural Resources Research, and Education Center of Kohkiloya va Boyer-Ahmad province, Yasaoj, Iran. 20 – Agricultural and Natural Resources Research, and Education Center of Isfahan province, Isfahan, Iran. 21 – Agricultural and Natural Resources Research, and Education Center of Markazi province, Arak, Iran. 22 – Agricultural and Natural Resources Research, and Education Center of Lorstan province, Khoram abad, Iran. 23 – Agricultural and Natural Resources Research, and Education Center of Yazd province, Yazd, Iran. 24 – Agricultural and Natural Resources Research, and Education Center of Hormozgan province, Bandar-Abas, Iran. 25 – Agricultural and Natural Resources Research, and Education Center of Boshehr province, Boshehr, Iran. 26 – Agricultural and Natural Resources Research, and Education Center of Semnan province, Semnan, Iran. 27 – Agricultural and Natural Resources Research, and Education Center of Khorasan Shomali province, Bojnord, Iran.

email: a.g.hassanzadeh@gmail.com

Castor bean is important oil crops. It is planting for aims of industrial and pharmaceutical. The 4-year studies in different provinces to collect identify and evaluate the genotypes of native castor bean in Iran. According to the results of this study, 186 local varieties of castor bean seed from different parts of the country were collected. Studies showed that the coefficient of variation and diversity index in Eco-geographical condition of collected area for castor bean local varieties including latitude, altitude, annual temperature, climate, rainfall, soil type, the slope of collected area very difference. The field study showed that exist high variation in different traits of castor bean local varieties, such as grain yield, oil content, 100 seed weight, leaf and stem weight and number of capsules per plant total weigh,. This variation can be modified and used to produce resistant varieties to adapted climatic conditions in each area for produce high yield. The improve local varieties and cultivated genotypes to suitable climatic conditions in each region benefit for maximum use of environmental resources such as light, water and nutrients for achieve greater performance.

ACCUMULATION OF ORGANIC ACIDS IN FRUIT OF CRATAEGUS AMBIGUA FROM DIFFERENT NATURAL POPULATIONS OF MANGISTAU

A.A. Imanbaeva, N.I. Duysenova, A.T. Tujakova, D. Jumakhan

Mangyshlak Experimental Botanical Garden, Aktau, Kazakhstan
e-mail: imangarden@mail.ru

Introduction new useful plants to the culture at Mangyshlak extra arid climate has important practical value. A perspective species for an introduction is *Crataegus ambigua*. It is endemic of Mangyshlak, which can be used as decorative, food and medical plant.

We carried out the analysis of accumulation of some organic acids in *Crataegus ambigua* fruits of different age periods and from various places of growth (Table 1).

In ripe fruits of *Crataegus ambigua* different places of growth (in terms of crude weight) accumulation of organic acidsare following: from Tulkili Say gorge in young generative oxalic acid – 0,005%, fumaric – 0,07%, apple-0,21%, lemon-0,15%, dairy-0,20%, in adult generative oxalic – 0,01%, fumaric - 0,07%, apple – 0,21%, lemon - 0,18%, dairy - 0,06%; from Kendirli gorge in young generative oxalic acid – 0,007%, fumaric – 0,09%, apple – 0,24%, lemon – 0,57%, dairy – 0,10%, in adult generative oxalic – 0,006%, fumaric - 0,06%, apple – 0,17%, lemon - 0,40%, dairy – 0,06%; from the gorge Karasay in young generative oxalic acid – 0,005%, fumaric – 0,06%, apple – 0,13%, lemon – 0,30%, dairy – 0,09%, in adult generative oxalic – 0,01%, fumaric – 0,08%, apple – 0,23%, lemon – 0,46%, dairy – 0,15%; from the gorge Emdikor-gan in young generative oxalic acid – 0,01%, fumaric – 0,17%, apple – 0,33%, lemon – 0,48%, dairy – 0,08%, at adults oxalic – 0,02%, fumaric – 0,10%, apple – 0,32%, lemon – 0,31%, dairy – 0,12%.

Our results showed that accumulating of organic acids were differs by high-quality and quantitative structure. The maximum accumulating is fixed for malic and citric acid, minimum for oxalic acid.

The maximum accumulation of organic acids is noted in fruits from the Emdikorgan gorge, minimum in Tulkili Say gorge. It is noted strict dependence of quantitative content from plants age.

Gathering of fruits with the maximum accumulating of organic acids needs to be carried out for plants from Emdikorgan gorge. Plants of this population can be entered into culture as perspective for implementation in food economic usage.

CREATION OF PRODUCTION FOR OBTAINING OF LANDING MATERIAL OF POPLAR BY USING MICROCLONAL PROPAGATION

A.A. Kakimzhanova, V.K. Karimova, A.S. Nurtaza

RSE «National Center for Biotechnology», Astana, Kazakhstan

e-mail: kakimzhanova@mail.ru

In the greening of cities, the problem of the death of *Populus alba* L. is appeared, due to the defeat of fungal and viral diseases. *Populus bolleana* L. is difficult to take root with cuttings, the percentage of survival rate is only 30%. The largest company JSC "Astana-Zelenstroy" has addressed with an acute problem to National center for biotechnology to provide clonal propagation of two species of poplars for greening of the Astana capital.

To solve this problem for three years, conducted research work on the development and introduction of the technology of microclonal propagation of male poplar *(Populus)* for greening.

On the basis of the studies results, the laboratorial reglament of microclonal propagation of poplar was developed to obtain seedlings, which consisted of the following stages: the introduction of *in vitro* explant, activation of axillary buds, multiplication of microshoots, rooting of micro shoots, planting and adaptation of test tubes plants in soil, obtainibg seedlings.

We also developed and introduced the technology of propagation of male copies *populus alba L.* and *populus Bolleana L.* with biotechnological methods. The developed technology of microclonal propagation is made possible to obtain test tubes plants, seedlings, seedlings and transfer them to the organization of JSC "Astana-Zelenstroy", LLP "Astana Ormany" for greening.

The technology of microclonal propagation of two species of poplar consists of the following stages:

Stage 1 - Collection of axillary buds of *Populus alba L.* and *Populus bolleana L.* Introduction of axillary buds to in vitro culture of by two-step sterilization;

Stage 2 - Cultivation of axillary buds of the two species on the WPM or MC nutrient medium with growth regulators of benzylaminopurine (BAP) 0.3 mg/l, 0.2 mg/l gibberic acid for obtaining the main shoot;

Stage 3 - Molecular genetic analysis for the identity of the multiplied poplar clones in comparison with the original form;

Stage 4 - Microclonal propagation of test tubes poplar plants on WPM medium or MS with BAP 0.2 mg/l, gibberic acid 0.2 mg/l;

Stage 5 - Cultivation of test tubes poplar plants at a temperature of 24-26°C and 70% of air humidity in the illuminated climatic chamber;

Stage 6 - Rooting microshoots of poplar on ½ WPM medium with growth hormone indolyl butyric acid (IBA) 0.01 mg/l;

7 stage - Adaptation of test tubes plants in peat with sand at room-temperature room with a 16-hour photoperiod, illumination - 4-5 kl, temperature 24-26ºC and humidity 70%;

8 stage - Propagating microshoots of poplar in the soil in greenhouse;

9 stage - Propagation of mini seedings of poplars in a foresty nursery for greening.

At present, a production is being established to produce competitive products in the form of ready-made seedlings and seedlings of *Populus alba L.* and *Bolleana L* for the urbanization of cities within the framework of the Program "Stimulation of productive innovations", under the subproject "Commercialization of Technologies for microclonal reproduction of woody plants for industrial use in urban greening ".

RYE CHROMATIN INTROGRESSION INTO WHEAT GENOME: CONTRIBUTION OF WHEAT-RYE CHROMOSOME SUBSTITUTIONS 1R/1A AND 6R/6A IN HYBRID GENOME STABILIZATION

O.G. Silkova[1], D.B. Loginova[1], Yu.N. Ivanova[1], E.A. Krivosheina[1], E.B. Bondarevich[2], L.A. Solovey[2], E.A. Sycheva[2], N.I. Dubovets[2]

[1]Institute of Cytology and Genetics, Novosibirsk, Russia
[2]Institute of Genetics and Cytology, Minsk, Belarus

e-mail: loginova@bionet.nsc.ru

Development of wheat introgressive lines with alien genetic material significantly expands this culture genetic potential. Rye has been successfully used in wheat breeding programs; its chromosomes carry genes controlling the valuable traits. Overcome the sterility of wheat-rye F_1 hybrids is the first step in successful transmission of rye chromatin into wheat genome. Further amphidiploids stabilization process is characterized by chromosome instability. In this connection, the information about the meiotic mechanisms of F_1 fertility restoration and amphidiploid genomes reorganization is significant for breeding as well as understanding the conditions for wheat and rye chromosomes co-existing in the same nucleus.

This work is a comprehensive study of the wheat-rye hybrid genomes formation. Molecular cytogenetic analysis of meiosis in F_1 hybrids *T. aestivum* L. x *S. cereale* L., in which genomes wheat chromosomes 1A and 6A replaced by rye homoeologs, revealed two mechanisms of viable gamete formation: mitosis-like division, and monopolar spindle organization. Seed set analysis of self-pollinated F_1 and F_2 progenies showed considerable variability between hybrid combinations and among single plant offsprings. To analyze karyotypes of the F_3 most productive plants, C-banding and FISH were used. Hybrids 1Rv(1A)xR with 2n=44 carried only three rye homologs 1R1R, 2RL2RL and 4R4R. Among hybrids 6R(6A)xR most plants contained 56 chromosome, the number of rye chromosomes ranged from 10 to 14. The number of chromosomes in the control hybrids Saratovskaya 29 x R variated from 42 to 56, rye chromosome number was also instable – from 4 to 13. Wheat chromosomes formed telocentrics in some plants. Meiosis in 6R(6A)xR and 1Rv(1A) was mainly stable, while in the Saratovskaya 29 x R, number of univalents per cell were significantly higher.

Thus, the chromosome substitutions 1R/1A and 6R/6A promote the same mechanisms of viable gamete formation, but revealed the individual contribution in hybrid genome stabilization.

This work was supported by RSF №16-16-00011 and BRFFR B15CO-030.

METABOLOMIC APPROACH TO RESISTANCE OF *AVENA* SPECIES TO FUSARIUM HEAD BLIGHT (FHB)

Igor G. Loskutov [1,2]

1 – N.I. Vavilov Institute of Plant Genetic Resources (VIR), St-Petersburg, Russia
2 – St-Petersburg State University, St-Petersburg, Russia

Creation of new agricultural crop cultivars possessing a complex of important traits, high yielding ability and product quality under different environmental conditions requires the well-studied initial material. A potentially high grain yield of agricultural crops should be combined with other economically important traits and resistance to biotic and abiotic factors. Diseases not only suppress plants and reduce the size of grains and yields per unit area, but also deteriorate the yield quality through the accumulation of pathogens waste products. Mycotoxins decrease the cost and consumption properties of oat grain and adversely influence human and animal health. Complex field and laboratory evaluation of accessions of cultivated and wild species of *Avena* collection VIR showed these results. Infection of *Fusarium* fungi was detected in analyzed oat accessions. Average grain infestation ranged from 6.1 to 18.7 %, the maximum value was 64.0 %. The group of relatively resistant genotypes to Fusarium infection and to accumulation mycotoxins was found. The assessment of large genetic diversity of wild *Avena* species by using DNA testing was shown. These indicators were linked to each other and to grain infection with *Fusarium* head blight. Metabolomics spectra of seeds of wild and cultivated oat species were investigated. The kernels of wild and cultivated species displayed the highest values for protein, for oil and for other biochemical components. Content and composition of organic and fatty acids, amino acids, polyatomic alcohols and sugar were analyzed. Positive correlations have been found to reliably exist between the studied kernel metabolomics spectra, *Fusarium* head blight resistance and mycotoxins accumulation.

This publication was funded by the Russian Scientific Foundation (project № 14-16-00072).

MICROCLONAL INVITRO PROPAGATION OF *NEPETA DENSIFLORA*

A. Myrzagaliyeva

S.Amanzholov East Kazakhstan State University, Ust'-Kamenogorsk, Kazakhstan

Along with studying the increase of the use efficiency of useful plants, currently there are no less relevant studies that aimed at finding new, perspective species and, of course, multiplying them with the aim of preserving their natural populations. The method of tissue culture has been recently widely used for the mass propagation of rare and endangered species of natural flora. The application of these methods will allow obtaining the necessary amount of planting material for introduction into natural conditions.

The genus *Nepeta* is one of the most important flowering plants of the family *Lamiaceae* Lindl. Most species of this genus are widely known as food, spicy-aromatic and medicinal plants. One of the most interesting species of the genus is the densely flowered catnip – *Nepeta densiflora* Kar.et Kir. It grows in the Altai, in the alpine belt on rocky places and near streams. It is found only on Mountain Zhaidak of Naryn Ridge in Southern Altai, at an altitude of 1990-2300 m above sea level, in the alpine belt. The coordinates of the GPS data are N 49003.952`, E 086 ° 55.264 '. The species occurs sporadically, along the banks of streams, dry riverbed.

The study of the peculiarities of the introduction of the densely flowered catnipinto in vitro culture becomes very important, since the species contains valuable essential oils that can be used in medicine, perfume industry and have not been studied to date with respect to the content of biologically active substances. Due to the inaccessibility and limited nature of the species distribution area, its use for practical purposes is possible only with sufficient raw materials. Therefore, we used a clonal propagation method for the densely flowered catnip. To introduce into the in vitro culture we used the hormone-free agar nutrient Murashige and Skoogmedium. Explants were cultivated with a 16-hour photoperiod, with an illumination intensity of 1000-1300 lux and an air temperature of 20-25°C. The explants underwent a complete sterilization process. An effective sterilizer was 5% sodium hypochlorite combined with 90% ethanol.Explants began to show viability on the 3rd day of cultivation. During 20 days of cultivation vegetative organs developed in the explants. After 34 days, cuttings of the obtained micro-plant were takenand planted in the liquid nutrient Murashige and Skoog medium without adding phytohormones. It was noted that the development of micro-plants in the liquid medium is faster, and the newly formed micro-plant is suitable for repeated propagation after 15 days. Root growth is activated on the 25th day of cultivation. Further, the obtained micro-plants were planted in the specially prepared soil. Thus, the use of the microclonal propagation method will solve the actual problem of the rapid reproduction of a rare economic plant, and its preservation by introducing it into a wide culture. Studies on the obtained catnip plants will be carried out on the identification of essential oils, with subsequent recommendations for practical use.

THE GENETIC POTENTIAL OF SOUTH CAUCASUS WHEAT

R.R. Sadoyan

Armenian State Pedagogical University, Yerevan, Armenia

e-mail: ruzannasad@mail.ru

Plants individual development is determined by their hereditary characteristics. The optimal way of genotypes identification is the examination of genotypically determined extensive changes of their phenotypes. One of actual approaches is the study of widely expanded spontaneous negative dominant mutations in wheat varieties with different ploidy and genome composition that results in depression or death of hybrid plants. The investigation of varietal, geographical, and biotypical localization of dominant genes of hybrid depression is an important issue for the profound study of wheat phylogenesis and implementation of seed breeding programs.

The presented research of hybrid depression phenomenon is based on the exploration of the linked genes, which determine the immunity and range of valuable features, having definite practical significance for the wheat selection. Hybrid depression genes, detected in wheat contemporary varieties have been also identified in Aegilops species and diploid forms of wheats, which are involved in the processes of morphogenesis within various phases of the evolution and strong allele combinations the phenomenon of lethality were defined as genetically isolating mechanism among varieties.

The South Caucasus is one of the regions, where the vast accumulations of different kinds of spontaneous negative dominant mutations are observed in cultivated wheat varieties. Our study of endemic and selective wheat varieties has determined that the majority of them are carriers of hybrid depression genes. The comparative analysis of wheat varieties from Armenia, the South Caucasus and world-wide collection has revealed the characters of their distribution, localization and allele's accumulation, correlated with their biotypes.

It has been determined that the genes of hybrid depression in wheat varieties of the South Caucasus are subjected to overall regularities according to their origin, varietal and biotypical localization. Nevertheless, there are definite differences in their frequency, strength of alleles and deletion of single genes of hybrid depression.

Based on genetic variability and potential of phenotype expression, the role and place of endemic and selective wheat varieties of Armenia in the Asia Anterior family of cultivated crops were determined.

REPRODUCTION OF GENETIC RESOURCES OF KAZAKHSTAN

E. Shadenova*[*1], *E. Zhumabekov, M. Sembekov

Institute of General genetics and cytology, Almaty, Kazakhstan

*e-mail: shadel08@mail.ru

The serious problem of the natural existence of forests and their genetic resources in Kazakhstan creates a growing trend in ageing plantations. According to the scientific-production center of forestry, even in the face of especially protected natural territories the most widely represented middle-aged stands and premature plantings.

Current methods of gene and genetic engineering in conjunction with forest biotechnologies are used to create trees that are resistant to various diseases and pests, which greatly increases the speed of their growth.

Therefore, particularly relevant and a priority direction of genetic and breeding studies in forestry is the development and implementation of ways to preserve the viability of the gene pool of seeds (germplasm) and accelerated technology of growing seedlings using standard culture in vitro of the main generic breeds in Kazakhstan and valuable introduction.

To this end, we studied populations of trees and bushes plants on territorial areas of the Caspian Sea (Atyrau and Mangystau region). Severe climatic conditions of the Caspian Sea, located at the junction of the northern and southern deserts, along with unfavourable soil (salinization, close underlain by rocks of the indigenous Sarmatian) the intensive solar radiation, accompanied by high temperatures and low humidity, as well as the intensive development of industry, difficult to form a favorable environment for the growing population of cities and towns, the inability to ensure the settlements defensive gardening because of the poverty of woody vegetation, dictate the need for further and enhanced development of green construction.

On this basis have developed methods of accelerated reproduction of the most important species of trees and shrubs-nitraria, Turanga, biota which good transfer fouling and falling asleep.

Work was carried out for the conservation and reproduction of the relic species on the verge of extinction-red Birch (birch Yarmolenko), a collection of 20 types of birch and Aspen trees represent wood-economic value. The study found that plants obtained by in vitro culture, faster pass the first stage of ontogenesis, on 5-th month cultivation seedling height reaches 50 cm, compared with plants from natural populations (2-4 cm). The increase in population is due to the regular passage, optimal soil acidity.

TRANSGRESSIONS IN RECIPROCAL INTERSPECIFIC CROSSES BETWEEN THE CULTIVATED PEA AND ITS WILD SPECIES

V. Dogdu, H. Canci, H. Sari, D. Sari, A. Adak, C. Toker

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

e-mail: toker@akdeniz.edu.tr

Transgression is described as the presence of progeny in segregating populations that fall beyond phenotypes of their parents. It is often found in the progeny derived from interspecific crosses. Interspecific transgression is significant with regard to crop evolution and improvement since it represents a potential source of novel genetic variation. As an outcome of cultivation for a long time, the cultivated pea (*Pisum sativum*) has lost some traits conferring to resistance for biotic and abiotic stresses. For expanding narrower genetic base of the cultivated pea, it was crossed with its wild relatives including *P. elatius*, *P. fulvum* and *P. abyssinicum* since wild *Pisum* species are generally considered as alternative resistant genetic resources for stresses. In the current study, reciprocal crosses between the cultivated pea and its wild species were performed (i) to obtain hybrid vigor (heterosis) and (ii) to produce transgressions and (iii) to compare reciprocal interspecific crosses for yield and yield related traits. For number of pods per plant, biological and seed yields, considerable hybrid vigor and transgressions were found in F_1s and in F_2 populations, respectively. F_1 plants were found to be superior to their parents and superior progeny in F_2 populations were higher values than those of F_1 plants indicating that super progeny would be created. The cultivated pea could be suggested as female parent in interspecific hybridization to increase yield and yield criteria since fruitful heterosis in F_2 were higher than that of F_1.

CONSERVATION AND EVALUATION OF OAT GENETIC RESOURCES IN CHINA

***Zhang Zongwen*[1,2]**

[1] Institute of Crop Science, Chinese academy of Agricultural sciences, Beijing, China;
[2] China Office, Bioversity International, Beijing, China

e-mail: Zhangzongwen@caas.cn; z.zhang@cgiar.org

Oat is a grain crop in China. It is widely cultivated in north, northwest and southwest parts of the country. Oat is the staple food for many local people in producing areas. It is also popularly used for animal feed. In the long history of cultivation, various types of local oat varieties were derived and remained under different agroecological environments in China. Since 1980s, over 5268 accessions of oat germplasm have been collected and conserved by the national genebank of China, including 2482 accessions of naked type, 2652 accessions of hulled type and 134 accessions of wild species. Morphological variation was characterized for the traits of plant, panicle, flower and grains of oat accessions. Passport and characterization data were documented and shared in National Information System of Crop Germplasm Resources. Efforts were made to evaluate the resistance to drought and salt for oat accessions. Multilocation trials in different environments were carried out to identify accessions with adaptation to the climate change. Genetic diversity of oat collection was assessed with molecular markers, such as AFLP and SSR. With the constructed genetic linkage maps, QTLs related to important traits such as β-glucan content, grain size and plant height were identified. The efforts in conservation and evaluation has promoted the sustainable use of oat germplasm and contributed to the development of oat industry in China.

EVALUATION OF GENETIC VARIATION IN RARE TULIP SPECIES FROM KAZAKHSTAN

S. Abugalieva [1], A. Amalova [1], S. Anuarbek [1], R. Kaparbay, A. Ivaschenko [2], Y. Turuspekov [1]

1 – Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan
e-mail: yerlant@yahoo.com
2 – Ile-Alatau National Nature Reserve, Almaty region, Kazakhstan

According to Flora of Kazakhstan this country is home for 35 Tulip species, and, therefore, it is naturally one of the symbols of flora in Kazakhstan. Despite tremendous work in botanical description of local scientists, there was little effort in assessment of molecular phylogeny of representatives of this genus growing in Kazakhstan. The molecular phylogeny analysis is particularly important for taxonomy evaluation of endemic and rare Tulip species. In this study leaf material of thirteen Tulip species were collected in six different regions of the country during 2015-2016, six of those species were rare and four were endemic. DNA samples were extracted using Qiagene kits and preserved at -80^{0}C. The genetic analysis of Tulip samples was done based on using ITS (internal transcribed spacers) and *matK* DNA barcodes. It is interesting that unlike other flora representatives no PCR amplification was recorded for matK marker, suggesting that there is a deletion region in this location of chloroplast genome in all Tulip species studied in this work. However, PCR amplification was successful for ITS marker for all studied samples. The phylogenetic tree was constructed based on Neighbor Joining method in MEGA 6.0 package.

The research was conducted in the framework of the Program 0237/PTF-14 supported by the Ministry of Education and Sciences of the Republic of Kazakhstan (duration: 2015-2017).

.

TAXONOMIC REASSESSMENT OF SOME ALLIUM SPECIES FROM KAZAKHSTAN BASED ON DNA BARCODING ANALYSIS

S.I. Abugalieva [1], L.A. Volkova [1], K. Amangeldinov [1], A.A. Ivaschenko [2], Y.A. Kotukhov [3], G.B. Sakauova [4], Y.K. Turuspekov [1*]

1 – Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan
2 – Ile-Alatau Mational Nature Reserve, Almaty, Kazakhstan
3 – Altai Botanical Garden, Ridder, Kazakhstan
4 – Karatau National Nature Reserve, Kentau, Kazakhstan

Email: yerlant@yahoo.com

As part of nation-wide project for DNA barcoding of flora, a separate study was undergo for taxonomy analysis of Allium species. In total, nineteen Allium species were collected in field trips in six different regions of Kazakhstan during 2015-2016. Most of species were collected in Eastern part of the country along of Altai Mountains (13 species), followed by South Kazakhstan, where 7 different species were collected in Karatau and Sairam-Ugam National Nature Reserves. Previously, in different other studies, ten out of nineteen studied species were identified as endemic to various Kazakhstan regions. The phylogeny of Allium species was well described in study by Friesen et al (2006). Still, that study was not covering all available Allium taxons, including those that grow in mountainous area of Kazakhstan. In this study the DNA barcoding approach was applied in order to reassess the taxonomic position of *Allium oreoscordum* Vved., which is an endemic species to South Kazakhstan. Two DNA markers used in this study were ITS (internal transcribed spacers) and matK, representing nuclear and chloroplast genomes, respectively. The alignment analyses of nucleotide sequences of those two markers precisely confirmed the clustering of Allium species obtained by Friesen and his co-authors. At the same time, both ITS and matK analyses suggest that *Allium oreoscordum,* which was missing in the study by Friesen and co-authors, is genetically closer to species in section Nigrimontana of subgenus Reticulatobulbosa. The sequences of Allium species were deposited to the NCBI database.

The research was conducted in the framework of the Program 0237/PTF-14 supported by the Ministry of Education and Sciences of the Republic of Kazakhstan (duration: 2015-2017).

CURRENT PROBLEMS OF STUDY AND PRESERVE OF WHEAT GENE POOL OF ARMENIA

R.E. Avalyan, L.A. Minasbekyan

Yerevan State University, Scientific Research Institute of Biology, Yerevan, Armenia

E-mail: re_avalyan@mail.ru, minlia@ysu.am

Armenia is a part of Near Eastern focus of crop species origin. On the territory of modern Armenia are located nature reserves, protected areas and parks. Armenia flora abounds with of biodiversity of medicinal herbs and plants, comprising over 3,500 species, 180 species of which are endemic to the Armenian highlands. Such moderate by its territory focus of origin of wild and cultivated cereals the territory of Erebouni Reserve – a unique place in the world on a diversity of growing here wild wheat and their relatives. The problem of the protection of plant resources, including wild relatives of cultivated plants, currently is a quite topical question and becomes particularly great importance due to reduction of the natural habitat of valuable species and the degradation of certain plant communities caused by human economic activity and the influence of technogenic factors (Gandilyan, Avagyan, 1998; 2001).

In natural ecosystems carried out the study of spontaneous mutational variability of wild species of wheat and barley as the indicators of effects of environment pollution in the natural plant communities. Also, endemic cereals investigated as an environmental biomonitors near the industrial pollution sources in order to establish and conduct genetic monitoring. Early we investigated reserve proteins (gliadins) of wheat with different ploidity as markers of phylogenic analyze for revealing the questions concerning the origin of hexaploid wheat separate species. The comparative investigation of electrophoretic polymorphism spectrum of gliadins have been carried out among six species of endemic wild wheat – *Tr. urartu, Tr. monococcum, Tr. diccocum, Tr. aestivum* and two species of Aegilops – *Aegilops cylindrica* and *Ae. tauschii.* The comparison of electrophoretic gliadin spectrums of diploid and tetraploid wheat species have been shown considerable occurrence of gliadin components in the *Tr. urartu* and *Tr. dicoccum* [Avalyan, 2001, 2009; Zaminyan, Avalyan, 2004].

To investigate the effects of the environment on the different varieties cultivated hexaploid wheat in modern conditions have been carried out a study on the effects of mm-waves on wheat seedlings, which gave us the opportunity to assess the possible changes in the genome over a dozen years. It has shown us how important the study of wild wheat and the preservation of their biodiversity in terms of the increasing number of anthropogenic sources of mm-wave with the development of civilization (Minasbekyan et al., 2013, 2016).

The genetic wealth is the most expensive strategically important capital of each country. Armenia is one of those few countries on the territory of which are still preserved wild relatives of important crops, the problem of the protection and use of which is of world significance. Nowadays is highly relevant and the extremely indispensable to study as many cultivated species of wheat in Armenia and their wild relatives, especially in the areas of their specific diversity, with the aim of studying the phylogenetic relationships between the species and the preservation of the wild wheat gene pool.

EFFECT OF COLCHICINE APPLICATIONS ON GERMINATION OF SOME FORAGE CROPS

M. Bilgen *, Z. Delibalta, A. Adak

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

*e-mail: bilgen@akdeniz.edu.tr

Colchicine applications are commonly preferred for increasing plant morphology and doubling the number of chromosomes in cell, referring to as polyploidy, in plant breeding. In this study, effect of colchicine on germination shoot and root lengths in some forage crops including *Medicago sativa*, *Trifolium alexandrinum*, *Onobrychis viciifolia*, *Lotus corniculatus, Dactylis glomerata*, *Chloris gayana*, *Agropyron cristatum*, *Agropyron intermedium*, *Phleum pratense* and *Phacelia tanacetifolia* were studied with colchicine solutions of 0.25% and 0.5%. Seeds were treated by each concentration as 2, 4 and 6 hours. The seed were germinated in trays content with vermiculite. Germination percentage, shoot and root lengths were recorded after treatments both in the treated seedlings and controls. Colchicine treatments slightly decreased in germination percentage in some species with the increasing doses and times.

STUDY OF SPECIFICS OF FORMATION THE SPIKELET NUMBER PER SPIKE OF VARIETIES OF SOFT SPRING WHEAT IN CONTRASTING YEARS

N. Boiko, V. Piskarev *, A. Timofeev, T. Kapko

SibRIPP&B- Branch ofICG SB RAS, Novosibirsk, Russia

*e-mail: piskaryov_v@mail.ru

The purpose - examine features of the formation of spikelet number per spike in wheat soft spring samples of different terms of maturation into various moisture- and heat provision according to years. The of spikelet number per spike were studied in 139 soft spring wheat varieties in contrasting years. The study was conducted in 2011-2013 at the experimental field of the laboratory of the gene pool of SibRIPP&B. The cultivars were divided into the following maturation groups: mid-early and early (31 plants), middle (94 plants) and mid-late (14 plants). The predecessor is clean fallow. During a vegetation of plants, phenological observations were carried out according to methodical instructions (Merezhko etc. 1999).

The average value of the spikelet number per spike increases in ripeness groups of 13.5 of pieces (early and mid-early groups of maturity) to 14.5 of pieces (meddle group of maturity).

The most stable by year found themselves the samples of meddle group – 64% of which were characterized by a significant variability (Cv=10%).A significant the variability was characterized one sample – Albidum 188 (Cv> 20.0%, middle-group).

A significant excess of the average value of spikelet number per spike, over 3 years (2011-2013) the study noted on samples of Enita and Bell. On variety Rosinka 1, Chebarkulskaya, Omskay 24 significant excess was observed in 2011 and 2012. Then how on the variety – Leningradskaya 97, Baganskaya 51 and Lada significant exceeding of the average value of this trait observed in 2012 and 2013.

Significant positive correlations of have observed between yield and the spikelet number per spike on the middle group of maturity and early, mid-early groups of maturity in 2011 ($r = 0,29$) and 2013 ($r = 0,49$), years, and on the a group of middle - 2013 ($r = 0,36$). In the mid-later group of maturity in all years of the study (2011-2013) correlation dependences of were does not significant.

The work was supported by the Russian Scientific Foundation (Project No. 16-16-00011).

PHYLOGENETIC ANALYSIS OF FOREIGN AND LOCAL ECOTYPES OF GENUS *AEGILOPS* L. USING EST-SSR MARKERS

A.P. Chirkin [1], ***N.A. Yurkevich*** [1], ***M.A. Yessimbekova*** [2], ***K.B. Mukin*** [2], ***G.A. Ismagulova*** [1]

[1] M.A.Aitkhozhin Institute of Molecular Biology and Biochemistry, Almaty, Kazakhstan, e-mail: chirkin_a@mail.ru

[2] Kazakh Scientific Research Institute of Agriculture and Plant Growing, Almalybak, Almaty reg., Kazakhstan

Study and conservation of wild relatives of cultivated plants as the source of valuable genetic material for modern varieties' selection is important due to loss of biodiversity of the cultivated species and decrease of their genetic potential as the result of loss of some genes or their alleles.

A phylogenetic analysis was carried out for 101 samples of genus *Aegilops* L. using 11 microsatellite EST-SSR markers (PK1, PK3, PK5, PK8, PK9, PK18, PK29, PK31, PK32, PK34 and PK57). Eight markers were found to be informative and polymorphous. Allele frequency and heterozygosity was calculated for each of them. The average allele number for the studied group was 2.73, and average heterozygosity was 20%. The most informative of all studied markers were PK1 and PK5. So, for example, presence of 5 allele variations was shown for marker PK1, while it was 6 for PK5. The remaining markers showed presence of 2 to 4 alleles. For hexaploid samples of species *Ae. trivialis*, *Ae. vavilovi* and *Ae. crassa* the presence of three allele variations simultaneously was established in marker PK9.

Based on the results collected in two years of research, the phylogenetic trees were constructed for each species separately and for all populations as a whole. Genetic distances between the studied species are calculated. It is established that populations' clustarization of various *Aegilops* species happens depending on the represented genomes. Populations' clusterization did not contradict the geographic distribution of the studied samples. All plant samples of Kazakhstan's populations of *Ae. cylindrica* and *Ae. tauschi* were divided into three big groups according to the distribution areas – Almaty, Zhambyl and South-Kazakhstan regions.

CHARACTERIZATION OF LIGULELESS MUTANTS OF TRITICEA SPECIES USING MOLECULAR GENETICS AND SCANNING ELECTRON MICROSCOPY

O.B. Dobrovolskaya [1,2], A.A. Ermakov [1], A.E. Dresvyannikova [2], Yu. Amagai [3], A.A. Krasnikov [4], N.P. Goncharov [1], N. Watanabe [3]

[1] Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
[2] Novosibirsk State University, Novosibirsk, Russia
[3] College of Agriculture, Ibaraki University, Inashiki, Ibaraki, Japan
[4] Central Siberian Botanical Garden SB RAS, Novosibirsk, Russia
*e-mail: ermakov@bionet.nsc.ru

The leaf of Triticeae grasses has a proximal sheath and distal blade separated by the ligule-auricle region. The sheath provides structural support and protects young leaves; whereas the main function of blade is photosynthesis. The auricles allow the blade to tilt back for optimal photosynthesis and determine the angle of a leaf. The ligule protects the stem from entering water and pests. Liguleless variants have upright leaf blade that raps around the culm. In wheat species, spontaneous liguleless variants were collected in Cyprus (durum wheat), Badakhshoni Kuhi and Tajikistan (bread wheat). Liguleless variants are also found in rye. A liguleless mutant was obtained in *Aegilops tauschii*. The genes that determined the liguleless phenotype in wheat, rye and *Ae. tauschii* were identified and mapped on homoeologous group-2 chromosomes. Here we report characterization of liguleless lines of wheat, *Ae. tauschii* and rye by means of scanning electron microscopy and molecular genetic tools. The orthologs of *Lg1* maize gene, whose mutations cause luguleless phenotype, were first isolated in the A, B, D genomes of tetraploid and hexaploid wheat species, the D genome of *Ae. tauschii* and the R genome of rye. These *Lg1*-orthologous genes of Triticeae species were mapped on wheat and rye chromosomes and their locations were compared with the previously reported location of liguleless morphological genes.

This work was supported by Russian Science Foundation (grant N 16-16-10021) and RFBR grant N 15-04-05371.

THE POTENTIAL OF USING OF PRACTICAL - VALUED PLANTS' RESOURCES OF THE CENTRAL KAZAKHSTAN'S FLORA

M.Yu. Ishmuratova

Karaganda State University named after academician Ye.A. Buketov, Karaganda, Kazakhstan;
e-mail: margarita.ishmur@mail.ru

Modern development of agricultural industry and branches of Kazakhstan, such as light, food, alcoholic, pharmaceutical and medical, determines before scientists the tasks of rational use of natural renewable resources of the republic such as vegetable cover. Studying of useful groups of plants allows to estimate their resources correctly and rationally to use them.

A variety of natural reliefs, considerable amplitude of temperatures, rainfall and humidity determined a variety of vegetation. So, on the territory of the Central Kazakhstan more than 1200 species of vascular plants grow which belong to 434 genes and 99 families.

Our researches determined that flora of the Karaganda region (the Central Kazakhstan) contained considerable number of species which had value in the economic relation.

The revealed plant species were divided into the following groups: technical, fodder, medicinal, essential oil, food, melliferous, ornamental-decorative, vitamin andfood.

The leading position belongs to herbs – 306 species (25.4% from all practical-valued plants) from 151 genes and 46 families. Among them: *Achillea nobilis, Artemisia vulgaris, Inula helenium, Tanacetum vulgare, Thymus marschallianus, Sanguisorba officinalis, Serratula coronata, Salvia stepposa, Asparagus officinalis, Rosa laxa, Ephedra distachya*, and others.

The second place is occupying essential-oil plants – 298 species (23.7%) from 106 genes and 27 families. The biggest amount of plants are in genus Artemisia, Achillea, Ferula, Seseli, Salvia, Thymus, Dragocephalum, Hyssopus, Tanacetum, Ajania, Eryngium, Bupleurum and etc.

The third position belongs to fodder plants (280 species from 151 genes and 46 families). They are such species as: *Dactylis glomerata, Festuca valesiaca, Agropyron cristatum, Eremopyrum triticeun, Filipendula ulmaria, Rheum tataricum, Beckmannia eruciformis, Althaea officinalis, Malva pusila, Polygonum aviculare, Anabasis salsa* and other.

On the forth position are technical plants (*Betula pendula, Pinus sylvestris, Isatistinctoria, Salsola collina, Artemisia frigida, Caragana pumila, Alnus glutinosa*) which are used as building and ornamental material, fuel, for the production of tannins, resins and paints.

There are a lot of species containing vitamins (168 species from 78 genes and 18 families) – *Artemisia dracunculus, Ribes nigrum, Rubus caesius, Rubus idaeus, Fragaria viridis, Fragaria vesca, Rosa spinosissima, Rosa bergeriana, Rumex acetosa, Viburnum opulus, Lonicera palassii*, etc.

Milleferous plants are belonging 166 species from 116 genes and 41 families. They are can be be a source as honey, so perga: *Caragana frutex, Amygdalus nana, Thymus serpyllum, Lonicera tatarica, Halimodendrom halodendron, Spiraea hypericifolia, Filipendula vulgaris*, etc.

Food plants include 151 species from 101 genes and 48 families. Among them are *Rubus saxatile, Rumex confertus, Elaeagnus angustifolia, Equisetum ramosissimum, Allium sativum, Allium galanthum, Solanum dulcamara*.

The minimum number of species belongs to decorative-ornamental plants – 126 species from 91 genes and 46 families. It should be noted that human application is found a small number of species – from 5 to 15% of the available potential resources.

Considerable potential use in the Central Kazakhstan belongs to herbs, essential oil and melliferous plants.

Thus, flora of the Karaganda region contains considerable number of useful species which use is limited now.

Researches are executed within the program 0237/PTF-14 (project "Molecular Systematization of Endemic, Rare and Practical-Valued Plant Species of the Western, Central and Eastern Kazakhstan").

MORPHOLOGICAL AND PHYLOGENETIC IDENTIFICATION OF THE *ANTHEMIS TROTZKIANA* CLAUS

K.S. Izbastina [1], ***M.S. Kurmanbayeva*** [1], ***S.I. Abugalieva*** [2]

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

email: izbastina.k@gmail.com

Anthemis trotzkiana Claus (Asteraceae) is rare species, subshrub, growing on the chalk cliffs and limestones and endemic to the Volga region and Western Kazakhstan. We are interested in studying this species, since this species of genus *Anthemis* L. was included in flora red books (The Red Book of the USSR, 1978 y., The Red Book of the Kazakh SSR, 1981 y., The Red Book of the RSFSR, 1988 y., The Red Book of Kazakhstan, 2014 y.). Descirption of this species is extremely limited, population structure of the species, anatomical and morphological features and genetic diversity were unstudied. Herbarium specimens of the species were collected in the Aktobe region, three kilometers from the cretaceous slopes of Akshatau. Rare specimens were found on Cretaceous deposits, the rhizome of the plant is almost horizontal, branched, with numerous subordinate roots. Above the rhizome leaves many furrows, cylindrical chalky-horny stems, averahe height is 27,06±9,9 cm.,roots are hard, arboreal, stems are unbranched, leaves twice pinnat-dissected, leaflets are mainly located on the lower part of the stem,color of leaves is dense-white, peduncle long with single baskets, in one plant 4-5 medium-sized baskets.In the baskets, the marginal flowers are reed with yellow corolla,in the middle, tubular flowers areandrogyne, with a crown. Seedlings are light, a short crest in the form of a crenellated crown, the data us obtained fully corresponded to the description of the species.

DNA analysis on phylogeny of *Anthemis trotzkiana* was conducted based on ITS (internal transcribed spacers) marker. DNA sequencing was conducted using DNA analyzer 3130 from the Applied Biosystems. Alignment of Antemis sequences was performed using nucleotide sequences available at the NCBI and MEGA 6 package. The phylogenetic tree constructed based on Neighbor Joining method. The results suggested that *A.trotzkiana* along with *A. marschalliana, A. futiculosa,* and *A. calcarea* form a single cluster within Tanacetum clade, while other Athemis species formed a separate Anthemis clade. Obtained results provide an important insights for evolutionary processes within Anthemis genus.

The work was supported by NTP 0237/PTF-14 granted by the Ministry of Education and Sciences of the Republic of Kazakhstan.

THE CONTENT OF OIL AND FATTY ACIDS IN BREEDING OF SUNFLOWER, SAFFLOWER, SOYBEAN, CANOLA AND LINEN: CULTIVARS GENE POOL AND GENETIC RESOURCES

A.I. Abugalieva *[1], A.I. Massimgaziyeva [1], T.B. Azhgaliev [2], A.Zh. Zhumahanova[2]

[1] The Kazakh Research Institute of Agriculture and Plant Growing, Almalybak, Kazakhstan
[2]SVTMA RK, Astana-Almaty, Kazakhstan

*e-mail: kiz_abugalieva@mail.ru

Cultivars resources of oil seeds in Kazakhstan by 54 varieties and hybrids of sunflower, safflower 6 varieties, 24 varieties ofcanola, 33 soy, and 7 linen from 1 to 4 varieties of castor bean, camelina and mustard. The aim of this work was to examine the fat content in the seeds of the test, prospective and admitted to the use of varieties of rapeseed, sunflower, soybean, safflower, flax domestic and foreign selection used in the Republic of Kazakhstan and determine the biological potential of oilseeds on fatty acid composition.

The fat content of sunflower seeds varies greatly from 31.2% to 52.8% (*Talmaz*). According to the oil collection per hectare allocated genotypes *Kandy, Brio, Kazakhstan 1, Jubilee 40, LH 5635, Printasol, ripening 87, PR 64 T-46, PR 63 A62*. The maximum fat content noted for sunflower samples: *P62LL109* (51.5%); *ECX9064* (48.0-50.4%); *Kazakhstan 95* (48,8-51,3%). Safflower oil seed samples and varieties ranges 20.0-43.3%. Safflower oil contains 76-82% of linoleic acid for high-quality gene pool. Oil content of the seeds on dry substance of 36%, 52.7% kernel. Linoleic acid content in varieties Kazakhstan ranges from 67.5% (*Akmai*) to 73.9% (*Nurlan*), the ratio of unsaturated / saturated varies from 5.79 (Akkyzyl and Akmai) to 7.69 (cv *Nurlan*). The content of erucic was minimal for cvs *Akmai* (0.04%) and a maximum for *AkKyzyl* variety (0.27%).In the competitive test of variety KazSRIA&PG (Gazke L., Meyrman G.T.) revealed two samples containing linoleic acid more than 84.0%, and in manual form identified with an almost equal ratio of linoleic to oleic acid (39.2-52.6 % / 39.7-49.4%).

The oil content in soybean varieties ranged from 18.0% to 26.9% in the SVT system, depending on the condition andyearof reproduction. The maximum oil content find for cv *Annushka* (22.2-25.4%) and *Mavka* (21.6-25.9%). *Almaty* soybean varietyis characterized by thehigh content ofoleic acid (35%), and cv *Zhalpaksay* high inlinoleicacid (47.5%) and VitaminFto 58.4%. In the collection nursery (Didorenko SV) the maximum content of oleic acid was for cvs *Maplepresto* 31.9% (000 groups); for genotype *Aldana* – 27.7% (00 groups); 0 group for genotype ripeness *Maplearrow* 24,8%; *Enterprize* (I gr.) – 21.6%; *K-11222* (II maturity group) - 22.8%; 2) linoleic acid varieties for *Nadezhda* - 58.1% (000 Group); *№6271* – 49.4% (00); *№431* - *KIZ* and *Altom* – 55.9% and 55.6% (0); 55.5% - *Enterprize* (I); 53.4% – *K-11222* (II).

Rape has elevated oleic acid content of 58.0% for the cultivars *Maibulak, Lipetsk* to 65.8% (*Gladiator*), and a high ratio of unsaturated / saturated fatty acids of 6.70 in the variety Lipetsk to 7.80 in the variety *Ubileinuy*. Negative for food use erucic acid is present in the range from of 0.17% cvs Jubilee to 1.83% in cvs *Maily* (Dolgich, Abugalieva, 2009).

The main varieties of linen in Kazakhstan: *North* and *Kostanaisky yantar* with a fat content of up to 43.8% (East) in the mountainous regions. The oil content of the variety *Kostanaisk yyantar* ranges from 36.4% to 42.8% at the level of the yield 14.3-16.0 c/ha climate - environment conditions can increase the production potential of oilseeds. By the diversity of crops (linen, sesame, castor) as informed research KSRA and Vavilov Institute (Udolskaya, Kolushev, 1970; Kuzmich, 1945). In Kazakhstan, promising oilseed such as castor oil (castor oil). In modern studies of tong oil content reaches 41.4 - 46.4%.

IDENTIFICATION OF PRODUCTIVITY AND QUALITY OAT GENOTYPES: AVENYNE, DNA MARKERS AND MORPHOLOGY (UPOV)

A.I. Abugalieva [1,2], M. Nurpeissov [2], B. S. Sariev [1], K. K. Zhundibaev [1]

[1] Kazakh Research Institute of Agriculture and Plant Growing, Kazakhstan
[2] Kazakh National Agrarian University, Kazakhstan

e-mail: kiz_abugalieva@mail.ru

Eleven genomic and expressed sequence tags (EST)-derived primer pairs were designed and selected according to their high polymorphism (Langdon,2014). The varieties and block of competitive variety testing (CVT) were classified as poly- and monomorphic according to the analysis of three microsatellite DNA loci. On the basis of 5 Kazakhstan varieties have been created pure-line materials by genetic (DNA) markers and morphological traits of UPOV (Zhorga, Baige, Pegas, Skakun, Alaman), avenyne electrophoresis.

It was revealed the dominance of genotype CVT (Kazakh Research Institute of Agriculture and Plant Growing -KazRIAPG) 06 / 03-1 and the genotype of the EVT (Ecological variety testing) 1185 H2 (Scientific Production Center of Grain Farming - SPCGF) by assessment of the forms for potential and adaptability.

The maximum accumulation of biomass (NDVI) by two genotypes 50/98-12 and 6/03-1 in the process of the growing season correlated with grain yield 0,70 ± 0,1 t/ha and 7,3 ± 0,2 t/ha regarding to standards Kazakhstanskyi 70 with a yield of 6,3 t/ha, and Alaman – 6,4 t/ha.

Block of naked oats is characterized by containing the protein between 15,7-18,9% and two samples with a very high value, above 19.0% (K-14832 and K-14537). The main part of the protein in husked oats was formed by fractions of glutenin and albumin + globulin, as the most assimilable. The ratio of protein fractions for naked oats shifted towards predominance of gluteline fractions and decrease avenyne. Naked oats surpass husked forms on the contents of protein, starch and fat, which is consistent with the data of breeders and researchers in this field. The ranking of varietal gene pool, genetic resources and breeding materials revealed a high glucan forms with more than 5.0% for varieties Alaman, Nicola, Pegas, Irtysh 15, K-14638, K-11247, K-13587, K-13544; K-14836.

This work was supported by grants № 0115RK02331 "Identification and marking of oats germplasm for breeding high-glucan and naked types of productive oat varieties" O.7221, project state registration №0115RK02312 "Phenotyping, genomics and biotechnology (biochemistry) in the creation of cereals, legumes and forage varieties with genetically identified stress indicator properties of productivity and quality".

DEVELOPMENT OF TECHNOLOGY FOR CLONAL MICROPROPAGATION OF *RHODIOLA ROSEA* L.

A.E. Orazov, A.M. Akzambek

S.Amanzholov East Kazakhstan State University

Rhodiola rosea is a perennial plant of the Tolstyankov family (*Crassulaceae* DC). The plant reaches a height of 20-30 cm. This is a valuable species, with a big decrease in number. It is listed in the Red Book. *Rhodiola rosea* contains an essential oil, flavour of which is reminiscent of pink. *Rhodiola rosea* has long been used in folk medicine, which was the reason for the reduction of its distribution area, so the study of the peculiarities of the introduction of rhodiolarosea into culture in vitro is of great importance (Flora of Kazakhstan).

To introduce it into in vitro culture we used buds of the regeneration of *Rhodiola rosea*, which were collected on the southwestern hills of the Sarynokai mountain of Altai Tarbagatai ridge, at an altitude of 2369 m above sea level, with coordinates (according to GPS): N 49008.854`; E 086 ° 11.898 '. The buds were separated from the rhizome.

It was decided to use the following agents for sterilization: a soap solution, sodium hypochlorite, ethanol and hydrogen peroxide. 15x15 cm four-layer bags were made from a sterile medical bandage. The material was treated with a soap solution and sodium hypochlorite outside the laminar box. The remaining manipulations with the materials were carried out under conditions of increased sterility (Kalinin F.L., 1992).

Apical parts of buds were isolated and placed in a nutrient medium.When introduced into in vitro culture, we used Murashige and Skoog (MS) nutrient media with various additives of growth regulators:

1) MS without growth regulators (number of explants 11, viable of them 0).

2) MS + IAA 1 mg/l, BAP 0,1 mg/l, kinetin 1 mg/l, gibberic acid 0,1 mg/l (number of explants 12, viable of them9).

3) MS + BAP 1 mg/l, kinetin 1 mg/l, gibbericacid 0,1 mg/l (number of explants 10, viable of them8).

On the 14th day of cultivation in a nutrient medium with the addition of BAP, kinetin and gibberellic acid, the explants began to develop leaves.

The conducted studies show the possibility of introduction into in vitro culture and further microclonal propagation of *Phodiola rosea L.* Callus formation can also be used in the future to isolate biologically active substances.

The optimum composition of the nutrient medium for a given plant species is the medium supplemented with BAP, kinetin and gibberellic acid. Thus, the study of the conditions of cultivation of *Rhodiola rosea* L. in vitro has shown the possibility of effective application of the buds for its propagation.

The research is carried out within the framework of grant financing of fundamental scientific research on the priorities of science development for 2015-2017 on the topic "Development of biotechnological methods for the preservation of endemic and medicinal plants in conditions of in vitro ". The research is funded by the Committee of Science of the Ministry of Education and Science of the Republic of Kazakhstan.

IDENTIFICATION OF THE GENETIC CONTROL OF THE 1000 GRAIN WEIGHT OF VARIETIES DIFFER OF SOFT SPRING WHEAT

***V. Piskarev* *, N. Boiko, T. Kapko, A. Timofeev**

SibRIPP&B- Branch ofICG SB RAS, Novosibirsk, Russia

e-mail: piskaryov_v@mail.ru

The purpose of the research was to determine the peculiarities of genetic control of the 1000 grain weight of the varieties differ of soft spring wheat. The study was conducted in 2016 at the experimental field of the laboratory of the gene pool of SibRIPP&B. Mathematical treatment of value of the 1000 grain weight of the varieties and the hybrids F_2 was carried out using the system of genetic analysis of quantitative traits Poligen A, developed by Merezhko A.F.

The parental forms Isheevskaya and Amu 65500 differ at the 3 genes controlling the trait with the expression of dominant epistasis A>B = 1,0. The parental forms Isheevskaya and Lutescens 112 different at the 1 gene controlling the trait. The degree of dominance is equal to -1,0 for the first generation hybrids. The parental forms Isheevskaya and Fenita differ at the 2 genes controlling the trait. The degree of dominance equal to -0,8 for the first generation hybrids. The recessive epistasis is a>B = 1,0. The parental forms Lutescens 85 and Amu 65500 differ by 4 genes that determine the trait. Dominant epistasis is A>B = 1.0 And A>C = 1. The parental forms Lutescens 85 and Lutescens 112 differ by 2 genes controlling the trait. The degree of dominance equal to -0,8 for the first generation hybrids. The parental forms Lutescens 85 and Fenita differ at the 2 genes controlling the trait. The degree of dominance equal to 0.8. The parental forms Shorthandinka 95 and Amu 65500 different by 2 genes controlling the trait. The degree of dominance is equal to -0,3. The parental forms Shorthandinka 95 and Lutescens 112 different by 2 genes controlling the trait. The degree of dominance equal to a 1.0. The parental forms Shorthandinka 95 and Fenita differ at the 3 genes controlling the trait. The degree of dominance is equal to -0,3.

The work was supported by the Russian Scientific Foundation (Project No. 16-16-00011).

GENOTYPIC AND AMPELOMETRIC CHARACTERIZATION OF KAZAKHSTAN GRAPEVINE CULTIVARS COMPARED TO EUROPEAN AND ASIAN CULTIVARS

A.S. Pozharskiy, K.P. Aubakirova, N.A. Ryabushkina

Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan

email: natrya7@yahoo.com

Grapevine is one of the most important and oldest fruit crops of temperate areas of the world. Development of viticulture in Kazakhstan started in late 1950s, but decreased since 1980s resulting from political, social and economic changes in the country. For now the aim of the Government programs is to recover vineyards in southern and south-eastern Kazakhstan' regions and increase grapevine productivity. For the region nowadays an important step in viticulture improvement is detailed genetic and phenotypic characteristics of perspective cultivars. 114 cultivars including 18 ones of Kazakhstan breeding, 21 and 56 cultivars of European and Asian origin, respectively, and 19 hybrids were genotyped using six SSR-markers, recommended by OIV International grapevine descriptor: VVS2, VVMD5 VVMD7, VVMD27, VrZag62, VrZag79. Genotypic data were analyzed using following software: STRUCTURE, IDENTITY 1.0, TFPGA 1.3, GenAlex. Analysis included UPGMA clustering with Nei's genetic distances, Bayesian structure analysis, descriptive and population statistics of alleles. Obtained results confirmed *a priori* data about cultivars' relations and pointed on some mistakes of attribution. As an approach complementing genetic analysis leaf ampelometric study was conducted. 16 leaf parameters according to OIV descriptor were measured using Gra.LE.D 2.04 software, also 12 relative parameters were computed and analyzed with R statistical programming language. 10 parameters most suitable for cultivars discrimination accordingly to statistical analysis were selected for clustering of cultivars. 17 landmarks of grapevine leaf were used to determine an average leaf shape for each cultivar by generalized Procrustes analysis (GPA). Results of ampelometric study showed that parameters of leaf shape can distinguish different grapevine varieties accordingly to their relations. Present study shows that, despite of development of molecular methods of fingerprinting for cultivars' classification, classical ampelometric methods linked with modern statistical approaches still remain relevant. Thus, molecular genetics' and morphometrical methods of characterization of grapevine varieties should be used in complex for more precise identification and classification. Such information is important for effective grapevine culture management and development of new cultivars with traits of interest.

This work was supported by Ministry of Education and Science of Republic of Kazakhstan (grant 1194/GF4).

RETROTRANSPOSONS-BASED GENETIC DIVERSITY AND RELATIONSHIP AMONG *RHODIOLA ROSEA*

D.S. Tagimanova *[1], ***O.N. Khapilina*** [1], ***A.N. Danilova*** [2], ***A.A. Amenov*** [1], ***R.N. Kalendar*** [1]

[1]National Center for Biotechnology, Astana, Kazaкhstan
[2]Altai Botanical Garden, Ridder, Kazakhstan

*e-mail: tagds@mail.ru

Genetic diversity of species is one of the most important parameters that determine the steady state populations and the preservation of mechanisms of adaptation to external environmental factors. This is especially true for small and isolated populations of rare and endangered species of plants that are sensitive to changes in climatic conditions. Molecular markers are essential in plant and animal breeding and biodiversity applications, in human forensics, and for map-based cloning of genes. The long terminal repeat (LTR) retrotransposons are well suited as molecular markers. As dispersed and ubiquitous transposable elements, their “copy and paste” life cycle of replicative transposition leads to new genome insertions without excision of the original element. Both the overall structure of retrotransposons and the domains responsible for the various phases of their replication are highly conserved in all eukaryotes. The method, iPBS amplification, is based on the virtually universal presence of a tRNA complement as a reverse transcriptase primer binding site (PBS) in LTR retrotransposons. To study the genetic diversity of geographical populations of Kazakhstan *Rhodiola* has been used *iPBS* amplification technique. Polymorphisms are defined as the presence-absence of electrophoretic spectra of specific DNA fragments, due to differences in the DNA sequences of primers planting places. In the study 60 accessions belonging to *Rhodiola* sp. A total of 155 scorable bands were detected out of were polymorphic (60 %), ranging in size from 100 to 3000 bp. The dendrogram constructed using the method of ME (Minimum Evolution), revealed a clear differentiation population of *Rhodiola*. The studies revealed that the molecular markers iPBS can be used as effective tools for clustering and inter-population used in research aimed at studying the genetic diversity of populations *Rhodiola rosea.* This study also demonstrates the utility of retrotransposons sequences, a ubiquitous part of eukaryotic genomes, for diversity studies in *Rhodiola rosea* and in *Rhodiola* sp.

IDENTIFICATION OF *GLU-D1* AND *GLU-A1* ALLELES IN BREAD WHEAT USING DNA MARKERS

M.A. Tikhonova, R. Koppel, A. Ingver

Estonian Crop Research Institute, Estonia
Email: marina.tikhonova@etki.ee

The bread-making quality of wheat (*Triticum aestivum* L.) is primarily influenced by its grain protein content and gluten quality. It was indicated that the unique visco-elastic properties of wheat dough could be accounted by variation in high molecular weight glutenin subunits (HMW-GS), the components of the gluten polymer.

The aim of the present study was to perform molecular-genetic analyses of allele composition of HMW glutenin loci *Glu-A1* and *Glu-D1* in 27 winter and 15 spring wheat cultivars originated from 9 countries of Europe using PCR method. Comparison of two methods, PCR and protein SDS-PAGE (by Tohver, 2007; Békés, Wrigley, 2013), of 18 winter and all spring cultivars was carried out.

It was determined that 17 winter and 11 spring cultivars had allele *Glu-D1d*, and 16 winter and 13 spring – *Glu-A1a* or *Glu-A1b* alleles, that have significant positive effects on dough properties (Table). In general, 16 cultivars combine these desirable alleles in their genotypes. It was found that investigated genes were polymorphic mainly in old Estonian cultivars (Joni, Jõgeva 22, Kehra, Luunja, Sani). Comparison of the HMW-GS SDS-PAGE results with those using allele-specific markers indicated complete disagreements for the *Glu-D1* in 2 winter and 5 spring cultivars and for the *Glu-A1* in 5 winter and 2 spring cultivars. Low resolution of SDS-PAGE presumably is the main reason for the discrepancy, as DNA analysis is considered to be more accurate. Other causes could be intravarietal polymorphism of investigated cultivars and labelling errors in seed collections.

Table. The results of PCR analysis for *Glu-D1* and *Glu-A1* HMW-GS in selected wheat cultivars

Cultivar		Alleles
Winter	Spring	
Glu-D1		
Ada, Bjørke, Ebi, Eka, Flair, Fredis, Kalvi, Korweta, Lars, LIA 0044, LIA 00134, Portal, Ramiro, Ritmo, Sani nui, Širvinta, Tarso	Baldus, Mahti, Manu, Monsun, Munk, Runar, Taifun Tjalve, Triso, Vinjett, Zebra	d
Gunbo, Joni, Jõgeva 22, Kehra, Kuusiku, Puuk, Sani B	Estrad, Helle, Meri	a
Luunja, Sani, Sani A	Satu	d/a
Glu-A1		
Fredis, Kuusiku, Lars, Luunja, Puuk, Ramiro, Sani nui, Širvinta	Baldus, Monsun	a
Gunbo, Eka, Kalvi, Sani A, Sani B	Estrad, Helle, Manu, Meri, Runar, Satu, Tjalve, Vinjett, Zebra	b
Ada, Bjørke, Ebi, Flair, Korweta, LIA 0044, LIA 00134, Ritmo	Munk, Taifun	c
Jõgeva 22, Kehra, Sani	Mahti, Triso	a/b
Portal	-	a/c
Joni, Tarso	-	b/c

VARIABILITY OF NUCLEAR GENOMES AND THE STATE OF ORGANELLE DNA IN ALLOPLASMIC (*HORDEUM*)-*T. AESTIVUM* LINES

N.V. Trubacheeva [*]***, T.S. Osadchaya, L.A. Pershina***

Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

[*]e.mail: natas@bionet.nsc.ru

Alloplasmic lines (ornuclear-cytoplasmichybrids) in which alien plasmonsare combined with given nuclear genomes through repeated substitution backcrosses, are valuable experimental tools for studying interaction of nuclear genomes and plasmons (organelle genomes) during the development of new genotypes derived from wide hybrids. The efficiency of viable and fertile hybrid plants formation is determined by the influence of nuclear-cytoplasmic interactions. The aim of this work was to study nuclear and organelle genomes in process of alloplasmic lines formation based on backcrossed and self-pollinated progenies of barley-wheat hybrids *H. marinum* subsp. *Gussoneanum* Hudson (2n=28) x *T. aestivum* L. (2n=42) and *H. vulgare* L. (2n=14) x *T. aestivum* L. (2n=42).

By using molecular and cytogenetic methods it was found out that the process of (*H. marinum* subsp. *gussoneanum*)-*T. aestivum* alloplasmic linesdevelopment involved either integration of wild barley chromosomes in wheat genome, which leads to formation of substituted and additional lines, or elimination of all barley chromosome from wheat genome. The genomes of alloplasmic (*H. vulgare*)-*T.aestivum* lines contained only wheat chromosomes. It was revealed that mitochondrial *cob, nad3-orf156, 18S/5S* and chloroplast *ndhH, rpoB, psaA, infA, ycf5* loci present in heteroplasmic (simultaneous presence of barley and wheat copies) and homoplasmic (copies of one parent) state in alloplasmic lines. Mitochondrial DNA heteroplasmy in (*H. marinum* subsp. *gussoneanum*)-*T. aestivum* lines associated with barley chromosomes in wheat genome irrespective of fertility level. As for (*H.vulgare*)-*T. aestivum* lines without barley chromosomes in nuclear genome, heteroplasmy was detected in partly fertile and sterile plants. The restoration of fertility accompanies with decrease of maternal barley copies and increase of paternal wheat copies. It was shown that only maternal mitochondrial and chloroplast copies expressed in plants with heteroplasmy.

Alloplasmic lines are suitable models for studying somaclonal variation mechanisms caused by changes in mitochondrial or chloroplast DNA.

This work was supported by Basic Project № 0324-2015-0005 and the RFBR (№ 17-04-01738).

GENE POLYMORPHISMS OF WHEAT SUPEROXIDE DISMUTASE GENE FAMILY

A.S. Turzhanova, R.N. Kalendar

RSE "National Center for Biotechnology", Astana, Kazakhstan

e-mail: ruslan.kalendar@mail.ru

Superoxide dismutase (SOD) is one of the main enzymes responsible for protection against stress effects, associated with the generation of ROS. These processes, which destructively affect cell structure and metabolism, are mutually connected and stimulate each other, which may result in a decreased efficiency of oxidation-reduction enzymes or the electron transport system leading to fast production of reactive oxygen species in the cell. Wheat species is the most important crop, and one of the most important objects in the field of genetics research, and molecular genetics. The aim of our work was to study the molecular genetic polymorphism of homologous gene families of SOD in the world collection of wheat, with a value in the breading of the root system. The polymerase chain reaction (PCR) based technique, 'exon-primed intron-crossing' (EPIC) has gained favour in plant and animal studies, and relies on design of primers selected to anneal to highly-conserved regions of the exons. Conservation of exonic regions allowed EPIC to be used to analyse intra- and interspecific polymorphism within SOD genes from multiple cereal species. Thus, genomic data obtained from one or more organisms can be effectively used to rapidly design EPIC-markers for additional related species. We have designed sets of PCR primers for detection of polymorphism genes of superoxide dismutase in wheat and other genetically related cereal species. The result of the research show the molecular-genetic polymorphism of the diversity of superoxide dismutase gene families of world collection of wheat. PCR based detection allelic variation of superoxide dismutase gene families were revealed in intra- and interspecific polymorphism. The greater the genetic distance were found between the studied wheat species (between *Triticum* sp. and *Aegilops*). This work demonstrates how EPIC can be used to determine inter- and intra-specific genetic variation within plant taxonomic groups, and could represent a useful tool for marker-assisted selection of novel SOD alleles within breeding programmes. Thus, new information can be used to improve existing varieties to enhance their adaptation properties, resistance to climatic factors, diseases and pests, analysis of the genome of this important culture for the characterization of varieties that will be used for practical purposes – for marker assisted selection.

ASSESSMENT OF DISTINCTIONS BETWEEN *GLYCYRRHIZA URALENSIS* AND *GLYCYRRHIZA GLABRA* BASED ON ANALYSIS OF ITS MARKER

L. Volkova [1], ***N. Gemedzhieva*** [2], ***S. Abugalieva*** [1], ***S. Zhanarbek*** [1], ***P. Veselova*** [2], ***G. Sitpayeva*** [2], ***Y. Turuspekov*** [1*]

[1] Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan
[2] Institute of Botany and Phytointroduction, Almaty, Kazakhstan
e-mail: yerlant@yahoo.com

The genus *Glycyrrhiza* consists of approximately 30 species, in which six species produce a sweet saponin glycyrrhizic acid (glycyrrhizin). Three representative species (*G.glabra, G.uralensis* and *G.aspera*) of this genus are growing in South-East, Center and West Kazakhstan. Among them *G.glabra* and *G.uralensis* are an important medicinal plants with industrial, ecological values and using as flavorings, sweeteners, for improving health, detoxification and cures for injury. Molecular genetics analysis was applied in order to differentiate these species. The ITS region is an effective marker for use in authenticating of the family *Fabaceae*. In this study the genetic diversity of three species of genus *Glycyrrhiza* L. has been characterized by using the nuclear rDNA internal transcribed spacer (ITS) region.The studied collection consisted from 10 populations, including 6 populations of *Glycyrrhiza glabra*, 3 populations of *G.uralensis* and 1 populations of *G.aspera*, collected in 5 regions of Kazakhstan. Direct sequencing of samples was carried out using Genetic Analyzer 3130 (Applied Biosystems, USA). Genetic distances between genotypes by analyzing genes were calculated using Neighbor-Joining method (Saitou and Nei, 1987). Phylogenetic tree was produced using Neighbor-Joining method and MEGA, version 5 (Tamura K. et al., 2011). The obtained results show polymorphism of nucleotide sequences among three *Glycyrrhiza* L. species, involved in this study. Four nucleotide substitutions were found at 161, 385, 386 and 387 nucleotide positions, which is helping to discriminate the species. Also, the analysis of nrDNA ITS sequences showed good resolution at the intraspecific level and allowed to identify hybrid samples in populations. In Kazakhstan, this was first study the populations of *Glycyrrhiza* L. by using the DNA sequencing of the nuclear rDNA internal transcribed spacer (ITS) region to infer phylogenetic relationships. The resulting information can be used in population genetic, molecular systematics and biogeography, and studies for identification of potentially new species.

The research was conducted in the framework of the Program 0237/PTF-14 supported by the Ministry of Education and Sciences of the Republic of Kazakhstan (duration: 2015-2017).

ANALYSIS OF GENETIC DIVERSITY OF COMMON BEAN FROM DIFFERENT REGION OF CHINA

Lei Lei, Lanfeng Wang, Shumin Wang*

Institute of Crop Sciences, Chinese Academy of Agricultural of Sciences, Beijing, China

*Corresponding author: wangshumin@caas.cn

Common bean (*Phaseolus vulgaris* L.) was introduced to China from the Americas in the fifteen century and presently is an important food legume crop which has been cultivated in many areas of China. This work aims to evaluate the genetic diversity of a Chinese common bean core collection by examining the variability of phaseolin, the major seed storage protein of common bean, throughe-dimensional sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS/PAGE) method. A total of 689 common bean accessions, including landraces, wild germplasms and modern varieties, were evaluated in this study. In terms of geographic representation, both the main common bean producing areas in China, such as Heilongjiang Province, Shanxi Province, Shaanxi Province, and the foreign germplasms were included. Of the total 689 accessions, 12 phaseolin patterns (S, Sb, Sd, B, M13, C, CA, T, PA, To, H, H1) were detected in 676 accessions, but no phaseolin pattern existence was proved in the remaining 13 accessions. Among those detected patterns, there were five patterns (S,Sb,Sd,B,M13) belong to the Mesoamerican gene pool, and seven patterns (C, CA, T, PA, To, H, H1) belong to the Andean gene pool. The most frequent pattern was T (31.2%), followed by Sb (25.6%). These phaseolin profiles were informative in determining the dissemination pathways of the common bean from Americas to China, as well as assessing the genetic diversity of Chinese common bean.

STUDY OF FLORAL GENETIC DIVERSITY IN THE STATE NATIONAL NATURAL PARKS OF BAYANAUL AND BURABAY IN KAZAKHSTAN

A. Yessimseitova, Zh. Zhanybekova, A. Kakimzhanova

National Center for Biotechnology, Astana, Kazakhstan

e-mail: asel_1388@bk.ru

Study and preservation by rational use of genetic resources of the wild flora in Kazakhstan is relevant due to the declining genetic diversity of plants, climate changes and anthropogenic influences. Molecular genotyping of the flora of the Natural Parks SNPP Bayanaul and Burabai is important because it allows comparing efficiency of the methods of species determination using the classic taxonomic approaches and molecular genetic methods based on DNA markers of the nuclear and chloroplast genomes.

The study was aimed at applying primers to amplify a portion of the nuclear (*ITS*) genome of rare plant species when determining a site suitable for the species identification and DNA-barcoding. DNA markers used for the DNA-barcoding have a relatively small size (up to 800 bp), with a presence of conservative flanking sequences, and are haracterized by the excess of interspecific variability over the intraspecific ones.

As a result of the study, when using the *ITS* primer to amplify a portion of the nuclear DNA, sizes of the amplified fragments were within acceptable limits (~700 bp). PCR amplification was carried out for 63 samples from 28 plant species using the *ITS* marker (annealing temperature 55°C). Separation of the amplification products was carried out in a 1.5% agarose gel and as a result electrophoretic profiles were obtained for each sample.

PCR amplification products of the *ITS* marker were subsequently used to sequester 63 populations of endemic, rare and economically valuable plant species. As a result of sequencing, the nucleotide sequences of the analyzed samples were collected and edited using the SeqMan program. Automatic alignment, counting the number of replacements per site, and building of a phylogenetic tree using the maximum likelihood method were carried out by using the software MEGA5 and Neighbor-joining method with a bootstrap function with 1000 replicates. Genetic distances between populations are calculated using the Maximum Composite Likelihood.

When using the marker of the nuclear genome (*ITS*), a phylogenetic tree was constructed for 63 samples representing 30 populations from 28 endemic, rare and economically valuable plant species in the Bayanaul and Burabai Natural Parks. The phylogenetic tree constructed on the *ITS* data reflects evolutionary relationships between populations within species, as well as for the species within families and between plant families. In the phylogenetic tree, 10 clusters are evident which also demonstrate families-dependent difefrences.

Level of the genetic diversity for 63 nucleotide sequences from plant samples from the Bayanaul and Burabai was determined using the *ITS* marker. The Tajima index was 0.469317.

Genetic diversity (using the *ITS* marker) was calculated for plant species belonging to the *Fabaceae* family, namely the species *Lathyrus pisiformis*, *Trifolium repens*, *Medicago falcata*, *Oxytropis floribunda*, *Glycyrrhiza uralensis*. The phylogenetic analysis revealed two clusters of five plant genera.

The research was supported by NT program 0237/PTF-14 granted from the Ministry of Education and Sciences of the Republic of Kazakhstan for duration 2015-2017.

TRANSCRIPTOMIC ANALYSIS OF A TRICHOMELESS MUTANT IN *AGRIOPHYLLUM SQUARROSUM*

J.W. Zhang [1,2], ***G.X. Chen*** [*1]

[1]Northwest Institute of Eco-Environment and Resources, Chinese Academy of Sciences, Lanzhou, China

[2]University of Chinese Academy of Sciences, Beijing, China

*e-mail: guoxiong@lzb.ac.cn

Agriophyllum squarrosum (sand rice) is a highly nutritious grain identified as an important potential crop. In order to get excellent agronomic characteristics, such as trichomeless, mutations were induced by EMS with the sand rice seeds. A trichomeless (tri) mutant (*tri1*) was identified in M2 and confirmed in M3 and M4.A comparative transcriptomic analysis of *tri1* and its wild type was conducted. There were 78117 unigenes assembled and 284 unigenes significantly differentially expressed. About 22923 putative SNPs were detected within 7955 unigenes and stringent post-processing reduced this number to 1283 putative SNPs within 859 unigenes. Meanwhile, we identified 158 orthologous genes related to trichome initiation and development in sand rice by the comparison with *Arabidopsis thaliana* using OrthoMCL. Among them, 18 genes contained the putative SNP. Combining the two approaches, 28 candidate genes were identified according to the gene annotationand the protein alteration.

Session 2.
Abiotic and Biotic Stress Resistance

DIVERSITY AND EVOLUTION OF DISEASE RESISTANCE GENES DERIVED FROM WILD EMMER WHEAT

***Tzion Fahima*[1], *Huang Lin*[1], *Elitsur Yaniv*[1,2], *Dina Raats*[1], *Valentina Klymiuk*[1], *Hanan Sela*[1,3], *Lihua Feng*[1], *Assaf Distelfeld*[3], *Tamar Kis-papo*[1], *Tamar Krugman*[1], *Jorge Dubcovsky*[4], *Boulos Chalhoub*[5], *Alan H. Schulman*[2], *Abraham B. Korol*[1]**

[1] Institute of Evolution, University of Haifa, Mt. Carmel, Haifa, Israel

[2] LUKE Natural Resources Institute and University of Helsinki, Helsinki, Finland

[3] Institute for Cereal Crops Improvement, Tel Aviv University, Ramat Aviv, Israel

[4] University of California, Davis, California, USA

[5] University of Evry Val d'Essonne, Evry, France

Wild emmer wheat, *Triticum dicoccoides*, the tetraploid progenitor of domesticated wheat, distributed along a wide range of eco-geographical conditions in the Fertile Crescent, has valuable "left behind" adaptive diversity to multiple diseases and environmental stresses. Segregating mapping populations, developed by crossing of selected *T. dicoccoides* genotypes with *T. durum* cultivars, revealed numerous loci associated with disease resistance, drought tolerance, high grain protein content, and yield. Furthermore, wild emmer is a promising source of resistance to stripe rust. For example, *Yr15* is a dominant gene that confers high resistance to stripe rust, while *Yr36* confers slow rusting quantitative resistance. Comparative genomics approaches were used to develop high resolution physical maps for *Yr15*, and for cloning of *Yr36*. *Yr36* has a unique architecture with a kinase and a START lipid-binding domains, designated *WKS* hereafter. The distribution and sequence conservation of *WKS* R-geneswere compared with those of NBS-LRR R-genes (e.g. *Lr10* and *Pm3*) among wild emmer natural populations. The sequence diversity of *WKS1* was much lower than that of *Lr10* and *Pm3*, indicating that these R-genes, representing different resistance mechanisms, are shaped by different evolutionary processes. Further work is underway to clone *Yr15* located on chromosome arm 1BS, using the complete 1BS physical map, constructed by our group, as well as the recently assembled wild emmer reference genome. These studies demonstrate the potential of wild emmer wheat gene pool for improvement of durum and bread wheats by exploitation of genes that were lost during domestication.

GLOBAL JOURNEYS OF ADAPTIVE WHEAT GENES

Simon Griffiths

John Innes Centre, Norwich, UK

The domestication of wheat, it's spread with agriculture, and increasingly systematic breeding approaches have led to fascinating variation in the developmental profile of cultivars adapted to environments that are very different to those encountered in the centre of wheat domestication. From the rapid flowering and maturing spring wheat varieties of Kazakhstan to UK winter wheat varieties which spread their development across a season of almost twelve months. In this presentation the origin of known heading date genes controlling this range will be described in relation to the current distribution of alleles in elite varieties. This will include allelic variants of *Ppd-1*, *Ppd-2*, *Vrn-1*, *Vrn-3*, and *EPS-1*. The potential for more efficient deployment of these alleles in breeding and the potential for the use of less well described genes and alleles will be discussed.

GENOMICS-BASED BREEDING USING GENETIC VARIATION OF ROOT SYSTEM ARCHITECTURE IMPROVES CROP PRODUCTIVITY UNDER ABIOTIC STRESS CONDITIONS

Yusaku Uga [1, 2]

[1] Breeding Material Development Unit, Division of Basic Research, Institute of Crop Science, National Agriculture and Food Research Organization (NARO), Tsukuba, Ibaraki, Japan, E-mail: yuga@affrc.go.jp

[2] Department of International Agricultural Development, Graduate School of Agricultre, Tokyo University of Agriculture, Tokyo, Japan

Crop production is greatly affected by environmental stresses such as drought, high salinity, and submergence as well as by nutrient deficiency. The global climate change that has occurred in recent years has exacerbated the effects of these stresses on plant growth. The root is an essential organ for absorbing water and nutrients from the ground. Especially, adequate root system architecture is important for plant growth under soil conditions where water and nutrients are deficient. Therefore, genetic improvement of the root system architecture has been recognized as an important approach to provide stabilization of crop production. In cultivated rice (*Oryza sativa* L.), the wide extent of natural variation of root system architecture has been revealed in previous studies. For example, upland rice typically shows thicker and deeper rooting than lowland rice. This diverse natural variation in rice could be a useful resource for improving on inadequate root system architecture to adapt to severe environmental conditions.

The root growth angle, which determines the direction of root elongation in the soil, affects the area in which roots capture water and nutrients. Our group have isolated *DRO1*, quantitative trait locus (QTL) controlling root growth angle, on chromosome 9 in rice. We also have developed a near-isogenic line (NIL) that carries a functional allele of *DRO1* derived from the deep-rooting cultivar 'Kinandang Patong' in the genetic background of the shallow-rooting parent variety 'IR64', which has a non-functional allele of *DRO1*. Using this NIL, we demonstrated that introducing of gene for root growth angle enhanced rice yield under conditions of water and nitrogen deficiencies. Recently, our group isolated another QTL for root growth angle, *qSOR1*, in rice. We developed four NILs having functional or non-functional *DRO1* and *qSOR1*. These lines showed several types of root growth angle, ranging from super shallow to deep roots, suggesting that we could make wide variation of root system architecture by using two allelic variations in only two QTLs. We also identified several QTLs for root length because root length also determines the area in which roots take up water and nutrients. These QTLs would be useful genetic resources for improving rice production under abiotic stresses.

MOLECULAR MARKERS AND HAPLOID BIOTECHNOLOGY IN RAPID SELECTION OF *TRITICUM AESTIVUM* L. FOR RESISTANCE TO RUST DISEASES IN THE CONDITIONS OF SOUTHERN KAZAKHSTAN

B.B. Anapiyayev [1], ***K.M. Iskakova*** [1], ***E.B. Beisenbek*** [1], ***A.T. Sarbayev*** [2], ***I.M. Dweikat*** [2], ***P.S. Baenziger*** [2]

[1] Institute of Engineering High Technologies, Almaty, Kazakhstan;
[2] Institute of Agriculture, Almalybak, Almaty region, Kazakhstan;
[3] University of Nebraska, NE, Lincoln, USA;
E-mail: bak_anapiyayev@mail.ru

The problem of cultural plants resistance to adverse environmental factors, along side with Earth population growth, is recognized as a global problem. Scientists have faced the important problem of new cultivars accelerated breeding of the basic food cultures which are steady to abiotic and biotic environmental factors.

Modern developments of androgenesis which is one of the haploid biotechnology directions and the basis of it is the method of isolated anthers and microspores culture, allow to create the constant homozygous double haploid lines from plant hybrid populations during 1-2 years while a traditional breeding method of stable lines reception demands about 8-10 years.

In our research was monitoring of wheat genotypes on rust diseases resistance was carried out in Southern Kazakhstan conditions in natural and infectious nursery. Races *Puccinia graminis, Puccinia striiformis, Puccinia recondita* were used as an infecting agent. Intensity of rust defeat was taken into account on Peterson et al scale visually on all plants of the plot. The following genotypes have shown a high stability to rust diseases: *Triticum kihara, Triticum diccocum, Triticum thimofeevi,* Almaly, Naz, Taza and others. The selected steady genotypes have been used for crossing and breeding of perspective inter-cultivar and inter-species remote hybrids. More than 120 hybrid combinations were created. Received hybrids were genetically stabilized by using haploid biotechnology methods on the basis of isolated anthers and microspores culture in vitro. The structures of nutrient mediums on Blaydes and №6 basis were modified through activated coal and amylodextrine addition. In the following experiments series rust-disease resistance and rust-disease susceptible parental forms, wheat hybrid forms and new doubled haploid lines were analyzed at DNA level using molecular markers method. As a result of the SSR-analysis and isogenic lines on the Thatcher basis it was established that rust-disease resistance genotypes and lines have Lr 24 gene. In a final stage new perspective dohaploid lines were tested on stability to rust diseases in natural and artificial conditions in two areas of Southern Kazakhstan (Almaty and Zhambyl). Among investigated doubled haploid lines the numbers DHL 1257, DHL 1250, DHL 1245 and DHL 1227 were allocated. They appeared rust-diseases resistance and are characterized with high productivity and grain quality.

On the basis of the carried out researches and use of haploid biotechnology for the first time in Kazakhstan a new high productive cultivar of common wheat "Nureke" which is zoned in Almaty and Zhambyl areas of Southern Kazakhstan. Also was created the model systems for the culture of isolated microspores in vitro and research the processes of plant regeneration for cereal crops.

DETERMINATION OF ASCORBATE PEROXIDASE GENE EXPRESSION IN THE LENTIL (*LENS CULINARIS* MEDIK) UNDER DROUGHT STRESS CONDITIONS

Meltem ÖZDERE, Melike BAKIR

Department of Agricultural Biotechnology, Seyrani Faculty of Agriculture, Erciyes University, Kayseri, Turkey

Ascorbate Peroxidase (APX) is a very important enzyme responsible for the detoxification of ROS family member H_2O_2 causing cellular damage. In this study, changes in the expression of APXI gene were investigated in the leaves and roots of drought-resistant lentils (*Lens culinaris* M *cv* Fırat-87) and drought-sensitive lentils (*Lens culinaris* M *cv* Özbek). For this purpose, lentils grown for 7 days were exposed to drought stress for 6, 13, 20 days without being irrigated. The effect of the stress was determined by measuring the relative water content (RWC). The relationship between drought stress and APXI gene expression was determined by quantitative real time PCR (Real Time qPCR). The increase in the APXI gene expression in the leaves was highest in the Fırat-87 variety on the 6^{th} day (2 fold higher compared to the control plants), whereas a statistically significant increase was observed only on the 20^{th} day of the Özbek variety known to be sensitive to drought. And this increase was relatively low compared to the Fırat-87 variety. Similar to the leaves, in the roots of the Fırat-87 variety, APXI gene expression reached the highest levels on 6^{th} day, but no increase was observed on the 13^{th} and 20^{th} days. In the Özbek variety, unlike to its leaves, APXI gene expression reached the highest levels on the 6^{th} and 13^{th} days, and similar to the Fırat-87 variety there was no increase on the 20^{th} day. In conclusion, in the present study, time-dependent relationship between drought stress and APXI gene expression was investigated in different varieties and tissues. The results of the present studies demonstrate that APXI gene expression is highly variable due to drought-induced stress in the leaves and roots.

This study was supported by Erciyes University Scientific Research Unit (Project No: FLY_2016_6684).

THE VARIABILITY OF THE PARAMETERS OF THE MORPHOGENETIC PROCESSES IN POPULATIONS OF *Triticum aestivum* L. UNDER THE INFLUENCE OF STRESS FACTORS

N.A. Bome* *[1], A.Ya. Bome [1], L.I. Weisfeld [2], N.N. Kolokolova [1], A.A. Petrova [1], A.A. Belozerova [1]

[1]Tyumen State University, Tyumen, Russia
[2]Emanuel Institute of Biochemical Physics of Russian Academy Sciences, Moscow, Russia
*e-mail: bomena@mail.ru

The projected climate changes could cause to an increase of extreme environmental conditions. The projected climate changes lead to an increase of extreme environmental conditions. An understanding of how genotypes of crops are respond to the adverse factors is crucial in the strategy for sustainable crop production. We conducted a series of laboratory experiments in which plants of spring wheat were subjected to chloride salinity, lack of moisture and low temperatures. Study of the molecular mechanisms of plant response to stress factors is usually preceded by a study of quantitative traits at the phenotypic level. Variability signs of seedlings can be used as a marker for selection in populations forms adapted to unfavorable factors. At high levels of individual simulated stress in most cases, there is a shift in the ratio of raw mass of roots and shoots. At the same time the varieties with a well-developed root system often were showing a higher tolerance to drought, salinity, and to cold. Calculation of the indexes of length of roots and shoots gives an indication of the dynamics of the adaptation processes to stress in early ontogenesis. The results obtained in the laboratory, in some cases, correlate with the results of field trials. However, to extrapolate them into agricultural practices necessary cautiously, supporting by field research. Expanded environmental test of varieties and hybrids of spring wheat in the soil and climatic conditions of the south of the Tyumen region (Russia), Baden-Württemberg and Lower Saxony (Germany), allowed to reveal individual and population sings which can be used as indicators the adaptation properties. In the creation and evaluation of new forms of plants resistant to hydrothermal stresses, seed germination and biological resistance of plants during all vegetation period serve as informative indicators a number of interrelated processes of ontogenesis reflecting changes in environmental conditions. As criteria of the ability of plants to withstand dehydration during arid periods serve the water-holding capacity of leaves, their length, width and area. The phenotypical variability of plant height, number and weight of grains per ear were determined by the terms of ecological and geographical points. Hybrid forms having the stable expression of the studied traits were identified. That allows recommending them as a valuable raw material for breeding. The deciduous diseases of plants (the pathogenic microorganisms: *Erysiphe graminis* DC, *Puccinia recondita* Rob. ex. Desm *f. sp. tritici* Eriks (=*P. triticina* Eriks.), *Alternaria* spp. и *Helminthosporium* spp.) contribute significant limitations in the production of wheat grains. Our studies have shown that the tolerance of plants to disease (for example, to powdery mildew) depends on the concentration of the pigments (Chl a, Chl b, and carotenoids) in cells of flag leaf. Rapid determination of the content of chlorophyll in the field using a Spad-502 Plus N-tester allows evaluating the dynamics of the spread of the disease from the onset of symptoms. Regulation of abiotic and biotic stress responses of plants, according to our data, it is possible with the help of genetic active, but free from mutational properties of para-amino benzoic acid (PABA). The genetic diversity of spring and winter wheat is achieved by a combination of the two methods – chemical mutagenesis and artificial hybridisation. The starting material we used samples of VIR world collection, which has large reserves of genotypic variability. We have determined the optimal dose of the mutagen for mutation breeding plants. In general, the offered methods may be useful for the receiving of stress-resistant varieties.

DROUGHT AS A MODULATOR OF GENE EXPRESSION FOR CMS AND APOMIXIS IN SORGHUM

L.A. Elkonin* [*1], V.V. Kozhemyakin [1], G.A. Gerashchenkov [2], E.V. Belyaeva [1], V.M. Panin [1], N.A. Rozhnova [2]

[1]Agricultural Research Institute of South-East Region, Saratov, Russia
[2] Institute of Biochemistry and Genetics, Ufa Research Centre, Russian Academy of Sciences, Ufa, Russia

*e-mail: lelkonin@gmail.com

Drought is one of the most powerful factors causing significant changes in plant epigenotype. Over the years we studied the impact of drought conditions on the expression of cytoplasmic male sterility (CMS) and apomixis in sorghum. We found that in some types of CMS-inducing cytoplasms, the common feature of which is a distortion of anther dehiscence (9E, A3, M35-1A), expression of fertility-restoring genes in genome of F1 hybrids is governed by the conditions of plant water availability, in particular, by air humidity. Male fertility "induced" by a high level of water availability stably inherited and manifested in self-pollination progeny of fertile hybrids, grown in drought conditions. The restoration of male fertility under the influence of the environment is not due to changes in the structure of genes involved in the control of CMS, but with a change of regulation in the genome of the hybrid plants under the influence of water availability. MSAP-analysis of genome of sterile F1 hybrids in the 9E cytoplasm and the fertile revertants derived from them showed that the reversion to fertility is accompanied by changes in the methylation of the gene of transcription regulator Myb46. These data suggested epigenetic mechanism regulating restoration of male fertility in this cytoplasmic system. This mechanism involved repression of nuclear fertility-restoring genes under drought stress by methylation of their nucleotide sequences and removing repression in high water availability. In the A3 cytoplasm, a strong correlation between restoration of male fertility and air vapor pressure deficit (VPD) at flowering ($r = -0.96$; $P<0.01$) was found suggesting VPD is a trigger for down-regulation of *Rf*-genes.

In sorghum lines (AS-1a, Atc), which are characterized by elements of apomixis – aposporous embryo-sacs, parthenogenetic pro-embryos, and maternal-type plants, – apomictic potentials distinctly manifested in the seasons with high daily temperatures and severe drought in the period of ovule and megagametophyte development, and almost disappear under high moisture and moderate temperature. Apparently, drought conditions regulate the expression of apomictic potentials in these lines by epigenetic changes in the genetic systems controlling megagametophyte development.

This work was partially supported by the Russian Foundation for Basic Research, grant 16-04-01131.

LEAF AND YELLOW RUST EVALUATION AND MOLECULAR SCREENING IN WHEAT CULTIVARS PRODUCED IN KAZAKHSTAN

A. Kokhmetova[1], E. Gultyaeva[2], A. Madenova[1], Galymbek K.[1,3], B. L. Purnhause[4]

[1]Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan
[2] All-Russian Research Institute of Plant Protection, St.Petersburg-Pushkin, Russia
[3]Kazakh National Agricultural University, Almaty, Kazakhstan
[4]Cereal Research Non-Profit Ltd. Co., Szeged, Hungary
e-mail: gen_kalma@mail.ru

Kazakhstan is one of the great wheat producers in Central Asia. Yield losses from rusts reached 30-50% in epidemic years. Resistance leaf rust *Puccinia triticina* Eriks. and yellow rust *Puccinia striiformis* f.sp. *tritici* are the most important objectives in Kazakhstan and are the major factor that adversely affects wheat yield and quality and causes considerable economic damage. To effectively use stripe (*Yr*) and leaf rust resistance genes (*Lr*), it is important for breeders to know the resistance genotype in current cultivars. In this study, 30 winter wheat cultivars grown and/or produced in Kazakhstan were investigated using molecular markers to determine the presence and absence of important *Lr* genes (*Lr1, Lr9, Lr10, Lr19, Lr28, Lr29, Lr68*), and some linked *Yr* genes (*Lr26/Sr31/Yr9/Pm8, Lr37/Yr17/Sr31*). Molecular screening of these genotypes showed contrasting differences in the frequencies of these genes. Among the 30 entries, 17 carried leaf rust resistance gene *Lr1,* six had *Lr26* and *Lr34,* and *Lr10* and *Lr37* were found in three cultivars. Two single cultivars separately carried *Lr19* and *Lr68*, while *Lr9* was not detected in any genotypes in this study. Field evaluation demonstrated that two of the most frequent two genes (*Lr1* and *Lr26*) to be ineffective. While *Lr34* provided some protection, the remaining effective *Lr* genes were found only in few genotypes: *Lr37* occurred in Kazakh genotypes L-1090 and Krasnovodapadskaya 210 and in the US cultivar Madsen; *Lr19* and *Lr68* were likely present only in Russian and Kazakh cultivars, Pallada and Yegemen, respectively. The highest resistance over three years of leaf rust testing was found in Kazakh cultivars, Karasay, Krasnovodapadskaya 210, L-1090, Arap and Yegmen, foreign cultivars Madsen, Pallada and the control Parula (*Lr68*). 20 near-isogenic Thatcher lines, each possessing a single *Lr* gene was used for virulence analysis of *P. triticina* populations in Kazakhstan in 2016. The high efficiency of gene *Lr19* and *Lr24* were revealed Virulence to gene *Lr9* was absent or occured rare in fungus populations from South Kazakhstan, but was observed in North Kazakhstan (mainly from wheat cultivars with *Lr9* gene). Variability in virulence frequencies were observed in Thatcher isogenic lines with genes *Lr2a, Lr11, Lr15, Lr16, Lr20* and *Lr26*. Virulence to *Lr1, Lr 2b, Lr2c, Lr3a, Lr3bg, Lr3ka, Lr14a, Lr14b, Lr17, Lr18* and *Lr30* was high both in South Kazakhstan and North Kazakhstan *P. triticina* populations. Data may assist breeders to incorporate effective *Lr* and *Yr* genes into new cultivars.

This work was financially supported by the Ministry of Education and Science Republic of Kazakhstan, research project grant funding №2120 and by the Ministry of Agriculture RK, research grant №O0721.

MARKER ASSISTED SELECTION (MAS) OF RICE ON RESISTANCE TO DISEASES, FLOODING AND SALINITY

P.I. Kostylev, E.V. Krasnova, A.A. Redkin, Yu.P. Kalievskaya

ARRI of Grain crops named after I.G. Kalinenko, Zernograd

The increase of rice productivity has always been the main purpose of all breeding programs. The potential productivity of new varieties reached its maximum of 10-12 t/ha, but the practical productivity is significantly lower because of different biotic and abiotic stress-factors, which become the main obstacles for productivity improvement. The principle stress-factors for rice are salinity, flooding, cold weather, drought, diseases, pests and weeds. Thus the transfer of genes of resistance into the genotypes of the main rice varieties is of primary importance. The use of biotechnologies contributes a lot into the identification of the genes and their introduction into new varieties.

The purpose of the research was to develop the initial material of rice for breeding of highly productive varieties with resistance to salinity, long-term water flooding and rice blast, using DNA-markers and PCR-analysis.

The initial material and methodology. The samples 'AGI' (Vietnam) have been taken as the sources of resistance to salinity and flooding, and the lines 'C101-A-51', 'C101-Lac', 'IR-58' and 'Moroberakan' as the sources of resistance to rice blast. The early maturing varieties 'Novator', 'Boyarin' and 'Virazh' have become the recipients. The identification of the genes has been carried out by the method of molecular marking based on PCR with the use of special primers.

The results of the researches. The development of varieties, resistant to blast and their quick introduction into production is the most promising decision in the fight against the disease. The combination of some efficient genes of resistance on genetic basis of basic varieties is a productive strategy of breeding on resistance to highly variable fungal pathogens. Due to the use of DNA-marking selection we have introduced 5 genes of resistance to rice blast into the domestic rice varieties adapted to agro climatic conditions of rice-growing in the south of Russia. The conducted hybridization allowed obtaining the rice lines on the basis of the varieties 'Boyarin' and 'Virazh' with the pyramiding genes of resistance to rice blast Pi-1, Pi-2, Pi-33, Pi-ta, Pi-b in the homozygous state. There have been obtained the hybrids of the variety 'Novator' with the Oriental rice varieties, possessing the gene 'Saltol'. The analysis of DNA of the 83 best crops F_2 showed that the segregation along the gene 'Saltol' was NSIC Rc 106 x Novator – 15ss: 13Ss: 2SS; IR 52713 x Novator 9ss: 18Ss: 2SS; IR 74099 x Novator 14ss: 8Ss: 2SS. There was a dominance of the plants with the recessive alleles of genes and heterozygotes, but the number of salt resistant dominant homozygotes was less than expected. It was due to a correlation of the genes 'Saltol' with the unfavourable for the plants genes of photosensitivity, later maturity, seeds fall and beardedness, and because the sample was not representative because of the artificial selection. There have been identified the best forms. The samples obtained from the hybridization of the variety 'Novator' and the donors of the gene Sub 1 in F_2 resistant to flooding possessed a great range of segregation in such traits as vegetation period, plant height, length and form of a panicle, number of spikelets and beardedness. During the analysis of the hybrids 'BR-11xNovator' the gene Sub 1A (in homozygous and heterozygous state) was available in nine hybrids, i.e. in the ratio 9:11, though it had to be 15:5 in a monohybrid segregation. In the hybrid combination 'CR-1009xNovator' the segregation F_2 was in the ratio 18:2, i.e. almost all selected plants had the gene Sub1. The segregation of the hybrids 'Inbara-3xNovator' and 'TDK-1xNovator' was in the ratio 14:6 or about 3:1, i.e. close to the mendelian. The deviation in the segregation of two combinations can be explained by the effect of the selection and correlation of the genes. The samples with the necessary genes have been reproduced in FSEF 'Proletarskoe' of the Rostov region, where there have been selected the best plants F_3-F_4.

EPIGENETIC EVENTS IN WHEAT SEEDLINGS NUCLEI ABIOTIC STRESS RESPONSES

L.A. Minasbekyan

Yerevan State University, Scientific Research Institute of Biology, E-mail:minlia@ysu.am

With the development of civilization and technology, our living space is filled with a variety of electromagnetic fields, the sources of which are computers, cell phones, various radiological diagnostic and physiotherapy equipment in medicine, cellular antenna amplifier, etc. The problem of electromagnetic safety becomes extremely relevant, since the most medical devices and technical devices radiate mm-wave in the range of 1-300 GHz. The plant's ability to respond to stresses largely depends on its capacity to modulate the transcriptome rapidly and specifically. Epigenetic mechanisms, including DNA methylation, chromatin dynamics and small RNAs, play an essential role in the regulation of stress-responsive gene expression. Stress induced both long –term and short-term effects on epigenetic mechanisms in plant germ cell development. Short – term responses to abiotic stresses include DNA-methylation alterations (Chen et al., 2016), miRNA disregulation (Babenko et al., 2012), heterochromatin de-condensation (Minasbekyan et al.2007) and transposon activation (Pecinka et al., 2010). Stress-related covalent modifications of DNA and histones can be passed on during mitosis and meiosis to the next generation and provide a memory that enables the plant and even its offspring to adopt better to a subsequent stress.

In our study of plant adaptation to abiotic stress, such as emission extremely high frequent of electromagnetic irradiation (EHF EMI) by different type of electromagnetic equipment and power station of cellular phone communication, have been investigated. Influence of EHF EMI in the mm-range (45-53 GHz) on nuclear envelope PL content and DNA methylation of wheat seedlings on 3 and 4 day after irradiation have been studied.

Under impact of EHF EMI we observed falling of nuclear membrane charge, due to decreasing of anionic PL in content of nuclear envelope and simultaneous increasing of this ones in nuclear soluble fraction, which can change direction of facilitate transport through nuclear envelope according to proposed by us physical model (Minasbekyan et al., 2007). Obtained data was compare with our early investigation PL content of nuclear envelope during germination, which leads to the increasing of anionic PL in content of nuclear membrane, and appropriate decreasing this one in nuclear soluble fraction. From the obtained data it can be concluded that decrease in the content of the anionic PL in the nuclear membrane under abiotic stress is a protective reaction of cells in response to mm-wave, which commonly means to enhance transport activity, as the reduction of the anionic PL in content of the nuclear envelope restrains increase transport activity through the nuclear envelope, playing the role of a kind of natural buffer.

Rearrangements in nuclear envelope reflected on the genome state. Although the genome often depicted as a static structure upon which protein-aqueous factors bind to control turn expression, the genome is actually highly mobile and capable of exploring the complex domain architecture of the nucleus, which in turn controls genome maintenance and gene expression. As direct stress response we investigated treated by mm-waves wheat seedlings of first generations on PL content of NE and Soluble nuclear fraction, as well on DNA methylation. For revealing long-term stress recponce we study alterations in DNA methylation of treated by EHF EMI seeds in next generation. As obtained by us part of methylated DNA sites preserved in the next generation. It is assumed, that symmetrical methylation pattern are stably inherited through mitotic and to some extent also through meiotic divisions, and it might facilitate the inheritance of a stress memory. So alteration in many direction of nuclear envelope and adjacent to it peripheral chromatin may alter and as we show in this study chromatin conformation may changes through DNA methylation of transposable elements of genome under EHF EMI influence.

THE CHANGE OF AN EXPRESSION OF PR AND HSP GENES OF *IN VITRO* POTATO PLANTS UNDER HEAT STRESS AND PATHOGENESIS OF RING ROT OF POTATO

A.I. Perfileva, E.Uy. Garnik, A.S. Stolbikov, V.N. Nurminsky

Siberian Institute of Plant Physiology and Biochemistry, Siberian Branch of Russian Academy of Sciences, Irkutsk, Russia
e-mail: alla.light@mail.ru

It was shown for the first time that high-temperature exposure of potato plants cultivated *in vitro* (39°C for 2 h) provokes maximum synthesis of heat shock proteins (HSP). The changes in HSP gene expressions in tissues of potato plants *in vitro* of two varieties (Lugovskoy and Lukyanovsky) under heat treatment (39°C for 2 h) and infection of *Clavibacter michiganensis* ssp. *sepedonicus* (*Cms*) with different sequences of treatments were investigated. *Cms* are phytopathogenic bacteria that cause the ring rot disease of potato. The changes were assessed at transcript and protein content levels. In check (control) experiments the plants of the two varieties showed no synthesis of proteins *HSP101* and *HSP17.6* at transcript and protein content levels. HSP synthesis in the infected plants had no varietal specificity. The heat treatment (39°C) induced HSP synthesis in tissues of potato plants of both varieties. The infection without addition of the heat treatment slightly induced HSP synthesis in potato plants of Lukyanovsky variety, while the presence of HSP was not observed in potato plants of Lugovskoy variety. This can be explained by the different dynamics of HSP level changes in plants of the two varieties. The infection slightly suppressed the activation of *HSP* expression under heat treatment.

The results obtained indicate that biotic stress is able to modulate plant protective response to thermal effects. It is consistent with the data concerning the change of expression level of genes encoding pathogenesis-related (PR) proteins that protect cell from the consequences of biotic stress. PR proteins are the extracellular proteins synthesized in plant cells under attack from pathogens, and their role in pathogenesis is significant and diverse. Some PR proteins provide the cell protection mechanism associated with increased formation of ROS in plant cell. In addition many of PR proteins have also fungicidal and bactericidal activity *in vivo*.

According to the results concerning the gene expressions of *PR2* (1,3-β-glucosidase) and *PR4* (hevein-like protein) in tissues of susceptible potato variety Lukyanovsky, it can be concluded that the expressions of these genes are increased in the pathogenesis of *Cms*, and the expression level of *PR2* gene under biotic stress is higher than that of *PR4*. Two- to threefold increases in the transcripts of these genes are considered as significant. Literature data indicate that the infection of *Clavibacter michiganensis* ssp. *michiganensis* (tomato pathogen) in tomato plants increases the content of such proteins as 1,3-β-glucosidase (*PR2*), endochitinase (*PR3*), hevein-like protein (*PR4*) and thaumatin/osmotin (*PR5*). The decreases in the transcript levels of both *PR2* and *PR4* genes under heat treatment were not observed. *PR4* gene transcript level increased significantly in plants under the combined impact of the stressors in comparison with that under only heat treatment, and *PR2* gene expression was unchanged.

Thus, this paper shows for the first time that infection of *Cms* activates the expression of *PR2* and *PR4* genes in potato. Heat shock does not suppress the expression of these genes in the infected plants, and on the contrary the expression of *PR4* gene increases.

The changes in the transcript levels of *HSP* genes may relate to those of *PR*-protein genes. So, an increase in *PR* gene expressions under biotic stress is observed, at the same time the *HSP* gene expressions are negligible. There is an increase of *HSP* and *PR* gene expressions under heat treatment, which can be explained by an increase in the synthesis of protective proteins as a non-specific defense response of plant to stress factors. Under the combined impact of the stressors the transcript levels of the majority of *HSP* genes investigated are lower than under only heat treatment, at the same time the transcript levels of *PR* genes increase.

The work was executed at financial support of Russian Foundation for basic research (RFBR), the Grant No. mol_a 16-34-00806.

Keynote

MAPPING AND RE-SEQUENCING OF *SDW1/DENSO* LOCUS AFFECTING PLANT HEIGHT AND HEADING DATE IN BARLEY

E.K. Potokina *, M.V. Lebedeva, S.B. Teplyakova, N.N. Ivanova, N.P. Voytsutskaya, O.N. Kovaleva

[1]Vavilov Institute of Plant Genetic Resources (VIR), St.Petersburg, Russia

*e-mail: e.potokina@vir.nw.ru

Molecular markers of genes that expose a significant pleiotropic effect are of a great importance for breeding programs. In the classic cases the genes are involved in a gibberellic acid (GA) metabolism influencing plant height, lodging resistance, and, consequently, harvest index. In barley, more than 30 types of dwarfs or semi-dwarfs have been described; among them the *sdw1.d* mutant (cv. Diamant) is documented in the pedigree of the famous European malting barley Triumph, which is known as the parental line for many malting barley varieties.

Searching for genetic factors affecting flowering time in barley we performed a large scale field evaluation of series of barley mapping populations in two very diverse environments separated from one another by 15° of latitude with changing day length. We were looking for steady QTLs, influencing heading date in barley independently on environment cue. The robust significant QTL was detected on 3H chromosome affecting heading date and plant height in DH lines from Morex/Barke and Morex/Triumph crosses. The position of the QTL peak on the Morex/Barke genetic map was proved to coincide with HvGA20ox2, the recently discovered candidate gene for the *sdw1/denso* locus in barley. Barke pedigree list can be traced back to Diamant via Triumph, which is known as a donor of *sdw1/denso* semi-dwarf allele. Combining the recently published findings in molecular characterization of barley HvGA20ox2 gene with our QTL mapping results we were focusing on the most likely functional polymorphism of the *sdw1.d* (*denso*) allele presented in cv. Barke and its ancestor cv. Triumph.

UNIQUE GENE STRUCTURE ENCODED A FAMILY OF HAIRPIN-LIKE DEFENSE PEPTIDES FROM BARNYARD GRASS (*ECHINOCHLOA CRUSGALLI* L. BEAUV.) SEEDS

E.A. Rogozhin [*1,2], ***D.Yu. Ryazantsev*** [1]

[1]Shemyakin and Ovchinnikov Institute of Bioorganic Chemistry RAS, Moscow, Russia
[2]Gause Institute of New Antibiotics, Moscow, Russia
*e-mail: rea21@list.ru

In complex studying of structure-functional characterization of the family of hairpin-like defense peptides (alpha-hairpinins) from barnyard grass (*E. crusgalli*) seeds an organization of DNA sequence that coding one of the novel previously isolated homologous members of the EcAMP peptides, has been determined. This polypeptide, named EcAMP6, consisted of a typical for all known alpha-hairpinins cysteine motif Xn-Cys1-X3-Cys2-Xn-Cys3-X3-Cys4-Xn (when X-any amino acid residue, n-any numbers of amino acid residues). It is suggested that it contains the same spatial conformation like other plant alpha-hairpinins – two alpha-helical regions (parallel of non-parallel) linked by a loop as beta-hairpin with non-structural N- and C-termini. It has been shown that EcAMP6 is characterized by a low primary structure homology with some previously described alpha-hairpins from *E. crusgalli* (EcAMP1-EcAMP5) (about 30-35% of identical amino acid residues or conserved substitutions); it is cationic peptide that possesses basic properties. A spectrum of biological activity of EcAMP6 involves antifungal and antibacterial; also this molecule is capable of noncompetitive inhibition activity of some serine proteases. Previously we estimated a full-length gene structure that coding a precursor consisted of all five EcAMP peptides that are exposed serially like tandem repeats according to their cysteine motifs, through linkers which are preliminary required for post-translational processing of the precursor followed by releasing of the mature hairpin-like peptides (Ryazantsev et al., 2014). Results obtained in the current stage of investigations completely confirmed a hypothesis about modular localization of plant alpha-hairpinins in kernels of cultivated wheat (*Triticum kiharae* Dorof. et Mugish.) (Utkina et al., 2013). A multiple amino acid sequence alignment EcAMP6 in comparison with translated gene structure, in which EcAMPs are localized, has not resulted any positive information, thus, probably, could be supposed that it belongs to the another group of polypeptides are situated in some divergent gene and, consequently, is processed as a result of post-translational modification of another protein precursor. Amplification of DNA fragment encoding EcAMP6 peptide, based on some specific primers are designed on GeneBank EST data from closely-related cereals (rice, millet, corn) could allow to receive one of dominant PCR fragment that is corresponded to the defined translated amino acid sequence, thus in the following, provided to determine the complete gene structure and protein precursor. This protein is represented a fragment of storage protein from cereal kernels (7S globulin-1) and, that is why, in the first time we demonstrated a homology of plant alpha-hairpins from cereals to seed storage proteins that previously was determined exclusively for peptides isolated from dicotyledonous plants (Marcus et al., 1999; Slavokhotova et al., 2014). Moreover, the additional novelty is consisted of an exception in the precursor discovered modular repeats that are typical for EcAMP1-5 group and other dicotyledonous plants. This fact is able to suppose some divergence in gene evolution coding hairpin-like peptides, at least for two basic directions.

This study was supported by Russian Science Foundation (project № 14-50-00131).

SCREENING OF BARLEY GENOTYPE FOR DETECTION OF RESISTANCE DONORS TO BARLEY POWDERY MILDEW

A.S. Rsaliyev, Zh.U. Pakhratdinova

Research Institute for Biological safety problems, Kazakhstan

e-mail: aralbek@mail.ru

Powdery mildew is a fungal disease caused by sac fungus *Erysiph egraminis* DC f. sp. *Horde i*Em. Marchal (synonym *Blumeria graminis* DC Speer f. sp. *hordei* em. Marchal) which belong to the harmful diseases of barley. Annually pathogen affects crops of winter and spring barley, the disease meets as on cultural and wild cereals in Kazakhstan. Powdery mildew in generally is spreaded on the productive crops of winter barley in the Almatinskiy, Zhambylskiy and South-Kazakhstanskiy regions. The most practical and economic approach in struggle with to barley powdery mildew is identification and use of resistance varieties to disease.

In 2015-2016 the commercial, collection varieties and perspective lines barley which are developed at the different selection RU of Kazakhstan are studiedon the artificial infectious background of powdery mildew. In total 120 barley varieties and lines were tested. In the field and laboratory conditions 116 examples of spring barley from the international nurseries created at the International Center for Agricultural Research in the Dry Areas (ICARDA): International Barley Yield Trial (IBYT), International Barley Observation Nursery (IBON), Early Maturity Barley Screening nursery (EMBSN), Hulless Barley Screening Nursery (HBSN) were also studied.

As a result, in Kazakhstan many cultivated commercial spring barley varieties are strongly affected by powdery mildew. At the same time, local die-off of the affected tissue areas ("resistance necrosis") was formedon the flag leaves of susceptible barley varieties. The reason of thisnecrosis – so-called reaction of epidermis hypersensitivity, i.e. the affected cells quickly died off, and "the ring of dead tissue" was formed around the place of introduction of inoculum. The separate varieties, samples and barley lines have field and partial resistance. During the researches the resistance samples comparatively more are noted in nurseries of IBON (11 example) and HBSN (14 example).

Providing of molecular screening of barley examples for detection of carriers of resistance genes to powdery mildew wasthe next stage of our work. 16 barley examples of the Kazakhstan selection and 26 lines of the foreign selection which are selected as productive and sources of resistance to disease in the conditions of Kazakhstan were served as object of research. Presence of the following Mlg, Mlo-5 and Mlo-9 resistance genes to powdery mildew was defined in their genome with use specific DNA-markers on the basis of polymerase chain reaction. Molecular screening showed that 6 barley examples of domestic and foreign selection have Mlg resistance gene, 5 examples – Mlo-5 and 18 examples – Mlo-9. Marker components of these genes for PCR were absent at other high resistance barley varieties and lines.

Work is executed with financial support of the Ministry of Education and Science of the Republic of Kazakhstan within the program of grant financing for 2015-2017 (grant # 1233/GF4).

Keynote

APPROACHES AND ACHIEVEMENTS IN MOLECULAR PRE-BREEDING FOR RUST RESISTANCE IN WEST SIBERIA

E.A. Salina, I.G. Adonina, A.I. Stasyuk, I.N. Leonova

Institute of Cytology Genetics, Siberian Branch, Russian Academy of Sciences, Novosibirsk, Russia,

e-mail: salina@bionet.nsc.ru

Wheat hybrids and varieties carrying translocations from related species or genera are an important source of rust resistance genes. Here we characterized Russian wheat varieties and hybrid lines with rust resistance genes and their using for molecular pre-breeding.

It was shown, that 1RS.1BL translocation is most common for Russian varieties resistant to fungal disease. Some varieties carry other types of introgressions that have not been identified yet, namely 2DS.2SL, 5BS.5BL-5GL, and 6BS.6BL-6GL translocations, 6D/6Agi substitution from *Agropyron intermedium* and introgression of *Aegilops tauschii* genetic material into 1D and 6D chromosomes. The chromosome 6D/6Agi of cultivar Tulaikovskaya possesses genes conferring resistance to leaf, stem, and yellow rusts and powdery mildew, which are not allelic to any known rust resistance genes. On the basis of EST analysis we selected markers specific for 6Agi chromosome for their subsequent use in molecular-assisted breeding.

Four lines with durable resistance to leaf rust were selected from 74 hybrid lines. Marker-assisted backcrossing was used for developing lines carrying a single *Ae. speltoides* and *T. timopheevii* translocations. It was shown that lines carrying the translocations from *Ae. speltoides* (21-4 with T5BS.5BL-5SL, 17-7 with T6BS.6BL-6SL) are resistant to leaf rust. The line11-8 with 7D/7S substitution is completely resistant to leaf rust and powdery mildew. The lines 5366-180 and 3862-5 with *T. timopheevii* translocations were resistant to leaf rust and stem rust, respectively. According to molecular analysis line 3862-5 may possess the *Sr36* gene. The *LrTt2* gene of 5366-180 may be allelic to *Lr18*. The rust resistance genes identified in other selected lines (21-4, 17-7, 11-8) haven't been described earlier.

The variety and lines with alien introgressions and genes of interest were used as donors of resistance genes in pre-breeding programs of spring and winter wheat.

The work was supported by the Russian Science Foundation (project №16-16-00011).

VARIATION FOR MICRONUTRIENT AND VITAMIN B CONTENTS OF TURKISH EINKORN AND EMMER WHEAT CANDIDATE LINES

***Mehmet Tekin*[1], *Mehmet Fatih Cengiz*[2], *Huseyin Canci*[1], *Ilknur Coskun*[1], *Aytekin Aksoy*[3], *Taner Akar*[1*]**

[1]Akdeniz University, Faculty of Agriculture, Department of Field Crops, Antalya, Turkey
[2]Akdeniz University, Food Safety and Agricultural Research Centre, Antalya, Turkey
[3]Tasaco Agriculture and Trade Company, Antalya, Turkey

[*]e-mail: tanerakar@akdeniz.edu.tr

Turkey is one of the important gene centres and has great cultivation experience for einkorn (*Triticum monococcum*) and emmer wheat (*Triticum dicoccon)*. Nowadays, they are still cultivated as population on marginal conditions by subsistence farmers of Black Sea Region. Einkorn and Emmer Wheat arepotential food sources due to their valuable protein, vitamin and mineral contents. Thus, the target of this study was to evaluate micro nutrient and B vitamin profiles of 36 einkorn and 49 emmer wheatadvanced lines collected from different provinces of Turkey and selected during the last five years. For this aim, two field experiments were established under augmented experimental design including three common durum wheat cultivars during 2015-16 season in Antalya province of Turkey. All candidate lines and three checks were analyzed for five micronutrients (Fe, Cu, Zn, Mn and Se) and four Vitamin B (B1, B2, B5, B6) including grain yield data for each genotype. There was great variation especially forFe and Zn content of einkorn and emmer wheat lines and mean Fe (41.70 ppm) and Zn (17.06 ppm) content of emmer wheat lines were higher than that of check durum wheat cultivars. The same amount of variation was also observed for Vitamin B complex for einkorn and emmer wheat advanced lines but only mean Vitamin B5 of emmer wheat (3.6 ppm) was higher than that of check cultivars.However, check durum wheat cultivars surpassed both einkorn and emmer wheat advanced lines in terms of mean grain yield as was expected. Grain yield changed 1.14 to 3.55 t ha^{-1} for einkorn advanced lines; 2.42 to 4.53 t ha^{-1} for emmer wheat advanced lines and 4.77 to 7.37 t ha^{-1} for durum wheat check cultivars. The first year of experiment showed that some promising emmer wheat advanced lines with reasonable grain yield, better micronutrient (Zn and Fe) and vitamin B5 content can be selected for further studies to improve the first cultivars for organic and low input agriculture in Turkey.

Acknowledgement: Financial contribution of TUBITAK under 214O401 project is kindly acknowledged.

GENETIC-STATISTICAL ANALYSIS THE AGRONOMIC TRAITS OF BARLEY BY TWO-TESTING METHOD

L.Tohetova, A. Demesinova, M. Bekova

Kazakh Research Institute of Rice Growing named after I.Zhahaev, Kyzylorda, Kazakhstan

Two-testing method consists of two parts: 1) test for the presence of epistasis; 2) study on the additive and dominant components if there is no epistasis. The study was conducted on the three schemes two-testing topcrosses on next traits: plants height, number of grains per ear, length of the growing season and the protein content of the grain, which is the determining in barley breeding under the salinity conditions of the Pri-Aral region. For comparison, we used data from similar studies conducted in Almaty region. In the first scheme, used by grade- testers (L_{1i} and L_{2i}): Odessky 100 and Saule; second - Saule and Donetsky 8; in the third Donetsky 8 and Odessky 100. Determinations of genetic and statistical parameters were performed.

Regardless from environmental conditions in all three testcrosses of the studied traits appeared fairly significant epistasis interaction «L_{1i} + L_{2i} - Pi». The study showed significant influence of additive and dominant components of genetic variance, but variance values of dominance effects in the Almaty conditions were higher. In general, the variability of additive component (D) has unequal numerical expressions and more expressed in the Kazakhstan Aral conditions and for the manifestation of the dominant effect was more favorable the Almaty region. On the basis of "length of the growing season," revealed different types of inheritance. More effective in selecting for earliness under the stress conditions was the third testcross in which an intermediate type of inheritance combined with a high proportion of additive and non-allelic epistasis effects, indicating the possibility of selections already in the F_2 generation.

The main direction of barley breeding under the conditions of Kazakhstan Aral region is the creation of feed varieties. In this connection, the search for sources and donors with high protein in grain is an important goal in the selection region. Genetic-statistical analyses have shown that the genetic system which controls the sign of "protein content" includes additive, dominant and epistasis gene interactions. For example, highly reliable values of general combining ability grade-testers Donetsky 8 and Odessky 100 with highly significant of no allelic interactions reflect the "additive x additive" type of epistasis, which will integrate in the single genotype of dominant genes additive action and conduct an effective selection in the early generations of hybrids.

The predominance in controlling the traits under stress conditions of Kazakhstan Aral region the additive gene interactions indicates the possibility of effective selection in the F2 generation, and favorable conditions of Almaty region due to the high determination of these signs dominant genes necessary to differentiate the population of hybrids and further selection carried out in several cycles before attainment of homozygosis loci. Therefore, the genetic contribution of additive and non-additive gene effects in inheritance and determination of the studied traits essentially depends from the growing conditions. The greatest practical interest have samples of Bi-17 (Iran), 5-7 (ICARDA) and the varieties Odessky 100, Saule with high effects of general and specific combining ability, which are widely used in hybridization programs as important donor selection parameters. Therefore, in the initial stages of the selection process to study the initial material is advisable to carry out using two-testing method to avoid loss of valuable genotypes during screening in early generations.

EVALUATION OF OPPORTUNITY FOR APPLYING THE BIOGENIC METALS ASPARTATES TO IMPROVE THE PROCESSES OF MUSHROOMS CULTIVATION

O.M. Tsivileva[1], V.V.Fadeev[1], S.P. Voronin[2], A.P. Gumenyuk[2], V.E. Nikitina[1]

[1]Institute of Biochemistry and Physiology of Plants and Microorganisms, RAS, Saratov, Russia
[2]ZAO "BioAmid", Saratov, Russia

Edible mushrooms are ubiquitous fungi existing in almost every ecosystem and playing key role in the biotransformation, utilization and recycling of organic waste natural materials. Rather low-scale mushrooms' commercial cultivation in Russia interferes their utility as food and medicinal agents. A good alternative to mushrooms' fruit bodies production is provided in this respect by the submerged fermentation. The process implements quite a lot of advantages, *e.g*. a fast growth and high biomass productivity, compact and controlled environment and shortened production time.

One of the ways of getting trace elements in their organic form to improve the processes of mushrooms cultivation is their binding to the essential amino acids. Two of us have invented the method of providing wide-scale synthesis of the biogenic metals(II) aspartates $M(Asp)_2$ [1], where M is, e.g., Cu, Mn, Fe, Zn, Co. Systematic studies within the framework of approach related to the biogenic metals chelates implementation to optimize the mineral nutrition of cultivable mushrooms were not carried out earlier. High potentialities of application of non-toxic aspartic acids chelates of metals (II) for obtaining the greater yield of fungal biomass, the more so characterized by the property of better adaptation to environmental factors, were revealed here for the first time.

Even the initial experiments allowed us to elucidate the promising consequences of implementing the metals(II) aspartates in mushroom cultivation to obtain the mycelial biomass with higher efficiency under the laboratory conditions. Searching for the favourable dosage of microelements as the supplements led us to the rational concentration values of about $1 \cdot 10^{-4}$ mol/l as the initial quantity in nutrient media.

The effect of *L*-aspartates on the fungal growth and development was dependent upon the mushroom culture age, as well as the composition of synthetic media. The above effect manifested itself as, e.g., intensity of fungal biomass accumulation, pigments and primordia formation in submerged cultures of *Ganoderma lucidum*, *Grifola umbellata*, *Laetiporus sulphureus*, *Lentinula edodes*, *Pleurotus ostreatus*. When the fungal seeding material was grown in the presence of some aspartates, the mycelia development period before the morphogenesis stage preceding the mushrooms fruiting was appreciably shorter. Survival rate at such unfavourable environmental factors as hyperthermia (up to 37°C) or the artificially decreased humidity, solid substrate dryness, etc., was observed to be considerably greater, especially in the cases of implementing $Cu(Asp)_2$ or $Zn(Asp)_2$.

For instance, the dependence of period before fruiting start for the *G. lucidum* culture in the presence of divalent copper cations in the chemical form of aspartate in liquid media when growing the seeding culture by means of submerged cultivation was explored. The essentially shortened period preceding the formation of primordia in liquid culture with this aspartate was detected, the same being observed for the appearance of mycelia yellow pigmentation and primordia of the mushroom on solid medium provided that this intermediate seeding culture was applied.

In general, the pioneering knowledge on the optimization of mineral nutrition of cultivated mushrooms with the use of *L*-aspartates has been contributed from the results obtained within the present work.

Reference

1. Voronin S.P., Golubov I.I., Gumenyuk A.P., Sinolitskii M.K. Bioavailable form of microelement supplementations to feed mixtures for animals and poultry. Patent no. 2411747 of the Russian Federation. Published 20.02.2011. Inventions. Useful Models, Bull. no. 5.

PREDICTION OF FLOWERING TIME AND GWAS OF YIELD COMPONENTS OF SPRING WHEAT IN KAZAKHSTAN

Y. Turuspekov [1], K. Yermekbayev [1], A. Baibulatova [1], S. Chapman [2], B. Zheng [2], M. Ganal [3], J. Plieske [3], S. Griffiths [4], S. Abugalieva [1]

1 – Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan
2 – CSIRO, St Lucia, QLD, Australia
3 – TraitGenetics GmbH, Gatersleben, Germany
4 – John Innes Centre, Norwich, UK

Email: yerlant@yahoo.com

Wheat is the major crop in Kazakhstan growing over 13 million hectares annually, more than 80% of sowing area is spring type of wheat. Due to harsh environmental conditions the average spring wheat yield in Kazakhstan is less than 1.3 t/ha. Main area of spring wheat growth is Northern Kazakhstan. Climate is continental, summer is dry (~250 mm precipitation) with long day photoperiod. The material consisted from 61 officially registered and 33 prospective cultivars in Kazakhstan, 38 cultivars from Europe, 60 CIMCOG lines, Avalon x Cadenza DH mapping population, 600 lines of wheat collection (Asia, Australia, Canada, Europe, USA and landraces). Field trials conducted in Northern, Central and Southern Kazakhstan. The collection from Kazakhstan and Europe was genotyped using KASP markers for flowering time and 90K Illumina SNP array. APSIM modeling was applied to predict flowering time based on Wheat-M and Wheat_G models to avoid drought and hot stresses during summer time. GWAS was performed using TASSEL and FARM CPU packages. The genotyping analysis of 134 wheat accessions allowed to select 3659 polymorphic SNPs for the GWAS (maf – 0.05). The STRUCTURE outputs suggested that there are five subgroups in studied collections. Identified markers were well spread on all seven groups of homeological chromosomes o wheat. Nine significant SNPs were identified at two or more locations. Overall 31 SNPs were identified for different plant growth stages and yield components. Locations of *Vrn1* genes on 5th group of chromosome based on analyses of vernalization sensetive indices are additionally confirming the significance of identified SNPs for studied traits.

The study was supported by ADAPTAWHEAT project funded by 7th EU FP and grant number 1784/GF funded by the Ministry of Education and Sciences of the Republic of Kazakhstan

ENERGETIC AND INFORMATION SYSTEMS OF PLANT CELLS AT TEMPERATURE FLUCTUATIONS

V.K. Voinikov

Siberian Institute of Plant Physiology and Biochemistry, Siberian Branch
of Russian Academy of Sciences, Irkutsk, Russia

During several passed years from a discovery of stress proteins of plants an undoubted progress was achieved. It is so far precisely established that a response reaction of a plant organism to a low-temperature stress, as well as a formation of tempered condition of a plant starts exactly with a moment of its cooling start and proceeds with the participation of certain proteins. Except a considerable number of the enzymes involved in these processes, some families of the proteins which have been specifically connected with these processes are so far singled out. These are chaperons and dehydrins, antifreeze proteins, multifunctional proteins regulating processes of translation and transcription and uncoupling proteins which separate oxidation and phosphorylation during low-temperature stress. Synthesis of these proteins is provided in most cases by nuclear genes expression of which is induced during a temperature stress and hardening and is defined by its conditions.

Though it should be noted that there are individual hypotheses of biochemical mechanisms of participation of proteins induced by low temperature in developments of cold resistant plants it is little known about the role of concrete proteins in these processes, except for representatives of several families of proteins, such as dehydrins, antifreeze proteins and some other.

In the last decades mechanisms of induction of an expression of genes at a hypothermia and specificity of these genes and proteins coded by them start being studied intensively. Research works in this field are intensively carried out today all over the world. Especially these research studies are being done intensively in connection with a carried-out full sequencing of genomes of plants. At the same time it should be noted that researches of genes expression during low-temperature stress are conducted not systematically and generally they consist of establishment of the fact of expression induction of a separate gene or family of genes or increase in the content of separate stress protein. In practice the interrelation between induction of separate genes or their families is not investigated and in conducted research works there is no integrated approach to the studied phenomenon. Only in the latest time "gene networks" connecting together the description of an expression of various genes in certain conditions start being created. This approach to research works is extremely perspective and allows to hope for a creation of gene network describing the complex response of a genome of plant upon a low-temperature stress henceforward.

At temperature stresses in plant cells the mitochondrial signaling is functioning which includes interaction of information and energetic systems of a cell functions. It is proven that temperature fluctuations cause changes in energetic activity of plant mitochondria.

ASSOCIATION MAPPING OF AGRONOMIC TRAITS IN SOYBEAN HARVESTED IN KAZAKHSTAN

A. Zatybekov [1], ***A. Rsaliyev*** [2], ***S. Didorenko*** [3], ***S. Abugalieva*** [1], ***Y. Turuspekov*** [1]

1 – Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan
2 – Research Institute for Biological Safety Problems, Gvardeiskiy vil, Dzhambul region, Kazakhstan
3 – Kazakh Research Institute of Agriculture and Plant Growing, Almalybak vil., Almaty region, Kazakhstan

Soybean is relatively new crop in Kazakhstan and yield productivity is affected by a number of important diseases. In this study GWAS approach was used for identification of QTL for several yield components, including plant height, number of fertile nodes, number of seeds per plant, weight of seeds per plant and thousand seeds weight. For this purpose the collection of 184 accessions representing 5 different regions of the World, including East Asia, East and West Europe, North America and Kazakhstan were tested in the fields of Dzhambul region (South Kazakhstan) and Kazakh Research Institute of Agriculture and Plant Growing (Almaty region, South-east Kazakhstan). The soybean collection was previously genotyped using 7K SNP Illumina array. SNP genotyping analysis was performed at TraitGenetics GmbH (Gatersleben, Germany) using an optimized soybean cluster file using the Illumina Genome Studio software. After quality control filtering of the SNP dataset 5,213 SNPs were selected for further analysis. The SNP dataset was filtered using a 10% cutoff for missing data and markers with minor allele frequency $\geq$0.10 were considered for GWAS. GWAS mapping of QTL governing yield components was performed using three different packages, TASSEL, FARM CPU and GAPIT. Results indicate that FARM CPU is most efficient package that avoiding identification of false positive and false negative SNP – trait associations. Identified SNP markers were converted to KASP markers and they are currently under validation using larger field experiments in different parts of Kazakhstan. Obtained results provide new tools for marker assistant breeding of soybean in different regions of Kazakhstan.

The research was supported by the Ministry of Education and Science of Republic of Kazakhstan (grant # 1108/GF4).

GENOTYPE AND ENVIRONMENT INTERACTION PATTERNS IN COLLECTION OF SOYBEAN GROWN IN KAZAKHSTAN

S. Abugalieva [1], S. Didorenko [2], Sh. Anuarbek [1], L. Volkova [1], Y. Gerasimova [3], I. Sidorik [4], A. Zatybekov [1], Y. Turuspekov [1]

[1] Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan
[2] Kazakh Research Institute of Agriculture, Almalybak vil., Almaty region, Kazakhstan
[3] East Kazakhstan Research Institute of Agriculture, VKO, Kazakhstan
[4]Kostanaiskyi Research Institute of Agriculture, Kostanai region, Kazakhstan

Understanding of genotype and environment interaction (GEI) patterns is very important for introduction of new cultivars of plant growth in expanding new zones. As soybean is relatively new crop for Kazakhstan, it is vital to determine adaptive genotypes to particular environments in Northern and Eastern parts of the country. In this study the collection of 120 accessions of world soybean collection was tested in three different regions of Kazakhstan – Almaty, Kostanai, and East Kazakhstan regions. The yield was used as a major trait to evaluate GEI patterns by using AMMI *(Additive Main Multiplicative Interaction)*, and GGE (genotype x genotype environment) Biplot methods. ANOVA (analysis of variance) as part of the AMMI study suggested that Environment contributed 89.52% and GGE added 10.48% to the total variation. Graphical visualization of AMMI suggested that PC1 was most effective contributor to the differentiation of East and South-east regions from North Kazakhstan, while PC2 allowed separation of East from South-east of Kazakhstan. Similar results were obtained using GGE bilpot approach, which is suggesting that in relationship to soybean yield, East and South-east regions are forming a single mega environment. Both methods allowed determining valuable genotypes, which demonstrated best yield scores in three environments. For instance the accession SD61 showed highest yield in Northern Kazakhstan, while SD74 and SD91 were most productive both in East and South-east regions.

The research was supported by the Ministry of Education and Science of Republic of Kazakhstan (grant # 1108/GF4).

INFLUENCE OF *DT1* GENE TO YIELD COMPONENTS OF SOYBEAN HARVESTED IN KAZAKHSTAN

Sh. Anuarbek [1], ***S. Abugalieva*** [1], ***S. Didorenko*** [2], ***Y. Gerasimova*** [3], ***I. Sidorik*** [4], ***Y. Turuspekov*** [1]

[1] Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan
[2] Kazakh Research Institute of Agriculture, Almalybak vil., Almaty region, Kazakhstan
[3] East Kazakhstan Research Institute of Agriculture, VKO, Kazakhstan
[4] Kostanaiskyi Research Institute of Agriculture, Kostanai region, Kazakhstan

Soybean stem growth habit is directly associated with yield components and may differentiated as indeterminate and determinate types. In indeterminate type flowering begins in lower nodes of the plant and progresses toward the top of the plant. In determinate type flowering begins at the middle of plant and progresses both ways. Indeterminate type is a negative trait in most regions of Kazakhstan since in the top of the plant most pods have immature seeds and lower pods difficult for machinery type of harvesting. Therefore, genetic factors controlling the stem growth habit are very important for improvement of soybean productivity. There are two known genes, *Dt1* and *Dt2*, which control the habit type in soybean, and *Dt1* is by far more important gene for controlling of the phenotype in comparison to *Dt2*. *Dt1* is also involved in the control of flowering time Therefore, in this study the collection of 120 soybean lines from different parts of the World, including from Kazakhstan, were genotyped using *Dt1*. Out of 120 tested soybean lines, 103 were genotypes with *Dt1* allele and 17 genotypes with *dt1* allele. Studied lines were also planted in South-East region, near Almaty city. The comparison between determinate and indeterminate lines showed significant difference in flowering and seed maturation time, plant height, number of nods per plant, and yield. DNA marker for *Dt1* gene was successfully converted to KASP marker and available for further large scale genotype screening in breeding lines.

The research was supported by the Ministry of Education and Science of Republic of Kazakhstan (grant # 1108/GF4).

IDENTIFICATION OF GENETIC CARRIERS OF WHEAT, STEADY AGAINST YELLOW RUST *PUCCINIA STRIIFORMIS* F. SP. *TRITICI*

M. Atishova*, *A. Kokhmetova*, *L. Typina*, *A. Madenova*, *K. Galymbek*, *Zh. Keishilov

Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan

Wheat is the most important cereal in Kazakhstan. Wheat (*Triticum aestivum* L.) rusts have been one of the main yield limiting factors in wheat cultivation throughout the world. Leaf and yellow rusts can severely reduce wheat yields by almost 63% and 46% of the wheat growing areas in the world, if susceptible cultivars are grown (Singh et al. 2004). Yellow rust, caused by the pathogen *Puccinia striiformis* f.sp *Tritici* is considered the most important diseases of wheat in Kazakhstan. Yellow rust negatively affects the quality and yield of wheat grain (Chen 2005). The preferred way of controlling the disease is through the use of resistant varieties. There more than 70 genes that can express resistance to this disease. The aim of the present study was to screen advanced line of wheat for the presence of *Yr*-genes effective to yellow rust. *Yr5* is located on chromosome arm 2BL, 21 cM away from the centromere. We used two STS (sequence-tagged site) molecular markers, namely S19M93 and S23M41 to detect the likely presence/absence of *Yr5* in 105 wheat lines. The STS markers S19M93-140 completely co-segregates with *Yr5*, whereas S23M41-310 maps at a distance of 0.7 cM. Marker S19M93 amplified a 100-bp fragment in 42 wheat lines, indicating the likely presence of Yr5 gene while the remaining 63 wheat lines and negative control did not show the 100-bp band, indicating the likely absence of *Yr5* gene. Marker S23M41 amplified a 275-bp fragment in 42 of 105 wheat lines and the positive control, suggesting the likely presence of *Yr5*, whereas 63 wheat lines and the negative control did not show the 275-bp fragment, indicating the likely absence of *Yr5* gene. The most promising lines are the following: 18-ICARDA-IPBB-2013 x *Yr18*/#275*T.spelta*, д.U11AGEC-7 x *Yr15*/#1093 9-ICARDA-IPBB-2013, F1(F5#23 x Купава x #1659д.1030Д620.F4 Улугбек x *Yr4* x Мереке) x *Yr5*/*T.spelta*). They indicated DNA fragment associated with presence *Yr5* and also have shown high level of field resistance. As a result of the PSR analysis of the 105 samples studied in 42 carries the gene *Yr5* was revealed. These results will assist the programs of gene pyramiding and Marker Assisted selection in the wheat breeding for improvement of yellow rust resistance.

This work was financially supported by the Ministry of Education and Science Republic of Kazakhstan, research project grant funding №2120.

THE ROLE OF SALICYLIC ACID IN THE INDUCTION OF WHEAT STABILITY TO STRESSERS

S. Bekkuzhina [1], ***A. Zhamekova*** [1], ***S. Kitaibekova*** [1], ***N. Apushev*** [2]

[1] S. Seifullin KATU, Astana, Kazakhstan
[2] LLP Berry Republic, Astana, Kazakhstan

It is known that Abscisic Acid (AA) plays an important role in the response of plants to stressful effects, in particular, with water deficiency. Our early works are devoted to the launching of plant response mechanisms in water deficiency and some positive and negative results were obtained on the use of AA in the variety of wheat pollen. The lack of unambiguous conclusions is probably due to the fact that AA launches a signaling network, interacting with other phytohormones at the cellular level.

In recent decades, many works have appeared on the mechanisms of stress-resistance at the level of genes, at the level of cells and at the level of the whole organism. In studies, close attention is paid to an equally important plant inducer too and which is an antagonist of AA to Salicylic Acid (SA).

Currently, attention is paid to the issues of indirect communication of SA, with proteins NPR1 (Natriuretic Peptide Receptor) NPR3, NPR4 synthesis of which depends on the concentration of SA. The role of ubiquitin as a conservative regulator, which in advance designates an eliminable protein, has been established.

Research at the level of the molecular mechanisms and functions of the above mentioned proteins attracts the interest of cellular biologists, breeders in the search of source material for resistance to stressors. Modern data about the effect of SA have led us to the idea of clarifying the concentration curves and their correlation in the *in vitro* and *in vivo* conditions.

The following varieties and lines of the wheat were used in the experiment: Akmola 2, Steppe 50, 93C, Steppe 2, Steppe 53, Erythrosperium 7A, Lutescens 2994, Lutescens 471H36, 101 / 88, 93c.

In the first series of experiments wheat seeds were germinated on filter paper, the second series of experiments were carried out by embryo culture, and in the third, concentration of SA was tested on callus culture.

As a result of the conducted studies, an increase in the length of the root was detected and varieties with a number of germinal roots more than 5 were identified. By the root length, in the treatment with SA with low concentrations on the third day the variety Steppe 2 differed to 2 cm compared to the variety Akmola-2-1.2, and in Lutescens, 2994, growth of roots decreased by 0.3. With the treatment of SA 0.03% and 0.05%, the process of root formation and shoot formation was depressed. In addition, the number of germinal roots was also selected single plants of variety L2994, Steppe 53, 93c where this indicator is equal to 6-7. In *in vitro* conditions, at the second passage for Steppe 2 and Steppe 50, the growth of the callus mass was observed, where the correlation coefficient in the control for the biomass increment was r = 0.95, in the SA 0.001% r = 0.98, and for SA 0.0001 % R = 0,87.

The results of our studies are consistent with the literature data that using SA in the induction of plant protective reactions, it is very important to select concentrations for the arrival of a matched signal with other growth regulators. In this connection, work continues with the complex use of growth regulators of auxin and cytokinin type of action for inducing an immunomodulatory effect of SA. In addition, in subsequent experiments, it is necessary to create conditions for water deficiency in the cell after establishing the concentration of SA.

REGULATION OF ABA METABOLISM BY TOR SIGNALING IN *ARABIDOPSIS THALIANA*

R.I. Bersimbaev*, *A.P. Kravchenko

L.N. Gumilyov Eurasian National University, Institute of Cell biology and Biotechnology
Astana, Kazakhstan

Basic cellular functions of living organisms are regulated by a complex network of biochemical processes and signaling pathways responsible for the regulation of cellular metabolism in response to external signals. The Target of Rapamycin (TOR) pathway is present in all eukaryotic organisms and plays a key role in regulation of various cellular processes like autophagy, translation, ribosome biogenesis, and metabolic adaptation in response to nutrients, growth factors and energy conditions [V. Albert et al., 2015].

The TOR protein kinase is a large protein (~250 kD) which belongs to the phosphatidylinositol kinase-related kinase (PIKK) family. In yeast and animals, TOR associates in two complexes TORC1 and TORC2 with different protein partners, namely LST8 and RAPTOR/KOG1 for TORC1, and LST8, RICTOR/AVO3 and SIN1/AVO1 for TORC2. TORC1 is sensitive to rapamycin and participates in the responses to favorable growth conditions by promoting energy-consuming processes like cell division, translation, ribosome biosynthesis and anabolic metabolism and repressing recycling mechanisms like autophagy [S. Wullschleger et al., 2006]. In Arabidopsis, a single TOR gene (*AtTOR*) and some of the TOR complex 1 (TORC1) partners have been identified including two homologs of the LST8 protein (*Lst8-1* and *Lst8-2* genes) and two genes encoding RAPTOR proteins (*Raptor3g* and *Raptor5g*). [D. Rexin et al., 2015].

Despite the growing interest in the plant TOR kinase, this link between ABA and the TOR signaling pathway has received hitherto little attention. Furthermore, although it is generally believed that TOR is only active in favorable external conditions, more and more studies suggest that the activity of the TOR complex is also needed for stress adaptation [S. Sengupta et al., 2010]. ABA plays also an essential role as regulator in many cellular processes including germination, seed development and environmental stress responses. The first committed steps of ABA biosynthesis take place in plastids and are catalyzed by zeaxanthin epoxidase (ZEP) and the 9-cis-epoxycarotenoid dioxygenase (NCED) which produces xanthoxin and is tought to be the main rate-limiting reaction. Xanthoxin then moves to the cytoplasm where it is converted to ABA-aldehyde. Finally the last step in ABA biosynthesis is catalyzed by aldehyde oxidases (AAO) localized in the cytosol. [E. Nambara et al., 2005]. Among the ABA catabolic pathways the C8'-methyl hydroxylation by cytochrome P450 monooxygenases (CYP707A) is considered as the major regulatory step. ABA level is thus the result of a balance between synthesis and degradation. Stress-induced ABA accumulation regulates the global metabolic network in Arabidopsis [T. Yoshida et al., 2015].

We used HPLC-MS/MS method to quantify ABA levels in the TORC1 mutants or after TOR inactivation by the specific inhibitor AZD-8055. The expression levels of the genes encoding the main enzyme of ABA metabolism measured by quantitative real-time PCR using specific primers. Our results showed that loss-of-function mutation in *Lst8-1* and *Raptor3g* genes or the inhibition of TOR complex activity cause a significant decrease in ABA level as well as in expression of *ZEP*, *NCED3* and *AAO3* genes involved in ABA biosynthesis in contrast to the ABA catabolic *CYP707A2* and *CYP707A3* genes which were induced. These results provide one step forward in understanding of TOR and ABA signaling networks collaboration in plant growth and metabolism. Finally these data suggest that TOR activity is needed in plants to synthesize ABA and therefore to mount efficient responses to environmental stresses. The role of the TOR signaling pathway in short term response to stress, and the molecular players involved in the relation between this kinase and ABA still remain to be discovered.

MOLECULAR EVOLUTION OF ANTIOXIDANT GENES IN PLANTS AND ITS RELATIONSHIP WITH CELLULAR LOCALIZATION OF PROTEIN PRODUCTS

A.V. Bobrovskikh [1,2], ***A.V. Doroshkov*** [1]

[1] Institute of Cytology and Genetics of the SB RAS, Novosibirsk, Russia
[2] Novosibirsk State University, Novosibirsk, Russia

In the very beginning of photosynthesis era, for all living cells became necessary to utilze reactive oxygen species (RAS). RAS molecules is dangerous for cellular methabolism and they can damage all membrane components in the cell. This problem mostly important for plant cells that produce a lot of RAS during the photosynthesis. Currently a several biochemical pathways of antioxidant defence system is well-known. Also, discovered a set of antioxidant enzyme classes, which are presented in genome in series of copies with different cellular localization. It was shown that activity of antioxidant system of plants is an important factor for defending against stress environmental conditions such as unbalanced salt and water composition of the soil, temperature changes.

On the one hand understanding the evolution of antioxidant system genes is a fundamental task. It is a perfect model to reveal how evolution features of identical component of enzyme system depending of their particular cellular localization. On the other hand this data allow us to identify the most important enzymes for use in marker-assisted selection of crop plants for resistance to stress.

Presented work contains phylogenetic analysis of five major antioxidant enzymes of plants: ascorbate peroxidase, glutathione reductase, superoxide dismutase, catalase and dehydroascorbate reductase. Revealed the time of gene duplication events previous to the formation of differences in localization. Estimated the synonymous per nonsynonymous substitution ratio, revealed its relationship with cellular localization of proteins.

Data of the DNA and protein sequences were extracted from NCBI and PLAZA databases. Samples of homologous genes are aligned by MAFFT algorithm. Reconstruction of phylogenic trees was perfomed by PhyML algorithm. Analysis of the patterns of synonymous and nonsynonymous substitution was made for orthological groups of flowering plants with intermediate reconstruction of ancestral taxa.

EXPRESSING THE *SUC2* YEAST INVERTASE GENE OF APOPLAST LOCALIZATIONS INCREASE THE COLD RESISTANCE OF POTATO PLANTS

A.N. Deryabin, T.I. Trunova

K. A. Timiryazev Institute of Plant Physiology of the Russian Academy of Sciences, Moscow, Russia
E-mail: anderyabin@mail.ru

Low temperature (LT) is a determinative environmental factor, which can affect all aspects of plant life. The first compartment of the plant cell, which gets LT signal and participates in its transduction and response, is the apoplast. The apoplast contains the cell-wall invertase (CWI) – the key enzyme of carbohydrate metabolism in plants, which catalyzes sucrose forming two monosaccharide molecules (glucose + fructose). CWI is involved in important physiological processes such as control over both sucrose outflow from leaves into other vegetative organs and transport of monosaccharide across the plasmalemma that increases total sugar contents in cells. The accumulation of soluble sugars in vegetative plant organs is one of obligate factors for forming plant resistance to LT.

The purpose of this study was to investigate the involvement of CWI (β-*D*-fructofuranoside-fructohydrolase, EC 3.2.1.26), into formation tolerance to LT of potato (*Solanum tuberosum* L., cv. Désirée) plants, which expressed the *SUC2* gene of *Saccharomyces cerevisiae* under the control of the patatin class I B33 promoter (B33-*inv*-plants). WT-potato plants served as the control (WT-plants). Plants were grown *in vitro* at 22°C and 16-hour long light day (illuminating intensity of 100 μmol photons/(m^2·s).

B33-*inv*-plants offer unique opportunities for research since the integrated *SUC2* gene encodes the invertase of yeast with an *N*-end-connected potato proteinase II inhibitor signal peptide, which provides apoplastic localization of foreign invertase. It was shown that the *SUC2* gene presence in the plant genome and its expression were shown using PCR and RT-PCR. Yeast invertase were identified by MALDI-TOF MS analysis. A soluble form of the yeast invertase was present in the apoplast, and it was weakly adsorbed onto the cellular wall (Deryabin et al., *Biol. Bull. Russ. Acad. Sci*. 2014;1:24-30). The activity of yeast invertase changed the intracellular sugars content in the leaves of the B33-*inv*-plants. The total content of sugars (sucrose, fructose, glucose) in the roots, leaves and apoplast was higher in the B33-*inv*-plants compared to those of the WT-plants. Prolonged cold exposure (5°C, 6 days) contributed to the increased activity of apoplastic invertase and contents sugar in the B33-*inv*-plants compared to that in the WT-plants. The increase in the essential CWI activity in the leaves, revealed during cold hardening indicates significant changes in the cellular carbohydrate metabolism and regulatory function of this enzyme. The activity of CWI induced by LT changed the composition and intracellular sugars in the roots and leaves of the potato plant. It can be assumed that glucose and fructose were actively transported from the apoplast into the cytosol, where they performed protective function and were used for energy and synthetic processes in the cell. Our data indicate higher resistance of B33-*inv*-plants to severe LT conditions compared to the WT-plants (Deryabin et al., *Biol. Bull. Russ. Acad. Sci*. 2016;1:26-33). It is known, that the enzyme substrate (sucrose) and the reaction products (fructose and glucose) are active multifunctional metabolites whose concentration in the cell and apoplast significantly affects the resistance forming of potato plants to LT. The fact allows us to consider CWI as an enzyme of carbohydrate metabolism playing an important regulatory role in the metabolic signaling upon forming increased potato plant resistance to LT.

The authors are grateful to Dr. L. Willmitzer (Max Planck Institute of Molecular Plant Physiology, Germany) and Dr. G.A. Romanov (Timiryazev Institute of Plant Physiology, Russia) for the potato plants provided for the research.

FAST-RIPENING SOMACLONAL LINES OF SOYBEAN WITHIN THE CONDITIONS OF NORTH AND SOUTH OF KAZAKHSTAN (PRODUCTIVITY, DROUGHT TOLERANCE AND GRAIN QUALITY)

S.V. Didorenko [1], ***A.I. Abugalieva*** [1,2], ***I.V. Sidorik*** [3]

[1] Kazakh Research Institute of Agriculture and Plant Growing, Almalybak, Kazakhstan
[2] Kazakh National Agrarian University,Almaty, Kazakhstan
[3] Kostanay Research Institute of Agriculture, Kostanay, Kazakhstan

e-mail: Svetl_did@mail.ru

New, ultra-fast somaclonal studied soybean lines for the conditions of Northern Kazakhstan on productivity and drought tolerance. Somaclonal line varieties SibNIIK 315 - *R198-12, R184-4, R*177-5, R 8 has an increased ability to form beans. These lines somaclonal sterile plants were found. We select the most productive line with a mass of seeds with plants 13,1-14,7 g - *R 176-5, R 165-11, R* 198-12, R 162-17, R 155-2.

In order to isolate the forms of drought-resistant somaclonal lines were grown under conditions of drought provoked in the greenhouse complex KazNIIZiR. The most productive patterns *R-177-5, R-165-11, R-186-8* , R-170-1 characterized as increased weight of seeds per plant, and increased the number of stomata in the flowering stage (12,8-17,6 pcs / box) and the number of hairs (20,0-24,5 pcs/box). Measurement of standardized difference vegetation index *(NDVI),* showed a high rate in the phase of loading beans from somaclonal lines *R-177-5, R-186-8, R-165-11* and *R-290-11 (0,79-0,* 81), whereas SibNIIK standard grade 315, he was in the same phase of development 0,74-0,75. *NDVI* measurements confirm the results on the accumulation of biomass a more intensive development of somaclonal lines compared with the standard.

The protein content in soybean grain was formed by 40,5% (R 155-2) to 45,7% (R 176-5) for ripening forms at the level of yields. Two rooms in addition to the maximum protein accumulate above 45.0% are non - R186-8 and R177-5, with respect to grade-standard - 44.7%. The fat content is formed at 19,0-21,0% with an average of 19.8% for the whole relative SibNIIK standard block 315 with a fat content of 19.3%. Collecting samples of the soybean crop years 2014-2016. analyzed for Fe content in the beans. Variation observed within 89-103 mg/kg. 100 mg/kg Fe content characterized by between 2 and 11% of the genotypes. Among them, high protein varieties and breeding patterns KazNIIZiR and Ukrainian selection (Lybid). The large amount of breeding material studied in these years, the level of the samples with Fe content greater than 100 mg/kg is practically very low (2-4%). The biochemical composition of grains estimated for protein, starch.

Research was carried out under the program O.0721 "Creation and implementation of cereal varieties with genetically identified stress light-governmental properties on the basis of molecular breeding, genomics and Biotechnology (Biochemistry) for efficient use of the country's soil and bioclimatic building" project state registration number 0115RK02312 " Phenotyping, genomics and biotechnology (biochemistry) in the creation of varieties of cereals, legumes and forage genetically iden-lated stress indicator of efficiency and quality properties".

THE MANIFESTATION AND PHYTOHORMONE RESPONSE OF LEAF PUBESCENCE GENES IN BREAD WHEAT

A.V. Doroshkov, A.V. Simonov, D.A. Afonnikov, T.A. Pshenichnikova

Institute of Cytology and Genetics Siberian Branch Russian Academy of Sciences, Russia

The leaves of many angiosperm species develop trichomes. This trait is known to make a significant contribution to the protection from pests and adaptation to environmental factors in bread wheat.

However the genetic basis of wheat trichome formation is poorly understood although a wide variation was found among *Triticeae* species with different ploidy level. Currently Catalogue of Gene Symbols for wheat contains only two loci associated with this trait: the gene *Hl1* in 4B chromosome and the gene $Hl2^{aesp}$ in 7B chromosome. Molecular function and regulation of these genes are currently not known.

The present research sought to establish the individual and joint effect on trichome patterning and growth of each of three wheat leaf pubescence genes (*Hl1,* $Hl2^{aesp}$ and new one - *Hl3*) under normal conditions and phytohormone treatment.

Various lines carrying *Hl1, Hl3* and $Hl2^{aesp}$ and specially created nearly isogenic lines were used to quantitatively compare leaf pubescence using a modern high throughput phenotyping method (wheatdb.org/lhdetect2). This method allows us to obtain rapidly quantitative characteristics of leaf pubescence (length of individual trichomes and their number) among many plants.

Studied genes differed in their effect on trichome formation. *Hl1* and *Hl3* more affected trichome initiation and growth, while $Hl2^{aesp}$ modified mostly trichome length. Their action was independent to a large extent. A model of the action and interaction of *Hl1, Hl3* and $Hl2^{aesp}$ has been proposed to explain the genetic basis of trichome length and number.

The effects of phytohormones on trichome cell growth and initiation while *Hl1, Hl3* and $Hl2^{aesp}$ genes manifestation were explored. The effects of auxin (IAA), gibberellic acid (GA), cytokinins (6-BAP, Kinetin), metyl jasmonate (MeJa), ethylene (ACC) have been investigated and described. Our data revealed a key role of GA and cytokinin signaling pathways in *Hl1* and *Hl2* gene manifestation. At the same time this genes differs in a character of responce to hormone action. This suggests a different position *Hl1, Hl3* and $Hl2^{aesp}$ genes in the network of trichome formation control.

This work was supported by Russian Science Foundation (RSCF) grant № 14-14-00734.

ASSESSMENT OF WHEAT-RYE HYBRIDS' BREEDING POTENTIAL WITH THE USE OF MOLECULAR MARKERS

N.I. Dubovets* [1], N.I. Drobot [1], O.G. Silkova [2], E.A. Sycheva [1], E.B. Bondarevich [1]

[1]Institute of Genetics and Cytology, National Academy of Sciences of Belarus, Minsk, Belarus

[2]Institute of Cytology and Genetics, Siberian Branch of the Russian Academy of Sciences, Novosibirsk, Russia

e-mail: N.I.Dubovets@igc.by

The analysis of the allelic composition of *Rht* dwarfing genes and *Vp-1B* gene regulated seed dormancy was carried out in the material of 8 wheat-rye substituted lines with different types of R(A)-, R(B)- and R(D)-chromosome substitutions (*RhtB1, Rht8, Rht-D1* and *Vp-1B* gene composition was analyzed) and 33 lines of recombinant triticale with different types of D(A)- and D(B)-substitutions (*RhtB1* and *Vp-1B* genes composition was analyzed). It was found that the substituted wheat lines and most triticale lines (22) contain *Vp-1Bc* allele in the homozygous state associated with resistance to pre-harvest sprouting. The mutant allele of *Rht-B1b* ensuring a significant reduction in plant height was detected in the homozygous state in 20 triticale lines. All substituted wheat lines contain wild alleles of *RhtB1* and *Rht8* genes and the vast majority of them are heterozygous for allelic composition of *Rht-D1*gene that generally indicates low breeding importance of this material in terms of development of resistant to lodging varieties. Based on the analysis results, 10 recombinant lines of triticale, which combine mutant alleles of *Rht-B1* gene and *Vp-1B* gene in their genotypes, were selected for further pre-breeding research.

The research work was partially supported by the BRFFR (grant № B15CO-030)

SELECTION GENETIC EVALUATION OF SOMACLONAL LINES OF SOYBEAN TOLERANT TO THE HEAVY METALS IONS

O.S. Efremova [1], ***G.A. Kodirova*** [2], ***P.V. Fisenko*** [1]

[1] Primorsky Scientific Research Institute of Agriculture, Ussuriysk, Russia

[2] All-Russian Scientific Research Institute of Soybean, Blagoveshchensk, Russia

e-mail: efremo.olga2010@yandex.ru

The goal selection of gene pool, and its diversity make it possible to identify genetic sources and donors of economically valuable traits for the different breeding programs. However, the traditional crop selection may not provide revolutionizing of plants. Thanks to biotechnological research methods there appeared new possibilities of expanding genetic diversity in soybean breeding. For the first time we held genetic evaluation of somaklonal soybean lines oforganogenic origin derived using nutritional medium of mutagenic factor-heavy metal ions. Subject of studies were 240 regenerant soybean lines from 10 source forms developed on selective medium with the addition of copper ions (Cu^{2+}) and cadmium (Cd^{2+}) as mutagenic factor. According to the results of the study in the control nursery nine lines exceeded the standard on productivity by 3,0 - 36,9%. According to biochemical parameters, the three lines developed on the medium containing ions of Cu^{2+} performed high content of oil and histidine in the seeds having a low index of linolenic acid (R 1485, R 1357, R 1490). Regenerant line R1357 was distinguished on the complex of reliably exceeded biochemical comopennts. Relative electrophoretic mobility of peroxidase with a zone of 0,36-0,40 Rf was revealed in forms: R 1357, R 1496, R 1524, R 109 and R 1490. The more mobile electrophoretic spectra were defined in R 1496 (0,43-0,45 Rf), R 1490 (0,48-0,50 Rf), and R 1518 (0,42 Rf; 0,47 Rf). Cadmium ions being applied in the experiment had practically inpibiting effect upon the regeneration process of certain genotypes of soybean source forms. Despite the low productivity of cotyledon's nodes, normally developed *in vitro* regenerants from six original forms were transferred ex *vitro.* We received 46 fertile plants that were reproduced to conduct genetic analysis. We conducted genetic analysis of four regenerant soybean lines involving six different primers for di-and trinucleotide micro satellite repetitions, which initiated 69 fragments, 17 of which were polymorphic (24.6%), the rest were monomorphic, i.e., they were observed in all spectra of the studied plants. The size of the identified fragments ranged from 300 to 1000 nucleotide pairs (p.n.), depending on the primer, the number of polymorphic fragments varied from 2 to 8. Based on the analysis of binary matrices there were calculated indices of genetic differences between the investigated lines. The largest value of genetic distances was found between the initial form Hudson and the regenerant line R1585 line (0.3321), the smallest gap was between the lines R1585 and R1597 (0.0392), as well as between R1571 and R1569 (0.0594). There were identified the regenerants reliable genetic differences from the initial form.

THE OBTAINMENT AND USE OF GENETICALLY MARKED COMMON WHEAT LINES FOR THE STUDY OF GENES CONTROLLING ADAPTATION AND RESISTANCE TO STRESS

T.T. Efremova, E.V. Chumanova, N.V. Trubacheeva

Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia

Email: efremova@bionet.nsc.ru

In recent years, there has been significant progress in the development of research focused on the possibility of gene transfer from wild species of cereals to improve the adaptability of bread wheat. In most studies shown the results for the production of wheat-alien substitution, introgression and translocation lines using cytogenetic and molecular methods for the identification of alien chromosomes. The sources of alien material are the *Aegilops*, *Agropyron, Secale, Hordeum* species. In this regard, interest to the obtainand study of a new wheat-alien lines is not reduced. We carry out research directed to developmenta new approach to targeted and precise replacement of common wheat individual chromosomes from taxonomically distant and unrelated species based on aneuploid lines carrying the genetic or cytological markers. Were developed the effective schemes to obtain the5R (5A), 5R(5D) wheat-rye substitution lines, as well as a large set of intervarietal lines with the substitution of chromosomes in fifth homoeologous group. Experimentally implemented the possibility of using synthetic amfiploid *T. timopheevii / T. tauschii* (GGAADD) as a donor of resistance to leaf rust and powdery mildew.

With the use of molecular genetic methods were established the location and size of the fragments in the genome of *T. timopheevii/T. tauschii* immune lines of wheat Saratovskaya 29. Were obtained the isogenic lines on varieties Saratovskaya 29 with marker genes from *T. polonicum*, *T. petropavlovskyi*, *Ag. elongatum* and *S. cereale*. First obtained wheat-barley *T. aestivum- H. marinum* ssp. *gussoneanum* Hudson 4 *x* substitution lines $7HL^{mar}$(7A), $7HL^{mar}$(7B), $7HL^{mar}$(7D). Were obtained introgression lines with combination of genes controlling morphological traits and disease resistance: T1RS.1BL (*Lr26/Pm8/Sr31*)+T5AS.5RL+T7DS.7DL-Ae#1L(*Lr19/Sr25*) and T1RS.1BL (*Lr26/Pm8/Sr31*)+5R(5D)+T7DS.7DL-Ae#1L(*Lr19/Sr25*). A significant part of our work is related to the study of the relation of individual cereals chromosomes with adaptive and valuable traits.So, on the basis of the obtained lines with intervarietal and alien substitution chromosomes studied the effects of donor chromosomes in fifth and seventh homoeologous group of wheat, rye and wild barley on the length of the growing season, type of development, winter hardiness, protein content and grain hardiness. Were established the presence of two alleles of the gene *Vrn-B1*, determining the difference the duration of seedling–heading time and studied the structure of these alleles. With the use of allele-specific primers developed for the *VRN1* loci, the allelic diversity of the *VRN-A1*, *VRN-B1*, and *VRN-D1* genes was studied in 148 spring common wheat cultivars cultivated under the conditions of Western Siberia. It was demonstrated that modern Western Siberian cultivars have the *VRN-A1a* allele, which is widely distributed in the world (alone or in combination with the *VRN-B1a* and *VRN-B1c* alleles).

DISCRETE FRAGMENTATION OF 18S rRNA 5'-TERMINUS MAY REGULATE PROTEIN SYNTHESIS IN PLANTS UNDER DIFFERENT STRESS CONDITIONS

A.V. Zhigailov, V.Y. Kislitsin, D.K. Beisenov, N.S. Polimbetova, B.K. Iskakov

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

e-mail: bulat.iskakov@mail.ru

Earlier in wheat germ small ribosomal subunits (WG 40S RSU) we detected new small RNA of 132 nucleotides (5.3S RNA) which exists also in all tested plants and amount of which increases several times under heat shock. We isolated, cloned and sequenced 5.3S RNA, which proved to be a discrete 5'-terminal fragment of 18S rRNA ($5.3S_{132}RNA^{18S}$).

To study the influence of 18S rRNA cleavage on function of 40S RSUs and on protein synthesis *in vitro*, we translated reporter mRNA with different 5'UTRs in WG cell-free system (CFS) that was pre-treated by micrococcal nuclease (MNase). Brief treatment of WG-extract by MNase induced several discrete fragments of 18S rRNA among which $5.3S_{132}RNA^{18S}$ was most prominent. In pre-treated WG-CFS, translation level of all mRNAs decreased 2-3 times, indicating that such cleavage inhibits protein synthesis.

To trace $5.3S_{132}RNA^{18S}$ induction in plants under different stresses we used oligonucleotide probe complementary to first 35 nucleotides of WG 18S rRNA. This probe was labelled by either radioactive or DIG labels to perform northern blot-hybridization after PAG-electrophoresis in denaturing conditions (8M urea) of total nucleic acids extracted from plants subjected to different stresses. Using such an approach we detected additional discrete 5'-terminal fragment of ~75 nucleotides ($5'F_{75}RNA^{18S}$) which was usually hidden by tRNAs, and also another fragment - $5'F_{190}RNA^{18S}$.

WG from dormant seeds contained the least amount of all mentioned fragments. In germinated WG the amounts of these fragments slightly increased. Treatment of germinated WG with H_2O_2 does not induce fragmentation, while cold shock obviously stimulates. Most pronounced induction of fragments was observed in germinated WG subjected to following stresses and treatments: drought, salinity, heat shock, UV irradiation, salicylic acid, histidinol.

This suggests that cleavage of 18S rRNA in definite sites may complement the mechanism based on phosphorylation of peIF2 (by pGCN2) in "braking" of translation initiation especially under stresses (heat shock, salinity) which are not accompanied by peIF2 phosphorylation.

THE STUDY OF RESISTANCE OF WHEAT GERMPLASMS TO STRIPE AND LEAF RUST USING MOLECULAR MARKERS

***A. Kokhmetova*[1], *M. Atishova*[1], *A. Madenova*[1], *K. Galymbek*[1], *Zh. Keyshilov*[1], *R. S. Sharma*[2], *M. Yessimbekova*[3], *R. Urazaliev*[3], *B. Aynebekova3*, *I. Lapochkina*[4], *A. Morgounov*[5]**

[1]Institute of Plant Biology and Biotechnology, Almaty, Kazakhsta
[2] ICARDA-Tashkent, Uzbekistan, Tashkent, Uzbekistan
[3] Kazakh Research Institute of Farming, Almalybak, Almaty Reg. Kazakhstan
[4]Agricultural Research Institute of Non-Chernozem Zon, Moscow region, Russia
[5]International Maize and Wheat Improvement Center (CIMMYT), Ankara, Turkey

e-mail: gen_kalma@mail.ru

Wheat leaf and stripe rust over the past several years has been the major factor in Kazakhstan that reduces wheat yield and quality and caused considerable economic damage. Utilization of foreign germplasms is the best way to solve the problem of development new rust resistant cultivars. The study of winter wheat germplasm from different national and international nurseries allowed to evaluate the value of the lines for genetic and breeding programs directed on improvement of wheat leaf and stripe rust resistance in Kazakhstan. Based on data from field test can be concluded that the most valuable sources, combined resistance to both leaf and stripe rust were 16 lines and cultivars (28.6%), including mainly entries from CIMMYT and ICARDA. Nineteen entries (30.6%) had high level of resistance to leaf rust in the field tests. Thirty-three entries (53%) were resistant to stripe rust in the field and have great effectiveness to control stripe rust. In our study 22% wheat accessions of 62 wheat entries studied had polymorphic band of linked STS marker F1.2245Lr10-6/r2 to leaf resistance gene *Lr10*, 3% entries had polymorphic band of linked STS marker *Gb* to leaf resistance gene *Lr19/Sr25,* 11% entries had polymorphic band of linked SSR marker Iag95 to *Lr26/Sr31/Yr9/Pm8* resistance gene block, 43% had polymorphic band of linked STS marker csLV34 to *Lr34/Yr18* APR resistance gene block, 12% entries had polymorphic band of linked LN2-Ventriup to *Lr37/Yr17/Sr38* resistance gene block, 17% had polymorphic band of linked marker csGS to *Lr68* leaf rust APR gene, 6% had polymorphic band of SCAR marker linked to *Yr10* stripe rust resistance gene, but all of sources of this gene appeared to be heterozygotes. Only one line from ICARDA showed presence of stripe rust resistance gene *Yr15*. The results obtained are used in Kazakhstan for developing varieties of wheat that are resistant to leaf and stripe rust. Four CIMMYT lines and thirteen ICARDA lines were resistant to leaf rust, nine CIMMYT lines and twenty two ICARDA lines were resistant to stripe rust. Introduction of new resistance genes is required to improve the field resistance of Kazakh winter wheat cultivars to leaf and stripe rust. In this context, gene pyramiding of effective *Lr* and *Yr* genes is probably the faster strategy to develop leaf rust resistant wheat cultivars. The results of our study create opportunities for transfer of breeding process in Kazakhstan to a new scientific level due to the application of molecular methods.

This work was financially supported by the Ministry of Education and Science Republic of Kazakhstan, research project grant funding №2120 and by the Ministry of Agriculture RK, research grant №O0721.

THE STRUCTURE OF THE PATHOGEN *PYRENOPHORA TRITICI-REPENTIS* POPULATION IN THE REPUBLIC OF KAZAKHSTAN AND NORTH CAUCASUS REGION OF RUSSIA

***A. Kokhmetova*[1], *O. Kremneva*[2], *G. Volkova*[2], *Zh.S. Keyshilov*[1], *K. Galymbek*[1], *M. Kumarbayeva*[1], *N.Zh. Sultanova*[3]**

[1]RSE Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan
[2]All-Russian Research Institute of Biological Plant Protection RAAS, Krasnodar, Russia
3 LLC Kazakh Research Institute of plant protection and quarantine, Almaty, Kazakhstan
e-mail: gen_kalma@mail.ru

Pyrenophora tritici-repentis, causal agent of tan spot on wheat. In recent years there has been increasing distribution and harmfulness of *P. tritici-repentis* on wheat. The aim of research was to study distribution, similarities and differences between populations of *P. tritici-repentis* in virulence and race structure of isolates obtained from wheat in the North Caucasus region of Russia and Republic of Kazakhstan. Route survey of wheat fields showed that wheat tan spot appears by mild to moderate level, depending on climatic conditions and the varietal characteristics of wheat. The greatest development and spread of the pathogen in Kazakhstan and Russia recorded in the zones with the highest humidity. These differences in the development of tan spot may be also associated with resistance to the disease of definite wheat cultivar and agricultural practices. In the process of studying the virulence and racial composition of pathogen populations 30 monosporic isolates of P. tritici-repentis were analyzed, including 17 isolates from wheat samples collected in the North Caucasus region; 13 isolates from samples collected in the Republic of Kazakhstan. The monosporic isolates of *P. tritici-repentis* originated from different regions of Kazakhstan and Russia were attributed to certain races based on their ability to produce necrosis/chlorosis symptoms on standard differentials (Glenlea, 6V662, 6V365). The isolates of *P. tritici-repentis* from Kazakhstan were most virulent; phenotypically more diverse were isolates from Russia. Races 1, 4 and 8 and virulence phenotypes of 77 and 35 occurred both in Kazakhstan, and the Russian of a pathogen. The virulence phenotypes 77 and 53 from Russia and 77 and 37 from Kazakhstan were the most frequent. It is shown that the dominant races are 1 and 8 of *P. tritici-repentis*. The variation was observed in the virulence of isolates: in Russia races 1, 2, 4 and 8 of a pathogen were identified, and in Kazakhstan races 1, 3, 4, 6 and 8 *P. tritici-repentis* were detected. Races 1 and 2 were being predominant races in the North Caucasus region of Russia, while races 1 and 8 were the most common in Kazakhstan. Race 8 was detected for the first time in Kazakhstan.

This study was supported by grant № 2170 of the Ministry of Education and Science of the Republic of Kazakhstan and by grant №16-44-230696 r_a of Russian Foundation for Basic Research and the administration of the Krasnodar Territory.

RESISTANCE OF SPRING AND WINTER WHEAT WITH THE INTROGRESSION OF GENETIC MATERIAL (T.*TIMOPHEEVI, T.KIHARAE, T.DICOCCOIDES, AE.TRIARISTATA, AE.CYLINDRICA*) TO ABIOTIC AND BIOTIC STRESS FACTORS OF THE ENVIRONMENT

K. Kozhahmetov [1], ***A.I. Abugalieva*** [1,2], ***A.S. Rsaliyev*** [3], ***V.A. Chudinov*** [4]

[1]*Kazakh Research Institute of Agriculture and Plant Growing, Kazakhstan*
[2]*Kazakh National Agrarian University, Kazakhstan*
[3]*Research Institute for Biological Safety Problems, Kazakhstan*
[4]*Karabalyk Agricultural Experimental Station, Kazakhstan*

Based on the screening of resource material transition (6 x 2 = 12), synthetic (25) and advanced (11) Forms of spring wheat with germplasm of wild relatives compiled a database of 1) the NDVI phenotyping in the 2-vegetation in the South region (KazSRIA&PG) and North (Karabalyk) for 7-11 measurements; 2) productive properties; 3) resistance to diseases; 4) indices of drought resistance.

Obtained 1) line - the sources of disease resistance (on a natural background) confirmed on an artificial background, and genetic analysis; 2) line of high NDVI potential, confirmed the high grain yield and converted into senior nursery selection process with simultaneous multiplication of the individual sibs; 3) genotypes for registration and patenting of new forms (of high and stable) on novelty, distinctness and uniformity: Tim-biday and Guntikum (application №20548 and №20549 from 15.06.2016).

In general, the dynamics of biomass accumulation *(NDVI)* reflects genotype response to stressful conditions (increased temperature, insufficient humidification, etc.). Wild relatives do not reduce *NDVI* under stress and are characterized by a smooth curve in the growing process. Spring common wheat varieties characterized by hopping curve under stress. Transient spring wheat synthetic forms depending on the specific genotype react to environmental conditions. The criterion for selection for stable physiology can be smooth curve at a high level.

As a result of screening material on disease resistance: a) among transitional forms and synthetic spring wheat held negative selection unit unstable form; accessions wheat obtained from crossing from wild relatives show high resistance to yellow and leaf rust in the defeat of standard grades of 100%, which indicates the high values of this material as a source of stability, although at less than productivity; b) among the varieties studied in the background of the strong development of stripe rust resistant samples were allocated *Bezostaya 1 x Ae.cylindrica, (Bezostaya 1 x T.militinae) x T.militinae; Zhetysu x T.timopheevi; Zhetysu x T.militinae; Bezostaya 1 x Ae.cylindrica and Erythrospermum 350 x T.kiharae.* High resistance aforementioned samples due to the presence of certain Yr-genes for resistance to yellow rust.

On an artificial infectious background of all samples analyzed, only 5 out of 60 samples, including standard-grade amazed leaf rust degree of manifestation of the disease which has reached 40-80%. The defeat of the sheet form Septoria and yellow spot in the middle was 15,9-20,4%, with a variation of 0-40% by accessions. High resistance to pathogens data showed samples (*Bezostaya 1 x T.militinae) x T.militinae; Karahan; Steklovidnaya 24 x T.timopheevi; (Bezostaya 1 x T.triaristata) x Karlygash; Erythrospermum 350 x T.kiharae*.

Samples of *Erythrospermum 350 x T.kiharae* (58,0-75,0 t/ha), *Zhetysu x T.timopheevi (49,0-61,5* t/ha) and Zhetysu x *T.militinae (48,5-61,* 1 kg/ha) showed increased stability of yields on long-term results, including infectious background Erythrospermum 350 x *T.militinae,* Bezostaya 1 x *Ae.cylindrica* and (Bezostaya 1 x *T.militinae)* x *T.militinae-9.*

The work was done in the project "Phenotyping, genomics and biotechnology (biochemistry) in the creation of varieties of cereals, legumes and forage genetically identified stress indicator of efficiency and quality properties" (State registration number 0115RK02312).

ASPARAGINE METABOLISM AND PROTEIN CONTENT IN THE DEVELOPING SOYBEAN SEEDS

T. Lee[1], Z. Spankulova[1], U.Orazbayeva[1], S. Didorenko[2]

1Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan
2Kazakh Institute of Agricultureand Crop Production, Almalybak, Kazakhstan

E-mail: tamaralee05@gmail.com

30 soybean lines were used in this study: 3 early-maturing (110-120 days) withthe standard Misula, 16 medium- maturing (121-130 days) with standard Zhansaya, 11 late- maturing (more than 130 days) with the standard Lastochka.

Since soy is a rich source of protein and oil, one of the main objective of breeders around the world is to enhance the nutritional quality of soybean seeds by the increase of protein content or oil. For successful breeding programs it is very important to understand the biochemical mechanisms of the accumulation of protein and oil in soybean

A positive correlation ($P \leq 0.05$) between free asparagine in developing cotyledons and protein content in mature seeds of soybean was confirmed in comparisonof the 5 growingin the fieldcrops, which is consistent with the hypothesis that the high protein content is determined in soybean embryo ability to synthesize proteins from available nitrogen sources.

Probably, the level of asparagine, closely-controlled inembryo of high protein lines, can serve as a metabolic nitrogen status signal in soybean seeds. The higher expression of asparagine synthetase *(ASNS,EC 6.3.5.4)*, the higher content of asparagine in developing soybean seeds, i.e. the higher concentration of protein in the mature seeds. In other words, high levels of free asparagine might be serve as a physiological marker associated with high protein content in soybean seeds.

The high content of total essential amino acids (EAA) was observed in the next varieties: B48/232;ZR13; ZR38; B37/153; V10/1012; A8/2-2; A9-562, notably Phenylalanine, Valine, Isoleucine.

Distinct positive correlation was established between the concentration of asparagine and total amino acids in soybean samples.

IDENTIFICATION OF GERMPLASM WINTER WHEAT FOR RESISTANCE TO YELLOW AND LEAF RUST

A.K. Madenova, A.M. Kokhmetova, M.N. Atishova, K. Galymbek, Zh. Keishilov

Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan

One of the main reasons for the high yield losses of grain Kazakhstan is the intensive development of fungal diseases. Yellow (*Puccinia striiformis* f. *Sp. Tritici*) and leaf (*Puccinia recondita Rob.et Desm* f. *Tritici* Eriks) rusts are the most widespread and dangerous diseases of wheat and are the major factor that adversely affects wheat yield and quality and causes considerable economic damage. To avoid economically significant crop losses from plant diseases, it is necessary to use genetically resistant varieties. A set of promising lines of breeding nursery (SP-1) as objects of this study was used. With the help of molecular markers csLV34, WMC44, Ventriup/LN2 breeding lines were screened for presence of resistance genes to yellow and leaf rust. The STS marker, csLV34 that maps 0.4 cM from *Lr34*, and was validated in many lines and cultivars from different breeding programs worldwide (Lagudah et al., 2006). Another rust resistance genes *Lr37*, *Sr38* and *Yr17* are located within a segment of Triticum ventricosum chromosome 2NS translocated to the short arm of bread wheat chromosome 2AS (Helguera et al., 2003). The 259-bp PCR product from primers VENTRIUP-LN2 is a dominant marker and therefore cannot differentiate heterozygous from homozygous 2NS individuals. The AFLP marker to map *Lr46* on the distal end of 1BL (William et al., 2003). The *Lr46* was tightly linked or pleiotropic to a stripe rust resistance gene designated *Yr29*. The tight linkage of a slow rusting gene to a stripe rust resistance gene was also found for the pair *Lr34/Yr18*. The marker Xwmc44 determined that the microsatellite locus is located 5.6-cM proximal to the putative QTL for *Lr46* (Suenaga et al.). As a result of molecular screening, it was shown that 4 promising lines consist of both gene complexes *Lr34/Yr18* and *Lr37/Sr38/Yr17*. In four wheat lines the gene complex *Lr34/Yr18* was observed: d.114 Novosibirskaya 22 x Omskaya 37 x 28-1, d.114 Novosibirskaya 22 x Omskaya 37 x 28-2, d.114 Novosibirskaya 22 x Omskaya 37 x 28-3, 897F5#25 Madsen x Almaly x #60 BWKLDN-9. In six lines genes *Lr37/Sr38*/*Yr17* were identified: d.114 Novosibirskaya 22 x Omskaya 37 x 28, d.114 Novosibirskaya 22 x Omskaya 37 x 28-1, d.114 Novosibirskaya 22 x Omskaya 37 x 28-2, d.114 Novosibirskaya 22 x Omskaya 37 x 28-3, d.114 Novosibirskaya 22 x Omskaya 37 x 28-4, 897 F5#25 Madsen x Almaly x #60 BWKLDN-9. *Lr46/Yr29* genes in two lines were identified: d.1777 Daryax1724 F1 1581x (d.807 F4 (Naz x Umanka)xAlmaly) x Zimorodok, #78 and 897 F5#25 Madsen x Almaly x #60 BWKLDN-9. Thus, molecular analysis allowed identify carriers of *Yr*- and *Lr*-genes, effective to yellow and leaf rust of wheat in our region. Identified sources of resistance to yellow and leaf rust recommended as donors in breeding programs to improve rust resistance of wheat.

This work was financially supported by the Ministry of Education and Science Republic of Kazakhstan, research project grant funding №2120 and by the Ministry of Agriculture RK, research grant №O0721.

JOINT EFFECT OF GROWTH STIMULATOR OF PLANTS C-2 AND EMI EHF ON PEROXIDASE TOTAL ACTIVITY OF WHEAT SEEDLINGS

A.V. Nerkararyan, L.A. Minasbekyan, M.A. Shahinyan

Yerevan State University, Faculty of Biology, Department of Biophysics, Yerevan, Armenia
e-mail: m.shahinyan@ysu.am

Plants are appropriate models compared to animals for realization of different kinds of experiments: they are immobile and therefore keep a constant orientation in the EMF and their specific scheme of development makes them ideally fitted to intercept electromagnetic field. Electromagnetic field exposure alters the activity of several enzymes, including those of reactive oxygen species (ROS) metabolism, a well-known marker of plant responses to various kinds of environmental factors [1, 2].

It was shown that the irradiation of wheat seedlings in range of 49-53 GHz impacts on peroxidase (PO) total activity change during growth process. The change of III class PO total activity can be judged by activity of 10 genes encoding enzyme synthesis [3]. Peroxidase possesses a pronounced polymorphism. Presence of number of isoforms permits it working in different conditions and realizing various functional loads [3].

Series of experiments directed to PO activity studies of wheat seedlings exposed to joint effect of growth stimulator C-2 [4] and electromagnetic irradiation with extremely high frequencies (EMI EHF) has been carried out.It was shown that pre-plant treatment of wheat seedlings by C-2 growth stimulator leads to increasing of PO total activity in seedlings up to 6^{th} day of germination, while in control samples the enzyme activity gradually decreases. At combination of stimulator and irradiation effects the following scene is observed: PO total activity increases up to 3^{rd} day of germination, then it decreases.

Similar regularity is observed in all variants of experiment. It was shown that the combination of physical and chemical factors preserves the common tendency; moreover the value of organism response to the effect depends on EMI frequency.

In the first days of growth the wheat seedlings perform higher sensitivity to the irradiation than to stimulator. It indicates that EMI EHF is a factor stimulating the growth. PO total activity decreasing in seedlings exposed to joint effect of chemical and physical factors compared to treatment of variants by only stimulator indicates that the irradiation acts as stress factor for plant. That is why in organism processes occur directed to stressor factor weakening.

1. Vian A., Davies E., Gendreud M., Bonnet P. Plant responses to high frequency electromagnetic fields. BioMedRes. Int., v. 2016, 2016, p. 1-13.
2. BalmoriA. Electromagneticpollutionfromphonemasts. Effectsonwildlife. Pathophysiology, v. 16, N2-3, 2009, p. 191-199.
3. Duroux L., Welinder K.G. The peroxidase gene family in plants: A phylogenetic overview. J. Mol. Evol., v. 57, 2003, p. 397-407.
4. Safrazbekyan E.E., Nerkararyan A.V., Kazumoev N.B. Amarant in Armenia. New and non-traditional plants and perspectives of their usage. V intern. Symp., June 9-14, 2003, Pushchino, Russia, p. 83-85.

HIGH MOLECULAR WEIGHT GLUTENIN SUBUNITS IN COMMON WHEAT LINES WITH ALIEN GENETIC MATERIAL INTROGRESSION

O.A. Orlovskaya, L.V. Milko, L.V. Khotyleva, A.V. Kilchevsky

Institute of Genetics and Cytology, National Academy of Sciences of Belarus, Minsk, Belarus

e-mail: O.Orlovskaya@igc.by

Nowadays, the world pays great attention to the development of the initial material for wheat breeding, including on the basis of the original sources of genetic plasma. It is known from the data in the literature that some species of *Triticum* genus contain new alleles of high molecular weight glutenin subunits (HMW-GS), which may positively affect wheat bread-making qualities. HMW glutenins are known to be encoded by genes in *Glu-1* loci located on long chromosome arms of the first homeologous group. In view of this, by use of molecular markers we evaluated the allelic composition of *Glu-1* loci in 11 common wheat lines with the introgression of *T. dicoccum*, *T. dicoccoides, T. spelta* genetic material and their parent forms. Parent wheat varieties contained *Glu-A1b* allele. *Glu-A1a* allele was found in *T. spelta* and *T. dicoccoides.* For *T. dicoccum,* we failed to identify specific for soft wheat alleles that indicates the presence of specific for this species alleles by *Glu-A1* locus. *Glu-A1* locus of hybrid lines contained both parent variety alleles (27,3%) and the alleles of wheat relatives (72,7%). When assessing the protein quality, subunits 1 and 2 *, encoded respectively by *Glu-A1a* and *Glu-A1b* alleles, are assigned the maximum for a given locus 3 points to. Since two genes (x- and y-types) are normally expressed in *Glu-B1* locus, we were identifying the alleles for each of them. *Bx6* gene was identified only in *T. spelta,* which passed to the lines developed with its participation. The other analyzed genotypes contained *Bx7* gene. *C*-allele, encoding a pair of subunits 7+9 (2 points), is specific for all parent wheat varieties by *Glu-B1* locus. In the studied *T. dicoccum* sample, we identified *Glu-B1b* allele, which determines the presence of subunits 7+8 (3 points). This allele was also identified in three lines with the introgression of *T. dicoccum* genetic material that improved their bread-making capacity as compared to the parent wheat variety. For *T. dicoccoides* and *T. spelta*, we failed to identify the allelic composition of y-type gene by the primers, identifying the specific for common wheat alleles. This indicates that these samples of wheat relatives are carriers of new *By* gene alleles. For the majority of the studied by *Glu-B1* locus hybrids, we identified the allelic variants specific for wheat relatives – 63,6%. In the studied hybrid material, we identified two allelic variants of *Glu-D1* locus: *Glu-D1a* (2 points) and *Glu-D1d* (4 points). 54,5% of introgressive lines contain the most valuable in dough quality Glu-*D1d* allele and 45,5% contain *Glu-D1a* allele.

The studied wheat lines with the introgression of alien genetic material contain alleles of *Glu-1* loci, specific for wheat varieties with good grain quality. The frequency of favorable *Glu-A1b* allele amounted to 27,3%, *Glu-B1b* – 27,3%, *Glu-B1c* – 36,4%, and *Glu-D1d* – 54,5%. In addition, for 63,6% of lines, except for high molecular weight subunits of glutenin alleles identical to common wheat, we identified new alleles of wheat relatives (*T. spelta, T. dicoccoides, T. dicoccum)*. New alleles are a source to enlarge the gene pool of wheat, determining bread-making qualities, and are of interest for further study.

FLOW CYTOMETRY FOR IDENTIFICATION OF PLANT GENOMIC RESPONSE IN ECOLOGICAL STUDIES

Isaak Rashal, Dace Grauda, Nikole Krasņevska, Inta Belogrudova, Jekaterina Voskresenska, Lada Bumbure, Anton Kolodinski

Institute of Biology, University of Latvia, LATVIA

Email: izaks.rasals@lu.lv

Ecological studies of plants, including endangered plant species in natural conditions and different types of plants growing in the urban environment, are among fast growing natural research fields. Growing plants are subject to the influence of different types of biotic and abiotic stresses. Depending of the stress character plant response could be cell damage, increase of cells oxidative stress, changing level of endopolyploidy etc.

The flow cytometry is a powerful investigation method on the cellular level, because it is based on measurement of relative cell fluorescence what reflected cell conditions. In ecology studies flow cytometry is used to determine cell ploidy and gender, to sort living cells from apoptotic, counting fluorescent nanoparticles, and to detect an overall impact of various factors on cells by examining cell self-fluorescence. Flow cytometry is a biophysical technology employed in cell counting, cell sorting, biomarker detection, and protein engineering. Flow cytometry works through suspending cells in a stream of special fluid, exciting them by laser light and passing them through a detection device. It allows making multiparametric (up to 20 parameters) analysis of thousands of cells per second.

In our laboratory we used BD FACSJazz® cell sorter (BD Biosciences, USA) with flow cytometer function to measure the relative fluorescence of plant cells. For cell excitation the 488 nm Coherent Sapphire Solid State (blue) laser are applied. Cells' relative fluorescence was measured at 530 nm and 585 nm. The information of mean fluorescence intensity from the purified cell suspension samples was recorded. Preliminarily, multiple gate sizes and shapes were tested to find the one with the lowest CV. Using flow cytometer BS FACS Software 1.0.0.650 cells plot was construed to determine the densest part that was later gated using oval-shaped gate. The gate included from 95 to 99% of all target cells.

Different naturally and in urban conditions growing plant species – Siberian ligularia *Ligularia sibirica*, lime trees *Tillia cordata,* white clover *Trifolium repens*, were included in investigations. In they turn, in experimental conditions influence of such factors, as the low frequency (50–60 Hz) electromagnetic field, UV irradiation and SiO_2 nanoparticles were studied on the cellular level in different types of plant tissue cultures of several species – lime trees (*Tillia cordata*), cyclamen (*Cyclamen persicum*), wheat (*Triticum aestivum*), barley (*Hordeum vulgare*), flax (*Linum usitatissimum*).

Our experience showed that the flow cytometry is an excellent method to define cell changes impacted by diverse factors. Some results of investigations using flow cytometry will be shown in the presentation.

Investigation was supported partly by the Latvian State Research Programme "EVIDEnT"

THE CREATION OF DROUGHT-RESISTANT WHEAT SAMPLES USING THE METHODS OF CLASSICAL GENETICS, TRADITIONAL AND MARKER SELECTION

A.I. Sedlovsky, L.N. Tjupina, A.I. Tjezhenova, M. Atishova

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

e-mail: gen_sai@mail.ru

The use of interspecific crosses one of the ways to create caltivars of wheat with high grain quality and resistance to stressful conditions. As objects of research in the work used wild relatives of wheat *Triticum spelta* (2n = 42 BAUD), *Triticum macha* (2n = 42 BAUD), *Triticum dicoccum* (2n = 28 BAU), *Triticum turgidum* (2n = 42 BAU), *Triticum Kiharae* (2n = 42 GAbD), *Triticum compactum* (2n = 42 BAUD), *Aegilops triaristatum*, wheat-pyrejnyj hybrid *Agropirum glaucum*, samples obtained from distant hybridization (80 samples) and promising samples that are in the final stages of the breeding process (41 samples).

To identify promising samples of wheat obtained from interspecific and intervarietal crosses of interest for breeding for drought tolerance, conducted laboratory evaluation of the degree of seed germination on solutions of sucrose. In addition held cytogenetic characteristic control of drought on the basis of the development of the male gametofita and plasmolysis of pollen grains associated with drought. In the course of work carried out a comprehensive assessment of the agronomic and physiological, because resistance caltivars varies significantly influenced by external conditions. In this regard, studies have been conducted in conditions of flat-steppe zone of Almaty oblast is KazNIIZiR (irrigation and rain-fed von-poluobespechennajabogara and Karoy).

The evaluation samples from populations of distant hybrids highlighted potentially more drought-tolerant designs and created collection of high-yielding, drought-resistant samples. Prospective samples evaluated under field conditions (using morphological markers that correlated with drought-tolerance-length podkoloskovogo internode, stem blight, gaining strength, vypolnennost' grain, grain quality, plant height, weight of 1000 grains). Based on the results of the tests in conditions of dry-unsecured Károypoluobespechennoj, dry and watering these samplesvyvleny the best performance to productivity with Piazza during the four years of testing at each point. The sample 1214 (*Ljutescens*-1272 x Saratov-70) on the productivity of Karoe reached 15.5 centner/ha, bogare – 27.7 centner/ha for irrigation – 40.8 centner/ha. The sample 1148 (Virgin-60 x Zhenis) productivity at Karoe was 15.8 centner/ha, bogare – 30.0 centner/ha and watering – 40.7 centner/ha. Score samples in kennel Competitive trials under conditions of irrigation and rainfed conditions, Károy allowed select samples of intensive type. Selected master responded well to the moisture and fertilizer. In the conditions of irrigation and rainfed conditions Károy 1148 samples and 1214 exceeded standard on productivity from 3 up to 6 t/ha. that testifies to their plasticity. Selected samples transferred to Control kennel and environmental testing. A study of the stability of perspective samples of allocated citogenetic samples 738/2713/SP-1 Zhenis x Aegilops triaristatum and 783/1269/SP-1 Zhenis x Aegilops triaristatum, who observed cytological uniformity of plants.

Molecular screening of perspective samples of wheat for the presence of rye translocation 1BL/1RS characterizes drought resistance revealed specimens 2713 SP-1 Zhenis x Aegilops triaristatum, 1269-1 Zhenis x Aegilops triaristatum, 1258/09 Icarus x Tr. macha, 1236 Virgin-60 x Zhenis, 526-1 Steppe-16 x Akmola-2.

The creation of drought-resistant wheat cultivars using germplasm of wild relatives with the holding of laboratory evaluation on the degree of germination on solutions of sucrose with conducting cytogenetic monitoring and assessing drought indicator FL based on the plasmolysis pollen grains associated with drought, and then their field test in stressful conditions and widespread use of environmental assessment perspective samples allows you to emphasize drought-resistant designs.

PI-LAMP ASSAY FOR DETECTION OF ERWINIA AMYLOVORA IN DIAGNOSIS OF FIRE BLIGHT

B.B. Smailov, M.E. Omasheva, N.N. Galiakparov

Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan

e-mail: ismail_kz@yahoo.com

Erwinia amylovora, a Gram-negative Enterobacterium, is the cause of fire blight in more than 200 species of the Rosaceae family, including economically important cultivars, such as pear and apple. Fire blight is one of the most serious diseases inpome industry worldwide. Treatment with antibiotics causeemergence of resistant strains and has unknown environmental hazards, therefore the most effective measure against fire blight is eradication of already infected plants and prevention of pathogen dispersal. Such drastic measures can lead to substantialeconomic damage.

LAMP (loop-mediated isothermal amplification)assay isa useful tool forrapid, accurate and cost-effective diagnosis of infectious diseases. The assay is faster and several times more sensitive than conventional PCR. It can be performed in field and application of cheap fluorescent DNA-intercalating dyes such as propidium iodide (PI)in LAMP allows to simply visualize results under UV-light.

Aset of 4 primers were designed for LAMP assay specific to unique DNA sequence in *E. amylovora* genome. The target site was selected on basis of genome-wide alignment of DNA from 19 different bacterial pathogens of apple trees, including *Bacillus spp., Pseudomonas spp., Erwinia spp.,* etc. Specificity of the assay was tested on DNA isolated from pure cultures of *E.amylovora.* A range of reaction parameters including temperature, DNA concentration and reaction time were tested in process of determining optimal conditions. The optimum temperature of the reaction was identified as 55^{o}C. The assay had detection limit of 7 to 10 copies of *E.amylovora* DNA with a 60-min incubation time, whereas PCR with internal primers detected about 750 copies. Resulting amplicons are visualized under UV-light by adding of 0.1 μg of PI toreaction tubes.Isolates from 45 apple trees from a local orchardwere analyzed using the LAMP method. About 75% (34/45) oftested samples were positive in LAMP analysis for presence of *E.amylovora*, though only 40% (18/45) of samples exhibited visible symptoms of fire blight in last 5 years.These results indicate that the PI-LAMP assay is a simple, convenient and sensitive diagnostic tool for fire blight.

RESULTS OF THE USE IN THE CROSSBREEDING OF REGENERANTED SOFT SPRING WHEAT FOR RECEIVING A NEW SOURCE MATERIAL OF WHEAT IN NORTH KAZAKHSTAN

A. Turganbayeva, A. Kakimzhanova, G. Shek, Zh. Zhanybekova, K. Ortaeva

National Center for Biotechnology, Astana, Kazakhstan

The climatic conditions of Northern Kazakhstan differ by large contrasts of the temperature and water regime during the vegetation period and high insolation. To increase the stability of yields of spring soft wheat as the main export culture of Kazakhstan, it is necessary to create new more plastic varieties on the basis of modern methods of genetics, biotechnology and selection. The increase in the plasticity of new varieties is possible with the combination in the genome of such contradictory properties as drought resistance and moisture resistance, heat resistance and endurance to high humidity at low temperatures, high regenerative capacity of plants after stressful situations (droughts, frosts, high insolation, salinity).

For the successful cultivation of bakers wheat, it is necessary to expand the adaptive capacity of the genotype of spring soft wheat, which is possible in the process of cell selection and recombinant genetic selection in the process of hybridizing of regenerant lines between themselves and with the best varieties.

The aim of the research was to hybridize hybrids, regenerants, varieties, and then to use F1 of complex hybrids obtained in hybridization experiments with each other. The aim was to increase the recombination of various complex genotypes obtained by hybridization, cell selection and haploidy to enhance the adaptive capabilities of the new spring soft wheat.

The subjects of the study were hybrids, regenerants from selective media (PEG-6000, mannitol, NaCl, culture filtrate from Alternaria alternata.

In our studies, in 2015-2017, 101 crosses of regenerants and hybrids between each other and the best varieties of Kazakhstan and Siberia were conducted in the field and in the greenhouse. In parallel, the possibility of obtaining haploid plants by in vitro culture of immature anthers was studied. As a result, positive results were obtained on the induction of haploid structures both from the anthers, and from wheat ovaries.

The percentage of success of crosses ranged from 3.1 to 92.3%, depending on the genotype of the components of crossing and weather conditions. The yields of new forms from the total number of explants averaged 16.1% and varied from 4.6% to 42.5%.

The most plastic hybrids in crosses (the percentage of success of crossing more than 40%) were 209/99, T.spelta/Pyrotriks 28, 35/06, 212/99, varieties - Tselinnaya 3S, Astana. The highest percentages of crosses were regenerants of spring soft wheat: Akmola field with 5% A.a. No. 5-1, 92/82-4 with 2% mannitol No. 1-1, 118/94-1 with 3% A.a. No.4-2, T.spelta/Pyrotriks 28 with 2% PEG No. 1-2, ´In memory of Aziev´ with 2% mannitol No. 1-2, 42/03 with MS → 2,5% PEG No. 1-1, 118/94-1 with 10% A.a. No. 2-2, 475/94-1 with 0.3% NaCl No. 6-1, 467/97 with 2% PEG No. 4-1-1.

Obtained F1 hybrids were crossbreeded to study and select hybrids of complex origin to enhance the adaptive genetic capabilities. From the obtained hybrid material F2, more than 2000 elite ears were selected, which will be tested in the field in the breeding nursery.

Thus, a new source material of spring soft wheat has been obtained, which is a complex hybrid nature and is promising for further selection to produce novel variety of wheat.

GENOTYPING OF SPRING HEXAPLOID WHEAT COLLECTION FROM KAZAKHSTAN USING *Vrn, Ppd* and *Eps* GENES

Y. Turuspekov [1], K. Yermekbayev [1], S. Griffiths [2]

1 – Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan
2 – John Innes Centre, Norwich, UK

Vernalization, photoperiod, and earliness *per se* genes are major genetic factors determining the adaptation of wheat to different ecological niches. In this study the collection of 96 commercial cultivars and promising lines of spring wheat from Kazakhstan were genotyped by a set of *Vrn, Ppd,* and *Eps* genes. The studied spring wheat panel consisted of 96 released and prospective cultivars from Kazakhstan. Currently, 40 cultivars from Kazakhstan and 21 cultivars from Russia in this genetic panel have been registered through the State Seed Trials Commission of the Republic of Kazakhstan (2015), and grown officially in Kazakhstan. The panel also included 19 and 10 prospective cultivars developed in Kazakhstan and Russia, respectively. Kompetative Allele Specific PCR (KASP) assays were run using LGC Genomics instructions. In *Vrn* loci the alleles *Vrn-A1a* and *Vrn-A1b* were determined using markers wMAS000033 and wMAS000035. The *Vrn-B1* alleles were identified using dominant wMAS000036 (*Vrn-B1a/Vrn-B1b*) and co-dominant wMAS000037 (*Vrn-B1b*) markers, and the *Vrn-D1* was distinguished using wMAS000039. Three KASP makers were used to identify photoperiod sensitive alleles in *Ppd-A1* (wMAS000029, wMAS000030, wMAS000031), one for *Ppd-B1* (wMAS000027), and three for *Ppd-D1* (wMAS000024, wMAS000025, wMAS000025). Three KASP markers (TAFT3-A1, TaFT3-B1, TaFT3-D1) were evaluated for *Eps* loci. The study revealed very little variation in the collection using all three analyzed groups of genes (*Vrn, Ppd, Eps*). The results suggest that wheat genetic material in Kazakhstan is very much fixed and more research is required for understanding of plant adaptation using alternative allelic combinations in various regions of this country.

The study supported by ADAPTAWHEAT project funded by 7th EU FP and grant number 1784/GF funded by the Ministry of Education and Sciences of the Republic of Kazakhstan

USING OF WHEAT WILD RELATIVES (*AEGILOPS* L.) DIVERSITY FOR BALANCED USE

M.A. Yessimbekova, Abugalieva A.I., Mukin K.B.

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

Email: minura.esimbekova@mail.ru

Most species of the genus *Aegilops L.* are resistant to fungal diseases. According to the materials of expeditions investigated the territory of Kazakhstan for rust infection has been found that some populations of genus *Aegilops L.* were infected with yellow rust (*Puccinia striformis*) one of the aggressive wheat diseases in Central Asia up to 80-100%. On plants of this species takes place preservation and formation of these rust species races. 38 local populations *Aegilops L.* (*cylindrica, tauschii, triuncialis, crassa*) gathering from 25 districts of Kazakhstan were studied on an artificial infectious background. 29 local populations of *Ae.triuncialis* and *Ae.tauschii* showed resistance (R) to yellow rust, 8 accessions were resistant (R - MR) to stem rust.

Large differences in the protein content of grain have been reported in wheat wild relatives. Among local population of *Ae.triuncialis and Ae.tauschii* were selected accessions with protein content in the grain up to 19%. According to the content of starch in the grain variability magnitude ranged from 53,5% (*Ae.triuncialis*) to 56,2% (*Ae.tauschii*). It was allocated 25 accessions according of high 1000 kernel weight (≥50,0 g); 3 accessions as early maturity (the period before heading - 133-136 days).

Analysis of the gliadin spectra showed heterogeneity and significant polymorphism of protein composition. In general, electrophoretic spectrum was presented by all gliadin zones, more components enriched in ω zone. For 20 accessions marked depletion of components or absence α-zone. For each genotype composed of gliadin formula, this proved its specificity.

The screening data base of *Aegilops* L. local populations ex situ collections, reflecting both within and between species diversity has been formed for useful traits.

INFLUENCE OF SALT STRESS ON BIOCHEMICAL PARAMETERS OF *WEIGELA FLORIDA* «VARIEGATA» MICROCLONES AND SUGAR BEET HYBRID COMPONENTS

O.A. Zemlyanuhina, N.N. Cherkasova, T.P. Zhuzhzhalova, V.N. Kalayev, V.S. Voronina

Federal State Budgetary Educational Institution of High Vocational Training "Voronezh State University" (FSBEI HVT "VGU")

For long-term three-stage adaptation to salt stress, microclones of *Weigela florida* «Variegata» and microclones of sugar beet main components (male sterility fixer – a plant normal cytoplasm and genetic sterility (MS; NZZXX), and a female plant with cytoplasmic male sterility (RF; SZZXX)) were used. Mathematically reliable changes in specific activity of enzymes of different metabolic cycles were studied. They were: peroxidase (PRX; E.C. 1.11.17); NADP-glucose-6-phosphate-dehydrogenaze (G6PDH; E.C. 1.1.1.49); NADH-dehydrogenaze (NADHDH; E.C. 1.6.99.1). Besides, two of four enzymes of malate dehydrogenase complex in tricarboxylic acids cycle, i.e. NADH-malate-dehydrogenase (MDG; E.C. 1.1.1.37) and malic enzyme (ME; E.C. 1.1.1.39), as well as isocitrate lyase (ICL; E.C. 4.1.3.1) – cytoplasmic enzyme functioning outside glyoxisomes were studied. Adaptation scheme consisted in putting plants into semi-lethal concentration of salts; 10 days later, they were transferred to control media for 30 days to recover. The long-time adaptation within three passages on selective medium using the same plants lasted 120 days. The results showed that plants of *Weigela* and sugar beet were much different in metabolic response to salt stress. Throughout the experiment, activity of peroxidase stress enzyme increased 1.3 times in *Weigela* plants, 2.4 times in microclones of MS-form sugar beet and 3.4 times in RF-form as compared to the control. NADP-glucose-6-phosphate-dehydrogenaze activity of *Weigela* clones showed a 2.5-fold decrease at the beginning of the experiment, but, by the end of 120 day, it achieved the control plant level. In sugar beet, both of MS- and RF-forms, enzyme activity did not depend on salt. Salinization did not influence upon activity of isocitrate lyase in plants of *Weigela* throughout the experiment. As for sugar beet forms, increase of the enzyme activity by 1.7 times for MS and 1.5 times for RF was registered. Specific activity of NADH-malate-dehydrogenase in adapted plants of *Weigela* is 1.4 times less than in the control ones. Salt does not influence upon the enzyme of MS-form, and activity of the RF-form enzyme shows 1.3-fold decrease. Salt stress does not influence upon NADH-dehydrogenaze of *Weigela*, but reduces the enzyme activity by 1.2 times in MS and 1.6 times in RF. Sugar beet is among the plants actively accumulating oxaloacetate. Functioning outside glyoxisomes isocitrate lyase plays the main role in this process. Besides, different action of malate dehydrogenase and malic enzyme in *Weigela* has been shown: in the course of ontogenesis, the malate dehydrogenase enzyme activity increases 9-12 times both in experimental and control plants, and activity of malic enzyme shows 2-fold (control) to 5-fold (experiment) decrease. For sugar beet plants, such phenomenon is not observed. It can be assumed that basic enzymes in adaptation reactions of *Weigela* plants are glucose-6-phosphate-dehydrogenase and complex of malate dehydrogenase and malic enzyme and, in plants accumulating oxalic acid, such an enzyme is isocitrate lyase. It has been shown that process of adaptation to salt stress is a multiple-factor one consisting, at least, of three-four components. It has been shown for the first time that free proline content was decreased below control plans becoming similar *in vivo* ones.

Session 3.

Genomics, Phenomics, and Bioinformatics

HIGH THROUGHPUT GENOTYPING FOR PLANT RESEARCH AND BREEDING

M.W. Ganal, E.-M. Graner, A. Polley, J. Plieske

TraitGenetics GmbH, Gatersleben, Germany

e-mail: ganal@traitgenetics.de

Array-based genotyping has become an important tool for diversity analyses, genetic mapping and plant breeding. TraitGenetics has been involved in the development, characterization and optimization of a number of genotyping arrays for important diploid crop plants such as maize, tomato, barley, sunflower and others. We have also been involved in the array development for allotetraploid oilseed rape (*Brassica napus*), cotton, and allohexaploid wheat. In many cases, we have analyzed large sets of varieties within internal projects using such genotyping arrays. We demonstrate the use of such marker databases for the generation of optimized marker sets based on technical quality, distribution along chromosomes, allele frequency and haplotype data. Such arrays containing a selected marker set provide non-redundant data at very low costs for genomic selection, association analysis, marker-assisted backcrossing, variety identification and material characterization. Examples for the continuous improvement of such optimized arrays with new highly polymorphic markers and genes for candidate genes are also presented.

GREEN GOALS AND GREEN TECHNOLOGIES IN PLANT BREEDING FOR GLOBAL FOOD SECURITY: THE RICE MODEL

Qifa Zhang

National Key Laboratory of Crop Genetic Improvement, Huazhong Agricultural University, Wuhan, China

Email: qifazh@mail.hzau.edu.cn

In the past half century, production of major food crops in the world has kept pace with the population increase. However, food production is still facing great challenges in the next half century because of high demands in both quantity and quality, and ever increasing pressures on resources and environments. Food production needs to be greatly increased to cope with the population increase, while the environmental sustainability requires reduction of input including chemical fertilizers, pesticides, water, labor and other resources. Increased awareness of the relation between nutrition and health also requires crop products to better meet the need of human population by producing more nutritious foods. The goals of plant breeding have to evolve accordingly to address all these needs, which I refer to as "green goals". In my presentation, I will use rice as a model to describe the demands for increased production for future needs, address the main issues that we have encountered as challenges, present current progress in rice genomics research, and provide examples and prospect on how the advance in research can be translated into technologies for rice genetic improvement especially for developing resource saving and environment friendly varieties (green technologies).

INTEGRATIVE BIOINFORMATICS APPROACHES FOR CELLULAR INTERACTOME MODELLING OF RICE

Ming Chen

Department of Bioinformatics; State Key Laboratory of Plant Physiology and Biochemistry, College of Life Sciences, Zhejiang University, Hangzhou, China

e-mail: mchen@zju.edu.cn

Multi-omics data brings us a challenge to develop appropriate integrateive bioinformatics approaches to model complex biological systems at spatial and temporal scales. In this talk, we will describe multi-omics data available for rice cellular interactome modeling. Biological networks on multiple levels such as gene regulations, protein interactions, noncoding RNA regulations and metabolic reactions are reconstructed. A systematic identification and quantification of rice proteins in various tissues and organs are introduced. To better understand the interactions of proteins in rice, we developed PRIN, a predicted rice interactome network. We presented a novel integrative approach (PSI) that derives the wisdom of multiple specialized predictors via a joint-approach of group decision making strategy and machine learning methods to achieve better prediction results of protein subcellular localization. A genome-wide multiple level of interactome model of rice is integratively built. Furthermore, a database RiceNetDB is developed for systematically storing and retrieving the genome-scale multi-level network of rice to facilitate biomolecular regulatory analysis and gene-metabolite mapping. A virtual rice cell model in three dimensions will be developed via international collaborations. Our goal is to build such a whole plant cell model that can describe how phenotype arises from genotype.

EVALUATING GENETIC DIVERSITY OF DURUM AND BREAD WHEAT GENOTYPES USING NEXT GENERATION SEQUENCING

***Mehraj Abbasov*[1], *Zeynal Akparov*[1], *Naib Aminov*[1], *Khanbala Rustamov*[1], *Fatma Sheykzamanova*[1], *Sveta Rzayeva*[1], *Robert Bowden* [2], *John Raupp* [3], *Sunish Sehgal*[4], *Bikram Gill* [2]**

[1] Genetic Resources Institute of ANAS, Baku, Azerbaijan
[2] USDA–ARS Hard Winter Wheat Genetics Research Unit, Manhattan, KS
[3] Department of Plant Pathology, Kansas State University
[4] Department of Agronomy, Horticulture & Plant Science, South Dakota State University

The bread wheat (*Triticum aestivum*, 2n=6x=42)) genome, 17 GB size and 124,201 genes, is considered to be one of the largest and the most complex genomes among crop plant species; it is also a polyploid consisting of three different subgenomes (AABBDD). De-novo and re-sequencing are both extremely complicated processes and require detailed bioinformatic data analyses. The genotyping-by-sequencing (GBS) is based on simplifying the complexity of genomes using restriction enzymes with no requirement for a reference genome for detecting SNPs. We used GBS for genotyping durum wheat (T. turgidum, 2n=4x=28, genomes AABB) and bread wheat accessions. Eighty-two durum wheat accessions belonging to 13 botanical varieties, mainly from Azerbaijan and Central Asia, were genotyped. We identified 1,058 SNPs with less that 50% missing data and studied the genetic variability in 71 accessions of *Triticum turgidum ssp durum*. A dendrogram was constructed that classified genotypes from the same plant variety into congenial clusters. Improved varieties of Azerbaijani origin were genetically close in contrast with the relatively different U.S. durum cultivar Langdon. We genotyped 102 accessions of *Triticum aestivum* using GBS and 411 SNPs with less than 50% missing data were used for diversity analysis.

PECULIARITIES OF LYCOPENE β-CYCLASE GENES EXPRESSION, DEPENDING ON THE COMBINATIONS OF ALLELES THAT DETERMINE THE ACCUMULATION OF PIGMENTS IN THE *SOLANACEAE*

O.G. Babak*, *N.A. Nekrashevich, T.V. Nikitinskaya, K.K. Yatsevich, A.V. Kilchevsky

The Institute of Genetics and Cytology, the National Academy of Science of Belarus; Minsk, Belarus
e-mail: babak_olga@mail.ru

Beta allele of *CYC-B* gene in tomato and *LCY-B* gene in sweet pepper encode synthesis of chloroplast-specific lycopene β-cyclase that determine β-carotene accumulation in fruit. Peculiarities of lycopene β-cyclase genes expression in the *Solanaceae* were studied in *Solanum lycopersicum* and *Capsicum annuum* at early stages of fruit ripening. RT-PCR was performed on Bio-Rad CFX96 thermocycler. The analysis of the transcript expression level was fulfilled by BioRad CFX Manager 3.1 program.

The expression levels of *CYC-B* gene in tomato and *LCY-B* gene in sweet pepper were evaluated depending on the combinations of fruit quality genes. The analysis was conducted in tomato samples with *B* (control), *B/nor*, *B/hp2^{dg}*, *B/nor/hp2^{dg}* allele combinations in the homozygous state, in sweet pepper samples with the following allele combinations: *LCY-B/Y^{-}* (control), *LCY-B/norc/Y^{-}*, *LCY-B/Y^{+}*; *LCY-B/norc/Y^{+}*.

Mutations *nor* (*non-ripening*) and *norc* (*nor capsicum*) in LeNAC-NOR transcription factor lead to inhibiting ripening in fruits. The effect of *hp2^{dg}* mutant is characterized by an increase in the number and sizes of chloroplasts that is the basis for an increase in the carotenoid synthesis in tomato fruits during maturation. *Y* gene alleles encode bifunctional capsanthin-capsorubin synthase enzyme (*Ccs*), its active allele (*Y^{+})* is involved in antheraxanthin to capsanthin and violaxanthin to capsorubin conversion in pepper fruit. The absence of an active allele (*Y)* in the genotype leads to the accumulation of yellow pigments – violaxanthin and neoxanthin.

A decrease in the level of *Beta* allele expression by 1.73 times was found in tomato genotype with *nor* allele. Adding *hp2^{dg}* allele in the genotype resulted in the expression level increase by 1.55 times in *B/hp^{2dg}* combination, and by 1.37 times in *B/nor/hp^{2dg}* combination as compared to the control one. The data confirm a decrease of *nor* allele negative influence on the carotenoid synthesis of tomato at genotype saturation with *hp^{2dg}* allele.

It was shown that the expression level of *LCY-B* gene of sweet pepper in the control (*LCY-B/Y^{-}*) is above 1.95 and 2.08 times, as compared to *LCY-B/norc/Y^{-}* and *LCY-B/norc/Y^{+}* allele combinations respectively, but by 1.82 times less than in *LCY-B/Y^{+}* combination. This shows a decline in the expression level of *LCY-B* allele under the influence of *norc* allele, and an increase of the expression level in the presence of active *Y^{+}* allele.

STUDY ON GENETIC CONTROL OF EARLY INFLORESCENCE DEVELOPMENT IN BREAD WHEAT (*T. aestivum* L.) THAT DETERMINES INFLORESCENCE ARCHITECTURE AND YIELD

O.B. Dobrovolskaya [1,2]***, K.I. Popova*** [1]***, Yu.L. Orlov*** [1,2]***, A.A. Krasnikov*** [3]***, P. Martinek*** [4]

[1] Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
[2] Novosibirsk State University, Novosibirsk, Russia
[3] Central Siberian Botanical Garden, SB RAS, Novosibirsk, Russia
[4] Agrotest Fyto, s.r.o., Kroměříž, Czech Republic
Email: oxanad@bionet.nsc.ru

Features of plant inflorescences development can influence the formation of economically valuable traits in important crops, which include bread wheat *Triticum aestivum* L. The inflorescence of wheat is a spike with the main axis (spike rachis) carrying lateral sessile spikelets that are directly attached to the rachis and a terminal spikelet. The study of the genetic factors that determine the structural features of the spikelet, a reduced branch bearing the reproductive organs (the florets), is important to understand the mechanisms underlying plant developmental processes and has obvious practical importance. In wheat, difference in the number of fertile florets per a spikelet is genetically determined by the level of ploidy and interspecific variability, but the genes that determine this trait are currently little studied. The aim of our research was to identify genes that control the development of the bread wheat inflorescence and affect the number of fertile florets in a spikelet. To identify the genetic factors that determine the formation of the fan-shaped “flabellum” multifloret spikelet in wheat, molecular-genetic mapping using the Illumina Infinium 15 k Wheat platform was performed. It was found that several genes located on chromosomes 5AL, 2AS, and 4D control the formation of fan-shaped «flabellum» spikelet in wheat. Results of SEM analysis showed that the formation of the "flabellum" spikelet was associated with the features of spikelet development.

This work was supported by RFBR grants N 15-04-05371.

CYTOGENOMIC PROBLEMS OF HETEROPLASMATIC HEXAPLOID TRITICALE

I.A. Gordei [1], O.M. Lyusikov [1], I.S. Gordei [1], Yu.A. Lipikhin [2], E.V. Evtushenko [2], A.V. Vershinin [2]

[1]Insitute of Genetics and Cytology NASB, Minsk, Belarus
[2]Institute of Molecular and Cellular Biology SB RAS, Novosibirsk

Triticale (x*Triticosecale* Wittm.) is a successful synthetic allopolyploid between wheat and rye with great productivity potential. Hexaploid triticale with the wheat cytoplasm (ssp. *Triticale Tscherm.,* $^{T/}$AABBRR, 2n=6x=42) is used in commercial objectives. However, the genetic potential of the rye adaptability is incompletely realized in these triticale. We aimed to obtain the rye-wheat amphidiploids with the rye cytoplasm – secalotriticum (ssp. *secalotricum* Rosenst., et Mittelst., syn. *secalotriticum*, $^{S/}$RRAABB, 2n=6x=42) in order to achieve the balanced expression of the original species genetic systems. Secalotriticum was created by hybridization of the tetraploid rye ($^{S/}$RRRR, 2n=4x=28) to hexaploid triticale ($^{T/}$AABBRR, 2n=6x=42) followed by a single backcross of the rye-triticale hybrids F_1 ($^{S/}$RRABR, 5x=42) to triticale. Here, triticale has been used as an intermediary species (bridge species) – a source of the wheat genomes, and the inhibitor of the rye S-RNase, allowing to overcome the one-way progamic rye-wheat incompatibility.

The bases of secalotriticum recombination potential are maximum preservation of hybrids F_1 genotypic specificity and rye genomes heterogeneity of various origins as a result of a single backcrossing. Formation of secalotriticum genome takes place on the basis of partially unreduced 21-chromosome gametes (pUG) of pentaploids F_1 that have the balanced chromosomes set of parent species haplogenomes (7(R) + 7(A) + 7(B)). The meiosis stability and genetic diversity of secalotriticum determined by the type of cytoplasm and cytogenetic factors inherited from the genotypes of rye-triticale hybrids F_1: mainly desynaptic univalent origin, preservation of a unipolar orientation of the centromere and the first meiotic reducing division, the second meiotic equational division and regular polar segregation of chromosomes. Secalotriticum is characterized by the meiotic stabilization in $F_{5\text{-}7}$ (15,2-16,7% abnormal meiocytes on the average) at the level of the original forms of hexaploid triticale (~4,6%) and tetraploid rye (12,9%) to 9,4% in the $F_{7\text{-}9}$. Recombination selection of secalotriticum is the most effective on the basis of rye cytoplasm because crossing with triticale reduce stability. Secalotriticum is a source of stability for triticale meiosis.

The correct chromosomes segregation during meiosis of the hybrid plants is largely determined by the structural and functional organization of parental centromeres. We analyzed the molecular structure of a key protein of the centromeres – centromeric histone H3 (CENN3). This protein is responsible for the kinetochore assembly and connection the chromosomes to the spindle at mitosis and meiosis. The molecular structure of the wheat and rye CENH3s is characterized by a high level of similarity, which achieves 99% under comparison between the rye cultivar “Verasen” and the triticale cultivar “Mihas” on nucleotides and aminoacides levels. We were able to identify the specific aminoacides in the structure of CENH3 that served as markers of the level of gene expression of the parental forms in TSENN3 secalotriticum. It was found that the both parental forms of CENH3 are synthesized in the genome of the hybrid plants. The level of the typical rye CENH3 transcripts of secalotriticum corresponded to the level of transcription in the original cultivar "Verasen" and showed a stable tendency to excess in comparison with the transcription level of the rye forms in triticale cultivar "Mihas".

Thus, we have obtained a stable secalotriticum that is comparable to or exceed the original triticale in terms of productivity, is characterized by a wider variability, and closer to rye in some morphological characters. The results of the research are the theoretical and experimental substantiation of breeding technology of secalotriticum.

MOBILE APPLICATION FOR HIGH THROUGHPUT GRAIN PHENOTYPING

M. A. Genaev [1*], ***E. G. Komyshev*** [1], ***D. A. Afonnikov*** [1,2]

[1] *Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia*
[2] *Novosibirsk National Research State University, Novosibirsk, Russia*

**e-mail: mag@bionet.nsc.ru*

Grains morphometry in cereals is an important step in selecting new high-yielding plants. The manual assessment of parameters such as the number of grains per ear and their size is laborious. The solution to this problem is image-based analysis, which can be performed using a desktop PC. The effectiveness of this analysis in the field can be improved through the use of mobile devices. We propose a method for the automated evaluation of phenotypic parameters of grains using mobile devices running the Android operational system. The experimental results show that this approach is efficient and sufficiently accurate for the large-scale analysis of phenotypic characteristics in wheat grains.

In this work, we present a mobile application, SeedCounter, for the Android platform that enables the automated calculation of morphological parameters of wheat grains using mobile devices "in the field" (conditions without computer facilities). The application estimates the number of grains scattered on a sheet of A4, Letter, Legal, A3, A4, A5, B4, B5 or B6 paper and morphological parameters such as the length, width, area, and distance between the geometric center of mass of the grain and the point of intersection of its principal axes.

The algorithm is implemented using the OpenCV image processing library and consists of several steps: 1) Paper sheet recognition; 2) Grains identification; 3) Grains morphometry. Grain recognition algorithm implemented on the Java programming language.

We conducted several seed counting tests under controlled lighting conditions and daylight to estimate the software performance. We demonstrated that the SeedCounter's performance enables it to estimate the number of grains in the image and their sizes with high accuracy, but the performance of the method is dependent on the lighting conditions.

The SeedCounter application is available on GooglePlay:
https://play.google.com/store/apps/details?id=org.wheatdb.seedcounter

The work supported by RFBR grants 16-37-00304, 16-34-00688.

IDENTIFICATION OF GENES CONTROLLING BLACK PIGMENTATION IN CEREALS

A.Y. Glagoleva [*1,2], ***G.V. Vasiliev*** [1], ***N.V. Shatskaya*** [1], ***N.A. Shmakov*** [1,2], ***D.A. Afonnikov*** [1,2], ***O.Y. Shoeva*** [1], ***A. Börner*** [3], ***E.K. Khlestkina*** [1,2]

[1] Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
[2] Novosibirsk State University, Novosibirsk, Russia
[3] Leibnitz-Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany

[*]e-mail:glagoleva@bionet.nsc.ru

Some crop species may have‘melanin-like’ black pigmentation of seed. Chemical nature of this ‘melanin-like’ black pigmenthas not been explored yet, because of its complex structure and with standing to almost all solvents. Identification of genetic networks participating in trait formation is a key to understanding metabolic processes (and probably substances) involved. Analysis of differentially expressed genes (DEGs) is necessary for this. Barley is a suitable model for investigation of ‘melanin-like’ black pigmentation of seed. The *Blp* locus associated with black pigmentation of lemma and pericarp has been mapped to the long arm of chromosome 1H, and near-isogenic lines (NILs) for this gene are available.

At the first step we elucidated the involvement of the flavonoid biosynthesis pathway in production of black pigment using NILs having different color of pericarp and lemma. Our data demonstrated that none of the six flavonoid biosynthesis genes analyzed (*Chs*, *Chi*, *F3h*, *F3’h*, *Dfr*, *Ans*) is expressed significantly in BLP (black lemma and pericarp), whereas these genes where up-regulated in PLP (purple lemma and pericarp) line. It can be concluded that neither anthocyanins nor any other flavonoids participate in black pigmentation of barley grain.

At the second step, RNA-seqwas exploited for identification of genes differently expressed in lemma and pericarp of the NILs having different alleles in the *Blp* locus.

Genes with high level of differential expression in BLP line were identified in following pathways: wax esters biosynthesis, flavonol biosynthesis, 2,4,6-trinitrotoluene degradation, cuticular wax biosynthesis, sphingolipid biosynthesis, cytokinin-O-glucosides biosynthesis. In the report, these results are discussed in relation to putative mechanisms of black pigment formation.

This study is supported by the Russian Science Foundation (No 16-14-00086).

THE APPLICATION OF GENOMIC INNOVATION IN PLANT

Jianbo Jian

BGI Genomics Co., Ltd, Shenzhen, China

With the development of sequencing technology and assembly software, most of the important crop reference genomes have been finished. With the sequencing and analysis cost decreased continuously, a new era of genomics is coming. More and more reference genomes will be updated based on comination technology. We have successful experience in the Rice, the Maize, the Soybean, the Wheat, the Lupin projects. Combined multiple components such as high-throughput techniques, HIC, 10 X, cost-effective protocols, global integration of genetic and environmental factors and precise knowledge of quantitative trait inheritance. The genetic maps of many crops are getting increasingly dense; HapMap and GWAS (Genome Wide Association Study) project have being done. All of those genomic technolgy would be a great innovation application in plant.

Here, we obtained the lupin reference genome and re-sequencing nine representative lupin cultivars.The re-sequencing data together with the reference genome sequence data were used in marker development, which revealed 180,596 to 795,735 SNP markers from pairwise comparisons among the cultivars. A total of 207,887 markers were anchored on the lupin genetic linkage map. Marker mining obtained an average of 387 SNP markers and 87 InDel markers for each of the 24 genome sequence assembly scaffolds bearing markers linked to 11 genes of agronomic interest. Using the R gene PhtjR conferring resistance to phomopsis stem blight disease as a test case, we discovered 17 candidate diagnostic markers by genotyping and selecting markers on a genetic linkage map. A further 243 candidate diagnostic markers were discovered by marker mining on a scaffold bearing non-diagnostic markers linked to the PhtjR gene. Nine out from the ten tested candidate diagnostic markers were confirmed as truly diagnostic on a broad range of commercial cultivars. Markers developed using these strategies meet the requirements for broad application in molecular plant breeding.

TRANSCRIPTOME SEQUENCING AND GENE EXPRESSION PROFILING OF WHEAT CELL CULTURE DURING TRANZITION TO SOMATIC EMBRYOGENESIS

N.K. Bishimbayeva*[1], U. Kairov[2], CY. Li[3], N.O. Nakisbekov[4], A.N. Begzat[1,6], A. Molkenov[2], A.S. Amirbekov[4], A.O. Smagul[4], T. Kapasuly[1], A. Mitra[5], I.R. Rakhimbayev[1]

[1] Institute of Plant Biology and Biotechnology (IPBB), SC MES RK, Almaty, Kazakhstan
[2] Laboratory of bioinformatics and computational system of biology, Center for Life Sciences, National Laboratory Astana, Nazarbayev University, Astana, Kazakhstan
[3] Beijing Genomics Institute (BGI), Shenzhen, China
[4] B.A. Atchabarov SRI of Fundamental and Applied Medicine, Asfendiarov Kazakh National Medical University, Almaty, Kazakhstan
[5] Plant Pathology Department of University of Nebraska- Lincoln, Nebraska, USA
[6]Al-Farabi Kazakh National University, Almaty, Kazakhstan
*e-mail: gen_jan@mail.ru

Today, the most modern approach for study the gene expression is profiling of the entire transcriptome. The cell identity is defined by its transcriptome, i.e., by a complete set of expressed RNA transcripts. Profiling of the whole transcriptome is widely used to assess the relative gene expression in cells, tissues, organisms, or under different conditions.The main goal of this investigation is identification of differentially expressed genes by whole-transcriptomesequencing of wheat cell culture samples during induction of somatic embryogenesis. For this purpose the transcriptomes of 7-days wheat (cv. Kazakhstanskaya-10)embryogenic callihave been compared with samples of controlnonembryogenic tissues. Initial globular callus, cultured on MS media with 5,0 mg/l 2,4-D with normal level of mineral salts have been used as a control nonebryogenic sample. Control variant were compared with globular callus, transferred forsomatic embryogenesis induction on the nutrient medium with doubled concentration of salts and 5,0 mg/l 2,4-D.

All samples have been sequenced on next generation sequencing platform Illumina HiSeq. 27.31 GB of the nucleotides were generated as a result of sequencing. Sequencing reads were assembled in 106084 unigenes with a total length of unigenes - 120,285,635 nucleotides and an average length of 1,133 nucleotides. Indicator of GC-pairs content amounted to 50.45%. In the result of bioinformatics analysis, 1808 differentially expressed genes have been detected, which can beinvolved in early stage of somatic embryogenesis induction. Differentially expressed genes were analyzed using genome of *A.thaliana.* It should be noted, that only 419 genes were identified among 974 genes with increased expression. Whereas only 403 genes were identifiedamong the 834 genes with decreased expression.

Overall, transcriptome analyses of our novel model wheat system reveled genes associated with dramatic phenotypic differences in our system. These genes will allow us to further dissect the molecular interplay leading to our observed phenotypic states.

It is also interesting to note that our analyses identified many genes that are not in the database. It is possible that these are wheat specific genes and these genes will provide a direct wheat target. Our next step is to study these genes to understand their roles in more detail. We will also check wheat reference genome for unrecognized gene sequences.

As phenomenon of somatic embryogenesis is appeared to be an extreme reaction to stress (D. Dudits et al., 1995) leading to the surviving and propagation of living systems these studies will eventually allow us to reveal genes responsible to stress resistance and high productivity. This, in turn, will allow to produce better wheat crop that can be grown efficiently and in an environmentally friendly manner in Kazakhstan.

This work performed in the framework of fundamental research program №0149, Target Program Funding, IPBB, Science Committee, Ministry of Education and Science, Republic of Kazakhstan (2015-2017).

Keynote

GENOME SIZE VARIATION AND LONG TANDEM ARRAYS OF LTR RETROELEMENTS IN PLANTS

R.N. Kalendar

National Center for Biotechnology, Astana, Kazaкhstan

Email: ruslan.kalendar@mail.ru

Retrotransposable elements are widely distributed and diverse in eukaryotes and are a source for considerable genomic variation through direct transposition and/or through ectopic (i.e. non-allelic homologous) recombination events between transposable element copies, resulting in genomic rearrangements. Recently, we have identified large, structurally uniform retrotransposon groups in which no member contains the gag, pol, or env internal domains. These non-autonomous groups have been named LARDs (LArge Retrotransposon Derivatives) and TRIMs (Terminal Repeats in Miniature). The LARD and TRIM phylogenies mirror those of the host organisms for close and distant species. Because of the lack of protein coding capacity, these groups are non-autonomous in replication, even if transcriptionally active. Cassandra element belongs to TRIM. These retrotransposons universally carry conserved 5S RNA sequences and associated RNA polymerase (pol) III promoters and terminators in their long terminal repeats (LTRs). In this study, we identified multiple and long tandem arrays for Cassandra retrotransposon within all studied plant species and ferns, consisting at least 12 copies of repeated LTR and central part, typical as the cellular 5S rRNA genes. Cassandra element is not unique in forming the tandem arrays, SINE elements and as well as MITEs also form tandem repeats. Secondary structure Cassandra retroelement forms super-loop, in which the two LTR complementary to each other and can initiate local recombination, leading to multi-copy LTR and central Cassandra retroelement, this structure is universal for all Cassandra retroelement of different species. We observed Cassandra retrotransposon long tandem repeats in number of blocks distributed within all the chromosomes. Our results suggest that recombination events are the cause of wide variation of Cassandra copy number. It is therefore likely that Cassandra elements generate tandem repeats by multiplication mechanism similar to 5S rRNA genes or the telomere tandem repeats. Some of the types of ectopic recombination indicated the common occurrence of concerted events. Cassandra tandems arrays are highly dynamic, and can be removed or appeared during meiosis and mitosis.

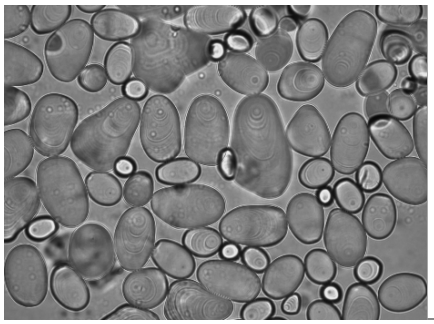
HIGH-THROUGHPUT MICROSCOPY-BASED PHENOTYPING OF POTATO STARCH GRANULES

Vadim K. Khlestkin

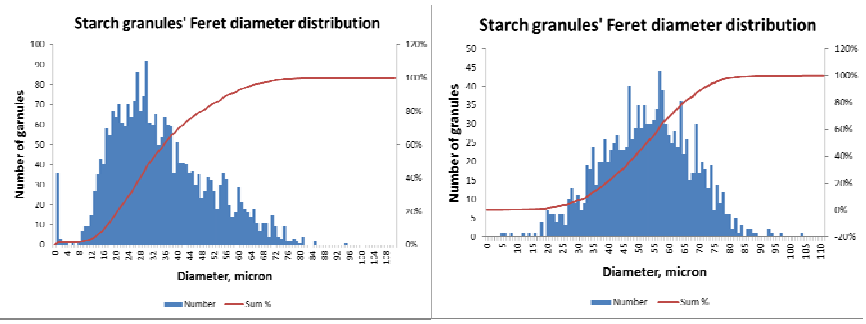
Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

Starch is an important organic feedstock easily available for human in industrial scale. Optimal physical and chemical properties of molecules comprising starch and starch granule morphology significantly vary in dependence on the technical scope. Molecular and supramolecular composition and structure are genetically regulated and may be considered as traits for selection. Combining genes in certain composition one may program potato plant to produce starch of predetermined structure and properties.

However, chemical and physical properties of potato starch as traits for selection are most often regulated by complicated gene network rather than single gene. In this work, we propose a high-throughput method for potato starch granules morphology measurement, tested on a set of ~ 50 cultivars and hybrids. This economical, simple, and easily available method based on microphotography and computer image analysis allows performing quick analysis of starch granules distribution by size and circularity with limited amount of starch. This method is suitable for phenotyping of large panels of potato cultivars used in genome-wide association studies (GWAS) or mapping populations in order to find QTLs related with starch granules. The proposed method also can be used for high-throughput phenotyping of hybrids during the breeding process aimed on development of cultivars for certain industrial starch application.



Microphotograph of potato starch granules



Granule size distribution difference for two potato hybrids

Keynote

GENETICS AND OMICS APPROACHES TO BETTER UNDERSTANDING REGULATION OF METABOLIC PATHWAYS UNDERLYING PIGMENTATION IN WHEAT AND BARLEY

O.Y. Shoeva [1], E.I. Gordeeva [1], N.A. Shmakov [1,2], K.V. Strygina [1,2], A.Y. Glagoleva [1,2], T.V. Kukoeva [1], N.V. Shatskaya [1], G.V. Vasiljev [1], A. Börner[3], D.A. Afonnikov [1,2], E.K. Khlestkina [1,2*]

[1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
[2]Novosibirsk State University, Novosibirsk, Russia
[3]Leibnitz-Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany

[*]e-mail: khlest@bionet.nsc.ru

Along with the main pigment chlorophyll plants can be colored with flavonoid or carotenoid pigments as well as other more rare pigments such as phytomelanins or betalains. These colored substances and their uncolored precursors are known as secondary metabolites required for the plant to survive in its environment (for communicating with other organisms or coping with abiotic stress). Here, we present results of comparative analysis of the sets of wheat and barley near-isogenic lines (NILs) differing by coloration traits as well as results of in silico analysis of flavonoid biosynthesis genes evolutionary rates. We have found that monocot and dicot plants differ by evolutionary patterns of the universal flavonoid biosynthesis genetic network. In addition some species-specific features were observed. Unexpectedly high selective pressure on certain gene in some species (such as F3h in wheat) is suggested to be an indirect evidence of importance of this gene activation as a key regulatory point of the pathway. We describe here for the first time the full sets of genes encoding for flavonoid biosynthesis MBW regulatory complexes in wheat and barley. We also identified genes related with poorly studied phytomelanin-like black and albino phenotypes of barley grain. In addition we present results of comparative physiological studies of the NILs, suggesting the coloration traits importance in coping with abiotic stress.

The study of evolutionary patterns of the FB genetic network was partially supported by RFBR (16-34-60052), the study of wheat MBW encoding genes was partially supported by RFBR (16-04-00912) and RAS Programme (0324-2015-0016), the study of phytomelanin-like black pigmentation of barley grain was partially supported by RSF (16-14-00086).

NEW ASPECTS OF WHEAT PHOTOPERIOD INSENSITIVE *PPD-B1* REGULATION AND INTERACTIONS

A.A. Kiseleva [1], ***E.A. Salina*** [1]

[1]Institute of Cytology and Genetics, Novosibirsk, Russia

e-mail: antkiseleva@bionet.nsc.ru

Wheat cultivars, different in photoperiod sensitivity up to total insensitivity, being well-adopted to environmental changes, were selected by breeders over extended periods. These cultivars have photoperiod insensitive *Ppd-1* genes, which are the key regulators of photoperiod sensitivity and flowering transaction of wheat. Different *Ppd-1* alleles result in variation of flowering time, supporting breeders to select appropriate cultivars with definite *Ppd-1* alleles for every environment. Photoperiod insensitive alleles of these genes are widely used in Europe, America, Australia and Asia. However, percent of cultivars with such alleles is very low in Russia.

In this study, we investigated early flowering cultivar Sonora and near-isogenic lines with photoperiod insensitive *Ppd-B1* allele. This allele has increased number of copies. We investigated structure of *Ppd-B1a* distinct copies and detected some SNPs confirmed difference between NILs and their sister lines with photoperiod sensitive *Ppd-B1* allele, the indel in promoter region distinguished the lines under investigation from other alleles with copy number increment, but revealed no polymorphisms between *Ppd-B1* gene copies.

Then we bioinformatically analyzed promoter regions of *Ppd-1* genes to identify cis-regulatory elements associated with flowering. Transcription factors, common for all the *Ppd-1* genes, were divided into three groups according to their input signal nature: circadian-clock regulated, light regulated and phytochrome regulated groups. Further improvement of its association is required. However, these transcription factors are to complement current scheme of wheat flowering transaction. We also detected regulatory elements, specific to *Ppd-B1* promoter. Among them, *MADS* genes are likely to be transcription factors, involved in *Ppd-B1a* expression regulation. The majority of *MADS* genes with binding sites in *Ppd-B1* promoter are known to be involved in flowering time repression. Therefore, we might propose *Ppd-B1a* with increased number of copies to continue expression in dark period because repressor quantity does not change.

To investigate interactions of *Ppd-B1* with other genes, we utilized quantitive Real-Time PCR and analyzed expression correlations of genes. We detected significant correlation of *Ppd-B1* and *Phy-C* in night period and proposed photoperiod insensitive *Ppd-B1* allele to influence *Phy-C* expression positively in dark. *Phy-C in silico* promoter analysis, together with data demonstrated increase of phytochrome protein quantity in lines with photoperiod insensitive *Ppd-1* alleles (Koshkin et al., 2004), supported this proposition.

We also detected difference in expression patterns of near-isogenic lines with photoperiod insensitive *Ppd-B1*. Line with introgression in 5B pericentromeric region from Sonora flowered three days earlier. Previously, using other genetic model we detected QTL in the discussed region of 5B chromosome and proposed some candidate genes to regulate wheat flowering time (Kiseleva et al., 2016). These findings provide us an opportunity to investigate 5B pericentromeric region in more details.

To sum up, detected gene interactions require further investigation and the discussed lines are a good model for the following study of wheat flowering pathways and a good source for improving modern wheat cultivars.

This study was supported by the Russian Scientific Foundation (Project No. 14-14-00161).

Keynote

BIOINFORMATICS ANALYSIS OF GENOME AND TRANSCRIPTOME STRUCTURES RELATED TO FREEZING AND DROUGHT RESISTANCE IN CROP PLANTS

Y.L. Orlov [1,2]***, O.B. Dobrovolskaya*** [1,2]***, A.O. Bragin*** [1]***, V.N. Babenko*** [1]***, M. Chen*** [3]

[1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
[2]Novosibirsk State University, Novosibirsk, Russia
[3]Zhejiang University, Hangzhou, China

e-mail: orlov@bionet.nsc.ru

Important problem of plant genomics is analysis of structure of transcripts and the genome organization of crop plants on the basis of integration of high-performance sequencing data. The analysis of structure of the genes connected with architecture of an ear in crop plants, morphological parameters of draught- and cold resistance for wheat can be added with the bioinformatics methods and data for model organisms. We present joint research project devoted to development of integrative computer platform for the analysis of high-performance sequencing data and publicly available computer genomics data. The mechanisms of drought resistance might be grouped into three categories: drought escape, drought avoidance and drought tolerance. However, crop plants use more than one mechanism at a time to resist drought. Drought escape is defined as the ability of a plant to complete its life cycle before serious soil and plant water deficits develop. Plants under drought condition survive by doing a balancing act between maintenance of turgor and reduction of water loss. The mechanisms of drought tolerance are maintenance of turgor through osmotic adjustment (a process which induces solute accumulation in cell), increase in elasticity in cell and decrease in cell size and desiccation tolerance by protoplasmic resistance. Such studies need molecular-genetics approaches and integration of available data. Fundamental basis of the researches is the analysis of molecular mechanisms of genes functioning connected with expression of cis-antisense transcripts. The expected results include development and adaptation of the computer database of potential genes and antis-sense transcripts in model organisms of plants – A.thaliana, rice, bread wheat. Integration of data in the project will include data of sequencing technologies RNA-seq and Hi-C (for Arabidopsis). With use of the developed programs and algorithms the general platform of the bioinformatics analysis in plant genomes using high-performance sequencing data will be developed.

The work was supported by RFBR (16-54-53064).

INVESTIGATING BARLEY NUCLEAR GENES CONTROLLING CHLOROPHYLL SYNTHESIS WITH RNA-SEQ

***N.A. Shmakov*[1,2], *G. V. Vasiliev*[1], *N. V. Shatskaya*[1], *A. V. Doroshkov*[1], *D.A. Afonnikov*[1,2], *E. K. Khlestkina*[1,2]**

[1] Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia;
[2] Novosibirsk State University, Novosibirsk, Russia
e-mail: shmakov@bionet.nsc.ru

Albinism in plants is characterized by lack of chlorophyll and results in photosynthesis impairment, abnormal plant development and premature death. These deviations are frequently encountered in interspecific crosses and tissue culture experiments. Analysis of albino mutant phenotypes with full or partial chlorophyll deficiency can shed light on genetic determinants and molecular mechanisms of albinism. One such mutant phenotype is barley i:Bw*Alm* line with tissue-specific albinism.

Poly-A RNA was extracted from spikelets of barley of Bowman line and i:Bw*Alm* line and sequenced using IonTorrent platform. Resulting short read libraries were mapped to *Hordeum vulgare* genome using TopHat and STAR aligners. Libraries were clustered with Cluster3 software. Differential expression search was conducted with cufflinks pipeline and edgeR package. Lists of genes with higher and lower level of expression in line i:Bw*Alm* were examined separately for enriched gene ontology terms from AgriGO database and significantly represented pathways from PlantCyc database. For a selected list of genes differential expression was checked with quantitative real-time PCR. Phenotypic characterization and chlorophyll distribution patterns were examined using chlorophyll fluorescence microscopy. *De novo* transcriptome assembly was performed using Trinity tool.

Microscopic analysis revealed segregation of cells in spikelets to chloroplast-containing and chloroplast-deficient. Our results demonstrate that plants of i:Bw*Alm* line have decreased expression levels of plastid genes. Statistically significant differential expression was observed for several plastid operons containing protein coding genes, rRNA and tRNA-coding genes. We identified nuclear genes with differential expression in two barley lines. Functional differentiation between genes with higher and lower levels of expression in i:Bw*Alm* line was detected. As was demonstrated with gene ontology analysis, genes with lower level of expression in i:Bw*Alm* line are mostly associated with photosynthesis and chlorophyll synthesis, while genes with higher expression level are functionally associated with vesicle transport. Differentially expressed genes are involved in a number of metabolic pathways, most represented being Calvin-Benson-Bassham cycle. Finally, *de novo* assembly of transcriptome contains several transcripts, not annotated in current *H. vulgare* genome version.

Our results provide new information about genes that could be involved in formation of albino lemma and pericarp phenotype. Results obtained demonstrate the interaction between nuclear and chloroplast genomes in this physiological process.

This work was supported by the RFBR (№ 16-34-00924, bioinformatics data analysis), RSF (№ 14-14-00734, microscopic images preparation and analysis).

NGS OF BARLEY ORGANELLE GENOMES

N.V. Lukhanina, M.G. Sinyavskaya, V.S. Pankratov, A.D. Liaudansky, I.M. Goloenko, A.M. Shymkevich, N.G. Danilenko, O.G. Davydenko

Institute of Genetics and Cytology, National Academy of Sciences of Belarus, Minsk, Belarus

e-mail: cytoplasmic@mail.ru

Presence of three interacting genetic systems: nucleus, mitochondria and chloroplasts, is a distinctive plant cell feature. In the present study, NGS (next generation sequencing) was performed to identify differences in organelle genome nucleotide sequence that mayimpact key processes of plant cell activity, photosynthesis and respiration. For this purpose we used the created the model of lines with substituted nuclear genomes – alloplasmic lines, that was formerly created in our laboratory.

Formerly we detected the diversity in RFLP profiles of mt and cp DNA in the collection of alloplasmic barley lines and their parental forms, then we showedthe differences in structural and functional characteristics of photosynthetic apparatus. Some of these lines - cultivar Visit (*Hordeum vulgare* ssp. *vulgare*) andalloplasmic lines Visit $(W3)^8$ (Atlit 37, Israel) and Visit $(W4)^8$ (Atlit 55, Israel) (with *Hordeum vulgare* ssp. *spontaneum* cytoplasm) were studied.

Paired-end sequencing of purified organelle DNA as a template was performed using Illumina MiSeq. Assembling complete genome sequence was performed by contig aligning according to the reference chloroplast (PubMed NC008590) and mitochondrial (PubMed AP017301) barley *H.v.* ssp. *vulgare* genomes. As a result, we obtained data on both cultural *H.v.* ssp. *vulgare* and wild *H.v. ssp*. *spontaneum* barley organelle genomesnucleotide sequence relative variability. 48 differences in the nucleotide sequence of chloroplast DNA were revealed, bothbetween chloroplast DNA of wild *H.v*. ssp. *spontaneum* and cultivar Visit (39), and between the lines with different cytoplasms of *H.v.* ssp. *spontaneum* (9), as well. Polymorphism was detected in both coding and noncoding regions of different genes, as well as in intergenic regions. Synonymous substitutions in exons were identified in transcription and translation apparatus genes (*rpoC2*, *infA*) and NADH dehydrogenase (*ndhD*, *ndhA*, *ndhH*).

Nonsynonymous substitution was found in the exon of *infA* gene (the position 76 884, G → A substitution leads to Ser→Leu) in the chloroplast genome of the lines with *H.v.* ssp. *spontaneum* W3 and W4cytoplasms. *InfA* gene is the chloroplast localized translation initiation factor 1.

In contrast to chloroplast DNA, mitochondrial DNA of the *H.v.* ssp. *spontaneum* displayed 9,6 times less differences from*H.v.* ssp. *vulgare*. All differences identified in mitochondrial DNA were observed between the *H.v.* ssp. *spontaneum* and cultivar Visit only, while *H.v.* ssp. *spontaneum* lines did not differ from each other. Point substitutions were found in noncoding regions only.

At present, the obtained results are verifying. A comparative study of DNA nucleotide sequencesin alloplasmic barley lines and parental varietiesis the starting point for further investigation of nuclear and cytoplasmic genome interaction mechanisms and their co-adaptation.

DUPLICATED GENES IN POLYPLOID PLANT SPECIES - CASE STUDIES IN WHEAT AND POTATO

K.V. Strygina, O.Y. Shoeva, E.I. Gordeeva, E.K. Khlestkina

Federal Research Center Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

e-mail: pushpandzhali@bionet.nsc.ru

Genomes of polyploid plant species, having an increased number of genes copies, are an attractive model for studying functional and evolutionary features of the duplicated genes. Here, we report results of a case study on flavonoid biosynthesis (FB) genes in allohexaploid wheat (*Triticum aestivum* L.) and autotetraploid potato (*Solanum tuberosum* L.). FB regulatory network is a convenient model system, underlying intraspecies variability by coloration traits. There are three types of FB regulatory factors MYB, bHLH and WD40, which compose MBW complex necessary for activation of the expression of FB structural genes in plants.

We used a wide range of bioinformatics and molecular genetics tools to characterize MBW components of wheat and potato. The bHLH-encoding gene (*TaMyc1*), necessary for activation of anthocyanins (colored flavonoids) biosynthesis in wheat grain pericarp, was isolated for the first time. A total of 10 copies of this gene were identified in homoeologous groups 2 and 4 chromosomes. Their transcriptional activity in different parts of wheat plant was investigated. The WD40-encoding genes (at least 2 copies) were also isolated and characterized for the first time in wheat. Annotation of 7 copies of the known wheat MYB-encoding gene *TaC1* was carried out. In potato, information about known MYB-encoding genes was used to identify allelic diversity among cultivars differing by tuber skin and flesh color and to develop allele-specific markers for expression analysis. Overall, the results obtained suggest that the duplicated FB genes are maintained in wheat and potato due to the copies diversification. The presence of duplicated regulatory genes is responsible for diverse patterns and combinations of coloration traits in the investigated species.

The part of the study on wheat genes was supported by RFBR (16-04-00912) and the RAS Programme (0324-2015-0016), the part of the study on potato genes was supported by the Russian Science Foundation (16-16-04073).

FACTORES AFFECTING SYNONYMOUS CODON USAGE BIAS IN CHLOROPLAST GENOME OF *GOSSYPIUM THURBERI* AND *GOSSYPIUM ARBOREUM*

S. Hasaninejad [1], ***F. Talat*** [2]

[1] Islamic Azad University of Urmia, Urmia, Iran
[2] West Azerbaijan Agricultural and Natural Resources Research and Education Center, AREEO, Urmia, Iran

email: farshid.talat@gmail.com

Analysis of codon usage is very important to optimize the production of proteins in gene expression system. Chloroplast has special importance due to its small size and high copy number of genome. *Gossypium spp.* is the most important fiber crop in the modern world. In this research, the complete nucleotide sequence of the chloroplast genomes of two wild cotton species was studied, and then analyzed using Codon W software. Synonymous codon usage of 57 protein coding genes in chloroplast genome of *Gossypium thurberi* and *Gossypium arboreum* was analyzed for the first time to find out the possible factors contributing codon bias. All preferred synonymous codons were found to use A/T ending codons as chloroplast genomes are rich in AT. Correspondence analysis and method of effective number of codon as Nc-plot were conducted to analyze synonymous codon usage. ENC Vs GC3 plot grouped majority of the analyzed genes on or just below the left side of the expected GC3 curve indicating the influence of base compositional constraints in regulating codon usage. According to the corresponding analysis, codon bias in the chloroplast genome of *Gossypium thurberi* and *Gossypium arboreum* are related to their gene length, mutation bias, gene hydropathy level of each protein, gene function and selection or gene expression only subtly affect codon usage. This study provided insights into the molecular evolution studies.

GENOTYPING OF POPULATION GENERATED BY*POPULUS TREMULA* × *P. ALBA* CROSS

***M. V. Lebedeva* [*1,2], *A. V. Zhigunov* [2], *P. S. Ulianich* [1,2], *D. M. Voitsekhovskii* [2], *E. K. Potokina* [1,2]**

[1] N. I. Vavilov Institute of Plant Genetic Resources (VIR)
[2] Saint-Peterburg State Forest Technical University

*E-mail: marilistik@mail.ru

The *Populus* genus has a significant ecological and economic importance. Some species of *Populus* are cultivated worldwide due to their fast growth, high stress tolerance, asexual reproductionand applicable to demands of pulp, paper and biofuel production.

In April of 2016 we carried out cross between *P. tremula* and *P. alba* – widely distributed Eurasian poplarspecies, whose hybrids are very promising in forest cultivation. Germinated seeds were planted in ground. After vegetation season we measured height of each 473 trees and collected leaves for DNA extraction. Nearly 100 trees were randomly chosen for genotyping as mapping population to construct a linkage map of the *P. tremula* and *P. alba.*

For population genotyping we used RADSeq (Restriction-site associated DNA sequencing) – a powerful NGS-based technology, which allows to reveal a large amount of SNP, single nucleotide polymorphism.

CONSTRUCTION AND UTILIZATION OF THE HEXAPLOID WHEAT GENETIC MAP *PAMYATI AZIEVA X PARAGON*

K. Yermekbayev [1], ***Y. Turuspekov*** [1], ***M. Ganal*** [2], ***J. Plieske*** [2], ***S. Griffiths*** [3]

[1] Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan
[2] TraitGenetics GmbH, Gatersleben, Germany
[3] John Innes Centre, Norwich, UK

The genetic map of 92 recombinant inbred lines (RILs) from the cross of Pamyati Azieva (Russia) and Paragon (UK) was constructed using 7K SNP Illumina array. Currently the genetic map is consisting from 4594 polymorphic SNP markers. The number of polymorphic SNP markers for 21 chromosomes varied from 401 markers in homeologic group 4 to 940 markers in homeologic group 2. The length of the map varied from 17 cM in chromosome 4D to 218 cM in chromosome 3B with total overall length 2724,4 cM for all chromosomes. In addition, 158 KASP markers were added to the genetic map in order to improve the genetic resolution.

The mapping population (F_8) was grown in greenhouse (Norwich, UK) and field (Almaty region, Kazakhstan) conditions. The initial trials allowed identification of three QTLs associated with plant height in GH condition. The plant height QTLs were mapped on chromosomes 2B, 5A and 6A. Genetic analysis of yield components from the field trials is underway. Seeds of the mapping population was multiplied and provided to breeders in Northern region of Kazakhstan for further use in identification of important QTLs associated with productivity and grain quality.

The study supported by ADAPTAWHEAT project funded by 7th EU FP and grant number 1784/GF funded by the Ministry of Education and Sciences of the Republic of Kazakhstan

GROWTH AND IMMUNITY STIMULATING ACTIVITY OF EXTRACELLULAR POLYSACCHARIDES FROMWHEAT CELL CULTURE

N.K. Bishimbayeva, M. Tastan, A. Murtazina, M. Rakhmedova, Z. Dossova, M. Yugai, M. Baimenov, S.D. Demesinova

RSE "Institute of Plant Biology and Biotechnology" MES RK, Almaty,
e-mail: gen_jan@mail.ru

Growth regulative and protective activity of extracellular polysaccharides (PS) isolated from wheat cell culture were investigated by the use of ten agricultural crops (wheat, barley, corn, rape, tomato, cucumber, watermelon, melon, soybean, cotton). For the investigation of growth-regulative activity seeds of agricultural crops werepreliminary soaked into polysaccharide solutions in different concentrations (0,1, 0,01, 0,001 and 0,0001 mkg/ml). Then seeds were removed from polysaccharide solution and growed up in water during 5 days at 26 C° and 16-hours photoperiod. During the growth process we studied the energy and percentage of seeds germination, measured the length of shoots and roots. To identify the protective activity of PS, we determined for each crop sublethal doses of stress factors – salt and osmotic, initiated by different concentrations of NaCl and saccharose, accordingly. Seeds, preliminary soaked in PS solutions, were grown in solutions with sublethal concentrations of NaCl and saccharose.

Considerable differences in growth-regulative and protective activity of PS have been showndepending on various plant species. Very low (nanomolar) concentrations of PS – 0,001 and 0,0001mkg/ml, showed stimulating effect on the seedlings growth of all investigated crops. As well as medium concentrations of PS – 0,01mkg/ml, stimulated the growth of seedlings in tomato, barley and cucumber. High concentration of PS – 0,1mkg/ml, stimulated the growth of seedlings in cotton and rape. In general, under the PS influence, the growth of shoots increased by 2-4 times, the growth of roots – from 0,5 to 5,5 times in comparison to control (H_2O without preliminary soaking in PS), depending on the crop. All tested concentrations of PS have shown to accelerate germination of seeds, particularly, very low (nanomolar) concentrations – 0,0001mkg/ml. For example, percentage of germination for tomato, watermelon and wheat elevated from 50 to 100%, for rape –from 20 to 75%.

Under the salt and osmotic stress all PS concentrations have been found to be a physiologically active, in particular, in medium (0,01mkg/ml) and very low (nanomolar 0,001; 0,0001mkg/ml) concentrations. During osmotic stress PS demonstrated protective activity as the growth of shoots increased 2-3 times, the growth of roots – 3-4 times, compared to control (saccharose without preliminary soaking in PS solutions). We have shown capability of extracellular PS to increase germination of seeds under the salt and osmotic stresses as well. Under the salt stress protective activity of PS was found in medium -0,01mkg/ml, and very low – 0,001 and 0,0001 mkg/ml concentrations. Seeds germination increased from 10-40% to 50-100%. Protective activity of PS during osmotic stress is being expressed in very low (nanomolar) concentrations – 0,001 and 0,0001 mkg/ml. Seeds germination, overall, increased from 12-35% to 60-75%, compared to control, depending upon the crop.

The data obtained make it possible to propose extracellular polysaccharides for use in biotechnology and agricultureas a biostimulants of plant growth and immunitywith the activity in nanomolar concentrations.

This work performed in the framework of fundamental research program №0149, Target Program Funding, IPBB, Science Committee, Ministry of Education and Science, Republic of Kazakhstan (2015-2017).

MOLECULAR EVOLUTION ANALYSIS OF GENETIC NETWORK RELATED TO PLANT TRICHOME DEVELOPMENT

D.K. Konstantinov [1,2], ***A.V. Doroshkov*** [2], ***D.A. Afonnikov*** [2]

[1]Novosibirsk State University, Novosibirsk, Russia

[2]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

Trichomes are involved in many significant functions such as the transpiration, thermoregulation and protection from insect attacks. On the other hand specialized cell formation is an fruitful model system for analyzing the molecular mechanisms of plant cell differentiation, including cell fate choices, cell cycle control, and cell morphogenesis. In plants, epidermal cells are easily accessible and allow in vivo study. Unicellular trichome formation is a classical experimental model for identification of the activator–inhibitor and the activator–depletion pattern formation models, studying the interplay between cell cycle and cell differentiation and numerous of genes involved in these processes were found. However, the evolution of specialized epidermal cell formation genetic network remains unclear. In this study, we analyze the phylogenetic relationships of genes associated with the formation of trichomes and root hairs from various species of flowering plants.

Using the text mining technology we reconstructed the network of interactions between known leaf pubescence genes using *A. thaliana* as a model organism. The genetic network model was clarified by the iterative improvement based on gene co-expression data. For each node was performed extraction of sets of homological sequences presets from databases was carried out using the reciprocal BLAST search. Multiple sequence alignment was conducted with MAFFT algorithm. The PhyML maximum likelihood algorithm was used to reconstruct the phylogeny and bootstrap resampling technique was used for testing the topology. Genetic networks containing target genes were reconstructed using Cytoscape and Pathway Studio software.

As a result, work has been traced the main stages of gene network evolution, predicted time of appearance of its components. Our results argue that there is a fraction of genes involved in the formation of trichomes passed several relatively young duplication events and do not reveal a direct correspondence between monocotyledonous and dicotyledonous plants. Also, this facts justify that part of the cellular morphogenesis mechanisms evolved independently in dicots and monocots which reflects morphology differences. At the same time, we observe a good correspondence between studied genes of cell morphogenesis inside dicotyledonous as well as monocotyledonous clades. This allowed us to find orthologous genes in wheat genomic sequences and predict its chromosome localization to compare with known leaf hairiness QTLs.

This study was funded by Russian Science Foundation grant №14-14-00734.

GENOTYPING WHEAT VARIETIES WITH DIFFERENT GENOTYPING ARRAYS

J. Plieske **, *E.-M. Graner, A. Polley, M.W. Ganal***

TraitGenetics GmbH. Gatersleben, Germany

e-mail: plieske@traitgenetics.de

An overview about the allelic diversity of hexaploid wheat (*Triticum aestivum*) with large marker sets is instrumental for a detailed analysis of allelic diversity in the genome and specific genomic regions linked to important agronomic traits. In order to obtain such information, we have genotyped a large set (>500) of wheat varieties with a number of genotyping arrays including the 90K Illumina Infinium array, the Affymetrix 35K Wheat Breeders array, and a new 135K Affymetrix array generated with SNPs identified from Exon sequence capture. Altogether significantly more than 100,000 polymorphic markers were evaluated with all three arrays together. We present results concerning the technical quality of the respective markers, the genomic distribution of the analyzed markers on the arrays and the general usefulness of the different technologies. Furthermore, we show data concerning the allelic diversity and haplotype structure that is detected with these three arrays in European wheat varieties. Implications of the results for the general genotyping of wheat and the use of genotyping arrays for wheat breeding are also discussed.

CHARACTERIZATION OF A CHLOROPHYLL MUTANT, *TIGRINA,* IN RYE

O.B. Dobrovolskaya [1,2] , K. Morozova [1,2], K.I. Popova [1], A.E. Dresvyannikova [2], A. Börner [3], M.S. Röder [3], E.B. Kiseleva [1], A.V. Voylokov [4]

[1] Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
[2] Novosibirsk State University, Novosibirsk, Russia
[3] Leibniz Institute of Plant Genetics and Crop Plant Research, Gatersleben, Germany
[4] Vavilov Institute of General Genetics RAS, St. Petersburg, Russia
[*]e-mail: oxanad@bionet.nsc.ru

Leaf is the main important plant photosynthetic organ, and efficiency of photosynthesis in leaves influences crop productivity. Leaf color mutants are important genetic resources for studying the molecular mechanisms that regulate leaf photosynthesis and photorespiration. The aim of the present study was to characterise a rye mutant, *tigrina,* using molecular genetic tools and electron microscopy. The rye *tigrina* mutant is characterised by transversal yellow stripes on leaves. It was shown that this trait is under the control of a recessive allele at a single locus. The *tigrina* (*ti*) locus was placed on chromosome 5R, using molecular-genetic mapping. Analysis of cell ultrastructure showed that morphological changes in the color of leaves were associated with structural disruptions of chloroplasts, photosynthetic organelles of the plant cell. These multiple changes of chloroplast structure included alterations of chloroplast membranes, organization of grana, length of intergranal thylakoids, number of starch granules and lipid droplets in the stroma. The characterized *tigrina* mutant will be useful for further isolation of novel genes that are involved in processes of photosynthesis.

GENETIC DIVERSITY OF GRAIN LEGUME STUDIES WITH VARIOUS MOLECULAR MARKERS FROM DIFFERENT GENOMIC ORIGIN

O.B. Raizer, O.N. Khapilina, A.P. Novakovskaya, A.A. Amenov, A.Z. Danyarov, A.S. Turzhanova, R.N. Kalendar

RSE "National Center for Biotechnology", Astana, Kazakhstan

e-mail: 2008olesya@mail.ru

Legumes (Fabaceae) represent the second most important family of crop plants after the grass family, Poaceae, all together with 800 genera and 20,000 species. The importance of legumes is evidenced by their high representation in ex situ germplasm collections, with more than 1,000,000 accessions worldwide. A detailed knowledge of the genetic of the Fabaceae is essential for understanding the origin and diversification of this economically and ecologically important family of angiosperms. Our research aims to study genetic diversity of germplasm of major legume crops by molecular markers that represented different part of genome (retrotransposons and genes). Genome-wide sequence data was used for developing the high-throughput genotyping technology based on repeats (retrotransposons) and non-protein-coding DNA genome sequences. These molecular markers were used for study of genetic diversity and to assist in designing strategies to utilize the genomic information for legume crop improvement. It was analysed the germplasm collections of legumes of different countries. Retrotransposons were isolated and sequenced; long terminal repeat (LTR) primers were designed to obtain Inter-Retrotransposon Amplified Polymorphism (IRAP) fingerprints for Legumes species. The genetic variability within accessions of legumes species of each accessed by IRAP markers allowed separation of legumes species according to their geographical origin and botanical variety respectively. The utilization of germplasm use, in crop breeding is most importantly, the association of alleles with targeted phenotyping traits potentially will provide sufficient knowledge to the crop community to decide which accession(s) and which genomic segment(s) they need to target for improving a given trait in a particular legume crop species. It is also important to mention that information generated regarding germplasm of, whether genotyping, genome sequencing or phenotyping, should be made available as open access data." This would link seeds and genetic stocks directly to passport, genomic and phenotypic information, thereby engaging the creativity of geneticists and breeders. This will help crop communities across the world make the best use of the information generated available for crop improvement.

CARTOGRAM OF ZN CONTENT IN THE GRAIN OF WHEAT, BARLEY AND OATS ON THE BACKGROUND OF PRODUCTIVITY AND DROUGHT RESISTANCE

T.V. Savin [1], ***A.I. Abugalieva*** [1.2], ***I. Cakmak*** [3]

[1]*Kazakh Research Institute of Agriculture and Plant Growing, Kazakhstan*
[2]*Kazakh National Agrarian University, Kazakhstan*
[3]*Sabanci University, Turkey*
e-mail: Savintimur_83@mail.ru

Identification of *Zn*-deficient and *Zn*-excessive regions has been performed using data from different regions for the standard variety - Saratovskaya 29. Selection of biofortification genotypes for spring wheat breeding at the level of 45 mg/kg has been recorded in the following varieties: Karabalykskaya 2, Karabalykskaya 3, Kazakhstanskaya early ripening, Kazakhstanskaya 4, Kazakhstanskaya 15, Korneevka and Pavlodarskaya 93. The volatility index as an indicator of variation of *Zn* content in grain within the single variety depending on growing conditions varied from 1.03 to 4.73 times. Variability model was applied for selection of breeding-significant genotypes, which combined classification of *Zn* content in the grain (1-5 grade) and frequency of class occurrence (%). Several varieties stood out with breeding-significant level of *Zn* in grain 45 mg/kg: Pavlodarskaya 93 (22% of all samples studied), Kazakhstan early ripening (11%), Kazakhstanskaya 15 (33%), Kazakhstanskaya 4 and Karabalykskaya 3 (16%), Gedera 125 and Intensive.

Zn content in spring wheat was varied across average background from 11-12 mg/kg to 41 mg/kg. The lowest *Zn* content in the grain was recorded at the three sites: Osakarov, Shortandy (10-13 mg/kg) and Kazan GSU (11-22 mg/kg), which correlates to drought problems in these regions. Maximum *Zn* content was recorded in the following sites: Alga, Aytekebi, Ruzaev, Shchuchin, Lenger and Gvardeysky (45-80 mg/kg). Background average was recorded at the Ruzaev site. Lenger and Ruzaev sites are characterized by high proportion of genotypes with grain *Zn* content of more than 41 mg/kg (50-65% of genotypes).

Aktubinsk region with KASIB spring wheat is characterized as low-level by zinc content, which is reduced to below 12 mg/kg, and thus *Zn*-deficient grain. A ranking of regions was established with decreasing *Zn* content in the grain of KASIB spring wheat: Fiton > Karabalyk > Pavlodar > Aktyubinsk.

In general, according to the results of dispersion analysis, *Zn* content in the grain is determined on 6-10% by genotype, on 57-82% - by regional growing conditions and on 5-10% - by interaction of these factors.

Zn-deficiency of certain spring wheat growing regions according to wheat data is confirmed by minimum *Zn* content values in barley (for Osakarov at 14-15 mg/kg and Urlyutyub, Arykbalyk at 17-19 mg/kg), which is associated with drought problem in these regions in general, regardless of the crop, and is presented by Zn cartogram across Republic of Kazakhstan.

Research has been carried out under the program O.0721 "Breeding and dissemination of cereal varieties with genetically identified stress indicator properties based on molecular breeding, genomics and biotechnology (biochemistry) for effective use of soil and bioclimatic potential of the country", project with state registration number 0115RK02313 "To investigate grain mineral content of synthetic forms of wheat and biochemical composition of dihaploid lines of wheat and barley, oats, sorghum and soybeans, relative to productivity, and to identify resources stable quality. To define the role of *Zn* in drought resistance of spring wheat and grain biofortification".

EVALUATION OF GENETIC VARIATION IN SPRING BARLEY COLLECTION USING SNP ILLUMINA ARRAY

Y. Turuspekov *[1], J. Genievskaya [1], B. Sariev [2], L. Tokhetova [3], V. Chudinov [4], A. Ortaev [5], V. Tsygankov [6], G. Sereda [7], A. Espanov [8]

1 – Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan
2 – Kazakh Research Institute of Agriculture and Plant production, Almaty region, Kazakhstan
3 – Kazakh Institute of Rice, Kyzylorda, Kazakhstan
4 – Karabalyk breeding station, Kostanai region, Kazakhstan
5 – Krasnovodopad breeding station, South Kazakhstan region, Kazakhstan
6 – Aktobe breeding station, Aktobe region, Kazakhstan
7 – Karaganda breeding station, Karaganda region, Kazakhstan
8 – Priaral breeding station by N. Vavilov, Aktobe region, Kazakhstan

Email: yerlant@yahoo.com

The collection of 104 spring barley accessions from Kazakhstan and 80 landraces from different parts of the world were genotyped using the 9K SNP iSelect array containing 7,842 SNPs. Genotyping revealed set of 6,670 storable SNPs (85.1% of success) with 72.85% variants being transitions and 27.15% transversions. After quality control filtering of the SNP dataset 5,050 SNPs (64.4% of success) were selected for genetic variation analysis. The total genetic length of the whole genome based on the genetic distances between mapped markers was 990.9 cM. The number of SNPs per chromosome with known positions ranged from 306 in chromosomes 1H and 4H to 608 in chromosome 5H, and suggested average coverage for each marker was 0.33 cM. Unbiased genetic diversity index was ranged from 0.333 in Europe to 0.394 in North America, while the index for Kazakh group of accessions was 0.35. Principal Coordinate analysis revealed that accessions from Kazakhstan were rather genetically closer to South and North American landraces in comparison to European and Asian accessions. The SNP data for all 184 accessions were prepared for genome-wide association study of QTL related to yield components and grain quality.

GWAS for mapping QTLs of flowering time and yield components was performed using TASSEL and FARM CPU packages. Overall 84 SNP markers that significantly associated with plant growth stages and yield components were identified. The identified markers are under validation using different hybrid populations with high generation progenies. The results can be effectively used in local barley breeding programs.

Session 4.

Genetic Engineering and Crop Improvement

THE POTENTIAL OF BARLEY/WHEAT ORTHOLOGY TO ADVANCE CEREAL GRAIN YIELD

Takao Komatsuda

Institute of Crop Science (NICS), National Agriculture and Food Research Organization (NARO), Tsukuba, Japan

About 12,000 years ago in the Near East, humans began the transition from hunter-gathering to agriculture-based societies. Barley was a founder crop in this process, and the most important steps in its domestication were mutations in two adjacent, dominant and complementary genes, *btr1* and *btr2*, through which grains were retained on the inflorescence at maturity, enabling effective harvesting. The early-domesticated barley had one fertile central and two sterile lateral spikelets at each rachis node, soon later cultivators of barley selected a phenotype with a six-rowed spike with all spikelets fertile that stably produced three times the usual grain number during domestication. This improved yield, generated by mutation at *vrs1* for a homeobox gene, established barley as a founder crop for the Near Eastern Neolithic civilization. Wheat has one-, two- or three sets of *vrs1* orthologous genes according to their ploidy. There was a significant variation of gene structure and gene expression correlated with the ploidy. Reduction of the *vrs1* function by either RNAi and natural variation and mutation alleles increased grain number of wheat.

GENOME ENGINEERING IN CEREALS

Jochen Kumlehn

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

e-mail: kumlehn@ipk-gatersleben.de

Genome engineering is a breakthrough technology that offers versatile novel possibilities for both the experimental elucidation of gene functions and the improvement of crop performance. Aiming to establish site-directed mutagenesis in cereals, target gene-specific transcription activator-like effector nucleases (TALENs) were designed and used pairwise to genetically transform barley. Owing to the haploid nature of immature pollen used for Agrobacterium-mediated gene transfer and their capability of undergoing cell proliferation, whole genome duplication and plant regeneration, some resultant primary mutants proved instantly homozygous. In a second approach, we produced two types of plant lines each carrying only one of the two required TALEN units. Crossings of these plants result in the combination of complementary TALENs and their heterodimerization/activation during early zygotic embryogenesis in hybrid caryopses, which facilitated site-directed mutagenesis with unprecedented efficiency in a cereal crop. By this principle, many mutations can be independently produced, even if only a few endonuclease-transgenic lines are available, e.g. in plant species that are not readily transformable. To allow for prevalidation and optimization of customized endonuclease constructs before investing in the laborious creation of stable transgenic plants, a transient expression test was established which indicates cleavage activity via frame shift reconstitution of a reporter gene positioned downstream of the target sequence. Site-directed mutagenesis was also established using RNA-guided Cas9 endonuclease. This platform has proved more reliable in generating barley mutant plants as compared with current TALEN technology. The proportion of plants carrying genetic modifications at the target site can be as high as 84 percent of the gRNA/Cas9 transgenics produced. A comparison of TALEN- and Cas9-mediated barley mutagenesis revealed platform-specific modification patterns. More sophisticated applications of customizable endonucleases involve the use of an artificial DNA repair template facilitating homology-directed repair (HDR) so as to create predefined rather than random DNA sequence modifications at the target locus. Homology-directed genome editing was exemplified by converting *GFP* stably residing in the barley genome into *YFP*, which is caused by a particular single amino acid exchange in the gene product.

RAPID GENE CLONING IN WHEAT AND BARLEY

Brande B.H. Wulff

John Innes Centre, Norwich, UK

e-mail: brande.wulff@jic.a.cuk

Molecular cloning of genes underpinning genetic variation in the wild ancestors of our domesticated crops opens up novel precision-deployment possibilities in elite cultivars via gene editing and transgenesis. However, large genomes, extensive regions of suppressed recombination, and long generation times, often impose significant barriers to gene cloning in crops and crop wild relatives. Using a series of case-studies in small-grain cereals, I will present a suite of enabling technologies that can overcome these obstacles and speed up gene cloning.

MAIN TRENDS IN CEREAL BREEDING IN KAZAKHSTAN

A. Abugalieva [1,2]***, B. Bashabayeva***

[1] Kazakh Research Institute of Agriculture, Almaty region, Kazakhstan
[2] Kazakh National Agrarian University, Kazakhstan

The Republic of Kazakhstan – number 9 largest in the world with an area of the territory of 2 million 724.9 thousand sq.km.

The territory of Kazakhstan is characterized by a general zonation and vertical zonation. Climatic zones: Kazakhsta distinguished by the landscape diversity. 58% of the state is desert or semi-desert 10% - mountains (the foothills). In the north of the country is dominated by steppe and forest steppe.

Agriculture is a priority sector for the Kazakhstan production. The total area of agricultural land is more than 222.4 million hectares of arable land under them – 24.2 mln.ga (10.9%), grasslands – 5.2 million hectares (2.3%), pastures – 188.4 million hectares (84.7%). In the forest – steppe and steppe zones – 10% of cultivated land, semi-desert and desert – about 60%. All agricultural zones of the country are characterized by low annual precipitation – 150-320 mm.

Cereals is the most important in human economic activity group of cultivated plants, giving the grain, the staple food of man, the raw material for many industries and feed for farm animals/ grains are divided into grain and legumes.

Problem: The stability of grain production in Kazakhstan.

Solution: Improved varieties and others.

Improving the efficiency of adaptive selection (complex breeding and genetic, physiological and biochemical work) on agro-climatic zoning, agro – ecological safety, yield and quality of grain. Agroclimatic zoning should be directed to agroekotipov grades.

Cereals production is the main area of farming activities in the country.

Spring wheat production is concentrated almost exclusively in Northern Kazakhstan and it comprises 75% of total wheat production. Total area under wheat in Kazakhstan is 11.8-13.5 mln ha producing 11.2-16.6 mln t of grain. Domestic consumption uses around 7.5 mnl t. Export varies from 3 to 8 mln t depending on year. Other important cereal crops are barley, oats, maize and millet. barley area varies from 1.6 to 2.1 mln ha and with average yield of 0.9-1.4 t/ha annual production reaches 1.5-2.8 mln t. Domestic consumption uses around 1.5 mnl t. Export is insignificant: 0.1-0.8 mln t. Maize area is around 0.1 mln ha producing total of 0.4 mln t of grain for domestic consumption. Cotton produces high yield in southern Kazakhstan and its share in agricultural export is 15%. The other important crops are sugar beet, tobacco, rice, safflower and potato.

The breeding history, achievement of breeding and important role breeding community in Kazakhstan was observed plays for maintaining regional food security. So far despite the organizational and other changes breeding programs remain productive and focused on farmers and their income as the ultimate goal of variety adoption. There is still support of more basic research to breeding from different groups in the country. It may not have realized in routine application of molecular or other modern techniques but it certainly maintains the overall level of research and critical mass of wheat scientists. This situation is likely to remain in the near future considering the recent tendency of rather substantial increase in funding of agricultural research and breeding specifically. The medium-long term future challenges are associated with maintenance of high precision field experimentation, practical application of modern tools and attraction and education of young generation of scientists and breeders (Abugalieva A., Morgounov A., 2016).

REGULATION OF SOMATIC EMBRYOGENESIS BY *WOX* GENES IN *MEDICAGO TRUNCATULA*

Y.A. Fedorova, V.E. Tvorogova, L.A.Lutova

Saint Petersburg State University, Saint Petersburg, Russia

e-mail: julchen.fedorowa@gmail.com

Somatic embryogenesis (SE) is a process by which somatic cells reverse their developmental program and become embryogenic. Among the various factors essential for this developmental switch, transcription factors are believed to play a central role.

WUSCHEL-related homeobox (WOX) family transcription factors are playing important roles in developmental processes during zygotic embryogenesis (ZE) and the expression of some *WOX* genes was shown to be associated with SE. However, involvement of many *WOX* genes in SE remains unstudied. In our previous research, we demonstrated that expression of *Medicago truncatula WOX* genes, *MtWOX11-like, STENOFOLIA (STF)* and *MtWOX9-1*, is associated with SE. In the present study, we mainly investigate the role of *STF* gene during SE.

In adult plants, *STF* expression was observed in the generative organs, fruits and flowers, suggesting that this gene may also be involved in ZE. The local analysis of *STF* expression during SE demonstrated that its promoter is activated directly in somatic embryos.

Overexpression of *STF* gene leads to increased embryogenic capacity of calli and correlates with decrease in expression levels of *MtGH3.6* and *MtHB1* genes, involved in auxin metabolism and abscisic acid response, respectively. We are planning to examine whether STF directly binds promoter regions of the *MtHB1* gene using yeast one-hybrid system.

Surprisingly, *STF* loss-of-function mutants showed slightly increased embryogenic capacity of calli, suggesting that this transcription factor is not strictly necessary for inducing SE and may influence SE in different pathways. To unravel mechanism of these pathways, we are going to identify STF targets by transcriptome analysis.

To understand functions of *STF,* we are identifying its interacting partners, involved in SE, by using yeast-two hybrid system. We already have shown that STF does not bind MtFUS3, MtSVP, MtAP3 and MtPI proteins.

This work was supported by the grant of the Russian Science Foundation (1.53.917.2016).

ECOLOGY AND ECONOMICAL IMPACT OF BARLEY STRIPE MOSAIC VIRUS (*VIRGAVIRIDAE*, *HORDEIVIRUS*) IN THE PRIMORSKY KRAI OF RUSSIA

A.V. Gapeka [1], ***A.A. Zelikova*** [1,2], ***S.K. Zhmurkina*** [2], ***T.I. Pleshakova*** [1], ***Yu.G. Volkov*** [1], ***N.N. Kakareka*** [1], ***M.Yu. Shchelkanov*** [1,2]

[1] Federal Scientific Center of the East Asia Terrestrial Biodiversity, Far Eastern Branch of Russian Academy of Sciences, Vladivostok, Russia;
[2] Far Eastern Federal University, Russian Ministry of Education and Science, Vladivostok, Russia

Barley stripe mosaic virus (BSMV) (*Virgaviridae*, *Hordeivirus*) is common in agrocenoses infecting wide spectrum of cereals with barley and wheat being described as the main hosts. The typical symptoms of BSMV-associated disease are from small light-green or chlorotic stripes or streaks to chlorosis and necrosis and stunted growth of plants. Unlike many phytoviruses BSMV is not proved to have any vectors – this virus could be transmitted by contact of sick and healthy plants, through the seeds and the pollen. But some important ecological aspects of BSMV and its harmfulness are yet to reveal nowadays. In order to obtain a higher yields these aspects need to be considered according to regional specifics.

Materials and methods. Annual phytovirological monitoring with visual assessment and a detailed accounting was carried out in the sown crops of winter and spring barley, winter wheat and spring wheat, spring oats, maize. Plants or leaves with viral infection-like symptoms were transported to the Laboratory of virology for identification by indirect ELISA with specific antisera, electron microscopy (Libra 200 FE HT in the Center for Electron Microscopy of Far Eastern Branch of Russian Academy of Sciences) and other standard virology methods. To determine the BSMV-infected maize yield loss, seeds of maze were planted out in experimental plot: 100 control seeds and 200 experimental seeds for inoculation. The experimental seedlings were infected on the 26-th day after planting, with the infection development being checked by indirect ELISA on the 14-th and 28-th day after the inoculation.

Results and discussion. We revealed that BSMV infects barley (14.3-41.6 %), oats (8.3-21.4 %) and wheat (16.7-59 %) more often in relation to other cereals and other cereal viruses on the territory of Primorsky krai. Infection load in the productive agricultural cereal crops is lower than in the selection and collection nurseries. It could be explained due to the ability of the virus to be transmitted through seeds and higher sowing density in productive agricultural cereal crops in comparison to experimental stations where low sowing density creates good conditions for potential active insect-vectors. Maize (*Zea mays*) is one of the most important cereal crops for the agricultural industry of Primorsky krai. Some authors mention maize as an experimental BSMV host. We have found plants of maize with yellow or white streak and identified BSMV-associated disease. Thus we have revealed that maize is a natural host of BSMV. Infection of productive agricultural crops of maize is significantly lower than the selection and collection nurseries of the experimental station of Primorsky Research Institute of Agriculture. We have found symptoms and proved BSMV-disease by laboratory methods in the surrounding weed *Setaria pumila (Poir.) Roem. Et Schult.(= S. Glauca (L.) Beauv.)* as well (51.6 % positive plants). This species was indicated as BSMV host for the very first time. There were no any observed mechanical contacts between maize and weed plants, which implies that virus vector took place. We have found flying and parthenogenesis forms of aphids on the glue traps in experimental plots, on experimental plants and on *S. pumila*. Under laboratory conditions BSMV was transmitted by aphids on wild plants of genus *Poaceae*: *Echinochloa crusgali* (L.) Roem. (*Echinochloa crus-galli*) and *Phleum pratense* L. The loss of maize yield is about 30-60 % which is the direct proportional dependence to the infection rate.

Conclusion. BSMV is a harmful viral disease, which can cause significant economic damage. Infected viral particles are determined in all parts of the seed and the pollen. Because of seed and mechanical transmission, the virus is involved in the selection process.

GENOME EDITING IN SIBERIAN BARLEY

S.V. Gerasimova, A.M. Korotkova, E.K. Khlestkina

Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

e-mail: gerson@bionet.nsc.ru

Cereals are of outstanding value among crop species. The application of new plant breeding techniques on monocot plants with large genomes, especially wheat and barley is an important challenge. The most basic research, transgenic plants development and genome editing are carrying out on model barley cultivar "Golden promise". There is a lack of information about amenability of local cultivars for genetic transformation and *in vitro* regeneration. The present work aims to overpass the barrier between model genome editing and practical breeding and introduce the valuable trait in local cultivar of *Hordeum vulgare* L. via CRISPR/Cas system.

Hulled (covered) barley trait is determined by a single gene *Nud* located on the chromosome 7H. The mutant *nud* provides free-threshing variant called naked (hulless) barley. The targeted mutagenesis of barley *Nud* gene using CRISPR/Cas system in Siberian cultivar is the task of this study.

The study consists of two main issues: the search of most suitable cultivars among the Russian collection of spring barley and the application of CRISPR/Cas genome editing technique on selected ones.

Ten most common Siberian barley cultivars have been chosen for the first *in vitro* regeneration test. It was shown that all selected cultivars are able to produce callus from immature embryos. The callus growth dynamics and regeneration ability vary among the cultivars. The best results comparable with control "Golden promise" cultivar were obtained for "Aley". This cultivar has been chosen for genome editing experiment.

The nucleotide sequence of *Nud* gene from "Aley" cultivar has been elucidated via Sanger sequencing. Using online target-design tools the few sgRNAs have been designed to pair with diverse sites of the *Nud* gene. The potential off-targets have been identified. The two genetic constructs carrying Cas9 nuclease and sgRNA targeting different sites in *Nud* gene have been developed. For the genetic transformation of immature embryos, both *Agrobacterim*-mediated transformation and biolistic technique have been implemented.

The work is supported by Russian Science Foundation (project 16-14-00086).

THE POSSIBILITY OF NANOCOMPOSITES APPLICATION IN AGRICULTURE

I.A. Graskova [1], ***A.I. Perfilieva*** [1], ***I.V. Klimenkov*** [2], ***B.G. Sukhov*** [3]

[1] Siberian Institute of Plant Physiology and Biochemistry SB RAS, Irkutsk, Russia
[2]Limnological Institute SB RAS, Irkutsk, Russia
[3] A.E. Favosky Irkutsk Institute of Chemistry, Irkutsk, Russia

e-mail: graskova@sifibr.irk.ru

Among the pathogenic gram-positive bacteria, the most common and significant are non-sporing bacteria of the genus *Clavibacter*, presenting single or united in pairs (as well as in the short chains) immobile rod-shaped bacteria. *Clavibacter michiganensis* subsp. S*epedonicus* (Spieck. et Kotth.) SkaptetBurkh *(C. michiganensis)* is the agent of the potato ring rot. As a result of the development of this disease crop losses account for 10-45%. To date there are no effective techniques of controlling *c. michiganensis* and all available methods are preventive and involve disinfection of packaging materials, implements and planting material. Such aggressive agents as formalin, hydrogen peroxide, hydrochloric acid, etc. are used as decontaminants.

Therefore the search for effective and safe methods of potato sanitation from the *C. michiganensis* is extremely important. In this connection it can be promising to use hybrid organic-inorganic nanocomposite of potentially antimicrobial elemental selenium (NKSe), obtained on the basis of natural geteropolisaccharide arabinogalactan, which is effective stabilizer of various types of nanoparticles, as a decontamination agent.

Two nanocomposites with different content of selenium were studied: NC 1, obtained by selenium oxide SeO_2 (1.23% Se) polymerization of arabinogalactan; NC 2 also obtained by bis (2 phenylethyl) sodium diselenophosphinate $(PhCH_2CH_2)_2PSe_2Na$(3.4% Se) polymerization of arabinogalactan. Selenium nanoparticles are well visible in transmission electron microscope, their form is close to spherical and dimensional distribution is rather narrow (50-80 nm, the average size of 67 nm).

After incubation of bacterial cells with nanocomposites the change of cells' morphology, production of mucus around them, cells adhesion in conglomerates as well as cell death due to arupture of a cell wall was noted. The use of techniques of scanning electron microscopy showed the presence of selenium particles on a cell wall of bacteria, which resulted in blocking of cells' vital activity. However adding nanocomposites in food solution for infected potato *in vitro* did not affect plants growth and development.

The researches show that selenium nanoparticles can be used for effective prevention and suppression of diseases of potato ring rot caused by *C.michiganensis*. Used nanocomposites consist of polymer arabinogalactan matrix, into which the selenium molecule is dipped. This combination is effective, as arabinogalactan is a polysaccharide which is digested by many microorganisms. Selenium has bactericidal properties but it is not toxic for plants in appropriate concentrations. All of this determines the prospects of the research for future application.

NUCLEAR DNA CONTENT IN RICE REGENERANTS, OBTAINED BY ANTHER CULTURE *IN VITRO* IN RUSSIAN FAR EAST

M.V. Ilyushko [1], ***M.V. Skaptsov*** [2], ***M.V. Romashova*** [1]

[1] Primorsky Scientific Research Institute of Agriculture, Ussurisk, Russia
[2] Altai State University, Barnaul, Russia

e-mail: ilyushkoiris@mail.ru

Rice is the important food culture for the south of the Russian Far East, therefore breeding is necessary for new varieties with high harvest and crop quality. Anther culture *in vitro* is successfully applied in breeding programs in rice-growing countries and in Russia. In anther culture *in vitro* flow cytometry has application for division of regenerants group on haploid, dihaploid and polyploid plants. There are data about clear divisible increase of chromosome set and position of peaks is represented as constant magnitude. Cytological investigations in plant tissue culture *in vitro* existence about not only genome variations from haploid to hexaploid but chromosome ones lead to aneuploidy and endopoliploidy. In this case a nuclear DNA content can not be constant value. We followed two aims in the work: to describe the population of androgenic rice regenerants on nuclear DNA content by flow cytometry; to estimate the applicability of the combination of anther culture *in vitro* and flow cytometry in the rice breeding. Rice regenerants (1099 ones), obtained in anther culture *in vitro* of single hybrid plant, separated on four groups on morphological features: haploids (sterile plants with very small flowers), dihaploids (plants with seeds), tetraploids (plants with very few large seeds, expressed keel and ribbing on floral scales), plants without seeds (flowers were normal size, but two or more sterile panicles); 176 plants from 1099 regenerants estimated by flow cytometry.

Group of plants without seeds was characterized by high nuclear DNA content the coefficient of variation – 32%. Probably, plants with double of chromosome set, triploids, tetraploids and pentaploids got into the group. Endopoliploidy phenomenon was observed in this regenerants, five plants had two peaks in detection of nuclear DNA content like haploids and diploids. 23 plants had chromosome set nuclear DNA content approximate to dihaploids (average value 2,00 pg). Obviously, aneuploidy phenomenon is characteristic for rice anther culture *in vitro* it can lead to aliquant changes in chromosome set of regenerants which incompatible with rice production. Groups of dihaploids and tetraploids was low variable (10,5 and 5,3%), average value nuclear DNA content was 1,88 and 3,75 pg respectively. Haploids was characterized by high variability of nuclear DNA content – 29%, average value – 0,89 pg.

Flow cytometry possible to apply for extraction tetraploids in complex with productive index in rice breeding. It can use for rejection of haploids and phase of their cultivation in conditions *ex vitro* as unpromising regenerants in rice breeding.

CREATION OF EXPRESSION PLATFORM BASED ON *WOLFFIA ARRHIZA* FOR PRODUCTION OF THERAPEUTIC PROTEINS IN THE EXAMPLE OF RECOMBINANT HUMAN GRANULOCYTE COLONY-STIMULATING FACTOR

P. Khvatkov [1,3], ***A. Firsov*** [1,2], ***L. Shaloiko*** [2], ***A. Pushin*** [1,2,3], ***I. Tarasenko*** [2], ***M. Chernobrovkina*** [1], ***S. Dolgov*** [1,2,3]

[1] All-Russia Research Institute of Agricultural Biotechnology, Moscow, Russia
[2] Branch of Shemyakin and Ovchinnikov Institute of Bioorganic Chemistry, Pushchino, Russia
[3] Nikita Botanical Gardens, Yalta, Russia

E-mail: khvatkov1987@gmail.com

Vaccines creation based on transgenic plants may be considered as a groundbreaking technology in modern vaccinology with the advantages as compared to bacterial and yeast systems, such as the lack of common human and animal pathogens, and high-level expression of heterologous proteins. To date the development of tissue culture systems in duckweeds is limited to species of the genus *Lemna* and *Spirodella*. Yet more promising target for biopharming is *Wolffia arrhiza* as an object for submerged cultivation in a fermenter. We have developed a two-step procedure of callus induction in *Wolffia*. The created protocols for callus induction and regeneration allow achieving not only the high efficiency at each stage, but also proceeding to the development of a protocol for *Wolffia arrhiza* stable transformation. The most efficient transgenesis and selection of the transgenic lines occures in the presence of hygromycin B. The successful transformation requires the presence both of 2,4-D and BA in the cultivation medium within 15 days. To induce regeneration, after 2 weeks the explants were transferred to SH medium without growth regulators. For transformation were used bacterial strains EHA105 harbouring plasmid pCamGCSF contains double *CaMV35S*-driven *hG-CSF* gene containing signal peptide the rice α-amylase and *ER*-signal (localization signal to the endoplasmic reticulum) and double *CaMV35S*-driven hygromycin phosphotransferase (*hpt*) selection gene allowing for Hyg selection of transgenic plant tissues, were used in agro inoculation experiments. In total, the experiments of agro transformation included 8095 explants, respectively, efficiency of 0.42% transgenes per 100 explants. As a result of investigations, 34 transgenic lines of *Wolffia* harbouring both granulocyte colony-stimulating factor genes were obtained. Integration of heterologous DNA was proved by molecular-biological analyzes (PCR and Southern blot analyzes). Western blot assay and ELISA confirmed expression of recombinant protein. Revealed two lines expressing G-CSF at 0.12 - 0.35% of the saturated protein (≈ 30 mg target protein per 1 kg green weight of *Wolffia arrhiza*).

EVALUATION OF THE MUTAGENIC EFFECT NITROSOETHYLUREA AND NITROZOZOGUANIDINA ON PLANTS OF FLAX *(LINUM USITATISSIMUM* L.)

K.P. Korolev [1], ***I.A.Golub*** [2]

[1] Tyumen State University, Tyumen, Russia

[2] Republican Scientific Subsidiary Unitary Enterprise "Institute Flax", Orsha district, Vitebsk region, Republic of Belarus

e-mail: corolev.konstantin2016@yandex.ru

In recent years, breeding of various crops in several countries widely used method of induced mutagenesis, which allows to change the features and properties of plants and to obtain new forms of (mutant) plants by exposing the mutagenic heredity factors. The selection of fiber flax, some theoretical and applied aspects of induced mutagenesis still not established, which causes the relevance of our work. For the development of mutation breeding flax - flax is necessary to include new mutagens. In this connection, in the present study aims to compare the classical (N-nitroso-N-methylurea) and not previously used in the flax-flax (N-nitroso-N-guanidine) mutagens. To find the optimal concentration of mutagen sensitivity of the varieties studied for phenotypic expression of traits. As a result of observations found that a small amount of chimeras manifested in phase, some seedlings later - in phase "budding" and "bloom". With increasing concentrations of a decrease in germination of seeds (except Class Grant, NMM, 6h. Exposure, 0.006% and 0.12% of exposure), the height of plants and plant survival during the growing season. It should be noted that in some embodiments, using nitrosoguanidine revealed complete destruction of the plants in the phase of full ripeness of flax seeds. Particularly high lethal effect is set at 12 and 18 hours of exposure to a concentration of 0.05%, 0.15% and 0.1%, 0.15%. During the phenological observations revealed features of plant growth and development of experimental and control options flax. If the control seedlings embodiments noted on day 6-8., In embodiments, the high exposure concentrations and exposure seedlings were only 10-14 days. Mutagenic chemical nature of the factors influenced the plant height, leaf area, internode length, number of pods and seeds. It should be noted that the storage ability of plants in the experimental variants differ in cleaning.

As a result, the work received 78 mutant population whose study will be continued.

Keynote

GENOMICS TOOLS FOR OAT BREEDING

M. Bisaga [1], I. Griffiths [1], R.Vickerstaff [1,6], E. Paczos-Grzeda [2], A. Abugalieva [3], Z. Dumlupinar [4], Y-F Huang [5], D. Giorgi [6], S. Lucretti [6], T. Langdon [1, 7]

[1] IBERS, Aberystwyth University, Aberystwyth UK
[2] Institute of Plant Genetics, Breeding and Biotechnology, University of Life Sciences in Lublin, Lublin, Poland
[3] Kazakh Research Institute of Agriculture and Crop Production, Almalybak, Kazakhstan
[4] Kahramanmaras Sutcu Imam University, Kahramanmaraş, Turkey
5 Depatyment of Agronomy, National Taiwan University, Taipei, Taiwan
[6] ENEA, Rome, Italy
[7] NIAB EMR, East Malling, UK
8 ttl@aber.ac.uk

High throughput genotyping platforms such as DArTseq, an Illumina 6k chip and genotyping-by-sequencing (GbS) have been developed and applied to hexaploid oat, with significant amounts of marker and associated phenotype data publically available at T3/oat (https://triticeaetoolbox.org/oat/). However, no hexaploid oat reference genome is yet available, complicating identification of candidate genes and refinement of markers to use in breeding programmes. We have established a genome zipper for the wild diploid species *Avena atlantica* as a proxy for the hexaploid A sub-genome. We have extended this to include orthologous hexaploid sequences recovered from specific isolated chromosome fractions from the European spring oat variety, Firth. Firth has been used as the common parent of a Nested Association Mapping population (NAM), with twelve other parents of specific sub-populations providing diversity representing modern and historical commercial cultivars, landraces and introgressions from wild species. GbS has been carried out on 632 lines, all of which have been grown and phenotyped in the field at IBERS over at least two years. A consensus map is being constructed, with additional data being provided by RNAseq of parents and field trials in Poland, Turkey and Kazakhstan. Specific subfamilies are being used to dissect yield component traits and identify major genes underlying relevant QTLs based on 'contig juggling' between hexaploid and diploid assemblies. The same approach is being used to identify genes involved in domestication, which are being mapped in wild and weed hybrid populations developed by the University of Life Sciences in Lublin.

TOMATO BUSHY STUNT VIRUS - BASED VECTOR FOR TRANSIENT EXPRESSION OF HETEROLOGOUS PROTEINS IN *NICOTIANA BENTHAMIANA* PLANTS

S.A. Manabayeva, A.T. Zhumabek, L.S. Abeuova, E.M. Ramankulov

National Center for Biotechnology, Astana, Kazakhstan

Increasing economic efficiency of use of plants as "biofactories" - producers of proteins – has served as the beginning of development of new technologies for the production of target proteins in non-transgenic plants at the highest level. One of them is using transient expression systems of target genes by self-replicating recombinant viral vectors. At the same time, there are still no accurate criteria of a choice of optimal vector system for an expression of target proteins. Considering this, an application of *Tomato bushy stunt virus* (TBSV) genome for creation of the genetically engineered designs providing a transient expression of heterologous proteins in plants is interesting. The fact that the TBSV genome encodes the p19 protein, capable of inhibition of posttranscriptional silencing and enhancing expression levels for each gene in the viral RNA (including heterologous ones), is a significant advantage of the TBSV vector system. In this approach, the CP gene in the developed TBSV vector was replaced by the codon optimized target genes (human granulocyte colony-stimulating factor (GenBank accession number M17706.1), 1,4-β-*endoglucanase E1* (GenBank accession number HQ541433.1) and glycoprotein gp51 of BLV (GenBank accession number FM209472.1) that were synthesized by a PCR-based gene synthesis method. The plant viral vector encoding target genes was delivered into 4-5 weeks old *N.benthamiana* plants by agroinfiltration. In order to facilitate purification of the rhG-CSF from plant materials the protein sequences were modified by the addition of the short amino acid tag (6 x His). Four days after infiltration, expression of heterologous proteins isolated by using metal affinity chromatography on Ni^{2+}-NTA agarose has been verified by western blotting procedures. The concentration of purified target proteins was determined by ELISA. Biological activity of heterologous proteins has been studied by using an appropriate methodology. The results indicate that the TBSV - based protein production system is suitable for transient production of proteins for biopharmaceutical and industrial uses.

AGROBACTERIUM MEDIATED TRANSFORMATION OF *POPULUS×BEROLIENSIS* BY *ATGA20OX1* GENE USING PRI 101-AN VECTOR

V.V. Pavlichenko [1], ***E.M. Bairamova*** [2], ***M.V. Protopopova*** [1], ***E.D Zolotovskaya.*** [2], ***V.K. Voinikov*** [1]

[1]Siberian Institute of Plant Physiology and Biochemistry SB RAS, Irkutsk, Russia
[2]Irkutsk State University, Irkutsk, Russia

e-mail: vpavlichenko@gmail.com

Genetic engineering technologies allow developing of the plants with enhanced growth hormones biosynthesis, which leads to a multiple increasing of growth rate and biomass accumulation. Application of these plants in wood plantations will allow significantly reducing of the production costs of wood raw. At the same time, the results of different research groups in the field of genetic transformation of plants by the genes of growth hormones biosynthesis are still insufficient and often contradictory.

Thus, the study was aimed to solving of the fundamental problem of plants genetic engineering - usage of the genetic transformation for the development of the woody plant forms, which are characterized by increased growth rate and biomass accumulation.

Populus×berolinensis Dippel, the hybrid of laurel-leaf poplar *(Populus laurifolia)* and black poplar *(Populus nigra)*, willow family *(Salicaceae)*, was chosen for the genetic transformation.

Plasmid vector for the Agrobacterium mediated transformation was performed on the basis of the commercial pRI 101-AN binary vector containing the general CaMV35S promoter, selective kanamycin resistance gene – *nptII* and 5'non-coding region (5'-UTR) of *Arabidopsis thaliana* alcohol dehydrogenase (ADH) gene as a translational enhancer.

As the gene of interest gibberellin 20-oxidase 1 from *Arabidopsis thaliana* (*AtGA20Ox1*) was used. Genetic transformation of the poplar was carried out by incubation of stem explants in the suspension of *A. tumefaciens* preliminary transformed by plasmid vector pRI 101-AN containing *AtGA20Ox1*. Stems were inoculated into suspension and placed on the solid media for 24 hours (darkness, 23°C). After incubation, the stem explants were incubated on the media containing 15 mg/L of kanamycin sulfate. The growing media was based on ½ MS with full norm of microelements and Fe-chelate and contained following components: thiamine (1 mg/L), pyridoxine (0,5 mg/L), nicotinic acid (0,5 mg/L), inositol (50 mg/L), kinetin (0,5 mg/L), indole butyric acid (0,05 mg/L), sucrose (20 g/L) and agar (7 g/L). An acidity of the media was adjusted to pH 5.7 and after sterilization kanamycin (15 mg/L) and cefotaxime (200 mg/L) were added. After 20 days of stems exposition, kanamycin was removed from the growing media and regenerates were obtained only in presents of cefotaxime purposed for inactivation of Agrobacterium. Obtained regenerates were propagated on the same media but with reduced concentration on kinetin (0,1 mg/L) and without indole butyric acid. Elongated regenerates were rooted on the media containing 0,15 mg/L of indole butyric acid.

At the end of micro propagation, 23 regenerates were obtained. The absence of plants contamination by *A. tumefaciens* was checked by incubation of leaves parts on the growing media for the bacteria. The PCR analysis showed the positive reaction on *nptII* and *AtGA20Ox1* genes in genomic DNA of all obtained transgenes. Genetically modified poplars will be grown up in the green house to estimate a physiological effect of *AtGA20Ox1* over expression on the growth speed and biomass accumulation of *Populus×berolinensis*. Further analyses such as qPCR and active gibberellins detection will be also applied.

The study was financially supported by Complex program of fundamental researches Siberian Branch of Russian Academy of Sciences (project No 0343-2015-0005), Russian Foundation for Basic Research (project No 14-04-31681 mol_a), scholarship of President of Russian Federation for young scientists (SP-3823.2015.1) and The Global Energy Non-profit Partnership.

ALLOPLASMIC WHEAT IN GENETIC RESEARCH AND BREEDING

L.A. Pershina [1, 2], ***I.A. Belan*** [3], ***L.P. Rosseeva*** [3], ***T.S. Osadchaya*** [1], ***L.A. Kravtsova*** [1], ***L.I. Belova*** [1], ***N.V. Trubacheeva*** [1]

[1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
[2]Novosibirsk State University, Novosibirsk, Russia
[3]Siberian Agricultural Research Institute, Omsk, Russia
e-mail: pershina@bionet.nsc.ru

The productivity of the plant and its adaptability to environmental factors largely determined by the coordinated interaction between the nucleus and cytoplasm. Nuclear-cytoplasmic interactions can influence on fertility and agronomic performance of interspecific hybrids and their progenies. Both cytoplasmic and nuclear genetic variations are potentially exploitable for practical purposes. It was shown that the replacement of wheat cytoplasm with the cytoplasm of related species leads to the formation of alloplasmic lines and affects nuclear-cytoplasmic interaction leading to transcript and metabolite alterations (C. Crosatti et al., 2013). Depression in plant development and cytoplasmic male sterility are manifested in the case of nuclear-cytoplasmic conflict. The fertility restoration of alloplasmic lines provided by the influence of *Rf*-genes. In our work, the peculiarities of fertility restoration in alloplasmic lines of common wheat resulted from backcrossing of barley-wheat hybrids *H.vulgare* (2n=14) x *T.aestivum* (2n=42) and *H. marinum* subsp. *gussoneanum* Hudson (2n=28) x *T. aestivum* L. (2n=42) with different varieties of wheat, were investigated. The role of genotypic diversity of common wheat and individual chromosomes for fertility restoration of barley-wheat hybrids and their alloplasmic lines was determined. The nuclear-cytoplasmic compatibility doesn't disrupt due to the introgression of the alien chromosomes into the nuclear genome of these alloplasmic recombinant fertile lines; the plants of introgressive lines are fertile and normally developed, and the states of the cpDNA and mtDNA regions correspond to their states in fertile recombinant lines. A variety of alloplasmic recombinant and introgressive lines (*Hordeum*)-*T.aestivum* with different levels of fertility has been obtained. It was revealed that the barley-wheat hybrids and their alloplasmic lines are suitable models for the study of organelle DNA transmission in wide hybridization. DH lines were produced from androgenic plants with spontaneously doubled chromosome numbers and restored fertility that induced in anther culture. Of the alloplasmic and their DH lines carrying wheat-alien translocations, the most promising with the exhibition of agronomic valuable traits and resistance to diseases were used in breeding programs. Currently, more than 1000 genotypes obtained with the participation of alloplasmic introgressive and alloplasmic DH lines are used in breeding. So, perspective selection lines Lyutescens (L) 310/00-2 and L-310/00-10 (carrying genes *Lr26+Lr19*, *Sr31+Sr25*) were produced using alloplasmic recombinant lines L-80 resulted from backcrossed progeny of BC_4-generations of barley-wheat hybrid (as maternal genotypes): (*H.vulgare,* line 319) × (*T.aestivum,* cv. Saratovskaya 29)/Sar29/Ul'yanovka/Sar29/Sar29. L-310/00-2 and L-310/00-10 which displayed a complex resistance to leaf and stem rust in different regions and serve as a source of genes to obtain new resistance genotypes. The promising form L-311/00-22 has the following origin: (alloplasmic dihaploid line L-17DH) × (Lai3302 × Druzhina). The line L-17DH was obtained by cultivation of anthers of alloplasmic recombinant line L-17, which was formed on the basis of a plant that was isolated from the BC_3-generation of the barley–wheat hybrid: (*H. vulgare* L. cv. Nepolegayushchi) × (*T. aestivum* L. cv. Saratovskaya 29)/Mironovskaya 808/Mir808/Sar29. Six promising lines selected from form L-311/00-22. One of these lines (L-311/00-22-5) as a spring common wheat var. Sigma was included in the State register of breeding achievements of the Russian Federation from 2016. The line L-311/00-22-4 as a spring common wheat var. Uralosibirskaya 2 is being tested in State variety trial.

This work was supported by Basic Project № 0324-2015-0005 and the RFBR (№ 17-04-01738).

PLANT VIRUSES AND THEIR INTERACTION WITH PLANT COMMUNITIES OF FAR EAST OF RUSSIA

T.I. Pleshakova, Z.N. Kozlovskaya, V.F. Tolkach, Y.G. Volkov, N.N. Kakareka, A.V. Gapeka, M.Y. Shchelkanov

Federal Scientific Center of the East Asia Terrestrial Biodiversity, Far Eastern Branch of Russian Academy of Sciences, Vladivostok, Russia

A large number of phytopathogenic viruses harmful for most agricultural plants is described here. Very important is the fact that besides direct harm to the productivity of plants these viruses reduce resistance against adverse habitat conditions – deficiency or excess of water, changes in insolation, higher content of pollutants, *etc*. Even latent viral infection in adverse conditions can cause a serious disease. Many viruses quickly penetrate into natural plant communities and form constant local foci of infection.

East Asia is recently notable for an intensive exchange of commercial agricultural products, as well as samples of agricultural and ornamental plant species. Since viruses can be transferred by vegetative parts and by true seeds, an invasion of these pathogens to new territories with planting stock is observed. These are the most dangerous being new for stable natural and anthropogenic plant communities.

We regularly monitored phytosanitary condition of agricultural crops and natural plant communities in farms cultivating large range of crops using seeds and planting material imported from other regions and from abroad. The list includes more than 10 crop cultures. We also studied farms and organizations involved in breeding, seed production, and marketing of their products. At the same time, a lot of plants with virus-like symptoms were revealed: garlic, pepper, tomato, eggplant, cucumber, cilantro, plantain, and commelina.

In addition, to detect viral diseases in many districts of Primorsky Krai industrial crops of most important cereals were surveyed, as well as adjacent forest stands and shelterbelts, meadows and silage grass, and selection and crop areas of wheat, barley and oats in Primorsky Research Institute of Agriculture. There were revealed several dozens of different isolates of virus diseases of cereals.

Also private collections of ornamental plants were surveyed: dahlias, asters, irises, gladioli, petunia hybrids, primroses, roses, hydrangea, peach-leaved campanula and lilies. A number of plants of these species with virus-like symptoms were detected.

Electron-microscopic analysis of preparations of most of the studied crops revealed various types of virions: filamentous, rod-shaped and isometric, indicating that phytoviruses are widespread among the introduced plant material.

Further studies revealed that some pathogens are new to the region or primarily encountered in the new hosts. Therefore, there were identified more than 10 new strains of cucumber mosaic virus, new strains of potyviruses. For the first time, tomato aspermia virus was identified in lettuce, carrot and parsley in the Russian Far East. Garlic cultivated from imported planting material revealed new harmful strains of onion yellow dwarf virus and latent garlic virus. Several strains of viruses new for the Far East were identified in cereal crops: dwarf corn mosaic, cucumber mosaic and tobacco ringspot. The agents of natural focal diseases are nepoviruses transmitted with soil that, according to our data, affect many horticultural crops.

It is concluded that all new viruses introduced with planting material cause serious diseases and often spread rapidly, forming local epiphytoties. On the other hand, imported plant material can be heavily infected by local strains and viruses, for example lagenaria and fenugreek imported for testing as new cultures.

Monitoring of collections and nurseries revealed that it is difficult and sometimes impossible to conduct breeding work to produce new varieties under transmission of viral infections.

Thus, to improve the quality of selection and seed-growing, the nurseries must be protected from invasion of phytoviruses.

AN EFFECTIVE AGROBACTERIUM-MEDIATED IN PLANTA TRANSFORMATION OF WHEAT (*TRITICUM AESTIVUM*)

B.R. Rezaeva, Z.T. Buriev, Kh.A. Ubaydullaeva, B.K. Rakhmanov, A.A. Tulanov, I.Y. Abdurakhmonov

Center of Genomics and Bioinformatics, Academy of Sciences of Uzbekistan, Tashkent, Uzbekistan
Email: rezaevabarno@gmail.com

Today, cereals make up around 50% of global food production. Wheat plant (Triticum aestivum) is the world's most important agricultural crop and it cultivates in large areas as food sources. Every year, large parts of the wheat yields are lost due to variety of biotic and abiotic stresses.

Hence, nowadays scientists and breeders are developing new strategies to fight against such plant pathogens and stresses via genetic engineering and biotechnologies. Most widely used techniques from those are gene gun bombardment, microinjection, polybrene, tissue culture, electroporation, *in planta* and agrobacterial transformation. *In planta* transformation is the most effective and inexpensive method, and it is a branch of tissue culture that can allow obtaining somoclonal lines of plants which are incapable to regenerate. This method is being used to obtain transgenic lines by directly transformation of genetic vector constructs.

Thus, *Agrobacterium*-mediated *in planta* transformation protocols have been optimized by us to improve range of traits of local Uzbek wheat varieties. As initial studies was used genetic vector construction that express *GUS* gene from gene bank collection of our research Center. To introduce this construct into wheat genome, *in planta* transformation were used and successfully obtained some transformants. In research experiments for inoculation with *Agrobacterium tumefaciens* one day old tissues of apical meristems were used. This is the easiest way to introduce T-DNA through apical meristem to cereal crops, which is considered as target for transformation. Further, tissues we subjected into media containing antibiotic cefotaxime in order to eliminate agrobacteria and kept them at + 4 ^{o}C for vernalization, and transformants were selected by kanamycin afterwards.

Transformed plants demonstrated successful transformation for 3% based on molecular determination, therefore now we are applying this agrobacterium-mediated *in planta* transformation method to obtain new wheat lines resistant to several pathogens and stresses.

Keynote

A KEY ENZYME OF ANIMAL STEROIDOGENESIS CAN FUNCTION IN PLANTS IMPROVING THEIR IMMUNITY AND INCREASING THE PROCESSES OF GROWTH AND DEVELOPMENT

G.V. Shpakovski* [*1], S.G. Spivak [2], I.N. Berdichevets [3], O.G. Babak [3], A.V. Kilchevsky [3], D.G. Shpakovski [1], M.R. Khaliluev [4], E.K. Shematorova [1]

[1] Shemyakin-Ovchinnikov Institute of Bioorganic Chemistry, Russian Academy of Sciences, Moscow, Russia
[2] Belarusian State Medical University, Minsk, Belarus
[3] Institute of Genetics and Cytology, National Academy of Sciences of Belarus, Minsk, Belarus
[4] Russian State Agrarian University – Moscow Timiryazev Agricultural Academy, Moscow, Russia

*e-mail: gvs@ibch.ru

In contrast to animal and yeast, where cholesterol and ergosterol, respectively, are prevalent, at least four different molecular species (sitosterol, campesterol, stigmasterol, and cholesterol) represent the most abundant sterol lipids (phytosterols) in plants. The initial stages of animal steroid hormones biosynthesis occure in the mitochondria of steroidogenic tissues, where cytochrome P450scc encoded by the CYP11A1 gene catalyzes the conversion of cholesterol into pregnenolone – the general precursor of all steroid hormones, starting with progesterone. This stage is missing in plants where mitochondrial cytochromes P450 (the mito CYP clan) have not been found. Instead, the biosynthetic pathway for campesterol provides the precursors for brassinosteroids, phytohormones involved in the regulation of plant growth and development. At the same time, number of animal steroid hormones (pregnenolone sulfate, progesterone, 17-hydroxyprogesterone, 16-dihydroxyprogesterone, androstenedione) and receptors which mediate mitochondrial cholesterol uptake in animal cells were also recently discovered in many divergent plant species. To more thoroughly compare steroidogenic systems of Plantae and Animalia, we have created and studied the transgenic tobacco and tomato plants efficiently expressing cDNA of mammalian CYP11A1. The detailed phenotypic characterization of plants obtained have shown that through four generations studied the transgenic tobacco plants have reduced period of vegetative development (early flowering and maturation of bolls), enlarged biomass and increased productivity (quantity and quality of seeds) compared to the only empty-vector containing or wild-type plants. Moreover, the CYP11A1 transgenic plants show resistance to such fungal pathogene as Botrytis cinerea. These two different valuable phenotypes are separated in two clearly distinct transgenic tomato lines expressing CYP11A1 cDNA: one line (#4) have an accelerated rate of vegetative development, while the other (#7) have enhanced immunity to abiotic and biotic stresses.

GENETIC PARAMETERS OF SPECIES REQUIRED FOR EFFECTIVE SELECTION

V.N. Stegniy, A.K. Sibataev, G.M. Abylkassymova

National Research Tomsk State University, Russia, Tomsk

In breeding there are cases when certain types of plants and animals used as source material, do not respond well to selection for the desired characteristics and do not exhibit the required level of adaptive genetic plasticity. The reason for this may be different circumstances and primarily genetic features Constitution of the species used for breeding. The study of the genetic aspects of speciation and adaptation, carried out in our laboratory allowed us to identify a number of genetic parameters, distinguishing evolutionarily labile species (generators speciation) and species evolutionary conservative (terminal links in the phylogenetic chains).

When the evolutionary development of the taxon in the horizontal direction (cladogenesis or adaptive radiation) signs of little specialisms evolutionary labile species genomes in each step of speciation have been gradually replaced in the process of progressive specialization on the characteristics of alternative (evolutionary conservative), reaching its highest expression in terminal types: a decrease in the number of acrocentrics (Robertsonian merge), polyploidy, the "dispersion" of heterochromatin, a sharp restriction of recombination, the formation of adaptive inversion polymorphism, the extension of the zones of attachment of chromosomes to the nuclear envelope (preservation of structure of the nucleus). These genetic parameters of the specialized types is also important in the selection, preference should be given to the types (among closely related groups), has the following parameters: a smaller number of chromosomes, the low level of recombination, high intraspecific chromosomal polymorphism, dispersed on chromosomes, heterochromatin, and transposable genetic elements, the presence of diffuse chromocenters.

Keynote

PRECISE AND EFFICIENT MUTAGENESIS IN CROPS VIA GENOME EDITING

Seiichi Toki[1,2]

[1] Plant Genome Engineering Research Unit, NARO Institute of Agrobiological Sciences, National Agriculture and Food Research Organization (NARO)
[2] Kihara Institute for Biological Research, Yokohama City University

e-mail: stoki@affrc.go.jp

Two types of genome editing technologies, targeted mutagenesis and gene targeting, are vigorously applied to several agronomicaly important crops. Targeted mutagenesis is useful if we want to knock-out a targeted gene. In contrast, gene targeting enables precise modification of the targeted gene using the specific template DNA. In both cases, finally we would like to remove transgene used for genome editing completely from the plant genome to leave a desired point mutation. In the case of a targeted mutagenesis in seed-propagated crops, once integrated into the genome as a transgene, sequence-specific nucleases (SSNs) genes such are ZFNs, TALENs and CRISPR/Cas9 expression cassette can be segregated out by self-pollination or back-crossing. However, in the case of crops that are propagated vegetatively, transgene should be removed without using genetic segregation. We found that piggyBack transposon can be used as a reversible transgenesis vector in plants to put SSNs IN and OUT without leaving any footprints. Alternatively, virus-mediated transient expression of Cas9 and gRNA provides an integration-free genome editing method. We revealed that split SaCas9 system successfully works in plants. We are currently trying to express pair of the split SaCas9 proteins using two kinds of plant viruses.

In the case of positive/negative selection mediated gene targeting method, a positive selection marker gene is left at the targeted gene. Recently, we succeeded in removing the positive selection marker gene completely using a piggyBack transposition. We can modify any sequence of the rice genome precisely using this system.

NEW PARTICIPANTS OF SOMATIC EMBRYOGENESIS IN *MEDICAGO TRUNCATULA*

V.E. Tvorogova, Y.A. Fedorova, T.A. Vaschkevich, L.A. Lutova

Saint Petersburg State University, Saint Petersburg, Russia

e-mail: krubaza@mail.ru

Somatic embryogenesis is a specific type of regeneration in plants, which includes formation of embryo-like structures from somatic cells. It is widely used in plant biotechnology and propagation. Many *in vitro* protocols for obtaining somatic embryos were developed, but there are a lot of undiscovered molecular mechanisms underlying this process.

WUSCHEL-related homeobox (WOX) family transcription factors and PIN auxin transporters are shown to play important and different roles in many aspects of plant development. The aim of our research is to find new somatic embryogenesis regulators among the members of these gene families.

According to our results, expression of three *Medicago truncatula WOX* family genes, *STENOFOLIA* (*STF*), *MtWOX9-1* and *MtWOX-11-like*, as well as expression of one *PIN* family gene *SMOOTH LEAF MARGIN 1 (SLM1),* is associated with somatic embryogenesis. In embryogenic calli, promoters of *STF*, *MtWOX9-1* and *SLM1* genes are active in somatic embryos and also in adjacent zones of calli. Overexpression of *MtWOX9-1* and *STENOFOLIA* genes leads to increased embryogenic capacity of calli and correlates with changes in expression levels of several embryogenesis-associated genes, including *MtWOX-11-like*, *SLM1* and several genes, involved in hormone signaling and metabolism.

We are planning to identify targets of discovered somatic embryogenesis regulators by using RNA-seq analysis, Y1H system and EMSA.

This work was supported by the grant of the Russian Science Foundation (1.53.917.2016) and by the grant of SPSU (1.42.1288.2014).

AGGLUTININ GENES AND THE PROCESS OF CREATING ARTIFICIAL SYMBIOTIC SYSTEMS

Z.R. Vershinina, L.R. Hakimova, G.R. Yasybaeva, A.M. Lavina, Al.Kh. Baimiev

Institute of biochemistry and genetics of Ufa science centre RAS, Department of Molecular Biology and Plant Physiology, Bashkortostan, Ufa, Russia

At present the whole potential of plant-microbial relationships is used for ecological farmingwhereby it is possible to increase the quality and quantity of the crop. In this regard interest in microbial biopreparations based on strains of PGPR-microorganisms (Plant Growth Promoting Rhizobacteria) naturally increases. The strains isolated from natural biocenoses do not pollute the environment and are safe for humans and animals. Such microorganisms include bacteria of the genus *Rhizobium* (nodule bacteria or rhizobia), which are one of the most effective nitrogen fixers in symbiosis with leguminous plants. However, rhizobia can act as associative PGPR microorganisms, contributing to the improvement of growth and development, as well as mineral nutrition of plants. One of the main disadvantages of biofertilizers, which worsen the effectiveness of their action, is the instability of PGPR-strains in the soil due to the negative influence of unfavorable environmental conditions and/or low competitiveness. Various methods are used for increase of the efficiency of formation new associative symbiotic systems, including the creation of transgenic plants that produce specific root exudates that determine the stage of recognition macrosymbiontmicrosymbionts. Natural mediators can be usedto attach bacterial cells to the surface of the root hairs. Such plant mediators are lectins of leguminous plants, which, being agglutinins, attach rhizobia to the root surface and influence various processes occurring at different stages of symbiosis formation. Thus, it was shown that the preliminary incubation of rhizobia with the lectin of the macrosymbiont plant increases the number of nodules and, consequently, the productivity of symbiosis. It is known that the specificity of the legume-rhizobia symbiosis changes in the presence of lectins. Thus, expression of the gene encoding pea lectin allowed to significantly increase the amount of rhizobia colonizing the roots of transgenic rice and other non-plant plants (Vershinina Z.R. et al. 2012). Another natural mediator is a bacterial adhesin RapA1, involved in the adsorption of bacteria on the surface of plant root hairs. Previously part *rap*A1 encoding gene (727 bp) was amplified from DNA of *Rhizobium leguminosarum* PVu5, obtained from bean nodules using Pfu-polymerase (Nigmatullina L.R. et al. 2015). Further *rap*A1 gene was cloned into the binary vector for plant transformation pCambia1301 with leader peptide (110 bp) from pea lectin*psl* under the control of the constitutive 35S promoter of cauliflower mosaic virus.Subsequentlycomposite tomato plant were obtainedusing *Agrobacterium rhizogenes* 15834 bacteria. The plants stably produced RapA1 protein in roots, this phenomenon was proved by Western blot analysis of proteins. In addition, immunofluorescence analysis was carried out, showing the localization of the target protein RapA1 on the surface of transgenic tomato roots.Further testing was devoted to adhesion of bacteria to the root hairs of composite plants. For this experiments,roots ofone-month-old composite and control seedlingswere inoculated with rhizobia *R. leguminosarum* PVu5, pre-labeled with red fluorescent protein (RFP).After incubation with roots bacteria within 24 hourswe counted the number of cells adhered on the roots of control and compositeplants. Analysis showed that transgenic roots of composite plantswith RapA1 sorbed on average 15 times more bacteria in comparison with the control plants.

These data leave no doubt that the bacterial adhesin RapA1 from *R. leguminosarum* is possible to use as a tool to create associative symbiotic systems de novo.

This work was supported by Russian Foundation for Basic Research № 14-04-97005; № 16-04-00902 A; № 16-34-01076.

CONSERVATION AND EVALUATION OF OAT GENETIC RESOURCES IN CHINA

***Zhang Zongwen*[1,2]**

[1] Institute of Crop Science, Chinese academy of Agricultural sciences, Beijing, China;

[2] China Office, Bioversity International, Beijing, China

Email: Zhangzongwen@caas.cn or z.zhang@cgiar.org

Oat is a grain crop in China. It is widely cultivated in north, northwest and southwest parts of the country. Oat is the staple food for many local people in producing areas. It is also popularly used for animal feed. In the long history of cultivation, various types of local oat varieties were derived and remained under different agroecological environments in China. Since 1980s, over 5268 accessions of oat germplasm have been collected and conserved by the national genebank of China, including 2482 accessions of naked type, 2652 accessions of hulled type and 134 accessions of wild species. Morphological variation was characterized for the traits of plant, panicle, flower and grains of oat accessions. Passport and characterization data were documented and shared in National Information System of Crop Germplasm Resources. Efforts were made to evaluate the resistance to drought and salt for oat accessions. Multilocation trials in different environments were carried out to identify accessions with adaptation to the climate change. Genetic diversity of oat collection was assessed with molecular markers, such as AFLP and SSR. With the constructed genetic linkage maps, QTLs related to important traits such as β-glucan content, grain size and plant height were identified. The efforts in conservation and evaluation has promoted the sustainable use of oat germplasm and contributed to the development of oat industry in China.

GRAIN QUALITY IN SPRING WHEAT, ITS WILD RELATIVES AND NEW PROMISING VARIETIES (INTROGRESSIVE FORMS)

A.I. Abugalieva [1,2]

[1]Kazakh Research Institute of Agriculture and Plant Growing, Almlybak, Kazakhstan,
[2]Kazakh National Agrarian University, Almaty, Kazakhstan
e-mail: kiz_abugalieva@mail.ru

The protein content in different types of wheat was formed due to the prevalence of various protein fractions: globulin in the grain of *Ae.triaristata* and *Tr.militinae;* gliadin in *Tr.dicoccoides, Tr.dicoccum* and *Tr.timopheevi.* Glutenin type protein (osborn alkali-soluble fraction), important for gluten formation, is marked on the minimum level of *14,3%* (*Tr.kiharae*) to 20,1% (*Tr.timopheevi*). The protein content in the grain of transitional forms within the north conditions meets the requirements of satisfactory improvers (≥14,0%) as well as for genotype Kazakhstanskaya 10 x *Tr.dicoccum* in the south conditions. The amount of gluten proteins over 50% allows to predict stable formation of gluten for transitional forms, and partly for wild relatives. The amount of gluten proteins, gliadin and glutenin, varies from 49.5% (Kazakhstanskaya 10 x *Tr.dicoccum)* to 56.9% (6583 x *Tr.timopheevi)* for transitional forms. For wild relatives the amount varies from 29,0 % (*Tr.kiharae; Tr.militinae*) to 55,5 % (*Tr.dicoccoides*). The ratio of gliadin to glutenin in wild relatives is typical in favor of gliadin from 1,03 (*Tr.militinae* and *Tr.kiharae)* to 2,34 (*Tr.dicoccoides*). In transitional forms prevalence in this ratio is observed both in favor of gliadin and glutenin (0,74-1,58).

Synthetic forms of spring wheat are suitable for bread-making with prognostic quality levels "Filler" and "Valuable". A number of samples of wild relatives are well suited for industrial use in their pure form. *Tr.kiharae* and *Tr.militinae* can be problematic in their pure form due to gluten content, and *Tr.dicoccoides* - due to gluten quality (very elastic), and most of them were sulfurdificient except *Tr.compactum; Tr.timopheevi; Tr.turgidum*, *Tr.aephiopicum.*Sulphur deficiency in grain according to *N:S* ratio was detected in the early reproductions of almost all synthetics, gradually decreasing in generations to 14,8-16,2 except in Erythrospermum 350 x *Tr.militinae* and Zhetysu x *Tr.militinae* genotypes.

Synthetic forms of winter wheat, according to bread-making type evaluation, are marked as "Valuable" and "Filler". According to physical properties of flour and dough, synthetics vary in dough dilution from 80 to 170 EF, at the level of "Filler" and "Weak" wheat with the best value for the following genotypes: Bezostaya 1 x *Ae.triaristata* and Erythrospermum 350 x *Tr.militinae (*49-45 farinograph units). Bread-making type evaluation shows that bread baked with flour from grain of synthetics is comparable in volume to varieties, including above standards of Almaly (720-760 ml) and Karahan (800 ml) in appearance, porosity and overall bread-baking evaluation.

Cultivars used in the crosses are characterized by valuable high molecular weight glutenin subunits alleles in terms of quality (score 9 and 10 by Payne scale). Identification, and thus and forecast of grain quality, in wild relatives is difficult because of their pronounced difference from the varieties gene pool. Synthetics are forecasted at high molecular weight glutenin subunits, grain hardness and 1B/R as a class for a strong 60% of the total unit.

Results of electrophoretic analysis of gliadin allowed to establish genotype specificity for the *Triticum* and *Aegilops* types. Using cluster analysis wild relatives were classified, and the most remote from the examined forms *Tr.monococcum* (a single diploid sample studied in the unit) and *Tr.ispanicae* were highlighted. The distribution of species across 3 clusters is determined by the absence of (full or of a majority) α-group for Aegilops, and the absence of ω9 and ω89 for tetraploid wheats and *Tr.compactum* (A^bGD).

Research was carried out for the project 0115RK00717 "Synthetic forms as a basis for preservation and usage of wild relatives gene pool for wheat grain quality (nutritional and technological aspects)".

DETECTION OF GENETICALLY MODIFIED ORGANISMS (GMOS) USING ISOTHERMAL AMPLIFICATION OF THE GENETIC CONSTRUCT DNA SEQUENCES

A.A. Amenov, R.N. Kalendar

RSE "National Center for Biotechnology", Astana, Kazakhstan

e-mail: ruslan.kalendar@mail.ru

Detection of genetically modified crops can be achieved by a nucleic acid detection (the amplification of GMO-specific DNA amplicons using PCR). GMO detecting target nucleic acid is inserted foreign gene, including the integration site of the foreign gene, a promoter, a terminator, a selection marker gene and the nucleic acid sequence the reporter gene, such as the cauliflower mosaic virus (CaMV) 35S promoter, the nopaline synthase terminator (NOS terminator) and so on. GMO detection current database has a list of PCR primers to detect all kinds of endogenous reference gene (http://gmo-crl.jrc.ec.europa.eu/gmomethods/). Here we have applied the loop-mediated isothermal amplification (LAMP) method to amplify the commonly-used motifs of the genetic construct (virus regulatory elements) DNA sequences. The isothermal techniques utilise DNA polymerases with strand-displacement activity and are used as a nucleic acid amplification method that can obviate the need for the repeated temperature cycles. Displacement primers help the formation of these hairpins at the ends of the DNA strands and once formed, these structures can be copied into a series of DNA fragments containing multiple units of the target sequence under isothermal conditions utilizing the displacement properties of *Bst* polymerase. The disadvantages of LAMP are complicated primer design and non-specific amplification can take place, where the target DNA is absent and there are low amounts of DNA present in the reaction. We have designed LAMP assays and demonstrated our FastPCR software (http://primerdigital.com/fastpcr.html) for efficient LAMP assays design. The chosen primers match motifs sufficiently conserved in the promoters to allow amplification of almost all targets in the genome. Target sequences for CaMV 35S and T-nos were chosen based upon common identity between different plasmids in the EMBL database containing the promoters and terminator. We have tested the specificity of the technique for use in GMO studies. This work shows that GMO detection can be carried out using LAMP for routine screening.

CELL TECHNOLOGY FOR CREATING PRECOCIOUS FORMS OF SOFT SPRING WHEAT

***N. K. Bishimbayeva*[1], *K. Baymagambetova*[2], *R.A. Urazaliev*[2], *I.A. Nurpeisov*[2], *V.A. Chudinov*[4], *G.A. Sereda*[3], *L.V. Bekenova*[5], *O.S. Gass*[6], *M.K. Karabayev*[7], *I.R. Rahimbayev*[1]**

[1] Institute of Plant Biology and Biotechnology (IPBB), SC MES RK, Almaty,Kazakhstan
[2] Kazakh Research Institute of Agriculture and Crop Production, Almalybak, Kazakhstan
[3] Karaganda Research Institute of Breeding and Crop Production, Kazakhstan
[4] Karabalyk Agricultural Experimental Station, Kostanai region, Kazakhstan
[5] Pavlodar Research Institute of Agriculture, Kazakhstan
[6] North-Kazakhstan experimental station, North Kazakhstan region, Kazakhstan
[7]CIMMYT-Kazakhstan, Astana, Kazakhstan

e-mail: gen_jan@mail.ru

The main areas of spring wheat cultivation are the northern regions of Kazakhstan, characterized by late spring, early autumn and short summer. Crop destruction of most commercial cultivars under the autumn rain and frostsbrings huge economic losses.Therefore, the creation of precocious lines and cultivars of main agricultural crop - spring wheat, is a very actual task.

We have developed cell technology for creation precocious forms of spring wheat with the complex of valuable economic-biological traits. This method was tested on 28 commercially important wheat varieties of new generation which are cultivated in Northern and Central Kazakhstan. 398 R0 plants were regenerated from long-term cultivated calli of 28 wheat varieties. From these 110 plants of 18 varieties brought up R1 seed generation. 47 lines (37%) from those 110 lines of R1 we selected that had accelerated term of maturation on 3-6 days compared to initial varieties. Ecological trial of selected lines in R2 generation at North and Central Kazakhstan conditions allowed to prove the expression of the precocity trait (accelerated development on 1-8 days) and to select the precocious forms (25-47,7% from the number of lines tested) with high productivity and drought resistance traits which were most prospective for each region.

In 2016 17 precocious lines (70,8%, 3-8 days earlier, than standart) were selected from 24 wheat lines of R4 generation in Pavlodar region, in Kustanay region - 15 precocious lines (44,1%, 2-4 days earlier) were chosen from 34 lines of R4 generation. Almost all selected precocious lines have either an increase of productivity or have similar level comparing withstandart.

It should be noted that the obtained output of precocious forms aremuch higher than output of transgenic forms with introduced useful genesobtained by genetic transformation (0,1-2,0%) (Liang Skinner, 2004). Therefore, we believe the cell technology developed in our laboratory is an effective alternative biotechnological method for the creating of precocious forms of spring wheat.

This work performed under the applied project № 1911 of GF1 program (2012-2014) and the Programm of fundamental research №0149 of Target Program Funding (2015-2017), SCMES, RK.

OBTAINING OF TRANSGENIC PLANTS OF MAIZE RESISTANT TO INCREASED DROUGHT

D.L. Daurov, O.V. Karpova, A.M. Alexandrova, R.M. Nargilova, K.Zh. Zhambakin, M.Kh. Shamekova

Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan
Email: Dias.Daurov@mail.ru

Gene expression of transcription factor DREB2A inside pathways signal transduction occurs in conditions of high temperatures and drought and requires post-translational modifications.

During the cloning, was conducted *in vitro* mutagenesis of the coding sequence of the gene DREB2A from *Arabidopsis thaliana,* the aim of deletions had a size of 90 nt in the central region to purchase Δ*AtDREB2A* gene, encoding the catalytically active form of the protein.

For the subsequent agrobacterium-mediated transformation of maize plants were used recombinant DNA construct containing gene coding sequence of the transcription factor Δ*AtDREB2A*, which was cloned in the composition of the agrobacterial binary vector pCAMBIA2300 under the control of inducible promoter *rd29A* gene of *Arabidopsis thaliana*, and different 5'-noncoding sequences (5'-TMV, 5'-PVY or 5'-AMV), 3'-NTP tobacco mosaic virus (3'-TMV) and the nopaline synthetase (nos) terminator gene, required for expression of the transgene in plant cells.

Transformation was performed by the method of cultivation of immature embryos of inbred lines of maize, which were kindly provided by A. Sh. Omarova (Scientific research Institute of agriculture and plant growing) on agrobacterium-mediated lawn. As a result of the transformation 47 plants was obtained, after screening on selective nutrient medium. The obtained plants were verified for the presence of DNA target gene Δ*AtDREB2A*, as well as RNA transcripts.

23-plants, which have shown a positive response to the presence of the transgene, have been landed in soil in controlled conditions, adapted to greenhouse conditions. From each plant have been selected a plant material for isolation of total RNA and conducted the reaction of reverse transcription to determine the presence of RNA transcripts corresponding to the target gene. A positive response was obtained from nine plants (variants of 5'and the TMV 5'-AMV).

Moreover in a laboratory conditions initiated testing the transgenic lines for resistance to drought conditions.

THE ROLE OF OAT GENE IN PLANT PROLIFERATING TISSUES

A.A. Egorova, P.S. Nikulin, S.S. Ibragimova, A.V. Kochetov, V.K. Shumny, S.V. Gerasimova

Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

e-mail: sealin-nsk2@yandex.ru

Ornithine aminotransferase (OAT) enzyme catalyzes the transfer of the delta-amino group from L-ornithine to oxo-glutarate. In plants, this reaction biochemically connects urea cycle, proline cycle, and poliamines biosynthesis pathway. OAT activity is usually associated with biotic and abiotic stress response and nitrogen metabolism.

To study the functions of plant OAT gene, a set of genetic models has been created in our lab: transgenic *N. tabacum* plants with overexpression and antisense suppression of OAT gene and transgenic *A. thaliana* plants with reporter gene system containing *E.coli* β-glucuronidase gene (GUS) under *A. thaliana* OAT gene promoter control. Our previous results show that OAT promoter activity is associated with growth zones, and transgenic *N. tabacum* plants with constitutive overexpression of OAT gene demonstrate high growth performance under salt stress.

The aim of present study is to investigate the role of the plant OAT gene in processes related to plant growth.

The transcriptional regulation of OAT gene was investigated on *A. thaliana* plants with reporter gene system. Seedlings were treated with different growth regulators; the promoter activity was analyzed histochemically. The reporter protein expression was observed in response to different forms of auxin (IAA, NAA, and 2,4D), cytokinin (6-BAP), and ethylene precursor (ACC). These results allow us to suggest the role of OAT gene in plant cell proliferation and expansion.

To investigate the role of OAT gene in cell proliferation a model system of *in vitro* crown gall formation was implicated. Crown gall is a plant tumor caused by *A. tumefaciens.* Leaf explants of model transgenic plants *N. tabacum* with overexpression and suppression of OAT gene were infected by *A. tumefaciens* virulent strain A281. The dynamics of gall formation was estimated. Preliminary results show gall formation is suppressed in transgenic *N. tabacum* plants with OAT gene constitutive overexpression.

The results show that OAT gene might be involved in plant cell proliferation processes.

The work is supported by № 0324-2015- 0005 Budget Project.

IDENTIFICATION, CHARACTERIZATION AND EXPRESSION ANALYSIS OF *CLE* GENES IN POTATO (*SOLANUM TUBEROSUM* L.)

M.S. Gancheva, I.E. Dodueva, L.A. Lutova

Saint-Petersburg State University, Saint-Petersburg, Russia

e-mail: vaiagan@mail.ru

CLE peptides (CLAVATA3/ENOSPERM SURROUNDING REGION) are small proteins that play a role in regulation of various types of meristems: shoot and root apical meristems, pro-/cambium, nodule meristem and tumors. Potato is the most important non-cereal in the world and the global production of potato tubers exceeds 300 million tons per year. In our work, we focused on the role of CLE-peptides in the tuber development in potato (*Solanum tuberosum* L.). We identified 12 *StCLE* genes from potato (*Solanum tuberosum* Group Phureja) genome and analyzed their phylogeny, gene structures and chromosome locations. Real-time PCR analysis showed that expression of some *StCLEs* changed after initiation of tuber development. In addition, we found cortex-, pith- and perimedullary region-specific expression of some *StCLEs*. We suggested that CLE peptides encoded by these genes regulate tuber development.

ANTHOCYANINS IN WHEAT: PLANT PROTECTION AND HEALTH BENEFIT

E. Gordeeva [1], ***O. Shoeva*** [1], ***R. Yudina*** [1], ***N. Usenko*** [2], ***Y. Otmakhova*** [2], ***T. Amstislavskaya*** [1], ***K Pavlov.*** [1], ***E. Khlestkina*** [1,2]

[1] The Federal research center Institute of Cytology and Genetics, Siberian Branch of the Russian Academy of Sciences, Novosibirsk, Russia

[2] National Research Novosibirsk State University, Novosibirsk, Russia

Email: elgordeeva@bionet.nsc.ru

Anthocyanins can be synthesized in wheat grains, leaves, culms, coleoptiles, auricles, glumes and anthers. A precise genetic model, such as NILs (near-isogenic lines), is useful for comparative studies aimed at finding out advantages (or disadvantages) of the presence of anthocyanins in different parts of wheat plant. Marker-assisted backcrossing approach based on the microsatellite DNA markers was used to develop a set of wheat NILs with different combinations of anthocyanin biosynthesis regulatory genes. By our estimates, the use of the DNA-markers at least twice decreased time needed for line development, and reduced sowing area needed for this at least 70 times. A current set of NILs derived from cultivar Saratovskaya 29 includes 10 lines. It was demonstrated that the presence of anthocyanins in coleoptiles has some protective effect on seedlings grown from seeds exposed to moderate irradiation dose (50 Gy), while their accumulation in grain pericarp has a potential for seed longevity. The NILs differing by the presence of anthocyanins in grains were also used to access influence of 'anthocyanin' diet on mice cognitive ability and to estimate its neuroprotective effects. Behavioral phenotyping showed that intact animals from the group that were get grains of NIL with anthocyanins, had higher rates for working memory assessment than animals receiving grains of NIL without anthocyanins. Further question was, whether good-quality bread can be obtained from anthocyanin-colored grains. Again, we compared NILs to distinguish the effect of anthocyanins from many other biochemical features, which could influence bread quality. It was shown, that bread-making quality and organoleptic properties of bakery products made from anthocyanin-colored grains, did not concede, or in some cases were higher than corresponding properties of products obtained from control NIL grains. It was demonstrated that anthocyanins are resistant to baking process. By our estimates one can get up to 1,03 mg of assimilable anthocyanins with 100 g of whole-grained bread produced from anthocyanin-colored grains.

Thus, the specific wheat genes responsible for anthocyanin pigmentation are an attractive target for future accelerated marker-assisted breeding.

The Russian Science Foundation (Project No 16-14-00086) supported comparative studies of the NILs under irradiation exposure and assessment of 'anthocyanin' diet effect in mice.

INSERTION OF 2A PEPTIDES BETWEEN ORF4 AND ORF5 OF GRAPEVINE VIRUS A

D.A Gritsenko*, N.N. Galiakparov

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

*e-mail: d.kopytina@gmail.com

Grapevine virus A (GVA) is responsible for considerable crop losses. GVA (a Vitivirus) is associated with the Kober Stem Grooving disease. Virus genome is positive RNA with 5 open reading frames (ORF). ORF3 incodes movement protein, ORF 4 is coat protein and ORF 5 is binding protein and involved in pathogenesis. The investigation of GVA molecular biology will allow to develop a viral vector for the production of heterologous genes in plants. Usually, the viral vectors for simultaneous expression of several proteins contain IRES or 2A peptides (self-cleaving peptides). In this work the insertion of T2A / T2A-E2A sequences between ORF4 and ORF5 of GVA was carried out to study the effect of the 2A peptides on the efficiency of the capsid protein and infection process. pCASSgva vector carrying the complete genome of GVA was used for modification of the grapevine virus A genome. The gene encoding the capsid protein was changed by using PCR mutagenesis for removing the stop codon. CP-T2A-ORF5 / CP-T2A-E2A-ORF5 constructs were developed; T2A-ORF5 / T2A-E2A-ORF5 were in frame with CP gene and under control of CP subgenomic promoter. The complete modified genome of grapevine virus A for two constructs was assembled in pCAMBIA 2300 binary vector. Proteins were isolated from infected leaves of N. benthamiana at 4 day after agroinfiltration and capsid protein expression was confirmed by western blotting. Expression results show that capsid protein and ORF 5 protein was cleaved but we could not behold any symptoms of infection on the upper leaf surfaces during 20 days.

DEVELOPMENT OF IN VITRO REGENERATION SYSTEM FOR OAT LOCAL VARIETIES

T. Kapasuly, Z.R. Muchitdinova, N.K. Bishimbayeva

Institute of Plant Biology and Biotechnology (IPBB), SC MES RK
Almaty, Kazakhstan

e-mail: gen_jan@mail.ru

Effective use of biotechnological methods in crop breeding depends on the development of *in vitro* plant regeneration systems. Oats is known as one of the most "difficult" grain crops, characterized by a low frequency and strong genotype dependence of embryogenic structures induction and plant regeneration. It was shown, that only one genotype from 15 oat genotypes has been selected as high embryogenic, and plant regeneration has been distinguished only for two genotypes (Birsin et al., 2001). Therefore one of the important tasks of modern plant biotechnology is the overcoming of genotype dependence of *in vitro* plant regeneration process in oat tissue culture. The aim of this work was to reveal common regularities of morphogenesis *in vitro* for different oat cultivars and to develop universal regeneration system acceptable for different genotypes. For this purpose we studied callus induction process, morphological heterogeneity, metamorphosis and regenerative potential of the induced tissues. All stages of investigation were accompanied by histological investigation of primary, long-term subcultivated tissues and tissues in the moment of methamorphosis.

Three oat cultivars of Kazakh Research Institute of Agriculture and Crop Production – Kulan, Jorhga, Kulager, were used as an object of investigation. It was established that callus induction and morphogenesis processes of all three genotypes depend on 2,4-D concentration. Maximum rate of callusogenesis is varied from 46.8 to 60.7 % depending on cultivar. There are two common morphological types of calli have been identified in oat tissue culture: friable nonembryogenic (NE) and globular embryogenic callus (EC). Friable tissue is more stable and produce embryogenic callus during methamorphosis in optimized media. EC induction ranges from 23.53% to 58,8% depending on genotype. Regeneration of plants from embryogenic callus has been achieved in optimized medium.

Histological study of EC revealed a common features: a huge amount of single embryogenic cells on the surface of the embryogenic tissue and globular embryoid separation, which indicate that in this type of callus, embryoids can have both unicellular and multicellular origin. On the surface and inside of EC the dense net of extracellular substances, stained by alcian blue, has been observed.

Thus, for the first time we have studied the processes of metamorphosis of oat callus tissues, identified morphologically stable tissue types universal for different genotypes. We have developed in vitro regeneration system for oat local varieties which can be used in plant transformation works as a recipient system for introduction of usefull genes into oat genome. Also this system is of great scientific interest as an object for the study of totipotency of plant cells *in vitro.*

This work performed in the framework of fundamental research program №0149, Target Program Funding, IPBB, Science Committee, Ministry of Education and Science, Republic of Kazakhstan (2015-2017).

ANTHER CULTURE METHOD FOR RAPID SELECTION OF WINTER TRITICALE VARIETIES FOR VOLGA REGION

T. I. Djatchouk, A. V. Pominov, I. A. Kibkalo, O. V. Khomyakova, V.N. Akinina, Yu. V. Italiyanskaya

Agriculturasl Research Institute of Southeast region, Saratov, Russia

e_mail: raiser_saratov@mail.ru

In the Volga region, as well as in Russia as a whole, the problem of the direct use of DH-lines as a elite selection lines is a new. The homogeneity of the varieties of haploid origin can address the problem of their adaptability in this unique climate region, primarily drought resistant.

By analysis of the advanced DH-lines and varieties in comparison with the official standard it was founded, that they are exceeded it at 0, 18-0, 50 t / ha. DH-line №9 was the leader in the grain yield in different years of studying. On the second indicator of adaptation - the 1000 grains weight - DH-lines were compared to inbred lines in arid Volga region.

A prerequisite of haploid breeding using is its ability to express different types of gametes that ensures the implementation of the potential genetic variability of hybrid population and its breeding value. In a comparative study of 10 DH-lines derived from one hybrid was revealed the different degree of selectable features - grain yield, 1000 grain weight, plant height and index of SDS-sedimentation. Genetic diversity of lines derived from this hybrid was reflects in the spectrum of storage proteins - gliadins and glutenins. A wide range of variability of traits of DH-lines reflected the numerous types of recombination in microspores.

Thus, in the arid Volga region triticale DH-lines compete with the standard and inbred lines for grain yield and 1000 grain weight as the primary adaptive traits. The possibility of obtaining positive transgression does not depend on the method of creating a breeding material. The potential genetic variability of the hybrid caused by genes recombination. At the same time it should be noted that the bottleneck of haploid biotechnology in cereals is a genotypic relationship in all phases of DH-lines production, which limits their use in a wide crosses.

CROP GENES MODIFIED USING CRISPR/CAS9 SYSTEM: SYSTEMATIC ANALYSIS OF PUBLISHED REPORTS

A.M. Korotkova, S.V. Gerasimova, V.K. Shumny, E.K. Khlestkina

The Federal Research Center Institute of Cytology and Genetics, Novosibirsk, Russia

e-mail: korotkova@bionet.nsc.ru

CRISPR/Cas9 system is the most promising among genome editing tools. When applied to crop genes, it can provide development of modified nontransgenic plants with possibility of simultaneous multiple modifications.

Systematic analysis of reports on the use of CRISPR/Cas9 in crops was carried out. From a total of 200 articles found for 42 crops by search for "CRISPR & crop name" within article titles, abstracts and keywords in Scopus database, only 87 has been recognized as original articles describing editing crop genes with CRISPR/Cas9 system, resulting in modification of 139 genes of 15 crop species with maximum in rice (76 genes). In these studies, ability to get modified nontransgenic plants was widely demonstrated. However, in most cases modifications have been done either to study gene function or to try/adjust/modify the technology to certain crop/genetic system. Less than 50 target genes were modified for potential crop improvement. In most of these cases, modifications resulted in knockout of the genes such as negative growth regulators or negative regulators of plant resistance. Knockout of these genes resulted in increased productivity and plant resistance, respectively. Other phenotype changes achieved by CRISPR-directed gene knockout are reduced height, which may have positive effect on plant productivity, and increased tolerance to herbicides. However, since estimated number of “negative regulators” is limited in plant genomes, the CRISPR-directed gene knockout has a restricted potential for crop improvement. Intensive application of CRISPR/Cas9 system for more complicate modifications such as replacement of defect alleles or insertion of desired gene is required. In addition, to provide a basis for broad practical application of genome editing, more cultivars of crop species should be involved in ongoing studies. Just a few genotypes have been used for CRISPR/Cas9-based gene modifications thus far.

In our studies, we focused on the use of CRISPR/Cas9 system to change cereal grain and spike morphology. Primary target genes selected for modification are barley *Nud* and *Vrs1* genes. Knockout of these genes is expected to transform hulled grains to naked and two-rowed spikes to six-rowed, respectively. Target genotypes are hulled two-rowed spring barley cultivars from the local collection of spring barley. The current results of ongoing large-scale screening of these cultivars for regeneration ability as well as development and application of constructs for CRISPR/Cas9-based knockout are presented and discussed.

The study was supported by the Russian Science Foundation (Project No 16-14-00086).

WHEAT TRANSFORMATION EFFICIENCY IN BREAD WHEAT CV. SARATOVSKAYA 29, KAZAKHSTANSKAYA 19 AND ALMALY

E.R. Maltseva, Y.A. Skiba, A.P. Chirkin, G.A. Iskakova, N.A. Yurkevich, S.S. Baizhumanova , D.A. Naizabayeva, R.E. Zhidkeyeva, G.A. Ismagulova

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

e-mail: elina_m@inbox.ru

The main index of plant transformation's success is its efficiency. It is especially important for biolistic method, where it is not high with accidental maximum shown in some studies. Biolistic transformation efficiency depends on bombardment's parameters, donor material's condition, and even more on the genotype of the plant chosen for the experiment.

In this study we have established stable transformation efficiency for three bread wheat varieties cultivated in Kazakhstan – spring wheat Saratovskaya 29 (St 29) and Kazakhstanskaya 19 (Kz 19), and winter wheat Almaly.

Minimal expression unit carried wheat chitinase gene with gene conferring resistance to hygromycin. The protocol of cell culture work and the conditions of bombardment are given in previous publications. The target gene insert was checked by PCR with specific primers.

A total of 2652 explants were used for biolistic transformation (St 29 – 468, Kz 19 – 732, Almaly - 1452). The experiment resulted in 14 transgenic plants with average efficiency of 0.53%. Both Kz 19 and Almaly showed 0.55% of efficiency with 4 and 8 plants correspondingly, while this index was lower for St 29 – 0.43% with 2 PCR-positive plants. In transformation experiments we should also account for the regeneration ability of wheat. The three studied varieties were chosen after preliminary experiments, which showed their fitness to cell culture work. The average regeneration effectiveness of the experiment, i.e. the ratio of plants produced for PCR analysis to the number of explants, was 3.1%, with Kz 19 expressing the lowest regeneration index of 1.8% and Almaly being most successful with 3.9%. The selection stage yielded 71 regenerant plants, only 14 of which (19.7%) were PCR-positive, meaning that hygromycin selection press must be stronger (100 mg/l) than recommended (50 mg/l).

Thus, three bread wheat varieties were found to be suitable for stable biolistic transformation and showed good results in transformation efficiency study. Further research of insert's stability is under way.

EFFICIENCY OF BIOLISTIC CO-TRANSFORMATION IN POTATO VARIETIES AKSOR AND NEVSKIY

Y.A. Skiba, E.R. Maltseva, A.P. Chirkin, N.A. Yurkevich, D.A. Naizabayeva, R.E. Zhidkeyeva, G.A. Ismagulova

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

e-mail: yuriy.skiba@gmail.com

A whole set of approaches is used for potato transformation, agrobacterial being the most popular. However, biolistic transformation offers an opportunity of introducing several genes with high co-transformation efficiency. At the same time, no backbone DNA is introduced since only minimal expression units are used.

The experimental series was focused on stable introduction of two genes – chitinase and b-1,3-glucanase – to potato varieties cultivated in Kazakhstan (Aksor and Nevskiy).

The regeneration abilities of various explant types were tested and internodes' callus was chosen for further use. Biolistic transformation was carried out using pBI121 vector with 100 ng of each target gene for minimal expression unit driven by CaMV-35S promotor. After the bombardment the explants were recovered on the medium with half dose of the osmotic agent and then subcultured to medium supplemented with 2,4-D and zeatin. The selection was carried out with kanamycin and resulting potato shoots analyzed by PCR with target gene-specific primers.

There were 5 experimental series 10 plates each, with total of 862 explants: 475 of Aksor variety and 387 of Nevskiy. The experiments resulted in six transformed plants: one carrying chitinase gene insert, one – glucanase gene insert, and four plants with both inserts. Both varieties were found suitable for biolistic approach and for selection with kanamycin, which is genotype-dependent and might make regeneration lower. The average transformation efficiency was found to be 0.7% with maximum of 0.96% for Aksor internodes. The efficiency of co-transformation was 66.7%, adding to the data of other authors who point out the high level of target genes' co-integration from two independent minimal expression units.

Biolistic transformation is still not very popular for potato, despite the advantages it offers. The information on the efficiency of this method is scarce and in many cases incomparable, making the data collected in this study valuable for comparison of the stable transformation efficiency in potato.

EXPRESSION IN PLANTS OF THE C-TERMINAL FRAGMENT OF THE HUMAN ALPHA-FETOPROTEIN

***G.E. Stanbekova* *[1,2], *L.T. Nadirova* [1,2], *Beisenov D.K.* [1,2], *B.K. Iskakov* [1,2]**

[1]Aitkhozhin Institute of Molecular Biology and Biochemistry, Almaty, Kazakhstan

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

*e-mail: gulshanst@yahoo.com

Human alpha-fetoprotein (hAFP) is an embryo-specific protein, also known as a tumor marker and could be found in some cases of liver and reproductive system cancers. The C-terminal fragment possesses essential properties of the full-size hAFP, such as the ability to bind to the AFP-specific receptor and to inhibit the proliferation of estrogen-dependent cells *in vitro.* Biological features of the hAFP offers great opportunities to develop various anticancer drugs that could be highly selective to the tumor cells. However, this promising perspective is limited to the complexity and the cost of the hAFP purification from the abortion serum. Plant-based production is the way to simplify and cheapen the production of hAFP.

The cDNA fragment corresponding to C-terminal 357-590 amino acids of hAFP was amplified by PCR using full-length cDNA as a template, which has been cloned earlier from AFP-producing human hepatocellular carcinoma (HepG2) cell line. The amplicon was cloned first into bacterial vector pET11d, expressed in *Escherichia coli* and then was transferred into plant vector pCAMBIA2300. Recombinant DNA construct in plant vector contained the following *cis*-regulatory sequences: 35S CaMV promoter; 5'-untranslated region of tobacco etch virus; transcription terminator 35S CAMV. This recombinant DNA construct was used for stable transformation of tobacco plants *Nicotiana benthamiana*. The transgenesis was confirmed by PCR analysis of genomic DNA extracted from kanamycin-resistant plants. Subsequent western blot analysis showed expression of the recombinant C-terminal fragment of AFP with molecular mass about 27 kDa in some transgenic plant lines.

MAPPING OF PHOTOPERIOD RESPONSE LOCI IN THE RILS POPULATION OF HEXAPLOID OAT

***P.S. Ulianich*, E.A. Grigoreva, V.A. Koshkin, I.G. Loskutov, E.K. Potokina**

[1]Vavilov Institute of Plant Genetic Resources (VIR), St.Petersburg, Russia

e-mail: Ulianich.P@inbox.ru

Photoperiodic sensitivity (PS) is one of the most important agronomic characteristics, which determines the performance of crops and their adaptation ability. The genes responsible for photoperiod reaction (Ppd) in hexaploid oats (*Avena sativa* L.) are not identified yet. Identification of Ppd genes for oat would significantly improve the selection of early ripening varieties, which are less affected by *Fusarium* toxins. On other hand, weak photoperiod sensitivity may enhance adaptation of oat cultivars followed by increasing acreage.

To map Ppd loci in oat, we employed the Recombinant Inbred Lines (RILs) population containing ~120 genotypes of F4 that are contrast in their photoperiod response: their heading date delay in short day (SD) conditions comparing to long day (LD) varied between 8-40 days. The RILS were obtained from the cross of photoperiod insensitive local variety Chihuahua (Mexico) and photoperiod sensitive cv. Anatolisher (Turkey). The RILs population was propagated and scored for heading date in Pushkin experimental station of VIR (St.Petersburg) under condition of long (16 hr) and short (12hr) photoperiod. From leaves of the plants total DNA and RNA was isolated. For genotyping of the RILs population the high-throughput RAD-seq method (Illumina) will be employed.

At the same time, we continued the *Ppd* candidate gene identification based on synteny approach. Employing the short ortholog sequence identified earlier (~ 130 bp) we used the Step-Out RACE method to define a full length sequence of *Ppd* loci in oat genome. The method allows obtaining data on the structure of the full-length transcript, based on a minimum of information about its sequence (30-50 bp). With this method, it is planned to identify the sequence of the candidate gene for *Ppd* and compare those sequences between lines and parental genotypes of RILs that are contrast in their photoperiod sensitivity to identify functional polymorphism. At the final stage of research, we will check whether the polymorphism of *Ppd* candidate genes segregates with photoperiod sensitivity of RILs. The results of molecular marking of Ppd genes may help breeders to predict the length of the vegetation period in oat genotypes in the very early stage of ontogeny.

OBTAINING OF DOUBLE HAPLOID LINES OF INTERSPECIFIC AND INTERGENERIC WHEAT SYNTETICS

R.S. Yerzhebayeva, A.I. Abugalieva, A.K.Danyarova

Kazakh Research Institute of Agriculture and Plant Growing, Kazakhstan

e-mail: raushan_2008@mail.ru

Production of double haploids plants through anther culture is a very important tool to accelerate plant breeding. Double haploids plants derived from microspores provide a quick way to obtain homozygous and homogeneous lines of important crops.

As part of the budget program O.7222 of MARK by the subproject «The creation and phenotyping of double haploid and somaclonal lines to stress resistance, productivity and quality of grain» was conducted research for the obtainingof double haploids lines of interspecific and intergeneric wheat syntetics. During the period of 2015-2016 years, using anther culture technology, were studied 74 winter and spring lines obtained by distant hybridization with wild relatives of wheat as *T.militinae Zhuk., T.timopheevii Zhuk., T.kihara Dorof. et Migusch., Ae. cylindrica L., Ae. triaristata Willd.* (Kozhahmetov, 2010).

The donor material was grown on a research field of Kazakh research institute of agriculture and plant growing and spikes were selected at the stage of medium mononuclear microspores. All spikes of donor plants were subjected to cold treatment at + 2- + 4 ° for 14 day sand aseptically transferred to two culture media to induce embryogenesis (150 anthers/Petri dish) – modifier MS (Murashige T., Skoog F, 1962) supplemented 90 g/l maltose, 2 mg/l 2,4-D and 50 g/l Ficoll 400 and AP (IsmagulA., et al, 2013).

Evaluation of the embryogenesis induction of 74 winter and spring wheat synthetics genotypes showed that the output of embryo-like structures (ELS) varied on different culture medias from 3 to 166 ELS/150 anthers of one Petri dish. On average, in one Petri dish formed 45.7 androgenic structures. Comparative analysis of induction of androgen structures on two culture medias AP and mMS showed that the highest induction of embryogenesis was observed for the AP, by prescribing ASPFG, where were fixed 200 ELS to one Petri dish.

According to the results valuation of androgenic structures of studied lines in two variants of culture media were isolated responsive genotypes: a) spring - 6625 x *T.timopheevii*-10 (150±56,4 ELS), 6569 x *T.militinae* (183±31,4 ELS); b) winter - (Erythrospermum 350 x *T.kihara*) x Erythrospermum 350-92 (210±53,7 ELS); (Bezostaya1 x *Ae.cylindrica) x Erythrospermum 350* (123±23,4 ELS).

On the basis of the method of anther culture and spontaneous doubling of the chromosomes were obtained 762 grains of 28 double haploids lines of interspecific and intergeneric wheat synthetics.

This research has foundation by project N0115PK02312 Ministry Agriculture Programme O.0721 “Molecular breeding, genomics and biotechnology in the cultivar creation of cereals”.

TRANSFER OF TRANSGENES TO VARIETIES AND RELATIVES OF RAPESEED

K.Zh. Zhambakin, M.Kh.Shamekova, A.K.Edilova

Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan

Email: zhambakin@gmail.com

Aim of the study: The cultivation of genetically modified (GM) crop varieties leads to the transfer of transgenes to other plants as a result of cross-pollination. As a result of increasing environmental risks, for which the possible significant change to biodiversity of wild flora and fauna, as well as agro-technical risks, such as decline in biodiversity among cultivars, and change of the properties of non-target qualities of varieties, the appearance of super-weeds. In addition, among the possible consequences of cross-pollination with transgenic plants an increase in the invasive potential of hybrids and weed and disappearance and assimilation of wild species are indicated.In this paper we studied the possibility of gene transfer from GM rapeseed to non-GM oilseed rape varieties and their wild relatives.

Materials for the study were GM Chris rapeseed cultivar *(Brassica napus)* with reporter gene 2GUS35S115x3GUS, derived from transgenic plants of 2015 rapeseed varieties Chris *(Brassica napus), Brassica juncea* Rocket variety *(Brassica juncea),* Golden and wild rapeseed varieties *(Brassica campestris),* and shepherd's purse *(Capsella bursa-pasroris)*. Experiments were carried out for 2 years (2015 and 2016). In a study of transgenes transfer experimental design was used, in which the central portion is surrounded by areas of GM with non-GM rapeseed.In a study in the first year of a central plot contained transgenic rapeseed Chris *(Brassica napus)* with 2GUS35S115x3GUS genome which was surrounded by several groups of non-genetically modified rapeseed plants at a distance of 1-10 meters. The first round of non-transgenic plants - the recipient was divided in the form of sectoral areas. On the experimental plot of the 2nd year (2016) rapeseed colza and mustard, as potential recipients sown oriented to the cardinal points (North, South, East, West, North-East, North-West, South-East and South-West). Rapeseed was sown sector, and rape and mustard rays at 18.3 meters from GM plants.After harvesting, the samples were screened on kanamycin, followed by an analysis of the seeds in the presence of a foreign gene in the studied varieties. Seeds were plated on a Petri dish with nutrient medium containing 50 mg / l kanamycin.

Analysis of the results showed the presence of cross-breeding between GM and non-GM varieties of oilseed rape. A significant effect of environmental conditions was revealed, depending on the year of cultivation. It was determined that the hybridization level of the transgenes in the 1st year amounted to 4.8% of the rapeseed *(Brassica napus),* 1,3% of mustard *(Brassica juncea),* and 0.9% with rapesedd*(Brassica campestris)*. In the 2nd year cross-pollination with transgene was 22.5% for the rapeseed (Brassica napus), 7,8% for mustard *(Brassica juncea)* and 6.8% for high-quality summer rapeseed *(Brassica campestris)*. Hybridization with shepherd's purse *(Capsella bursa-pasroris)* and wild rapeseed were not found. At the same time, the largest cross-pollination with transgenic canola rapeseed varieties at a distance in the first year, from 2 to 7 meters, and in the second year, from 2 to 13 meters.

These studies are carried out within the framework of funding for Kazakhstan scientific technical program 0.0677 “Development of biotechnological bases for the creation and monitoring of genetically modified plants with improved economically valuable traits” for 2015-2017.

DEVELOPMENT OF ANDROGENIC TECHNOLOGY FOR OAT AND BARLEY

R.S. Erzhebayeva *[2], A.K. Daniyarova [2], B.S. Sariyev [2], A. Zhumakayev [1], N.K. Bishimbayeva [1]

[1]Institute of Plant Biology and Biotechnology (IPPB), SC MES RK, Almaty, Kazakhstan
[2]Kazakh Research Institute of Agriculture and Crop Production, Almaty region, Almalybak, Kazakhstan

*e-mail: raushan_2008@mail.ru

Barley and oat are multipurpose crops due to their food, fodder and technical values. Currently, demand for barley and oat grain, as for sources of concentrated and roughaged fodder, has increased sharply with the rapid development of animal husbandry and processing industry of Kazakhstan. According to the Governmantal Program of Kazakhstan's Agro-Industrial Complex Development for 2017-2021, among target indicators to achieve is an increase of barley production up to 4004 thousand tons and oat production up to 517 thousand tons per year. Due to the fact that homozygous lines are available for selection in the first generation hybrids (F1), haploid technology has the potential for significant acceleratation of plant breeding. We carried out a research on the development of androgenic technology for plant breeding of barley and oat cultivars of Kazakh Research Institute of Agriculture and Crop Production.

In order to select the most responsive genotypes to the *in vitro* morphogenesis we have studied embryogenesis and regeneration in anther culture of 7 barley varieties (Arna, Asem, Birlik-20, North-1, Turan-2, Ula and Elik) and 7 varieties of oats (Alaman, Donen, Jorha, Kulager, Kazakhstani-70, Kulan, Baige). As a result, the most responsive genotypes have been selected: for barley - Asem (52 androgenic structures/100 anthers), for oat - Alman (23 androgenic structures/100 anthers).

Selection of optimal medium for anther culture of barley and oat is conducted on five liquid nutrient media with different mineral composition and balance of phytohormones in the anther culture: FHG (Kasha K.J. et.al., 2001); KFWC (Parminder K.Sidhy, 2009); W14 (Ponitka A. et.al., 2009); AP (Ismagul A. et al., 2013).

According to the obtained results liquid nutrient medium FHG (Kasha K. J et al., 2001) was selected for barley, where barley genotypes formed 22,2 androgenic structures/100 anthers in average. The nutrient medium W14 (Ponitka A. et.al., 2009) was selected for oat where oat genotypes was formed 15,6 androgenic structures/100 anthers in average. The developed model systems were used for histological and ultrastructural investigation of cytophysiologic regularities of androgenesis *in vitro* as well as for optimizing media composition for plant regeneration.

This work performed in the framework of fundamental research program №0149, Target Program Funding, IPBB, Science Committee, Ministry of Education and Science, Republic of Kazakhstan (2015-2017).

CURRENT STATE OF CISGENESIS AND RAPID CROP CYCLE BREEDING IN GERMAN FRUIT BREEDING RESEARCH

Flachowsky H.*, Hanke M.-V.**

[1]Julius Kühn-Institut, Federal Research Center for Cultivated Plants, Institute for Breeding Research on Fruit Crops, Dresden, Germany

*e-mail: viola.hanke@julius-kuehn.de

Genetic engineering provides promising tools for improving the efficiency of fruit tree breeding. Beside classical transgenic and intragenic approaches cisgenesis and rapid crop cycle breeding have recently aroused considerable attention as New Plant Breeding Techniques in Europe. Both strategies allow genetic improvement in a very smart way, but the final products are free of foreign DNA from outside the natural gene pool.

Cisgenesis offers the opportunity to equip well established apple cultivars with additional beneficial traits (e.g. genes), such as resistances to different pathogens for example. In Germany much effort has been made in this direction and an efficient protocol for producing cisgenic apple plants was successfully established. Using this protocol different cisgenic apple lines containing resistances to apple scab caused by *Venturia inaequalis* and fire blight caused by *Erwinia amylovora* were created. These lines were tested on their cisgenic state by molecular standard techniques such as PCR, Southern blot and qRT-PCR. Their resistance was tested by artificial inoculation in the greenhouse using strains differing in their virulence.

Rapid crop cycle breeding is aimed to overcome the long-lasting juvenile period of apple seedlings, which is the most time-consuming process making fruit tree breeding inefficient and expensive. Transgenic early flowering plants seem to be a promising idea to overcome this problem. Recently it was shown that the BpMADS4 gene of silver birch induces early flowering in apple. The transgenic early flowering line T1190 was selected and used as crossbred parent in a breeding program aimed on the introgression of resistance genes from wild apple species to the cultivated apple. This breeding program combines the advantages of transgenic early flowering trees and molecular markers as an efficient tool to speed up the selection process.

RESISTANCE TO FUNGAL DISEASES OF SPRING WHEAT VARIETIES FROM DIFFERENT RUSSIAN REGIONS

Leonova I.N., Skolotneva E.S., Salina E.A.

Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

*e-mail: leonova@bionet.nsc.ru

Fungal diseases cause significant losses of yield and quality of common wheat (*T. aestivum* L.) in many counties where wheat is cultivated. Development and cultivation of genetically resistant varieties is one of the most effective ways for wheat protection against plant pathogens. A set of 95 spring wheat varieties growing in different regions of the Russian Federation has been investigated for resistance to powdery mildew (*Blumeria graminis*), leaf rust (*Puccinia triticina*) and stem rust (*Puccinia graminis*). Fungal disease resistance was evaluated under natural infection background of pathogen populations specific to West Siberian region of Russia. Evaluation of susceptibility of wheat varieties to powdery mildew showed that eleven cultivars demonstrated resistant and medium resistant infection types. Screening for leaf rust resistance indicated that 66 varieties demonstrate from medium to highly susceptible reaction against pathogen, 20 moderate resistant varieties differed in the degree of the disease development, and 9 varieties were not affected by leaf rust. Scoring of the wheat cultivars on resistance to stem rust identified 38 cultivars with resistant and moderate resistant type of reaction. According to the phytopathological evaluation six varieties (Tulaikovskaya golden, Tulaikovskaya 10, Kinelskaya 60, Volgouralskaya, Erythrospermum 72 and Lutescens 101) were found to have complex resistance to all three diseases, among them 4 cultivars belong to the group of Samara region. A genome-wide association study (GWAS) was undertaken with Illumina Infinium 15K wheat array (www.traitgenetics.de). A single-nucleotide polymorphism (SNP) was provided by 13007 SNPs. Population structure was evaluated with 4900 markers, which classified the wheat varieties into seven subgroups. GWAS using the general linear model identified from 55 to 98 SNP markers significantly associated with resistance to different pathogens. Several markers were found to be associated with multiple disease resistance. This study provides new knowledge which can be exploited for utilizing of fungal disease resistance in breeding.

The work was supported by Russian Science Foundation (project № 16-16-00011).

RESISTANCE TO WHEAT YELLOW MOSAIC VIRUS IN MADSEN WHEAT IS CONTROLLED BY TWO MAJOR COMPLEMENTARY QTLS

Takako Suzuki

Agricultural Research Department, Hokkaido Research Organization, Hokkaido, Japan

Wheat yellow mosaic, caused by Wheat yellow mosaic virus (WYMV), is one of the most serious wheat diseases in East Asia. In this study, recombinant inbred lines (RILs, F9) from a cross between cultivars Madsen (resistant) and Hokushin (susceptible) grown in a WYMV-infected nursery field were tested for the presence of WYMV in leaves by enzyme-linked immunosorbent assay (ELISA) and genotyped by using genome-wide molecular markers. Two major QTLs were detected: Qym1 located between Xgwm539 and Xgwm349 on chromosome 2DL and Qym2 located between Xbarc147 and Xwmc623 on chromosome 3BS. The resistance alleles for both QTLs originated from Madsen. The third QTL Qym3 located near Xwmc457 on chromosome 4D, where the resistant allele for this QTL originated from Hokushin. Although the Qym3 was rather minor, it was essential to complement Qym1 and Qym2 for complete avoidance of WYMV infection. Nearisogenic lines carrying the resistance QTLs were developed by repeated backcrosses using Madsen as the donor parent and Hokushin as the recurrent parent. The lines that were resistant to WYMV (as tested by ELISA) were homozygous for the Madsen alleles at both Qym1 and Qym2. Qym1 dominance was partial, whereas that of Qym2 was nearly complete. Qym1 was closely linked to Xwmc41; Qym2 was closely linked to Xwmc754. These markers will be useful in marker-assisted selection in wheat breeding for WYMV resistance; this study will facilitate cloning the WYMV resistance genes. Now we had made the fine map of 3B resistance gene and are trying to isolate it.

BREEDING POTATO VARIETY ASTANALYK FOR RECEIVING IMPROVED SEED PLANTING MATERIAL

Magzumova G.K., Abdildaeva S.K., Kakimzhanova A.A.

RSE "National Center for Biotechnology", Astana
e-mail: kakimzhanova@mail.ru

In the Republic of Kazakhstan, the distribution of potato areas is 186,900 hectares [http://www.stat.gov.kz], however, due to low yield, the gross harvest of tubers does not meet the need for agriculture. The export of potatoes from foreign countries does not justify itself economically and strategically, because many well-known and highly productive varieties of foreign selection in conditions of hot and arid climate of most regions of Kazakhstan and the spread of severe forms of viral diseases, in the second or third year of reproduction, sharply reduce yields, seed quality degenerates. One of the ways to solve this problem is to conduct seed farming of local potato varieties, that are resistant to diseases.

Currently, microclonal propagation is used actively to obtain a healthy planting stock of potatoes, which allows to improve and multiply plants in test tube in a short period of time.

As an initial material, the variety of potato Astanalyk *(Solanum tuberosum*), resistant to dry fusarial putridity, which has been obtained with method cell selection by using 20% of the culture filtrate of the fungus *Fusarium solani* from a variety of potatoes Karasai.

The following biotechnological methods were used: thermotherapy of tubers, isolation and cultivation of apical meristems, testing of meristem systems for the presence of viruses, microclonal reproduction, propagation of plants in the greenhouse and field nursery for obtaining healthy potato seeds.

As a result of the research, 57 apical meristems of the Astanalyk potato were isolated and cultivated on the nutrient medium of Murashige and Skoog (MS) with phytohormones. Analysis of meristem lines using enzyme immunoassay (EIA) to determine 5 types of potato viruses in accordance with the manufacturer's recommendations (AG Lorch Research Institute of Potato Farming). The results of the analysis of 39 meristem lines of Astanalyk showed no with viruses infection.

After composition of nutrient medium MS for Rapid growth and of test tubes plants rooting, were microclonally propagated 4700 plants, of which 3980 plants were planted in the soil in a film greenhouse of the branch of the RSE "National Center for Biotechnology" (Stepnogorsk).

After 30 and 60 days, the morphometric parameters of the growth and development of potato, that were obtained by using microclonal propagation. Accounting and structure of the tubers yield of the potato variety of "Astanalyk " were cunduct by weighing the commodity fraction from one bush, the number of tubers from one bush was counted. On the average, the number of tubers from one bush was 12.1.

The collected cultivated tubers of the Astanalyk variety were propagated in the field. The kennel of the first year was transferred to the State Commission for the Variety Testing of Agricultural Crops for Variety Testing.

OPTIMIZATION OF CONDITIONS OF MICROCLONAL PROPAGATION OF *MALUS NJEDZWETZKYANA*

Nurtaza A., Karimova V., Kakimzhanova A.

RSE «National Center for Biotechnology», Astana
e-mail: Aid306@mail.ru

Complex natural and climatic conditions of Kazakhstan requires to observe recommendation for creating and maintaining green planting. The success of greening in a great measure depends on the correct selection of ornamental trees and shrubs. One such promising species of woody crops is the wild-growing small-fruited apple tree of *Malus njedzwetzkyana*. This is due to the complex of biological signs and properties, such as drought resistance, winter hardness, freezing tolerance and a long flowering period.

However, *Malus njedzwetzkyana* refers to very rare species that are endangered. For the preservation and breeding of this culture, the traditional methods are not effective enough. Cuttings of apple tree take root very difficult and requires special attention to the period, season and temperature. The seedlings of *Malus njedzwetzkyana*, obtained from seeds, are not always the same as their parent plant, only 10% of 100 seeds rise.

Proceeding from this, it is expedient to use methods of biotechnology. One of such methods is microclonal propagation of plants. This method allow to get rapidly, spread around, improve, root, reduce the cost and shorten the time for obtaining planting material. As objects of research for microclonal propagation, the auxiliary buds of the *Malus njedzwetzkyana*, growing in the dendrological garden of the city of Astana, were used. The following biotechnological methods were used: introduction into the *in vitro* culture of axillary buds, microclonal multiplication of microshoots.

For *in vitro* administration, the mode of sterilization of axillary buds has been optimized. Various concentrations of peroxide of hydrogen, commercial “Domestos” and “Belizna” were investigated as sterilizing agents.

With the introduction of *in vitro* axillary buds, we faced the problem of active extraction of phenolic compounds. This process does not possibility to growth and cause plant material to die. To prevent this process, antibiotic nystatin at a concentration of 0.2 mg / l and activated charcoal 1 g/l was added to the nutrient media.

In order to induce the growth of the main shoot of *Malus njedzwetzkyana in vitro* culture, the nutrient media of Murasige-Skoog (MS) and Kvorin Lepuavr with different concentrations of phytohormones were studied. As a result of the studies, the sterilization was optimized. The most suitable sterilizing agent is 12% peroxide of hydrogen. When sterilized with this reagent, the axillary buds of the *Malus njedzwetzkyana* were 95% pure of infections and ere viable.

Analysis of the studies showed that the addition of the antibiotic nystatin to nutrient media suppresses phenolic metabolism in the axillary buds. In 80% of the plant material there was no pigment, thus the growth of axillary buds was not inhibited.

To growth of the microshoots from the axillary buds of the *Malus njedzwetzkyana*, MC nutrient medium was optimizated with the addition of 0.5 mg /l benzylaminopurine (BAP); 0.01 mg/l indolyl butyric acid (IBA) and 1 mg/l gibberic acid. At present, obtained microshoots of the *Malus njedzwetzkyana* are used for the multiplication of plants.

MONITORING OF PLANT SPREADING OF *AGRIOPHYLLUM* L. (KUMARCHAK)

Zhubanysheva A.U., Zhubanyshev A.B., Titova B.U.

LLP "Agricultural Experimental Station of Aktobe city"

Email: aktobeopyt@gmail.com

The research work on the creation of maps with places of growth and spreading areas of wild-growing *Agriophyllum, L.* (also known as "Kumarchak") across Aktobe and Western-Kazakhstan regions, together with work on definition of forage productivity of *Agriophyllum, L.,* held for the first time in Western Kazakhstan. Basis of this scientific work comprised of on-field research expeditions in Aktobe and Western-Kazakhstan regions.

Wild *Agriophyllum, L.* is of great interest for the introduction to the culture in order to create autumn pastures and hay fields, where in autumn can be harvested considerable amount of valuable hay containing a significant amount of seed that is readily eaten by sheep in winter. *Agriophyllum, L.* develops in the sandy desert, which belongs to the dry salt grasses (Salsola). These kinds of salt grasses begin its developing in the spring and complete the development in August and September; thus, the autumn gives a good forage and pasture herbage.

All kinds of the young plants of *Agriophyllum, L.* are good as fodder for grazing sheep, cattle and camels. 100 kg of green mass contains about 25 fodder units and 3.7 kg of digestible protein. Yields are up to 20 quintals of green mass and 30 kg of seeds per 1 hectare.

Composition of the plant at the time of fruiting is following: water 9.9%, fiber 22,5-25%, crude protein 5.5-6.2% pure protein 5,3-5,9%, fat 2,1-2,3%, nitrogen-free extractives 50-55,5% and ash 9,9-11,0%. Starch equivalent of the plant is quite high: 34-37, 6.

Sandy desert species are widely distributed in western Kazakhstan. Kazakhs have long used the seeds of edible plants as a delicacy in the form of lightly toasted and for making flour tortillas. It is not difficult to judge the economic importance of species, because in good years seeds of plants were collected in an amount not less than 500 000-700 000.kg. In such years, raw, unprocessed seeds *Agriophyllum, L.* valued at 30% more than millet and 15-20% more expensive than rye and wheat flour.

Dry seeds of *Agriophyllum, L.* contain 16-17% protein, 6-10% fat edible and semidrying oil and 60% of carbohydrates, mainly starch, in an amount up to 87% of the substances perfectly metabolized by human body. 100 g of the food-used-substance contain 343 Kcal, which makes *Agriophyllum, L.* closer to wheat flour, which is about 344 calories. The oil obtained by pressing of the seeds - a semi-liquid, taste resembles a sunflower oil, and the composition is close to sesame. Yields of *Agriophyllum, L.* in the best years reached 30-32 kg per 1 ha and about 15-20 cwt plant mass.

In the south of Aktobe and the southeast of the Western-Kazakhstan regions large areas occupied by shifting sands, which will cause huge damage to agriculture. As the main reasons for the formation of new areas of mobile sand is unconscionable grazing or plowing overgrown sands and sandy loam soils, they should be secured. *Agriophyllum, L.* deserved to be called an "indicator plant". If the crop has taken roots- then sands fixing process has started.

Basis of cattle breeding's fodder base in western Kazakhstan is natural pastures that fall within zones of deserts and semi-deserts. Productivity of arid pastures is low. Annual growth rate of fodder is from 2 to 6 t / ha of dry mass, which hinders the further development of sheep and cattle breeding in general. Existing range of forage plants do not currently meet the requirements of the radical transformation of vegetation cover of low-yield pastures in deserts, semi-deserts and dry steppes. Therefore, it is necessary to engage new varieties of plants. One of them is Kumarchak or *Agriophyllum,L.* wild-growing plant, that do have valuable fodder properties.

MOLECULAR CHARACTERIZATION OF DURUM WHEAT AND ITS TETRAPLOID WILD RELATIVES FOR CADMIUM ACCUMULATION

Mehmet TEKIN[1], Ilknur COSKUN[1], Gulizar MANAV[1], Ahmet CAT[2], Sahriye SONMEZ[3], Taner AKAR[1*]

[1]Department of Field Crops, Faculty of Agriculture, Akdeniz University, Antalya, Turkey
[2]Department of Plant Protection, Faculty of Agriculture, Siirt University, Siirt, Turkey
[3]Department of Soil Science, Faculty of Agriculture, Akdeniz University, Antalya, Turkey

[*]e- mail:tanerakar@akdeniz.edu.tr

Cadmium (Cd) is a trace element that exists naturally in the soils and it threats to both human and animal health due to its toxicity. Cd accumulation in the soils is mainly increasing with anthropogenic sources such as atmospheric reasons and applications and phosphorous fertilizers day after day. Cd can accumulate in the human body through food consumption, mainly thanks to a high intake of cereals. Especially in durum wheat (*Triticum durum* Desf.), there is a large genetic variation for Cd and it has commonly higher Cd accumulation than another cool season cereals (rye<barley<oat<bread wheat<durum wheat). Cd accumulation is controlled by a major gene called as *Cdu1* in durum wheat. In recent years, several molecular markers have been developed to screen this gene for Cd content in grain and co-dominant CAPS marker "*usw47*" is commonly used for markerassisted selection among them. We also used *usw47*marker in order to determine Cd accumulation of 71 Turkish durum wheat cultivars with 2 universal checks and 35genotypes of its wild relatives (24emmer and 11 wild emmer). According to results, 32 durum wheat cultivars, 1 emmer and 4 wild emmer genotypes were found as high Cd accumulator in grain whileother genotypes were found as low Cd accumulator. Moreover, the first phenotypic data on seedling stage (Z13) from greenhouse experiment generally overlapped to molecular data. In conclusion, *usw47* marker successfully classified these genotypes into either high or low accumulators and these results can be useful to be conducted breeding programsin durum wheat for low Cd accumulation.

Keywords: Molecular characterization, cadmium, durum wheat, wild relatives, *Cdu1* gene, breeding

Acknowledgements:This research was financially supported by the Akdeniz University Scientific Research Projects Coordination Unit, Turkey (FBA-2017-2402).

THE TETRAPLOID WHEAT SPECIES AS SOURCES HIGHLY RESISTANT TO ABIOTIC STRESSES

***N. Terletskaya*[1], *N. Zobova*[2], *V. Stupko*[2], *A. Iskakova* [1], *S. Lugovtsova*[2], *M. Kurmanbayeva* [3]**

[1] Institute of Plant Biology and Biotechnology of Science Committee of the Ministry of Education and Science of the Republic of Kazakhstan, Almaty, Kazakhstan, e-mail: teni02@mail.ru

[2] Federal State Institution of Science "Krasnoyarsk Research Institute of Agriculture", Krasnoyarsk, Russia, e-mail: zobovnat@mail.ru

[3] Al Farabi Kazakh National University, Kazakhstan Almaty, Kazakhstan, e-mail: kurmanbaevakz@mail.ru

Studies have revealed a number of general and specific patterns on the regulation of growth and photosynthetic activity of plant tissues different wheat species in response to drought and salt stress as *in vivo*, and *in vitro*.

It is noted that the tetraploid species of wheat capable of rapid adaptation to drought and salt stress and restore growth.There are shown the maximum area of the first leaf during drought for them (*T. dicoccum* (83%) and salt stress (*T. polonicum* (84%) and *T. dicoccum* (100%).

It revealed a higher adaptability tetraploid species of wheat *T. dicoccum*, *T. polonicum* and T. *aethiopicum* compared with hexaploid anatomical parameters of leafs.It was noted that indicators such as the increase in the size of the protective and mechanical tissue and mesophyll under stress can be good selection criteria stress-resistant forms of wheat in its early stages of ontogenesis.

Showing differences between species in the distribution of trichomes and stomatas on the surface of both the first and the flag leaves. The highest xeromorphic flag leaf in terms of the number of stomata was typical for tetraploid, the lowest – for hexaploid wheat species.The tetraploid species *T. dicoccum* had the largest area of the flag and subflagleaves in dry conditions with relation to the control. In the earing the maximum thickness of the abaxial epidermis characterized by tetraploid species *T. dicoccum* and *T. macha* (24.8 и 27.4μмrespectively) in drought conditions. The maximum dimensions of the central vascular bundle observed in the same species (19775.12μm). Consequently, these tetraploid species can be characterized as the most drought-resistant in the later stages of ontogeny. The tetraploid species *T. dicoccum* was characterized by high resistance to drought on indicators CO_2 assimilation and transpiration in leafsof seedlings. The fluorescence quantum yield of photosystem II and electron transport rate through the photosystem II (ETR) was studied. The analysis of other PA components revealed that some tolerant tetraploid species could be distinguished, *T. aethiopicum* to drought and *T. aethiopicum*, *T. Dicoccum*and *T. polonicum*to salinity, which may possess dynamic tolerance to drought according to their high level of Y(NPQ).

In an in vitro culture showed that calluses tetraploid species T. *dicoccum*, *T. polonicum*, *T. aethiopicum* significantly superior to other species in the growth of the raw biomass. It is noted that in a drought-induced depression callus biomass has also been less pronounced in tetraploid forms of wheat and tetraploid form of *T. macha* demonstrated greater stability of the photosynthetic apparatus under the influence of stressors *in vitro*.

Thus, the tetraploid species of wheat may be of great interest for genetic research in the field of stress cereals, as well as sources of high drought and salt tolerance for involvement in the selection process.

Research was carried out in the framework of the project 1104/GF4 ‘Study of stability of photosynthetic apparatus of wheat (*T. aestivum* L.) and its wild congeners to abiotic stress *in vivo and in vitro*’.This grant are funding by the Ministry of Education and Science of the Republic of Kazakhstan.

The International Science and Technology Center

The International Science and Technology Center (ISTC) is an intergovernmental organization connecting scientists from Kazakhstan, Armenia, Tajikistan, Kyrgyzstan, and Georgia with their peers and research organizations in the EU, Japan, Republic of Korea, Norway and the United States.

ISTC facilitates international science projects and assists the global scientific and business community to source and engage with CIS and Georgian institutes that develop or possess an excellence of scientific know-how.

http://www.istc.int/en/

VELD

Товарищество с ограниченной ответственностью Научно-производственная фирма "VELD"

050004, Республика Казахстан,
г. Алматы, ул. Сейфуллина, 410
тел 8-727-2952270, 952269
факс 8-727-2794926
E-mail: info@veld.kz

Seifullin Str. 410, 050004 Almaty,
Republic of Kazakhstan,
tel/fax +7-727-2952270, 952269
tel +7-727-2794926
E-mail: info@veld.kz

ОСНАЩЕНИЕ ЛАБОРАТОРИЙ РАЗЛИЧНОГО НАПРАВЛЕНИЯ
БЫСТРАЯ ПОСТАВКА СО СКЛАДОВ В АЛМАТЫ:

- **ЛАБОРАТОРНОГО ОБОРУДОВАНИЯ**
- **ХИМИЧЕСКИХ РЕАКТИВОВ ДЛЯ МОЛЕКУЛЯРНОЙ БИОЛОГИИ И БИОТЕХНОЛОГИИ**
- **ЛАБОРАТОРНОЙ ПОСУДЫ**
- **ДИАГНОСТИЧЕСКИХ НАБОРОВ ТЕСТ-СИСТЕМ**

ТОО Научно-производственная фирма "VELD" с 1994 года занимается оснащением различных лабораторий лабораторным оборудованием и расходными материалами в различные лаборатории на территории Республики Казахстан, Киргизии и Узбекистан. Спецификой работы нашей фирмы является большие товарные запасы (лабораторного оборудования, химических реагентов, лабораторной посуды, тест-систем и других товаров, необходимых для полноценной работы лаборатории), находящиеся на складе в г. Алматы. Это позволяет нам в короткие сроки обеспечить любую лабораторию всем необходимым для работы. Мы поставляем также лабораторное оборудование и расходные материалы под заказ. Являясь дистрибьютором крупнейших мировых производителей, мы имеем возможность поставки до 250000 наименований лабораторного оборудования и расходных материалов.

Одним из главных направлений фирмы является продвижение наукоемких технологий в Республике Казахстан. Специалисты фирмы осуществляют постоянный скрининг новых технологий, регулярно посещая международные выставки. После реализации новых методов и методик в приборе и программном продукте наши специалисты проходят подготовку в фирмах, наладивших производство, и начинают продвижение новых технологий на территории Казахстана.

Мы имеем достаточный штат сервисных инженеров, прошедших обучение на заводах-производителях по установке и обслуживанию. При поставке оборудования, мы обеспечиваем установку оборудования, обучение специалистов работе на оборудование. Сервисные инженеры осуществляют гарантийный и послегарантийный ремонт и сервисное обслуживание.

Наша компания сертифицирована на соответствие СТ РК ИСО 9001-2001 «Системы менеджмента качества».

Обращайтесь к менеджерам по продажам нашей фирмы и они с удовольствием помогут решить Ваши проблемы в лаборатории.

ТОО Научно-производственная фирма "VELD" официально представляет на территории Казахстана продукцию всемирно известных компаний: **Eppendorf, Esco, BINDER.**

Eppendorf представляет новые и новаторские продукты, которые помогут упростить процессы работы с жидкостями, клетками и образцами и тем самым облегчить вашу работу в лаборатории.

Благодаря инновационным технологиям и первоклассным продуктам вот уже почти 70 лет Eppendorf вносит важный вклад в улучшение рабочих процессов при работе с жидкостями, клетками, образцами в лабораториях и научно-исследовательских учреждениях. Продукты Eppendorf помогают сделать рутинные лабораторные процедуры настолько простыми, надежными и эффективными, насколько это возможно. Благодаря сочетанию глубокого понимания прикладных задач и процессов и высоких требований по качеству Eppendorf гарантирует, что продукты и услуги приносят пользу клиентам из различных прикладных областей. Постоянно растущий ассортимент продукции высоко востребован в фармацевтической и биотехнологической промышленности, в производстве вакцин и проведении диагностики, а также и в лабораториях аграрной, пищевой промышленности и в производстве биотоплива.

Оборудование для биотехнологий предназначено для использования в этих областях: биореакторы и системы контроля биопроцессов, а также ПО для управления и анализа данных позволяет производить масштабирование и расширение. Благодаря многолетнему, насчитывающему не один десяток лет, опыту работы со сложными полимерными продуктами, своей компетентности в биотехнологии и за счет применения в процессе разработки и изготовления новейших данных из самых разных научных областей. Eppendorf разрабатывает инновационные продукты для биотехнологий.

Esco представляет инновационные конструкции, которые отвечают высочайшим стандартам с 1978 года. Группа компаний Esco посвящена созданию инновационных решений для клинических, медико-биологических, исследовательских, промышленных, лабораторных, фармацевтических и ЭКО направлений. Имея самую разветвленную продуктовую линейку в своей отрасли, наши продукты прошли сертификацию на ряд международных стандартов и сертификатов. Esco работает в соответствии с ISO 9001, ISO 14001 и ISO 13485. Штаб-квартира компании находится в Сингапуре, а производственные мощности расположены в Азии и Европе. Исследования и разработки проводятся в научных центрах по всему миру, включая США, Европу и Азию. Представительства и сервисные центры расположены в 12 крупных регионах, включая США, Великобританию, Японию, Китай, Россию и Индию.

Благодаря нашему присутствию по всему миру, Вы можете быть уверены, что Esco находится в пределах Вашей досягаемости. Наши клиенты уверены, что они могут быть уверены в точности своих исследований и процедур только с высококачественными и надежными продуктами. Многофункциональные команды Esco с производства, из департаментов исследований, обеспечения качества, а также высшего руководства регулярно собираются для рассмотрения и реализации областей для совершенствования.

Esco заботится о вашей безопасности. Esco фокусируется на обеспечении безопасности не только Ваших образцов, но и самих пользователей. Esco заботится о вашем комфорте.

Комфорт наших пользователей обеспечивается путем создания эргономичной конструкции и снижения уровня шума приборов. Esco заботится об окружающей среде.

Медико-биологическое лабораторное оборудование:

Компания Esco как мировой лидер в производстве боксов биологической безопасности предлагает широкий ассортимент продукции, уже установленной в тысячах ведущих лабораторий в более чем 100 странах мира. Боксы биологической безопасности Esco заработали больше независимых сертификатов в большем количестве стран на большем количестве языков, чем любой другой продукт, что демонстрирует нашу приверженность безопасности и качеству.

Особенности

• Энергоэффективный DC ECM вентилятор*
• Антимикробное порошковое покрытие ISOCIDE
• ULPA фильтр с > 99,999% эффективностью для частиц размером
0,1-0,3 мкм
• Большая производительность
• Эргономичный дизайн
• Низкий уровень шума
• Легко чистить

Линейки продукта

• Боксы биологической безопасности, класс I*Модели: Airstream®
• Боксы биологической безопасности, класс II, тип A2
* Модели: eSafe, NordicSafe, Airstream, Labculture, Reliant, Airstream
• Боксы биологической безопасности, класс II, тип B2
* Модели: Labculture
• Боксы биологической безопасности, класс III
*Модели: Airstream
• Боксы биологической безопасности со свинцовыми пластинами, класс II
*Модели: Cytoculture
• Боксы пищевой безопасности
*Модели: AgriSafe

Компания Esco является мировым лидером в развитии профессиональных качественных ламинарных боксов для мирового рынка медико-
биологических наук. Учитывая десятки тысяч проданных по всему миру единиц оборудования, компания Esco усилила свою репутацию
надежностью, обеспечивая надежную защиту образцов и рабочих процессов в самых разных областях применения.

Ассортимент ламинарных боксов с вертикальным и горизонтальным потоками воздуха, а также боксов специального назначения предлагает широкий выбор вариантов для установок, где имеет важное значение высокое качество. Ламинарные боксы сконструированы с учетом аэродинамических свойств и используют только ULPA фильтры высокого качества со встроенными двигателями / вентиляторами для тихой работы и долгого срока службы.

Линейки продукта

• Ламинарные боксы с горизонтальным потоком воздуха
• Ламинарные боксы с обратным потоком воздуха
• Ламинарные боксы с вертикальным потоком воздух

Рабочие станции для работы с лабораторными животными

Исследования с применением лабораторных животных, смена клеток и удаление подстилок теперь проще, безопаснее и продуктивнее с рабочими станциями VIVA®

от Esco. Опыт компании в производстве чистого воздуха и технологий аэродинамических барьеров распространяется и на продукты для работы с лабораторными животными, чтобы помочь защитить исследователя, технический персонал, самих животных и окружающую среду в ходе исследования, смены клеток и удаления подстилок.Продукты для работы с лабораторными животными VIVA® помогают лаборатории выполнять рекомендации NIOSH по созданию более безопасной, здоровой и продуктивной рабочей среды, а уверенность, что защита оператора и окружающей среды обеспечивается каждой рабочей станцией VIVA®, создается благодаря анализу ELISA.

Для моделирования использования рабочих станций были выполнены настоящие работы по смене клеток и удалению подстилок, а затем были взяты пробы на концентрацию аллергенов в рабочей зоне. Концентрация аллергенов была оценена сэндвичным методом ELISA.

Линейки продукта:

Рабочие станции для удаления подстилок

Универсальные рабочие станции для работы с лабораторными животными

Рабочие станции для работы с лабораторными животными двойного доступа

Анализ образцов

Компания Esco предлагает выбор моделей обычных амплификаторов, созданных для удовлетворения критических требований практически для всех видов ПЦР таких, как градиентный ПЦР, ступенчатая ПЦР, ПЦР с высокой пропускной способностью, in situ ПЦР и т.д. Конфигурации блока доступны для различных форм образцов, пробирок, полосок, тарелочек и пластин.

Особенности

• Отличная температурная однородность и стабильность

• Подходит для различных форматов образцов, которые могут упростить эксперименты

• Удобные средства управления и эксплуатации

Химические исследования

• Автономные вытяжные шкафы

• Лабораторные вытяжные шкафы

• Контроль воздушного потока в вытяжном шкафу

• Вентиляторы

• Боксы для весов для взвешивания

• Шкафы для хранения одежды

Хранение образцов и решения для их защиты

Серия морозильников ультранизких температур Lexicon® II включает в себя лучшую и наиболее полную защиту образца, а также систему организации образцов любого производителя морозильников ультранизких температур. Такие морозильники широко используются в научных исследованиях для долгосрочного хранения образцов. Так как морозильники часто работают при температуре -80°C непрерывно в течение года, то надежность имеет первостепенное значение для исследователей. Для проведения стресс теста большого количества морозильников ультранизких температур Esco использует принятое в отрасли Ускоренное ресурсное испытание (HALT). Все морозильники Esco прошли эти экстремальные стресс-тесты, и их конструкция дает уверенность в том, что она оптимизирована для защиты Ваших образцов.

Серия HP лабораторных холодильников и морозильников – это высопроизводительные модели, сконструированные для обеспечения высокого уровня защиты образцов, используемых в научных исследованиях и клинических приложени

Общелабораторное оборудование

Термостатирующее лабораторное оборудование
• Лабораторные печи
• Лабораторные инкубаторы
• Охлаждаемые инкубаторы
Фармацевтическое оборудование
Сдерживание воздушного потока
• Стенды с нисходящим воздушным потоком
• Потолочные приборы ламинарного потока
• Передвижные боксы ламинарного горизонтального потока
• Передвижные боксы ламинарного вертикального потока
• Ламинарные сборочные станции
Изолирование
• Изолятор асептического сдерживания (ACTI)
• Изолятор для взвешивания и дозирования (WDCI)
• Изолятор для общих процессов (GPPI)
Встроенная барьерная защита от перекрестного загрязнения
• Воздушный душ для чистых помещений
• Передаточное окно для чистых помещений
• Переходный люк для чистых помещений
• Передаточные окна
• Чистые помещения с мягкими стенами
• Динамические передаточные окна и динамически
Барьерная изоляционная технология
• Сдерживающие изоляторы (рециркулирующие)
• Фармацевтические смешивающие асептические изоляторы
• Цитотоксические боксы безопасности

Компания BINDER полностью сфокусирована на камерах для моделирования условий окружающей среды. BINDER являемся крупнейшим в мире специализированным предприятием по выпуску камер для моделирования условий окружающей среды для научных и промышленных лабораторий. Более 22 000 камер выходит каждый год с завода в Тутлингене. Совершенные передовые технологии, инновации и абсолютная точность - таков портрет BINDER на рынке. В фокусе нашего внимания - идеальное моделирование биологических, химических и физических воздействий окружающей среды для множества Камеры для моделирования условий окружающей среды BINDER выполняют сложные лабораторные задачи с абсолютной надежностью. Они разрабатываются и изготавливаются исключительно в отделении компании в городе Тутлингене, в высокотехнологичном городе Южной Германии. От точной штамповки, биговки и сварки до изоляции и тщательного монтажа выполняются все производственные этапы на своем заводе и таким образом гарантируется качество всей производственной линии. Интенсивный контроль качества обеспечивает превосходный стандарт BINDER отраслей. Будь это культивирование клеток или

тканей, долговременное хранение, испытания продуктов или материалов: практически все ведущие компании и исследовательские учреждения делают ставку на камеры для моделирования условий окружающей среды компании BINDER с характерным красным треугольником. Широкий ассортимент камер BINDER включает инкубаторы, камеры роста, морозильные шкафы сверхглубокой заморозки, сушильные шкафы и нагревательные камеры, а также климатические камеры и, таким образом, превосходно покрывает многочисленные запросы разных отраслей и рынков.

Мы являемся ***официальными дистрибьюторами*** расходных материалов таких производителей, как:

Brand GmBH, Германия, известный производитель и поставщик лабораторных расходных материалов с 1949 года;

Nuova Aptaca s.r.l., Италия, профессиональный производитель одноразовых расходных материалов для лаборатории с 1976года.Компания выпускает широкий ассортимент продукции для клинической химии, серологии, гематологии, криогеники, микробиологии и бактериологии.

Nerbe plus, Германия, производитель лабораторной пластиковой посуды для клинической и микробиологической лабораторий с 1976года.

Sarstedt AG, Германия, наш партнер по поставки лабораторных принадлежностей для медицины и науки.

FL Medical s.r.l., Италия, профессиональный производитель лабораторных и медицинских продуктов с 1979года.

ТОО НПФ «VELD» является эксклюзивным и единственным дистрибьютором компании **Hain Lifescience GmbH** (Германия) на территории Республики Казахстан. Hain Lifescience GmbH признанный и авторитетный производитель продукции для молекулярно-биологической диагностики в условиях in vitro, имеющая заводы в Нерене (Германия), Мидранде (Южная Африка), Найроби (Кения), Байфлите (Англия), Виго-Понтеведре (Испания) и Бандоле (Франция). Компания была основана в 1986 году. Hain Lifescience GmbH сертифицирована по ISO 9001 и ISO 13485 и соответствует европейским рекомендациям по диагностике in vitro (98/79/EG).

Продукция **Hain Lifescience GmbH**

Подтвержденная и эффективная диагностика является наилучшим предварительным условием для быстрого и надежного выявления заболеваний. Современная, всесторонняя и безопасная диагностика позволяет эффективно лечить, специально адаптированная к конкретному пациенту. Это дает наибольший шанс для выздоровления. Только удобные и практичные методы диагностики могут быть выполнены точно и надежно в лаборатории и, таким образом, гарантируют надежные результаты. Продукты Hain Lifescience GmbH соответствуют всем этим критериям и, следовательно, обеспечивают оптимальную лабораторную диагностику, чтобы вылечить пациентов и избежать распространения резистентности и инфекций.

Компания **Merck KGaA** (Германия), основанная в 1668 году в Дармштадте, является производителем химической продукции высокого качества. Компания уделяет основное внимание качеству, надежности и инновации, концентрируясь на потребности клиентов. От разработки до поставки действуют с максимальной тщательностью для обеспечения превосходного качества, особенно в чувствительной сфере реагентов для анализа.

Компания предлагает несколько сотен неорганических химических реагентов для анализа – в частности, кислоты, соли, щелочи, основания, индикаторы и специальные реагенты. Фактически, ни один другой производитель не поставляет такого широкого ассортимента продукции.

Кроме того, вы можете быть уверены, что работаете с подходящими реагентами для ваших специфических задач, отвечающими всем требованиям по качеству. Реагенты для фармакопейного анализа не только соответствуют стандарту ACS, но также стандартам реагентов по Европейской фармакопее. Поэтому продукты соответствуют всем спецификациям реагентов, описанным как Американской, так и Европейской фармакопеей.

Через обеспечение соответствия этим всесторонним стандартам компания создает новый уровень качества аналитических реагентов, обеспечивая вам наивысший возможный уровень надежности – по всему миру.

Titan Biotech Limited (Индия) является ведущим производителем и поставщиком различных питательных сред для микробиологии.

Система управления качеством компании Titan Biotech Limited сертифицирована по стандарту ISO 9001:2000, ISO 13485:2003, WHO GMP, Европейскому стандарту качества (CE). Выпускаемая компанией продукция соответствует требованиям Фармакопеи США, Европейской Фармакопеи и Британской Фармакопеи.

Обладая самой современной инфраструктурой, новейшими технологиями и опытным подразделением, компания может предоставить различные среды для культивирования по самым конкурентным ценам.

Общее количество выпускаемых сред составляет около полутора тысяч. Ко многим средам выпускаются стерильные, готовые к применению, добавки. Titan Biotech Limited поставляет различные виды сырья для биотехнологии, такие как пептоны (ферментативный, бактериологический, соевый, микологический, протеозный, специальный и т.д.), агары (бактериологический, ультрачистый, для иммуноэлектрофореза и т.д.), экстракты (мясной, дрожжевой, печеночный), гидролизаты (казеина и лактальбумина), а также другие компоненты питательных сред.

ТОО "Zalma Ltd." (Цалма Лтд.)
РК, г. Алматы, ул. Богенбай батыра, 305а
тел.: +7 (727) 374-35-87 факс: +7 (727) 374-35-67
info@zalma.org

АФ ТОО "Zalma Ltd."
РК, г. Астана, р-н Алматы, ЖК «Сказочный мир»,
ул. 23-15, дом 11, блок А, кв.132;
тел.: 8 (7172) 25-99-75; info.astana@zalma.org

ZALMA
www.zalma.org

Компания "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.

Под «системными решениями» мы понимаем комплексное оснащение конкретной лаборатории сложным специализированным и общелабораторным оборудованием, лабораторной мебелью, посудой, аксессуарами и расходными материалами; методическую и сервисную (гарантийную и послегарантийную) поддержку, обучение персонала лаборатории, как на базе заказчика, так и на базе производителя оборудования; проведение проектирования, помощь в получении всех необходимых разрешительных документов и государственной аккредитации лаборатории.

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™, Affymetrix™, Gibco™, Molecular Probes™, eBioscience™ and Ion Torrent™** 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.

ThermoFisher SCIENTIFIC AB Applied Biosystems

У нас стабильные хорошие отношения с нашими поставщиками, но мы постоянно ищем новые возможности для диверсификации и открыты для сотрудничества с новыми партнерами. Мы плодотворно сотрудничаем с различными лабораториями медицинской, судебной, аграрной и пищевой отраслей, а также с различными 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 нашего сервисного отдела проходят регулярное обучение на тренингах компаний-производителей. Наши сервисные инженеры сертифицированы на проведение IQ, OQ/PQ, ремонта и регулярного сервисного обслуживания.

Различные исследования в генетике и клеточной биологии производятся на базе нашей демонстрационной лаборатории, в г. Алматы. Сотрудниками отдела научной и методической поддержки компании разрабатываются новые методики анализа.

Компания «Zalma LTD» регулярно организует научно-практические семинары, посвященные использованию современного генетического и аналитического оборудования. Мы активно участвуем в выставках, семинарах и конференциях, которые соответствуют нашим профессиональным интересам.

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.

РЕШЕНИЯ ДЛЯ ГЕНОТИПИРОВАНИЯ В АГРОГЕНОМИКЕ

Легкие, гибкие, автоматизированные решения для ускорения наших программ геномного отбора и селекции. Единая платформа для каждого этапа исследования.

Решения для генотипироваия в Агрогеномике от Affymetrix обеспечивает селекционеров и ученых мощным и гибким набором инструментов генотипирования для экономически эффективной идентификации, проверки и скрининга сложных генетических признаков у растений и животных.

Инструменты для генетического анализа Affymetrix дают Вам возможность:

- Определять генетическое разнообразие de novo посредством технологий генетического анализа
- Делать анализ структуры популяции
- Определять генетические маркеры, связанные с желаемыми признаками
- Подтверждать ассоциации маркеров-признаков
- Понимать генетическую адаптацию к окружающей среде
- Использовать генетическую информацию для контроля желаемых результатов
- Проводить отбор растений и животных для желаемых признаков
- Ускорить генетический прогресс с высокой точностью

ПРЕИМУЩЕСТВА ГЕНОТИПИРОВАНИЯ НА ОСНОВЕ МАТРИЦ

Доступность

- Экономичные инструменты генотипирования

affymetrix
Biology for a better world

Упрощенные инструменты для генотипирования

- Объединяйте несколько приложений для генотипирования на одной технологической платформе
- Прост в использовании и простой рабочий процесс
- Получайте точные ответы генотипирования в течение нескольких часов

Гибкость

- Высокопроизводительные инструменты генотипирования для приложений в таргет генотипировании и генотипировании с высокой плотностью
- Анализ для безусловного генотипирования **всех** соответствующих маркеров, представляющих интерес

- Низкая приверженность выборке

Продукция для генотипирования на основе матриц от Affymetrix предлагает комплексные решения для приложений от геномного анализа до рутинного скрининга с высокой точностью и воспроизводимостью, простотой рабочего процесса и низкой стоимостью.

РЕШЕНИЯ ДЛЯ ГЕНОТИПИРОВАНИЯ AXIOM - Ускорьте процесс ассоциации фенотип-признака и их отбора с надежной технологией

Решения для генотипирования для агрогеномики включает матрицы с генотип-тестированным материалом из геномной базы данных Axiom® или de novo маркеры, которые важны для Вас.

Мощный

- Генотипируйте любые виды, любого размера генома и уровня
- Анализ Axiom® определяет инсерции/делеции и гарантирует включение всех потенциальных ОНП с соседними ОНП в пределах 20 н.п., что позволяет более эффективный анализ ЛКП

Надежный

- Можно генотипировать с 100 нг выделенного ДНК из различного вида образцов
- Коэффициенты генотипирования ≥99%

Масштабируемый

- Полностью автоматизированный рабочий процесс с возможностью обработки до 8 образцов в неделю с помощью одного прибора GeneTitan® MC
- Высокопроизводительный и гибкий дизайн матрицы для 96 или 384 образцов на планшет

ГЕНОТИПИРОВАНИЕ РАСТЕНИЙ

Получите доступ к экспертным дизайнам для интересующих вас видов

Affymetrix сотрудничает с учеными из научно-исследовательских институтов и коммерческих семеноводческих компаний для дизайна матриц для различных растений, включая картофель, соя, клубника, пшеница, кукуруза и декоративные растения.

Рабочий процесс Axiom® обеспечивает автоматизированное программное обеспечение для определения генотипов, устраняя утомительный ручной процесс определения генотипов.

- Программное обеспечение Axiom® предлагает адаптивную динамическую кластеризацию, которая использует статистические методы для точного генотипирования диплоидных и полиплоидных видов
- Пользовательские матрицы для генотипирования Axiom myDesign™ могут быть использованы для исслдеований по валидации секвенирования, полного, и рутинного генотипирования для селекционныз целей.

ГЕНОТИПИРОВАНИЕ АКВАКУЛЬТУРЫ

Affymetrix сотрудничает с рядом исследователей аквакультуры, включая Aqua Gen, Center for Integrative Genomics (CIGENE), USDA и Landcatch, для комплексного исследования признаков и геномного отбора, чтобы улучшить программы разведения во множестве видов аквакультуры, таких как сом, карп и форель.

- Пользовательская технология генотипирования Axiom myDesign обеспечивает дизайн матриц для генотипирования ОНП сложных мозаичных геномов, таких как у лосося.
- Программное обеспечение для анализа данных Affymetrix включает адаптируемые инструменты, которые могут быть применены к различным видам аквакультуры.

ГЕНОТИПИРОВАНИЕ ЖИВОТНЫХ

Выберите из нашего каталога матрицу высокой плотности

Матрица для полногеномного генотипирования куриц Axiom®

- Набор для генотипирования с высокой плотностью для куриц, который доступен для общественного использования, предназначен для бройлеров, несушек белых яйц, несушек коричневых яиц и беспородных некоммерческих пород,
- Набор разработан в сотрудничестве с проектом German Synbreed, финансируемый BMBF в рамках частно-государственного партнерства, которое включает проект LINK, финансируемый BBSRC, между Институтом Рослина, Aviagen Ltd, Hy-Line International и Affymetrix.

BOS 1 матрица для полногеномного генотипирования КРС Axiom®

- Наивысший геномный охват для Bos taurus, Bos indicus с большим количеством пород Зебу и более пригодными ОНП для вашего использования,
- Разработанная в сотрудничестве с 10 ведущими исследователями крупного рогатого скота и с помощью базы данных Affymetrix’ по 3 млн. генотип-тестированных ОНП,
- Интеллектуальная матрица, которая использует стратегию выбора ОНП на основе блоков гаплотипов.

Матрица для генотипирования буйволов Axiom

Предназначена для широкого спектра применений: от комплексных исследований признаков и молекулярной селекции до сохранения и биоразнообразия

- Включает общие и редкие маркеры водяного буйвола (*B. Bubalis bubalis*),

- Представлены многочисленные породы — Mediterranean, Murrah, Jaffarabadi, and Nili-Ravi.

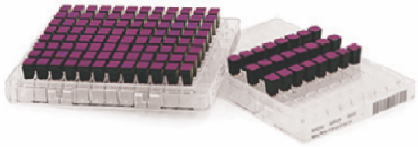
ПРИБОР GENETITAN – ПЕРВЫЙ И ЕДИНСТВЕННЫЙ ПОЛНОСТЬЮ ИНТЕГРИРОВАННЫЙ ИНСТРУМЕНТ МИКРОЧИПОВ ДЛЯ БЕЗ РУЧНОЙ ОБРАБОТКИ МАТРИЦ

Трансформируйте свою лабораторию с инструментом GeneTitan и ощутите непревзойденную мощь оптимизации обработки матриц для обнаружения, исследовани и скрининга. Оба инструмента, GeneTitan для экспрессии и GeneTitan® Multi-Channel (MC) Instrument для экспрессии и генотипирования плавно интегрируют процессы гибридизации, промывки и визуализации в единый инструмент для обеспечения без ручной обработки процессов array - независимо от того, выполняете ли вы основные или прикладные исследования.

- **Масштабируемость** – Соответствует потребностям как средне, так и высокопроизводительной способности, обеспечивает самое быстрое получение данных и требует минимальных ресурсов.
- Эффективность – Сокращает время обработки до 30 минут, дает снимки матриц менее чем за пять минут и работает без присмотра в течение ночи.
- Гибкость – Поддерживает исследования экспрессии генов и генотипирования на многоформатных матричных планшетах.
- Точность – Каждый раз обеспечивает высокое качество согласованных данных путем обработки нескольких выборок при одинаковых условиях.
- Адаптационность – Создает гибкие рабочие процессы и регистрацию образцов с помощью Программного обеспечения (AGCC) Affymetrix® GeneChip® Command Console® .

Гибкость, которую Вы желаете – множество форматов и индивидуальные решения для исследований экспрессии генов и генотипирования

GeneTitan® Instruments вместе с индустриально-признанными высокопроизводительными матричными планшетами Affymetrix®) обеспечивает первое не ручное, автоматизированное решение для обработки микрочипов. Благодаря широкому выбору форматов матричных планшетов вы можете легко перейти от открытий с помощью полногеномного генотипирования ОНП, к комплексным исследованиям профилей экспрессии генов, относящихся к важным биологическим фенотипам, таким как ответная реакция на препараты или заболевания.



Предварительно сконструированные и настраиваемые матричные планшеты, для 24- и 96-форматов, обеспечивают высочайшую производительность с масштабируемой производительностью .

GeneTitan Instruments вместе с Affymetrix Array Plates предоставляют широкий ассортимент применения в исследованиях генной экспрессии и генотипирования.

Множество форматов:

- **Affymetrix матричные планшеты для экспрессии** идеально подходят для лабораторий средней и высокой производительности; Доступны в форматах для 16-, 24- 96 образцов;
- **Axiom® матричные планшеты для генотипирования** доступны в нескольких форматах, для обработки от 24 до 96 образцов на планшету.

Масштабируемая производительность :

- **Процесс от 16 до 192 образцов в день.** Позволяет увеличить масштаб производительности без дополнительной рабочей силы или инструментов,
- **Достижение высокой производительности.** Матричные планшеты сокращают время ручной обработки, сводят к минимуму вмешательство пользователя и обрабатываются без присмотра в течение ночи.

Индивидуальные решения:

- **Матричные планшеты для экспресии MyGeneChip™** Индивидуальные решения для человеческих и модельных и прикладных исследовательских организмов,
- **Матричные планшеты генотипирования Axiom® myDesign™** Геномный охват специально сконструированный для человеческих и агрокультурных популяций, с фокусом на интересующие Вас ОНП.

Россия, 117997, г. Москва, ул. Миклухо-Маклая, д. 16/10
Тел. / факс: +7 (499) 724-8872, +7 (495) 223-4815
sales@labinstruments.ru
www.labinstruments.ru

Компания ЛабИнструментс занимается поставкой аналитических приборов, лабораторного оборудования, расходных материалов и реагентов для исследований в области экологии, биологии, химии, биотехнологии и смежных отраслей.
Компания ЛабИнструментс является официальным представителем в РФ и странах СНГ многих ведущих производителей из Америки и Европы, таких как: LI-COR (США), Eppendorf (/Newbrunswick) (Германия), Labconco (США), Wheaton (США), Sonics & Materials (США), Fibercell Systems (США), Linseis (Германия), VWR USA (США) и др.
Кроме того, компания ЛабИнструментс поставляет продукцию таких производителей как Merck, Millipore, Sigma, Beckman, Agilent, GE Healthcare и др.
Также компания ЛабИнструментс предлагает товары по американским каталогам: VWR International (США) (крупнейший мировой поставщик лабораторного оборудования) (https://us.vwr.com), Fisher Sci. (США) и др.
Компания имеет возможность поставки практически любого лабораторного оборудования от производителей из Америки и Европы, не представленных на местном рынке. Специалисты компании ЛабИнструментс имеют большой опыт и всегда рады оказать поддержку клиентам по вопросам выбора оборудования.
Сбалансированный портфель компании ЛабИнструментс позволяет комплектовать под ключ лаборатории любого профиля: от биореакторов и вытяжных шкафов до микропробирок и наконечников для пипеток.
Компания ЛабИнструментс располагает складскими помещениями в Москве, где всегда в наличии расходные материалы и наиболее ходовое оборудование.
Компания располагает штатом высококвалифицированных инженеров, готовых провести ввод оборудования в эксплуатацию, обучение персонала Заказчика, а также сервисное, гарантийное и послегарантийное обслуживание оборудования.
Основная цель компании ЛабИнструментс – предложить Вам, нашему клиенту, максимально широкий ассортимент высококачественной продукции, а также комфортабельный и профессиональный сервис.
Благодаря многолетнему опыту мы имеем возможность предложить Вам оптимальные технические решения по самым выгодным ценам.
Сегодня мы рады представить Вашему вниманию продукцию компании **LI-COR** (США) (www.licor.com). Компания LI-COR является мировым лидером в производстве оборудования для измерения газообмена растений и почв, изучения фотосинтеза, для экологического мониторинга, а также имаджинговых систем для документации и анализа вестерн-блотов и др., систем для in vivo имаджинга процессов в организмах мелких лабораторных животных и многого другого.

Новая система измерения газообмена растений LI-COR LI-6800

Универсальная система имаджинга LI-COR Odyssey CLx

LI-COR® ЛАБ Инструментс

Подразделение **LI-COR Environmental** компании **LI-COR** (США) (www.licor.com) является ведущим производителем приборов для изучения растений, включая системы изучения процессов фотосинтеза (измерение флуоресценции хлорофилла, измерение газообмена растений), приборов для измерения площади листьев и листового индекса (покрытия кроны), датчиком уровня освещенности и регистраторов к ним, а также профессиональных газоанализаторов и комплексных систем экологического мониторинга атмосферы и почвы и др.

Новая портативная система анализа процессов фотосинтеза
LI-COR LI-6800
Беспрецедентные возможности для измерения параметров газообмена растений и флуоресценции хлорофилла.
Новое поколение самой цитируемой системы в мире.

Портативная система анализа процессов фотосинтеза
LI-COR LI-6400
Проверенное временем качество и надежность, широкий спектр возможностей, широкий ассортимент рабочих камер.

Анализатор проективного покрытия кроны *LI-COR LAI-2200C*
Быстрый и точный неразрушающий анализ листового индекса трав, кустарников и древесных насаждений.

Регистраторы освещенности *LI-COR LI-250A* и *LI-COR LI-1500*
***LI-COR LI-250A* – одноканальный регистратор для записи сигнала**
***LI-COR LI-1500* – трехканальный регистратор для записи и анализа сигналов**
Интуитивный интерфейс, надежность, ударопрочность, водонепроницаемость.

Датчики уровня освещенности, температуры, влажности и др.
Наземные и подводные датчики ФАР, радиометры, фотометрические датчики, пиранометрические датчики, датчики температуры воздуха / почвы, датчики влажности воздуха / почвы, и многие другие.

Анализаторы площади листовой поверхности и других параметров листа
***LI-COR LI-3000C* - портативный анализатор площади листа**
***LI-COR LI-3100C* – лабораторный анализатор площади листа**
Анализ площади, длины, максимальной ширины и усредненной ширины листа.

Компания ЛабИнструментс - официальный эксклюзивный представитель компании LI-COR в РФ и странах СНГ

Россия, 117997, г. Москва, ул. Миклухо-Маклая, д.16/10 (ИБХ РАН), оф. 32-306
Тел./факс: +7 (499) 72-488-72, +7 (495) 223-2815, +7 (495) 669-2094
Ответственный представитель поставщика:
к.х.н. Анцыпович Сергей Игоревич
sa@labinstruments.ru www.labinstruments.ru

Подразделение **LI-COR Biotechnology** компании **LI-COR** (США) (www.licor.com) является ведущим производителем систем визуализации и анализа изображений вестерн-блотов и др. (имаджинговых систем), а также соответствующих реагентов и аксессуаров. В ассортименте:

Серия многофункциональных имаджинговых систем Li-Cor Odyssey для документации и анализа изображений (вестерн-блоты и др.)
Высокочувствительный количественный анализ блотов и др. методом детекции флуоресценции в ближней ИК-области одновременно по двум каналам, широчайший динамический диапазон, высокая точность и воспроизводимость.

Система Li-Cor Odyssey CLx (ИК-флуоресценция по двум каналам одновременно)
Мощная многофункциональная система высочайшей чувствительности. Истинный количественный анализ блотов, анализ гелей окрашенных Кумасси, анализ гелей ДНК/РНК, анализ клеточных вестернов (In- / On-Cell Western), EMSA, ELISA, FLISA, и многое другое!

Система Li-Cor Odyssey Fc (ИК-флуоресценция по двум каналам одновременно и хемилюминесценция)
Универсальная система по доступной цене. Истинный количественный анализ блотов, анализ гелей окрашенных Кумасси, анализ гелей ДНК/РНК и многое другое!

Высокоскоростной цифровой сканер хемилюминесцентных блотов LI-COR C-DiGit
Мгновенное получение высококачественных изображений вестерн-блотов без использования пленки. Сканирование нажатием одной кнопки. Чувствительность как у пленки или лучше. Одновременное обнаружение сигналов высокой и низкой интенсивности без перенасыщения полос.

Реагенты Li-Cor для блоттинга, имаджинга и др.
Метки и реагенты для ИК-флуоресценции и хемилюминесценции, квенчеры, метки видимого диапазона и др., реагенты для хемилюминесцентных и ИК-флуоресцентных вестерн-блотов, первичные и вторичные меченые антитела, белковые маркеры, субстраты, буферные смеси, реагенты для EMSA, ELISA, FLISA и многое другое!

Компания ЛабИнструментс - официальный эксклюзивный представитель компании LI-COR в РФ и странах СНГ
Россия, 117997, г. Москва, ул. Миклухо-Маклая, д.16/10 (ИБХ РАН), оф. 32-306
Тел./факс: +7 (499) 72-488-72, +7 (495) 223-2815, +7 (495) 669-2094
Ответственный представитель поставщика:
к.х.н. Анцыпович Сергей Игоревич
sa@labinstruments.ru www.labinstruments.ru

ЛАБ Инструментс

eppendorf

New Brunswick an eppendorf company

Компания Eppendorf (Германия) занимается разработкой, производством и продажей продукции премиум-класса и услуг для лабораторий по всему миру и является одним из лидеров на рынке высокотехнологичного оборудования. Продукция Eppendorf используется в лабораториях самых различных профилей: академических, отраслевых научно-исследовательских, клинико-диагностических, экологических, криминалистических, а также в фармацевтической, биотехнологической, химической и пищевой промышленности и в лабораториях на промышленных предприятиях, которым необходим контроль качества и анализ производственного процесса. ЛабИнструментс является дилером Eppendorf в РФ.

Продукция Eppendorf представлена в трех направлениях:

LIQUID HANDLING:
Механические и электронные дозаторы;
Наконечники для дозаторов;
Механические и электронные диспенсеры;
Бутылочные дозаторы, цифровые бюретки;
Станции автоматического дозирования.

SAMPLE HANDLING:
Миксеры, термомиксеры и термостаты;
Пробирки и планшеты;
Центрифуги и роторы;
Амплификаторы и расходные материалы для ПЦР;
Низкотемпературные морозильные камеры.

CELL HANDLING:
Биореакторы, ферментеры.
CO2-инкубаторы, шейкеры;
Фотометры, спектрофотометры;
Микроманипуляторы, микроинъекторы
Расходные материалы для культивирования клеток и микроскопии

Protecting your laboratory environment
LABCONCO

Компания Labconco (США) является признанным мировым лидером в производстве общелабораторного оборудования. Labconco - один из старейших мировых производителей оборудования для лабораторий химического и биологического профиля. Продукция компании отличается исключительной надежностью в эксплуатации, высоким уровнем безопасности, эргономичностью и передовыми техническими характеристиками. Компания ЛабИнструментс является официальным представителем компании Labconco в России и странах СНГ.
В ассортименте компании: - вытяжные шкафы, - ламинарные боксы, - лиофильные сушки, - вакуумные концентраторы, - перчаточные боксы, - лабораторные посудомоечные машины, - лабораторные системы водоподготовки и др.

ООО «Компания ЛабИнструментс»
Россия, 117997, г. Москва, ул. Миклухо-Маклая, д. 16/10 (ИБХ РАН), корпус 32, офис 306
Телефон: +7 (495) 762-0236; 223-4815, тел./факс: +7 (495) 223-4815; +7 (499) 724-8872

华大基因
BGI

Service Offerings and Specifications*

BGI provides 24/7, round-the-clock technical support across the US, Europe and Asia Pacific to our clients. From sample to results, BGI provides a complete solution to enable rapid discovery.

- **Genomics Services, including:**
  - Exome Sequencing
  - Target Region Sequencing
  - Human Whole Genome Sequencing
  - Plant and Animal De Novo Sequencing and Re-sequencing
  - Single-Cell DNA Sequencing
- **Transcriptomics Services, including:**
  - Whole Transcriptome Sequencing
  - RNA-Sequencing (Quantification)
  - Small RNA Sequencing
  - Single-Cell DNA Sequencing
- **Epigenomics Services, including:**
  - Bisulfite Sequencing
  - ChIP-Seq
  - MeDIP
- **Genotyping**
- **Proteomics Services**
- **Meta-omics Services**

- **Genotyping**
- **Proteomics Services**
- **Meta-omics Services**

- **Immune Repetoire Sequencing**
- **Tumor Profiling**
- **Wide Portfolio of Genetic Testing Services**
- **Bioinformatics Services**

Join BGI in the Genomic Revolution

With a rich portfolio of genomic products and services, BGI is committed to providing customers with NGS services to support the needs of the research and clinical markets.

For more information please contact us at **info@bgi-international.com**.
Alternatively, please visit **www.bgi.com**.

*Available services vary by area. Clinical services are available in select areas outside the United States. Contact your local representative for more details on the service menu in your area.

Published, March 2016, BR-COV-02

BGISEQ-500 System Specification

Operating Environment	Instrument Control PC	Power Requirements
Temperature: 19℃~22℃ Humidity: Non-condensing 35%RH~80%RH relative humidity Altitude: Less than 2000m	CPU: Intel Xeon E5 10Core * 2 2.3GHz Memory: 128GB Storage: 12TB Operating System: Windows 7(64-bit)	200-240VAC, 50/60Hz Power Consumption: 1200VA
Dimensions		**Weight**
W×D×H: 1228mm×734mm×723mm		200kg

华大基因 BGI

If you are interested in Next Generation Sequencing (NGS), please visit www.seq500.com for more relevant information on your research applications.

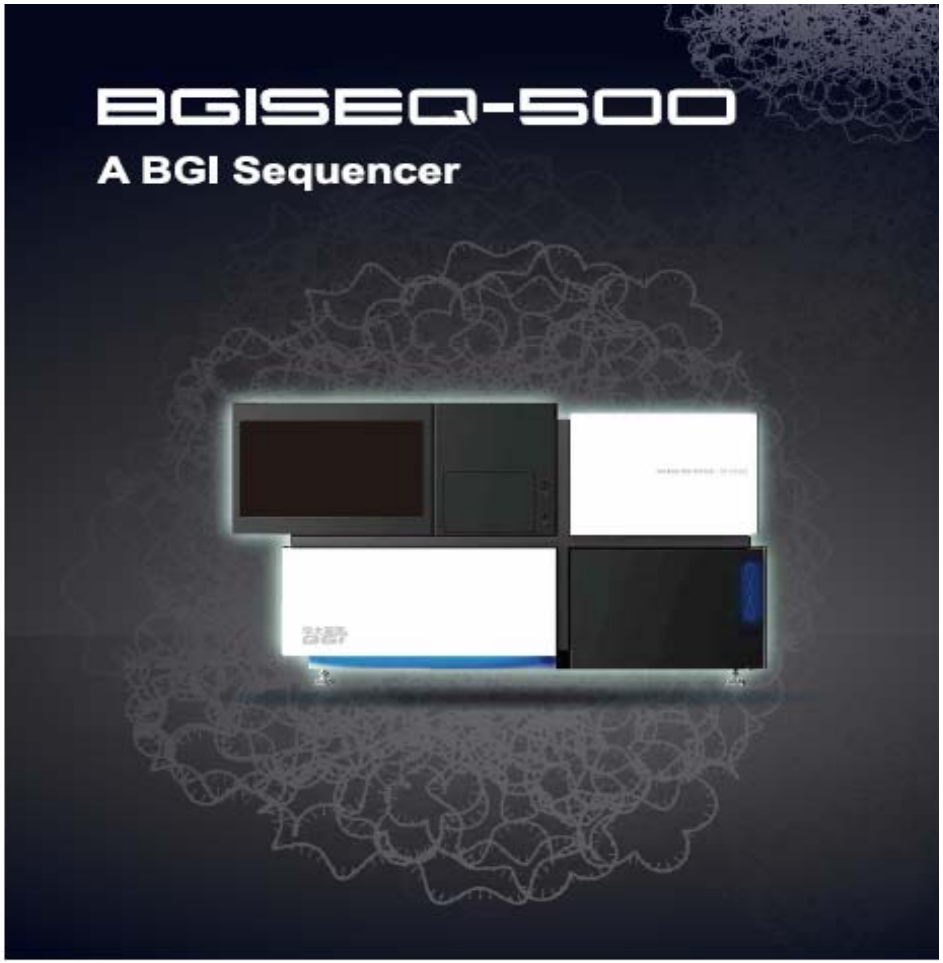
Service & Support

As a subsidiary of BGI, MGI has accumulated rich experience in gene sequencing with an excellent team of scientists and engineers, who are committed to providing comprehensive technical support in each section: from the installation, testing and operation, training, maintenance to subsequent upgrades, as well as the laboratory system construction, experiment scheme design and sequencing data analysis. You will experience an unprecedented journey of sequencing.

Contact Us

MGI Tech Co., Ltd.
Address: Building#11, Beishan Industrial Zone, Yantian District, Shenzhen, CHINA 518083
Email: MGI-service@genomics.cn
Website: www.seq500.com
Tel: 4000-965-988

CLINICAL USE IS SUBJECT TO REGULATORY APPROVAL

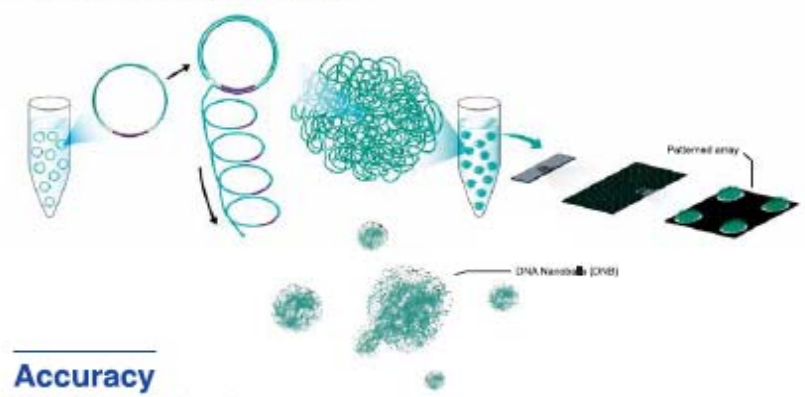


Next Generation Sequencing
Next Generation Experience

华大基因 BGI

BGI's NGS system | BGISEQ-500

A benchtop high-throughput open sequencing platform that provides end-to-end solutions



Accuracy

DNA Nanoballs (DNB)
Patterned array

BGISEQ-500 is an industry leading high-throughput sequencing solution, powered by combinatorial Probe-Anchor Synthesis (cPAS) and improved DNA Nanoballs (DNB) technology. The cPAS chemistry works by incorporating a fluorescent probe to a DNA anchor on the DNB, followed by high-resolution digital imaging. This combination of linear amplification and DNB technology reduces the error rate while enhancing the signal. In addition, the size of the DNB is controlled in such a way that only one DNB is bound per active site. This patterned array technology not only provides sequencing accuracy, but it also increases the chip utilization and sample density.

Simplicity

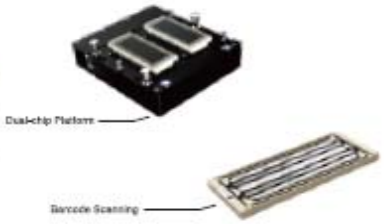
One-touch sequencing
Automation application analysis

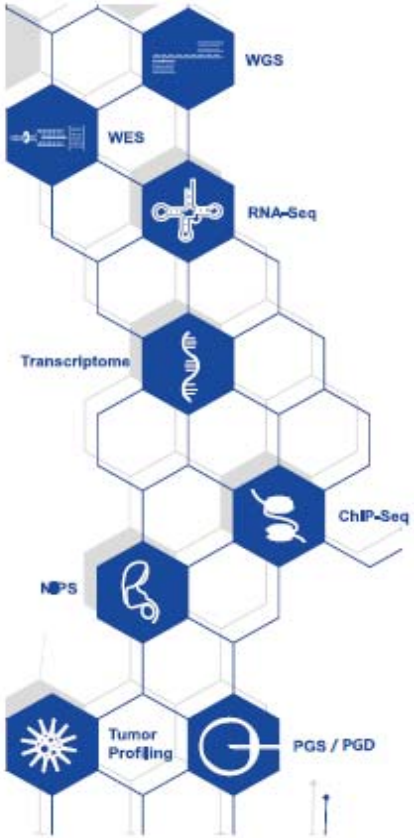
BGISEQ-500 is equipped with an intelligent, touch-sensitive interface providing simple, user-friendly operation. The automated tracking capabilities for samples, chips and reagents make lab information management simple, secure and traceable.

Speed

End-to-end sequencing operation
The fastest turn around time 24 hours

BGISEQ-500 provides a clear end-to-end sequencing work flow and allows for complete analysis of samples from input to the final result in as little as 24 hours when combined with the optional automatic library preparation and sample loading instruments.





Flexibility

Independent dual-chip platform
Optional multi-mode throughput

Each BGISEQ-500 can process two chips in a single run, with each chip capable of running different conditions on independent samples. In addition, we have developed two different types of chips: the high-throughput chip is well suited for analyzing many different sample types and provides large read output per run (200 Gb), whereas the fast-throughput chip is optimized for short turn-around-time applications, such as clinical exames, or for more economical runs where less data is required. These flexibilities will meet a variety of customers' sequencing needs; therefore, bring the best value to our users.

Expandability

Open-ended platform
Meet various sequencing requirements

BGISEQ-500 has an optional automatic library preparation and sample loading system supporting a variety of library preparation strategies. For each library method, specific reagent cartridges are formulated to maximize system performance and make the operation smooth and seamless. We've built flexibility into the system so as applications expand into new scientific and clinical areas, so will BGISEQ-500.

ТОО «БиоХимПрибор»

050002. г. Алматы, ул. Макатаева, 34
Телефон/факс:
+ 7 (727) 397-75-01 (-02, -04)
e-mail: biohimpribor@mail.ru

ТОО «БиоХимПрибор» создано в 2003 г. и в настоящий момент является поставщиком оборудования, расходных материалов, реактивов зарубежных производителей.
Наши клиенты – сотрудники лабораторий: биологических, химических, ветеринарных, экологических, контроля качества пищевых продуктов, контроля качества строительных лабораторий, государственные и контрольные службы.
Мы предлагаем своим клиентам комплексное оснащение, поэтому, наряду с продажей лабораторного оборудования, поставляем, также, и все, что требуется для его нормального использования – от расходных материалов, посуды и мебели до лабораторных животных.

НАПРАВЛЕНИЯ ДЕЯТЕЛЬНОСТИ КОМПАНИИ

✓ Химические реактивы

Компания "БиоХим Прибор" занимается поставкой химических реактивов под заказ по каталогам и является официальным дилером мирового производителя Sigma-Aldrich (бренды Sigma, Aldrich, Fluka, Supelco, SAFC, Riedel-de-Haen и др.). Ассортимент продукции насчитывает более 200 тысяч позиций.
Каталог сайта фирмы Сигма-Алдрич
SIGMA-ALDRICH http://www.sigmaaldrich.com/european-export.html

✓ Биореагенты

Реагенты для исследований в области молекулярной биологии, клеточного культивирования, биотехнологии. Пептиды и реагенты для пептидного синтеза. Питательные среды и их компоненты. Фетальные сыворотки. Наборы для выделения/очистки ДНК и РНК. Ферменты. Антитела. Олигонуклеотиды (праймера и пробы, производства SigmaGenoSys)

✓ Расходные материалы для лабораторий

Посуда стеклянная и пластиковая, термометры, ареометры, пикнометры, измерительная посуда, пипетки автоматические, дозаторы, фильтры из разных материалов, широкого диапазона, размеров и пористости, индикаторная бумага от лучших западных производителей.

✓ Общелабораторное оборудование

Центрифуги. Роторные испарители. Муфельные печи. Нагревательные приборы. Весы. Перемешивающие и диспергирующие приборы. Вакуумные насосы и датчики. Термостаты и автоклавы. Холодильное и морозильное оборудование. Микроскопы. Ультразвуковые бани. Спектрофотометры.

✓ Специальное лабораторное оборудование и сервис

- Приборы и аналитические системы для анализа сложных смесей органических соединений
- Приборы для анализа объектов натурального и синтетического происхождения, биообъектов
- Приборы для анализа диоксинов
- Методы и приборы для контроля безопасности пищевых продуктов
- Приборы для изотопного анализа в геологии, геохимии, и в ядерной энергетике
- Приборы для элементного анализа и изотопного скрининга
- Мы можем поставлять приборы отдельно и готовыми комплексными решениями Сервис высочайшего качества, методические и технические консультации.

✓Лабораторная мебель

Мы производим лабораторную мебель, это шкафы - вытяжные, медицинские, специальные для хранения химических реактивов; столы – химические, биологические, приборные, весовые, титровальные, островные, столы-мойки; делаем различные приспособления для лабораторий. Каркас нашей мебели из нержавеющей стали, поверхности столешниц могут быть из разных материалов. Заказы выполняются индивидуально, учитывая пожелания клиента.

✓Технический сервис и сертификация ШББ

Наша компания располагает собственным сервисным подразделением, которое осуществляет гарантийное и пост-гарантийное обслуживание, а также ремонт оборудования, методические и технические консультации.
Сертификация Шкафов Биологической Безопасности (ШББ) осуществляется согласно международным стандартам.

✓Ветеринарные тест-системы

Одно из главных направлений нашей компании является поставка ветеринарных тест-систем от ведущих мировых производителей ПЦР-диагностики и ИФА: Svanova (Швеция), BioNote (Южная Корея), Tetracore (США), Ingenaza (Испания), Intron Bytechnology (Южная Корея), ИнтерЛабСервис (ФГУН «ЦНИИ эпидемиологии» Роспотребнадзора, РФ), Prionics (Нидерланды) и др.

✓ Поставка лабораторных животных

Мы работаем с лучшими американскими и европейскими питомниками, поставляем лабораторных животных (аутбредных, инбредных, гибридных, мутантных, конгенных и трансгенных животных).

ТОО «БиоХим Прибор» имеет следующие лицензии:

Лицензия на занятие деятельности в области ветеринарии
Лицензия на занятие фармацевтической деятельностью
Лицензия на занятие ремонтом средств измерений
Лицензия на оборот и хранение прекурсоров
Лицензия на оборот и хранение ядов

Мы рады видеть Вас среди наших клиентов и партнеров.

Наши координаты: Казахстан,
г. Алматы, ул. Макатаева, 34

Адрес для писем:
050002. г. Алматы, ул. Макатаева, 34
Время работы:
Пн — Пт, с 09.00 до 18.00
Перерыв 13-00 до 14-00
Телефон/факс:
+ 7 (727) 397-75-01 (-02, -04)
e-mail: biohimpribor@mail.ru

SkyGen

THE LIFE SCIENCE TRADE & SERVICES COMPANY

Мы поставляем оборудование, реагенты и расходные материалы для исследовательских и биотехнологических лабораторий и производств.

Мы находим, разрабатываем и внедряем высокотехнологичные решения в генетике и геномике.

Наша цель – успех исследований наших покупателей.

НАША СТРАТЕГИЯ - МОЛЕКУЛЯРНЫЕ РЕШЕНИЯ «ПОД КЛЮЧ» ОТ ПОСТАНОВКИ ЗАДАЧИ ДО ИНТЕРПРЕТАЦИИ ДАННЫХ

БЛИЖЕ К КАЖДОМУ!

Более 3000 лабораторий работают с нами.

Доверяют и рекомендуют.

Территория Россия и страны СНГ

Исследовательские лаборатории

- Академии Наук
- Министерства Здравоохранения
- Криминалистики & судебной медицины
- Фарм производств & Биотеха

Ветеринарные лаборатории

Лаборатории пищевой безопасности

5 ПРИЧИН ВЫБРАТЬ SKYGEN

- Доступ к высококачественной продукции
- Быстрая логистика и складская программа
- Удобное и взаимовыгодное сотрудничество
- Высококвалифицированная поддержка
- Мы устанавливаем адекватные цены


НАШИ КОМПЕТЕНЦИИ
ФАРМАЦЕВТИЧЕСКОЕ ПРОИЗВОДСТВО
Европейская фармакопея и фармакопея США
Стандарты биодобавок и пищевых ингредиентов
Низкомолекулярные и органические реактивы
ГЕННАЯ ИНЖЕНЕРИЯ
Клонирование
CRISPR/Cas9
Синтез олигонуклеотидов и генов
БИОТЕХНОЛОГИЧЕСКОЕ ПРОИЗВОДСТВО
Штаммы и среды
Хим. реактивы
Поверка систем дозирования
МОЛЕКУЛЯРНАЯ ГЕНЕТИКА И ЦИТОГЕНЕТИКА
ПЦР, FISH анализ, биочипы
Анализ одиночных клеток
ПГД
SkyGen
Молекулярно Просто
ВЕТЕРИНАРНАЯ ДИАГНОСТИКА
Автоматизация ИФА
Оборудование для ПЦР
Тест-системы
NGS
Автоматизация пробоподготовки
Реагенты для создания библиотек
Секвенаторы NGS и биоинформатика
КРИМИНАЛИСТИКА
Экстракция ДНК из объектов
Автоматизация анализа
Капиллярное секвенирование
ПРОТЕОМИКА
Выделение белков
Масс-спектрометрия
Хроматография

SkyGen

THE LIFE SCIENCE TRADE & SERVICES COMPANY

КАРТА РЕШЕНИЙ

ПРОИЗВОДИТЕЛЬНОСТЬ (КОЛИЧЕСТВО ОБРАЗЦОВ / ЗАПУСК)

Боксы, шейкеры, термостаты, центрифуги, Biosan

Гомогенизатор TissueLyser II, QIAGEN

Гомогенизатор TissueLyser LT, QIAGEN

Гомогенизатор TissueRuptor, QIAGEN

Реагенты QIAGEN

Реагенты MN

Реагенты NEB

QIAcube, QIAGEN

Nimbus для пробоподготовки NGS, Hamilton

Персональные роботы Opentrons

Станция для ИФА Crocodile, Titertek-Berthold

Раскапывающая станция PIRO, Dornier-LTF

Классический амплификатор SureCycler 8800 (96/384), Agilent

6-канальный real-time амплификатор AriaMx (96), Agilent

4-канальный real-time амплификатор с HRM Mic (48), BMS

ПРОЦЕСС

Пробоподготовка	Выделение нуклеиновых кислот	Дозирование жидкостей и сборка ПЦР смесей	ПЦР

ToxScreener, Bruker

Сканер биочипов SureScan, Agilent

Система 4200 TapeStation (96), Agilent

Секвенатор NGS GeneReader, QIAGEN

MALDI Biotyper, Bruker

KREATECH DIAGNOSTICS

ДНК-зонды для диагностики, Kreatech

Спектрофотометр QIAxpert (16), QIAGEN

Обогащение для NGS, Agilent

SureFISH

ДНК-зонды SureFish, Agilent

NEW ENGLAND BioLabs

Реагенты для пробоподготовки NGS для illumina и ThermoFisher

microflex LT/SH, Bruker

Прямые, инвертированные и флуоресцентные микроскопы, Nikon

Биоанализатор 2100 (12), Agilent

Капиллярный секвенатор НАНОФОР-05, Синтол

Спектрофотометр Colibri (1), Titertek-Berthold

Реагенты для секвенаторов ABI, Nimagen & EdgeBio

Масс-спектрометрия | Цитогенетический анализ | Контроль качества | Секвенирование

Ғылыми – өндірістік фирмасы «Медилэнд»
Научно – производственная фирма «Медилэнд»

Юридический адрес: 050061, г. Алматы, ул. Ташкентская 417А;
Почтовый адрес: 050061, г. Алматы, пр. Райымбека 417А
Тел.: 8 (727) 222-00-55 (многоканальный);
Факс: 8 (727) 222-00-56;
E-mail: mail@mediland.kz

ТОО «НПФ Медилэнд» является частной казахстанской компанией с дислокацией в г. Алматы. Компания организована в 1993 году и имеет специализацию в области поставок сложной медицинской и лабораторной техники, а также расходных материалов для приборов клинической и функциональной диагностики и последующее их сервисное обслуживание.

Являясь официальным дистрибьютором на территории Казахстана таких ведущих мировых производителей, как «Sigma» (Германия), «Systec» (Германия), «Memmert» (Германия), «Heidolph» (Германия), «GFL» (Германия), «Brand» (Германия), «Kern» (Германия), «Bandelin» (Германия), «Siemens» (Германия), «Nabertherm» (Германия), «Martin Christ» (Германия), «Sartorius» (Германия), «Arctiko» (Дания), «Kojair» (Финляндия), и многих других, мы занимаемся поставкой в РК медицинского и лабораторного оборудования для оснащения медицинских и научных лабораторий, расходных лабораторных материалов и хим. реагентов. Все специалисты компании регулярно проходят обучение и повышают свою квалификацию на заводах компаний-производителей и имеют соответствующие сертификаты.

Мы имеем постоянно действующий склад расходных материалов и реагентов для предлагаемого нами лабораторного оборудования. С 1996 г. наша компания успешно участвует в тендерах по закупке медицинского, лабораторного оборудования и расходных материалов. Мы обеспечиваем бесплатное сервисное обслуживание в пределах гарантийного срока и последующее постгарантийное обслуживание на поставленное нами оборудование, обучение специалистов организаций-заказчиков методикам работы на приборах и консультационную поддержку по поставляемому нами оборудованию в различных областях применения. Кроме того, нами создана разветвленная сеть дилеров по всему Казахстану, своевременно реализующих поставляемую нами продукцию. В настоящее время штат компании составляет более 70 сотрудников, из них 3 кандидаты биологических наук, 10 магистров, 5 специалистов по продукции, имеющих медицинское, фармацевтическое, биологическое, химическое высшее образование, 9 сервис-инженеров. С 2000 года объем продаж вырос в 8 раз и составил в 2007 году более 1,7 миллиарда тенге.

В числе наших клиентов крупнейшие медицинские и научные центры Республики: Медицинский Центр Управления делами Президента РК, Научный центр

хирургии им. А. Н. Сызганова, НИИ Урологии им. Джарбусынова, НИИ Кардиологии и внутренних болезней, Центральный военный клинический госпиталь, Научный Центр Акушерства, Гинекологии и Перинаталогии, Республиканский НИИ Проблем Туберкулеза, НИИ Кожно-венерологических заболеваний, Институт глазных болезней, Институт Молекулярной Биологии и Биохимии АН-МН РК, Институт Общей Генетики и Цитологии РК, Республиканская СЭС, Республиканский Центр СПИД, Республиканский Центр Крови, Научный Центр Противоинфекционных препаратов, Научный Центр Педиатрии и Детской Хирургии, НИИ Травматологии и Ортопедии и многие другие. Нами оснащены лаборатории Областного Диагностического Центра в г.Павлодаре, лаборатории строящихся объектов Медицинского Кластера в г.Астана. В текущем году мы завершили проекты оснащения «под ключ» бактериологической лаборатории Медицинского Центра Управления делами Президента РК и лаборатории Научного Центра Животноводства и Ветеринарии.

В качестве консультанта ТОО «НПФ Медилэнд» привлекалось к разработке государственной Программы «Здоровье народа», участвует в техническом обеспечении программ «Предупреждение заболеваний, передаваемых половым путем» и «Туберкулез».

Мы видим своей целью внедрение инновационных технологий в области медицины и исследовательского оборудования, предоставляя в распоряжение наших клиентов последние технические разработки наряду с приборами, уже зарекомендовавшими себя и проверенными обширной практикой пользователей. Учитывая все возрастающий интерес и большое прогрессивное значение исследований стволовых клеток и пуповинной крови, мы представляем полное аппаратное обеспечение для работы лабораторий на этапах получения пробы, выделения, типирования и стандартизации образцов в соответствии с международными требованиями, а также их долгосрочного хранения.

Мы осуществляем консультирование нашего 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 нами оборудования;
- оказания консультативно-методической и практической помощи пользователям оборудования;
- регулярного информирования о новинках в методиках, технологиях и оборудовании для проведения учеными научно-исследовательских работ.

И во время и после истечения гарантийного срока эксплуатации предлагаемых нами приборов сертифицированные специалисты нашей сервисной службы сделают всё возможное для того, чтобы наши заказчики могли работать на поставленном нами оборудовании с максимальной эффективностью.

Нашей сервисной службой осуществляются консультации по телефону или оперативный выезд специалиста для срочного выявления и устранения неисправности приборов, а также гарантийное и послегарантийное обслуживание поставленного нами оборудования по договору с заказчиком.

ТОО «NURMEDINVEST» коммерческая компания, основанная в 2009 г. За годы стабильного роста компания приобрела опыт в области оснащения медицинских учреждений Республики Казахстан. За это время у нас сложились прочные деловые связи с отечественными и зарубежными производителями медицинской техники, расходных материалов и изделий медицинского назначения.

О результатах нашей работы свидетельствуют положительные отзывы клиентов, дипломы международных, российских выставок и конференций. Наша дилерская сеть охватывает всю территорию Республики Казахстан.

Мы находим для наших клиентов оптимальное решение поставленных задач и обеспечиваем техническую поддержку. Конструктивное долгосрочное сотрудничество и доверительные отношения с партнерами для нас важнее сиюминутной выгоды.

Наша компания предлагает широкий выбор продукции, включающий качественный лабораторный расходный материал, медицинские перчатки, центрифуги, термостаты, пластиковую и стеклянную посуду для лабораторий.

Мы являемся эксклюзивным представителем на территории Республики Казахстан:

HangzhouRollmedCo., Ltd (Китай) – китайскаякомпания, одна из самых профессиональных поставщиков лабораторной, диагностической, медицинской и стоматологической продукции. Завод находится в Провинции Цзяну. Так же имеется совместное предприятие в Провинции Чжэцзян. Принцип работы компании – обеспечение клиентов качественной и доступной продукцией.

У нас Вы можете приобрести товар, произведенный компанией HangzhouRollmedCo., Ltd (Китай): наконечники для дозаторов; центрифужные пробирки; криопробирки; штативы для пробирок; пипетки Пастера; предметные и покровные стекла; тампоны со средами Amies, CaryBlair, Stuart, с углем и без угля; тампоны без среды; контейнеры для биологического материала; стоматологические салфетки; наконечники для слюноотсосов; спиртовые салфетки; пакеты для стерилизации; бахилы; маски; шапочки, виниловые перчатки.

MercatorMedical (Thailand) Ltd–производитель медицинских диагностических и хирургических перчаток, поставщик медицинских расходных материалов. Имеются филиалы в Польше, Центральной и Восточной Европе, а так же и в России, поэтому продукция доступна по всему миру. Девиз компании: «Качество и ответственность - ключевые факторы для нас во всех областях».

Представляем следующие виды медицинских перчаток:

Перчатки диагностические **nitrylex®PF**, нитриловые, нестерильные, неопудренные

Перчатки диагностические **dermaGEL®**, латексные, текстурированные, с внутренним синтетическим покрытием, нестерильные, неопудренные
Перчатки диагностические **santex®**, латексные, нестерильные, опудренные
Также мы сотрудничаем с российскими компаниями:

ИнтерЛабСервис **ООО «Интерласервис»** является официальным дистрибьютором наборов реагентов для ПЦР-диагностики торговой марки АмплиСенс, а также продукции ряда ведущих производителей лабораторного оборудования, реагентов и лабораторного пластика (QIAGEN, Illumina, Axygen, Xiril, SPM, BeckmanCoulter и др.)

НПО Прибор Компания **НПО «Прибор» (Россия)** основана в 1990 г. как структурное подразделение Всесоюзной Ассоциации специалистов по охране труда (Постановление Совета Министров СССР и ВЦСПС декабрь 1989 г.) По техническому заданию, согласованному с Минздравом, Минэнерго и Агрохимом, впервые разработало универсальный газоанализатор для автоматического непрерывного контроля ГАНК-4 на базе сменных химкассет. В 1998 г., при доработке прибора для орбитальной космической станции «МИР», его функции были существенно расширены. Были встроены датчики с различными физическими принципами действия. В результате прибор стал контролировать не только неорганические, но и органические вещества, а также физфакторы.

ОТКРЫТОЕ АКЦИОНЕРНОЕ ОБЩЕСТВО Смоленское СКТБ СПУ Основанное в 1993 году, предприятие **ОАО «Смоленское СКТБ СПУ»** ведёт успешную деятельность по разработке и производству термостатического оборудования – лабораторной и медицинской техники для оснащения медицины, научно-исследовательских, аналитических, испытательных и производственных лабораторий предприятий легкой и тяжёлой промышленности, строительных предприятий и организаций муниципальной сферы, учебных учреждений, НИИ

Выпускаемое ОАО «Смоленское СКТБ СПУ» оборудование предназначено для выполнения лабораторно-аналитических работ, проведения бактериологических и серологических исследований, стерилизации, сушки и хранения медицинского инструмента, испытаний качеств пищевых продуктов, термической обработки различных материалов.

АО «ЛОИП» Лабораторное Оборудование и Приборы

ЗАО «Лабораторное Оборудование и Приборы» – производственно-коммерческая компания, основанная в 1996 г. одна из ведущих компаний, работающих в области комплексного оснащения лабораторий. Собственное производство лабораторной мебели, общелабораторного оборудования, специализированных приборов для анализа нефтепродуктов, позволило стать лидером среди российских производителей лабораторной продукции.

Свяжитесь с нашими специалистами – мы работаем по вашим запросам и делаем все для наиболее полного удовлетворения потребностей наших заказчиков.

г. Алматы, ул. Умбетбаева 190, 050057, тел: 266-20-94

CONTENT

Session 1. Genetic Resources and Evolution

PLENARY SESSION

Goncharov N. P. Taxonomy, architectonic of plant and molecular phylogeny of the genus *Triticum* L. 6

Blattner F.R., Bernhardt N. The evolution of the wheat grasses: Cenogenome vs. taxonomic diversification 7

Tanaka T. Barley genetic resources and development of genotyping infrastucture 8

ORAL SESSION

Abugalieva S., Ivaschenko A., Ishmuratova M., Kotukhov Y., Danilova A., Myrzagalieva A., Veselova P., Kudabayeva G., Sitpayeva G., Imanbayeva A., Sakauova G., Kakimzhanova A., Turuspekov Y. Collection and evaluation of endemic and rare species of flora in Kazakhstan 9

Gurkan K., Demirel F., Tekin M., **Akar T.** Molecular and Agro-Morphologic Characterization of Einkorn (*T. monococcum*) and Emmer (*T. dicoccon*) Hulled Wheat Landraces 10

Almerekova Sh.S., Mukhitdinov N.M., Kurmanbayeva M.S. Phylogenetic analysis of endemic species *Oxytropis almaatensis* Bajt. from Kazakhstan 11

Boika O. Plant development type and its correlation with other traits in Lunara genus (Cruciferae) 12

Börner A., Nagel M., Agacka-Mołdoch M., Börner M., Lohwasser U., Riewe D., Wiebach J., Altmann T., Pshenichnikova T.A., Khlestkina E. Genetic resources for food and agriculture- conservation and utilisation 13

Chen G., Zhao J., Zhao X., Zhao P., Zhang J. A potential food crop *Agriophyllum squarrosum* 14

Abugalieva S., **Genievskaya Y.,** Shamshadin D., Zhubanysheva A., Turuspekov Y. Genetic variation of sand rice (*Agrophillium squarosum* L.) collected from two different regions of Kazakhstan 15

Hassanzadeh Ghorttapeh A., Abasali M., Ghanavati F., Allahyari N., Khakizad G.R.,Mirakhorli A., Alitabar R.A., Taheripor A., Kanani R., Kyani M.R., Fanaei H.R.,Habibifar H. Ghojig S., Nakhaei A., Karami M.J., Abadoz G.R., Abbasi K.,Hamzehnegad A., Safari S., Asgari SH, Azizi H., Manochehri H., Fathi A., Asadi-Pour M., Soltani A., Asgari A.H., Kazerani N., Foromadi N., Samani M. Geographical variation and evaluation of Iranian landraces of *Ricinus communis* L. 16

Imanbaeva A.A., Duysenova N.I., Tujakova A.T., Jumakhan D. Accumulation of organic acids in fruit of *Crataegus ambigua* from different natural populations of Mangistau 17

Kakimzhanova A.A., Karimova V.K., Nurtaza A.S. Creation of production for obtaining of landing material of Poplar by using microclonal propagation 18

Silkova O.G., **Loginova D.B.,** Ivanova Yu.N., Krivosheina E.A., Bondarevich E.B., Solovey L.A., Sycheva E.A., Dubovets N.I. Rye chromatin introgression into wheat genome: contribution of wheat- rye chromosome substitutions 1R/1A and 6R/6A in hybrid genome stabilization 19

Loskutov I.G. Metabolomic approach to resistance of *Avena* species to Fusarium head blight (FHB) 20

Myrzagaliyeva A. Microclonal *in vitro* propagation of *Nepeta densiflora* 21

Sadoyan R.R. The genetic potential of south Caucasus wheat 22

Shadenova E., Zhumabekov E., Sembekov M. Reproduction of genetic resources of Kazakhstan 23

Dogdu V., Canci H., Sari H., Sari D., Adak A., **Toker C.** Transgressions in reciprocal interspecific crosses between the cultivated pea and its wild species 24

Zhang Z. Conservation and Evaluation of Oat Genetic Resources in China 25

POSTER SESSION

Abugalieva S., **Amalova A.,** Anuarbek S., Ivaschenko A., Turuspekov Y. 26
Evaluation of genetic variation in rare Tulip species from Kazakhstan

Abugalieva S., Volkova L., **Amangeldinov K.,** Ivaschenko A., Kotukhov Y., Sakauova G., Turuspekov Y. Taxonomic reassessment of some Allium species from Kazakhstan based on DNA barcoding analysis 27

Avalyan R.E, Minasbekyan L.A. Current problems of study and preserve of wheat gene pool of Armenia 28

Bilgen M., Delibalta Z., Adak A. Effect of colchicine applications on germination of some forage crops 29

Boiko N., Piskarev V., Timofeev A., Kapko T. Study of specifics of formation the spikelet number per spike of varieties of soft spring wheat in contrasting years 30

Chirkin A.P., Yurkevich N.A., Yessimbekova M.A., Mukin K.B. , Ismagulova G.A. Phylogenetic analysis of foreign and local ecotypes of genus *Aegilops* L. using EST-SSR markers 31

Dobrovolskaya O.B., **Ermakov A.A.,** Dresvyannikova A.E., Amagai Yu., Krasnikov A.A., Goncharov N.P., Watanabe N. Characterization of liguleless mutants of Triticea species using molecular genetics and scanning electron microscopy 32

Ishmuratova M.Yu. The potential of using of practical- valued plants' resources of the central Kazakhstan's flora 33

Izbastina K.S., Kurmanbayeva M.S., Abugalieva S.I. Morphological and phylogenetic identification of the *Anthemis trotzkiana* Claus 34

Abugalieva A.I., **Massimgaziyeva A.I.,** Azhgaliev T.B., Zhumahanova A.Zh. 35
The content of oil and fatty acids in breeding of sunflower, safflower, soybean, canola and linen: cultivars gene pool and genetic resources

Magzumova G.K., Abdildaeva S.K., Kakimzhanova A.A. Breeding potato variety Astanalyk for receiving improved seed planting material 172

Nurtaza A., Karimova V., Kakimzhanova A. Optimization of conditions of microclonal propagation of *Malus Njedzwetzkyana* 173

Abugalieva A.I., **Nurpeissov M.,** Sariev B.S., Zhundibaev K.K. Identification of productivity and quality oat genotypes: avenyne, DNA markers and morphology (UPOV) 36

Orazov A. E., Akzambek A.M. Development of technology for clonal micropropagation *Rhodiola rosea* L. 37

Piskarev V., Boiko N., KapkoT., Timofeev A. Identification of the genetic control of the 1000 grain weight of varieties differ of soft spring wheat 38

Pozharskiy A.S., Aubakirova K.P., **Ryabushkina N.A.** Genotyping and ampelometric characterization of Kazakhstan grapevine cultivars compared to European and Asian cultivars 39

Tagimanova D.S., Khapilina O.N., Danilova A.N., Amenov A.A., Kalendar R.N. Retrotransposons- based genetic diversity and relationship among *Rhodiola rosea* 40

Tekin M., Coskun I., Manav G., Cat A., Sonmez S., **Akar T.** Molecular Characterization of Durum Wheat and Its Tetraploid Wild Relatives for Cadmium Accumulation 175

Tikhonova M.A., Koppel R., Ingver A. Identification of *Glu- D1* and *Glu- A1* alleles in bread wheat using DNA markers 41

Trubacheeva N.V., Osadchaya T.S., Pershina L.A. Variability of nuclear genomes and the state of organelle DNA in alloplasmic (Hordeum)- *T. aestivum* lines 42

Turzhanova A.S., Kalendar R.N. Gene polymorphisms of wheat superoxide dismutase gene family 43

Volkova L., Gemedzhieva N., Abugalieva S., Zhanarbek S., Sitpayeva G., Turuspekov Y. Assessment of distinctions between *Glycyrrhiza uralensis* and *Glycyrrhiza glabra* based on analysis of ITS marker 44

Lei L., **Wang L.,** Wang Sh. Analysis of genetic diversity of Common bean from different region of China 45

Yessimseitova A., Zhanybekova Zh., Kakimzhanova A. Study of floral genetic diversity in the state national natural parks of Bayanaul and Burabay in Kazakhstan 46

Zhang J.W., Chen G.X. Transcriptomic analysis of a Trichomeless mutant in *Agriophyllum squarrosum* 47

Zhubanysheva A.U., Zhubanyshev A.B., Titova B.U. monitoring of plant spreading of *Agriophyllum* L. (Kumarchak) 174

Session 2. Abiotic and Biotic Stress Resistance

PLENARY SESSION

Fahima T., Huang Lin, Yaniv E., Raats D., Klymiuk V., Hanan Sela, Feng L., Distelfeld A., Tamar Kis-papo, Krugman T., Dubcovsky J., Chalhoub B., Schulman A. H., Korol A.B. Diversity and evolution of disease resistance genes derived from wild emmer wheat 49

Griffiths S. Global journeys of adaptive wheat genes 50

Uga Yu. Genomics-based breeding using genetic variation of root system architecture improves crop productivity under abiotic stress conditions 51

ORAL SESSION

Anapiyayev B.B., Iskakova K.M., Beisenbek E.B., Sarbayev A.T., Dweikat I.M., Baenziger P.S. Molecular markers and haploid biotechnology in rapid selection of *Triticum aestivum* L. for resistance to rust diseases in the conditions of Southern Kazakhstan 52

Özdere M., **Bakir M.** Determination of Ascorbate Peroxidase Gene expression in the Lentil (*Lens culinaris* Medik) under drought stress conditions 53

Bome N.A., Bome A.Ya., Weisfeld L.I., Kolokolova N.N., Petrova A.A., Belozerova A.A. The variability of the parameters of the morphogenetic processes in populations of *Triticum aestivum* L. under the influence of stress factors 54

Elkonin L.A., Kozhemyakin V.V., Gerashchenkov G.A., Belyaeva E.V., Panin V.M., Rozhnova N.A. Drought as a modulator of gene expression for CMS and apomixis in sorghum 55

Kokhmetova A., Gultyaeva E., Madenova A., Galymbek K., Purnhause B.L. Leaf and yellow rust evaluation and molecular screening in wheat cultivars produced in Kazakhstan 56

Kostylev P.I., Krasnova E.V., Redkin A.A., Kalievskaya Yu.P. Marker Assisted Selection (MAS) of rice on resistance to diseases, flooding and salinity 57

Leonova I.N., Skolotneva E.S., Salina E.A. Resistance to fungal diseases of spring wheat 170

varieties from different Russian regions

Minasbekyan L.A. Epigenetic events in wheat seedlings nuclei abiotic stress responces 58

Perfileva A.I., Garnik E.Uy., Stolbikov A.S., Nurminsky V.N. The change of an expression of PR and HSP genes of *in vitro* potato plants under heat stress and pathogenesis of ring rot of potato 59

Potokina E.K., Lebedeva M.V., Teplyakova S.B., Ivanova N.N., Voytsutskaya N.P., Kovaleva O.N. Mapping and re- sequencing of *SDW1/DENSO* locus affecting plant height and heading date in barley 60

Rogozhin E.A., Ryazantsev D.Yu. Unique gene structure encoded a family of hairpin-like defense peptides from barnyard grass (*Echinochloa crusgalli* L.Beauv.) seeds 61

Rsaliyev A.S., Pakhratdinova Zh.U. Screening of barley genotype for detection of resistance donors to barley powdery mildew 62

Salina E.A, Adonina I.G., Stasyuk A.I., Leonova I.N. Approaches and achievements in molecular pre- breeding for rust resistance in West Siberia 63

Suzuki T. Resistance to wheat yellow mosaic virus in Madsen wheat is controlled by two major complementary QTLs 171

Tekin M., Cengiz M. Fatih, Canci H., Coskun I., Aksoy A., Akar T. Variation for micronutrient and vitamin B contents of Turkish Einkorn and Emmer Wheat candidate lines 64

Tohetova L., Demesinova A., Bekova M. Genetic-statistical analysis the agronomic traits of barley by two-testing method 65

Tsivileva O.M., Fadeev V.V., Voronin S.P., Gumenyuk A.P., Nikitina V.E. Evaluation of opportunity for applying the biogenic metals aspartates to improve the processes of mushrooms cultivation 66

Turuspekov Y., Yermekbayev K., Baibulatova A., Chapman S., Zheng B., Ganal M., Plieske J., Griffiths S., Abugalieva S. Prediction of flowering time and GWAS of yield components of spring wheat in Kazakhstan 67

Voinikov V.K. Energetic and information systems of plant cells at temperature fluctuations 68

Zatybekov A., Rsaliyev A., Didorenko S., Abugalieva S., Turuspekov Y. Association mapping of agronomic traits in soybean harvested in Kazakhstan 69

POSTER SESSION

Abugalieva S., Didorenko S., **Anuarbek Sh.,** Volkova L., Gerasimova Y., Sidorik I., Zatybekov A., Turuspekov Y. Genotype and environment interaction patterns in collection of soybean grown in Kazakhstan 70

Anuarbek Sh., Abugalieva S., Didorenko S., Gerasimova Y., Sidorik I., Turuspekov Y. Influence of *Dt1* gene to yield components of soybean harvested in Kazakhstan 71

Atishova M., Kokhmetova A., Typina L., Madenova A., Galymbek K., Keishilov Zh. Identification of genetic carriers of wheat, steady against yellow rust *Puccinia striiformis* F. sp. tritici 72

Bekkuzhina S., Zhamekova A., Kitaibekova S., Apushev N. The role of salicylic acid in the induction of wheat stability to stressers 73

Bersimbaev R.I., Kravchenko A.P. Regulation of ABA metabolism by TOR signaling in *Arabidopsis thaliana* 74

Bobrovskikh A.V., Doroshkov A.V. Molecular evolution of antioxidant genes in plants and its relationship with cellular localization of protein products 75

Deryabin A.N., Trunova T.I. Expressing the *SUC2* yeast invertase gene of apoplast 76

localizations increase the cold resistance of potato plants

Didorenko S.V., Abugalieva A.I., Sidorik I.V. Fast- ripening somaclonal lines of soybean within the conditions of north and south of Kazakhstan (productivity, drought tolerance and grain quality) 77

Doroshkov A.V., Simonov A.V., Afonnikov D.A., Pshenichnikova T.A. The manifestation and phytohormone response of leaf pubescence genes in bread wheat 78

Dubovets N.I., **Drobot N.I.,** Silkova O.G., Sycheva E.A., Bondarevich E.B. Assessment of wheat- rye hybrids' breeding potential with the use of molecular markers 79

Efremova O.S., Kodirova G.A., Fisenko P.V. Selection genetic evaluation of somaclonal lines of soybean tolerant to the heavy metals ions 80

Efremova T.T., Chumanova E.V., Trubacheeva N.V. The obtainment and use of genetically marked common wheat lines for the study of genes controlling adaptation and resistance to stress 81

Zhigailov A.V., Kislitsin V.Y., Beisenov D.K., Polimbetova N.S., **Iskakov B.K.** Discrete fragmentation of 18S rRNA 5'-terminus may regulate protein synthesis in plants under different stress conditions 82

Kokhmetova A., Atishova M., Madenova A., Galymbek K., Keyshilov Zh., Sharma R. S., Yessimbekova M., Urazaliev R., Aynebekova B., Lapochkina I., Morgounov A. The study of resistance of wheat germplasms to stripe and leaf rust using molecular markers 83

Kokhmetova A., Kremneva O.,Volkova G., Keyshilov Zh.S., Galymbek K., Kumarbayeva M., Sultanova N.Zh. The structure of the pathogen *Pyrenophora tritici-repentis* population in the Republic of Kazakhstan and North Caucasus region of Russia 84

Kozhahmetov K., Abugalieva A.I., Rsaliyev A.S., Chudinov V.A. Resistance of spring and winter wheat with the introgression of genetic material (*T. timopheevi, T. kinarae, T. dicoccoides, Ae. triaristata, Ae. cylindrica*) to abiotic and biotic stress factors of the environment 85

Lee T., Spankulova Z., Orazbayeva U., Didorenko S. Asparagine metabolism and protein content in the developing soybean seeds 86

Madenova A.K., Kokhmetova A.M., Atishova M.N., Galymbek K., Keishilov Zh. Identification of germplasm winter wheat for resistance to yellow and leaf rust 87

Nerkararyan A.V., Minasbekyan L.A., Shahinyan M.A. Joint effect of growth stimulator of plants C-2 and EMI ENF on peroxidase total activity of wheat seedlings 88

Orlovskaya O.A., Milko L.V., Khotyleva L.V., Kilchevsky A.V. High molecular weight glutein subunits in common wheat lines with alien genetic material introgression 89

Rashal I., Grauda D., Krasņevska N., Belogrudova I., Voskresenska Je., Lada B., Kolodinski A. Flow cytometry for identification of plant genomic response in ecological studies 90

Sedlovsky A.I., Tjupina L.N, Tjezhenova A.I, Atishova M. The creation of drought-resistant wheat samples using the methods of Classical genetics, traditional and marker selection 91

Smailov B.B., Omasheva M.E., Galiakparov N.N. PI-LAMP assay for detection of *Erwinia amylovora* in diagnosis of fire blight 92

Terletskaya N., Zobova N., Stupko V., Iskakova A., Lugovtsova S., Kurmanbayeva M. The tetraploid wheat species as source highly resistant to abiotic stresses 175

Turganbayeva A., Kakimzhanova A., Shek G., Zhanybekova Zh., Ortaeva K. Results of the use in the crossbreeding of regeneranted soft spring wheat for receiving a new source 93

material of wheat in North Kazakhstan

Turuspekov Y., **Yermekbayev K.,** Griffiths S**.** Genotyping of spring hexaploid wheat collection from Kazakhstan using *Vrn, Ppd* and *Eps* genes 94

Yessimbekova M.A., Abugalieva A.I., Mukin K.B. Using of wheat wild relatives (*Aegilops* L.) diversity for balanced use 95

Zemlyanuhina O.A., Cherkasova N.N., Zhuzhzhalova T.P., Kalayev V.N., Voronina V.S. Influence of salt stress on biochemical parameters of *Weigela florida* «Variegata» microclones and sugar beet hybrid components 96

Session 3. Genomics, Phenomics, and Bioinformatics

PLENARY SESSION

Ganal M.W, Graner E.-M., Polley A., Plieske J. High throughput genotyping for plant research and breeding 98

Zhang Q. Green goals and green technologies in plant breeding for global food security: the rice model 99

Chen M. Integrative bioinformatics approaches for cellular interactome modelling of rice 100

ORAL SESSION

Abbasov M., Akparov Z., Aminov N., Rustamov Kh., Sheykzamanova F., Rzayeva S., Bowden R., Raupp J., Sehgal S., Gill B. Evaluating genetic diversity of durum and bread wheat genotypes using next generation sequencing. 101

Babak O.G., Nekrashevich N.A., Nikitinskaya T.V., Yatsevich K.K., Kilchevsky A.V. Peculiarities of lycopene β-cyclase genes expression, depending on the combinations of alleles that determine the accumulation of pigments in the *Solanaceae* 102

Dobrovolskaya O.B., Popova K.I., Orlov Yu.L., Krasnikov A.A., Martinek P. Study on genetic control of early inflorescence development in bread wheat (*T. aestivum* L.) that determines inflorescence architecture and yield. 103

Gordei I.A., Lyusikov O.M., Gordei I.S., Lipikhina Yu.A., **Evtushenko E.V.,** Vershinin A.V. Cytogenomic problems of heteroplasmatic hexaploid triticale 104

Genaev M.A., Komyshev **E.G.**, Afonnikov D.A. Mobile application for high throughput grain phenotyping 105

Glagoleva A.Y., Vasiliev G.V., Shatskaya N. V., Shmakov N.A., Afonnikov D.A., Shoeva O.Y., Börner A., Khlestkina E.K. Identification of genes controlling black pigmentation in cereals. 106

Jian J. The application of genomic innovation in plant 107

Bishimbayeva N.K., **Kairov U.,** Li C.Y., Nakisbekov N.O., Begzat A., Molkenov A., Amirbekov A.S., Smagul A.O., Kapasuly T., Mitra A., Rakhimbayev I.R. Transcriptome sequencing and gene expression profiling of wheat cell culture during transition to somatic embryogenesis 108

Kalendar R.N. Genome size variation and long tandem arrays of LTR retroelements in plants 109

Khlestkin V.K. High- throughput microscopy- based phenotyping of potato starch granules 110

Shoeva O.Y., Gordeeva E.I., Shmakov N.A., Strygina K.V., Glagoleva A.Y., Kukoeva T.V., Shatskaya N.V., Vasiljev G.V., Börner A., Afonnikov D.A., **Khlestkina E.K.** 111

Genetics and omics approaches to better understanding regulation of metabolic pathways underlying pigmentation in wheat and barley

Kiseleva A.A., Salina E.A. New aspects of wheat photoperiod insensitive *PPD-B1* regulation and interactions 112

Orlov Y.L., Dobrovolskaya O.B., Bragin A.O., Babenko V.N., Chen M. Bioinformatics analysis of genome and transcriptome structures related to freezing and draught resistance in crop plants 113

Shmakov N.A., Vasiliev G. V., Shatskaya N. V., Doroshkov A. V., Afonnikov D.A., Khlestkina E. K. Investigating barley nuclear genes controlling chlorophyll synthesis with RNA- SEQ 114

Lukhanina N.V., **Sinyavskaya M.G.,** Pankratov V.S., Liaudansky A.D., Goloenko I.M., Shymkevich A.M., Danilenko N.G. Davydenko O.G. NGS of barley organelle genomes 115

Strygina K.V., Shoeva O.Y., Gordeeva E.I., Khlestkina E.K. Duplicated genes in polyploid plant species- case studies in wheat and potato 116

Hasaninejad S., **Talat F.** Factories affecting synonymous codon usage bias in chloroplast genome of *Gossypium thurberi* and *Gossypium arboreum* 117

Lebedeva M.V., Zhigunov A.V., **Ulianich P.S.,** Voitsekhovskii D.M., Potokina E.K. Genotyping of population generated by *Populus tremula* × *P. alba* cross 118

Yermekbayev K., Turuspekov Y., Ganal M., Plieske J., Griffiths S. Construction and utilization of the hexaploid wheat genetic map *Pamyati Azieva x Paragon* 119

POSTER SESSION

Bishimbayeva N.K., Tastan M., Murtazina A., Rakhmedova M**., Dossova Z.,** Yugai M., Baimenov M., Demesinova S.D. Growth and immunity stimulating activity of extracellular polysaccharides from wheat cell culture 120

Konstantinov D.K., Doroshkov A.V., Afonnikov D.A. Molecular evolution analysis of genetic network related to plant trichome development 121

Plieske J., Graner E.-M., Polley A., Ganal M.W. Genotyping wheat varieties with different genotyping arrays 122

Dobrovolskaya O.B., Morozova K., **Popova K.I.,** Dresvyannikova A.E., Börner A., Röder M.S., Kiseleva E.B., Voylokov A.V. Characterization of a chlorophyll mutant, *Tigrina*, in rye 123

Raizer O.B., Khapilina O.N., Novakovskaya A.P., Amenov A.A., Danyarov A.Z., Turzhanova A.S., Kalendar R.N. Genetic diversity of grain legume studies with various molecular markers from different genomic origin 124

Savin T.V., Abugalieva A.I., Cakmak I. Cartogram of Zn content in the grain of wheat, barley and oats on the background of productivity and drought resistance 125

Turuspekov Y., Genievskaya J., Sariev B., Tokhetova L., Chudinov V., Ortaev A., Tsygankov V., Sereda G., Espanov A. Evaluation of genetic variation in spring barley collection using SNP Illumina array 126

Session 4. Genetic Engineering and Crop Improvement

PLENARY SESSION

Komatsuda T. The potential of barley/wheat orthology to advance cereal grain yield 128

Kumlehn J. Genome engineering in cereals 129

Wulff B.B.H. Rapid gene cloning in wheat and barley 130

ORAL SESSION

Abugalieva A., Bashabayeva B. Main trends in cereal breeding in Kazakhstan 131

Fedorova Y.A., Tvorogova V.E., Lutova L.A. Regulation of somatic embryogenesis by *WOX* genes in *Medicago truncatula* 132

Flachowsky H.[1], Hanke M.-V. Current state of CISgenesis and rapid crop cycle breeding in German fruit breeding research 169

Gapeka A.V., Zelikova A.A., Zhmurkina S.K., Pleshakova T.I., Volkov Yu.G., Kakareka N.N., Shchelkanov M.Yu. Ecology and economical impact of barley stripe mosaic virus (*Virgaviridae, Hordeivirus)* in the Primorsky krai of Russia 133

Gerasimova S.V., Korotkova A.M., Khlestkina E.K. Genome editing in Siberian barley 134

Graskova I.A., Perfilieva A.I., Klimenkov I.V., Sukhov B.G. The possibility of nanocomposites application in agriculture 135

Ilyushko M.V., Skaptsov M.V., Romashova M.V. Nuclear DNA content in rice regenerants, obtained by anther culture *in vitro* on Russian Far East 136

Khvatkov P., Firsov A., Shaloiko L., Pushin A., Tarasenko I., Chernobrovkina M., Dolgov S. Creation of expression platform based on *Wolffia arrhiza* for production of therapeutic proteins in the example of recombinant human granulacyte colony-stimulating factor 137

Korolev K.P., Golub I.A. Evaluation of the mutagenic effect nitrosoethylurea and nitrozozoguanidina on plants of flax (*Linum usitatissimum* L.) 138

Bisaga M., Griffiths I., Vickerstaff R., Paczos-Grzeda E., Abugalieva A., Dumlupinar Z., Huang Y-F, Giorgi D., Lucretti S., **Langdon T.** Genomics tools for oat breeding 139

Manabayeva S.A., Zhumabek A.T., Abeuova L.S., Ramankulov E.M. Tomato bushy stunt virus - based vector for transient expression of heterologous proteins in *Nicotiana benthamiana* plants 140

Pavlichenko V.V., Bairamova E.M., Protopopova M.V., Zolotovskaya E.D., Voinikov V.K. Agrobacterium mediated transformation of *Populus* × *Beroliensis* by *ATGA20OX1* gene using PRI 101-AN vector 141

Pershina L.A., Belan I.A., Rosseeva L.P., Osadchaya T.S., Kravtsova L.A., Belova L.I., Trubacheeva N.V. Alloplasmic wheat in genetic research and breeding 142

Pleshakova T.I., Kozlovskaya Z.N., Tolkach V.F., Volkov Y.G., Kakareka N.N., Gapeka A.V., Shchelkanov M.Y. Plant viruses and their interaction with plant communities of Far East of Russia 143

Rezaeva B.R., Buriev Z.T, Ubaydullaeva Kh.A., Rakhmanov B.K., Tulanov A.A, Abdurakhmonov I.Y. An effective Agrobacterium- mediated *in planta* transformation of wheat (*Triticum aestivum*) 144

Shpakovski G.V., Spivak S.G., Berdichevets I.N., Babak O.G., Kilchevsky A.V., Shpakovski D.G., Khaliluev M.R., Shematorova E.K. A key enzyme of animal steroidogenesis can function in plants improving their immunity and increasing the processes of growth and development 145

Stegniy V.N., Sibataev A.K., Abylkassymova G.M. Genetic parameters of species required for effective selection 146

Toki S. Precise and efficient Mutagenesis in Crops via Genome editing 147

Tvorogova V.E., Fedorova Y.A., Vaschkevich T.A., Lutova L.A. New participants of somatic embryogenesis in *Medicago truncatula* 148

Vershinina Z.R., Hakimova L.R., Yasybaeva G.R., Lavina A.M., Baimiev Al.Kh. 149

Agglutinin genes and the process of creating artificial symbiotic systems

Zhang Z. Conservation and evaluation of Oat Genetic Resources in China 150

POSTER SESSION

Abugalieva A.I. Grain quality in spring wheat, its wild relatives and new promising varieties (introgressive forms) 151

Amenov A.A., Kalendar R.N. Detection of genetically modified organisms (GMOS) using isothermal amplification of the genetic construct DNA sequences. 152

Bishimbayeva N.K., Baymagambetova K., Urazaliev R.A., Nurpeisov I.A., Chudinov V.A., Sereda G.A., Bekenova L.V., Gass O.S., Karabayev M.K., Rahimbayev I.R. Cell technology for creating precocious forms of soft spring wheat 153

Daurov D.L., Karpova O.V., Alexandrova A.M., Nargilova R.M., Zhambakin K.Zh., Shamekova M.Kh. Obtaining of transgenic plants of maize resistant to increased drought 154

Egorova A.A., Nikulin P.S., Ibragimova S.S., Kochetov A.V., Shumny V.K., Gerasimova S.V. The role of OAT gene in plant proliferating tissues 155

Gancheva M.S., Dodueva I.E., Lutova L.A. Identification, characterization and expression analysis of *CLE* genes in potato (*Solanum tuberosum* L.) 156

Gordeeva E., Shoeva O., Yudina R., Usenko N., Otmakhova Y., Amstislavskaya T., Pavlov K., Khlestkina E. Anthocyanins in wheat: plant protection and health benefit 157

Gritsenko D.A., Galiakparov N.N. Insertion of 2A peptides between ORF4 and ORF5 of grapevine virus A 158

Kapasuly T., Muchitdinova Z.R., Bishimbayeva N.K. Development of *in vitro* regeneration system for oat local varieties 159

Djatchouk T.I, Pominov A.V., Kibkalo I.A., **Khomyakova O.V.,** Akinina V.N., Italiyanskaya Yu.V. Anther culture method for rapid selection of winter Triticale varieties for Volga region 160

Korotkova A.M., Gerasimova S.V., Shumny V.K., Khlestkina E.K. Crop genes modified using CRISPR/CAS9 system: systematic analysis of published reports 161

Maltseva E.R., Skiba Y.A., Chirkin A.P., Iskakova G.A., Yurkevich N.A., Baizhumanova S.S., Naizabayeva D.A., Zhidkeyeva R.E., Ismagulova G.A. Wheat transformation efficiency in bread wheat cv. Saratovskaya 29, Kazakhstanskaya 19 and Almaly 162

Skiba Y.A., Maltseva E.R., Chirkin A.P., Yurkevich N.A., Naizabayeva D.A., Zhidkeyeva R.E., Ismagulova G.A. Efficiency of biolistic co- transformation in potato varieties Aksor and Nevskiy 163

Stanbekova G.E., Nadirova L.T., Beisenov D.K., Iskakov B.K. Expression in plants of the C- terminal fragment of the human Alpha- fetoprotein 164

Ulianich P.S., Grigoreva E.A., Koshkin V.A., Loskutov I.G., Potokina E.K. Mapping of photoperiod response loci in the RILS population of hexaploid oat. 165

Yerzhebayeva R.S., Abugalieva A.I., Danyarova A.K. Obtaining of double haploid lines of interspecific and intergeneric wheat syntetics 166

Zhambakin K.Zh., Shamekova M.Kh., Edilova A.K. Transfer of transgenes to varieties and relatives of rapeseed. 167

Erzhebayeva R.S., Daniyarova A.K., Sariyev B.S., **Zhumakayev A.,** Bishimbayeva N.K. Development of androgenic technology for oat and barley 168

AUTHORS INDEX

A

Abadoz G.R. 16
Abasali M. 16
Abbasi K. 16
Abbasov M. 101
Abdildaeva S.K. 172
Abdurakhmonov I.Y. 144
Abeuova L.S. 140
Abugalieva A.I. 35, 36, 77, 85, 95, 125, 131, 139, 151, 166
Abugalieva S.I. 9, 15, 26, 27, 34, 44, 67, 69, 70, 71
Abylkassymova G.M. 146
Adak A. 24, 29
Adonina I.G. 63
Afonnikov D.A. 78, 105, 106, 111, 114, 121
Agacka-Mołdoch M. 13
Akar T. 10, 64, 175
Akinina V.N. 160
Akparov Z. 101
Aksoy A. 64
Akzambek A.M. 37
Alexandrova A.M. 154
Alitabar R.A. 16
Allahyari N. 16
Almerekova Sh.S. 11
Altmann T. 13
Amagai Yu. 32
Amalova A. 26
Amangeldinov K. 27
Amenov A.A. 40, 124, 152
Aminov N. 101
Amirbekov A.S. 108
Amstislavskaya T. 157
Anapiyayev B.B. 52
Anuarbek Sh. 26, 70, 71
Apushev N. 73
Asadi-Pour M. 16
Asgari A.H. 16
Asgari S.H. 16
Atishova M.N. 72, 83, 87, 91
Aubakirova K.P. 39
Avalyan R.E. 28
Aynebekova B. 83
Azhgaliev T.B. 35
Azizi H. 16

B

Babak O.G. 102, 145
Babenko V.N. 113
Baenziger P.S. 52
Baibulatova A. 67
Baimenov M. 120
Baimiev Al.Kh. 149
Bairamova E.M. 141
Baizhumanova S.S. 162
Bakir M. 53
Bashabayeva B. 131
Baymagambetova K. 153
Begzat A.N. 108
Beisenbek E.B. 52
Beisenov D.K. 82, 164
Bekenova L.V. 153
Bekova M. 65
Belan I.A. 142
Belogrudova I. 90
Belova L.I. 142
Belozerova A.A. 54
Belyaeva E.V. 55
Berdichevets I.N. 145
Bernhardt N. 7
Bersimbaev R.I. 74
Bilgen M. 29, 139
Bishimbayeva N.K. 108, 120, 153, 159, 168
Blattner F.R. 7
Bobrovskikh A.V. 75
Boika O. 12
Boiko N. 30, 38
Bome A.Ya. 54
Bome N.A. 54
Bondarevich E.B. 19, 79
Börner A. 13, 106, 111, 123
Börner M. 13
Bowden R. 101
Bragin A.O. 113
Buriev Z.T 144

C

Cakmak I. 125
Canci H. 24,64
Cat A. 175
Cengiz M. Fatih 64
Chalhoub B. 49
Chapman S. 67
Chen G.X. 14, 47
Chen M. 100, 113
Cherkasova N.N. 96
Chernobrovkina M. 137
Chirkin A.P. 31, 162, 163
Chudinov V.A. 85, 126, 153

Chumanova E.V. 81
Coskun I. 64, 175

D
Danilenko N.G. 115
Danilova A.N. 9, 40
Daniyarova A.K. 166, 168
Danyarov A.Z. 124
Daurov D.L. 154
Davydenko O.G. 115
Delibalta Z. 29
Demesinova A. 65
Demesinova S.D. 120
Demirel F. 10
Deryabin A.N. 76
Didorenko S. 69, 70, 71, 77, 86
Distelfeld A. 49
Djatchouk T. I 160
Dobrovolskaya O.B. 32, 103, 113, 123
Dodueva I.E. 156
Dogdu V. 24
Dolgov S. 137
Doroshkov A.V. 75, 78, 114, 121
Dossova Z. 119
Dresvyannikova A.E. 32, 123
Drobot N.I. 79
Dubcovsky J. 49
Dubovets N.I 19, 79
Dumlupinar Z. 139
Duysenova N.I. 17
Dweikat I.M. 52

E
Edilova A.K. 167
Efremova O.S. 80
Efremova T.T. 81
Egorova A.A. 155
Elkonin L.A. 55
Ermakov A.A. 32
Erzhebayeva R.S. 168
Espanov A. 126
Evtushenko E.V. 104

F
Fadeev V.V. 66
Fahima T. 49
Fanaei H.R. 16
Fathi A. 16
Fedorova Y.A. 132, 148
Feng L. 49
Firsov A. 137
Fisenko P.V. 80
Flachowsky H. 169
Foromadi N. 16

G
Galiakparov N.N. 92, 158
Galymbek K. 56, 72, 83, 84, 87
Ganal M.W 67, 98, 119, 122
Gancheva M.S. 156
Gapeka A.V. 133, 143
Garnik E.Uy. 59
Gass O.S. 153
Gemedzhieva N. 44
Genaev M. A. 105
Genievskaya Y. 15, 126
Gerashchenkov G.A. 55
Gerasimova S.V. 134, 155
Gerasimova Y. 70, 71
Ghanavati F. 16
Ghojig S. 16
Gill B. 101
Giorgi D. 139
Glagoleva A.Y. 106, 111
Goloenko I.M. 115
Golub I.A. 138
Goncharov N. P. 6, 32
Gordeeva E.I. 111, 116, 157
Gordei I.A. 104
Gordei I.S. 104
Graner E.-M. 98, 122
Graskova I.A. 135
Grauda D. 90
Griffiths I. 139
Griffiths S. 50, 67, 94, 119
Grigoreva E.A. 165
Gritsenko D.A. 158
Gultyaeva E. 56
Gumenyuk A.P. 66
Gurkan K. 10

H
Habibifar H. 16
Hakimova L.R. 149
Hamzehnegad A. 16
Hanke M.-V. 169
Hasaninejad S. 117
Hassanzadeh Ghorttapeh A. 16
Huang Y-F. 139

I
Ibragimova S.S. 155
Ilyushko M.V. 136
Imanbaeva A.A. 9, 17
Ingver A. 41
Ishmuratova M.Yu. 9, 33
Iskakova A. 175
Iskakov B.K. 82, 164
Iskakova G.A. 162

Iskakova K.M. 52
Ismagulova G.A. 31, 162, 163
Italiyanskaya Yu.V. 160
Ivanova N.N. 60
Ivanova Yu.N. 19
Ivaschenko A. 9, 26, 27
Izbastina K.S. 34

J
Jian J. 107
Jumakhan D. 17

K
Kairov U. 108
Kakareka N.N. 133, 143
Kakimzhanova A.A. 9, 18, 46, 93, 172, 173
Kalayev V.N. 96
Kalendar R.N. 40, 43, 109, 124, 152
Kalievskaya Yu.P. 57
Kanani R. 16
Kapasuly T. 108, 159
Kapko T. 30, 38
Karabayev M.K. 153
Karami M.J. 16
Karimova V.K. 18, 173
Karpova O.V. 154
Kazerani N. 16
Keyshilov Zh.S. 73, 83, 84, 87
Khakizad G.R. 16
Khaliluev M.R. 145
Khapilina O.N. 40, 124
Khlestkin V.K. 110
Khlestkina E.K. 13, 106, 111, 114, 116, 134, 157, 161
Khomyakova O.V. 160
Khotyleva L.V. 89
Khvatkov P. 137
Kibkalo I. A. 160
Kilchevsky A.V. 89, 102, 145
Kis-papo T. 49
Kiseleva A.A. 112
Kiseleva E.B. 122
Kislitsin V.Y. 82
Kitaibekova S. 73

Klimenkov I.V. 135
Klymiuk V. 49
Kochetov A.V. 155
Kodirova G.A. 80
Kokhmetova A.M. 56, 72, 83, 84, 87
Kolodinski A. 90
Kolokolova N.N. 54
Komatsuda T. 128
Komyshev E. G. 105
Konstantinov D.K. 121
Koppel R. 41
Korol A.B. 49
Korolev K.P. 138
Korotkova A.M. 134, 161
Koshkin V.A. 165
Kostylev P.I. 57
Kotukhov Y. 9, 27
Kovaleva O.N. 60
Kozhahmetov K. 85
Kozhemyakin V.V. 55
Kozlovskaya Z.N. 143
Krasņevska N. 90
Krasnikov A.A. 32, 103
Krasnova E.V. 57
Kravchenko A.P. 74
Kravtsova L.A. 142
Kremneva O. 84
Krivosheina E.A. 19
Krugman T. 49
Kudabayeva G. 9
Kukoeva T.V. 111
Kumarbayeva M. 84
Kumlehn J. 129
Kurmanbayeva M.S. 11, 34, 175
Kyani M.R. 16

L
Lada B. 90
Langdon T. 139
Lapochkina I. 83
Lavina A.M. 149
Lebedeva M.V. 60, 118

Lee T. 86
Lei L. 45
Leonova I.N. 63, 170
Li C.Y. 108
Liaudansky A.D. 115
Lin H. 49
Lipikhina Yu.A. 104
Loginova D.B. 19
Lohwasser U. 13
Loskutov I.G. 20, 65
Lucretti S. 139
Lugovtsova S. 175
Lukhanina N.V. 115
Lutova L.A. 132, 148, 156
Lyusikov O.M. 104

M
Madenova A. 56, 72, 83, 87
Maltseva E.R. 162, 163
Magzumova G.K. 172

Manabayeva S.A. 140
Manav G. 175
Manochehri H. 16
Martinek P. 103
Massimgaziyeva A.I. 35
Milko L.V. 89
Minasbekyan L.A. 28, 58, 88
Mirakhorli A. 16
Mitra A. 108
Molkenov A. 108
Morgounov A. 83
Morozova K. 123
Muchitdinova Z.R. 159
Mukhitdinov N.M. 11
Mukin K.B. 31, 95
Murtazina A. 120
Myrzagaliyeva A. 9, 21

N
Nadirova L.T. 164
Nagel M., 13
Naizabayeva D.A. 162, 163
Nakhaei A., 16
Nakisbekov N.O. 108
Nargilova R.M. 154
Nekrashevich N.A. 102
Nerkararyan A.V. 88
Nikitina V.E. 66
Nikitinskaya T.V. 102
Nikulin P.S. 155
Novakovskaya A.P. 124
Nurminsky V.N. 59
Nurpeisov I.A. 153
Nurpeissov M. 36
Nurtaza A.S. 18

O
Omasheva M.E. 92
Orazbayeva U. 86
Orazov A. E. 37
Orlov Yu.L. 103, 113
Orlovskaya O.A. 89
Ortaev A. 126
Ortaeva K. 93
Osadchaya T.S. 42, 142
Otmakhova Y. 157
Özdere M. 53

P
Paczos-Grzeda E. 139
Pakhratdinova Zh.U. 62
Panin V.M. 55
Pankratov V.S. 115
Pavlichenko V.V. 141
Pavlov K. 157
Perfileva A.I. 59, 135
Pershina L.A. 42, 142
Petrova A.A. 54
Piskarev V. 30, 38
Pleshakova T.I. 133, 143
Plieske J. 67, 98, 119, 122
Polimbetova N.S. 82
Polley A. 98, 122
Pominov A. V. 160
Popova K.I. 103, 123
Potokina E.K. 60, 118, 165
Pozharskiy A.S. 39
Protopopova M.V. 141
Pshenichnikova T.A. 13, 78
Purnhause B.L. 56
Pushin A. 137

R
Raats D. 49
Rahimbayev I.R. 153
Raizer O.B. 124
Rakhimbayev I.R. 108
Rakhmanov B.K. 144
Rakhmedova M. 120
Ramankulov E.M. 140
Rashal I. 90
Raupp J. 101
Redkin A.A. 57
Rezaeva B.R. 144
Riewe D. 13
Röder M.S. 123
Rogozhin E.A. 61
Romashova M.V. 136
Rosseeva L.P. 142
Rozhnova N.A. 55
Rsaliyev A.S. 62, 69, 85
Rustamov Kh. 101
Ryabushkina N.A. 39
Ryazantsev D.Yu. 61
Rzayeva S. 101

S
Sadoyan R.R. 22
Safari S. 16
Sakauova G. 9, 27
Salina E.A 63, 112, 170
Samani M. 16
Sarbayev A.T. 52
Sari D. 24
Sari H. 24
Sariev B.S. 36, 126, 168

Savin T.V. 125
Schulman A.H. 49
Sedlovsky A.I. 91
Sehgal S. 101
Sela H. 49
Sembekov M. 23
Sereda G.A. 126, 153
Shadenova E. 23
Shahinyan M.A. 88
Shaloiko L. 137
Shamekova M.Kh. 154, 167
Shamshadin D. 15
Sharma R. S. 83
Shatskaya N. V. 106, 111, 114
Shchelkanov M.Yu. 133, 143
Shek G. 93
Shematorova E.K. 145
Sheykzamanova F. 101
Shmakov N.A. 106, 111, 114
Shoeva O.Y. 106, 111, 116, 157
Shpakovski D.G. 145
Shpakovski G.V. 145
Shumny V.K. 155, 161
Shymkevich A.M. 115
Sibataev A.K. 146
Sidorik I.V. 70, 71, 77
Silkova O.G. 19, 79
Simonov A.V. 78
Sinyavskaya M.G. 115
Sitpayeva G. 9, 44
Skaptsov M.V. 136
Skiba Y.A. 162, 163
Skolotneva E.S. 170
Smagul A.O. 108
Smailov B.B. 92
Solovey L.A. 19
Soltani A. 16
Sonmez S. 175
Spankulova Z. 86
Spivak S.G. 145
Stanbekova G.E. 164
Stasyuk A.I. 63
Stegniy V.N. 146
Stolbikov A.S. 59
Strygina K.V. 111, 116
Stupko V. 175
Sukhov B.G. 135
Sultanova N.Zh. 84
Suzuki T. 171
Sycheva E.A. 19, 79

T
Tagimanova D.S. 40
Taheripor A. 16
Tanaka T. 8
Tarasenko I. 137
Tastan M. 120
Tekin M. 10, 64, 175
Teplyakova S.B. 60
Terletskaya N. 175
Tikhonova M.A. 41
Timofeev A. 30, 38
Tjezhenova A.I 91
Tjupina L.N 91
Tokhetova L. 65, 126
Toker C. 24
Toki S. 147
Tolkach V.F. 143
Trubacheeva N.V. 42, 81, 142
Trunova T.I. 76
Tsivileva O.M. 66
Tsygankov V. 126
Tujakova A.T. 17
Tulanov A.A 144
Turganbayeva A. 93
Turuspekov Y. 9, 15, 26, 27, 44, 67, 69, 70, 71, 94, 119, 126
Turzhanova A.S. 43, 124
Tvorogova V.E. 132, 148
Typina L. 72

U
Ubaydullaeva Kh.A. 144
Uga Yu. 51
Ulianich P.S. 118, 165
Urazaliev R.A. 83, 153
Usenko N. 157

V
Vaschkevich T.A. 148
Vasiliev G. V. 106, 111, 114
Vershinin A.V. 104
Vershinina Z.R. 149
Veselova P., 9
Vickerstaff R. 139
Voinikov V.K. 68, 141
Voitsekhovskii D.M. 118
Volkov Yu.G. 133, 143
Volkova G. 84
Volkova L.A. 27, 44, 70
Voronin S.P. 66
Voronina V.S. 96
Voskresenska Je. 90
Voylokov A.V. 123
Voytsutskaya N.P. 60

W
Wang L. 45
Wang Sh. 45
Watanabe N. 32
Weisfeld L.I. 54
Wiebach J. 13
Wulff B.B.H. 130

Y
Yaniv E. 49
Yasybaeva G.R. 149
Yatsevich K.K. 102
Yermekbayev K. 67, 94, 119
Yerzhebayeva R.S. 166
Yessimbekova M.A. 31, 46, 83, 95
Yudina R. 157
Yugai M. 120
Yurkevich N.A. 31, 162, 163

Z
Zatybekov A. 69, 70
Zelikova A.A. 133
Zemlyanuhina O.A. 96
Zhambakin K.Zh. 154, 167
Zhamekova A. 73
Zhanarbek S. 44
Zhang J.W. 14, 47
Zhang Q. 99
Zhang Z. 25, 150
Zhanybekova Zh. 46, 93
Zhao J. 14
Zhao P. 14
Zhao X. 14
Zheng B. 67
Zhidkeyeva R.E. 162, 163
Zhigailov A.V. 82
Zhigunov A.V. 118
Zhmurkina S.K. 133
Zhubanysheva A.U. 15, 174
Zhubanyshev A.B. 174
Zhumabek A.T. 140
Zhumabekov E. 23
Zhumahanova A.Zh. 35
Zhumakayev A. 168
Zhundibaev K. K. 36
Zhuzhzhalova T.P. 96
Zobova N. 175
Zolotovskaya E.D. 141