PLANTGEN'23

10–15 July
Kazan, Tatarstan, Russia

KAZAN
2023
PLANTGEN

Abstracts

VII International scientific conference

PLANT GENETICS, GENOMICS, BIOINFORMATICS & BIOTECHNOLOGY

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Vavilov Society of Geneticists and Breeders
Russian Society of Plant Physiologists
Federal State Budgetary Institution of Science "Kazan Scientific Center of Russian Academy of Sciences"
Institute of Cytology and Genetics,
Siberian Branch of the Russian Academy of Sciences

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Сборник содержит тезисы докладов, представленных в рамках VII Международной научной конференции «Генетика, Геномика, Биоинформатика и Биотехнология растений» (PLANTGEN 2023), которая состоялась в Казани на базе Федерального исследовательского центра «Казанский научный центр Российской академии наук».

Научная программа конференции посвящена результатам исследований в области геномных технологий, генетических ресурсов растений, физиологической и экологической генетики растений, генетики устойчивости к стрессовым факторам окружающей среды, фундаментальных и прикладных аспектов изучения организации и эволюции генома растений. Часть представленных сообщений освещает вопросы селекции в изменяющихся условиях окружающей среды, генетической инженерии, клеточной биотехнологии и улучшения сельскохозяйственных культур. Все представленные тезисы докладов отражают современный уровень состояния генетики растений, ориентируют ученых на будущие тенденции развития фундаментальной науки и прикладных исследований на решение стоящих перед нами глобальных проблем.

Для широкого круга специалистов в сфере работ с биологов, генетиков, биотехнологов, селекционеров, специалистов, занимающихся генетическими ресурсами растений, и студентов биологического и сельскохозяйственного профиля, в том числе студентов, аспирантов и молодых ученых. Тезисы публикуются в авторской редакции. За объективность и достоверность представленных данных ответственность несут авторы (соавторы) публикуемых тезисов.

The Proceedings include the abstracts of papers presented at the VII International Scientific Conference "Genetics, Genomics, Bioinformatics and Plant Biotechnology" (PLANTGEN 2023), which was held in Kazan at the Federal Research Centre "Kazan Scientific Centre of the Russian Academy of Sciences".

The scientific program of the PLANTGEN 2023 conference is dedicated to the results of research in the field of genomic technologies, plant genetic resources, physiological and ecological genetics of plants, genetics of resistance to environmental stress factors, fundamental and applied aspects of studying the organization and evolution of the plant genome. Some of the submissions cover the issues of breeding under changing environmental conditions, genetic engineering, cell biotechnology, and crop improvement. The presented reports reflect the current state of plant genetics, orient scientists to future trends in the development of fundamental science and applied research to solve the global problems facing us. For a wide range of specialists in the field of works with biologists, geneticists, biotechnologists, breeders, specialists involved in plant genetic resources, and students of biological and agricultural profile, including students, postgraduates, and young scientists. Abstracts are published in the author's edition. The authors (co-authors) of published abstracts are responsible for the objectivity and reliability of the data presented.

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DEAR COLLEAGUES!

On behalf of the Organizing Committee, we are pleased to welcome the participants to the International Scientific Conference "Genetics, Genomics, Bioinformatics and Plant Biotechnology" (PLANTGEN 2023), which will be held in Kazan on July 10-15, 2023

Traditionally, the PLANTGEN Conference is a significant event in the scientific life of the scientists from all regions of Russia and many foreign countries whose professional activities focus on plant genetics. In recent years, our conference has become one of the outstanding events in Russian science and deservedly included in the list of the world's most important scientific conferences dedicated to plant genetics, breeding and biotechnology.

The 2023 Conference will continue the best traditions established by the Institute of Cytology and Genetics in organization the event and will attempt to introduce new ideas and trends. The greatest achievement of the upcoming PLANTGEN 2023 is the high demand, great interest in the Conference and its scale: the number of participants is more than 600 persons from 15 countries, which is twice as much as in all previous conferences. The geography of participants from Russia is also extensive and includes leading scientific and educational organizations from Karelia to the Far East. This demonstrates the attention of the wide public to the achievements and problems of our science, the desire to expand and consolidate scientific connections, and the growing popularity of plant genetics and related sciences among researchers.

The central objective of the conference is to develop the scientific basis and analysis of modern achievements and fundamental developments for food security, which are inextricably linked to the development of genetics and national breeding, which is important both for the Russian Federation and many countries around the world.

The program of the International Scientific Conference PLANTGEN 2023 includes a wide range of research areas of modern plant genetics, which are inextricably linked to a number of other areas of biological science and the development and use of genetic technology and breeding. It presents the results of the latest research and achievements in plant genetics, genomics, bioinformatics, and plant biotechnology, and will discuss promising research directions (including collaborative research) on fundamental and applied aspects of plant genome studies. We will discuss at the Conference these and other topics related to the impact of new genetic technologies on the main object of our research - the plant.

In addition to the scientific aspects, the International Scientific Conference PLANTGEN 2023 is an open communication platform in the field of experimental plant biology,where we have to discuss problems and evaluate the results of very serious research in recent years, including those conducted with the help of modern equipment. We have to determine the most promising directions of scientific thought and outline new trends in the development of the discussed problems, which can lead to a qualitative breakthrough in their development as soon as tomorrow. The congress will present these issues in 17 plenary lectures, 130 oral presentations in the form of section presentations, compact flash presentations and presentations by young scientists in a special section. In addition, there will be a large poster session with over 300 posters.

The pre-conference will be preceded by a young scientists' school on the most recent areas of plant genetics: genomic selection, recombinant proteins, genetic engineering and genome editing, and biomolecule modelling. Well-known scientists in the fields of genetics, plant physiology, biotechnology and breeding will give scientific lectures and workshops. A separate youth section is also planned, where very young scientists will present their results in the form of oral presentations to stimulate their interest in further research.

We have tried to fill the conference schedule as much as possible with important and informative discussions and activities to make your work interesting and fruitful. We want to create a good atmosphere for communication and exchange of scientific information in the fields of genetics and breeding, bioinformatics, and plant biotechnology. We strongly believe that the results of the conference will be useful for all participants and will be applied in the further scientific activities of each of them

In conclusion, dear colleagues, we would like to thank all of you for your interest and participation in this scientific forum and wish you creative and productive work, interesting discussions, new scientific contacts, activity, optimism, and an unforgettable impression of the ancient and modern Kazan. We wish all of you to achieve your goals!

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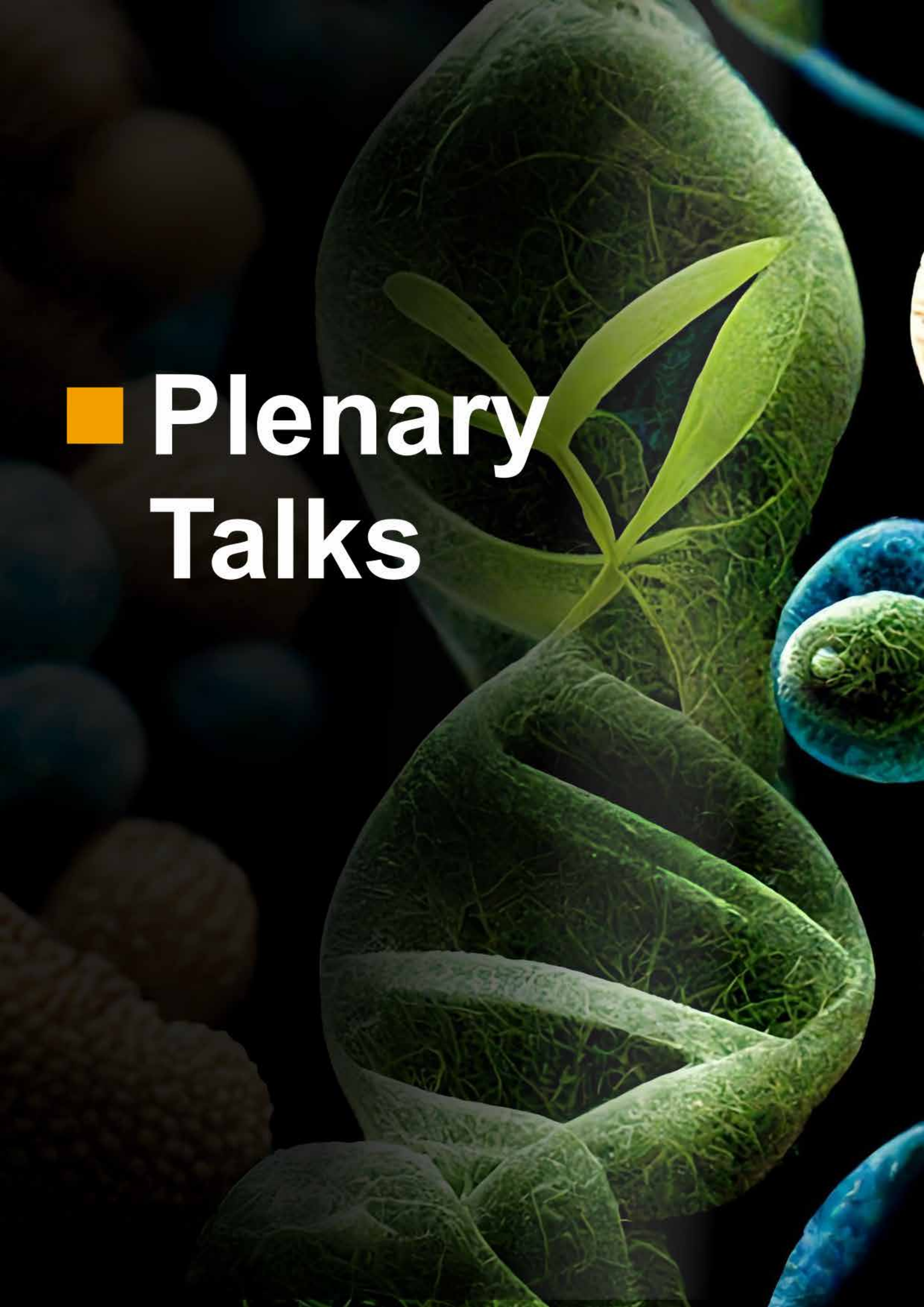
Organizing Committee
Vice-President of the Vavilov
Society of
Geneticists and Breeders
Professor
Ponomareva M. L

Plenary Talks



Current state of research on genetics of barley resistance to hemi-biotrophic pathogens

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A total of 99 pathogens were registered on barley, of which 46 are hemi- biotrophic micromycetes. Among the epidemic dangerous hemibiotrophic fungi, the causal agents of leaf blights Pyrenophora teres f. teres, P. teres f. maculata, and Bipolaris sorokiniana are widespread and harmful on barley. The world achievements in identifying the genetic diversity of barley resistance to pathogens are based mainly on the use of genome wide association studies (GWAS). By now the results of GWAS in different barley collections including several hundred of barley cultivars and landraces on resistance to net- and spot- forms of net blotch and spot blotch have been published in the global literature. A large number of quantitative (QTL) and qualitative resistance loci and their associated markers distributed throughout the barley genome have been revealed. However, information on the verification of the identified markers in another genetic environment for the majority of the identified genes is absent. The study of resistance and markers co-segregation in barley hybrid populations revealed effective markers for the identification of major resistance genes on chromosomes 3H and 6H.

The main publications of authors on the subject of the abstract:

Afanasenko O. et al. Validation of Molecular Markers of Barley Net Blotch Resistance Loci on Chromosome 3H for Marker-Assisted Selection // Agriculture (2022) 12(4): 439. DOI: 10.3390/agriculture12040439.

Take-home message:

1. Global data on genetic of barley resistance to leaf blights
2. Validation of effective markers for the identification of major resistance genes on chromosomes 3H and 6H.

Approaches to crop phenotyping using image analysis techniques

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Plant phenomics is the novel research area in the plant sciences aiming to solve the bottleneck in the analysis of the relationships between the genotype and phenotype. It is based mainly on the high throughput automated approaches of image analysis. In the report, we describe the successful implementation of the high throughput phenotyping for the analysis of plant leaf hairiness (in wheat, potato, and tobacco), wheat seed size, shape and color characteristics. These approaches allowed us to identify candidate genes for the complex plant traits and evaluate of the traits changes with respect to changing environmental conditions.

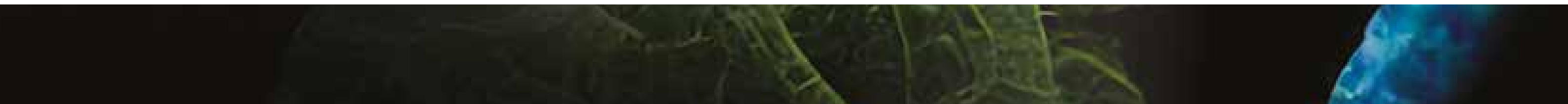
The work was funded by the Kurchatov Genome Center of the ICG SB RAS (project no. 075-15-2019-1662).

The main publications of authors on the subject of the abstract:

Afonnikov, D. A., Genaev, M. A., Doroshkov, A. V., Komyshev, E. G., & Pshenichnikova, T. A. (2016). Methods of high-throughput plant phenotyping for large-scale breeding and genetic experiments. Russian journal of genetics, 52(7), 688-701.

Take-home message:

The success of the development of the plant phenomics tools will provide efficient determination of the genes controlling various plant traits important for breeding.



Efficiency of integration of conventional and molecular methods in wheat breeding

Bespalova L.A., Agaeva E.V., Guenkova E.A., Puzirnaya O.U., Filobok V.A., Davoyan E.R., Divashuk M.G.*

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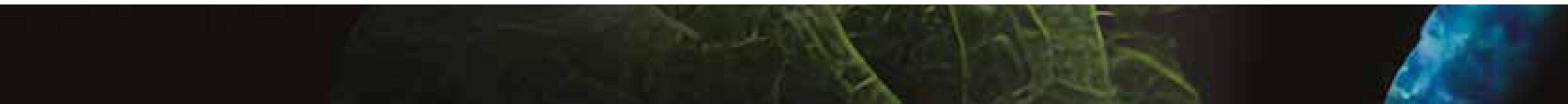

The hidden half of plants: molecular and genetic mechanisms of root branching plasticity

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Plants need to constantly modify their development to adapt to the ever-changing conditions and thus optimize the use of available resources. Over millions of years of evolution, plants have developed sophisticated mechanisms that allow them to integrate the information from external stimuli with their own internal programs to generate appropriate developmental outputs. Plant root systems are indispensable for water and nutrient foraging and as such a major evolutionary achievement for plants to cope with dry land conditions. During this colonization, different forms of root branching evolved, reinforcing step by step the phenotypic plasticity of the root system. Whereas the lycophytes, the most ancient land plants with roots, are only branching at the root tip, ferns and seed plants are able to form lateral roots along the main root. Despite the dissimilarities between the different clades, a number of genetic modules (GATA23; LBD16, 18, 30; RALF34; CEP) seem to be co-opted in order to acquire root branching capacity. We review root branching in the different land plant lineages and discuss the hitherto described genetic modules that contribute to their root branching capacity.

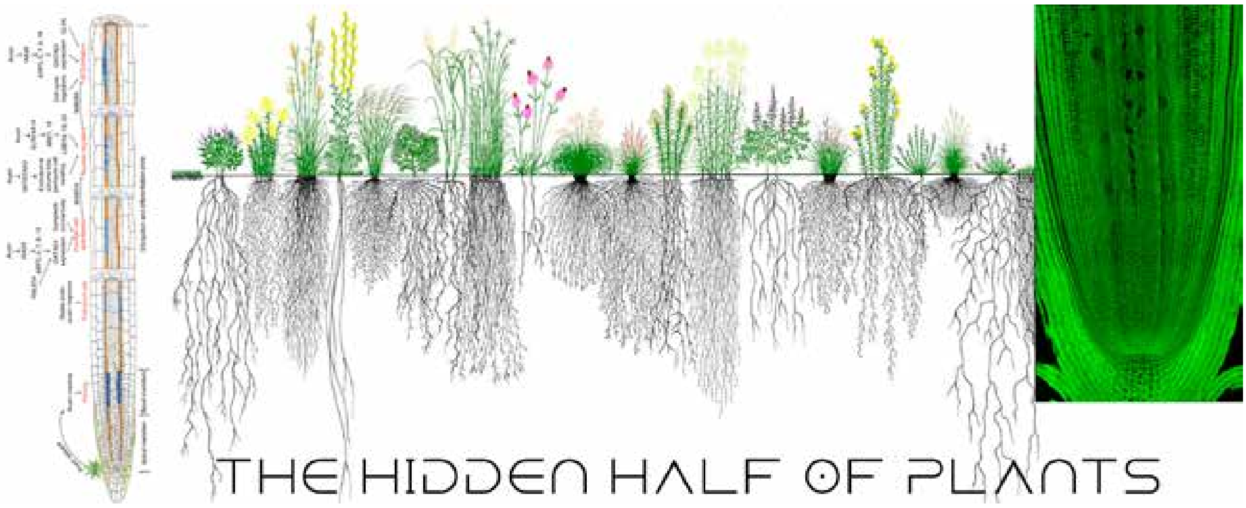
The main publications of authors on the subject of the abstract:

Kiryushkin A.S., … Pawlowski K., Demchenko K.N. Lateral root initiation in the parental root meristem of cucurbits: Old players in a new position // Front Plant Sci. (2019) 10(365): 1-16. doi: 10.3389/fpls.2019.00365.

Shumilina J., Kiryushkin A.S., … Frolov A., Demchenko K.N. Integrative proteomics and metabolomics analysis reveals the role of small signaling peptide Rapid Alkalinization Factor 34 (RALF34) in cucumber roots // Int J Mol Sci.(2023) 24(8): 7654. doi: 10.3390/ijms24087654.

Take-home message:

We try to get insight into how land plants have acquired an increasing root branching plasticity during evolution that contributed to the successful colonization of our planet by seed plants.



Unlocking Plant Adaptation: Envirotyping and Whole-Genome Approaches help shed light on plants' response to environmental challenges

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Plants, as sessile organisms, adapt to environmental fluctuations for species reproduction and persistence. The ability to express different phenotypes depending on the growing environment is called phenotypic plasticity. This trait allows plants to thrive in new locations, adjust to changing climatic conditions, and respond to seasonal variations, maximizing fitness or productivity.

Climate change and variability threaten sustainable food production. Many traits relevant to adaptation and productivity result from the complex interplay between genes and the environment. However, comprehensive analysis of genetic pathways and physiological effects across diverse backgrounds and conditions is often impractical. Recent advancements in genomic technologies offer innovative gene discovery methods in crops.

We will discuss how integrating envirotyping techniques and whole-genome based methods, such as GWAS, can enhance our understanding of plant responses to environmental changes. Utilizing these approaches can provide solutions for breeding crops suited to future climates.

Experimental and theoretical tools for monitoring the translational efficiency of plant mRNA: their relevance to functional genomics and plant biotechnology

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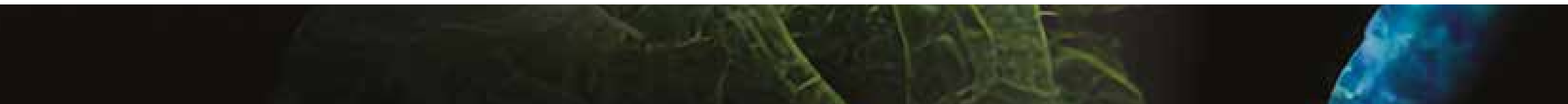
The paradox of the discrepancy between the levels of mRNA and their protein products in eukaryotic cells, including plants, directs the efforts of researchers to study the subtle mechanisms of translation. Translational control is one of the key steps in the regulation of gene expression, which contributes to the plasticity of plant metabolism, which allows them to survive in a dynamic environment. The importance of translaminar studies should be emphasized, namely, it is necessary to analyze and evaluate the efficiency of translation of organ-specific genes, which will help to find out what exact molecular mechanisms underlie the formation of unique morphological and physiological properties of certain tissues and organs during ontogenesis. A systematic study of translation control in plants during ontogenesis, as well as tissue and organ specificity of translation control, can clarify many fundamental issues and are necessary to clarify the mechanisms that ensure the uniqueness of each organ and tissue. In addition, compiling lists of tissue-specifically translated mRNAs has an important practical goal: determining target genes for exposure to genetic manipulations in order to increase economic productivity.

Research has been supported by the grants the Russian Science Foundation, RSF 22-14-00057



The role of genetics technologies in plant breeding

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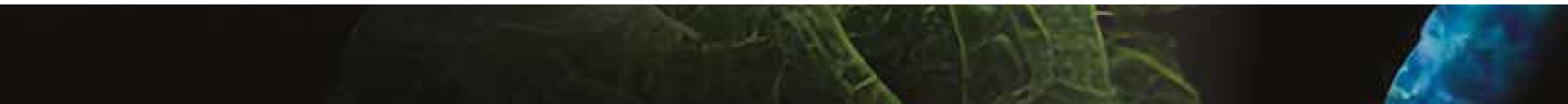
In recent years, genetic technologies have developed rapidly and play an important role in modern plant breeding. The modern plant breeding requires the effective use of recent innovations in genetics technologies and involves some of the world's most sophisticated technologies for the rapid and precise development of new crop varieties. In this context, recent advances in GM crops, genome editing, gene transfer using distant hybridization, genomic selection, marker assisted selection (MAS), digital phenotyping, speed breeding and other genetic technologies will be discussed.

The main publications of authors on the subject of the abstract:

Miroshnichenko D, Timerbaev V, Klementyeva A, Pushin A, Sidorova T, Litvinov D, Nazarova L, Shulga O, Divashuk M, Karlov G, Salina E and Dolgov S (2022) CRISPR/Cas9-induced modification of the conservative promoter region of VRN-A1 alters the heading time of hexaploid bread wheat. Front. Plant Sci. 13:1048695. doi: 10.3389/fpls.2022.1048695

Bazhenov, M.S.; Chernook, A.G.; Bespalova, L.A.; Gritsay, T.I.; Polevikova, N.A.; Karlov, G.I.; Nazarova, L.A.; Divashuk, M.G. Alleles of the GRF3-2A Gene in Wheat and Their Agronomic Value. Int. J. Mol. Sci. 2021, 22, 12376. https://doi.org/10.3390/ijms222212376



Genetic technologies-based development and assessement of novel lines of crop plants

Khlestkina E.K.[1], Ukhatova Yu.V.[1], Agakhanov M.M.[1], Antonova E.V.[1,2], Glagoleva A.Yu.[1,3], Gordeeva E.I.[1,3], Gerasimova S.V.[1,3], Egorova A.A.[1,3], Erastenkova M.V.[1], Zykova T.I.[1], Inozemtseva A.V.[1], Kolosovskaya E.V.[1,3], Krylova E.A.[1], Kumlehn J.[4], Mikhailova A.S.[1], Popov V.S.[1], Putina O.V. [1], Rakhmangulov R.S. [1], RozanovaI.V.[1], Semilet T.V.[1], Sokolova D.V.[1], Tikhonova N.G.[1], Ul'yanov A.V.[1], Khatefov E.B.[1], Hertig C.W., Shvachko N.A.[1], Shimalina N.S.[1,2], Shoeva O.Yu.[1,3]

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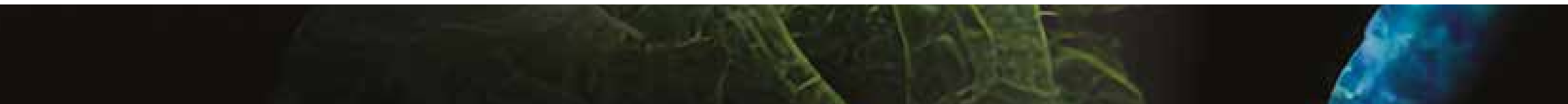
The aim of the study is CRISPR/Cas-based modification of cereal, legume, vegetable, fruit and berry plants in order to improve grain/ fruit quality or plant architecture, to control yield or ripeness period. In dicots, target genes (*BvDODA1* (beet), *SBEI и SBEII* (peas), *TFL1* (cowpea), *E4* (soybean), *MybA1* (actinidia and grapes), *IdnDH* (grapes), *ClFS1* (watermelon)) were selected and re-sequenced in cultivars chosen. Constructs for their editing were developed. In monocots, (1) the constructs for maize waxy endosperm (*wx*) и amylase extender (ae) genes editing were developed and tested by protoplast transfection; (2) barley mutants with edited genes *Myc2, Cle3* and *Ant2* were obtained; (3) the complex phenotyping of the earlier obtained barley mutants with the *Nud* and *Win1* genes knockouts was performed. Therefore, the work on modification/ preparation for modification of the number cultivated species varieties was carried out in order to obtain genotypes with desired traits, as well as pleiotropic effects of some mutations were tested using the precise isogenic lines obtained by genome editing.

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



Application of genetics and genomics in innovative plant breeding

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Ensuring a sustainable global supply of high-quality food and renewable biomass is a key priority for both European and global society. Plant breeding will play a central role in accomplishing these challenges in the coming decades and achieving this goal will depend heavily on the generation and use of new knowledge as well as the use of innovations in crop breeding.

In this context, genomics, and particularly its related molecular genetic technologies, play an important role in developing new plant varieties that optimally combine high and stable yields with resistance to abiotic stresses and biotic growing conditions. The availability of new molecular tools and technologies has a significant impact on the planning and development of critical steps in breeding to speed up this long and time-consuming process. The targeted use of plant genetic resources, examples of applications of molecular markers in cereal breeding, the potential of genomic selection and gene editing in cereal breeding will be presented and discussed.

The main publications of authors on the subject of the abstract:

Miedaner T. and V. Korzun (Book Editors): Applications of Genetics and Genomics Research in Cereals. Woodhead Publishing Series in Food Science, Technology and Nutrition, Elselver (2018), 1-349

Rabanus-Wallace T. M., …V. Korzun et al. (2021). Chromosome-scale genome asse bly provides insights into rye biology, evolution, and agronomic potential. Nature Genet 53:564–573 https://doi.org/10.1038/s41588-021-00807-0

Dendrogenomics - a new interdisciplinary field of research integrating dendrochronology, dendroecology, dendroclimatology and genomics

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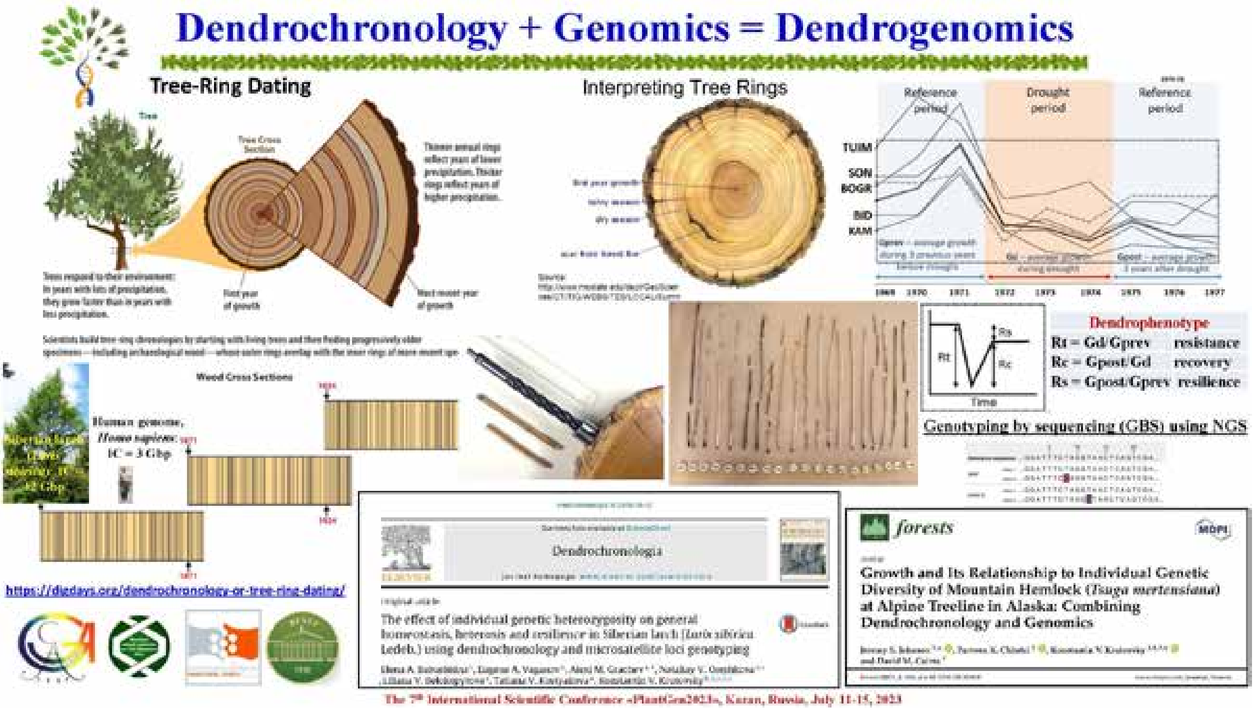
Dendrogenomics is a new interdisciplinary field of research that integrates dendrochronology, dendroecology, dendroclimatology, genetics and genomics. This novel approach allows joint analyses of dendrological and genomic data and opens new ways to study temporal dynamics of forest treelines, to delineate spatial and temporal population structure and, most of all, to study the adaptive genetic potential of forest tree populations. These problems are especially relevant to predicting how climate change will shape distribution of boreal forest species.

The main publications of authors on the subject of the abstract:

Krutovsky K. V. Dendrogenomics is a new interdisciplinary field of research of the adaptive genetic potential of forest tree populations integrating dendrochronology, dendroecology, dendroclimatology and genomics // Russian Journal of Genetics (2022) 58(11): 1273–1286. https://doi.org/10.1134/S1022795422110059

Take-home message:

Dendrogenomics is a new interdisciplinary field of research that allows joint analyses of dendrological and genomic data and opens new ways to study individual response of trees to the abiotic and biotic stresses.



Dendrochronology + Genomics = Dendrogenomics

Tree-Ring Dating

Interpreting Tree Rings

Dendrophenotype
Rt = Gd/Gprev resistance
Rc = Gpost/Gd recovery
Rs = Gpost/Gprev resilience

Genotyping by sequencing (GBS) using NGS

https://digdays.org/dendrochronology-or-tree-ring-dating/

Dendrochronologia

The effect of individual genetic heterozygosity on general homeostasis, heterosis and resilience in Siberian larch (*Larix sibirica* Ledeb.) using dendrochronology and microsatellite loci genotyping

forests

Growth and Its Relationship to Individual Genetic Diversity of Mountain Hemlock (*Tsuga mertensiana*) at Alpine Treeline in Alaska: Combining Dendrochronology and Genomics

The 7th International Scientific Conference «PlantGen2023», Kazan, Russia, July 11-15, 2023

Generation of multiple mutations in genes responsible for starch accumulation in hexaploid triticale using CRISPR/Cas9

Miroshnichenko D.*, Timerbaev V.*, Pushin A., Alekseeva V.***, Kroupin P., Bazhenov M., Samarina M., Ermolaev A., Karlov G.****, Divashuk M., Dolgov S.***

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Hexaploid triticale (× *Triticosecale*), is a hybrid of rye and wheat that combines the yield potential of wheat with the disease/environmental resistance of rye, but is characterized by a lower grain quality. Starch is an important component of cereal seeds, and changing its composition could make triticale a more desirable crop. We have achieved an efficient CRISPR/Cas9-mediated mutagenesis of genes involved in grain starch composition such as *GBSSI, SBEIIa, SSIIa, ISA1* and *RSR1*. To ensure knockout, polycistronic constructs were designed consisting of four sets of three guide RNAs targeting A, B and R alleles of each target genes. The vectors were delivered by a gene gun into embryogenic cells together with the vector encoding the Cas9 nuclease (Miroshnichenko et al., 2022), and a number of genome-edited triticale plants were generated. The combination of HRFA and NGS methods confirmed the successful editing of native sequences, and simultaneous mutations in two, three and four target genes were found in various plants. The described approach can be used to create polyploid cereals with various combinations of new alleles of functionally related or unrelated candidate genes.

The main publications of authors on the subject of the abstract:

Miroshnichenko D. et al. CRISPR/Cas9-induced modification of the conservative promoter region of VRN-A1 alters
the heading time of hexaploid bread wheat // Frontiers in Plant Science (2022) 13:1048695.
doi: 10.3389/fpls.2022.1048695

Transcription factors involved in plant cell wall regulation

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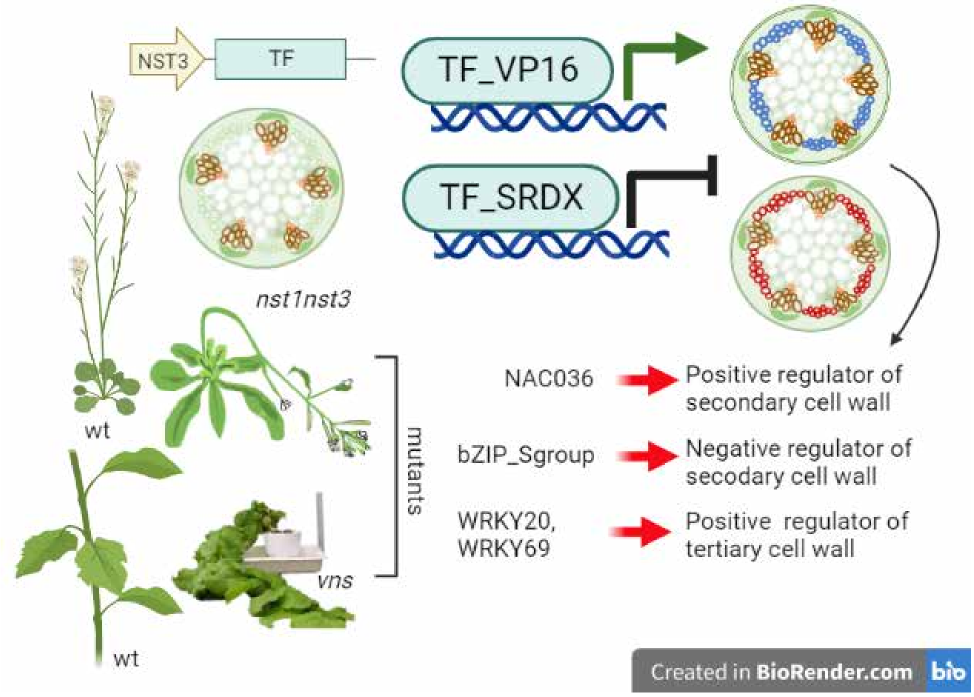
The modern boost in genome technology essentially affects plant biology. The published genomes and increased number of transcriptomic data for numerous plant species made the analysis of gene expression routine from one side and demanded the systematization and conceptualization of the obtained data from the other. Moreover, there is a switch to studying gene coexpression and regulators rather than actors (structural proteins and enzymes). The biosynthesis of the cell wall, one of the key plant cell compartments, is regulated by a complicated network of transcription factors. This network is well described for secondary cell walls, which comprise the bulk of wood. Among transcription factors regulating the primary cell wall, only ethylene-responsive factors were described (see poster by Syrchina N). Transcription factors regulating tertiary cell wall formation in plant fibers are not known at all. We used Arabidopsis and poplar mutants to search for potential factors involved in tertiary cell wall formation. Our approach allowed us to reveal factors (members of the NAC, WRKY, and bZIP families) involved in thickening cell walls; those functions were not described previously.

The main publications of authors on the subject of the abstract:

This work was supported by grant from the Russian Science Foundation, Project #20-44-07005 (RNA-Seq data analysis)

Take-home message:

Arabidopsis and poplar mutants lacking secondary cell walls in fibers are efficient models for studying transcription factors regulating cell wall formation; potential regulators of tertiary cell wall induction in plant fibers were revealed.



3D genomics

Razin S.V.

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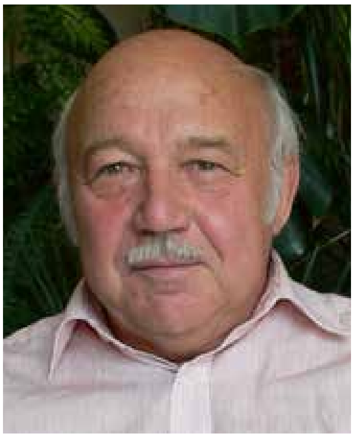

В лекции будет представлен обзор современных представлений о том, как формируется 3D геном и каковы основные структурные элементы 3D генома (петли ДНК, ТАДы и компартменты). Будет показана роль пространственных контактов между удаленными участками генома в установлении коммуникации между энхансерами и промоторами. Будут представлены новые результаты, демонстрирующие, что для большинства экспериментально подтвержденных пар энхансер-промотор характерно пространственное сближение этих элементов, осуществляемое посредством выпетливания разделяющего их сегмента хроматиновой фибриллы. Предметом обсуждения будет также роль контактных доменов хроматина (топологически ассоциированных доменов) в ограничении сферы действия энхансеров. В этом контексте будет рассмотрена эволюция представлений о доменной организации эукариотического генома. Также будут представлены собственные данные, демонстрирующие вариабельность 3D генома в индивидуальных клетках. В заключительной части лекции будут обсуждены различные стратегии направленной модификации 3D генома, такие, как принудительное замыкание хроматиновых петель и создание новых границ контактных доменов хроматина.

Allopolyploidization as a driving force of chromosome reorganization of *Triticum* species

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Allopolyploidization is one of the basic processes leading to an increase in genetic diversity and contributing to the domestication of plants. The genus *Triticum* is the most significant in terms of domesticated allopolyploid species. The study of the structural organization of the chromosomes of common wheat (BBAADD genome) and its progenitors was carried out by genetic and physical mapping, genotyping and sequencing of individual chromosomes.

It is shown that the integration of diploid species genomes in one nucleus is accompanied by deletions of repeated DNA sequences and chromosome loci, the transfer of mobile elements, translocations, and chromosome inversions.

The main direction in the reorganization of chromosomes A, B and D genomes during evolution and breeding were noted. The influence of chromosomal rearrangements on the manifestation of agricultural important traits is discussed.

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

The main publications of authors on the subject of the abstract:

Salina, *E., Muterko, A., Kiseleva, A., Liu, Z., Korol, A. Dissection of Structural Reorganization of Wheat 5B Chromosome Associated With Interspecies Recombination Suppression // Frontiers in Plant Science, 2022, 13, 884632*

The International Wheat Genome Sequencing Consortium (IWGSC), <…>, 5BS BAC sequencing and assembly: Elena Salina et al. Shifting the limits in wheat research and breeding using a fully annotated reference genome //SCIENCE, 2018, Vol. 361, Issue 6403, eaar7191.

Take-home message:

Allopolyploidization of *Triticum* species is accompanied by deletions of repeated DNA sequences and chromosome loci, the transfer of mobile elements, translocations, and chromosome inversions.

Identification of QTL for agronomic traits to enhance regional wheat and barley breeding projects in Kazakhstan

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The success of crop production is largely dependent on local breeding projects that focus on developing high-yielding cultivars using novel molecular tools. Genome-wide association study (GWAS) and biparental mapping (BM) are two powerful approaches for the identification of QTLs (quantitative trait loci) for key agronomic traits. Our multiyear and multi-environment GWAS and BM projects of wheat and barley allowed the identification of over 100 stable QTLs for plant adaptation traits, abiotic and biotic stress resistances, grain quality, and yield components in each of these crops. Identified SNP markers in marker-trait associations were converted to KASP assays and successfully tested in local breeding projects.

This research was partially funded by the Ministry of Agriculture of the Republic of Kazakhstan (grants number BR10765056, KATY-project) and the Ministry of Science and Higher Education of the Republic of Kazakhstan (grant number AP14871383, KASP-project).

The creation of genetically modified plants is just another effective way of breeding

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Genetically modified organisms (GMO) are organisms whose genetic material has been altered using genetic engineering techniques. They range from genome-edited organisms to metabolically engineered ones. But in any case, target gene can be carefully controlled by the organ- and stage-specific expression. More than 430 varieties of 32 GM crops are grown on the field, demonstrating increased resistance to herbicides, diseases and pests, or improved yield quality. GM plants also can be used as bioreactors for the synthesis of pharmacologically significant compounds and biopolymers [1]. The appearance of GM crops on the market formed a negative attitude towards GMOs in public opinion, which was largely inflated by mass media. Most of the scandalous studies on GMO dangers have methodological inaccuracies. DNA transformation is a natural process commonly widespread among prokaryotes. More than 50 years of use of GM bacteria was harmless to humans and environment, and did not cause any significant objections from society. An analysis of sequenced genomes shows about 6% of dicots are natural GMOs that have been used by humans throughout their history [2].

Supported by RSF 21-14-00050

The main publications of authors on the subject of the abstract:

1) Saveleva N.V., Burlakovskiy M.S., Yemelyanov V.V., Lutova L.A. Transgenic plants as bioreactors to produce substances for medical and veterinary uses. Russ. J. Genet. Appl. Res. 2016. 6(6): 712–724. doi: 10.1134/S2079059716060071

2) Matveeva T.V., Otten L. Widespread occurrence of natural genetic transformation of plants by Agrobacterium. Plant Mol. Biol. 2019. 101(4-5): 415–437. doi: 10.1007/s11103-019-00913-y

Take-home message:

The creation of genetically modified crops is a high-tech, relatively safe and targeted breeding method that allows to speed up and diversify obtaining of new cultivars. Do not be afraid of GMOs, which are naturally common among bacteria and plants.

Participants' Talks

In vitro micropropagation of Pomegranate

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Гранат — это целый витаминно-минеральный комплекс. В соке граната обнаружены уникальные аминокислоты, которые содержатся еще только в мясе и незаменимы для человеческого организма.

Название "гранат" происходит от латинского granatus – зернистый. В Древнем Риме у него было еще одно имя – malum granatum, то есть "зернистое яблоко". Яблоком его до сих пор называют и на других языках: по-немецки – Granatapfel, по-итальянски – melograna (apfel, mela – яблоко). Итальянцы считают, что именно гранат был тем райским яблоком, которым соблазнилась Ева.

В процессе культивирования растения в них накапливается вирусы и бактерии, которые влияют на урожайность и жизнеспособности растений.

В связи с этим нами было начато введение в культуру гранат без косточек in vitro и восстановление сортов гранат, традиционно культивируемых в Узбекистане.

Для получения узловых эксплантов использовали молодые весенние побеги 6 летного сорта граната без косточек.

Применение биотехнологических методов позволит получить посадочный материал, свободный от грибных, бактериальных и вирусных инфекций за короткое время и в достаточном количестве.

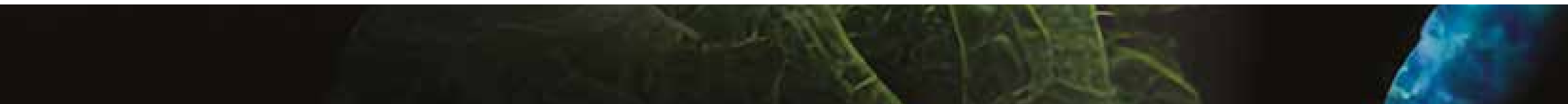
The main publications of authors on the subject of the abstract:

Yakubov M., Abdurazzakov K., Xasanov X., Nasirova G., Halmuratov E. Getting of sterile material depending on the growing conditions of the source material // Abstracts Book of International Conference Plant Cell & Tissue Culture in Vitro IV July 4 - 5, 2022, Vienna, Austria, P.43-44.

Якубов М.Д., Абдуразаков К. Введение в культуру in vitro и восстановление диких форм винограда //Сборник меж-ой научной конф-ии молодых ученых «НАУКА И ИННОВАЦИИ», 20 октября 2022, Ташкент, Узбекистан, С.177-178

Take-home message:

Нами было начато введение в культуру in vitro сорта гранат традиционно культивируемых в Узбекистане. Это позволит получить посадочный материал, свободный от грибных, бактериальных и вирусных инфекций за короткое время и в достаточном количестве.



Synthetic amphiploids - a potential source of common wheat genetic diversity in economically valuable traits

Adonina I. G.*, Zorina M.V., Mehdiyeva S.P., Leonova I.N., Komyshev E.G., Timonova E.M.*, Salina E.A.***

Federal Research Center Institute of Cytology and Genetics, Siberian Branch of Russian Academy of Sciences, Novosibirsk, Russia,
*Kurchatov Genomic Center, Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia,
**Genetic Resources Institute of ANAS, Baku, Azerbaijan
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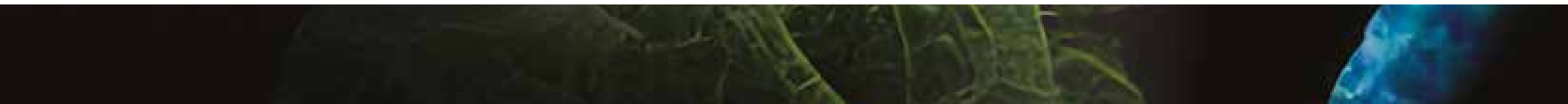
Synthetic amphiploids combine the genetic potential of several species, which can be used to expand the genetic diversity of wheat. Line 1102 was isolated from a population obtained by crossing a triticale (AABBRR) and a synthetic amphiploid (AADDSS). It was shown that her karyotype corresponds to hexaploid wheat (AABBDD). Breeding important characteristics of this line are short stem, spherical grains and high micronutrient, in particular, iron and zinc. To map the loci associated with plant height, grain shape, and microelement content, line 1102 was crossed with the common wheat cultivar Lutescens 85, which is contrasting according to these traits. Analysis of the F2 population revealed three QTLs for grain shape *Qsp.icg-5A, Qsp.icg-3B* and *Qsp.icg-6B* on chromosomes 5A, 3B and 6B. The *Qht.icg-4A* locus associated with the plant height was mapped to chromosome 4AS. Loci on chromosomes 5A, 6B and 4A were described for the first time. Short-stemmed, micronutrient-rich lines with spherical grains, obtained from crossing 1102×Lutescens 85, will be used in breeding. Acknowledgment: The work was supported by the Kurchatov Genomic Center of the ICG SB RAS (Agreement No. 075-15-2019-1662).

<u>The main publications of authors on the subject of the abstract:</u>

Adonina I.G., et al. Genetic features of triticale–wheat hybrids with vaviloid-type spike branching // Plants (2022), 11, 58. https://doi.org/10.3390/plants11010058



Study of grain shape, color and pre-harvest sprouting in population of winter bread wheat cultivated in Russia

Afonnikova S.D., Kiseleva A.A., Fedyaeva A.V., Afonnikov D.A., Salina E.A.

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Grain color and shape of bread wheat can affect yield, quality of flour characteristics and the nutritional value of the final product. Moreover, it was shown that grain color correlates with tolerance to pre-harvest sprouting (PHS), a process leading to a loss of yield and product quality decrease. Hence, the search for genetic variants responsible for grain color and shape is an urgent task of modern breeding.

We have analyzed single nucleotide polymorphisms and characteristics related to grain properties in winter wheat plants cultivated in Russia, Europe and America from the ICG SB RAS collection: grain size, shape and color, Growth index, α-amylase activity and Falling Number. The correlation analysis of traits showed significant correlation between α-amylase activity in mature grains and some both size and color traits. Population structure analysis showed that European and American genotypes form several distinct genetic groups.

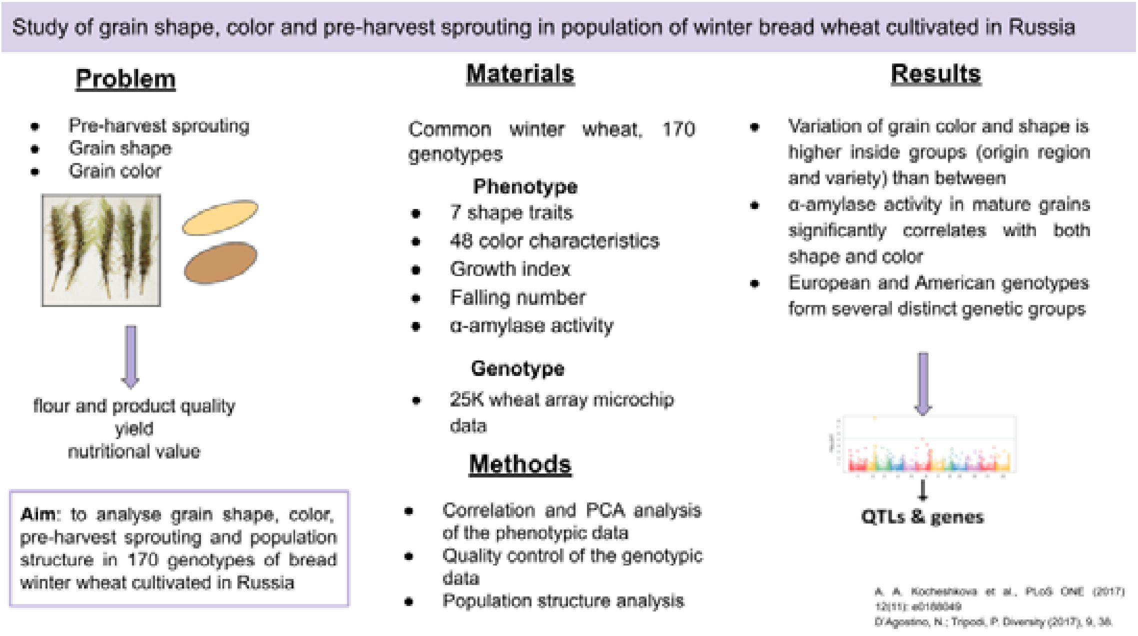
The results obtained will be used in genome-wide association analysis to find candidate genes linked to traits of interest.

Funding: The reported study was funded by the RSF (Russian Science Foundation) projects № 21-76-30003 and№075-15-2019-1662

Take-home message:

In population of winter bread wheat significant correlations between pre-harvest sprouting estimates and grain color and shape were observed only for α-amylase activity.

The studied population (170 samples) genetic structure is heterogenous.



Study of grain shape, color and pre-harvest sprouting in population of winter bread wheat cultivated in Russia

Problem

- Pre-harvest sprouting
- Grain shape
- Grain color

flour and product quality
yield
nutritional value

Aim: to analyse grain shape, color, pre-harvest sprouting and population structure in 170 genotypes of bread winter wheat cultivated in Russia

Materials

Common winter wheat, 170 genotypes

Phenotype

- 7 shape traits
- 48 color characteristics
- Growth index
- Falling number
- α-amylase activity

Genotype

- 25K wheat array microchip data

Methods

- Correlation and PCA analysis of the phenotypic data
- Quality control of the genotypic data
- Population structure analysis

Results

- Variation of grain color and shape is higher inside groups (origin region and variety) than between
- α-amylase activity in mature grains significantly correlates with both shape and color
- European and American genotypes form several distinct genetic groups

QTLs & genes

A. A. Kocheshkova et al., PLoS ONE (2017) 12(11): e0188049
D'Agostino, N.; Tripodi, P. Diversity (2017), 9, 38.

New genes which are involved in the regulation of the telomere length in model plant *Arabidopsis thaliana*

Agabekian I.A., Lushnenko A.U., Valeeva L.R, Abdulkina L.R., Shakirov E.V.*

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Теломеры - это нуклеопротеиновые структуры на концах эукариотических хромосом, которые защищают хромосомы от прогрессирующего укорочения. Теломерная ДНК состоит из коротких нуклеотидных повторов. Известно, что определенное количество теломерных повторов предопределяет способность большинства соматических клеток к пролиферации. Главная задача наших исследований - поиск и анализ генетических факторов, ответственных за регуляцию длины теломер растений Arabidopsis thaliana. Проведенные нами ранее эксперименты по изучению длины теломер позволили идентифицировать ген *OLI2,* контролирующий длину теломер. Ген *OLI2* ранее был также идентифицирован как часть генетического пути *OLIGOCELLULA (OLI)*. Однако вклад других *OLI* генов в регуляцию длины теломер ранее не изучался. Анализ гомозиготных мутантов по гену *OLI1* показал, что длина теломер мутантных растений увеличивалась. Анализ длины теломер гомозиготных мутантов по гену *OLI5* показал, что длина теломер у мутантов была стабильно короче, чем у дикого типа. Длина теломер мутантов по гену *OLI7* уменьшалась незначительно из поколение в поколение. Исследование выполнено в рамках программы К(П)ФУ (ПРИОРИТЕТ-2030) за счет гранта РНФ 21-14-00147.

The main publications of authors on the subject of the abstract:

Abdulkina LR et al, Components of the ribosome biogenesis pathway underlie establishment of telomere length set point in Arabidopsis. Nat Commun 2019 https://doi.org/10.1038/s41467-019-13448-z

Jae YC et al, Natural variation in plant telomere length is associated with flowering time. The Plant Cell 2021https://doi.org/10.1093/plcell/koab022

Valeeva LR et al, TELOMERE BIOLOGY AND RIBOSOME BIOGENESIS: STRUCTURAL AND FUNCTIONAL INTERCONNECTIONS. Biochem Cell Biol. 2023 doi: 10.1139/bcb-2022-0383

Effectiveness of Leaf rust resistance in the north Caucasus in 2011-2020

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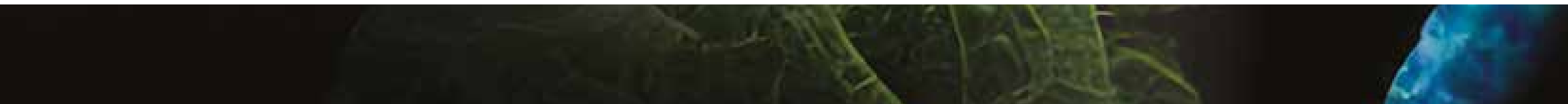
Leaf rust, caused by *Puccinia triticina,* is the most common rust disease of wheat. In this report was researched the effectiveness of 52 NILs of cv. Thatcher with Lr genes in field trials and 41 NILs – in the juvenile phase in a glasshouse during 2011-2020. In this work, we studied the efficiency of NILs of cv. Thatcher with Lr genes in different phases of ontogeny during 2011–2020. The disease was registered according to the CYMMIT (2018) scale in the adult plant phase and according to the Mains and Jackson (1926) scale in the juvenile phase. Therefore, the lines with *Lr9, Lr42* and *Lr43+24* genes remained immune in the juvenile and adult phases during ten years of research and NILs with *Lr* genes: 19, 24, 29, 36, 37, 38, 43, 45, 47, 50 showed efficiency in field tests. The line with the *Lr9* gene was immune up to 2020; *Lr19* and *Lr41* – up to 2015; *Lr42* – up to 2018, and *Lr50* – up to 2019. A increase in the frequencies of virulent isolates was recorded in 2018-2020 due to unfavorable weather in the growing seasons. This indicates the ability of a dangerous pathogen to rapidly evolve in response to biotic and abiotic stresses.

The main publications of authors on the subject of the abstract:

Volkova G, Kudinova O, Vaganova O, Agapova V. Effectiveness of Leaf Rust Resistance Genes in the Adult and Juvenile Stages in Southern Russia in 2011–2020 // Plants (2022) 11(6):793. https://doi.org/10.3390/plants11060793



Growing Maize Root: Lectins Involved in Consecutive Stages of Cell Development

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The abundance of various polysaccharides in the plant kingdom matches the great diversity of carbohydrate-binding proteins (lectins) that are represented in plant organisms. The great bulk of carbohydrates are concentrated in plant cell wall, and alterations in the polysaccharide backbone of cell wall are characteristic of elongation growth of plant cells.

In order to investigate the role of lectins in this process, we performed a genome-wide screening of lectin motifs in the genome of maize (Z. *mays*). We identified 306 genes putatively encoding proteins with lectin domains from 12 different families. Additionally, we analyzed the differential expression of these genes in the maize root whose cells were at different growth stages.

A bunch of differentially expressed genes encoded lectin receptor-like kinases (mainly malectin-like proteins) whose extracellular domain has direct access to the cell wall. Differential expression was also characteristic of a group of extracellular proteins (like jacalins or EULs). These various proteins are presumed to be potentially involved in the early stages of root morphogenesis.

The study was partially supported by RSF grant #20-64-47036.

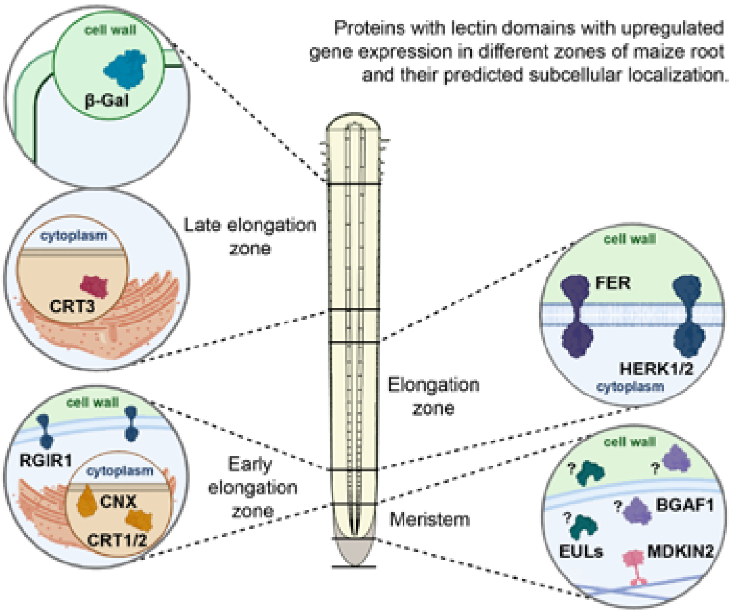
The main publications of authors on the subject of the abstract:

Aglyamova A. et al. Growing Maize Root: Lectins Involved in Consecutive Stages of Cell Development // Plants (2022) 11: 1799. https://doi.org/10.3390/plants11141799

Take-home message:

306 genes putatively encoding proteins with lectin domains from 12 different protein families were identified in maize genome

Their differential expression was analyzed in different zones of maize root, where cells were at different growth stages.



The source material for the selection of soft spring wheat for resistance to pre-harvest germination of grain in the ear

Aitbaeva R.N., Novohatin V.V., Shelomentseva T.V.

The Research Institute of Agriculture of the Northern Trans-Urals is a branch of the Federal State Budgetary Institution of Science of the Federal Research Center of the Tyumen Scientific Center of the Siberian Branch of the Russian Academy of Sciences, Tyumen, Russia
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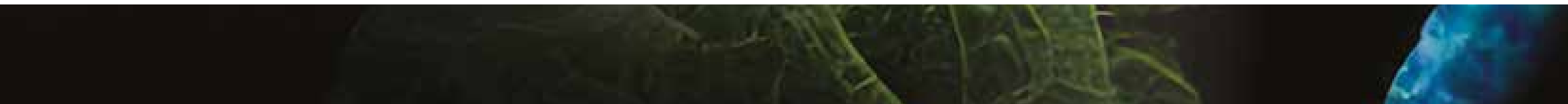
Влажные условия снижают физические, биохимические показатели зерна. Отмечается отрицательная корреляция прорастания зерна с урожаем – r = -0,57; -0,602, массой зерна (-0,394; -0,518), озернённостью колоса (-0,382; -0,419), массой колоса (-0,540; -0,578), натурой зерна (-0,494; -0,629), полеганием (-0,394; -0,490). Прорастание связано с активностью изофермента α-амилазы (r = 0,735-0,816). Наличие в красных колосковых чешуях кахетина и кахетеина ингибирует синтез α-амилазы. Себарин, семенной оболочки красного зерна препятствует воздушно-водному обмену. Белозёрные сорта отличаются высоким содержанием α-амилазы. Из 362 сортообразцов коллекции ВИР, устойчивостью к предуборочному прорастанию зерна в колосе, выделилось 15: KWS Torridon (к-66273), Атлант (к-66352), Toronit (к-66032), Greina (к-66031), Мажор (к-65271), Aletch (к-65011), Струна Мироновская (к-65016), Libertina (к-66401), Calispero (к-66393), KW 240-3-13 (к-66375), Odeta (к-66394), Heines Peko (к-38429), Weibulls 5583 (к-44786), Pompe (к-46563), Монастырская (к-65001) и 7 местных сортов: Лютесценс 70, Рикс, Гренада, АВИАДа, Атланта-1, Кристина, Эритроспермум 1119.



Bacterial endophytic community of the aerial part of pea (*Pisum sativum* L.): patterns of formation and plant growth-promoting activity

Akhtemova G.A., Vasileva E.N., Afonin A.M., Kichigina N.E., Sulima A.S., Zhukov V.A.

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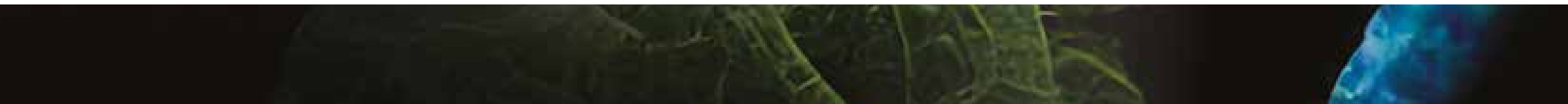
The patterns of formation of the bacterial endophytic community inhabiting the tissues and organs of the aerial parts of pea plants (*Pisum sativum L.*) have been studied. Diagnostic fragments (16S-rRNA gene) were sequenced on the Illumina MiSeq system. Analysis of the 16S-rRNA gene sequences revealed the "core microbiome" of stems of pea plants. Both pure bacterial cultures and consortia dominated by bacteria of the genus *Rahnella* were isolated from tissues of various genotypes of pea. The studied consortia had different effects on plants. Genotype K-8274 responds positively to inoculation with a pure culture of *Rahnella* sp. (KV13) and the KV17 consortium. Plants of the K-3358 genotype demonstrated an increase in growth parameters when inoculated with the KV72 consortium. Joint inoculation of plants with nodule bacteria and endophytic consortiums KV17 or KV72 did not have any synergistic effect, since rhizobia masked the growth-stimulating activity of endophytes. This work was supported by the Grant of RFBR № 19-016-00194

The main publications of authors on the subject of the abstract:

1. Vasileva EN, Akhtemova GA, Afonin AM., et al. Culturable endophytic bacteria from stemsand leaves of garden pea (Pisum sativum L.). Ecological genetics. 2020: 18(2):169-184. https://doi.org/10.17816/ecogen17915

2. Vasileva, E.N., Akhtemova, G.A., Zhukov, V.A., Tikhonovich, I.A. Endophytic microorganisms in fundamental research and agriculture // Ecological Genetics, Volume 17, Issue 1, 2019, Pages 19-32, doi: 10.17816/ecogen17119-32



Comparison of the level of PIP2 aquaporins and their gene transcripts in an ABA-deficient barley mutant and plants of its original genotype

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ABA is able to influence the water relations of plants not only by closing the stomata, but also through the regulation of the hydraulic conductivity of the roots. It has been shown that exogenous ABA increases the expression of aquaporin genes, as well as their activity due to phosphorylation/dephosphorylation and translocation from the cytoplasm to the plasmolemma, which explains the effect of ABA on hydraulic conductivity. To confirm the relationship between the change in the level of this hormone and the level of aquaporins, as well as the level of hydraulic conductivity of plants, the Az34 barley mutant with a reduced level of ABA and plants of its original Steptoe genotype were used. Immunolocalization of aquaporins showed higher amount of PIP2;1, PIP2;2, PIP2;5 proteins in Steptoe plants compared to the mutant. These data are consistent with the increased expression of PIP2;1, PIP2;2, PIP2;5 and a high level of hydraulic conductivity in Steptoe plants. The obtained information confirms the importance of ABA in the regulation of water relations.

This work was supported by the RSF grant № 21-14-00070.

The main publications of authors on the subject of the abstract:

Akhtyamova Z., Arkhipova T., Martynenko E., Nuzhnaya T., Kuzmina L. et al. Growth-Promoting Effect of Rhizobacterium (B. subtilis IB-22) in Salt-Stressed Barley Depends on ABA Accumulation in the Roots // Int. J. Mol. Sci. (2021) 22. 10680

Arkhipova T., Sharipova G., Akhiyarova G., Kuzmina L., Galin I. et al. The Effects of Rhizosphere Inoculation with P. mandelii on Formation of Apoplast Barriers, HvPIP2 Aquaporins and Hydraulic Conductance of Barley. Microorganisms (2022) 10: 935.

Take-home message:

In Steptoe plants, a more pronounced expression of PIP2 genes and immunolocalization of PIP2 proteins were observed than in its ABA mutant Az34. Wild-type plants showed high hydraulic conductivity, which confirms the role of ABA in water relations.

Phytochemical composition and antioxidant status of *Humulus lupulus* L with different processing methods

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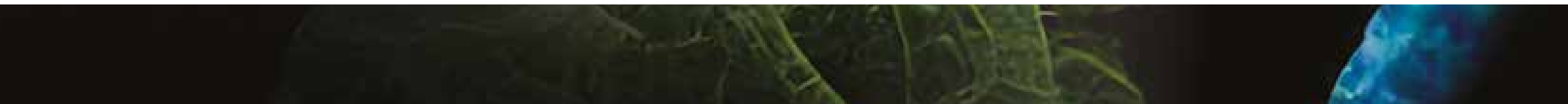
Хмель обыкновенный Humulus lupulus L. — двудомное многолетнее вьющееся растение, относящееся к семейству Cannabaceae. Хмель содержит много биологических активных соединений, благодаря чему его первоначальное применение было в лечебных целях и только позже начали использовали в производстве пива.

Цель работы состояла в выявлении особенностей действия регуляторов роста (гибберсиб и эпин-экстра) и также биоудобрения (пудрет) на фитохимический состав и антиоксидантную активность в листьях и шишках Humulus lupulus L .

Посадку корневищных черенков хмеля проводили в начале мая 2022 года в защищенном грунте. Через 4 недели все варианты пересадили в открытый грунт. Листья для анализа отбирали через 4,8,12,16 недель, шишки - через 12 недель.

Фитохимический состав листьев определяли спектрофотометрическим методом.

В контрольных растениях содержание фенольных соединений и витамина С достигали самых больших значений на двенадцатой неделе после посадки. Пудрет в большее степени повышал содержание витаминов и белков, в то время как регуляторы роста увеличивали содержание фенольных соединений и сахаров, особенно под влиянием гибберсиба.



Search for perspective endophytic bacteria for the protection of wheat plants against Greenbug (*Schizaphis graminum*)

Alekseev V.Y., Rumyantsev S.D., Sorokan A.V., Burkhanova G.F., Veselova S.V., Maksimov I.V.

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Beneficial endophytic bacteria can suppress the development of pests through direct antagonism, with the help of metabolites, or indirectly by the induction of systemic resistance through the regulation of hormonal signaling pathways. In this work, we studied nine isolates of bacteria isolated from the internal tissues of cultivated and wild wheat, potatoes, and parsley. Sequencing of the 16S rRNA gene showed that all isolates belong to the genus Bacillus. The genes of lipopeptide synthetase—phosphopantheteinyl transferase (BsSfp), surfactin synthetase (BsSrf), iturin synthetase (BsItuA, BsItuB, BsItuD) and fengycin synthetase (BsFenD)—were identified in all bacterial isolates using PCR. All isolates were aphicidal activity against Greenbug (Schizaphis graminum). Four isolates of Bacillus sp. Tas1, Tas8.2, Ttl2, Stl7, which showed high aphicidal activity, and the reference strain B. subtilis 26D were tested for the ability to induce systemic resistance against Greenbug, which manifested itself in the regulation of redox metabolism and the transcripts accumulation of genes PR1, PR2, PR3, PR6, PR9. The study was supported by grant MK-2543.2022.1.4.

The main publications of authors on the subject of the abstract:

Rumyantsev, S.D. et al. Additive Effect of the Composition of Endophytic Bacteria Bacillus subtilis on Systemic Resistance of Wheat against Greenbug Aphid Schizaphis graminum Due to Lipopeptides // Life (2023) 13, 214. doi: 10.3390/life13010214

Take-home message:

Bacteria of the genus Bacillus producing lipopeptides are able to protect plants against aphids due to the insecticidal effect and indirectly through the induction of systemic resistance.

Creation of doubled haploid lines of bread wheat with different alleles combination of waxy genes

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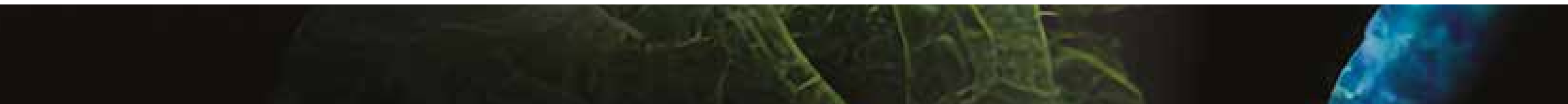
One of the most important technological properties of wheat grain is starch formation, which is influenced by the waxy genes encoding the enzyme granule-bound starch synthetase I (GBSSI). The waxy genes are located in each of the three wheat subgenomes. Doubled haploid technologies can be an effective method to help manipulate the combination of these alleles to create new wheat lines with different starch characteristics suitable for different food productions.

In our work, four F_1 hybrids of winter bread wheat developed by crossing parent plants with different waxy alleles were used for anther culture. The flow cytometry analysis shows that plants have different ploidy levels: haploids, plants with typical ploidy levels, aneuploids and polyploids. After regeneration, adaptation *in vivo* and colchicine treatment, 46 viable lines were obtained. The genotyping of *Waxy* allele was done using different pairs of primers for each of the three subgenomes. The produced lines are valuable material for breeders and geneticists to create new high-quality wheat cultivars.



Activation of TADHN dehydrin gene by NO-treatment in wheat plants under dehydration

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Nitric oxide (NO) is a signaling molecule functioning in plant ontogenesis and adaptation to stress factors, in particular to drought. An important role in the plant drought resistance belongs to the dehydrins proteins. However their participation in the NO-induced drought tolerance is poorly studied. We investigated the *TADHN* dehydrin gene activity in two wheat (*Triticum aestivum L.*) varieties differing in drought tolerance: Salavat Yulaev (SY - susceptible) and Ekada-70 (E-70 - resistant) under NO-pretreatment (200 µM SNP) followed by dehydration (PEG 12%). Dehydration activated *TADHN* gene, especially in E-70 plants, in which the 3-fold increasing of *TADHN* transcript content were detected by 6 h and maintained at this level until 9 h. In SY-plants expression of *TADHN* gene increased about 2- and 2.5-fold by 6 and 9 h, respectively. SNP contributed to additional accumulation of *TADHN* transcripts so their content by 9 h increased 3- and 4-fold in SY- and E-70 plants, respectively. These results may indicate the *TADHN* dehydrin involvement in NO-induced drought tolerance of different wheat cultivars. The work was supported by the Russian Science Foundation grant No 22-24-00196.

The main publications of authors on the subject of the abstract:

Аллагулова Ч. Р., Авальбаев А. М., Лубянова. А Р., Ласточкина О. В., Шакирова Ф. М. Современные представления о механизмах образования оксида азота в растениях. Физиология растений. 2022. Т. 69. С. 339-351

Аллагулова Ч. Р., Юлдашев Р. А., Авальбаев А. М. Участие оксида азота в регуляции развития растений и их устойчивости к дефициту влаги. Физиология растений. 2023. Т. 70. С. 115-132.

Genetic analysis and population structure of winter wheat accessions from Central Asia

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*S. Seifullin Kazakh Agrotechnical University, Astana, Kazakhstan
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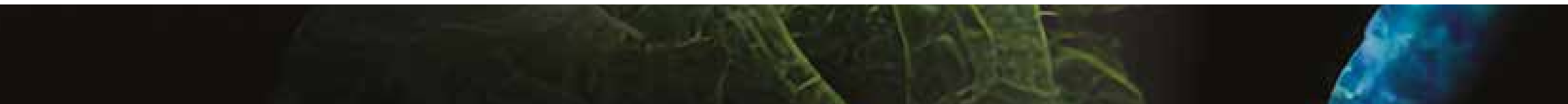
Despite the importance of winter wheat in Central Asian countries, there are limited reports describing their diversity within this region. The population structures of 115 winter wheat cultivars from four Central Asian countries (Kazakhstan, Kyrgyzstan, Tajikistan, and Uzbekistan) were compared to 552 accessions from six other geographic origins using 10,746 polymorphic SNP (single nucleotide polymorphism) markers. Application of the STRUCTURE package showed that accessions from Kazakhstan and Kyrgyzstan were grouped with samples from Russia, while Tajikistan's and Uzbekistan's accessions were clustered with samples from Afghanistan. The mean value of Nei's genetic diversity for the germplasm from four groups from Central Asia was 0.261, which is comparable to that of the six other groups studied: Europe, Australia, the USA, Afghanistan, Turkey, and Russia. The Principal Coordinate Analysis showed that samples from Kyrgyzstan, Tajikistan, and Uzbekistan were close to samples from Turkey, while Kazakh accessions were positioned near samples from Russia.

This research was funded by the Ministry of Science and Higher Education of the Republic of Kazakhstan (grant AP09259168).



Physiological and genetic bases of pea breeding of agricultural crops: an example of pea

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At present, in plant breeding in addition to traditional descriptors, it is necessary to take into account many physiological properties and characteristics of plants. Due to this, comprehensive long-term studies were carried out on the material of more than 100 varieties of peas, corresponding to the period of the crop breeding from wild forms to the best contemporary varieties. The methodological basis of the research was a complex approach. The aim was to develop physiological methods and techniques for increasing the efficiency of selection.

The experimental data obtained made it possible to conclude that the physiological basis for the breeding of agricultural crops is a well-developed system of compensatory mechanisms that allows to achieve the result required, i.e. the increasing yield of the crop in various growing conditions, using variability of morphophysiological organization of the production process of plants. However, the effectiveness of the chosen direction in each case will be different, since any compensatory mechanisms act in a certain frame, and, therefore, they cannot always provide the required level of strength of the biological system.

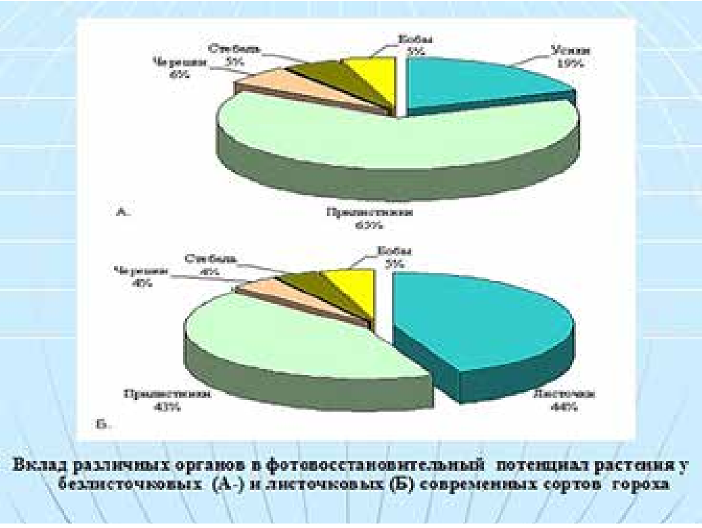
The main publications of authors on the subject of the abstract:

Амелин А.В. Физиологические аспекты создания высокопродуктивных сортов гороха усатого типа.// Вестник РАСХН. – 1998. - №1.- с. 54. (Amelin A.V. Physiological aspects of the creation of highly productive varieties of mustachioed peas.// Bulletin of RASKHN. – 1998. - No. 1.- p. 54.)

Амелин А.В. Физиологические особенности селекции зернового гороха листочкового морфотипа.// Вестник РАСХН. – 2001. - №4. - с. 29.

Take-home message:

The physiological basis of breeding is a well-developed system of compensatory mechanisms, which, due to the variability in morphophysiological organization of the production process of plants, allow to increase the crop productivity.



Вклад различных органов в фотовосстановительный потенциал растения у безлисточковых (А-) и листочковых (Б) современных сортов гороха

Flavonoid synthesis genes in rye *Secale cereale L.*

Andreeva E.A., Zykin P.A.*, Tsvetkova N.V.*, Bulanov A.N.*, Voylokov A.V.

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Sequencing of rye genome in 2021 gave research community a great opportunity for identifying specific genes underlying previously described mutations. Our interest is in flavonoid biosynthesis in rye grain. Previously, six mutations causing absence of anthocyanins color in grain and other organs and also different flavonoid content in rye grains were identified. Based on genomic sequences of two published rye genomes a new annotation and search for genes involved in flavonoid synthesis were performed. To confirm functionality of the genes trancriptomic data were also used in research. Resulting map of flavonoid synthesis genes on rye chromosomes is a powerful tool for identifying candidate genes for anthocyaninless mutations.

The work was supported by the Ministry of Science and Higher Education of the Russian Federation in accordance with agreement No. 075-15-2022-322 date 22.04.2022 on providing a grant in the form of subsidies from the Federal budget of Russian Federation.

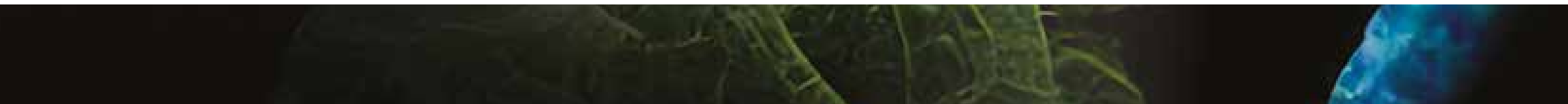
The main publications of authors on the subject of the abstract:

Zykin PA, Andreeva EA, Lykholay AN, Tsvetkova NV, Voylokov AV. Anthocyanin Composition and Content in Rye Plants with Different Grain Color. Molecules. 2018 Apr 19;23(4):948. doi: 10.3390/molecules23040948M.

Timothy Rabanus-Wallace, Bernd Hackauf, .., Natalia Tsvetkova, Anatoly V. Voylokov,.. Nils Stein. Chromosome-scale genome assembly provides insights into rye biology, evolution and agronomic potential. Nat Genet. 2021 53, 564–573. https://doi.org/10.1038/s41588-021-00807-0

Take-home message:

Chromosome map of flavonoid synthesis genes was constructed based on published rye genomes.



A methodology for assessing wheat grain asymmetry to improve phenotyping programmes

Aniskina T.S., Baranova E.N.

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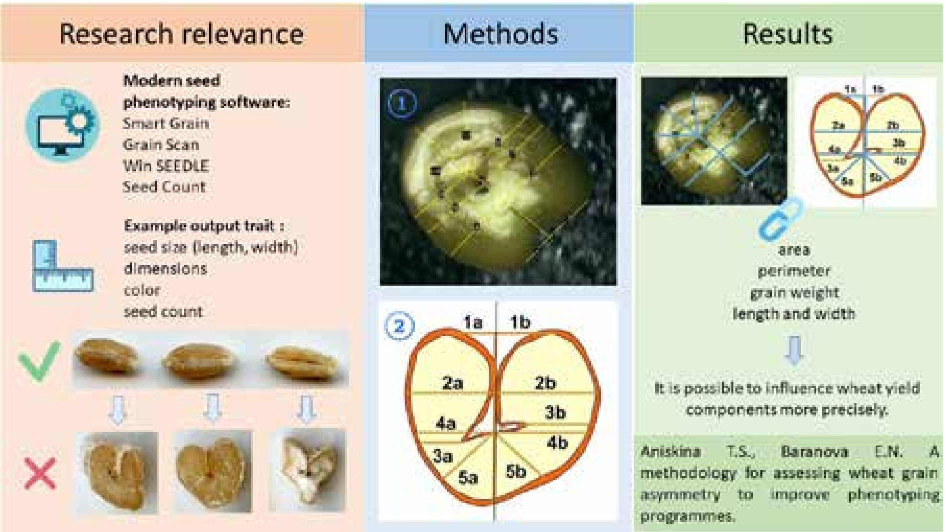
Wheat is one of the most important crops for mankind, and increasing its yields remains a priority. Grain number, shape, colour, length and width have a significant role in wheat yield-oriented phenotypes. To date, software has been developed for phenotyping grains according to these traits (Smart Grain, Grain Scan). However, it is possible to improve them by adding transverse grain size and asymmetry parameters, which will allow estimating the degree of distortion of parts of the object from ideal shapes due to stress effects. The aim of this work is to develop a methodology for estimating the asymmetry of wheat grains. It was found that grain depth, perpendicular length (PL) from the top of the endosperm fold to the symmetry axis (SA), PL from grain edge to SA through the wide part of the grain, PL from grain edge to the endosperm cavity have significant relationships with grain weight, area, perimeter, length and width. Grain symmetry and fullness in the experiments with low salt concentrations are higher than in the control variant. These parameters can be useful in the study of the genetics of yield components, in breeding and for analysis of response to stress.

<u>The main publications of authors on the subject of the abstract:</u>

- *Aniskina, T.S., Baranova, E.N. et al. Unexpected Effects of Sulfate and Sodium Chloride Application on Yield Qualitative Characteristics and Symmetry Indicators of Hard and Soft Wheat Kernels. Plants 2023, 12, 980. doi: 10.3390/plants12050980*
- *Baranova, E.N., Aniskina, T.S. et al. Evaluation of the Heterogeneity of Wheat Kernels as a Traditional Model Object in Connection with the Asymmetry of Development. Symmetry 2022, 14, 1124.doi: 10.3390/sym14061124*

<u>Take-home message:</u>

A number of transverse grain dimensions and asymmetry parameters have been proposed that may be useful for improving wheat grain phenotyping programmes.



It is possible to influence wheat yield components more precisely.

Aniskina T.S., Baranova E.N. A methodology for assessing wheat grain asymmetry to improve phenotyping programmes.

The Role of methylation of CpG-dinucleotide promoters of glutamate dehydrogenase genes in the Functional Regulation of Energy and Plastic Metabolism during Plant Cell Adaptation to Salt Stress

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Aminating GDH activity was determined spectrophotometrically.The analysis of the relative level of transcripts of the *GDH1* and *GDH2* was carried out by Real time PCR. Methyl-specific PCR was performed with DNA converted in the presence of NaHSO3.

An increase in GDH activity under salt stress is due to the changes in genes expression:the increase in *GDH1* expression from 6 h of salt stress is associated with promoter demethylation;the increase in the relative level of *GDH2* transcripts in the first 6 h was accompanied by a demethylation.The inactivation from 12 h of *GDH2* was due to the increase in the degree of methylation.

In salinized maize leaves, the change in the degree of methylation of the promoters of the *GDH1* and *GDH2* genes plays the key role in the regulation of GDH activity,which switches the flow of 2-oxoglutarate beetween TCA and GABA shunt.

Take-home message:

In salinized maize leaves, the change in the degree of methylation of the promoters of the *GDH1* and *GDH2* genes plays the key role in the regulation of GDH activity, which switches the flow of 2-oxoglutarate beetween TCA and GABA shunt.

Identification of polymorphisms in the eIF4E genes of wild potato species

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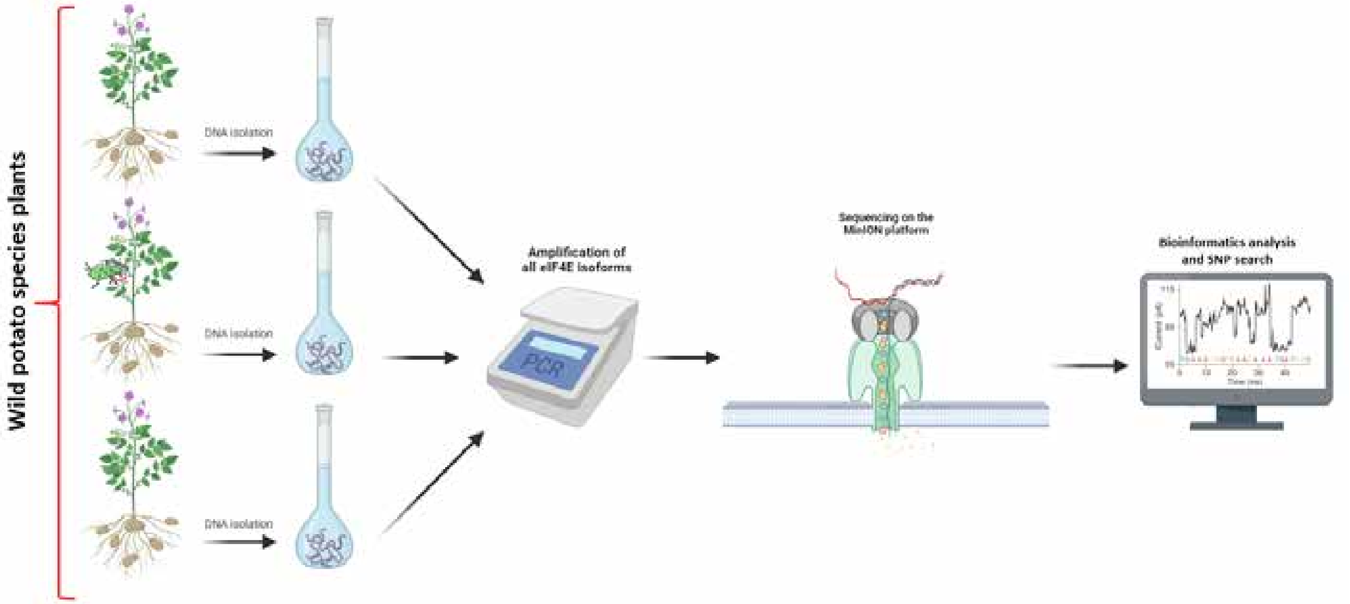
Eukaryotic translation initiation factor 4E (eIF4E) is protein that involved in translation in cells. The eIF4E proteins can be used by some viruses to replicate themselves. For the potatoes the Y virus can be considered as the most dangerous viral disease today. Recent studies of the biodiversity of eIF4E in pepper and tomato showed the presence of allelic variants of the eIF4E genes, which confer plant resistance to the Y virus. However there are no published data on the presence of resistant eIF4E alleles in potatoes. The aim of this study was to sequence all isoforms eIF4E in wild potato species: S.pinnatisectum, S.chacoense, S.phureja and S.stenotomum. All 4 isoforms of eIF4E were amplified from genomic DNA by PCR and obtained in a purified form. Sequencing of full-length sequences was performed using MinION. The results of the analysis of consensus sequences of exon regions of 4 eIF4E isoforms of all wild species showed that in addition to the presence of a small number of polymorphisms in individual plants, there are polymorphisms that occur in all plants of the same species. The study was supported by the RSF project №21-76-10050



Developing genome annotating pipeline and database for agriculturally important bacteria

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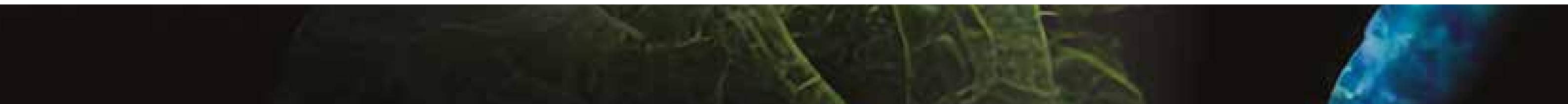
The bacterium *Bacillus thuringiensis* and some other strains from the Bacillus genus are actively used in biotechnology due to their ability to protect crops from insects, bacteria and fungi. The usage of biological agents decreases the ecological burden of agriculture. Despite the significance of these bacteria, genomic regions responsible for their properties are poorly characterized, which makes it difficult to determine the properties of newly isolated bacteria by their genome sequences. To facilitate the screening of bacteria from the *Bacillus* genus, which might be suitable for agriculture, we have developed the pipeline BacPack. This pipeline can process the raw sequencing data including short and long reads, and already assembled genomes. As a result, it identifies the potential insecticidal, bactericidal and fungicidal activities which the strain might possess. BacPack has been also integrated into the online available database, collecting information about *Bacillus* strains. The instruments developed will facilitate the genome annotation process and make it available to a wide range of investigators.

This work was supported by the Russian Science Foundation (20-76-10044).

Take-home message:

Bacteria are actively used in biotechnology as plant protection agents. Developing the pipeline for annotating their genomes and collecting the data regarding the bacteria facilitates screening for new bacterial strains suitable for agriculture.



Germination and growth characteristics of the *nud* knockout and *win1* knockout barley lines under salt stress

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The genes *NUD* and *WIN1* play a regulatory role in cuticle organization in barley. A knockout (KO) of each gene may alter plant mechanisms of adaptation to adverse environmental conditions. Our aim was to evaluate early stages of development of the *NUD* or *WIN1* barley KO lines under salt stress (50, 100, 200 μmol/l). Approximately 30 physiological parameters were evaluated, combined into groups: (1) viability, (2) salt tolerance, and (3) mutability of barley seed progeny. Seed germination and seedling survival were similar for all barley lines. In terms of growth characteristics, *nud* KO lines were inferior to *win1* and wild-type (WT) lines, while the root lengths of all *win1* KO lines were maximum. According to the majority of growth characteristics, the lines *nud* 01-4 and *nud* 05-4 were the tolerant to salinity. At the same time, a stimulating effect was observed in these lines at the minimum dose (50 μmol/l). The WT line turned out to be the most sensitive to salt stress.

The experiments and data analysis were supported by the Russian Science Foundation (21-66-00012).

The main publications of authors on the subject of the abstract:

Antonova E.V., Khlestkina E.K. Radiosensitivity and mutability of wheat seed progeny cultivated under adverse environments Plant Physiology and Biochemistry 2019; 137: 162–168. https://doi.org/10.1016/j.plaphy.2019.02.011

Antonova E.V. et al. Seedling biometry of the nud knockout and win1 knockout barley lines under ionizing radiation. Plants 2022; 11: 2474. https://doi.org/10.3390/plants11192474

Evaluation of the efficiency of computational approaches to identify epitopes on the surface of globular proteins for the binding of sulphated polysaccharides

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Сульфатированные полисахариды (СП) в человеческом организме определяют развитие и морфологию клеток, как в норме, так и при патологии, регулируют взаимодействия с бактериальными и вирусными патогенами. Широкий спектр функций СП указывает на потенциальную значимость их источников. Большое разнообразие СП (фуканы, каррагинаны, ульваны) представлено в водорослях, а именно в коричневых, красных и зеленых. СП из водорослей уже продемонстрировали сильные антиоксидантные, противоопухолевые и иммуномодулирующие свойства в медицине. Для использования СП необходимо точное понимание молекулярных механизмов, лежащих в основе процессов, в которых они участвуют. Эти процессы осуществляются через взаимодействия с белками. Однако в настоящее время экспериментальных данных о таких комплексах мало в связи со сложностью получения. Преодолению экспериментальных ограничений способствуют методы биоинформатики и in silico дизайна. На основании аннотированных баз данных с генетическими последовательностями, кодирующими соответствующие белки, была создана модель машинного обучения “случайный лес” для предсказания потенциальных сайтов связывания СП на поверхности белков.

The Expression Response of Carbohydrate Metabolism Genes to Cold Stress in *Zea mays* Inbred Lines

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Carbohydrate metabolism genes are among the first to be activated in plants in response to cold stress, resulting in an increase in the sugar content in tissues, which contributes to plant adaptation to low temperatures. In the study, the expression of key carbohydrate metabolism genes (starch synthase SSIIb, β-amylase BAM3, α-glucan water dikinase GWD, and sucrose-phosphatase 1 SPP1) was determined in the leaves of four maize inbred lines in response to cold stress (1, 12, and 24 h; +4°C) and during recovery (24 and 48 h; +22°C). All analyzed genes were found to be upregulated in response to cold. The genes differed in response rate: SSIIb and SPP1 were characterized by a rapid increase with an expression maximum after 1 h at +4°C and a subsequent decrease in the transcription level, while BAM3 and GWD were activated later (after 12-24 h, +4°C). All genes were characterized by a repeated increase in expression 24 h after returning to normal conditions (+22°C). Sequential activation of carbohydrate metabolism genes may be related to the efficiency of maize lines adaptation to cold stress.

This work was supported by the RSF grant 21-16-00008.

Glume pubescence classification of wheat using computer vision techniques

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Pubescence is an important phenotypic feature of plants. Plants with pubescence have increased resistance to drought, frost, insect pests and other adverse environmental conditions [1], which can be an important morphological marker in particular for wheat. The problem requires to involve an expert, moreover methods without using a microscope are quite subjective.

In this paper, we will propose alternative methods for determining the feature of pubescence using convolutional neural networks. Deep learning has already been used, for example, to classify plants based on hairiness. The article [2] considered the classification of soybean plots into different types of pubescence. At the same time, it should be emphasized that the problem of predicting the presence or absence of the feature itself has not been previously studied.

Final results: efficient-net_b1, accuracy: 0,85; precision 0,81; auc: 0.85;

The work supported by RSF project № 23-14-00150.

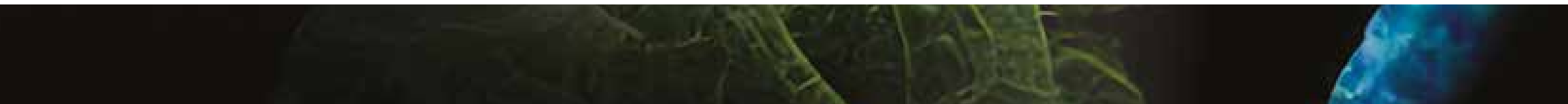
The main publications of authors on the subject of the abstract:

[1] Johnson H.B. Plant pubescence: an ecological perspective // The Botanical Review, 1975, Vol. 41, pp.233-258.

[2] Robert W. Bruce. Istvan Rajcan. John Sulik. Classification of Soybean Pubescence from multispectral aerial Imagery // Plant Phenomics, 2021.

Take-home message:

Pubescence is an important phenotypic feature of plants. Plants with pubescence have increased resistance to adverse environmental conditions. How good could neural networks distinguish wheat by that feature? Better than expert? We've found out!



Study of the effect of GmESR1 overexpression on somatic embryogenesis in *Medicago truncatula*

Artemiuk A.M., Tvorogova V.E., Lutova L.A., Jiao Y.*

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Somatic embryogenesis (SE) is the formation of embryos from a plant's somatic cells. It is widely used in biotechnology for the transformation of plants and their reproduction. The search and study of SE stimulators are important for improving the methods of obtaining somatic embryos.

We investigate the effect of overexpression of the *Glycine max* gene *ESR1* and its homologue in *Medicago truncatula - ERF74,* on the SE in *Medicago truncatula*. For their orthologue, the *ESR1 Arabidopsis thaliana* gene, a stimulating effect on the regeneration of shoots has been shown. We assume that these *ESR* genes can stimulate SE in *Fabaceae.*

At the moment, we have created constructions for overexpression and transformed explants.

To simplify the search for regulators of SE, we are also developing a system for cultivating explants in a liquid medium for the transformation and formation of somatic embryos for *Medicago truncatula*. It should allow the use of petioles as explants, simplify the renewal of the medium, and also replace disposable cultivation containers with reusable ones.

According to our preliminary results, the 1 mg/l concentration of hygromycin (selective agent) is sufficient.

The main publications of authors on the subject of the abstract:

Tvorogova, V.E. et al. The WUSCHEL-related homeobox transcription factor MtWOX9-1 stimulates somatic embryogenesis in Medicago truncatula // Plant Cell Tiss Organ Cult (2019) 138: 517-527. doi: 10.1007/s11240-019-01648-w

Assessment of resistance to powdery mildew in Indian dwarf wheat varieties

Askhadullin Danil, Askhadullin Damir, Vasilova N., Khusainova I., Khairullina A., Lysenko N.*

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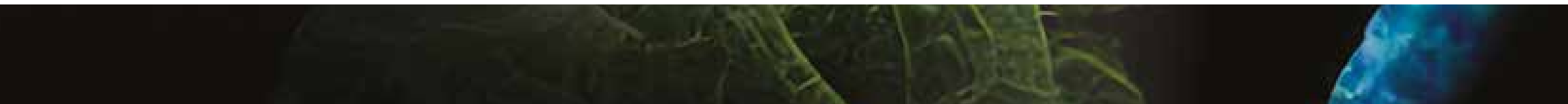
E-mail: tatnii-rape@mail.ru

When breeding for quality and productivity, one of the important indicators is the resistance of plants to diseases. A long-term study of the specimens of dwarf Indian wheat *Triticum sphaerococcum* (TSph) from the VIR collection, endemic to Hindustan, showed high susceptibility to powdery mildew (PM) in the conditions of the Middle Volga region. An epiphytotaxy of powdery mildew was observed in 2022 and the degree of plant infestation was 10-100%. In the course of the evaluation, the lines weakly susceptible to powdery mildew in both mild and shorofert wheat were identified and used in most crossing combinations. Prospective lines of dwarf wheat with "weak" *Blumeria graminis* infestation were obtained. In field trials, the lines obtained by us showed lesions on internodes and leaves of the lower tier, while similar specimens of TSph showed "moderate" and "strong" lesions on the upper internodes and leaves. Thus, the created hybrid lines, retained morphological and technological traits from TSph and inherited resistance to PM from the lines of spring type of soft wheat development.

The research was performed within the frameworks of the state tasks: 122112500039-4 and FGEM-2022-009.



Sources of spring bread wheat resistance to leaf and stem rust

Askhadullin Damir, Askhadullin Danil, Vasilova N., Tazutdinova M., Gayfullina G., Zuev E.*

Tatar Scientific Research Institute of Agriculture, FRC Kazan Scientific Center RAS, Kazan, Russia,
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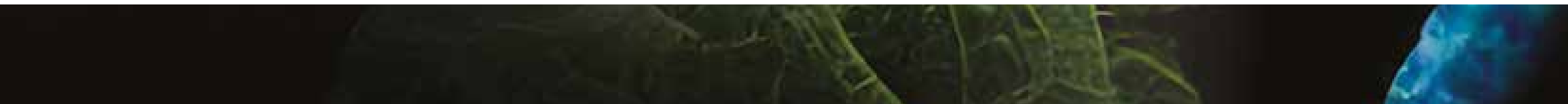
Leaf and stem rust are the most dangerous fungal diseases of spring bread wheat in the Republic of Tatarstan. For a number of years, 704 wheat accessions of the collection nursery were studied, represented mainly by samples from the VIR collection. In the conditions of the region, during the years of epiphytotic, leaf rust, 19% of the samples remained weakly susceptible to the disease. During the epiphytotic years of stem rust, 17% of the collection samples of spring bread wheat remained weakly susceptible to the disease. Screening of samples with known genes of resistance to brown rust showed that samples carrying the genes *Lr19, Lr47, LrAg#1 (T6Agi.6D)* and *LrAg#2* genes are not susceptible to the disease for a long time. Samples bearing the *Sr31* and *Sr24* genes widely used in breeding program for bread wheat breeding continue to remain immune to stem rust.

The research was performed within the frameworks of the state tasks according to the theme plans of: Tatar RIA-FRC KazRC RAS Project No.122011800138-7 and VIR, Project No. FGEM-2022-0009



In vitro rooting of microshoots and acclimatization of *Scrophularia umbrosa* Dumort

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Successful acclimatization of plantlets obtained from in vitro cultures plays a crucial role in a micropropagation protocol. For the transfer of plants cultivated in vitro to ex vitro conditions, a well-developed root system and the selection of an optimal substrate for acclimatization are necessary. In this work, the effect of phytohormones on in vitro rooting of Scrophularia umbrosa microshoots and their acclimatization ex vitro was analyzed.

Microshoots obtained from *S. umbrosa* under *in vitro* conditions were cultivated on full and half strength MS media (Murashige and Skoog) containing 20 g/l sucrose, 0.5 mg/l BAP, as well as indoleacetic acid (IAA) and indolebutyric acid (IBA). Rooted microshoots were transferred to the following substrate: soil: vermiculite: perlite (2: 1: 1); soil:vermiculite (2:1) and soil:perlite to acclimatize them to *in situ* conditions.

The highest number of roots (0.5 mg/l IAA combined with 1.0 mg/l IBA) and the development of longer roots were observed on full-strengthMS medium compared to half MS. Acclimatization of plantlets in *ex vitro* conditions was mostly successful (91%) on the soil:perlite substrate (2:1).

Take-home message:

A protocol for rapid *in vitro* propagation of *Scrophularia umbrosa* has been developed.

New molecular markers to assist the breeding process aimed at improving the quality of fruits in the Solanaceae

Babak O.G., Drozd E.V., Nekrashevich N.A., Anisimova N.V., Yatsevich K.K., Kilchevsky A.V.

Institute of Genetics and Cytology of National Academy of Science of Belarus, Minsk, Belarus
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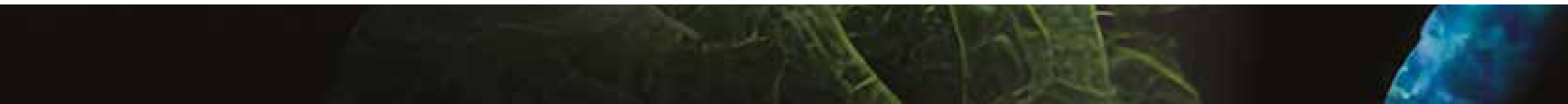
Development of DNA markers based on the polymorphism of pigment synthesis genes enhancing antioxidant properties of fruits is important in the crop breeding to obtain functional food products. Our study aimed to search for the polymorphisms of new genes that affect carotenoid and anthocyanin accumulation, the total number of pigments at the mRNA expression level, as well as post-transcriptional regulation.

The study included PCR analysis, gene sequencing, DNA markers' development, and the phenotypic assessment of manifestation of fruit pigment accumulation traits. *Ant1* and *An2* genes of R2R3Myb transcription factors regulating anthocyanins accumulation were resequenced. Three new markers were developed to type known alleles of *An2* in *S lycopersicon*. The SCAR marker An2-2 was developed to type the *An2* allele in *S. peruvianum.*

DNA and cDNA sequencing of the GLK2 GARP TF gene in S. *lycopersicon* allowed identifying a new *U-del52* allele. Splicing is disrupted and the 2nd exon dropout is observed in the allele. Its phenotypic manifestation was revealed: light green fruits with slightly increased chlorophyll concentration at the stalk compared to the normal *U* allele of the *GLK2* gene.

The main publications of authors on the subject of the abstract:

О.Г. Бабак и др. Новый аллель гена Golden 2-Like, его фенотипическое проявление и селекционное значение у Solanum lycopersicum // Молекулярная и прикладная генетика, 2023 Т . 34, стр. 19-29.



Assessment of morphometric parameters of *A. thaliana* plants of the cml 39 line after exposure to one or two stress factors

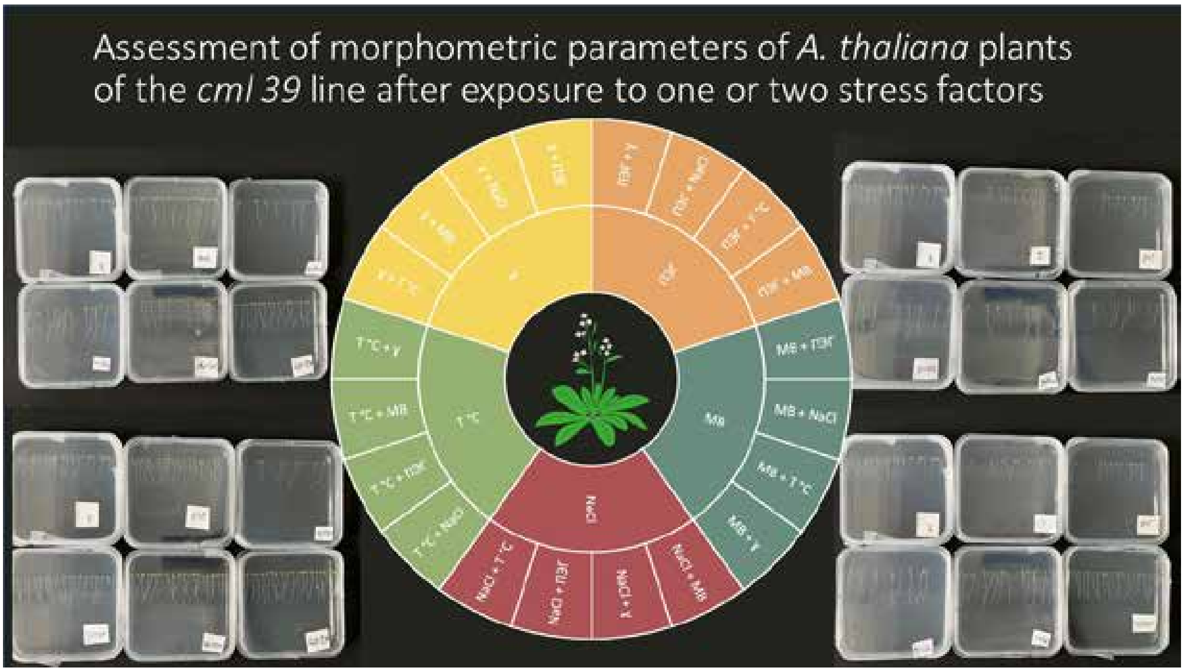
Babina D. D., Korol M. Yu., Blinova Ya. A., Prazyan A.A., Bondarenko E.V.

Russian Institute of Radiology and Agroecology, Obninsk, Russia
E-mail: babinadd@gmail.com

The study investigated the influence of abiotic stress factors, such as radiation, salinity, high temperature, oxidative and osmotic stress, and their combinations, on the morphometric parameters of juvenile plants Arabidopsis thaliana mutant line cml39 in comparison with wild type Col-0. Seeds of both genotypes were exposed to γ-radiation at 25 Gy, hyperthermic treatment at 50 ^{0}for 2 hours, osmotic stress with polyethylene glycol (PEG) at 1%, oxidative stress with methyl viologen (MV) at 0.001 μM, salinity with NaCl at 5 mM, as well as pairwise combinations of stress factors. To assess morphometric parameters, leaf surface area (LSA), primary root length (PRL) at 5 and 7 days after germination, and the average weight of one seedling on day 18 were measured. The results confirm the important role of the calcium sensor CML39 in signal transduction and induction of physiological processes in response to various abiotic factors, including γ-radiation.

The main publications of authors on the subject of the abstract:

Babina D., Podobed M., Bondarenko E., et al. Seed gamma irradiation of arabidopsis thaliana aba-mutant lines alters germination and does not inhibit the photosynthetic efficiency of juvenile plants // Dose Response. 2020. Vol. 18(4). 1559325820979249. doi:10.1177/1559325820979249



The study of the content of inulin in common chicory *Cichorium intybus* hairy roots by spectrophotometric method

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Shvets D.Yu.*, Kuluev B.R.

Institute of Biochemistry and Genetics – Subdivision of the Ufa Federal Research Centre of the Russian Academy of Sciences, Ufa, Russia,
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E-mail: elvina.baimuhametova@yandex.ru

Inulin is a natural polysaccharide with anticarcinogenic, immunomodulatory and bifidogenic properties. Obtaining inulin by the plantation method from natural sources - the roots of Jerusalem artichoke and chicory, is associated with a number of characteristic difficulties. An alternative way to obtain valuable metabolites is biotechnological, based on the cultivation of hairy roots. The purpose of this study was to obtain hairy roots of chicory, followed by a study of the content of inulin in them. For this, 12 lines of wild chicory roots and Kofeek variety were obtained by agrobacterial transformation with bacteria of the species *Agrobacterium rhizogenes* strain A4. The content of inulin in the roots was determined by the spectrophotometric method, which showed the presence of inulin in them, the content of which increased during cultivation, at least for 90 days. The results of the study indicate that hairy roots are able to preserve the biosynthesis of a root-specific metabolite. Average content of inulin in hairy roots of wild C. *intybus* was 1.46±0.46% and the variety Kofeek – 1.34±0.34%.

Take-home message:

Spectrophotometric analysis showed that the hairy roots of chicory contain inulin in amounts comparable to the content of inulin in the lateral roots of plants growing on the soil.

Genetic protection of wheat against stem rust in the Volga region

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*Federal Center of Agriculture Research of the South - East Region, Saratov, Russia
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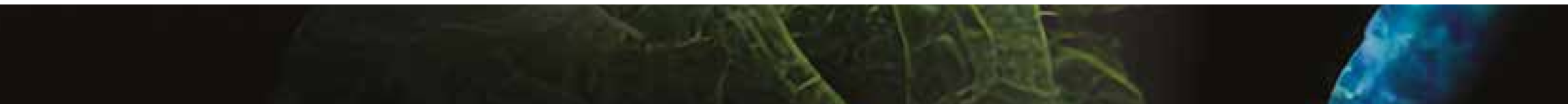
Recently, harmfulness of wheat stem rust caused by *Puccinia graminis* f. sp. *tritici* has increased in the Volga region (the main grain-producing region of Russia). In this regard, the analysis of the resistance and diversity of the Sr genes in the wheat cultivars and breeding lines is very important. In this work 126 wheat cultivars, approved for use in the Volga region and 150 spring bread wheat introgression lines developed by FCARSER were evaluated for resistance to stem rust at the seedling stage and analyzed for the presence of resistance genes (*Sr24, Sr25, Sr26, Sr28, Sr31, Sr32, Sr36, Sr38, Sr39* and *Sr57*) using molecular markers. Highly resistant cultivars (30 from 126) and lines (100 from 150) were identified. In wheat cultivars and introgression lines the genes *Sr31* (in 19 cultivars and 51 lines), *Sr24* (in one cultivar and 12 lines), *Sr25* (in 16 cultivars and 80 lines), *Sr28* (in 6 cultivars), *Sr38* (in 2 cultivars and 18 lines), *Sr57* (in 15 cultivars and 5 lines), *Sr39* (in one line) and their combinations were identified. The obtained results may be used in Russian breeding programs for immunity. This research was funded by Russian Science Foundation grant№ 22-26-00172.

The main publications of authors on the subject of the abstract:

Baranova O.A., Sibikeev S.N., Konkova E.A. Analysis of resistance to stem rust and identification of Sr genes in introgressive lines of spring bread wheat // Proceedings on Applied Botany, Genetics and Breeding (2023) 184(1):177-186. doi:10.30901/2227-8834-2023-1-177-186

Baranova O.A. et al. Evaluation of Resistance to Stem Rust and Identification of Sr Genes in Russian Spring and Winter Wheat Cultivars in the Volga Region // Agriculture (2023) 13:635. doi:10.3390/agriculture13030635



Regulation of illumination and temperature ranges in the synergotron experimental system for accelerated selection by epigenetic susceptibility of plant biosensors

Baranova E.N., Lutushkin V.V., Gavrilov S.V., Novikov V.B., Zelenkov V.N., Sudarikov K.A., Vernik P.A.

Independent NPO Institute for Socio-Economic Strategies and Development, Moscow, Russia
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Sugar beet and common wheat plants were grown under complete climate control in the closed system Synergotron ISR1. A wide range of spectrum changes were investigated (far red, blue, ultraviolet and green). This changes the metabolism of plant cells, affecting transport, changing the habitus of individual parts of the plant. For accelerated selection, the regulation of the formation of large reserves of metabolites in the desired organs is important. In the absence of light regulation, this task is unattainable. Previously, it was not possible to accumulation of seed nutrients during accelerated cultivation, due to the fact that immature seeds were collected. The maximum results, for early-ripening wheat varieties are up to 6, for plants with a long cycle, up to 2-3 generations per year. Closed climate control systems allow you to take the next step in accelerating generation. With the help of modulations of light and temperature, it is possible to “deceive” nature for several more days or even tens of days. It's a first steps. We offer to join the experiments. Now, we present a system for regulation plant development through the use of their climate-light biosensors.

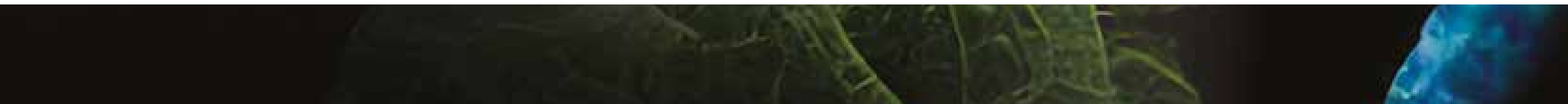
The main publications of authors on the subject of the abstract:

Zelenkov, V. N., Vernik, P. A., Latushkin, V. V. (2021). The Software Digital Complex “Sinergotron” for Research and Development: Breakthrough Technologies in the Cultivation of Agricultural Crops. In Complex Systems: Innovation and Sustainability in the Digital Age: Volume 2 (pp. 483-491).

Волков, М. Ю., Зеленков, В. Н., Латушкин, В. В., & Верник, П. А. (2019). Способ дезинфекции замкнутых агробиотехносистем.

Take-home message:

The synergotron closed system путем using the possibilities of adjusting the parameters of illumination and regulating the spectrum, temperature and humidity, can provide a significant breakthrough in accelerated selection and targeted plantzoning.



On the question of the selection of grain crops for the north-eastern territories of Russia

Batalova G.A., Lisitsyn E.M.

Federal Agricultural Research Center of the North-East named N.V. Rudnitsky, Kirov, Russia
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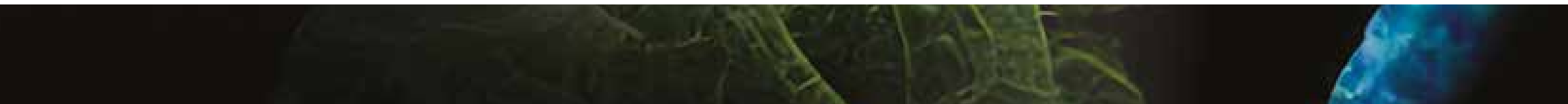
In breeding, various technologies are used to obtain new breeding forms: hybridization in the field on plants, on cut stems and stems selected with a root system in the laboratory, hybridization on plants grown in vessels with pruning of scales and substitution of vessels with a paternal component to maternal plants. Biotechnologies are used to create stable genotypes – obtaining regenerants on selective media based on signs of resistance to drought, soil acidity, the presence of heavy metals, and molecular biology research is being developed in immunity breeding. Molecular technologists shorten the period of obtaining new breeding forms, but not dramatically, as is often indicated in publications and reports, since these breeding forms in the field for the most part do not give the expected result in productivity, quality, efficiency of photosynthesis, and growing in a number of years in the field against the background of the formative process of pathogens leads to loss of resistance to biostressors, while maintaining resistance to stressors of inanimate nature. It is necessary to pay attention to obtaining genotypes capable of maintaining resistance to diseases for a long period.



Clonal micropropagation of technical grape varieties

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The purpose of the research is to study the effect of growth regulators in vitro. The research was carried out on grape varieties: Gift of Magarach and Cabernet Franc. At the end of May, two-eyed shoot tops were cut off, sterilized, meristems were isolated and introduced into in vitro culture. Growth regulators were introduced into the modified MS nutrient medium: 6-BAP (1 mg/l; 1.5 mg/l) - at the first planting of meristem apexes, 6-BAP (1 mg/l) in combination with GK3 (0.5 mg/l; 1 mg /l) - at the stage of actual micropropagation of clones and IAA (from 0.2 mg/l; 0.5 mg/l) - at the stage of rooting of test-tube plants. The growth with the addition of 6-BAP in both grape combs is significantly higher than in the control. At the next stage of micropropagation of grapes, it was added to its composition together with 6-BAP and GK3 at concentrations of 1.5 mg/l and 1 mg/l. The combination of 6-BAP with gibberellin strongly stimulates the growth of stems, by lengthening the internodes, and by increasing their number, since cytokinin growth regulators promote cell division and differentiation, and gibberellin affects cell elongation and division.

The main publications of authors on the subject of the abstract:

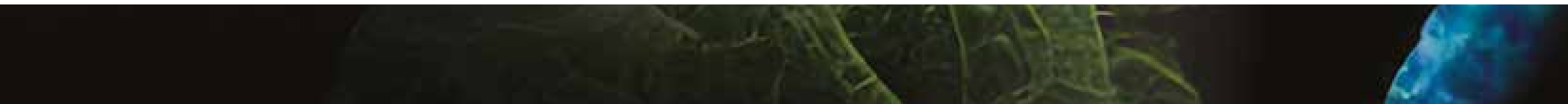
Batukaev A.A., Palaeva D.O., Batukaev M.S. Optimization of the main elements of grape propagation by the biotechnological method - Monograph. Makhachkala. 2021. 151p.

Batukaev A.A., Mukailov M.D., Batukaev M.S., Minkina T. Sushkova S. Use of growth regulators in grapes grinding by in vitro method.. // International Multidisciplinary Scientific GeoConference SGEM. T.18. №6.2. P.783-790.

DOI:10.5593/sgem2018/6.2/S25.103

Take-home message:

Growth regulators and minerals have a positive effect on the determination of grape varieties in vitro. Inclusion in the composition of the nutrient medium of increasing incidence, stimulating the growth and development of grape plants in vitro.



Genetic editing of the genes involved in flowering initiation in Capsella bursa-pastoris

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Transition to flowering is a crucially important process determining reproductive success of plants. A good model for studying it is *Capsella bursa-pastoris,* a recent polyploid of hybrid origin, a cosmopolitan species with remarkable phenotypic plasticity. The purpose of the study was to identify the role of differentially expressed homeologous genes responsible for flowering time in *C. bursa-pastoris* in the context of polyploid genome evolution. We identified the orthologs of regulators of flowering initiation in *C. bursa-pastoris (CO, FT and SVP).* To learn about the influence of these homeologous genes on flowering and unravel whether they did undergo sub- or neofunctionalization, we introduced knockout mutations in the open reading frame of selected genes. For this purpose, we used the CRISPR/Cas9 genome-editing system. Also we analyzed the natural diversity of C. bursa-pastoris and found some variation in these genes, in particular, the accession lel4 carries frameshifting deletion in *CO-O* gene.

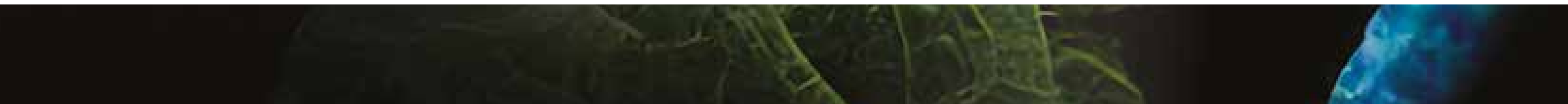
The study is supported by the project #075-15-2021-1064

The main publications of authors on the subject of the abstract:

Kasianov, Artem S., et al. "High-quality genome assembly of Capsella bursa-pastoris reveals asymmetry of regulatory elements at early stages of polyploid genome evolution." The Plant Journal *91.2 (2017): 278-291*

Take-home message:

The purpose of the study was to identify the role of differentially expressed homeologous genes responsible for flowering time in C. bursa-pastoris in the context of polyploid genome evolution.



Investigation of the structural and functional state of *Hordeum vulgare* L. with dark-colored grains

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The most important source of genetic diversity of cultivated plants is the formation of collections for basic research and implementation of breeding programs. Of special interest are varieties of barley (Hordeum vulgare L.) originating from Ethiopia with dark-colored ears. The dark pigmentation gives the plants a number of advantages (resistance to drought, diseases, low and high temperatures). In the barley collection represented by 35 accessions, 6 accessions (var. rubrum, griseinudiinerme, macrolepis, steudelii, nigripallidum) have dark coloring of the ear and grains. In field trials, these accessions had relatively high biological resistance, the manifestation of quantitative traits (height and plant resistance to lodging, the change of chlorophyll in the leaves, ear productivity) were at the level of the standard varieties. However, the selection of valuable genotypes cannot be complete without studying the morphological variability of the ear and grains qualitative features (color variation, pubescence, shape) in relationship with environmental factors. The studied accessions showed significant morphological variations depending on the origin and belonging to the variety.

Работа выполнена в рамках Государственного задания Министерства науки и высшего образования РФ «Адаптивная способность сельскохозяйственных растений в экстремальных условиях Северного Зауралья» (№ FEWZ-2021-0007).

The work was carried out within the framework of the State task of the Ministry of Science and Higher Education of the Russian Federation "Adaptive ability of agricultural plants in the extreme conditions of the Northern Trans-Urals" (No. FEWZ-2021-0007).

Take-home message:

Morphological variability of quantitative and qualitative characteristics of Hordeum vulgare L. in the Northern Trans-Urals

Creation of a hybrid material of spring barley and its use for testing DNA markers for the Run genes that control infection with *Ustilago nuda (Jens) Kell. Et Sw.*

Behtold N.P., Orlova E.A., Glagoleva A.Yu.*, Kukoeva T.V.*, Shoeva O.Yu.*

Siberian reserch institute of Plant Production and Breeding - Branch of Federal State Budget Scientific Institution "The Federal Research Center Institute of Cytology and Genetics of siberian Branch of the Russian Academy of Sciences", Novosibirsk, Russia,

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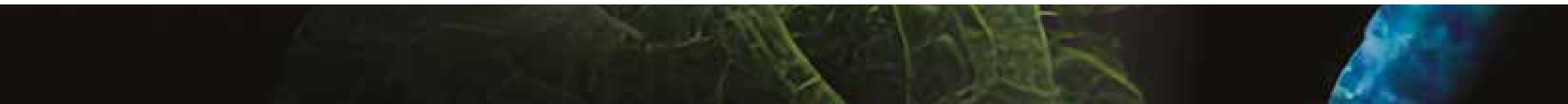
At present, more and more attention is being paid to the genetic protection of barley varieties from the pathogen Ustilago nuda. One of the effective methods for analyzing stable structures is the widespread use of classical techniques based on hybridization of gene donors, the stability with recipient methods of analysis, and the creation of selection methods using molecular markers. In the work for hybridization a were chosen he varieties Bioma, Tanai, Zeus and sensitive to the pathogen variety Grace. Varieties with identified genes Run 3+ Run 6 (Jet, Bonanza) and Run 8 (Effendi, Vestnik, Elf and Raushan) are used as donor stability. As a result of crossings, 9 hybrid combinations were obtained. Using PCR performed on the DNA of the selected samples, allelic polymorphism was detected in the tested markers. Subsequent testing of the resistance of hybrids to the dusty brain and their genotyping using polymorphic DNA markers makes it possible to evaluate the diagnostic efficiency of the use of markers.

This work was supported by the budget project No. FVNR-2022-0018 of the ICG SB RAS and the Kurchatov genomic centre of the ICG SB RAS (agreement No. 075-15-2019-1662).

The main publications of authors on the subject of the abstract:

Bekhtold N.P.,Orlova E.A. Genetics of resistance of spring barley to the agent Ustilago nuda//PlantsGen 2021-017. doi 10.18699

Behtold N.P., Orlova E.A., Grigoriev Yu.N. Virulence of the pathogen of covered smut of oats Ustilago kolleri in the Novosibirsk region. Pisma v Vavilovskii Zhurnal Genetiki i Selektsii = Letters to Vavilov Journal of Genetics and Breeding. 2023;9(1):15-20.DOI 10.18699



New variety of spring bread wheat Sigma 5 based on a doubled haploid line

Belan I.A*[1], Rosseeva L.P. [1], Blokhina N.P.[1], Muhina Y.V., Trubacheeva N.V[2], Pershina L.A.[2]

Omsk Agrarian Scientific Center, Omsk, Russia,
*Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia
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The variety is one of the main factors in the sustainable production of wheat grain. Climate change in Western Siberia, the emergence of new virulent biotypes and races of pathogens requires the accelerated creation of new varieties of spring bread wheat that can adapt to changing growing conditions. It takes 12 to 15 years to develop a commercial variety. The use of DH lines in breeding can significantly reduce the breeding process. The spring bread wheat variety Sigma 5 was derived from the DH line 48-3, which carries a combination of resistance genes to fungal pathogens Lr26/Sr31/Yr9/Pm8, as well as the Lr and Pm genes introgressed into bread wheat from *T. diccocoides*. The Sigma 5 variety was created in 6 years and in 2021 it was submitted to the state variety trial and is being tested in 9-11 regions of the Russian Federation. The main advantage is high yield (> 6.0 t/ha), resistance to leaf and stem rust, powdery mildew and uniformity in morphological characteristics, high grain quality: grain size 749 g/l, weight of 1000 grains 38.7 g, crude gluten content 32.6%, protein 16.21%, flour strength 446 a.u., total baking score 4.4 points.

The main publications of authors on the subject of the abstract:

Development of varieties of spring bread wheat using DH lines in Western Siberia/I.A. Belan, L.P. Rosseeva, N.P. Blokhina et al. The 6th International Scientific Conference; Abstracts. DOI 10.18699/PlantGen2021-018.

Alloplasmic recombinant lines (H. vulgare)-T. aestivum with 1RS.1BL translocation: initial genotypes for production of common wheat varieties /L.A. Pershina, L.I. Belova, N.V. Trubacheeva et al. Vavilov Journal of Genetics and Breeding. 2018. DOI 10.18699/VJ18.393.

Take-home message:

Сорт пшеницы мягкой Сигма 5 создан за 6 лет путем использования ДГ-линий. Основное достоинство –высокая урожайность (> 6,0 т/га), устойчивость к листовым патогенам, однородность по морфологическим признакам и высокие показатели качества зерна.

The role of rhizobacteria in adaptation of plants to toxic aluminum and acid soils

Belimov A.A., Shaposhnikov A.I., Azarova T.S., Yuzikhin O.S., Sekste E.A., Safronova V.I., Tikhonovich I.A.

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Aluminum (Al) is a major negative factor in acid soils responsible growth inhibition of agricultural crops. Plant growth-promoting rhizobacteria (PGPR) increase tolerance of plants to abiotic stresses, however counteraction of Al toxicity received little attention. The effects of PGPR were investigated using pea genotypes contrasting in Al tolerance, cultivar Sparkle and its Al-sensitive mutant E107(brz). The PGPR promoted growth of plants cultivated in hydroponics and in soil in the presence of toxic Al, immobilized Al in the root zone and decreased Al concentration in plant roots. The mutant E107(brz) showed upregulated exudation of organic acids, amino acids and sugars in the absence or presence of Al. Bacteria actively colonized root surface. Exudation of tryptophan and the production of IAA by PGPR in the root zone of the Al-treated plants were observed. Aluminum disturbed concentrations of nutrients in plants, but inoculation partially restored such negative effects. Thus, PGPR play important role in protecting plants against Al toxicity and the mechanisms involved into these plant-microbe interactions are discussed. The work supported by the RSF (19-16-00097; 22-26-00341).

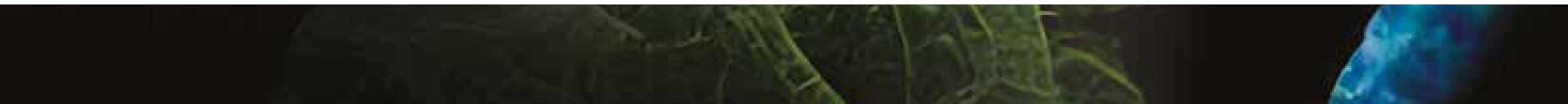
The main publications of authors on the subject of the abstract:

Belimov A.A. et al. Rhizobacteria mitigate the negative effect of aluminum on pea growth by immobilizing the toxicant and modulating root exudation. Plants 2022, 11(18), 2416. https://doi.org/10.3390/plants11182416.

Shaposhnikov A.I. et al. Beneficial aluminum immobilizing microorganisms inhabiting the rhizosphere of pea. Biological Communications. 2023, (in Press).

Take-home message:

Rhizobacteria counteract Al toxicity for plants via immobilization of Al and modulation of root exudation, hormonal status and nutrient uptake of plants.



Varietal features of resistance of subtropical plants to hydrothermal stressors

Belous O.G., Lagoshina A.G., Omarova Z.M., Platonova N.B., Kunina V.A.

Federal Research Centre the Subtropical Scientific Centre of the Russian Academy of Sciences,
Sochi, Russia
E-mail: oksana191962@mail.ru

Проводятся исследования устойчивости субтропических растений к абиотическим факторам в условиях влажного субтропического климата, определяется возможность использования агрохимикатов регуляторного действия, изучается зависимость степени устойчивости культур от уровня физиолого-биохимических параметров. Показано изменение в зрелых листьях чая содержания танинов и аскорбиновой кислоты, принимающих участие в адаптационных реакциях растений на стрессовый фактор. Обработки растений мандарина приводили к снижению водного дефицита листьев и повышению чистой продуктивности фотосинтеза. Обработка опытных растений чая активизирует продукционные процессы, прибавка урожая составляет 2,6 ц/га по сравнению с контролем. У растений мандарина на варианте с обработками прибавка составила от 1,04 до 2,66 кг/дер. (на контроле 0,32 кг/дер.).

Анализ динамики флуоресценции листьев разных сортов фейхоа выявил зависимость спектров флуоресценции не только от содержания хлорофиллов, но и от абиотических факторов. Корреляционный анализ показал тесную зависимость показателей от влажности воздуха и количества осадков и не вывил связи состояния фотосинтетического аппарата растений от температуры воздуха.

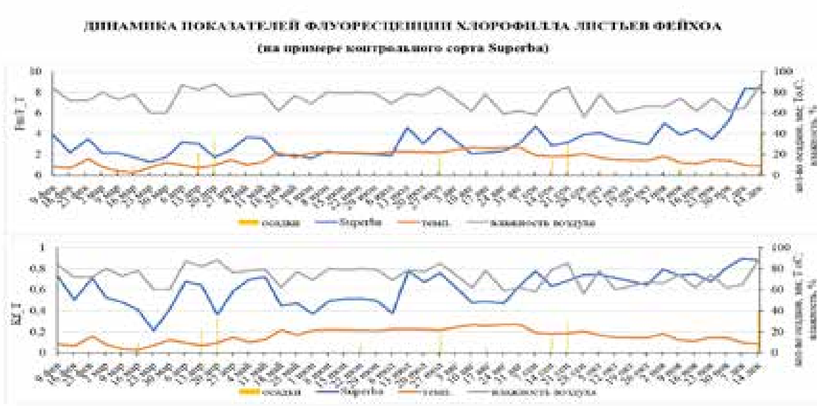
The main publications of authors on the subject of the abstract:

Belous O., Lagoshina A., Pchihachev E. Accumulation of biological active substances in Camellia sinensis (L.) Kuntze under the influence of innovative forms of fertilizers // Acta Horticulturae (2022) 1333: 255-260. doi:10.17660/ActaHortic.2022.1333.33

Кунина В.А., Белоус О.Г. Изменение листовых параметров карликового мандарина под влиянием регуляторов роста // Субтропическое и декоративное садоводство (2022) 82: 145-157. doi: 10.31360/2225-3068-2022-82-146-157

Take-home message:

Разрабатываются способы регулирования функционального состояния растений, обеспечивающие повышение урожайности и её стабильности в варьирующих климатических условиях; определяется сортимент, адаптивный в условиях влажных субтропиков России.



Liverworts as producers of neuroactive amines

Belyshenko A.Y., Morgunova M.M., Malygina E.V., Dmitrieva M.E., Imidoeva N.A., Shelkovnikova V.N., Axenov-Gribanov D.V.

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While the chemistry of plants is widely researched, there has been relatively little study of the natural products found in mosses. Mosses show great promise as a source for the biosynthesis of known natural products as well as the discovery of new biologically active compounds.

We used moss explants obtained from *Marchantia polymorpha* L. Samples were collected from both explants that grew in their natural habitat and from mosses cultured in a 10% Tamiya liquid medium. Secondary metabolites were extracted from the samples. We analyzed the extracts to determine the presence of neuroactive amines including dopamine, histamine, tryptamine, and tyramine. Neuroactive amines were identified via HPLC-MS in MRM mode using the Agilent Infiniti II complex and a mass-spectrometric detector QQQ 6470B.

We observed that *M. polymorpha* moss produces dopamine, tryptamine, and tyramine both in its natural habitat and under liquid cultivation. Furthermore, histamine was detected in the metabolome of *M. polymorpha* that was cultured in a liquid environment.

The study was supported by the Ministry of Education and Science of the Russian Federation, Project ID FZZE 2021-0013.

Take-home message:

This study demonstrated the ability of moss plants to produce neuroactive biogenic amines.

Responses to combined biotic/abiotic stresses: effect of increased temperature and salt stress on response to Verticillium wilt in Medicago spp

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*Project Center for Agro Technologies (Skoltech Agro), Skolkovo Institute of Science and Technology, Moscow, Russia,
**Laboratoire Ecologie Fonctionnelle et Environnement, Université de Toulouse, CNRS, Toulouse, France,
***Centre of Biotechnology of Borj Cedria, Hammam-Lif, Tunisia,
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To better understand interaction between biotic and abiotic stresses in plants, we assessed resistance to Verticillium wilt under increasing temperature and salinity in Medicago sp.

Experimental adaptation of *V. alfalfae* to higher temperature in *M. truncatula* resulted in increased aggressiveness, even in crop-relative alfalfa, suggesting root pathogenic interactions are influenced by global warming, with hot-adapted pathogens posing potential threats due to wider host range and increased aggressiveness. GWAS revealed a shift towards higher susceptibility and mostly different genetic control in response to a 'warm' Iranian strain versus a 'temperate' French strain at 2 temperatures. Salinity also affected plant response to Verticillium. GWAS showed different genetic architectures for the response to infection alone and combined with salt stress, with no overlap between both conditions.

Plant response to combined stresses is not only additive but depends on the interaction between plant genotype and stress conditions. Exploring ecologically-relevant germplasm and adapted pathogenic strains is essential to discover new sources of resistance and guide breeding for future conditions.

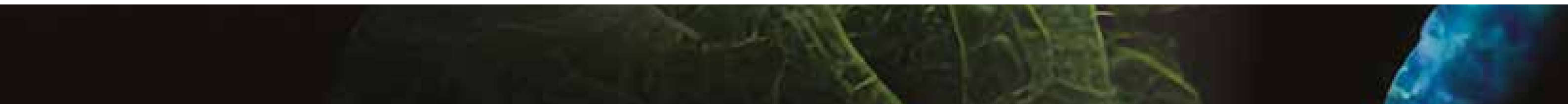
The main publications of authors on the subject of the abstract:

Sbeiti A. et al. Temperature increase modifies susceptibility to Verticillium wilt in Medicago spp and may contribute to the emergence of more aggressive pathogenic strains. // Frontiers in Plant Science (2023) Volume 14. doi: 10.3389/fpls.2023.1109154

Fartash A.H. et al. Medicago truncatula quantitative resistance to a new strain of Verticillium alfalfae from Iran revealed by a Genome-wide association study // Frontiers in Plant Science (2023) Volume 14. doi: 10.3389/fpls.2023.1125551

Take-home message:

Plant response to combined stresses is not only additive but depends on Genotype X Stress interaction. Exploring ecologically-relevant germplasm and newly adapted pathogens is essential to find new sources of resistance and guide breeding for future.



QTL analysis for heading time and grain-filling period in *Triticum aestivum* L.

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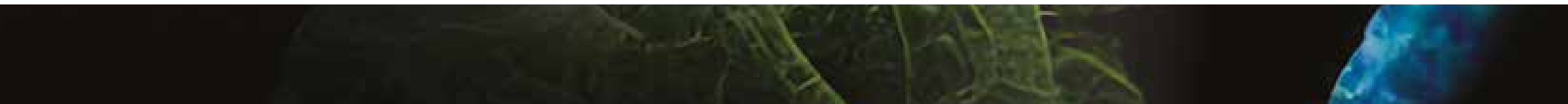
The study of the heading time and maturity in wheat is a topic of pivotal importance because these traits influence the adaptability and yield of the crop. The aim of the present study was to apply the QTL analysis to map the loci underlying the heading time, grain-filling period and maturity. The F2 mapping population was created from a cross between late wheat line 124-1 and early wheat cultivar Novosibirskaya 31 and evaluated in glasshouse. The experiment was then repeated in field conditions in two years using the F2:3 population. The F2 population was genotyped using the Illumina Infinium 25k Wheat array and the linkage map was constructed. A total of 17 QTLs were mapped on 10 wheat chromosomes. The QTL found on the 7B chromosome was detected in both glasshouse and field and it most likely corresponded to the VRN-B3 gene *(FLOWERING LOCUS T)*. The studied population segregated for the SNP G/C within the first exon of this gene, resulting in 2.2 days difference ($p < 0.001$). The other probable candidate genes are an SPL family gene and an ortholog of the CHE transcription factor.

Funding: The reported study was funded by the RSF (Russian Science Foundation) project №21-76-30003.

Take-home message:

The heading QTL corresponding to the VRN3 gene is defined by a non-synonymous SNP.

17 QTLs were mapped on 10 chromosomes. The probable candidate genes for the most environmentally stable QTLs are a SPL family gene and a CHE transcription factor.



Perspective methods for increasing the productivity of transgenic plants-producers of recombinant proteins

Bityukova O.V., Orlova V.A, Burlakovsky M.S., Timonin V.D., Lutova L.A, Padkina M.V.

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E-mail: 79292693255o@gmail.com

In recent years, there has been a growing interest in the use of transgenic plants as sources of valuable recombinant proteins. Plants as producers of immunomodulators have several advantages over alternative expression systems. Direct insertion of a foreign gene into the plant expression system often leads to an insufficient yield of recombinant proteins and to a product with low or undesirable activity. Many improvements of expression systems have been made to solve this problem. A popular way to improve transcription is by combining two promoters in tandem. Combining the two terminators also provides a significant increase in target protein production by reducing end-to-end transcription, resulting in reduced gene silencing. Codon optimization of recombinant protein sequences in favour of codons used by the expression hosts prevents the occurrence of translation pause or translation interruption.

A method for enhancing the productivity of transgenic plants based on the use of double terminators and a bovine interferon gene sequence obtained by codon optimization will be demonstrated.

The main publications of authors on the subject of the abstract:

Burlakovskiy, M. et al.//The Structure of T-DNA Insertions in Transgenic Toba co Plants Producing Bovine Interferon-Gamma. Appl. Sci. 2022, 12, 761.doi:10.3390/app12020761 Beyene, G. et.//Unprecedented enhancement of transient gene expression from minimal cassettes using a double terminator. Plant Cell Rep 30, 13–25 (2011). doi:10.1007/s00299-010-0936-3

Take-home message:

The use of two terminators in a transgene and codon optimization provides a significant increase in the production of the target protein.

To refine the methods we have created plant transformation vectors based on previously tested constructs.

Float culture of triticale anthers: features, embryogenesis, application

Blinkov A.O., Alkubesi M., Kroupina A.Yu., Kozar E.V.*, Rubets V.S., Feodorova T.A.***, Divashuk M.G.**

All-Russia Research Institute of Agricultural Biotechnology, Moscow, Russia,
*Federal State Budgetary Scientific Institution Federal Scientific Vegetable Center (FSVC), Moscow region, Russia,
**Russian State Agrarian University- Moscow Timiryazev Agricultural Academy, Moscow, Russia,
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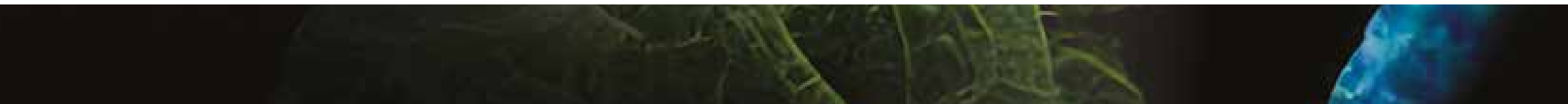
Haploid technologies are useful tools for different breeding, genetics, and biotechnology methods. Unfortunately, haploid production is linked with difficulties such as dependence on the genotype, low regeneration capacity, and mortality after chromosomes doubling. So it is important to investigate approaches to increase the efficiency of methods.

Some parameters influencing float culture's success have been researched: basal medium, maltose concentration, adding plant growth regulations, anther density, and time of transferring embryos.

From the first day of anther cultivation, pollen sacs begin to dehiscence and microspores are released into the liquid medium. After nine days of anther cultivation, almost all microspores leave pollen sacs. Microspores are with high viability. In the liquid medium, microspores start dividing and usually develop through direct embryogenesis. A few embryos are polyembryoids.

Regenerated plants with different ploidy levels were obtained: 21, 42, and more than 42 chromosomes. Seeds from doubled haploid plants are sown in the field for estimation. All lines were aligned according to morphological features.



Selection of pea interspecific hybrids with introgressive alleles of convicilin

Bobkov S.V., Selikhova T.N.

Federal Scientific Center of Legumes and Groat Crops, Orel, Russia
E-mail: svbobkov@gmail.com

Convicilin, vicilin and legumin are the main storage proteins in pea. Conservative convicilin isoforms of cultivated pea hinder gel formation in protein isolates restricting their use in food industry. There are no pea accessions without convicilin. But early we revealed light convicilin isoforms in two accessions of pea wild species *Pisum fulvum*. Objective of current study consisted in introgression of convicilin light isoform coding alleles from wild parents into germplasm of cultivated pea for use in breeding on high protein quality. Interspecific hybrids were obtained in crosses between plants of pea varieties and *P. fulvum* accessions k-2523 and k-6070 from VIR collection. For conducting marker-assisted selection each seed of interspecific hybrids was divided into two cotyledons. Cotyledon with attached axis was marked and sown into soil. Second cotyledon was used for extraction and separation of storage proteins in polyacrylamide gel (SDS-PAGE). Three phenotypic patterns of convicilin isoform bands allow selection interspecific hybrids with “wild” and “cultural” alleles of specified protein in homozygotic and heterozygotic state.

The main publications of authors on the subject of the abstract:

Selikhova T.N., Bobkov, S.V. Polymorphism of Storage Proteins in Accessions of Pea Wild Taxa // (2013) 39: 428-430. https://doi.org/10.3103/S1068367413060177

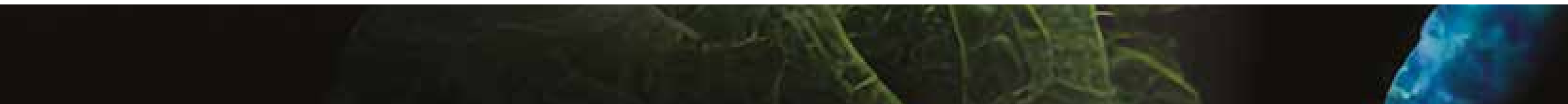
Bobkov S.V., Selikhova T.N. Obtaining of Interspecific Hybrids for Pea Introgressive Breeding // (2015) 13(3): 40-49. https://doi.org/10.17816/ecogen13340-49

Bobkov S., Selikhova T. (2022). Marker-assisted Selection of Pea Interspecific Hybrids with Introgressive Alleles of Convicilin. https://doi.org/10.1007/978-981-16-8731-0_28

Take-home message:

Light isoform of convicilin revealed in Pisum fulvum accessions could improve pea protein complex for use in food industry.

Interspecific hybrids with introgressive alleles of convicilin selected with use of biochemical markers.



The study of the nature of the introgression of alien chromosomes into the cotton genome *G.hirsutum* L.

Bobokhujayev Sh.U., Sanamyan M.F.

National University of Uzbekistan named after M. Ulugbek, Tashkent, Uzbekistan
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Substitution of specific chromosomes of cotton *G.hirsutum* L. with chromosomes of *G.barbadense* L. has a positive effect on fiber quality and length. To create new lines of cotton G. hirsutum with chromosome substitution, it is necessary to analyze the nature of the introgression of alien chromosomes during backcrossing. As a result of a molecular genetic study of backcross hybrids obtained from crossing monosomic lines of cotton *G.hirsutum* with different monosomic hybrids, genetic differences were found in the profile of chromosome-specific SSR markers. The predominant introgression of chromosomes **4, 6, 12** of the A_t-subgenome and **22** of the D - subgenome of *G. barbadense* was revealed, while chromosomes **2, 7** of the A_t-subgenome and **18** of the D - subgenome were characterized by elimination, among them chromosomes **7** and **18** were already eliminated in BC_1F_1, and chromosome **2** is in BC_2F_1. Chromosomes **4** and **6** of the At-subgenome were eliminated only in some backcross variants of BC_3F_1, which indicated the peculiarities in the introgression of chromosomes of the cotton *G. barbadense* into the *G. hirsutum* genome.

The study was financially supported by the Ministry of Higher Education, Science and Innovation of the Republic of Uzbekistan within the framework of the F-OT-2021-155 project.

The main publications of authors on the subject of the abstract:

Sanamyan M.F., Petlyakova J., Rakhmatullina E.M., Sharipova E. World Cotton Germplasm Resources. Chapter 10. Cytogenetic Collection of Uzbekistan. – Intech. – Croatia. – 2014. - P. - 247-287.

Sanamyan M.F., Bobokhujaev Sh.U., Abdukarimov Sh.S., Makamov Kh.A., Silkova O.G. Features of Chromosome Introgression from Gossypium barbadense L. into G. Hirsutum L. during the Development of Alien Substitution Lines.//Plants. 2022. 11(4):542. https://doi.org/10.3390/ plants11040542

Take-home message:

The predominant introgression of chromosomes **4, 6, 12** of the A_t-subgenome and **22** of the D_t-subgenome of *G. barbadense* was revealed, while chromosomes **2, 7** of the A_t-subgenome and **18** of the D_t-subgenome were characterized by elimination.

Development of a computational pipeline to search and analyze genes of multidomain protein families in plant genomes

Bocharnikova M.E., Afonnikov D.A.*

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Modern sequencing technologies have led to a huge flow of data on plant genome sequences. This data requires a high-performance computer annotation to determine protein functions. In this paper, we propose the OrthoDom computational pipeline, which is aimed at searching for orthologous proteins taking into account their domain composition. The pipeline is implemented based on the Snakemike system. Protein sequences of genomes, sets of reference proteins for which functions and domains are known, as well as HMM profiles for the domains of these proteins are fed to the input of the pipeline. The pipeline outputs a list of orthologous sequences for these reference proteins, as well as information about their domain composition and phylogenetic trees for the identified orthologous families. The pipeline was used to identify orthologs in the genomes of cereals.

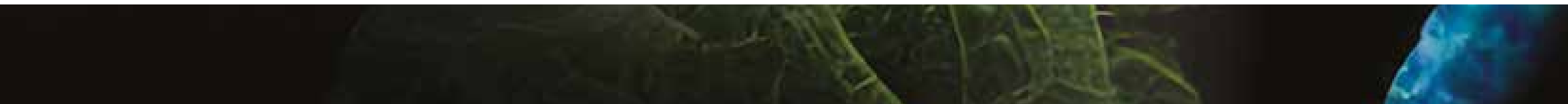
The work was funded by the Kurchatov Genome Center of the ICG SB RAS (project no. 075-15-2019-1662).

The main publications of authors on the subject of the abstract:

Turnaev I. I., Bocharnikova M. E., Afonnikov D. A. Human phospholipases A2: functional and evolutionary analysis //Vavilov Journal of Genetics and Breeding. - 2023. - T. 26. - №. 8. - C. 787-797.

Take-home message:

We propose the OrthoDom computational pipeline, which is aimed at searching for orthologous proteins taking into account their domain composition. We tested the systems accuracy and implemented it for plant protein analysis.



Complex system for comparative evaluation of tomato genotypes by salt tolerance *in vitro*

Bogoutdinova L.R., Kononenko N.V., Chaban I.A., Smirnova E.A.*, Gulevich A.A., Shelepova O.V., Baranova E.A.**, Khaliluev M.R.*****

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*M.V. Lomonosov Moscow State University & All-Russia Research Institute of Agricultural Biotechnology, Moscow, Russia,
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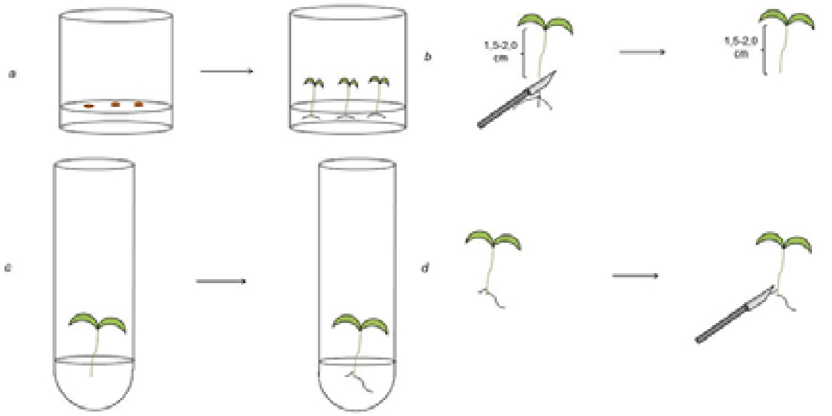
A necessary part of many studies is the study of the mechanisms of salt tolerance of plants as a complex trait. The aim of the work was a comparative assessment of tomato genotypes in terms of salt tolerance by a complex method using seedlings with regenerated roots. The object of research were 8 genotypes of tomato differing in salinity regions: Central and Nizhnevolzhsky. Plants were cultivated on Murashige-Skoog agar nutrient medium supplemented with 150 mM NaCl. The experiment included three repetitions of 30 plants each. An analysis was made of the content of secondary metabolites in the shoot part of seedlings, as well as a cytological analysis of hypocotyls and cotyledons.

The results of the experiment were evaluated after 7 days of cultivation by a set of indicators - morphometric; biochemical and cytological. Differences were shown in biomass as well as in the percentage of secondary metabolites. Scanning electron microscopy revealed differences at the cellular level in transverse sections of the hypocotyl. Thus, the proposed methodological approach can be used to screen promising varieties at early stages of development for resistance to abiotic factors.

The main publications of authors on the subject of the abstract:

Khaliluev, Marat R., et al. A simple and effective bioassay method suitable to comparative in vitro study of tomato salt tolerance at early development stages.Methods and Protocols 5.1 (2022):11. https://doi.org/10.3390/mps5010011

Bogoutdinova, Liliya R., et al. Characteristics of Root Cells during In Vitro Rhizogenesis under Action of NaCl in Two Tomato Genotypes Differing in Salt Tolerance. International Journal of Plant Biology 14.1 (2023): 104119. https://doi.org/10.3390/ijpb14010010



a - seed germination on the MS medium, b - transfer of the shoot part to induce rhizogenesis on the MS medium, c - root formation on the ½MS medium, with the addition of sucrose, 0.7% agar, 0.2 mg/l concentrations of 150 mM NaCl, d - biochemical, anatomical, morphometric and cytological characteristics of seedlings

This approach allowed:
1. Align the cultivated plant material in terms of size and stage of development.
2. Obtain additional parameters for evaluation - the frequency of rhizogenesis and the start time of the formation of regenerated roots

Genetic composition of wheat leaf rust population in Western Siberia in 2022

Boiko Natal'ya*, Sochalova Lyubov, Morozova Evgeniya, Skolotneva Ekaterina, Piskarev Vyacheslav, Shcherban Andrey

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*Siberian reserch institute of Plant Production and Breeding - Branch of Federal State Budget Scientific Institution "The Federal Research Center Institute of Cytology and Genetics of siberian Branch of the Russian Academy of Sciences", Novosibirsk, Russia
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Virulence survey of leaf rust population is a preliminary and necessary procedure before

identifying effective wheat genes. Infectious material was collected on the fields of the Western Siberia in 2022. The infection types of pathogen on wheat was assessed using the Mason E.B. and Jackson H.S. scale (1926) on seedlings. Most of the isolates were virulent on wheat lines with genes *Lr1, Lr14a, Lr14b, Lr15* and were avirulent on lines with *Lr9, Lr47*. Some genes differentiated regional populations of the fungus, these are the following: *Lr24* and *Lr45* (ineffective only in the Novosibirsk region), *Lr11* (ineffective against isolates from the Tomsk and Omsk regions). According to the literature data, the gene *Lr9 l*ost effectiveness in the region, but no virulent isolates were found in the screening samples. Virulent isolates to the line with *Lr19* were found, but the gene was effective in the region earlier. In relation to *Lr19*, there is a change in the genetic structure of the leaf rust population in the region in 2022. The line with the gene *Lr45* was affected by only single isolate from the Novosibirsk region.

This work was supported by FWNR-2022-0018

The study was funded by the RSF grant № 23-16-00119

The main publications of authors on the subject of the abstract:

Skolotneva E.S. et.al. Effectiveness of leaf rust resistance genes against puccinia triticina populations in Western Siberia during 2008-2017// Journal of Plant Diseases and Protection (2018) T.125.№6: 549-555. doi:10.1007/s41348-018-0191-3

Сколотнева Е.С. и др. Расовый состав новосибирской популяции puccinia graminis f. sp. tritici// Микология и фитопатология (2020) 54№1: 49-58. doi:10.31857/S0026364820010092

Induction of Genetic Variability of *Triticum aestivum L.* by a Chemical Mutagen

Bome N.A., Saleh S., Utebayev M.U.*, Weisfeld L.I.**

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**N.M. Emanuel Institute of Biochemical Physics after Russian Academy of Sciences, Moscow, Russia

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Search continues for chemicals that have mutagenic properties and can effectively change the hereditary nature of cultivated plants. We study the regularities of the mutagenic action of phosphemide (sin. phosphazine, diethyleneimide of 2-amidopyrimidyl-phosphoric acid).

Seeds of spring wheat cultivars Cara (Mexico), Scant 3 (Russia), hybrid F4 (Cara x Scant 3) were treated with a solution of phosphemide (0.002; 0.01%), exposure 3 hours. In the M_2 generation, a wide range of mutations (12 types) was revealed: with a frequency of 30% in the hybrid and 15-29% in the cultivars. Field trials at the experimental site of the biological station of the Tyumen State University "Lake Kuchak" (57°20'57.3"N 66°03'21.8"E), 29 mutant samples M_5 , M_6 revealed significant variations in quantitative characteristics.

Electrophoretic analysis of gliadin in mutant samples showed the predominance of blocks controlled by the *Gli-A1*c and *Gli-D2b* alleles. Attention should be paid to the gliadin block controlled by the Gli-B1l allele and being a marker of the wheat-rye translocation 1RS.1BL, which may be associated with wheat resistance to powdery mildew (Pm8), yellow (Yr9), stem (Sr31), leaf rust (Lr26).

Работа выполнена в рамках Государственного задания Министерства науки и высшего образования РФ «Адаптивная способность сельскохозяйственных растений в экстремальных условиях Северного Зауралья» (№ FEWZ-2021-0007).

The work was carried out within the framework of the State task of the Ministry of Science and Higher Education of the Russian Federation "Adaptive ability of agricultural plants in the extreme conditions of the Northern Trans-Urals" (No. FEWZ-2021-0007).

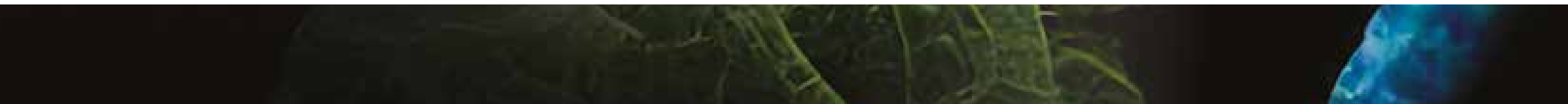
The main publications of authors on the subject of the abstract:

Bome N.A. et al. Agrobiological characteristics of spring soft wheat (Triticum aestivum L.) during seed treatment with chemical mutagen phosphamide // Agricultural biology. – 2017, Vol. 52, No. 3, pp. 570-579. doi.org/10.15389/agrobiology.2017.3.570rus

Saleh S., Bome N.A., Weisfeld L.I. Evaluation of mutant genotypes of Triticum aestivum L. under conditions of water and temperature stress // Agro-food policy of Russia. 2022. No. 2-3, pp. 20-24.

Take-home message:

The adaptation potential of spring common wheat (*Triticum aestivum* L.) in the extreme conditions of the Northern Trans-Urals can be increased by using the genetic variability of mutant populations created using the chemical mutagen phosphemide.



Annotation of the Siberian larch (*Larix sibirica Ledeb.*) reference genome and prediction of transcription start sites in giant genomes of conifer species

Bondar E.I., Tatarinova T.V.*, Putintseva Y.A., Miroshnikova K.A., Sharov V.V., Oreshkova N.V., Kuzmin D.A.**, Krutovsky K.V.*****

Federal Research Center Krasnoyarsk Science Center of SB RAS, Krasnoyarsk, Russia,
*University of La Verne, La Verne, USA,
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The Siberian larch (*Larix sibirica* Ledeb.) is one of the primary boreal tree species in Eurasia. We will present our data for this species, including the annotations of its chloroplast, mitochondrial, and nuclear genomes and a comprehensive repeatome analysis. We also improved the existing genome annotations of the three conifer species, *Pinus taeda*, *Picea glauca*, and *Picea abies*, by predicting transcription start sites (TSSs) and delineating 5'-UTRs.

Among the predicted gene models, 87% had homology to the *Arabidopsis* annotated proteins, and 78% had at least one GO term assignment. About 66% of the larch genome consists of repeats, and the wave of retrotransposon insertions into the larch genome was estimated to occur around 4-5 MYA. A comprehensive repeat library was generated and is available for free use to identify and mask repeats in other tree species. The availability of the draft reference assembly of the Siberian larch genome allowed us to identify microsatellite loci (SSRs) and develop a set of 14 reliable polymorphic nuclear SSR markers that can be used for further population genetic studies, breeding programs, and timber origin identification.

The main publications of authors on the subject of the abstract:

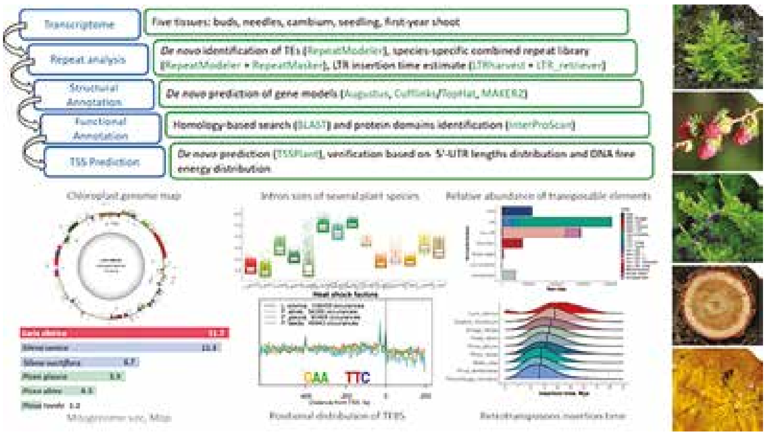
Kuzmin D.A. et al. Stepwise large genome assembly approach: A case of Siberian larch (Larix sibirica Ledeb.) // BMC Bioinformatics (2019) 20: 37

Bondar E.I. et al. Annotation of Siberian larch (Larix sibirica Ledeb.) nuclear genome—one of the most cold-resistant tree species in the only deciduous genus in Pinaceae // Plants (2022) 11(15): 2062

Bondar E.I. et al. Genome-wide prediction of transcription start sites in conifers // Int. J. Mol. Sci. (2022) 23(3): 1735

Take-home message:

The sizes of the both nuclear and mitochondrial genomes of Siberian larch are huge — 12 Gb and 11.7 Mbp, respectively. We sequenced and annotated them, developed a set of polymorphic SSR markers, and predicted TSS in several conifer species genomes.



The biological and agronomically-important traits of sorghum plants

Borisenko N.V., Elkonin L.A., Kenzhegulov O.A., Sarsenova S. Kh., Selivanov N.Yu.*

Federal Center of Agriculture Research of the South-East Region, Saratov, Russia,
*Institute of Biochemistry and Physiology of Plants and Microorganisms – Subdivision of the Federal State Budgetary Research Institution Saratov Federal Scientific Centre of the Russian Academy of Sciences (IBPPM RAS)., Saratov, Russia
E-mail: borisencko-n.v@yandex.ru

Among biotechnology methods, genetic transformation with RNAi-inducing constructs is one of the most effective approaches to regulate synthesis of the seed storage proteins. We used this approach to modify the synthesis of sorghum kafirins, which resistance to proteolytic digestion reduces the nutritional value of this crop as a source of feed and food protein. In the grain sorghum variety Avans (digestibility 63-67%), we obtained stable transgenic lines carrying the NRKAFSIL construct for RNA-silencing of the γ-kafirin gene (*gKAF1*), which are distinguished by improved digestibility of endosperm proteins (up to 90%), an increased proportion of lysine (by 75%), and a modified endosperm type with suppressed development of the vitreous layer. Segregation for the marker gene bar and for the endosperm type indicates the presence of two copies of the RNA-silencing construct. Field experiments have shown that the introduced construct has a number of pleiotropic effects, reducing plant height, weight of 1000 grains and grain yield per panicle. The T3 line was selected with high protein digestibility (81%) and a minimal decrease in agronomically-important traits (by 5-7%).

<u>The main publications of authors on the subject of the abstract:</u>

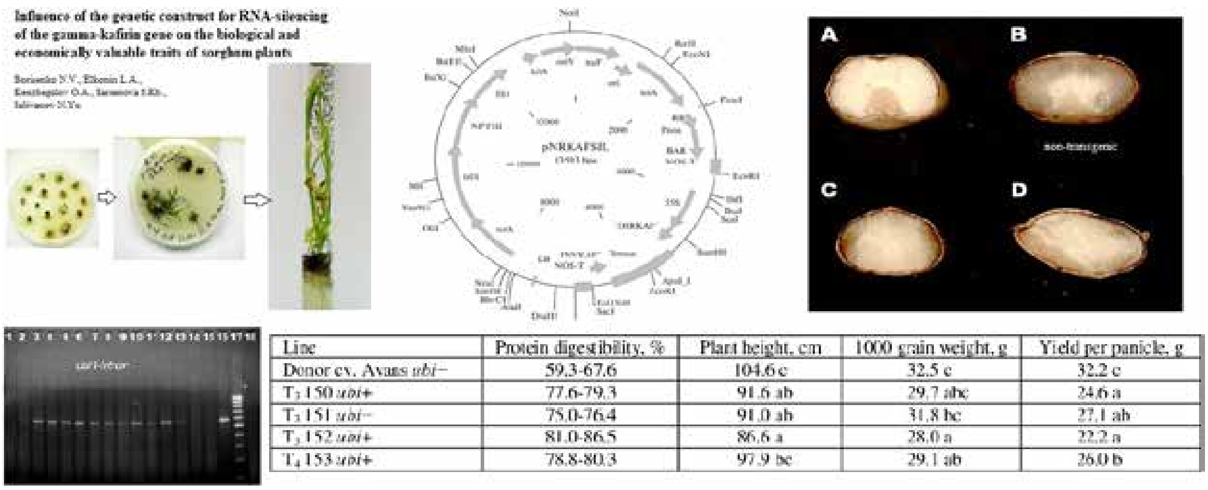
Elkonin L.A., Panin V.M., Kenzhegulov O.A., Sarsenova S.Kh. RNAi-Mutants of Sorghum bicolor (L.) Moench with Improved Digestibility of Seed Storage Proteins // In: Grain and Seed Proteins Funct. Intech Open Ltd., 2021.

DOI:10.5772/intechopen.96204

Borisenko N., Elkonin L., Kenzhegulov O. Inheritance of the genetic construct for RNA-silencing of the γ-kafirin gene (gKAF1) in the progeny of transgenic sorghum plants // BIO Web of Conf. 2022, 43, 03015.//doi.org/10.1051/bioconf/20224303015

<u>Take-home message:</u>

The genetic construct for RNAi of sorghum γ-kafirin gene improves grain protein digestibility, reduces plant height, 1000 grain weight and grain yield per panicle. The T_3 line was selected with a minimal decrease in agronomically-important traits.



Influence of the genetic construct for RNA-silencing of the gamma-kafirin gene on the biological and economically valuable traits of sorghum plants

Borisenko N.V., Elkonin L.A., Kenzhegulov O.A., Sarsenova S.Kh., Selivanov N.Yu.

Line	Protein digestibility, %	Plant height, cm	1000 grain weight, g	Yield per panicle, g
Donor cv. Avans *ubi*−	59.3-67.6	104.6 c	32.5 c	32.2 c
T_3 150 *ubi*+	77.6-79.3	91.6 ab	29.7 abc	24.6 a
T_3 151 *ubi*−	75.0-76.4	91.0 ab	31.8 bc	27.1 ab
T_3 152 *ubi*+	81.0-86.5	86.6 a	28.0 a	22.2 a
T_4 153 *ubi*+	78.8-80.3	97.9 bc	29.1 ab	26.0 b

Inositol phosphates' biosynthesis in pea *Pisum sativum* L. root seedlings at the early stages after rhizobial inoculation

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*Федеральное государственное унитарное предприятие "Научно-исследовательский институт гигиены, профпатологии и экологии человека"
Федерального медико-биологического агентства (ФГУП «НИИ ГПЭЧ» ФМБА России), Leningrad districtict, Kuz'molovskiy, Russia
E-mail: dol2helen@yahoo.com

The investigation of the inositol phosphates (IPs)' role in the signal exchange between legume plants and rhizobia is of great interest, since these compounds can affect the calcium metabolism in roots upon recognition of symbiont signal molecules. The regulation of this process is one of the key events in the control of symbiosis development but remains poorly understood. In our work, a significant increase of IP6 content in response to Nod factor perception was found, therefore in plants, unlike animals, this form may be important for signal transduction. This is consistent with the data that the receptor for IP3 has not been found in plants.

Gene expression analysis showed stimulation of the *PsITPK1* gene expression involved in the phospholipid-independent pathway. Previously, phospholipid-dependent IP biosynthesis pathway was evidenced by the stimulation of phospholipase C genes identified by analyzing the *Pisum sativum* and *Medicago truncatula* transcriptomes of the roots treated with Nod factors. Thus, in plants, in contrast to animals, IP synthesis pathways may be more diverse that indicates the plasticity of signal pathways.

The work was supported by RSF grant 21-16-00106

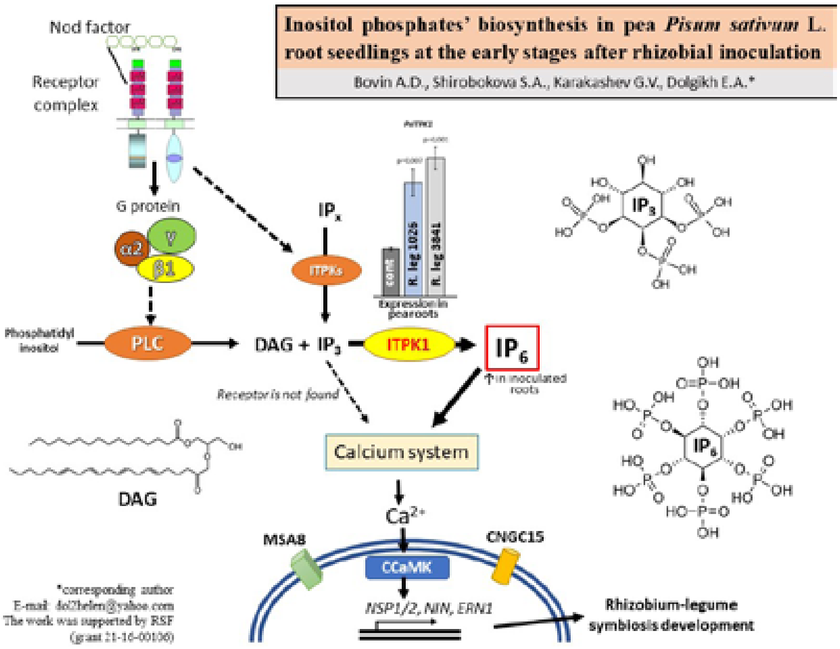
<u>The main publications of authors on the subject of the abstract:</u>

Bovin A.D., Shirobokova S.A., Karakashev G.V., Dolgikh E.A. Inositol phosphates' synthesis in pea Pisum sativum L. root seedlings at the early stages after Rhizobium leguminosarum bv. viciae inoculation // Ecological genetics. - 2023. - Vol. 21. - N. 1. doi: 10.17816/ecogen117412

<u>Take-home message:</u>

A significant increase of IP6 content in response to Nod factor perception was found.

Gene expression analysis showed stimulation of the *PsITPK1* gene expression involved in the phospholipid-independent IPs synthesis pathway.



Inositol phosphates' biosynthesis in pea *Pisum sativum* L. root seedlings at the early stages after rhizobial inoculation

Bovin A.D., Shirobokova S.A., Karakashev G.V., Dolgikh E.A.*

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The work was supported by RSF
(grant 21-16-00106)

Analysis of phenolics synthesis gene expression in blueberry leaves, calluses, and suspension cells

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Голубика - известный источник фенольных соединений, прежде всего катехинов и проантоцианидинов. Нами проведен сравнительный анализ уровня транскриптов генов фенилаланинаммиаклиазы (PAL), халконсинтазы (CHS) и лейкоантоцианидинредуктазы (LAR) в листьях, каллусах и суспензионных клетках *Vaccinium corymbosum* L. Каллусы инициировали из листьев маточных растений на среде WPM с 2,4-Д/БАП 0.5/0,5 мг/л, суспензионные клетки – из каллусов в жидкой среде такого же состава. Экспрессию генов оценивали с помощью ПЦР в реальном времени, методом $RQ=2-\Delta\Delta Ct$. В качестве референсного гена использовался актин. По сравнению с листьями уровень экспрессии PAL, переключающей первичный обмен на синтез фенолов, в каллусах снижен в 10 раз, а у суспензионных клеток - 16,6. Экспрессия CHS - ключевого фермента синтеза флавоноидов, преобладающих в фенольном комплексе голубики, напротив, значительно возрастает в каллусах в 29 раз, в суспензионных клетках в 14 раз, уровень транскрипции гена LAR, отвечающей за синтез катехинов, напротив падает в 4 раза. Вероятной причиной таких изменений экспрессии генов может быть дедифференцировка клеток, вызванная фитогормонами.

Работа поддержана грантом РНФ 23-24-00403.

The main publications of authors on the subject of the abstract:

Berezina E.V., et all // Scientia Horticulturae. (2017) 218: 139-146. doi.: 10.1016/j.scienta.2017.01.020

Березина Е.В. и др. // Физиология растений (2019) 66.1: 35-45. doi:10.1134/S1021443718050035

Take-home message:

Экспрессия генов халконсинтазы (CHS) усиливается в каллусах и суспензионных клетках голубики щитковой, что открывает перспективы для повышенной продукции фенольных соединений.

Study of the MYC family genes regulating flavonoid biosynthesis in rye *Secale cereale* L.

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Rye, Secale cereale L., is an important cereal crop that has received increased attention due to its wide natural variety, including anthocyanin pigmentation of different organs and tissues. Flavonoids, including anthocyanins, perform a set of important functions in plants and are widely used by humans. However, genetic control of the biosynthesis of flavonoids in rye is not yet well understood. We have found the evidence that Vs (*Violet seed*) gene controlling purple anthocyanin pigmentation of caryopsis codes MYC family protein. It is known that flavonoid biosynthesis in plants is regulated by MYC, MYB and WDR transcription regulators. We have analyzed five alleles of Vs differ in their pigmentation phenotype. For better understanding of this gene properties and traits associated with it we have performed the study of 13 closely related transcriptionally active MYC coding genes of rye. Thus, we have firstly described the gene of MYC transcription factor regulating flavonoid biosynthesis, Vs, and have compared it with other rye MYC family genes.

This work was supported by the Government of the Russian Federation in accordance with agreement No. 075-15-2022-322 date 22.04.2022.

The main publications of authors on the subject of the abstract:

Voylokov A.V. et al. Peterhof collection of rye and its use in genetic studies // Ecol Genet (2018) 16(2):40-49. doi:10.17816/ecogen16240-49

Zykin P.A. et al. Composition and content in rye plants with different grain color // Molecules (2018) 23(4):948. doi:10.3390/molecules23040948

Rabanus-Wallace M.T. et al. Chromosome-scale genome assembly provides insights into rye biology, evolution and agronomic potential // Nature Genetics (2021) 53:564–573. doi:10.1038/s41588-021-00807-0

Adaptive value for common wheat (*Triticum aestivum*) of the gene $Hl2^{aesp}$ leaf hairiness introgressed from *Aegilops speltoides*

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Pshenichnikova T.A.**

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Morphological features of leaf pubescence in common wheat have a significant impact on its photosynthetic activity (Pshenichnikova et al. 2019). The present study is devoted to the $Hl2^{aesp}$ gene introgressed from Aegilops speltoides that forms rare trichomes over 400 μm long on the leaf surface. The gene was introduced into the line 102/00i (Arsenal collection) on chromosome 7B(7S)of cv. Rodina which lacks leaf pubescence. When crossing this line and the original variety the recombinant lines were obtained with and without pubescence. The selection was accompanied by a control for *Xgwm400* microsatellite marker associated with $Hl2^{aesp}$gene. It was shown that when grown under conditions of controlled drought, the line rec:Rodina $Hl2^{aesp}$ the line evaporates water 20% less, but also absorbs carbon dioxide one third more slowly. With sufficient watering, the difference in CO_2 uptake and transpiration is not so contrasting. The germination-heading period is delayed by 3-4 days in the line with pubescence and it is more productive under normal watering and filed growing. Financial support: Russian Science Foundation (23-24-10029) and Novosibirsk Region (p-63).

<u>The main publications of authors on the subject of the abstract:</u>

Pshenichnikova T.A., et al. Quantitative characteristics of pubescence in wheat (Triticum aestivum L.) are associated with photosynthetic parameters under conditions of normal and limited water supply // PLANTA (2019) 3(243): 839-847

Genotyping of apricot cultivars from the Nikitsky Botanical Garden collection using SSR markers

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The results of studying the genetic structure of apricot cultivars with different ecological and geographical origin from the collection of FSFIS “NBG-NSC” using SSR markers were presented. Investigation relevance is due to the poorly studied gene pool collection of apricot at the genetic level and the need to develop genetic passports for cultivars as domestic breeding. Twenty apricot accessions were included in the study. Nine nucleotide SSR markers were used for analysis. According to our results, all primers were polymorphic. Based on obtained data, polyploidy is also supposed for some cultivars. However, the analysis revealed the difficulty of using only di-nucleotide SSR markers due to the error in estimating the amplicon length and, as a consequence, incorrect determination of alleles. The data obtained show the necessity of using three-, and tetra-nucleotide motifs in genetic passporting, as well as obligatory preliminary ploidy level determination. The study was supported by the Kurchatov Genomic Center of Nikitsky Botanical Garden -National Scientific Center of RAS (075-15-2019-1670).

Take-home message:

The work on the creation of a database of DNA passports of stone fruit crops of the South of Russia was started. 20 apricot cultivars from the “NBG-NSC” collection were examined using nine SSR markers. Possible polyploids were detected.

Hyperspectral Image Analysis Pipeline

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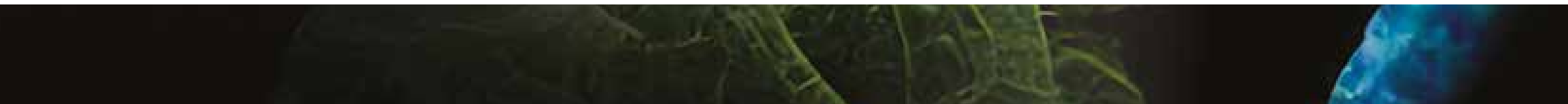
The analysis of hyperspectral images is of great interest in the problems of plant research. Hyperspectral technologies are used to assess the concentration of mineral elements in wild barley grain (Herzig P. et al., 2019), to classify viable and non-viable wheat seeds (Zhang T. et. al., 2018), to identify barley germinated at an early stage (Arngren M. et al., 2011). This work presents a hyperspectral image analysis pipeline. The Python pipeline includes: basic statistical analysis, visualization of a multichannel hyperspectral image, solving a classification problem using classical machine learning methods. Methods for constructing a confidence interval for the difference in sample means, checking the equality of distributions of two classes of hyperspectral images based on Pearson's chi-square test, visualization in two-dimensional space using PCA and Umap, classification using logistic regression or ridge regression, random forest and catbbost were implemented. The developed pipeline was tested in the task of determining the pigment composition of barley grains. The results of the analysis showed significant differences in the studied target groups.

The work was supported by the Russian Science Foundation, the project 22-74-00122, https://rscf.ru/project/22-74-00122/



Peroxidases in peach: gene expression change in response to low temperature stress

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Peroxidase (POD) is the antioxidant enzymes and plays a huge role in the response to stress. 60 genes encoding this protein was identified in the peach genome. As the temperature is limiting factor in growing this crop, the aim of our work was to analyze the expression of all PODs based on transcriptomic data and the relative expression of three PODs by RT-PCR in different cultivars under cold stress.

The transcriptomic data revealed the down-regulated peroxidase genes which were expressed at normal temperature and the up-regulated peroxidase genes which were not expressed at normal temperature occurred when crossing the cold threshold. As well analysis of the relative expression shown the decreasing of POD expression in cold-tolerant cultivars, while in cold-sensitive cultivars the increasing of POD expression was observed after 24-h cold stress.

We hypothesize that the expression of PODs is switched between different genes upon reaching cold thresholds. In cold-sensitive cultivars, the temperature thresholds are lower, so we observe an increase in POD expression already in the 1-st day.

The study is supported by the Kurchatov Genomic Centre of the NBG–NSC (075-15-2019-1670).

Take-home message:

The study revealed the mechanism of expression switching between peroxidase encoding genes in peach when temperature thresholds are reached. It explains the differences in the POD expression pattern in peach cultivars with different cold tolerance

Results of wide-genome sequencing and assembly of the *de novo* genome of the Siberian silkworm

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The paper considers whole genome sequencing and de novo assembly of the Siberian silkworm genome.

At the first stage, a method for determining the sex of an insect, based on morphological features, was studied. only females have WZ chromosomes, males usually have only two ZZ chromosomes.

At the second stage, DNA was isolated from a Siberian silkworm pupa, purified, the quality of the isolated DNA was assessed, and it was sent for sequencing to BGI (Hong Kong). The sequencing results were obtained on the DNBSEQ platform and amounted to 3.97 GB by paired reads, short reads up to 150 bp.

At the third stage, the analysis of the assemblers used to assemble the genomes was carried out, which made it possible to stop at the SPAdes genomic assembler.

The genome of the Siberian silkworm was assembled, about 420 Mb in size. Work is underway on the annotation of the genome. Having deciphered the genome, we will be able to study the expression of those genes that contribute to the adaptation of the pest to new unfavorable conditions. As a result, we will be able to develop approaches to the fight against the Siberian silkworm using genetic technologies.

The main publications of authors on the subject of the abstract:

Chemezova A.A. Whole genome sequencing and assembly of the De Novo genome of the Siberian silkworm // School section: Mathematics. Physics. Chemistry. Biology. Humanitarian sciences. Engineering design. Information Technology. Digital technologies: Proceedings of the 60th Intern. scientific stud. conf. April 10–20, 2022 / Novosib. state un-t. - Novosibirsk: CPI NGU, 2022. - P. 252.

Analyzing influence of the TaGrf3-2B gene on agronomically valuable traits in semi-dwarf spring triticale

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Wheat, rice and corn are "the main breads of mankind", recently scientists have added triticale (wheat-rye hybrid) to them. Growth regulation factors (GRF) are transcriptional proteins that play an important role in plant growth regulation and development (Knaap et al,2000). It has been shown in rice and corn that an increase in *Grf* genes expression leads to an increase in grain and leaves size (Che et al,2015; Nelissen et al,2015). Reducing height of plants, to prevent lodging, is achieved by introducing dwarfing genes. In triticale, *Ddw1* is a common such gene (Kroupin et al,2019). However, this gene negatively affects some economically valuable plant traits (Divashuk et al,2018).

We sequenced the *TaGrf3-2B* gene and created a co-dominant molecular marker. In semi-dwarf triticale plants *TaGrf3-2B(188)* allele increased number of grains per spike by 5 pc, thousand grains weight by 3.2 g, and reduced number of days from sowing to flowering and heading by 2 days (compared to allele *161*). This and our previous works show the promise of studying *Grf* genes in cereals and provide a rationale for their inclusion in breeding process. Study was supported by State Assignment FGUM-2022-0007.

<u>The main publications of authors on the subject of the abstract:</u>

Chernook A.G.et al.Compensatory effect of the ScGrf3-2R gene in semi-dwarf spring triticale(xTriticosecale Wittmack)//Plants(2022)11(22):3032.doi:10.3390/plants11223032

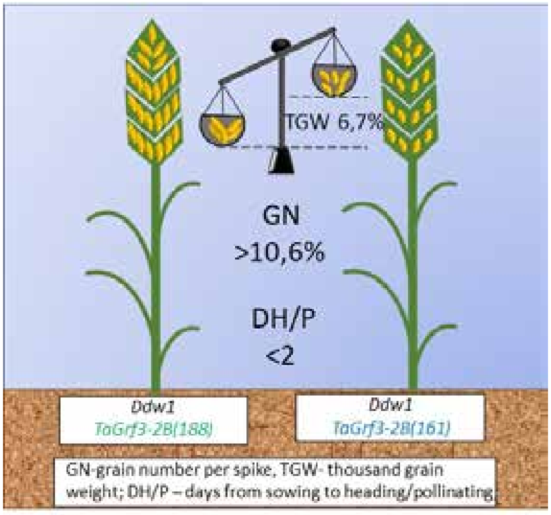
DivashukM.G.etal.TaGRF3-2Aimprovessomeagronomicallyvaluabletraitsinsemi-dwarfspringtriticale//Plants(2021)10(10):2012.doi:10.3390/plants10102012

Kroupin P.Yu.et al.Allele mining of TaGRF-2D gene 5'-UTR in Triticum aestivum and Aegilops tauschii genotypes//PloSOne(2020)15(4):e0231704.doi:10.1371/journal.pone.0231704

<u>Take-home message:</u>

The positive compensatory effect of *TaGgf3-2B* gene on important semi-dwarf spring triticales agronomically valuable traits was shown (*Ddw1* gene presence).

An accessible co-dominant molecular marker for *TaGgf3-2B* has been created.



Development of fiber-like cells in moss gametophytes

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The Laboratory of Plant Cell Growth Mechanisms, Kazan Institute of Biochemistry and Biophysics, FRC Kazan Scientific Center of RAS, Kazan, Russia,
*Microscopy Cabinet, Kazan Institute of Biochemistry and Biophysics, FRC Kazan Scientific Center of RAS, Kazan, Russia, **Lebedev Institute of Physics of Russian Academy of Sciences, Moscow, Russia, ***Department of Biology and Environment, Faculty of Natural Sciences, University of Haifa-Oranim, Tivon, Israel
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With the beginning of land colonization on Earth, plants had to specialize their cells and develop tissues. To characterize the first steps in the evolution of mechanical tissues in terrestrial plants, we used extant bryophytes and analyzed the cell walls of seven taxonomically distant true moss species (*Polytrichum juniperinum, Dicranum sp., Rhodobryum roseum, Eurhynchiadelphus sp., Climacium dendroides, Hylocomium splendens and Physcomitrium patens*). In all of them, the outer stem cortex of the leafy gametophytic generation had fiber-like cells with a thickened cell wall. Such cells had a spindle-like shape with pointed tips, which could arise from intrusive elongation. The cell walls of such cells are mannan-based and contain additional cell wall sublayer that differ in cellulose microfibril orientation and specific polymer composition, including 1,4-β-galactans. Finally, we compared the transcriptomes of *Physcomitrium patens* and *Linum usitatissimum* (a plant that produces long fibers with a thickened cell wall), which allowed us to outline further steps in studying the evolution of plant fiber growth mechanisms.

The work was supported by the RSF, project 19-14-00361.

Development of *Pinus sylvestris* L. megagametophytes depending on the genotype of the donor plant and the content of growth regulators in the cultivation medium

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Scots pine is one of the most economically valuable woody plants. However, this species is difficult to propagate using somatic embryogenesis. The key factors on which the initiation success depends are the nutrient medium containing optimum growth regulators amount and genotype of the explant donor plant. There were five variants of MSG media with different phytohormone content studied: 1) 13,6 µM 2,4-D+9 µM BA; 2) 13,6 µM 2,4-D +2.2 µM BA; 3) 15,8 µM 2,4-D +9 µM BA; 4) 18 µM 2,4-D+9 µM BA; 5) 2,7 µM NAA+9 µM BA. A total of 764 megagametophytes with mature embryo, collected from 4 plus tree clones (1026; 876; 864; 856) growing in the Petrozavodsk seed orchard (PSO), were cultured. Callus formation was most frequently recorded on medium №5 (5.7±1.7%), less frequently callus was formed on substrate №4 (1.4±1%). Explants collected from clone 864-1 initiated callus formation on all media, but from tree 1026-2 only on medium №5.Thus, substrate containing 2,7 µM NAA and 9 µM BA is the most optimal for callus induction from explants collected from *Pinus sylvestris* clones in PSO. Donor plants have been identified that are probably more responsive to the somatic embryogenesis initiation.

<u>The main publications of authors on the subject of the abstract:</u>

Pinus sylvestris L. mature seeds megagamethophytes cultured in vitro. Influence of the genotype and the growth regulators content in nutrient medium on the initiation of callus formation Chirva O. V., Ignatenko R. V., Ershova M. A. Plant Cell, Tissue and Organ Culture (PCTOC). 2022.

ОПТИМИЗАЦИЯ УСЛОВИЙ СТЕРИЛИЗАЦИИ И КУЛЬТИВИРОВАНИЯ ЭКСПЛАНТОВ PINUS SYLVESTRIS (PINACEAE) Ершова М.А., Игнатенко Р.В., Новичонок Е.В., Чирва О.В., Галибина Н.А. Растительные ресурсы, 2022, Т. 58, № 4. 2022.

<u>Take-home message:</u>

*Both genotype and culture medium content have significant influence on SE initiation success.

Effects of interaction between alleles of *Vrn-A1* and *Vrn-B1* loci on the heading time of bread wheat lines of the winter cultivar Bezostaya 1

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The allelic diversity of Vrn genes largely determines the broad adaptation of wheat to environmental conditions. It is important to study the effect of *VRN-1* alleles and their combinations influencing the heading time. This work presents the results of studying the heading time and duration of development phases of Bezostaya 1 (Bez1) lines with different combinations of dominant alleles *Vrn-A1a, Vrn-A1L, Vrn-B1a* and *Vrn-B1c*. The combination of *Vrn-A1a*, which determines early heading, with *Vrn-B1a* and *Vrn-B1c*, and *Vrn-A1L*, which determines late heading, led to a decrease in the period to the first node and ear emergence relative to the initial NILs. The lines with the combination of *Vrn-A1a* and *Vrn-B1a/Vrn-B1c* did not differ from each other in the duration of the phases studied, whereas *Bez1 Vrn-A1L Vrn-B1c* was more precocious than *Bez1 Vrn-A1L Vrn-B1a*. At the same time, *Bez1 Vrn-A1L Vrn-B1c* was virtually indistinguishable from *Vrn-A1a. Thus, Vrn-A1L* can be successfully used in selection for precocity as a result of combination with dominant alleles of *Vrn-B1* locus.

This study was supported by the Russian Science Foundation (Grant No. 22-26-00085).

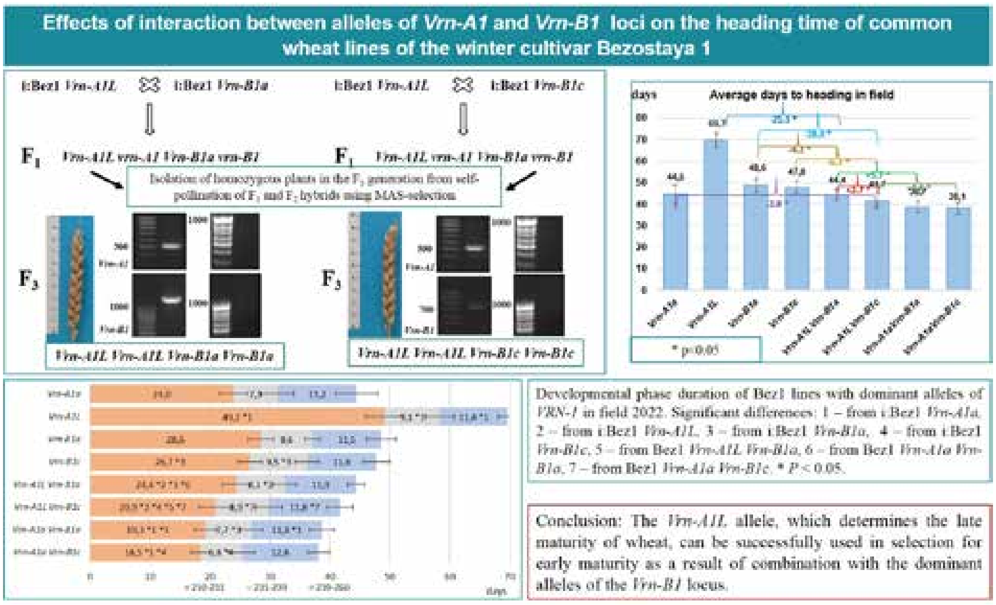
The main publications of authors on the subject of the abstract:

Chumanova E.V. et al. The effect of different dominant VRN alleles and their combinations on the duration of developmental phases and productivity in common wheat lines // Russian Journal of Genetics (2020) 56: 822–834. doi: 10.1134/S1022795420070029

Chumanova E.V. et al. Characterization of the VRN-A1 allele introgressed from T. aestivum ssp. petropavlovskyi that influences the heading time in bread wheat // Euphytica (2023) 219:53. doi: 10.1007/s10681-023-03178-1

Take-home message:

The *Vrn-A1L* allele, which determines the late maturity of wheat, can be successfully used in selection for early maturity as a result of combination with the dominant alleles of the *Vrn-B1* locus.



Effects of interaction between alleles of *Vrn-A1* and *Vrn-B1* loci on the heading time of common wheat lines of the winter cultivar Bezostaya 1

Isolation of homozygous plants in the F_3 generation from self-pollination of F_1 and F_2 hybrids using MAS-selection

Developmental phase duration of Bez1 lines with dominant alleles of *VRN-1* in field 2022. Significant differences: 1 – from i:Bez1 *Vrn-A1a*, 2 – from i:Bez1 *Vrn-A1L*, 3 – from i:Bez1 *Vrn-B1a*, 4 – from i:Bez1 *Vrn-B1c*, 5 – from Bez1 *Vrn-A1L Vrn-B1a*, 6 – from Bez1 *Vrn-A1a Vrn-B1a*, 7 – from Bez1 *Vrn-A1a Vrn-B1c*. * $P < 0.05$.

Conclusion: The *Vrn-A1L* allele, which determines the late maturity of wheat, can be successfully used in selection for early maturity as a result of combination with the dominant alleles of the *Vrn-B1* locus.

Interaction model between *Nicotiana tabacum* eIF4E factors and *Potato virus Y* VPg protein

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Potato virus Y (PVY) is a crop pathogen that affects *Nicotiana tabacum* L. and other members of the Solanaceae family. PVY infection relies on the interaction between viral genome-linked protein (VPg) and host-encoded eukaryotic initiation translation factors (eIF4E). Tobacco possesses an eIF4E multigene family, however it is unknown which tobacco factors can interact with VPg. In this study, we used the yeast two hybrid (YTH) assay to test the interaction between 10 tobacco factors eIF4E and 11 VPg obtained from PVY - resistant tobacco cultivars. The results showed that VPg interacts mainly with eIF4E-1, therefore mutagenesis PCR was used to introduce missense mutations in this factor and generate three mutant factors: eIF4E-1 FL, eIF4E-1 PS and eIF4E-1 GR. The functionality of these factors was tested through complementation assay and YTH assay was used to assess their interaction with VPg. As result all mutant factors were functional, however only eIF4E-1 PS was able to disrupt the interaction with VPg, thus this factor may provide resistance to PVY. In conclusion, eIF4E-1 is a promising target to increase the resistance of Tobacco to PVY using gene editing technology.

Take-home message:

The tobacco eukaryotic initiation translation factor eIF4E-1 is a promising target to increase the resistance of *Nicotiana tabacum* to PVY using gene editing technology.

This work was funded by State Task no. FGUM-2022-0004.

Bioinformatics search for bacilli genes responsible for the induction of systemic resistance (ISR) in plants

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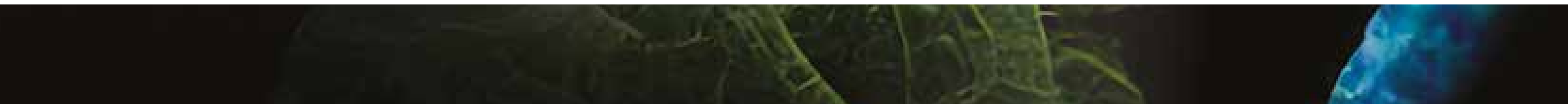
Bacillus spp. способны синтезировать экзополисахариды, сидерофоры, сурфактанты, играющие особую роль в жизни растений. Биологический контроль может быть достигнут путем направленной генетической модификации биоконтрольных штаммов.

Геномы штаммов B. *pumilus* 7P, B. *intestinalis* GM2 и B. *subtilis* GM5 депонированы в базе данных NCBI. Геном штамма B. *subtilis* 168 использовали как контрольный. Аннотацию геномов выполняли с помощью автоматического аннотатора NCBI PGAP и программы Prokka v.1.12. Используя базы данных IMG ER_v5.0, RAST_v2.0 и сервер antiSMASH во всех геномах был идентифицирован ген биосинтеза бациллибакцина (*dhbF)*. В геноме штамма B. *pumilus* 7P был идентифицирован кластер биосинтеза лихенизина (*lchA*). В остальных штаммах найден кластер биосинтеза сурфактина, состоящий из трех генов (*srfAA, srfAB, srfAC*). Для оценки вклада найденных генов в индукцию ISR растений, планируется провести редактирование геномов исследуемых штаммов, путем удаления найденных генов с помощью системы CRISPR/Cas9.

Исследование выполнено за счет средств гранта РНФ №22-16-00138 на исследовательской базе Программы стратегического академического лидерства Казанского федерального университета (ПРИОРИТЕТ-2030).



The use of a genome substituted form of Avrodes to expand the genetic diversity of common wheat

Davoyan R.O., Bebykina I.V., Davoyan E.R., Zubanova Y.S., Boldakov D.M., Zinchenco A.N., Salina E.A.*, Badaeva E.D., Adonina I.G.***

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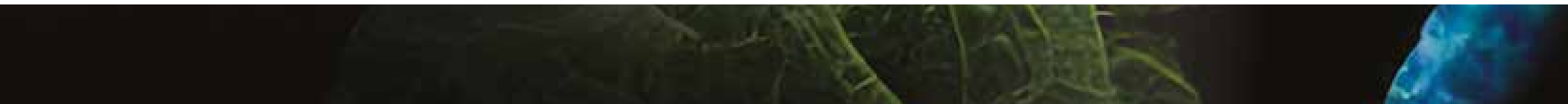
The synthetic form of Avrodes (BBAASS) and secondary synthetic recombinant forms (RS- forms) was used to obtain of the lines with resistance to diseases. Using the C-banding and FISH methods 50 lines have been studied to date. Rearrangements mainly affected the chromosomes of the D genome. In four lines obtained using RS-forms the transfer of genetic material from two species simultaneously was established. Translocations of T2DS.2DL-2UL from Ae. umbellulata, translocation T7SS.7SL-7DL, T5BS.5BL-5SL and substitution 1S(1B) from Ae. speltoides has been determined in line 4626. Line 3379 has translocation T7DL.7DS-7US from Ae. umbellulata, translocations T1DS.1DL-1SL, T2DS.2DL-2SL, T5BS.5BL-5SL and the substitution of 4S(4D) from Ae. speltoides. Translocations of T5BS.5SL from Ae. speltoides and T5DL.5DS-5US from Ae. umbellulata were detected in line 4938 p-17. Substituted chromosomes 6D(6Dt) from Ae. tauschii and 7D(7S) from Ae. speltoides were found in the 5791n17 line. The resulting translocations and chromosome substitution are new. Translocations on chromosomes 2A, 1D, 2D, 3D and 5D obtained from Ae. speltoides also belong to the new ones.

The main publications of authors on the subject of the abstract:

Давоян, Р.О. и др. Создание и изучение интрогрессивных линий мягкой пшеницы, полученных на основе синтетической формы RS7 // Вавиловский журнал генетики и селекции. 2019. Т. 23. № 7. С. 827-835.

Давоян, Р.О. и др. Использование синтетической формы RS5 для получения новых интрогрессивных линий мягкой пшеницы // Вавиловский журнал генетики и селекции. 2021. Т. 25. № 7. С. 770-777.



The study of an introgressive common wheat line with the T3DS.3DL-3SL translocation from Ae. speltoides

Davoyan E.R., Boldakov D.M., Zubanova Y.S., Basov V.I., Kresamova A.A., Zinchenco A.N., Davoyan R.O., Davoyan R.O., Adonina I.G.*

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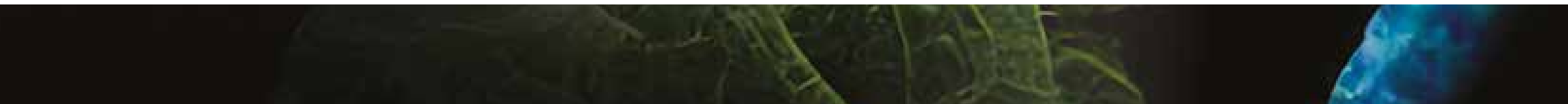
A selection and genetic study of the introgressive line of common wheat 4567RD obtained using a synthetic genome-substituted form Avrodes (BBAASS) was carried out. Using the method of fluorescent *in situ* hybridization (FISH), the wheat-rye translocation 1RS.1BL was identified in the line, as well as the previously unstudied translocation T3DS.3DL-3SL from *Aegilops speltoides* Tausch. Presence of 1RS.1BL confirmed by molecular methods using the SMC9 DNA- marker. Along with this, the line consist markers Lrk10 and S30-13L/AGA7-759R linked to leaf rust resistance genes *Lr10* and *Lr51* respectively. The leaf rust resistance level ranged from 1 (resistant) to 2 (moderately resistant) over the years. The line differed from the recipient cultivars in the spindle shape of the spike and had significant differences in such characteristics as the length of the spike and the number of spikelets in the spike. The yield components were at the level of the values obtained for the high yielding variety Krasnodarskaya 99. The line has high protein and gluten content of 15.9% and 32.4%, respectively. The score of bread maiking cvoliti was 4.5 points.

The main publications of authors on the subject of the abstract:

Давоян, Э.Р. и др. Изучение интрогрессивных линий мягкой пшеницы с генетическим материалом Aegilops tauschii по устойчивости к листовой ржавчине // Вавиловский журнал генетики и селекции. 2018. Т. 22. № 1. С. 97-101.

Davoyan, E.R. et al. Allelic variants for Waxy genes in common wheat lines bred at the Lukyanenko national grain center // Vavilov Journal of Genetics and Breeding. 2019. T. 23. № 7. C. 910-915.



Mechanism and genetic origin of stress-induced electrolyte leakage from plant cells

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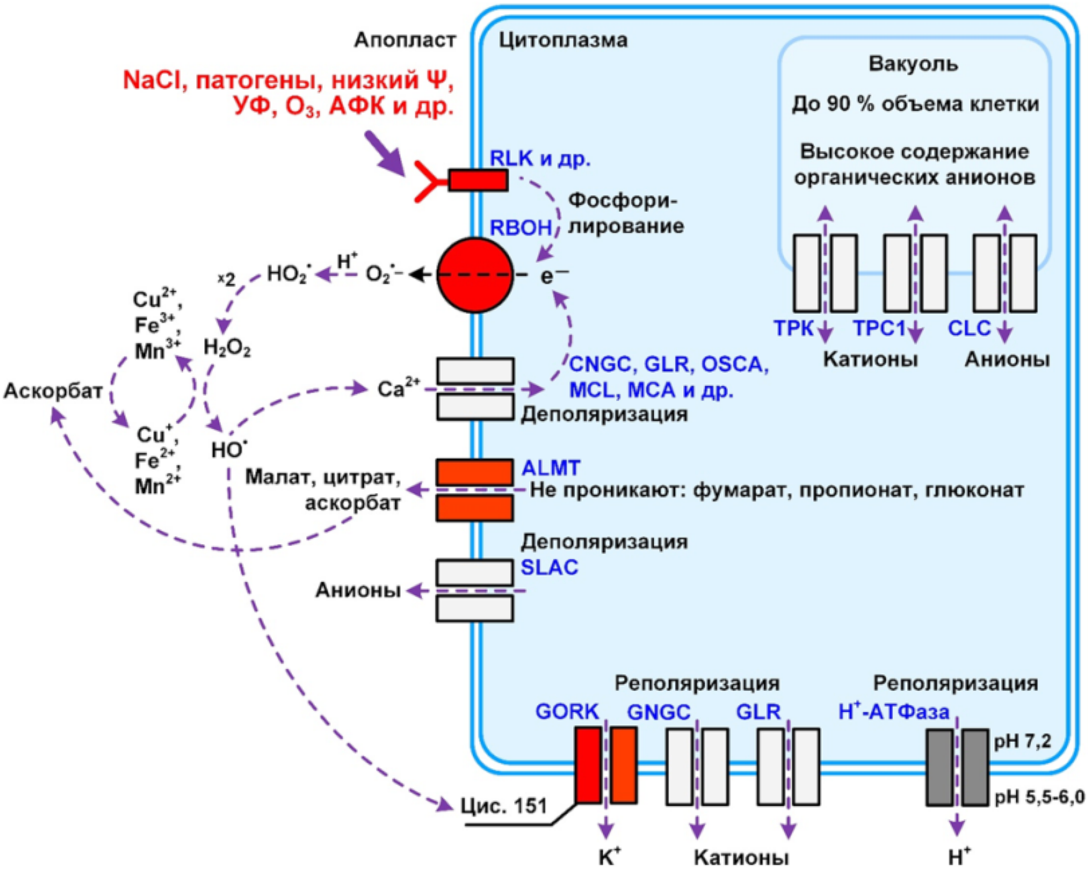
Electrolyte leakage is a marker of plant stress, such as salinity, pathogen attack, drought and extreme temperatures. Together with elevation of cytosolic $Ca^{2+}$and accumulation of ROS, this reaction is the earliest stress response of the plant. Recent research shows that electrolyte leakage induced by non-lethal stressesis related tothe ion-channel-mediated processes rather than non-specific permeabilization of the cell membrane. This study presents evidence that root cell electrolyte leakage is associated with activation of K^+ channels encoded by Gork gene and anionic channels encoded by Almt1 gene. Using reverse genetic approach and electrophysiology, we show a molecular mechanism of GORK opening,in the presence of ROS. We also report for the first time the properties of root ALMT1 channel, demonstrating that this channel is well permeable to malate, citrate and ascorbate, but poorly permeable to propionate, gluconate and fumarate. ALMT1 also revealed low permeability to chloride, suggesting that plant stress-responsive electrolyte leakage machinery mainly relies on organic anions. Overall, our study sheds the light onto the origin of the fundamental stress reaction in plants.



Новые тесты RT-PCR для идентификации *Pseudomonas fuscovaginae*

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Ключевые слова: *Pseudomonas fuscovaginae,* ПЦР в реальном времени, разработка молекулярно-генетических методов диагностики.

Актуальность: Возбудитель бурой гнили листовой оболочки пшеницы *Pseudomonas fuscovaginae* представляет серьезную опасность злаковым культурам. Бактериоз регулируется требованиями импортеров отечественной пшеницы – Египта и Пакистана. Для анализа распространенности фитопатогена необходима его идентификация. Одним из методов является ПЦР в реальном времени. Целью исследования было определение специфичного участка генома *Pseudomonas fuscovaginae* и подбор системы праймеров и зонда для ПЦР.

Основные методические подходы: сравнивали специфичность мишеней генома *Pseudomonas fuscovaginae* при использовании праймеров F3/B3, PfF3/PfR3 и Pfs207-F/Pfs207-R. Последовательности ПЦР-мишеней сравнивали с последовательностями, размещёнными в GenBank. На специфичную мишень подбирали праймеры и зонды.

Результаты исследования: На участке генома типового штамма бактерии LMG 2158 (chrom I) были подобраны оригинальные праймеры Pfs207-F/Pfs207-R и зонды Pfs207-P1, Pfs207-P2, которые могут использоваться для детекции *Pseudomonas fuscovaginae* методом ПЦР в реальном времени.

Take-home message:
ПЦР в реальном времени является эффективным методом для иденнтификации Pseudomonas fuscovaginae. Нами были подобраны оригинальные праймеры (Pfs207-F, Pfs207-R) и зонды (Pfs207-P1 Pfs207-P2) для детекции *Pseudomonas fuscovaginae* методом ПЦР.

Разработка ПЦР-теста в режиме «реального времени» для идентификации *Pseudomonas fuscovaginae*

ПЦР в реальном времени является эффективным методом для иденнтификации *Pseudomonas fuscovaginae*. Нами были подобраны оригинальные праймеры (Pfs207-F, Pfs207-R) и зонды (Pfs207-P1 Pfs207-P2) для детекции *Pseudomonas fuscovaginae* методом ПЦР.

Возбудитель бурой гнили листовой оболочки пшеницы *Pseudomonas fuscovaginae* представляет серьезную опасность злаковым культурам. Бактериоз регулируется требованиями импортеров отечественной пшеницы – Египта и Пакистана. Для анализа распространенности фитопатогена необходима его идентификация. Одним из методов является ПЦР в реальном времени. Целью исследования было определение специфичного участка генома *Pseudomonas fuscovaginae* и подбор системы праймеров и зонда для ПЦР.

В работе сравнивали специфичность мишеней генома *Pseudomonas fuscovaginae*, обнаруживаемых с помощью пар праймеров F3_B3, PfF3_PfR3 и Pfs207-F_ Pfs207-R. Нуклеотидные последовательности ПЦР-мишеней сравнивали с последовательностями, размещёнными в GenBank с помощью BLAST. Наиболее специфичную мишень использовали для подбора праймеров и зондов. Апробацию ПЦР-РВ проводили с ДНК целевой бактерии.

Мишени обнаруживаемые с помощью пар праймеров:
1. F3_B3
2. PfF3_PfR3
3. Pfs207-F_ Pfs207-R

На участке генома типового штамма бактерии Pseudomonas fuscovaginae strain LMG 2158 chromosome I были подобраны оригинальные праймеры (Pfs207 F, Pfs207 R) и зонды (Pfs207 P1 Pfs207-P2). Праймеры и соответствующие зонды могут быть использованы для детекции *Pseudomonas fuscovaginae* методом ПЦР в реальном времени в зерновой продукции и растительном материале.

Pseudomonas fuscovaginae strain LMG 2158 chromosome I

Праймеры Pfs207-F_ Pfs207-R

Зонды Pfs207-P1 Pfs207-P2

Десятерик А.А., Бондаренко Г.Н., Словарева О.Ю.

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Development of a plasmid for CRISPR/Cas9 editing of phytocyanin gene in *Marchantia polymorpha*

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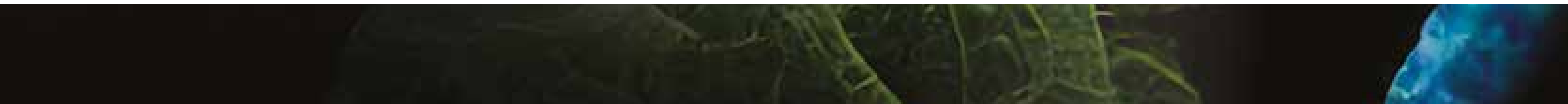
Phytocyanin (PC) gene family are plant-specific blue copper proteins which function as electron transporters but also are involved in processes which explicitly characterize multicellular organization: cell differentiation, plant reproductive structures formation, and somatic embryogenesis. However, the evolution of regulatory pathways in which PCs could be involved are not deeply studied yet. Liverworts, including well known *Marchantia polymorpha*, are a great model systems for evolutionary and molecular genetics. The long term aim of this study was to analyze the role of PCs in the development of *M. polymorpha*. We developed the binary plasmid for PC gene (Mapoly0037s0115) mutation via CRISPR/Cas9 genome editing method. gRNA coding sequences were inserted into the pMpGE_En03 vector under the control of MpU6 promoter. The MpU6:gRNA sequence were subcloned into the binary vector pMpGE011 for the transformation of plants. The following development of knockout plants will allow us to find out the role of PCs in developmental processes in multicellular plants. This work was supported by the President Scholarship PS-3391.2021.4 under the PRIORITY-2030 Program of Kazan Federal University.

Take-home message:

Previous studies have indicated that phytocyanins are involved in cell differentiation and reorganization. The aim of this study was to generate the plasmid for a phytocyanin CRISPR/Cas9 mediated muation for the further plant transformation.



Practical experience in acceleration of plant development under controlled growing conditions

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Speed breeding, a combination of genetic technology and controlled growing conditions (temperature, light, humidity, gas environment composition), allows scientists to accelerate the shift of developmental stages of plants (ontogenesis) and produce several generations per year. The technology is increasingly in demand in plant science not only as an applied breeding tool, but also as an accelerated way to develop recombinant inbred lines, pre-breeding, hybridological analysis and other research. We engineered the unique speed-breeding facility FSD-1 which provides controlled lighting (including far-red), duration of dark and light period, humidity, CO_2 level and other parameters, being equipped with sensor systems and remote access. Preliminary pilot studies on spring wheat, spring triticale, soybean, maize, and sunflower were carried out using FSD-1. Positive results were obtained for all tested crops, except for maize, which makes the use of FSD-1 promising for the implementation of scientific and applied projects in the field of speed breeding. The work was supported by the Ministry of Education and Science of Russia (Government Assignment FGUM-2022-0008).

The main publications of authors on the subject of the abstract:

Miroshnichenko, D. et al., CRISPR/Cas9-induced modification of the conservative promoter region of VRN-A1 alters the heading time of hexaploid bread wheat//Frontiers in Plant Science , 2022, 13, 1048695

Biodiversity and ecology of fungi associated with wilt disease of alfalfa in the oases of Southern Tunisia

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*Project Center for Agro Technologies (Skoltech Agro), Skolkovo Institute of Science and Technology, Skolkovo, Russia,
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This study aims to identify the causal agents of alfalfa wilting disease in the oases of the south region of Tunisia, along with their ecology of infestation. Seventy nine fungal strains were isolated from roots, collars, and stems of alfalfa. The inoculation of the fungal strains on alfalfa cultivar El-Hamma, *Medicago truncatula* lines A17 and F83005.5 induced different reactions in plants depending on the inoculated *Medicago* species and accession. The majority of the strains did not affect plant growth (59-86 %), the second group enhanced plant growth (6-16 %), and the third group induced disease symptoms associated with a reduction of seedlings growth (8-24 %). The results showed that alfalfa wilting disease is caused by a complex of four *Fusarium* complexes, associated with secondary pathogens of *Alternaria, Rhizoctonia*, and *Aaosphaeria species*. In addaition, the pathogenicity tests on date palm seedlings showed that *Rhizoctonia solani* and *Fusarium acutatum* species reduced the growth of plants, with this later species reported for the first time infecting date palm seedlings, suggesting that alfalfa constitute an alternate host for these pathogens.

Take-home message:

Alfalfa wilting disease is caused mainly by four *Fusarium* complexes i.e. *F. oxysporum, F. solani, F. Fujikuroi,* and *F. incarnatum-equiseti.* Alfalfa constitute an alternate host for some root pathogens of date palm in the Tunisian oases.

Shiny R Application for Distributed Gene Regulatory Network computing: ACase Study in Grapevine

Dolgaleva D.S., Pelagalli C.*, Pilati S., Blanzieri E.***, Cavecchia V.****, Astafiev S.N., Rumyantsev A.S.**

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The ever increasing availability of transcriptomic data and analytical software for data mining allowed the development of in-silico gene regulatory network (GRN) studies. These models can effectively support the biologist in gene function discovery, metabolic pathway regulation and the molecular description of physiological events. GRN computation based on causal relationship discovery (CRD) allows to produce a directed graph of GRN starting from a set of genes, identified as the most associated ones. A big limitation of this approach is the computational power required. A parallel CRD resource available to wide number of researchers is Distributed Computing (DC).

In this talk we briefly review the software and methods of in-silico CRD. We present an approach to distributed CRD processing by means of Shiny web application, R package for the PC algorithm of CRD, RBOINC interface to BOINC-based DC system and virtualization. A case study of the CRD in grapevine (Vitis vinifera) is presented, based on the gene expansion lists from a genome-wide BOINC-based (TN-Grid platform https://gene.disi.unitn.it/test) CRD project called OneGenE (http://vitis.onegenexp.eu) and VESPUCCI projects.

The research described in this publication was made possible in part by R&D Support Program for undergraduate and graduate students and postdoctoral researcher of PetrSU, funded by the Government of the Republic of Karelia.

<u>The main publications of authors on the subject of the abstract:</u>

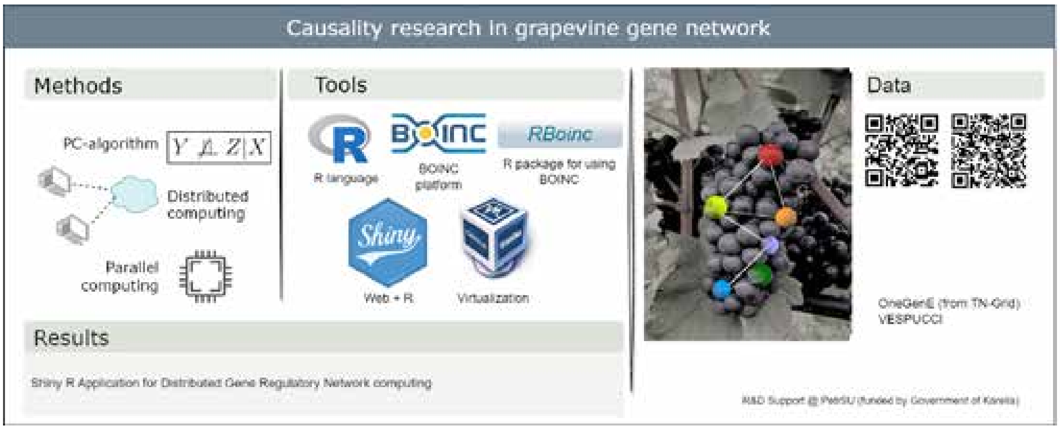
Dolgaleva D. et al. Distributed Computing for Gene Network Expansion in R Environment. 2022 DOI: 10.1007/978-3-031-22941-1_47

Pilati S. et al. Vitis OneGenE: A Causality-Based Approach to Generate Gene Networks in Vitis vinifera Sheds Light on the Laccase and Dirigent Gene Families. 2021 DOI: 10.3390/biom11121744

Blanzieri E. et al. A Computing System for Discovering Causal Relationships Among Human Genes to Improve Drug Repositioning. 2021 DOI: 10.1109/TETC.2020.3031024

<u>Take-home message:</u>

Gene Regulatory Network computation based on Causal Relationship discovery can be performed in parallel using Distributed Computing. Our solution: Shiny + R + PC + RBOINC + BOINC + VirtualBox. Case: grapevine. Data: OneGenE (from TN-Grid) + VESPUCCI.



The Role of the BELL1-2 transcription factor in the control of nitrogen-fixing nodule development in legumes

Dolgikh A.V., Dymo A.M., Kantsurova E.S., Dolgikh E.A.

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Single three-amino acid loop extension (TALE) homeodomain proteins regulate different developmental processes. In plants this group of proteins includes the KNOTTED-like (KNOX) and BEL-like (BELL) families. Whereas the role of KNOX transcription factors in the control of symbiosis was studied early, BELL transcription factors have received less attention. We found out that among all BELL genes, *BELL1-2* gene is the most significantly upregulated in the inoculated roots and nodules of such legume plants as *Medicago truncatula G.* and *Pisum sativum L.* We detected the ability of the PsBELL1-2 transcription factor to form complex with PsKNOX9. In addition, we showed that PsBELL1-2 can interact with the PsDELLA1 (LA) protein-regulator of the gibberellin pathway, which has a previously demonstrated important role in symbiosis development. Looking for possible target of BELL1-2 we found that expression of GA20ox and *IPT1* can be possibly regulated by this transcription factor.Taken together, these data indicate the important role of *BELL1-2* in the control of the symbiotic nodule formation.

This work was supported by grant RSF 22-26-00279

The main publications of authors on the subject of the abstract:

Dolgikh A.V. et al. Identification of BELL Transcription Factors Involved in Nodule Initiation and Development in the Legumes Pisum sativum and Medicago truncatula // Plants (2020) vol. 9,12 1808. doi:10.3390/plants9121808

Take-home message:

BELL1-2 can possibly influence of gibberellic acid metabolism through interaction with DELLA1 or through regulation of GA20ox expression.

BELL1-2 can influence on expression of genes associated with cytokinin metabolism.

Regulation of the immune response in legume-rhizobial symbiosis development

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Recent studies of the effect of nodule bacteria signal molecules, the Nod factors, revealed their ability to suppress the immune response in a wide range of plants. However, the receptors and regulators of this process in legume plants still remain unknown. It has been suggested that the suppression of immune response by Nod factors may be related to their effect on stability of the pattern-recognizing receptors (PRR) and activity of main regulators of signal pathways, the mitogen-activated protein kinases (MAP kinases). Using transcriptomic approach, the several candidates for the role of PRR and MAP kinases' stability regulators such as E3–ubiquitin ligase and two phosphatases were identified. It is known that the AtLYK3 receptor is involved in the recognition of Nod factors and immunity suppression in Arabidopsis, so its closest homologues in legumes were searched. As a result, a new LysM-containing receptor was identified as well as its effect on immunity suppression during symbiosis development in Pisum sativum and Medicago truncatula composite plants was investigated.

The work was supported by a grant from RSF (grant 21-16-00106).

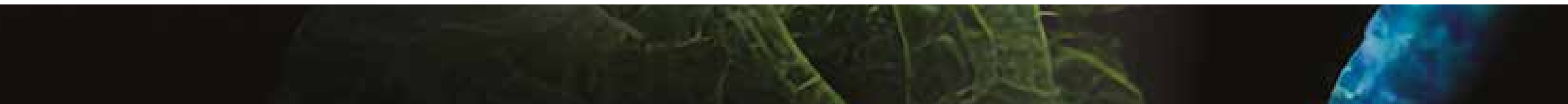
The main publications of authors on the subject of the abstract:

Kozyulina P.Y., Pavlova O.A., Kantsurova (Rudaya) E.S., Bovin A.D., Shirobokova S.A., Dolgikh A.V., Dymo A.M., Dolgikh E.A. Transcriptomic analysis of pea plant responses to chitooligosaccharides' treatment revealed stimulation of mitogen-activated protein kinase cascade // Front Plant Sci. (2023) 14: 1092013. doi: 10.3389/fpls.2023.1092013.

Take-home message:

Using transcriptomic approach, the several candidates for the role of PRR and MAP kinases' stability regulators were identified.

A new LysM-containing receptor involved in immunity suppression was found.



Identification of functional transcription factor binding motifs in the *Arabidopsis thaliana* ChIP-seq data

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Transcription factors (TFs) regulate the expression of target genes by binding to cis-regulatory elements (CREs) in their promoters. Such regulation is controlled by several types of mechanisms, including (I) physical interactions between TF and DNA and oligo-/multimerization of TFs. For correct binding of TF complexes with DNA, gene promoters contain complex CREs. Thus, promoters contain cis-regulatory modules (CREs) of two or more CREs. In addition, one TF can bind several alternative CREs. The intricate structure of CRMs makes it difficult to systematic experimental research. Bioinformatics integration of ChIP-seq data (that represents the CRE of the TF under study and its partners) with RNA-seq data (reflecting the transcriptional response of potential TF targets) can facilitate such researches. In this work, we have developed a pipeline SFMotif for identifying functional CREs and CRMs based on the integration of ChIP-seq and RNA-seq data. We used genome-wide ChIP-seq data on binding the key phytohormone ethylene TF EIN3, and the ethylene-induced transcriptome data, to assess the functionality of the pipeline.

This work was supported by the RSF grant no. 20-14-00140

<u>The main publications of authors on the subject of the abstract:</u>

Dolgikh VA, Wiebe DS, Levitsky VG, Zemlyanskaya EV Integration of ChIP-seq and RNA-seq data in structure-function analysis of cis-regulatory elements // Bioinformatics of Genome Regulation and Structure/Systems Biology (BGRS/SB-2022) Abstracts – Novosibirsk: ICG SB RAS, 2022. – 599 p DOI 10.18699/BGRS/SB-2022-000.

<u>Take-home message:</u>

Our pipeline SFMotif is able to determine the major transcription factor binding motif, its alternative structural variants, binding motifs of potential partner transcription factors, and functional cis-regulatory modules between them.

Effect of Gene Silencing of Translation Initiation Factors eIF(iso)4G and eIF(iso)4E on Sour Cherry Rootstock Resistance to Sharka Disease

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Sharka disease, caused by the Plum pox virus (PPV), is one of the most harmful viral diseases that affect stone fruit crops. The absence of natural resistance to the virus in stone fruits has become a decisive factor for the use of genetic transformation methods to obtain stable forms. The eIF(iso)4G and eIF(iso)4E genes encode translation initiation factors used in the PPV life cycle. In the presented study, the effect of silencing these genes using the RNA interference method on the resistance of sour cherry rootstock 146-2 plants (Prunus pumila L. x Prunus tomentosa Thunb) to the sharka disease was studied. The silencing of the eIF(iso)4G and eIF(iso)4E genes in transgenic plants was confirmed by the quantitative PCR. The presence of specific small interfering siRNAs was confirmed by the method of Northern blotting.. The ELISA results showed that silencing the eIF(iso)4G gene did not lead to increased resistance while silencing the eIF(iso)4E factor gene led to increased resistance to the PPV. The work demonstrates a approach in which the creation of stone cultures resistant to the plum pox virus can be achieved by suppressing the genes of translation initiation factors.

The main publications of authors on the subject of the abstract:

Mourenets, L.; Pushin, A.; Timerbaev, V.; Khmelnitskaya, T.; Gribkov, E.; Andreev, N.; Dolgov, S. Effect of Gene Silencing of Translation Initiation Factors eIF(iso)4G and eIF(iso)4E on Sour Cherry Rootstock Resistance to Sharka Disease // Int. J. Mol. Sci. 2023, 24, 360. https://doi.org/10.3390/ijms24010360

Evolution of leaf development in land plants: a bioinformatic approach

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Origin of specific photosynthetic organs - leaves, that greatly influenced the ecology of Earth is enigmatic. Leaves of angiosperms develop via specific meristems. Transcriptional polarization of adaxial (ARP, C3HDZ) and abaxial (YABBY, KANADI) determinants is prerequisite for the origin of marginal and plate meristems that are in turn regulated by the members of T3 clade of WOX TFs. To address regulation of leaf development in evolutionary context we have searched the homologs of abovementioned TFs in the available genomes and transcriptomes of bryophytes, lycophytes and ferns. We have revealed that two adaxial and two abaxial determinants are present in bryophytes; ARP was likely lost in Lycopodiales and YABBY in Selaginellales; both ARP and YABBY were likely lost in ferns. T3 clade of WOX TFs has independently originated in Polypodiopsida and seed plants. Incorporation of anatomical data into molecular context suggests that ARP, C3HDZ, YABBY and KANADI likely do not act as polarity genes in lycophytes and supports independent origin of marginal meristem in Polypodiopsida and spermatophytes.

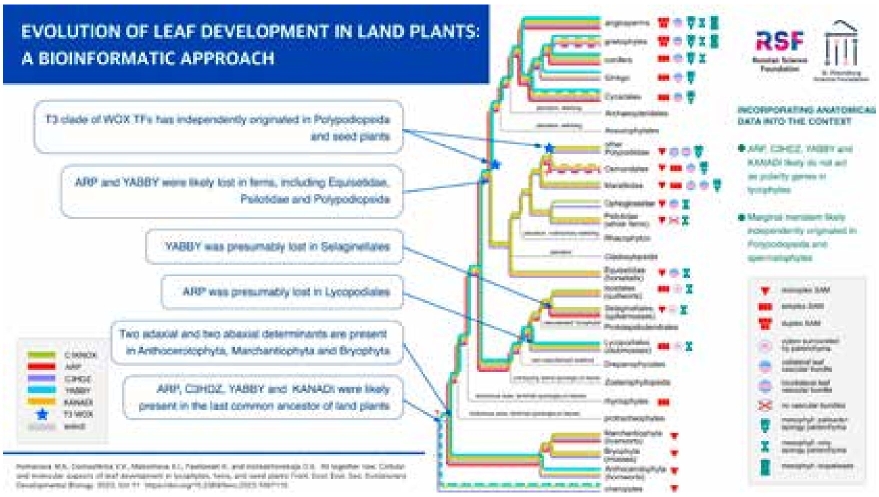
Research is supported by RSF, project 22-24-20049 and St-Petersburg Science Foundation.

The main publications of authors on the subject of the abstract:

Romanova M.A., Domashkina V.V., Maksimova A.I., Pawlowski K. and Voitsekhovskaja O.V. All together now: Cellular and molecular aspects of leaf development in lycophytes, ferns, and seed plants Front. Ecol. Evol. Sec. Evolutionary Developmental Biology. 2023, Vol 11 https://doi.org/10.3389/fevo.2023.1097115

Take-home message:

The leaf development toolkit composed of ARP, C3HDZ, YABBY and KANADI transcription factors was already present in the common ancestor of land plants; different components of this toolkit were lost in Lycododiales, Selaginellales and Polypodiophyta.



EVOLUTION OF LEAF DEVELOPMENT IN LAND PLANTS: A BIOINFORMATIC APPROACH

T3 clade of WOX TFs has independently originated in Polypodiopsida and seed plants

ARP and YABBY were likely lost in ferns, including Equisetidae, Psilotidae and Polypodiopsida

YABBY was presumably lost in Selaginellales

ARP was presumably lost in Lycopodiales

Two adaxial and two abaxial determinants are present in Anthocerotophyta, Marchantiophyta and Bryophyta

ARP, C3HDZ, YABBY and KANADI were likely present in the last common ancestor of land plants

INCORPORATING ANATOMICAL DATA INTO THE CONTEXT

- ARP, C3HDZ, YABBY and KANADI likely do not act as polarity genes in lycophytes
- Marginal meristem likely independently originated in Polypodiopsida and spermatophytes

Analysis of some Asteráceae plants microbial activity towards brown rot of potato pathogen

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На сегодняшний день в мире есть потребность в сохранении урожаев, на которые негативно влияют фитопатогенные организмы, постоянно приспосабливающиеся к уже использующимся в практике препаратам. Разработка технологии получения природного антибактериального препарата может помочь профилактике и уничтожению очагов болезней сельскохозяйственных культур.

Было показано, что соединения ряда тиофенов, вырабатываемые растениями семейства Астровые, угнетающе действуют на возбудителя карантинного бактериоза бурой бактериальной гнили *Ralstonia solanacearum*.

В моем исследовании сравнивается действие экстрактов из различных растений семейства Астровые на чистую культуру *R. solanacearum* в условиях *in vivo* с помощью метода посева пуассонером на плотную среду и метода дисков с дальнейшим анализом зоны подавления роста. Разрабатывается метод наиболее эффективной экстракции тиофенов из надземных и подземных частей растений.

Ожидается, что экстракт корней Мордовника шароголового *Echinops sphaerocephalus* будет обладать наиболее сильной антибиотической активностью, исходя из литературных данных по содержанию в нем тиофенов, хотя впервые такую активность заметили на растениях бархатцев.

DNA-technologies in rice and vegetable crops breeding

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Sustainable growth of competitive agricultural products is possible due to the acceleration of the breeding process. In this regard, biotechnological approaches are becoming relevant. In the laboratory of the IDB of the FNC of Rice, work is underway to create rice varieties resistant to pyriculariosis using MAS. Together with the breeders of the center and the ANC "Donskoy", a number of varieties with Pi genes have been created that ensure the resistance of rice to pyriculariosis. Scientific research is underway to develop and implement marker systems that provide control of target genes and their allelic state in the hybrid material of rice and vegetable crops. Marker systems for the identification of Sub genes for rice responsible for tolerance to prolonged flooding and SSR for the Waxy gene responsible for the nutritional and technological qualities of cooked rice are identified. A methodology has been developed for evaluating white cabbage for resistance to vascular bacteriosis and fusarium on the basis of DNA labeling. Scientific work has been carried out on the identification of genes for resistance to TMV, fusarium, late blight, tomato alternariasis using marker systems.

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Dubina E.V. et al. The study of polymorphism of SSR loci of resistance to Xanthomonas campestris pv. campestris in white cabbage.-Rice growing.-2021-No.3(52).-P.43-48

Dubina E.V. et al. The use of SSR-markers in rice breeding for resistance to blast and submergence tolerance. Agronomy Research.–2022.-vol.20.№3.-P.531–548

Take-home message:

A search was made for DNA-markers for identifying genes of resistance to diseases of tomatoes, white cabbage; genes of resistance to blast and tolerance to prolonged flooding on rice.

Simultaneous application of five exogenous dsRNAs for the regulation of anthocyanin metabolism-related genes and anthocyanin biosynthesis *in Arabidopsis thaliana*

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Exogenous application of double-stranded RNAs (dsRNAs) to plant surfaces has emerged as a promising tool for gene silencing in plants. However, regulation of plant endogenous

genes via external dsRNA treatments has not been sufficiently investigated. In this study, we targeted 5 genes in Arabidopsis thaliana, including 3 transcription factor (*AtCPC, AtMybL2, AtANAC032*), a calmodulin-binding protein (*AtCBP60g*), and an anthocyanidin reductase (*AtANR*) genes, which are all known as negative regulators of anthocyanin accumulation. dsRNAs encoding these 5 genes were exogenously applied both separately and simultaneusly to the foliar surface of A. thaliana. Expression of the target genes was analyzed by qRT-PCR, and anthocyanin levels were monitored by HPLC-MS. All exogenous dsRNAs considerably downregulated the 5 genes and induced anthocyanin accumulation. Simultaneous application of the dsRNAs activated the accumulation of anthocyanins more efficiently than any one of these dsRNAs separately. The data are important for plant biotechnology and gene functional studies. This work was supported by a grant 23-26-00253 of the Russian Science Foundation.

The main publications of authors on the subject of the abstract:

Kiselev, K.V.; Suprun, A.R.; Aleynova, O.A.; Ogneva, Z.V.; Kalachev, A.V.; Dubrovina, A.S. External dsRNA downregulates anthocyanin biosynthesis-related genes and affects anthocyanin accumulation in Arabidopsis thaliana // Int. J. Mol. Sci. (2021) 22: 6749.

Nityagovsky, N.N.; Kiselev, K.V.; Suprun, A.R.; Dubrovina, A.S. Exogenous dsRNA induces RNA interference of a chalcone synthase gene in Arabidopsis thaliana // Int. J. Mol. Sci. (2022) 23: 5325

Take-home message:

The gene-specific exogenous dsRNAs considerably downregulated 5 target genes and induced anthocyanin accumulation in Arabidopsis both separately and simulaneously. Simultaneus application was more efficient.

Study of spring triticale glutenin genes

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Today, the main efforts of triticale breeders are aimed at obtaining varieties with flour quality indicators close to wheat. In particular, special importance is attached to the study of high-molecular glutenins, which are important in the field of bakery production due to their influence on the elasticity of bread.

We conducted a screening of the spring triticale collection to study the diversity of the collection for high-molecular-weight gluten. Approaches have been developed for sequencing variable regions of glutenin genes in order to identify allelic variants of Glu Bx. Thanks to this, we were able to distinguish alleles that have an important baking value, namely: BX7, Bx14, Bx7. When studying the structure of genes, we revealed a high level of polymorphism in the promoter region of this gene.

We conducted a study of the triticale collection on the genetic diversity of the promoter region of the Glu Bx1 gene, among which four screening variants were found, which we designated: L, M, MS, S.

Thus, the study of allelic variants and the relationship of the promoter region of the Glu Bx1 gene will allow us to identify and evaluate their relationship with the baking qualities of triticale.

Funding: This research was funded by the Ministry of Education and Science of Russian Federation (Goszadanie No. FGUM-2022-0005)

The main publications of authors on the subject of the abstract:

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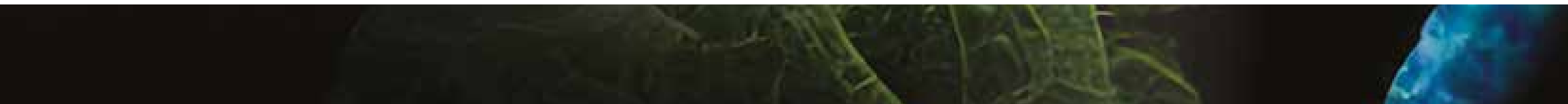

SAD and FAD genes expression in seeds of *Linum usitatissimum* L.

Dvorianinova E.M., Pushkova E.N., Rozhmina T.A.*, Povkhova L.V., Novakovskiy R.O., Dmitriev A.A., Melnikova N.V.

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*Federal Research Center for Bast Fiber Crops, Torzhok, Russia
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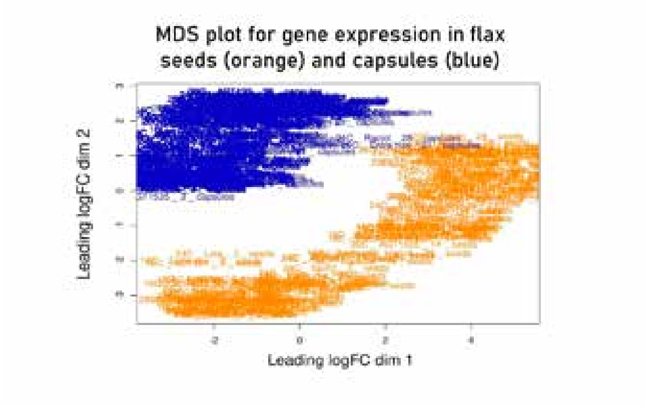
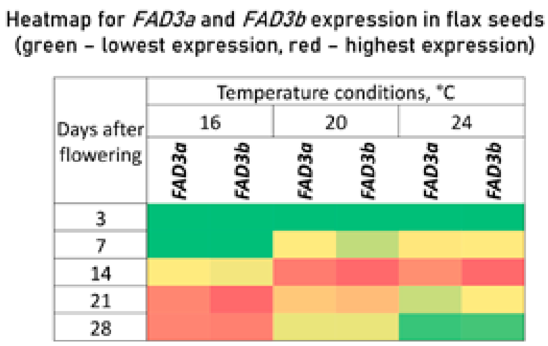
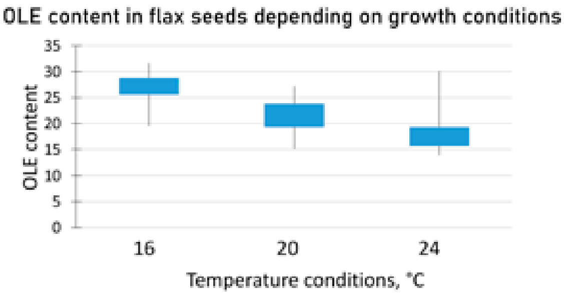
Linseed (*Linum usitatissimum* L.) is a source of valuable oil. Fatty acid synthesis in flax seeds is regulated by the SAD and FAD genes. At five time points after flowering, seeds were collected from typical representatives of nine varieties planted under different conditions of temperature (16, 20, 24°C) and irrigation (abundant, normal, poor). On sequencing, 8 million Illumina reads per sample were obtained on average. We established expression profiles of *SAD2-1, SAD2-2, SAD3-1, SAD3-2, FAD2a-1, FAD2a-2, FAD2b-1, FAD2b-2, FAD2c-1, FAD2c-2, FAD2d-1, FAD2d-2, FAD2e-1, FAD2e-2, FAD2f-1, FAD2f-2, FAD2g-1, FAD2g-2, FAD2h, FAD3a, FAD3b, FAD3c-1, FAD3c-2, FAD3d-1*, and *FAD3d-2* genes. The *SAD3-1* gene had increased expression compared to the other *SAD* genes. Among the *FAD2* genes, *FAD2b-2* had the highest expression. Expression of *FAD3a* and *FAD3b* was the greatest of the *FAD3* genes. The analysed genes with the highest expression within each group might have the greatest impact on the synthesis of oleic, linoleic, and linolenic acids in flax seeds. Our data contribute to understanding processes regulating the conversion of linseed oil fatty acids. The work was funded by RSF, grant 21-16-00111.







Regulation of the immune response during development of the legume-rhizobial symbiosis

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All-Russia Research Institute for Agricultural Microbiology, Saint-Petersburg, Russia
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Recent studies of the influence of nodule bacteria signal molecules, the Nod factors, revealed their ability to suppress the immune response in a wide range of plants. However, the receptors and regulators of this process in legume plants still remain unknown. It has been suggested that the suppression of immune response by Nod factors may be related to their effect on stability of the pattern-recognizing receptors (PRR) and activity of main regulators of signal pathways, the mitogen-activated protein kinases (MAP kinases). Using transcriptomic approach, the several candidates for the role of PRR and MAP kinases' stability regulators such as E3–ubiquitin ligase and two phosphatases were identified. It is known that the AtLYK3 receptor is involved in the recognition of Nod factors and immunity suppression in Arabidopsis, so its closest homologues in legumes were searched. As a result, a new LysM-containing receptor was identified as well as its effect on immunity suppression during symbiosis development in *Pisum sativum* and *Medicago truncatula* composite plants was investigated

The work was supported by RSF grant 21-16-00106

The main publications of authors on the subject of the abstract:

Kozyulina P.Y., Pavlova O.A., Kantsurova (Rudaya) E.S., Bovin A.D., Shirobokova S.A., Dolgikh A.V., Dymo A.M., Dolgikh E.A. Transcriptomic analysis of pea plant responses to chitooligosaccharides' treatment revealed stimulation of mitogen-activated protein kinase cascade // Front Plant Sci. 2023. V. 14: 1092013. doi: 10.3389/fpls.2023.1092013.

Take-home message:

1. The new receptor is a possible regulator involved in the control of the immune response in peas.
2. Possible targets of the action of Nod factors in peas have been identified - E2-ubiquitin-conjugating enzyme and two phosphatases.

Extracellular secondary metabolites of the moss *Ceratodon purpureus* as a source of new antibacterial compounds

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The uncontrolled increase in antibiotic resistance among pathogenic microorganisms is a major global health threat, required the search for new antibacterial compounds. Thereby, Bryophytes are of great interest due to their potential as a source of bioactive compounds with antibacterial, antifungal, antioxidant and anticancer activity. The goal of the current study was to analyze the moss *Ceratodon purpureus'* metabolites' antibacterial activity.

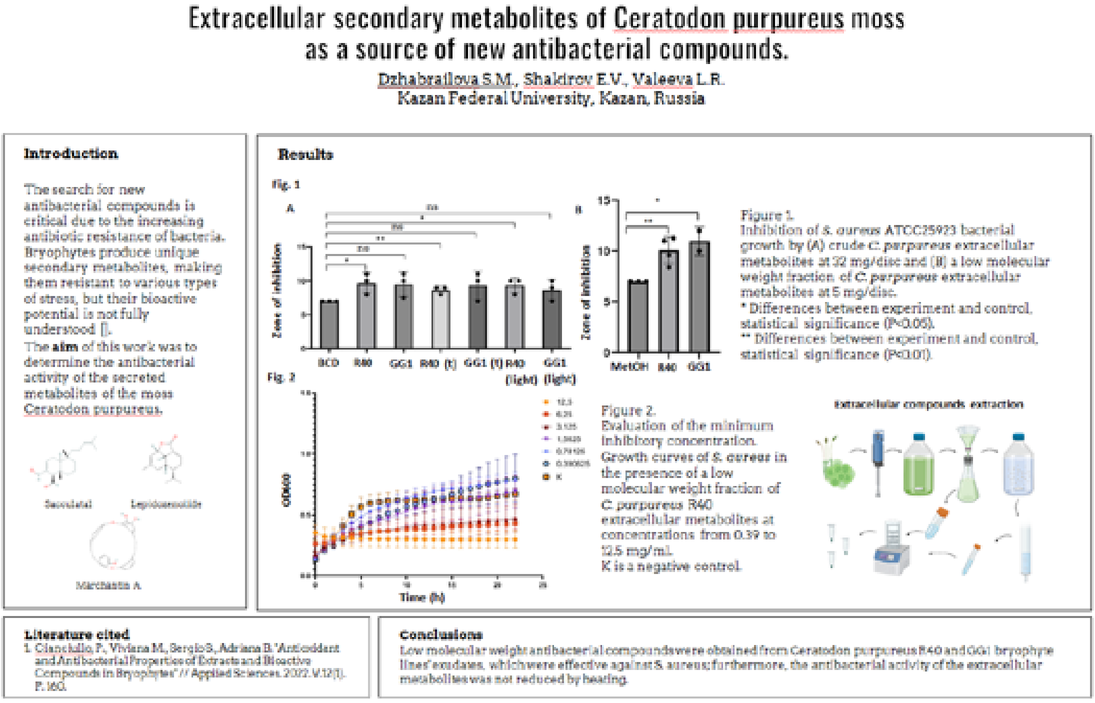
Low molecular weight metabolites from moss exudates was purified using ion-exchange resin. Metabolites of both C. *purpureus* lines, R40 and GG1, inhibited the growth of gram-positive *S. aureus* ATCC25923 at 5 mg dry matter/disc, while no antibacterial activity was observed against gram-negative *S. marcescens* SM6. The minimal inhibitory concentration for the R40 line's metabolites against *S. aureus* was 12.5 mg/ml.

Thus, we have found new moss-derived low molecular weight secreted compounds with antibacterial activity against Gram-positive bacteria *S. aureus.*

This work was supported by the President Scholarship PS-3391.2021.4 under the Strategic Academic Leadership Program of Kazan (Volga Region) Federal University (PRIORITY-2030).

Take-home message:

The antibacterial properties of extracellular metabolites secreted by a moss *C. purpureus* were studied. The inhibitory activity of purified low molecular weight metabolites against gram-positive *S. aureus was shown.*



Extracellular secondary metabolites of Ceratodon purpureus moss
as a source of new antibacterial compounds.
Dzhabrailova S.M., Shakirov E.V., Valeeva L.R.
Kazan Federal University, Kazan, Russia

Introduction

The search for new antibacterial compounds is critical due to the increasing antibiotic resistance of bacteria. Bryophytes produce unique secondary metabolites, making them resistant to various types of stress, but their bioactive potential is not fully understood [].
The **aim** of this work was to determine the antibacterial activity of the secreted metabolites of the moss Ceratodon purpureus.

Results

Figure 1.
Inhibition of *S. aureus* ATCC25923 bacterial growth by (A) crude *C. purpureus* extracellular metabolites at 32 mg/disc and (B) a low molecular weight fraction of *C. purpureus* extracellular metabolites at 5 mg/disc.
* Differences between experiment and control, statistical significance (P<0.05).
** Differences between experiment and control, statistical significance (P<0.01).

Figure 2.
Evaluation of the minimum inhibitory concentration.
Growth curves of *S. aureus* in the presence of a low molecular weight fraction of *C. purpureus* R40 extracellular metabolites at concentrations from 0.39 to 12.5 mg/ml.
K is a negative control.

Literature cited

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Conclusions

Low molecular weight antibacterial compoundswere obtained from Ceratodon purpureus R40 and GG1 bryophyte lines' exudates, which were effective against S. aureus; furthermore, the antibacterial activity of the extracellular metabolites was not reduced by heating.

Genetic diversity in *Amaranthaceae* species in stress-tolerance context

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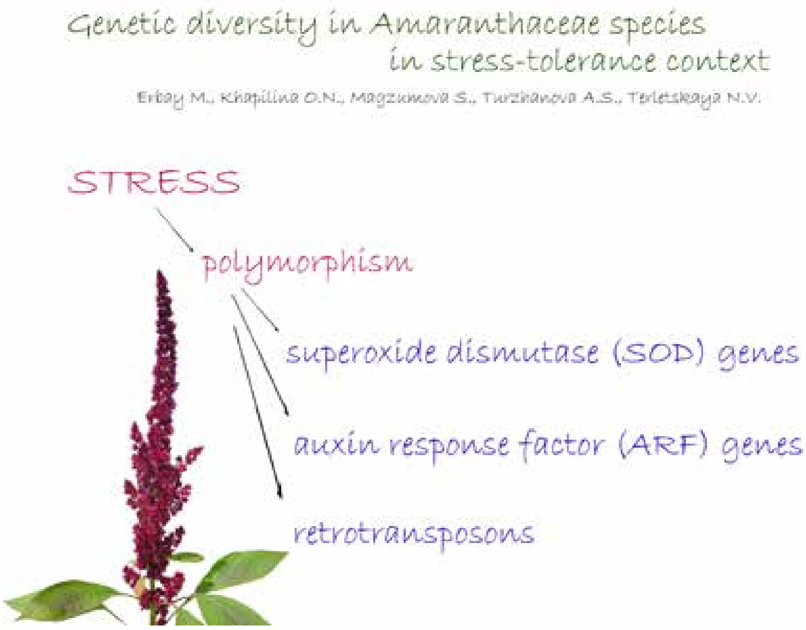
In the arid conditions the adaptive potential and biochemical properties of the Amaranthaceae sp. can contribute to their introduction into agricultural industry and promotion in the market. The analysis of molecular genetic polymorphism is one of the most significant tools for analyzing plant resources. Our work aimed to look at the polymorphisms of allelic variations of the auxin response factor (ARF) and superoxide dismutase (SOD) gene families, as well as the genetic diversity of six Amaranthaceae species, using the retrotransposons-based fingerprinting approach. We implemented the multi-locus exon-primed intron-crossing (EPIC-PCR) profiling approach we used to examine allelic variations in the ARF and SOD gene families. The inter-primer binding site (iPBS) PCR amplification technique was used for genome profiling, which demonstrated a differences in genetic diversity of the Amaranthaceae samples studied. It is shown that the genetic diversity of Amaranthaceae sp. is a factor in their increased tolerance to adverse environmental conditions. Further studies of gene flow in the context of abiotic factors may be useful in understanding the observed patterns of genetic diversity.

<u>The main publications of authors on the subject of the abstract:</u>

Terletskaya, N.V.; Turzhanova, A.S.; Khapilina, O.N.; Zhumagul, M.Z.; Meduntseva, N.D.; Kudrina, N.O.; Korbozova, N.K.; Kubentayev, S.A.; Kalendar, R. Genetic Diversity in Natural Populations of Rhodiola Species of Different Adaptation Strategies. Genes 2023, 14, 794. https://doi.org/10.3390/genes1404079

<u>Take-home message:</u>

We studied the polymorphisms of the ARF and SOD gene families, as well as the genetic diversity of six Amaranthaceae species, using the retrotransposons-based fingerprinting approach. It's interesting for understanding of stress-tolerance.



Идентификация высокоолеиновых генотипов ядер подсолнечника в сегрегирующем потомстве с помощью ИК-спектрометрии

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Содержание олеиновой кислоты в подсолнечном масле в высокоолеиновых генотипах контролируется мутантным доминантным геном Ol. Было показано, что на экспрессию этого гена влияют ген-модификатор, ген-супрессор и мозаичное распределение олеиновой кислоты в тканях семядолей подсолнечника. Идентификация мутантных генотипов семян необходима для повышения эффективности селекции высокоолеиновых форм. Альтернативным методом определения содержания олеиновой кислоты в подсолнечном масле является использование ИК-анализатора MATRIX-I. В Лаборатории биохимии ВНИИМК была разработана калибровочная модель для определения содержания олеиновой кислоты в подсолнечном масле. Используя эту технику, мы отобрали ядра с различным содержанием олеиновой кислоты в диапазоне от 36 до 91%. Затем ядра разделили на три части: две семядоли и одну геммулу. Химический анализ семядолей показал, что неполная пенетрантность гена Ol составляла от 45 до 91% олеиновой кислоты, а мозаичность достигала 22%. Содержание олеиновой кислоты в геммуле находилось в пределах 80-90%. Используя ИК-спектрометрию, можно отбирать высокоолеиновые зерна с хорошим проявлением признака при высокой скорости.

The main publications of authors on the subject of the abstract:

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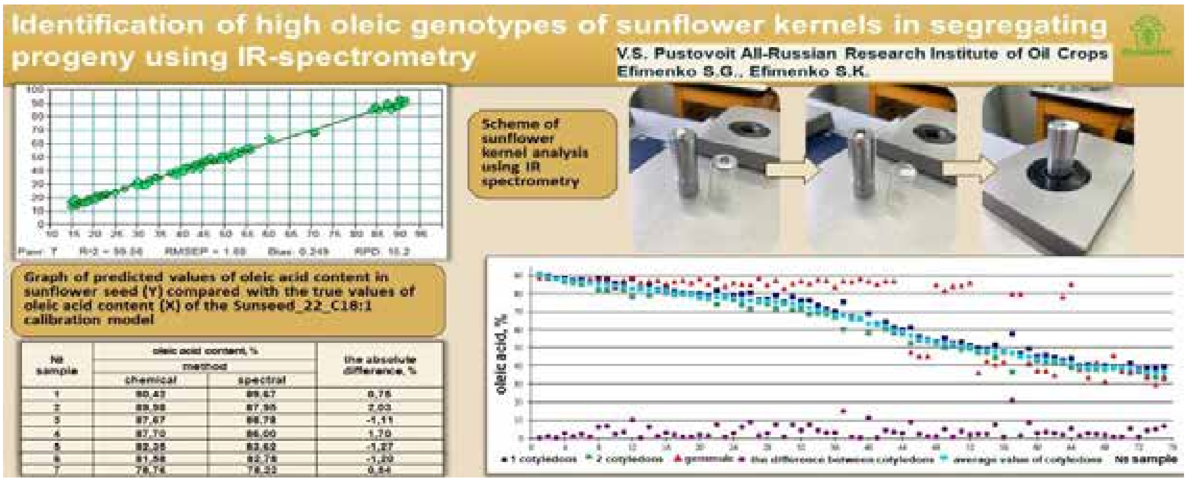
Take-home message:

Для ИК-анализатора MATRIX-I была разработана калибровочная модель для определения содержания олеиновой кислоты в масле косточек подсолнечника. Используя ИК-спектрометрию, можно отбирать высокоолеиновые зерна с хорошим проявлением признака при высокой скорости.



Identification of high oleic genotypes of sunflower kernels in segregating progeny using IR-spectrometry

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Efimenko S.G., Efimenko S.K.

Scheme of sunflower kernel analysis using IR spectrometry

Graph of predicted values of oleic acid content in sunflower seed (Y) compared with the true values of oleic acid content (X) of the Sunseed_22_C18:1 calibration model

№ sample	oleic acid content, %		the absolute difference, %
	method		
	chemical	spectral	
1	90,42	89,67	0,75
2	89,98	87,95	2,03
3	87,67	88,78	-1,11
4	87,70	86,00	1,70
5	82,35	83,62	-1,27
6	81,58	82,78	-1,20
7	78,76	78,22	0,54

Influence of environmental conditions on the duration of ontogenesis phases in wheat-rye 5R(5A) substituted lines

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Homoeologous group 5 chromosomes of wheat and rye possess genes that have a significant influence on the time of earing, growth habit and frost tolerance. The aim of this study is to investigate the effects of dominant and recessive alleles of the rye VRN-R1 gene in the wheat-rye 5R(5A) substituted lines on duration of interphase periods, growth habit and winter hardiness. The lines were growth in greenhouse, spring and winter sowing in the forest-steppe conditions near Novosibirsk. It has been established that by replacing chromosome 5A with chromosome 5R, depending on the genetic background of wheat can change the growth habit and influence winter hardiness. It has been shown that spring lines differ from the recipient varieties in the rate of development in ontogenesis and significantly differ in the duration of "tillering-first node" stage.

The research work was supported by the Russian Science Foundation (grant № 22-26-00085).

The main publications of authors on the subject of the abstract:

Efremova T.T., Chumanova E.V., Zhukova I. M. Winter hardiness analysis of wheat-rye 5R(5A)-substituted lines in Western Siberia // Cereal Research Communications (2022) 50: 25-35 doi.org/10.1007/s42976-021-00147-z

The WOX genes in the regulation of somatic embryogenesis in the *Medicago truncatula*

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Plant somatic cells can be reprogrammed into totipotent embryonic cells that are able to form differentiated embryos in a process called somatic embryogenesis (SE). SE can occur naturally in some plant species and it is widely used for plant biotechnology. This process is regulated by hormone treatment and many proteins, among which WUSCHEL-related homeobox (WOX) transcription factors are believed to play crucial roles. Our previous studies have shown that *MtWOX9-1* stimulates SE in *Medicago truncatula.* The aim of the present research is to search for new *MtWOX* genes regulating SE. Using transcriptomic data and literature analysis, we selected several genes with an increased expression level during SE or in the generative organs and have obtained calli with the overexpression of these *MtWOX*. At the moment we examine their effect on capacity to SE.

Acknowledgements: The research was supported by the grant from the Ministry of Science and Higher Education of the Russian Federation for the creation of the NCMU “Agrotechnologies for the Future” no. 075-15-2022-322.

The main publications of authors on the subject of the abstract:

Tvorogova V.E. et al. The WUSCHEL-Related Homeobox Transcription Factor MtWOX9-1 Stimulates Somatic Embryogenesis in Medicago truncatula // Plant Cell, Tissue and Organ Culture (2019) 3: 517–527. https://doi.org/10.1007/s11240-019-01648-w

Kudriashov A.A. et al. MtCLE08, MtCLE16, and MtCLE18 Transcription Patterns and Their Possible Functions in the Embryogenic Calli of Medicago Truncatula // Plants (2023) 3: 435. https://doi.org/10.3390/plants12030435.

RAPD analysis of variability and relationships of representatives of the genus *Thymus* L. Yakutia.

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One of the topical areas is the study of phylogenetic relationships of plants, where RAPD analysis is actively used. The genus *Thymus* L. is an important source of biologically active compounds. We collected aboveground phytomass of wild *Thymus* species growing in different regions of Yakutia and species introduced in the Botanical Garden. Genomic DNA was isolated using DNeasy Plant Kit, sample quality and purity was determined on SpectroStar and Qubit. RAPD analysis was performed using a selected nonspecific primer. In the electrophoregram of PCR-products of DNA samples of the *Thymus* species examined 86 RAPD-bands were detected, 93.02% of which were polymorphic. The dendrogram obtained by PyElph UPGMA clustering showed a close kinship between *Thymus sibiricus* and *Thymus extremus*, as well as between *Thymus karavaevii* and *Thymus pavlovii*, respectively. Conducted RAPD-analysis and UPGMA clustering allowed to obtain important data on genetic variability of different species of the genus *Thymus*. The results can be used to better understand the biological history of the genus *Thymus* L., as well as to develop strategies for conservation and improvement of cultural forms.

Effect of salicylic acid on the expression of the jasmonate signaling genes in pea roots

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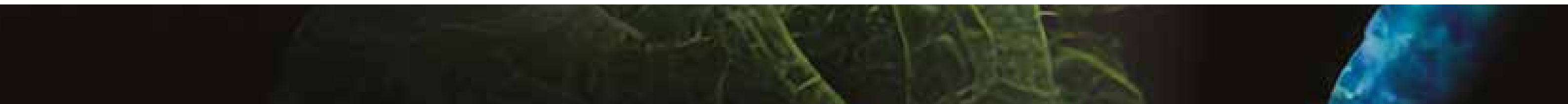
Salicylic acid (SA) can effect jasmonic acid (JA) signaling at the level of its synthesis, signaling and transcription factors that regulates expression of JA dependent proteins. Transcriptome analysis of the effect of SA on the expression of genes encoding JA pathway members was conducted. Analysis ot the expression of key genes involved in the synthesis of the JA – 13-LOX, AOS, AOC, OPR3 and JAZ1 catalyzing formation of JA and its active form J-Ile, showed that the SA does not inhibits its synthesis. SA also do not effect on the expression of the COI1 – JA receptor. MYC2 transcription factor regulates expression of the JA-dependent VSP2 gene. SA upregulates expression of the MYC2 gene more than two times. This led to increased expression of VSP1 gene under the action of SA. Thus, transcriptome analysis of the SA effect on the JA signaling genes showed that one cannot talk about the inhibition of the JA signaling pathway in the pea roots at the level of its synthesis, reception and signal transmission and regulation of the marker genes expression.



The development of potato with reduced cold-induced sweetening facilitated by genome editing

Egorova A., Zykova T., Kostina N., Saboiev I., Koeppel I.*, Hertig C.*, Hiekel S.*, Chamas S.*, Kumlehn J.*, Chalaya N., Rogosina E.**, Kochetov A., Gerasimova S.**

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Storing potatoes at low temperatures results in the accumulation of reducing sugars, known as cold-induced sweetening (CIS). When these sugars react with free amino acids during high-temperature processing, they produce brownish and bitter-tasting substances. Here, two strategies have been pursued to develop new varieties resistant to CIS. The first is to knock out the vacuolar invertase *(PAIN1)* gene in the potato variety Symfonia. Vacuolar invertase contributes to the accumulation of reducing sugars. Multiplex *cas9*/gRNA vectors were created and used for *Agrobacterium*-mediated DNA transfer to leaf explants, which resulted in 10 PAIN1-mutant lines. Tubers from three knockout lines showed reduced levels of glucose and fructose after 90 days of cold storage. The second strategy is to develop CIS-resistant donors from wild potato genotypes. Screening of our collection showed that *Solanum chacoense* has strong resistance to CIS but is toxic due to high levels of steroidal glycoalkaloids (SGAs). Several candidate genes were selected for the reduction of SGAs in potato. The use of respective *cas9*/gRNA vectors was demonstrated to result in targeted mutagenesis in S. *chacoense* cells.

The study is supported by the ICG Kurchatov Genomics Centre (075-15-2019-1662).

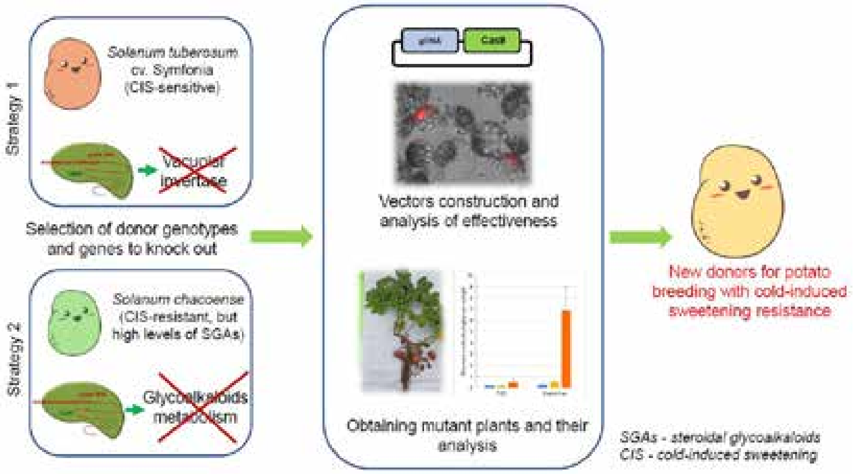
<u>The main publications of authors on the subject of the abstract:</u>

Egorova A.A. et al. Genotype-Specific Features of Cold-Induced Sweetening Process Regulation in Potato Varieties Nikulinsky, Symfonia, and Nevsky // Mol Biol (2023) 57, 193-203. https://doi.org/10.1134/S0026893323020061

Egorova A. A. et al. De Novo Domestication Concept for Potato Germplasm Enhancement // Agronomy (2022) 12 (2) 462. https://doi.org/10.3390/agronomy12020462

<u>Take-home message:</u>

Two strategies have been pursued to develop new varieties resistant to cold-induced sweetening (CIS). The first is to knock out PAIN1 gene in the elite potato variety. The second strategy is to develop CIS-resistant donors from wild potato genotypes.



Use of CRISPR/Cas technology to improve the nutritional value of grain sorghum

Elkonin L.A., Gerashchenkov G.A.*, Borisenko N.V., Kenzhegulov O.A., Sarsenova S.Kh., Rozhnova N.A.*, Panin V.M.

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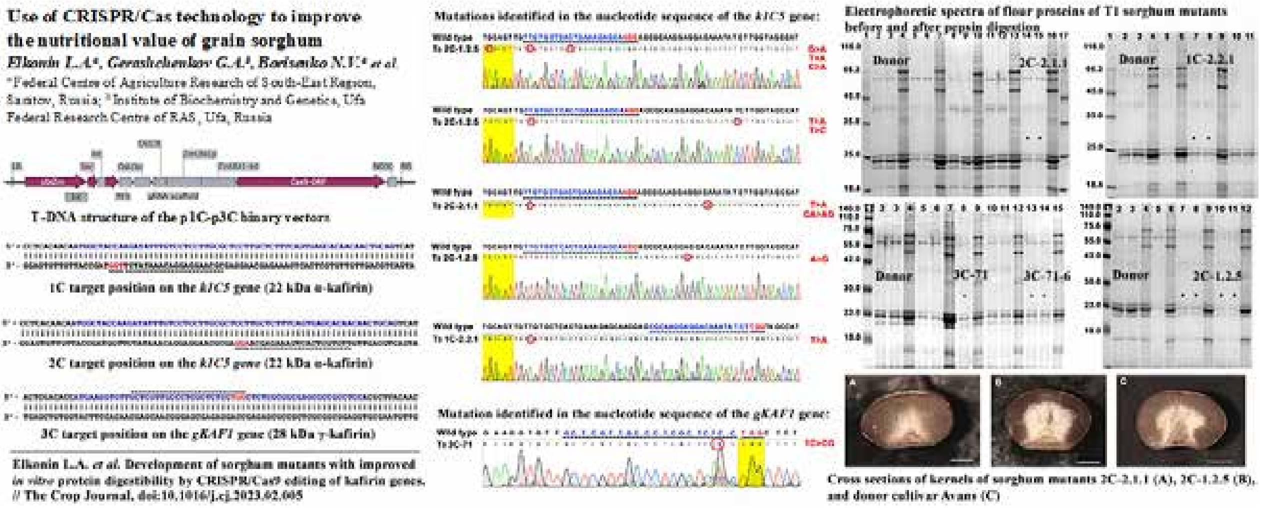
In the context of global warming, one of the main tasks of plant breeding is to increase the drought and heat tolerance of cereal crops. Sorghum is one of such crops, which is a reliable source of food grain for millions of people and fodder production in dry regions of the Globe. However, compared to other cereals, most of the currently cultivated sorghum cultivars and hybrids have a low nutritional value. This problem can be solved using genome editing technology. For this purpose, we have created a series of binary vectors (p1C-p3C) carried genetic constructs for inducing mutations in the nucleotide sequences encoding signal polypeptides of 22kDa α- and 28kDa γ-kafirins (*k1C5* and *gKAF1* genes). By Agrobacterium-mediated genetic transformation these constructs were introduced in genome of grain sorghum cv. Avans. Sequencing of 6 regenerants revealed 5 plants with mutations. T_1 progeny of these mutants had higher *in vitro* digestibility of endosperm proteins (76%–92%), in comparison with the donor cultivar (63%–67%). Some of these plants lacked the cas9 and bar genes that indicate the production of mutants, which did not carry the genetic constructs that induced these mutations.

<u>The main publications of authors on the subject of the abstract:</u>

Elkonin L.A., Gerashchenkov G.A, Borisenko N.V. et al. Development of sorghum mutants with improved in vitro protein digestibility by CRISPR/Cas9 editing of kafirin genes. // The Crop Journal, 2023, doi:10.1016/j.cj.2023.02.005 Gerashchenkov G.A., Elkonin L.A., Gerashchenkov K.G. et al. Binary vector construction for site-directed mutagenesis of kafirin genes in sorghum // Amer. J. Plant Sci. 2021. V. 12. P.1276-1287. doi:10.4236/ajps.2021.128089

<u>Take-home message:</u>

Using CRISPR/Cas technology we obtained sorghum mutants with mutations in the nucleotide sequences encoding signal polypeptides of 22kDa α- and 28kDa γ-kafirins. Some of them are characterized by improved *in vitro* digestibility of endosperm proteins.



Use of CRISPR/Cas technology to improve the nutritional value of grain sorghum

Elkonin L.A.[a], Gerashchenkov G.A.[b], Borisenko N.V.[a] et al.

[a]Federal Centre of Agriculture Research of South-East Region, Saratov, Russia; [b]Institute of Biochemistry and Genetics, Ufa Federal Research Centre of RAS, Ufa, Russia

T-DNA structure of the p1C-p3C binary vectors

1C target position on the *k1C5* gene (22 kDa α-kafirin)

2C target position on the *k1C5* gene (22 kDa α-kafirin)

3C target position on the *gKAF1* gene (28 kDa γ-kafirin)

Elkonin L.A. *et al.* Development of sorghum mutants with improved *in vitro* protein digestibility by CRISPR/Cas9 editing of kafirin genes. // The Crop Journal, doi:10.1016/j.cj.2023.02.005

Mutations identified in the nucleotide sequence of the *k1C5* gene:

Mutation identified in the nucleotide sequence of the *gKAF1* gene:

Electrophoretic spectra of flour proteins of T1 sorghum mutants before and after pepsin digestion

Cross sections of kernels of sorghum mutants 2C-2.1.1 (A), 2C-1.2.5 (B), and donor cultivar Avans (C)

Prospects of vegetable beans (*Phaséolus vulgáris* L.) breeding for resistance to the bean common mosaic virus (Potyviridae, Potyvirus) in the conditions of the Moscow region

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Stability of *Phaséolus vulgáris L.* Bean common mosaic virus - BCMV is controlled by seven resistance genes - strain-nonspecific dominant gene I and six strain-specific recessive genes *bc-u, bc-1, bc-12, bc-2, bc-22* and *bc-3*. Research on the search for sources of sustainability was carried out in 2016-2022. DNA labeling of resistance genes using the appropriate markers *SW13, SBD5* and *ROC11* according to the developed protocols.

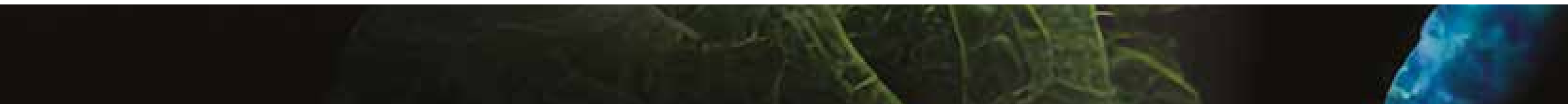
The study of the biological features of the Moscow region BCMV isolate made it possible to establish the influence of temperatures above 26^0C in conditions of artificial infection and high precipitation combined with low temperatures - in natural conditions. A high level of resistance to the virus was provided by the combined combination of the dominant gene I with recessive *bc-12* and bc-3. Recessive resistance without a dominant gene also provided resistance. The virus enters the cell, causing mosaic symptoms, but its systemic spread does not occur. The analysis of compliance with criterion χ2 revealed a more significant effect of the *bc-*1^2 gene on the level of field resistance of common bean samples to BCMV in the conditions of the Moscow region.

The main publications of authors on the subject of the abstract:

Engalycheva I.A., Kozar E.G., Domblides A.S., Antoshkin A.A., Pivovarov V.F., Ushakov A. A., Ushakov V. A. Development peculiarities of bean common mosaic virus (Potyvirus, Potyviridae) in Moscow region and initial material for resistance breeding//Agricultural Biology (2020) 5: 901-919. doi: 10.15389/agrobiology.2020.5.901rus

Take-home message:

For the first time in the Russian Federation, modern varieties of *Phaseolus vulgaris* L to Bean common mosaic virus were evaluated using molecular labeling and phenotyping methods.



Характер наследования хозяйственных признаков овса при скрещивании местных и зарубежных сортов

Eremin D.I.

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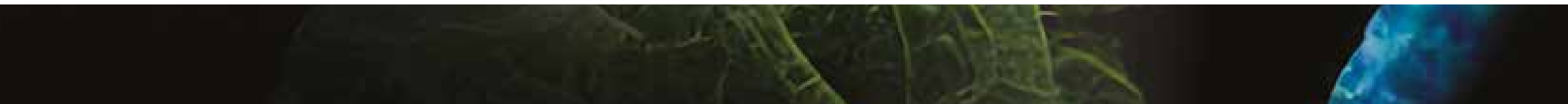
Использование в селекционном процессе в качестве родительских форм сортов местной селекции и зарубежных стран имеет неоспоримое преимущество. Местные сорта максимально адаптированы к условиям региона, но зачастую, проигрывают иностранцам по урожайности и качеству получаемой продукции. Особенно это сильно проявляется у зерновых культур, в том числе и овса. В опыте были использованы сорта овса местной селекции: Отрада, Талисман и Фома. Зарубежные – Ensiler (США), Sang (Швеция), Solidor (Германия). Степень доминирования определяли для гибридов второго поколения. Установлено, что при скрещивании Ensiler с местными сортами, потомство F2 наследует позднеспелость (hp = 1). При скрещивании раннеспелых иностранных сортов, F2 становятся более скороспелым при отрицательной степени доминирования. Скрещивание местных сортов с Sang, не приводит к изменению вегетационного периода, но отмечается сверходоминирование по массе зерна в главной метелке. В комбинациях Отрада, Фома с раннеспелым сортом Solidor выявлена депрессия по элементам структуры урожая, тогда как при скрещивании с Ensiler –проявляется сверхдоминирование по урожайности.



Role of β-glucosidase in isosuccinimide-β-glycoside metabolization of pea plants (*Pisum sativum* L.)

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Pea plant specific isosuccinimide-b-glycoside was discovered (IS-glycoside). Applying quantum-chemical methods including molecular orbitals and MOL MOD and HMO4.BAS software packages the spatial structure of IS-glycoside molecule was created. It was shown that O-glycoside bond between aglycone and D-glucopyranoside collapsed first under metabolization of IS-glycoside. Activity and properties of b-glucosidase in pea plants breaking down O-glycosidic bond were studied. By salting out and column chromatography methods electrophoretically homogenous samples of b-glucosidase were obtained. It was shown that the enzyme constitutes monomer with molecular mass 63kDa, optimum pH 5.6 and temperature +30oC. Under highest speed the enzyme hydrolyzed IS-glycoside (Km 0,58мМ) and also was able to break down other aryl- and alkyl-glucopyranosides (pNPG, methyl-b-D-glucopyranoside, salicin) but not a- and b-D-galactopyranosides compare to other plant glucosidases. Releasing glucose can fast enter into respiratory metabolism while aglycon – into organic and amino acids exchange. The data obtained broadens understanding of IS-glycoside metabolization ways in pea cells and the role of b-glucosidase.

The main publications of authors on the subject of the abstract:

Ershova A.N., Barkalova O. Identification of catalytically active groups of pea (Pisum sativum L.) β- glucosidase//Applied Biochemistry and Microbiology. 2011. Vol.47. No3, P.234–238 DOI:10.1134 S0003683811030057

Ershova A.N. et al. Effect of Phytohormones of Kinetin and Epibrassinolide on Content and Intracellular Localization of Glucosides and Free Amino Acids in Pea Plants Cells (Pisum sativum L.)//International Journal of Secondary Metabolite. 2018. Vol.5. No.2, P.156–162 DOI:10.21448/ijsm.422077

Take-home message:

By applied software a spatial structure of specific isosuccinimide-b-glycoside in pea plants was created and lability of bonds in its molecule was estimated.

Activity and properties of b-glucosidase participated in its metabolization were studied.

Novel cellular factor of *Nicotiana benthamiana* susceptibility to tobamoviral infection

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E-mail: ershovanatalie@gmail.com

Viral infection begins with virion penetration into the cell through the damaged cell wall. After the entry the virion uncoats and synthesis of non-structural viral proteins begins. Further steps include active reproduction, intercellular and systemic spread of the infection. Due to the restricted genome size and thus limited coding potential, viruses are to exploit cellular factors of their hosts at all stages of infection. *Nicotiana benthamiana* Kunitz peptidase inhibitor-like protein (KPILP) is one of the cellular factors that is involved in the regulation of chloroplast retrograde signaling and intercellular transport during potato virus X infection. The aim of the current study is to elucidate KPILP role in the development of tobamoviral infection. It was shown that N. *benthamiana KPILP* expression suppression leads to (1) an increase in plant lifespan and a decrease in the severity of symptoms of tobacco mosaic virus (TMV) and cruciferous-infecting tobamovirus (crTMV) infection; (2) development of resistance to TMV. Thus, KPILP could be regarded as one of N. *benthamiana susceptibility* factors to tobamoviral infection.

This work was supported by the RSF grant no. 19-74-20031.

<u>The main publications of authors on the subject of the abstract:</u>

Ershova N. et al. Nicotiana benthamiana Kunitz peptidase inhibitor-like protein involved in chloroplast-to-nucleus regulatory pathway in plant-virus interaction // Front Plant Sci. (2022) 13:1041867. doi: 10.3389/fpls.2022.1041867

<u>Take-home message:</u>

Nicotiana benthamiana Kunitz peptidase inhibitor-like protein is a cellular susceptibility factor to tobamoviral infection

Retention and evolution of centromeric histone paralogs in rye: essential for the organization of chromosomes in rye meiosis

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*Institute of Cytology and Genetics of the Siberian Branch of the Russian Academy of Sciences, Novosibirsk, Russia
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The functional centromeres of eukaryotic chromosomes are responsible for the assembly of the microtubule binding kinetochore and faithful segregation during cell division of sister chromatids and homologous chromosomes, respectively. The centromeric histone H3, called CENH3 in plants, is a key component of centromeres functioning. Most of studied cereal species have only one copy of the *CENH3* gene. However, similarly to other Triticeae species, two genes, aCENH3 and βCENH3, were revealed in rye (Secale cereale L.). We determined the organization of the CENH3 locus in rye, using the rye genome assembly. We compared the expression of these genes at different stages of plant development using quantitative real-time PCR. The transcription of both variants CENH3 reaches its highest in the generative tissue. Using CENH3 variant-specific antibodies, we revealed that meiotic nuclei had much brighter βCENH3 fluorescence compared with the smaller signals in mitotic nuclei from. It is possible that the advantage of having two functional CENH3 genes is to increase the loading of CENH3 proteins into the centromeric chromatin to ensure chromosome clustering during the first meiotic division.

This work was supported by the Russian Science Foundation (project № 19-14-00051-П).

The main publications of authors on the subject of the abstract:

Elisafenko E.A. et al. The origin and evolution of a two-component system of paralogous genes encoding the centromeric histone CENH3 in cereals // BMC Plant Biol. (2021) 21:541. doi: 10.1186/s12870-021-03264-3

Evtushenko E.V. et al. Expression of Two Rye CENH3 Variants and Their Loading into Centromeres // Plants (2021) 10:2043. doi:10.3390/plants10102043

Сорта озимой пшеницы для республики Татарстан

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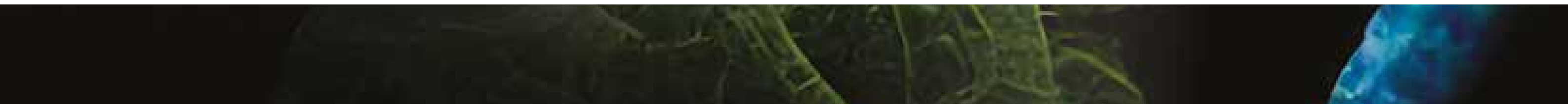
Озимая пшеница – одна из урожайных зерновых культур на полях Татарстана. Для получения стабильных урожаев зерна необходимы сорта, приспособленные к условиям конкретного региона. Проведена оценка урожайности и качества зерна 17 сортов озимой пшеницы различного происхождения. Урожайность в 2018-2022 г варьировала от 4,01 т/га до 6,23 т/га. Выделены высокоурожайные сорта с наименьшей изменчивостью признака от 2,5 до 10%: Универсиада, Дарина, Московская 39, Эритроспермум 2200. Содержание белка в зерне варьировало от 12,1 до 14,0 %. Максимальное содержание клейковины в зерне 32% получено у сорта Московская 39. Значимые эффекты на показатель признака «урожайность» оказывали генотип (27,7 %) и условия среды (39,8%). В контрастных метеоусловиях в годы изучения взаимодействие «генотип × среда» на урожайность оказывало значительное влияние (31,8 %). Показатели качества зерна в большей степени генетически детерминированы: сортовые различия на 65,1% определяли формирование качества клейковины (ИДК); на 52,1% – массы 1000 зерен; на 49,4% – массовой доли белка в зерне; на 48,1%. – массовая доля клейковины в зерне.

The main publications of authors on the subject of the abstract:

Фадеева И.Д., Тагиров М.Ш., Газизов И.Н. Оценка адаптивных свойств сортов озимой мягкой пшеницы Татарского НИИСХ// Достижения науки и техники АПК.- 2018.-Т.32.- №6.-С.46-48

Фадеева И.Д., Тагиров М.Ш., Газизов И.Н., Никифорова И.Ю., Сайфутдинова Д.Д. Изучение сортов и линий озимой пшеницы по хозяйственно ценным признакам// Вестник КазГАУ - 2019. – 3(54)– С.65 – 70. DOI 10.12737/article_5db95d3a953f93.66947300



Glycosylated peroxidases of gravistimulated flax fiber

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The study of the stem N-glycoproteome after gravistimulation of flax plants (Linum usitatissimum L.) was carried out. The evaluation of the amount of glycosylated proteins in different tissues of the stem revealed their higher content in the phloem part compared to the xylem part. After electrophoretic separation and processing with PNGases, the proteins were identified using mass spectrometry (ESI- MS). Among the identified proteins, peroxidases were prevailed having a molecular mass range from 33 to 38 kDa. At the same time, peroxidases with molecular masses of 33-34 kDa were specific for proteins of the phloem part of the stem associated with the cell wall. The content of these peroxidases in the xylem part was insignificant. Analysis of differential gene expression under gravistimulation of flax seedlings revealed 38 peroxidase genes the expression of which changes during exposure. It was noted that the tissue-specific expression of the genes of the identified enzymes correlated ambiguously with the level of their glycosylation. The reason may be related to the large variability of the isozyme composition of peroxidases.

The study of the influence of various factors on the germination index in the collection of soft winter wheat (*Triticum aestivum* L.)

Fedyaeva A.V., Afonnikova S.D., Afonnikov D.A., Deeva V.N.*, Pryanishnikov A.I., Salina E.A.**

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Pre-harvest sprouting leads to significant economic losses. The red-grain varieties wheat are more resistant pre-harvest sprouting than white-grain varieties wheat. Red color in wheat is controlled by the dominant alleles of the grain color genes (*Tamyb10*). The purpose of this study is to investigate 169 varieties of soft winter wheat for pre-harvest sprouting resistance. In this study were used different methods, such as determination of the germination index (GI), α-amylase (AA) activity, and falling numbers (FN); assessment of grain color using the SeedCounter application, PCR analysis to determine *Tamyb*10 alleles.

The analysis showed that there is a negative correlation between GI and FN, as well as between FN and AA activity. The study of allelic variants of the *Tamyb10* gene showed that the presence of even one dominant allele in one of the three wheat subgenomes A, B and D leads to a significant decrease in the germination index, and thus pre-harvest sprouting resistance.

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

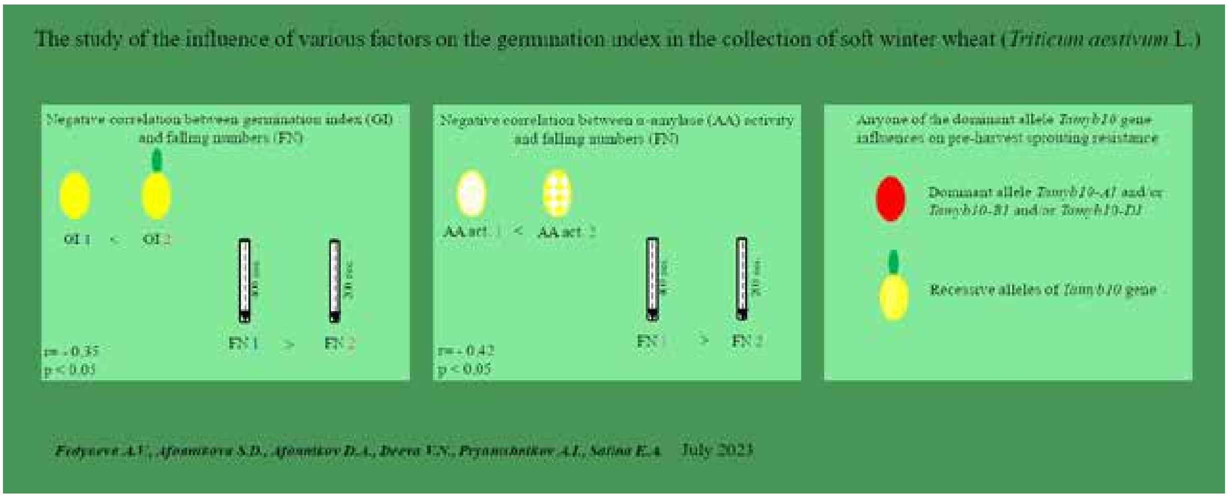
<u>The main publications of authors on the subject of the abstract:</u>

Федяева, А.В., Салина Е.А. Оценка полиморфизма коллекции озимой пшеницы по устойчивости к прорастанию зерна на корню // Генофонд и селекция растений : Сборник матер. 6-й Межд. конф., Новосибирск, 23–25 ноября 2022 года. – С. 202-205.

Федяева, А.В., Салина Е.А., Шумный В.К. Факторы, влияющие на прорастание зерна на корню у мягкой пшеницы (Triticum aestivum L.), и методы их оценки // Генетика. – 2023. – Т. 59, № 1. – С. 5-17. – DOI 10.31857/S0016675823010058.

<u>Take-home message:</u>

The relationship between the germination index (GI), α-amylase activity, falling numbers (FN) and the dominant alleles of the gene Tamyb10 (Tam) which determining wheat grain red color in 169 wheat varieties was studied.



Differences in expression and metabolomic responses in garlic (*Allium sativum* L.) cultivars, contrasting in Fusarium rot resistance, to *Fusarium proliferatum* infectionn

Filyushin M.A., Anisimova O.K., Kochieva E.Z., Shchennikova A.V.

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Fungi of the genus Fusarium are the most harmful garlic pathogens, causing bulb rot and leaf wilt. In this work, for the first time, genes of various families related to the biotic stress response were identified in the A. *sativum* genome and characterized: Pathogenesis-Related (PR1, PR2, PR3, PR4, and PR5 families), flavin-containing monooxygenases (FMO), monodehydroascorbate reductases (MDHAR), soluble sugar uniporters (SWEET) and DREB transcription factors. In garlic cv. Sarmat and Strelets, contrasting in *Fusarium* rot resistance, the expression response of the studied gene families to *F. proliferatum* infection was determined. It was found that in the resistant cv. Sarmat, the expression of most of the genes is significantly (100-3000 times) upregulated by the infection, while in the susceptible cv. Strelets, gene expression does not change or significantly decreases. A number of DEGs were characterized in terms of coding and regulatory sequence variability. Metabolome profiling showed a change in the content of organosulfur compounds in garlic roots in response to *F. proliferatum* infection.

This work was supported by the RSF grant no. 21-76-00007.

The main publications of authors on the subject of the abstract:

Anisimova et al. Thaumatin-like Protein (TLP) Genes in Garlic (Allium sativum L.): Genome-Wide Identification, Characterization, and Expression in Response to Fusarium proliferatum Infection // Plants (2022) 11: 748. 10.3390/plants11060748

Anisimova et al. Pathogenesis-Related Genes of PR1, PR2, PR4 and PR5 Families Are Involved in the Response to Fusarium Infection in Garlic (Allium sativum L.) // Int. J. Mol. Sci. (2021) 22: 6688. 10.3390/ijms22136688

Effect of salt stress on succinate dehydrogenase: enzyme activity, gene expression, and promoter analysis in leaves of *Triticum aestivum* and *Zea mays*

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The effect of short-term salt stress on the activity of the succinate dehydrogenase (SDH) enzyme and the expression of its genes in leaves of *Triticum aestivum* and *Zea mays* was studied. Changes were observed in the activity of SDH and in the expression of the genes that encode SDH after 6, 12, and 24 h of incubation in a 150 mM NaCl solution. The rate of SDH functioning in wheat leaves increased significantly after 6 h in NaCl, remaining stable after 24 h with a 175%increase. SDH activity increased more slowly in maize leaves, being almost double in stressed plants after 24 h. The expression of the ZmSdh1-2 and ZmSdh2-3 genes increased 2-3 times after 12-24 h of incubation. ZmSdh3-1 increased significantly in the first 6 h, while ZmSdh4 showed no significant changes. For the TaSdh1 gene, a strong 12-fold increase was observed at 24 h, while for TaSdh2 the increase was double after 12 h. A bioinformatic review was carried out to detect cis-regulatory regions in the promoter region of the studied genes, 900 bp upstream, finding binding sites for transcription factors bZIP, C2H2, WRKY, MYB, NAC, AP2, ERF involved in gene regulation under biotic and abiotic stress conditions.

The main publications of authors on the subject of the abstract:

Fedorin DN, Eprintsev AT, Florez Caro OJ, Igamberdiev AU. Effect of Salt Stress on the Activity, Expression, and Promoter Methylation of Succinate Dehydrogenase and Succinic Semialdehyde Dehydrogenase in Maize (Zea mays L.) Leaves. Plants. 2023; 12(1):68. https://doi.org/10.3390/plants12010068

Tissue-specific translation in *Arabidopsis thaliana*

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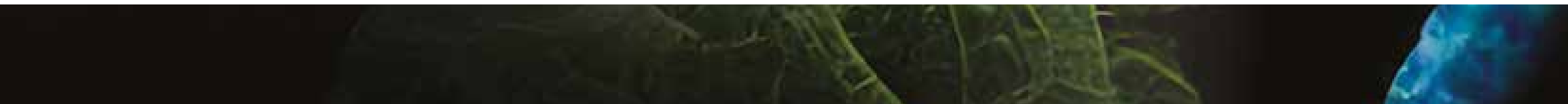
Работа направлена на изучение дифференциальной трансляции у растений A.thaliana в разных компартментах и в масштабе всего генома. Путь от ДНК к белку – многоэтапный процесс с регуляцией на каждом этапе. Особую значимость имеет регуляция экспрессии на уровне трансляции, поскольку именно после нее формируется протеом клетки. Разработано несколько важных методов анализа трансляции, основанных на сравнительном анализе транслятома и его фракций с разной трансляционной эффективностью, которые применены для анализа биоматериала различных органов растений A.thaliana. Образцы подвергали полисомному профилированию, получая фракции транскриптома, различающиеся по уровню трансляции, а также образцы суммарной транслируемой мРНК ультрацентрифугированием на сахарозной подушке. мРНК и нормализованные библиотеки кДНК секвенировали на платформах Illumina и ONT, соответственно. Эти данные позволили установить наборы транслируемых РНК и оценить их уровень трансляции для различных органов растений A.thaliana. В докладе будут представлены результаты поиска транслируемых РНК общих и уникальных для разных органов и частей растений с оценкой эффективности их трансляции.



Intensive cultivation of microalgae in flat-panel photobioreactors: from a laboratory to an industrial scale

Gabrielyan D.A., Sinetova M.A., Gabel B.V., Gabrielian A.K., Markelova A.G., Leusenko P.A., Shcherbakova N.V., Los D.A.

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Since the 1940s algal biomass was considered as a source for food supplements, animal foods, and pharmaceuticals. Nowadays, microalgae are widely applied for wastewater treatment, CO2 utilization, and the production of biofuels. The main point is to develop a technology of intensive cultivation in controlled conditions for effective biomass production. This work is devoted to photobioreactors (PBRs) designed at the IPP RAS in recent years and shows the technological line for the production of microalgae biomass from vessels to industrial volumes in flat-panel PBRs. The main advantage of the PBRs is the variability and mobility in creating conditions for the cultivation of microalgae and cyanobacteria according to the specified parameters: ambient temperature, intensity and spectral composition of the light, CO_2 content in the gas-air mixture and etc. The results of intensive cultivation of microalgae *Chlorella sorokoniana* IPPAS C-1, *Neochlorella semenenkoi* IPPAS C-1210 and mutant strain of the cyanobacterium *Synechococcus sp.* PCC 7942 producing polyunsaturated fatty acids are presented. This research was funded by the Russian Science Foundation (RSF grants no. 21-74-30003).

The main publications of authors on the subject of the abstract:

Gabrielyan, D.A. et al. Cultivation of Chlorella sorokiniana IPPAS C-1 in Flat-Panel Photobioreactors: From a Laboratory to a Pilot Scale. Life 2022, 12, 1469.

Gabrielyan, D.A. et al. Optimization of CO2 Supply for the Intensive Cultivation of Chlorella sorokiniana IPPAS C-1 in the Laboratory and Pilot-Scale Flat-Panel Photobioreactors. Life 2022, 12, 1469.

Cambium stem cells functioning and their derivatives differentiation programs at different stages of woody plant ontogenesis

**Galibina N.A., Moshchenskaya Y.L.,
Tarelkina T.V., Nikerova K.M.,
Korzhenevskii M.A., Serkova A.A.,
Afoshin N.V., Semenova L.I., Ivanova D.S.**

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Wood is the most important renewable energy source, and it is also becoming increasingly important as an industrial raw material for the production of many products. On a planetary scale, the wood formation is of great importance for climate regulation. Elements of the CLE41/44-PXY-WOX signaling module, are involved in regulating cambial activity, organization of "vascular pattern" and xylem differentiation, have been identified in several angiosperm and gymnosperm species of woody plants. Scientists usually study seedlings that form one or two rings of juvenile wood. In our work, we selected as objects of study two forms of *Betula pendula* (silver birch, Karelian birch) and adult Pinus sylvestris trees aged from 30 to 180 years, growing under natural conditions. The level of *CLE41/44-PXY- WOXs* gene transcripts in a radial row «the conductive phloem/ the cambial zone – the differentiating xylem» considered depending on (1) xylogenesis scenario, (2) cambial growth stage, (3) ontogeny stage, (4) cambial age (within one trunk).

Acknowledgments: The work is supported by the grant from the Russian Scientific Foundation (project No. 21-14-00204)

The main publications of authors on the subject of the abstract:

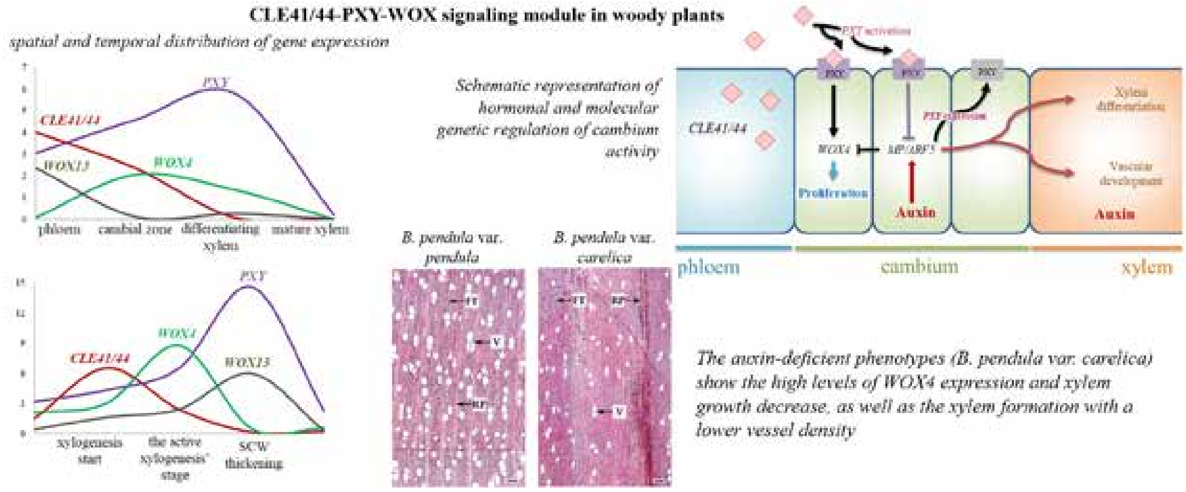
Galibina NA, Moshchenskaya YL, Tarelkina TV, Nikerova KM et al. Identification and expression profile of CLE41/44-PXY-WOX genes in Pinus sylvestris L. trunk tissues as a pattern of the cambial activity // Plants2023 https://doi.org/10.3390/plants12040835

Galibina NA, Moshchenskaya YL, Tarelkina TV, Chirva OV, Nikerova KM et al. Changes in the Activity of the CLE41/PXY/WOX Signaling Pathway in the Birch Cambial Zone under Different Xylogenesis Patterns // Plants2022 DOI:10.3390/plants11131727

Take-home message:

The expression maximum of CLE41 precedes the maximum PXY.

The auxin-deficient phenotypes of trees show high levels of WOX4 expression and a decrease in xylem growth, as well as the formation of xylem with a lower vessel density.



New chelating agent for micronutrient fertilizer improves lettuce yield and does not significantly alter endophytic microbiome

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Use of EDTA-chelates leads to many significant negative environmental effects. New alternatives to substitute EDTA have been searched. This study is dedicated to GLDA effects, which is known chelating agent but not previously used in agriculture, on growth and endophytic microbiome of lettuce grown on hydroponics. It was demonstrated that both GLDA- and EDTA- complexes increase the lettuce biomass by 7 and 6 fold. The number of bacterial OTUs revealed in control, GLDA and EDTA samples was 231, 256, 187 for hydroponic water, 93, 77, 120 in root endosphere and 25, 8, 25 in leaf endosphere.In control variant, bacteria of the genus Sphingomonas were dominant in the hydroponic water, root and leaf endosphere of lettuce. The use of GLDA and EDTA led to the dominance of the bacterial genera Pseudarthrobacter in the water, Anticatalyst in the root endosphere. The use of GLDA led to an abundance increase of bacteria from genus Sphinhomonas and Lactobacillus up to 67 and 15% in the endosphere. It can be concluded that GLDA is a promising chelate for microelemental fertilizer since it improves the yield but does not lead to significant changes in plant endospheric bacterial community.

The main publications of authors on the subject of the abstract:

Galieva, G. с соавт Monitoring Soil Bacteria with Community-Level Physiological Profiles Using BiologTM ECO-Plates in the Republic of Tatarstan (Russia). IOP Conference Series: Earth and Environmental Science. 107, (2018)

Galieva, G. с соавт Lipopeptides Produced by Bacillus mojavensis P1709 as an Efficient Tool to Maintain Postharvest Cherry Tomato Quality and Quantity. Agriculture (Switzerland). 12, 609 (2022).

The identification of immune peptides in plant stress transcriptomes

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Signal peptides play a crucial role in both plant development and the stress response to pathogen invasion. Their small size and mode of action make them a promising environmentally friendly alternative to chemical plant protection products. However, it is still a challenging task to search for novel biologically active peptides and to study their diversity in various plant taxa.

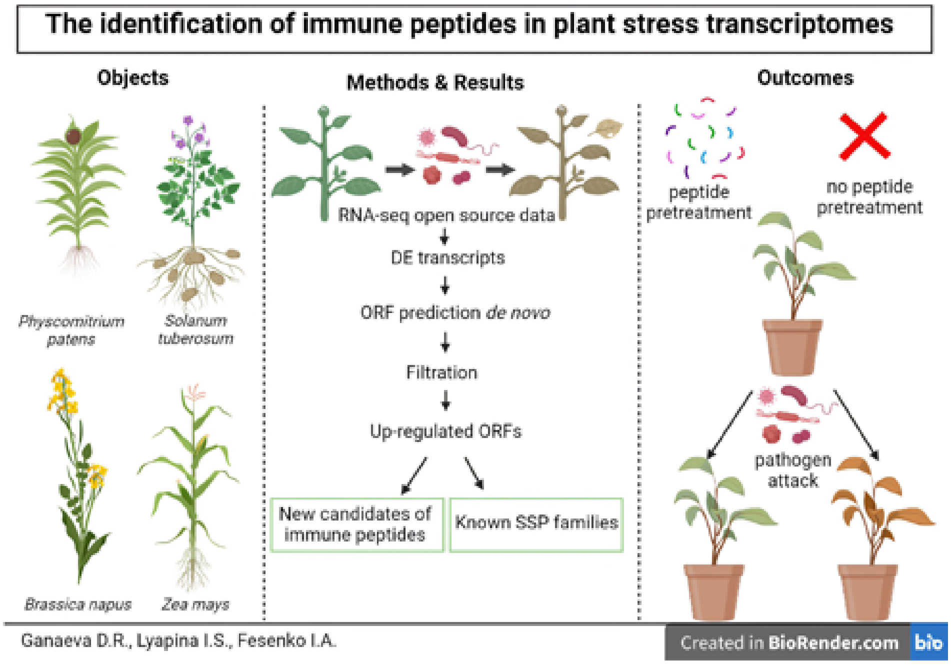
Based on the analysis of transcriptomic data obtained from plants infected with pathogens, we developed an algorithm for searching for signal peptides involved in the regulation of plant immune response. This algorithm was applied to the model organism moss Physcomitrium patens and several crops such as Zea mays, Brassica napus, Solanum tuberosum. Our pipeline includes the prediction of open reading frames that may encode short proteins and the search for conserved motifs associated with the activity of known signal peptide families. We identified peptides belonging to known families that are involved in the regulation of the plant immune response, as well as novel candidates that may play a role in the plant's response to biotic stress.

The main publications of authors on the subject of the abstract:

Lyapina, I.S., et al. Possible role of small secreted peptides (SSPs) in immune signaling in bryophytes // Plant Mol Biol (2021) 106:123–143. doi: https://doi.org/10.1007/s11103-021-01133-z

Take-home message:

Signal peptides play a crucial role in plant immunity by controlling defense responses. Using the analysis of plant stress transcriptomes, our research focuses on identifying novel immune peptides.



Nitrogen-mediated CLE4 peptide regulates shoot apical meristem development and tuber initiation in potato

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High levels of nitrogen in potato can cause excessive vegetative growth instead of tuber development, leading to lower yield and poor quality tubers. Our research shows that N-mediated CLE4 has a positive effect on root length in nitrogen-deficient conditions and has negative effect on normal shoot apex development. By analyzing the transgenic plant's transcriptome, we discovered that overexpression of *CLE4* represses *IT1*, a regulator of potato tuber initiation, in the leaves. Futhermore, during tuber initiation, overexpressing *CLE4* stolons did not swell but instead transformed into branches. In addition to this, based on motifs described in the other studies we found that *CLE4* could be regulated by NIN-like transcription factors, which are key regulators of nitrate signaling. Our data suggest that CLE peptides could be potentially involved in nitrogen-dependent regulation of tuberization.

The work was supported by the Russian Science Foundation (grant no. 22-76-00022).

The main publications of authors on the subject of the abstract:

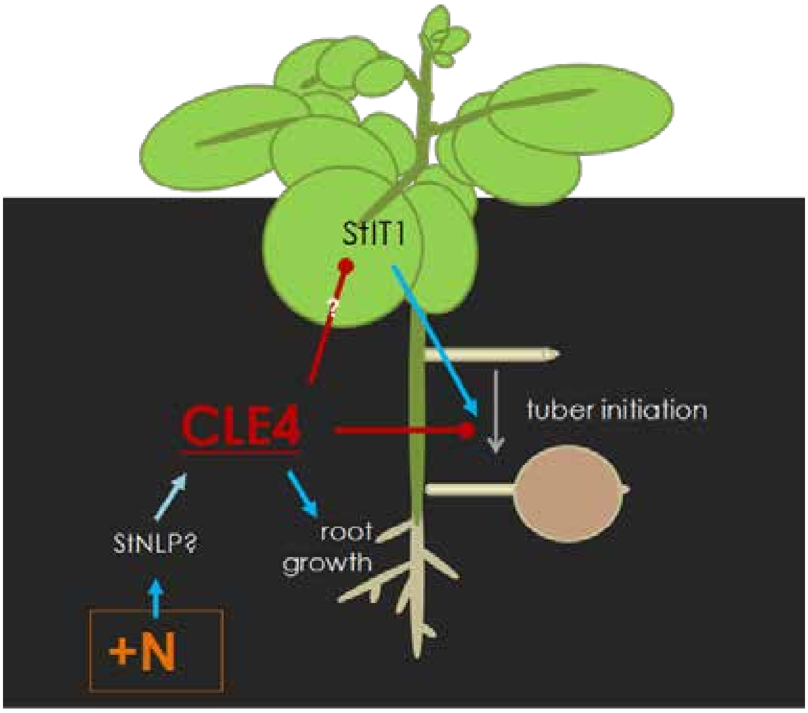
Gancheva M., Dodueva I., Lebedeva M., Lutova L. CLAVATA3/EMBRYO SURROUNDING REGION (CLE) Gene Family in Potato (Solanum tuberosum L.): Identification and Expression Analysis // Agronomy (2021) 11, 984. doi: 10.3390/agronomy11050984.

Take-home message:

The expression of *CLE4* was induced by nitrogen supply.

The *CLE4* overexpressing stolons were converted into branches, instead of swelling.

Overexpression of *CLE4* represses IT1, a regulator of potato tuber initiation.



Plasmodiophorol A: obtaining and studying of antibacterial activity

Garaeva D.I., Smirnova E.O.*, Lantsova N.V.*, Toporkova Y.Y.*, Grechkin A.N.*

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The lipoxygenase cascade is a source of oxidized derivatives of PUFAs — oxylipins. The key enzymes of lipoxygenase cascade are lipoxygenases and nonclassical cytochromes P450 of CYP74 clan.

Two genes encoding cytochromes P450 are expressed in the genome of the clubroot desease pathogen *Plasmodiophora brassicae*, which belong to the CYP74 clan. The cDNA of CYP50918A1 was cloned and protein was obtained in *E.coli* cells. The recombinant enzyme was purified by metal affinity chromatography. The preferred substrate is 13-hydroperoxide α-linolenic acid. The enzyme has been characterized as a hydroperoxyde bicyclase and produced three oxylipins, the main one was plasmodiophorol A.

The aim was to verify the presence of antimicrobial properties in plasmodiophorol A. It was shown that at concentration of 0.5 mM, plasmodiophorol A has a bacteriostatic effect during the first 24 hours. *Bacillus subtilis* cells proved to be the most sensitive. Using this microorganism, an experiment was conducted to determine the dynamics of cell growth during the 12 hours.

Work on the production of recombinant enzyme CYP50918A1 was supported by grant from the Russian Science Foundation project No.23-14-00350.

Take-home message:

Plasmodiophorol A is an incubation product of CYP50918A1 and α-linolenic acid 13-hydroperoxide.

Plasmodiophorol A is a new bicyclic oxylipine that has bacteriostatic action against some Gram-positive and Gram-negative bacteria.

Isolation and cultivation of sunflower protoplasts

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Sunflower *(Helianthus annuus L.)* is one of the valuable agricultural crops. For a wider use of sunflower, it is necessary to create new and genetic improvement of already known varieties, lines and hybrids, including methods of molecular biotechnology. Due to the low regenerative capacity of sunflower, obtaining regenerating plants using isolated protoplasts seems to be an urgent task. The sunflower variety SPK was selected for the study. Young leaves of 3-week-old aseptic plants were used as explants for isolating protoplasts. The regenerative ability of plants in vitro depends not only on the genotype, the type of explant, but also on the composition of the nutrient medium, several variants of nutrient media were used for the cultivation of the obtained protoplasts, including basic nutrien ts, osmotic stabilizer and plant growth regulators 2,4-D, 6-BAP, IAA, zeatin and NAA in concentrations of 0.2; 0.5 and 1 mg/l.

After 2 months of cultivation in a liquid nutrient medium, callus formation was observed, and after 4 months on an agarized nutrient medium including zeatin (1 mg/l) and IAA (0.1 mg/l), the formation of regenerants from morphogenic callus.

Preconditions and methods of precision engineering of the endophytic microbiome of cultivated plants

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A common strategy in the breeding of growth-promoting bacteria is to look for super-producers of phytohormones or plant growth promoters. In our study, it was found that *B. subtilis* strains with a high level of indolyl-3-acetic acid (IAA) production and activating the growth of wheat plants, when interacting with pea plants, were ineffective or stimulated growth and yield only when inoculated in strictly defined low doses.

The revealed differences in the reaction of different plant species and varieties to inoculation with endophytic bacteria necessitate the identification of physiological mechanisms of such specificity, the markers of which can be indicators of phytoimmune reactions, for example, the content of proline, malondialdehyde etc.

Treatment with *B. subtilis* strains which produce different levels of IAA/ cytokinins, change the root and shoot architecture, which have a selective advantage under different conditions of moisture ability. It seems promising to use a "smart capsule" that would "unarchive" exactly those components of the microbiome that are in demand under certain conditions of environment.

The work was supported by a grant from the Russian Science Foundation 23-24-00602.

The main publications of authors on the subject of the abstract:

Ivanchina N.V. et al. Effect of cell doses of Bacillus subtilis endophytic strains producing indolyl-3-acetic acid on growth and productivity of pea (Pisum sativum L.) // Agrohimia (2018) 4: 39-44. DOI: 10.7868/S0002188118040051

Garipova S.R.et al. Malondialdehyde and proline content in bean cultivars following the inoculation with endophytic bacteria // Acta Physiologiae Plantarum (2022) 44 (7): 89. doi.org/10.1007/s11738-022-03427-1

Take-home message:

A lot is not always good. Less is better. Find the optimum exogenous intake of IAA

An effective symbiosis should not cause a surge in immune defenses

From universal biologics to individualized microbiome, packaged in a "smart" capsule

Mechanisms underlying the compensation effect upon the suppression of mitochondrial alternative oxidase

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Alternative oxidase (AOX) maintains redox balance in the mitochondrial electron transport chain thereby alleviating the production of reactive oxygen species (ROS). *AOX1a* knockout is an effective approach to study AOX function. Triggers of genetic compensation for gene knockout at the transcriptional level are DNA lesions and mutant mRNAs that induce the expression of other "defense" genes. *AOX1a* suppression leads to decrease in functionally active AOX in mitochondria. The latter can be the reason of an increase in levels of ROS, a decrease in the mitochondrial membrane potential and a decline in ascorbate synthesis in mitochondria. All of these events can be possible triggers of retrograde signaling pathways from mitochondria to induce the ROS scavenging system. Compensation for AOX deficiency by enhancing cellular antioxidant defense leads to a decrease in ROS production. On the other hand, reaching a certain threshold of ROS formation provokes oxidative stress. A decrease in the relative amount of reduced ascorbate at stable levels of ROS as a result of compensation in *AOX-suppressed* plants may be a sign of stress development.

This research was funded by the RSF (22-24-01082).

The main publications of authors on the subject of the abstract:

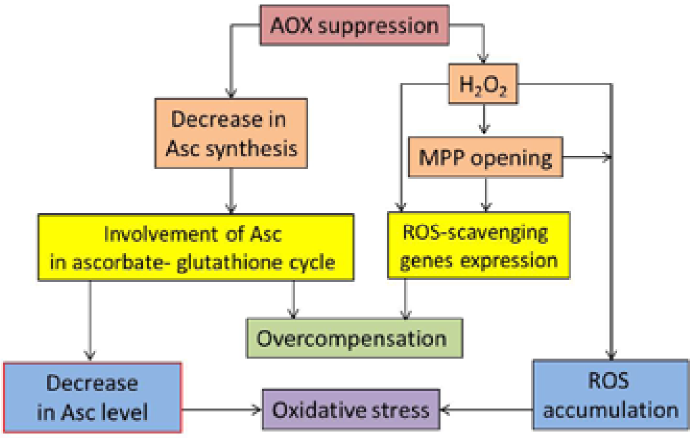
Garmash E.V. Suppression of mitochondrial alternative oxidase can result in upregulation of the ROS scavenging network: some possible mechanisms underlying the compensation effect// Plant Biology. 2022. doi:10.1111/plb.13477

Garmash, E.V.; Dymova, O.V.; Silina, E.V. et al. AOX1a expression in Arabidopsis thaliana affects the state of chloroplast photoprotective systems under moderately high light conditions // Plants. 2022, 11, 3030. https://doi.org/10.3390/plants11223030

Take-home message:

A decrease in the relative amount of reduced ascorbate, namely the ascorbate/dehydroascorbate ratio of at stable levels of reactive oxygen species due to a compensatory effect in plants with *AOX1a* suppression may be a sign of stress development.

A hypothetical scheme of mechanisms
during compensation of AOX deficiency in plants under stress



Disorder in auxin transport in Arabidopsis genome uncoupled mutant plants grown in the chloroplast biogenesis arrest conditions

Garnik E.Yu., Shmakov V.N., Vlasova A.A.*, Tarasenko V.I., Konstantinov Yu.M.**

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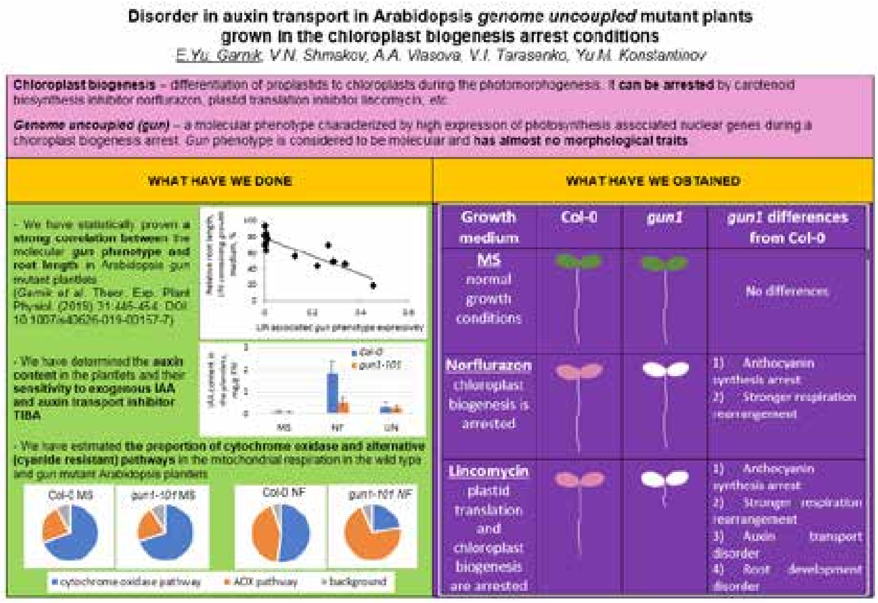
Genome uncoupled (gun) is a plant molecular phenotype with relatively strong expression of photosynthesis associated nuclear genes in young plantlets grown in chloroplast biogenesis arrest conditions (lincomycin, norflurazon, etc.). There are six genes in Arabidopsis genome named *GUN1* to *GUN6* that may lead to *gun* phenotype when mutated. Earlier we have described a root growth retardation in two Arabidopsis mutant lines with mutation in *GUN1* gene. Now we show that *gun1* plantlets grown on lincomycin or norflurazon demonstrate signs of auxin transport disorder: (a) lower IAA and higher TIBA sensitivity, (b) no induction of auxin marker genes *ARF7* and *LBD33* in the roots, (c) changes in expression patterns of auxin basipetal transport genes *PGP* in the shoots. Also, we found much higher induction of *AOX1a* gene expression and increase of cyanide resistant respiration pathway up to 70% in the *gun1* Arabidopsis plantlets grown on lincomycin or norflurazon, without so much changes in the wild type plantlets in the same conditions. The data obtained prove auxin transport disorder in Arabidopsis *gun1* plants and indicate their higher sensitivity to lincomycin and norflurazon stress.

The main publications of authors on the subject of the abstract:

Garnik E.Y. et al. Genome uncoupled (gun) phenotype is associated with root growth retardation in Arabidopsis seedlings grown on lincomycin // Theoretical and Experimental Plant Physiology (2019) 31(4): 445-454. DOI: 10.1007/s40626-019-00157-7

Take-home message:

We found evidence of auxin transport disorder in Arabidopsis *gun1* mutant plants grown on lincomycin or norflurazon:(a) lower IAA and higher TIBA sensitivity, (b) no induction of some auxin marker genes, (c) rise in auxin transport genes expression.



Disorder in auxin transport in Arabidopsis *genome uncoupled* mutant plants grown in the chloroplast biogenesis arrest conditions

E.Yu. Garnik, V.N. Shmakov, A.A. Vlasova, V.I. Tarasenko, Yu.M. Konstantinov

Chloroplast biogenesis – differentiation of proplastids to chloroplasts during the photomorphogenesis. It **can be arrested** by carotenoid biosynthesis inhibitor norflurazon, plastid translation inhibitor lincomycin, etc.

Genome uncoupled (gun) – a molecular phenotype characterized by high expression of photosynthesis associated nuclear genes during a chloroplast biogenesis arrest. Gun phenotype is considered to be molecular and **has almost no morphological traits**

WHAT HAVE WE DONE

- We have statistically proven a **strong correlation between** the molecular **gun phenotype and root length** in Arabidopsis gun mutant plantlets (Garnik et al. Theor. Exp. Plant Physiol. (2019) 31:445-454. DOI 10.1007/s40626-019-00157-7)

- We have determined the **auxin content** in the plantlets and their **sensitivity to exogenous IAA and auxin transport inhibitor TIBA**

- We have estimated **the proportion of cytochrome oxidase and alternative (cyanide resistant) pathways** in the mitochondrial respiration in the wild type and gun mutant Arabidopsis plantlets

WHAT HAVE WE OBTAINED

Growth medium	Col-0	*gun1*	*gun1* differences from Col-0
MS normal growth conditions			No differences
Norflurazon chloroplast biogenesis is arrested			1) Anthocyanin synthesis arrest 2) Stronger respiration rearrangement
Lincomycin plastid translation and chloroplast biogenesis are arrested			1) Anthocyanin synthesis arrest 2) Stronger respiration rearrangement 3) Auxin transport disorder 4) Root development disorder

Development of faulty leaf disease causes on winter wheat varieties of different susceptibility depending on weather conditions

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Для своевременного выявления возбудителей болезней необходимо получать данные о фитосанитарной обстановке агроценозов в максимально короткие сроки, что возможно за счет использования технических средств мониторинга. Целью работы стало изучение развития грибных листовых болезней пшеницы в зависимости от погодных условий и фактора восприимчивости сорта с применением приборного метода фитосанитарного мониторинга. Для определения видового состава грибных болезней пшеницы использовалось устройство для определения заспоренности растений и классическая визуальная оценка степени развития болезней. В результате, установлено и статистически доказано влияние погодных условий и фактора сорта на развитие и распространение грибных листовых болезней пшеницы. Проведенные исследования позволяют заключить, что момент первичного проявления болезней на посевах озимой пшеницы возможно выявить с помощью спороулавливающего устройства и предопределить дальнейшее развитие патогенов с учетом факторов сорта и погодных условий.

Исследование выполнено за счет средств гранта Российского научного фонда и Кубанского научного фонда № 22-26-20119.

The main publications of authors on the subject of the abstract:

Kremneva, O.; Danilov, R.; Gasiyan, K.; Ponomarev, A. Spore-Trapping Device: An Efficient Tool to Manage Fungal Diseases in Winter Wheat Crops // Plants (2023), 12,391. https://doi.org/10.3390/plants12020391

Кремнева О.Ю., Гасиян К.Э. Применение спороулавливающей аппаратуры для обнаружения болезней зерновых культур (обзор) // Зерновое хозяйство России (2023); (1):94-98. https://doi.org/10.31367/2079-8725-2023-84-1-94-98

Take-home message:

Момент первичного проявления болезней на посевах озимой пшеницы возможно выявить с помощью спороулавливающего устройства, что позволяет предопределить дальнейшее развитие патогенов с учетом факторов сорта и погодных условий.

Phylogenetic analysis of maize malate dehydrogenases from different cellular localization

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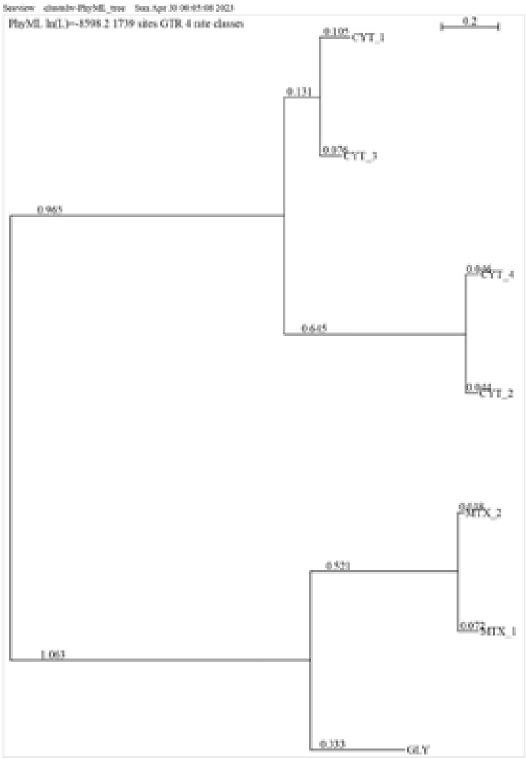
Построение филогенетического древа позволяет установить происхождение изучаемых белков и предположить их свойства. В связи с этим был проведен анализ последовательностей, кодирующих различные МДГ.

Последовательности генов растения *Zea mays* были взятые из GenBank. Выявление гомологии генов проводили с помощью BLAST и Clustal Omega. Филогенетическое древо было построено с помощью программы Seaview методом наибольшего правдоподобия (PhyML (GTR)).

Были обнаружены 4 цитоплазматических, 2 митохондриальных и глиоксисомальный гены, кодирующие НАД+-зависимую малатдегидрогеназу кукурузы.

Степень гомологии цитоплазматических генов составила 82%; митохондриального и глиоксисомального – 41%. Полученные результаты позволяют разделить малатдегидрогеназные гены на две большие группы: 1) цитозольные и цитоплазматические формы и 2) митохондриальные и глиоксисомальные МДГ.

Таким образом, эволюция генов малатдегидрогеназы, полученная при сравнении аминокислотных последовательностей, хорошо вписывается в теорию эндосимбиотического происхождения митохондрий и хлоропластов. Это объясняет различия в первичной последовательности аминокислот, сборке и свойствах изучаемых ферментов.



Genetic and epigenetic mechanisms of Scotch pine adaptation to chronic radiation exposure

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The main results of long-term observations on Scots pine populations inhabiting sites affected by the Chernobyl accident are presented. Populations growing for many years under chronic radiation exposure are characterized by the enhanced mutation rates, increased genetic diversity, changes in the gene expression and in the level of genome-wide methylation, alterations in the temporal dynamics of cytogenetic abnormalities and genetic structure of populations. However, significant changes at the genetic level had no effects on enzymatic activity, and morphological abnormalities of pine trees. The seed progeny of chronically exposed Scots pine populations is characterized by an increased frequency of cytogenetic abnormalities and abortive seeds, as well as reduced germination. At the same time, these seeds are characterized by increased resistance to additional γ-irradiation. Thus, the current levels of radiation exposure at the Chernobyl exclusion zone can inhibit the reproductive capacity of Scots pine and serve as a selection factor for increased resistance to radiation. This study was funded by Russian Science Foundation (grant number 21-16-00004)

The main publications of authors on the subject of the abstract:

Geras'kin S. et al. Multifaceted effects of chronic radiation exposure in Japanese red pines from Fukushima prefecture // Science of the Total Environment (2021) 763: 142946. doi.org/10.1016/j.scitotenv.2020.142946

Geras'kin S. et al. Scots pine as a promising indicator organism for biomonitoring of the polluted environment: A case study on chronically irradiated populations // Mutation Research (2019) 842: 3-13. doi.org/10.1016/j.mrgentox.2018.12.011

Take-home message:

The current levels of radiation exposure at the Chernobyl exclusion zone enhance mutation rates, increase genetic diversity, inhibit the reproductive capacity of Scots pine and serve as a selection factor for increased resistance to radiation.

Арабиноксиланы ржи – целевой показатель для селекции

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Дифференцирующим показателем, определяющим качество и направление использования зерна озимой ржи, служат структура, состав и содержание арабиноксиланов (АК). АК содержатся во всех частях злаковых растений и сочетают в себе биоактивные для здоровья человека свойства и важные технологические функции. Создание сортов разнообразного назначения является приоритетной задачей в селекции озимой ржи.

Для реализации этого направления проведена фенотипическая оценка содержания водорастворимой фракции АК в зерне и вязкости водного экстракта на широкой панели низкопентозановых самоопыленных линий, современных популяционных сортов собственной и российской селекции, генколлекции ВИГРР им. Н.И.Вавилова. Выделены доноры высокого и низкого содержания пентозанов.

Уровень содержания АК обусловлен как генетическими, так и средовыми факторами. Наименьшие величины АК и размах их варьирования отмечены в годы с избыточным увлажнением. Установлено, что общая и водорастворимая фракция арабиноксиланов ржи проявляет большую структурную гетерогенность в разные фенологические фазы развития растений и в разных частях формирующегося зерна. Создан разнообразный селекционный материал для создания сортов озимой ржи различного направления использования.

Assembly and annotation of the Far-Eastern Actinidia species chloroplast genomes

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Представители рода *Actinidia* являются ценными плодовыми культурами, известными высоким содержанием витамина С, антиоксидантов и других полезных веществ. Обширная коллекция видов и сортов актинидии собрана в ФГБНУ ФНЦ Садоводства и не оценивалась с генетической точки зрения.

Изучение хлоропластной ДНК (хпДНК) широко используется для анализа геномного разнообразия, оценки гетерогенной изменчивости и уточнения филогенетических взаимоотношений.

Для получения пластидных геномов были отобраны четыре вида: *A. arguta, A. kolomikta, A. polygama, A. purpurea.* Библиотеки секвенированы как для длинных чтений (на приборе ONT), так и для коротких (на приборе MGI).

Собранные геномы хлоропластов имеют длину ~156 т.п.н., состоят из большого (LSC, ~110 т.п.н.), малого (SSC, ~40 т.п.н.) участков и инвертированных повторов (IR, ~6 т.п.н.). Филогенетический анализ показал, что *A. kolomikta* и *A. arguta* образуют один кластер с *A. kolomikta* из GenBank. Последовательность *A. polygama* показала наибольшее сходство с хпДНК *A. valvata* и *A. polygama* из GenBank. Пластом *A. purpurea* на филогенетическом дереве сформировал отдельную ветвь.

Работа выполнена при поддержке гранта РНФ №22-16-00074.

Buckwheat callus induction and plant regeneration: culture media optimisation and selecting a variety for genetic transformation

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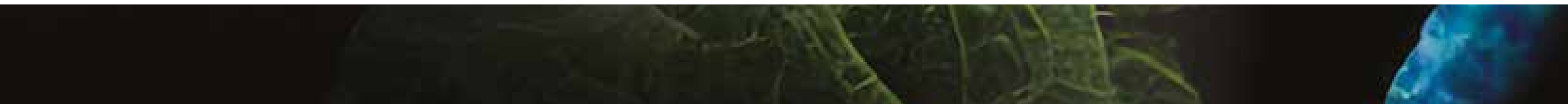
Transformation using plant cell cultures and isolated tissues is commonly employed to obtain genetically modified plants. The selection of optimal cultivation conditions at different stages, including *in vitro* culture obtainment, induction of morphogenesis, and regeneration of whole plants, is critical for successful plant transformation. We evaluated the callus formation ability and regenerative capacity of 10 varieties of *Fagopyrum esculentum* and *Fagopyrum* tataricum and selected the most promising ones for regenerated plant production: Batyr, Shinano, and KK8. The optimal medium for callus formation contained 2 mg/L 2,4-Dichlorophenoxyacetic acid and 2 mg/L Kinetin. The medium for plant regeneration contained 6-Benzylaminopurine (2 mg/L), Kinetin (0.2 mg/L), and Indole-3-acetic acid (0.2 mg/L). Regenerated plants of the Batyr variety were successfully acclimated to non-sterile soil conditions. This protocol can be used for the genetic transformation of buckwheat in future studies. Supported by the Ministry of Science and Higher Education, project #075-15-2021-1064

Take-home message:

We evaluated the callus formation ability and regeneration capacity of 10 varieties of *Fagopyrum esculentum* and *Fagopyrum* tataricum and selected the most promising ones for regenerated plant production: Batyr, Shinano, and KK8.



Transcriptomic landscape and metatranscriptomes of pathosystems

Gogolev Y.V., Gorshkov V.Y., Gogoleva N.E., Osipova E.V., Konnova T.A., Hamo H.*, Balkin A.C.**

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The study of bacterial RNA showed that bacterial transcriptomes have a very complex structure. A significant proportion of them is non-coding RNA (ncRNA). Bacterial ncRNAs have been shown to act as negative regulators of gene activity and may also serve as immunity factors. However, the functional role of most of the ncRNAs remains unclear.

The difficulty in studying pathosystems lies in the fact that the proportion of bacterial RNA in total preparations is less than a few percent. The development of the Capable-Seq method provides additional opportunities for the study of complex transcriptomes. We have performed RNA sequencing of pathogenic bacteria *Pectobacterium atrosepticum* and *Salmonella enterica* directly in tissues and cells of eukaryotic host organisms – *Nicotiana tabacum* L. and *Acanthamoeba castellanii* Neff, respectively. As a result, the differential activity of bacterial RNA transcription during infection development was characterized. Transcription start sites (TSS) were mapped with an accuracy of one nucleotide. More than 20,000 new TSSs have been identified and classified according to their position relative to the regulatory elements of genes and operons.

The main publications of authors on the subject of the abstract:

Gogolev Y.V. et al. OMICs, Epigenetics and Genome Editing Techniques for Food and Nutritional Security // Plants (2021) 10: 1423. doi: 10.3390/plants10071423

Tsers I. et al. Plant Soft Rot Development and Regulation from the Viewpoint of Transcriptomic Profiling // Plants (2020) 9: 1176. doi: 10.3390/plants9091176

Recombinant plasmids for the synthesis of dsRNA elicitin genes inf1 and inf2 for plant protection against *Phytophthora infestans*

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Spray-induced gene silencing (SIGS) is a promising approach for plant protection against pathogens. dsRNAs trigger degradation their complementary mRNA. This effect allows turn off the genes of both the plant and the pathogen at the level of translation.

We have selected *Phytophthora* genes, elicitins, the switching off of which will potentially lead to reduce pathogenicity, and tested various methods of processing potato exogenous dsRNA. The question of the effectiveness of SIGS against Phytophthora is being actively investigated, therefore determination of promising targets and processing parameters is our current task.

For the production of dsRNA genes *inf1* and *inf4* we constructed two expression vectors based on the plasmid L4440, dsRNA was developed in E. *coli* HT115. For processing, we used potato plants 6 weeks old. Control plants were treated with water, experimental ones with a solution of dsRNA of one of the genes or their combination. It has been shown that the treatment of plants protects them from phytophthora

The work supported by a grant from the President of the Russian Federation (MK-4311.2022.5).

The main publications of authors on the subject of the abstract:

Ivanov A.A.; Ukladov E.O.; Golubeva T.S. Phytophthora infestans: An Overview of Methods and Attempts to Combat Late Blight // J. Fungi (2021) 7: 1071. doi:10.3390/jof7121071

Ivanov A.A.; Tyapkin A.V.; Golubeva T.S. How Does the Sample Preparation of Phytophthora infestans Mycelium Affect the Quality of Isolated RNA? // Curr. Issues Mol. Biol. (2023) 45: 3517-3524. doi:10.3390/cimb45040230

Take-home message:

Two expression vectors based on the plasmid L4440 were constructed for the production of dsRNA genes inf1 and inf4

The treatment with dsRNA of inf1 and inf4 protects plants from Phytophthora infestans

Study of the effect of physiological parameters on a prolonged submergence tolerance of rice

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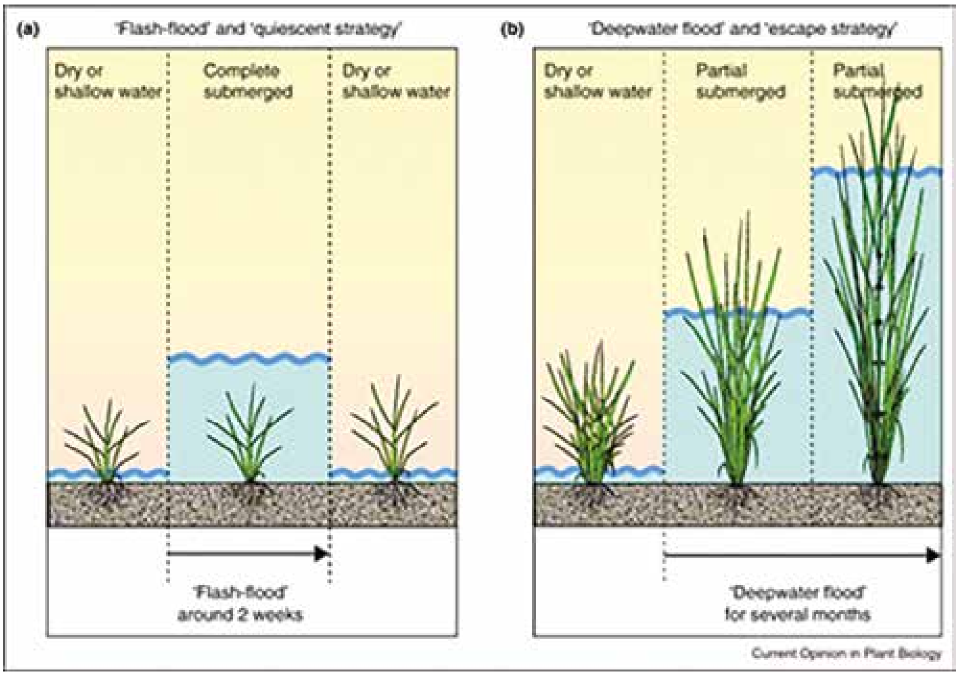
The report presents the results of the study of physiological parameters (germination, germination power, growth rate, as well as assessing the degree of development of the conducting system of the flag leaves of rice plants.) that affect a prolonged submergence tolerance of rice.A number of the studied samples revealed the potential to grow rapidly, overcome a large layer of water and accumulate vegetative mass. As a result of the evaluation of the conducting system of the flag leaf of rice plants, it was found that in plants with the Sub1 flood resistance gene, the conducting bundles were smaller in size compared to other samples, which means that stable samples use the restructuring of the conducting system as a resistance mechanism.The purpose of the study was to estimate the physiological parameters that affect a prolonged submergence tolerance of rice and vigorous emergency from under a layer of water.For the study there have been selected 180 rice varieties and samples, which were identified during crossing domestic varieties with Asian flood resistance genedonors in the laboratory of rice breeding and seed production of the ARC “Donskoy”.

The materials were prepared within the framework of the competition of the Russian Science Foundation in 2021 "Conducting fundamental scientific research and exploratory scientific research by small individual scientific groups" (Agreement No. 22-26-00246 of 12/21/2022).

The main publications of authors on the subject of the abstract:

П. И. Костылев, В. А. Голубова, Н. В. Калинина, Н. Н. Вожжова Влияние физиологических параметров растений риса на толерантность к длительному погружению в воду, Достижение науки и техники в АПК№1, 2023, стр. 4 doi: 10.53859/02352451_2023_37_1_4



Current Opinion in Plant Biology

Comparative study of germination of wheat grain distinguished by pericarp anthocyanin coloring under conditions of natural and induced aging

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Anthocyanins are biologically active secondary metabolites of plant. As natural antioxidants, anthocyanins neutralize cell-damaging reactive oxygen species under the influence of adverse environmental factors. In wheat (Triticum L.), despite the relevance of research, the relationship between the synthesis of secondary metabolites with protective adaptive functions and the molecular and genetic mechanisms of seed viability after long-term storage remains unstudied. To date, there is a well-characterized set of wheat genotypes based on the model variety Saratovskaya 29, which presents a different combination of alleles at the loci *Pp3* and *Pp-D1 (Purple pericarp)*, determining anthocyanin coloring of coleoptiles and pericarp. Such lines, which differ from each other only in anthocyanin coloration (and are similar in all other traits), are best suited for comparative physiological studies. The results showed a neutral role of anthocyanins in long-term seed longevities for 7-9 years under natural conditions of +20°C and +25°C. It was differ from the results obtained after artificial induced aging with elevated temperature of 48°C and 100% humidity for 72 hours (ISTA seed testing), where germination of anthocyanin-stained seeds was 20% higher than that of lines without anthocyanin pigment.

The study was supported by RSF 21-76-10024.

The main publications of authors on the subject of the abstract:

Gordeeva, E. I., Shoeva, O. Y., & Khlestkina, E. K. Marker-assisted development of bread wheat near-isogenic lines carrying various combinations of purple pericarp (Pp) alleles // Euphytica (2015) 203: 469-476. doi:10.1007/s10681-014-1317-8

Effect of single amino acid substitutions on the catalytic properties of asparagus divinyl ether synthase (AoDES)

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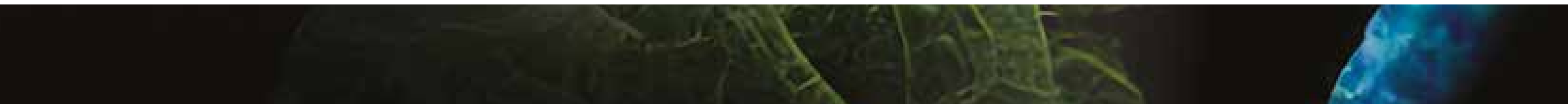
Divinyl ether synthases (DESs) are the enzymes catalysing the dehydration of fatty acid hydroperoxides to divinyl ether oxylipins, which exhibit antimicrobial and fungicidal activity. DESs, along with three other enzymes, namely allene oxide synthases (AOSs), hydroperoxide lyases (HPLs) and epoxyalcohol synthases (EASs), are members of the CYP74 clan of unusual P450 monooxygenases. AoDES is the first DES to biosynthesize the (1'Z)-isomers of divinyl ethers. Bioinformatic analysis allowed us to determine the hypothetical determinants of AoDES catalysis. Mutant forms with single substitutions retained DES activity, but the spectrum of divinyl ether isomers changed, and minor amounts of EAS and AOS products appeared. The combination of both mutations dramatically changed AoDES catalysis. Divinyl ethers were not detected. One of the main products was LTB4-like diol.

Bioinformatics analysis was carried out with financial support from the state assignment of the Federal Research Center "Kazan Scientific Center of the Russian Academy of Sciences". Catalytic studies of the AoDES mutant forms were performed under support of grant 23-14-00350 from Russian Science Foundation.

The main publications of authors on the subject of the abstract:

Gorina S.S. et al. Detection of divinyl eth er synthase CYP74H2 biosynthesizing (11Z)-etheroleic and (1'Z)-colnelenic acids in asparagus (Asparagus officinalis L.) // Phytochemistry (2022) 200:113212. doi: 10.1016/j.phytochem.2022.113212.



The induced susceptibility of plants to phytopathogens: physiological bases, regulation, consequences

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Plant susceptibility to pathogens is usually considered from the perspective of the loss of resistance. However, susceptibility cannot be equated with plant passivity since active host cooperation is required for the pathogen to propagate and cause disease. This cooperation consists of the induction of reactions called susceptible responses (SRs). Based on multiple transcriptome profiling studies, we predicted a set of plant SRs to the soft rot-causing phytopathogenic bacterium *Pectobacterium atrosepticum* and then verified some of these responses using biochemical, physiological, and molecular approaches. Based on the obtained results and systemic analysis of the literature, we highlighted two main categories of SRs according to their consequences. The SRs of the first type improve pathogen fitness in planta without promoting symptom manifestation, whereas those of the second type facilitate symptom development. Thus, we developed a theory of plant susceptible responses and clarified that their exogenous control is a promising disease management strategy. The work was supported by RSF (19-14-00194) and a government assignment for FRC KSC RAS.

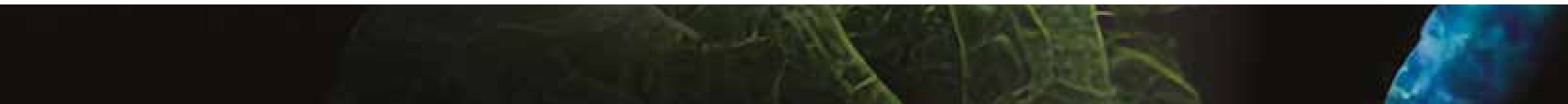
The main publications of authors on the subject of the abstract:

Gorshkov V. et al. Host plant physiological transformation and microbial population heterogeneity as important determinants of the Soft Rot Pectobacteriaceae–plant interactions // Seminars in Cell & Developmental Biology (2023). doi: 10.1016/j.semcdb.2023.01.002

Gorshkov V. et al. Plant susceptible responses: the underestimated side of plant–pathogen interactions // Biological Reviews (2022) 97 (1): 45-66. doi: 10.1111/brv.12789

Take-home message:

1. Plant susceptibility to pathogens arises only when a specific set of susceptible responses is induced.
2. Understanding susceptible responses in greater depth has high potential for the development of novel plant-protection approaches.



Comparative analysis of the transcriptome profiles of oilseed flax CDC Bethune and its mutant rdf1 with reduced fibre growth

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The identification of the molecular actors that carry out and regulate the key stages of plant fibre (PF) development - intrusive growth (IG) and cell wall thickening - is extremely relevant for understanding the growth and specialization processes of plant cells. In this regard, a comparative analysis of the transcriptomes of oilseed flax (CDC Bethune), and its mutant - reduced fibre 1 (rdf1), with reduced growth of PFs in both phloem and xylem is of considerable interest. Samples of different tissue types and stages of PF development were used to generate RNAseq data followed by bioinformatics analysis (HiSat2/StringTie/DESeq2). The intrusively growing phloem and xylem fibres were also characterized using immunochemistry and AFM techniques. The results of transcriptomic analysis combined with data on the composition and structure of fibre cell walls made it possible to form a pool of potential triggers affecting the growth and development of PFs. The data obtained provide a promising basis for further analysis of the functional specificity of gene products exhibiting differential expression in the rdf1 mutant.

Supported by the Russian Science Foundation (project №21-74-10131).

The main publications of authors on the subject of the abstract:

Gorshkov, O., Mokshina, N., Gorshkov, V. et al. Transcriptome portrait of cellulose-enriched flax fibres at advanced stage of specialization. Plant Mol Biol 93, 431–449 (2017). https://doi.org/10.1007/s11103-016-0571-7

Gorshkova, T., Chernova, T., Mokshina, N. et al. Transcriptome Analysis of Intrusively Growing Flax Fibers Isolated by Laser Microdissection. Sci Rep 8, 14570 (2018). https://doi.org/10.1038/s41598-018-32869-2

Transcriptomics as a basis to choose perspective genes for manipulations to improve crops

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The goal of any plant breeding program is to improve the quality of a target crop. Crop quality is a comprehensive feature largely determined by biological background. The toolbox is suggested to search for genes suitable for the effective manipulation of crop quality parameters. A key step is to identify the genes with spatial and temporal pattern of expression that suits the development of the targeted parameter. The whole pipeline includes: a) identification of the temporal and spatial localization of the key stages of the target crop parameter development; b) transcriptomic analysis of the corresponding tissues and stages; c) identification of genes with tissue-and/or stage-specific expression patterns, d) characterization of the relationship between target parameters of crop quality and expression of genes important at the key stages in the process development on a statistically justified number of genotypes over several seasons, e) characterization of the selected gene polymorphism in different genotypes and chromosome mapping for breeding purposes; f) modification of the set and level of gene expression using traditional breeding or genomic editing approaches. Supported by RSF grant #19-04-00361.

The main publications of authors on the subject of the abstract:

Galinousky D., Mokshina N., Padvitski T., Ageeva M., Bogdan V., Kilchevsky A., Gorshkova T. The Toolbox for Fiber Flax Breeding: A Pipeline From Gene Expression to Fiber Quality // Frontiers in Genetics. – 2020. doi:10.3389/fgene.2020.589881

Mokshina N. et al. FIBexDB: a new online transcriptome platform to analyze development of plant cellulosic fibers. New Phytologist, 2021;231:512–515.

CuO nanoparticles in clonal micropropagation of woody plants

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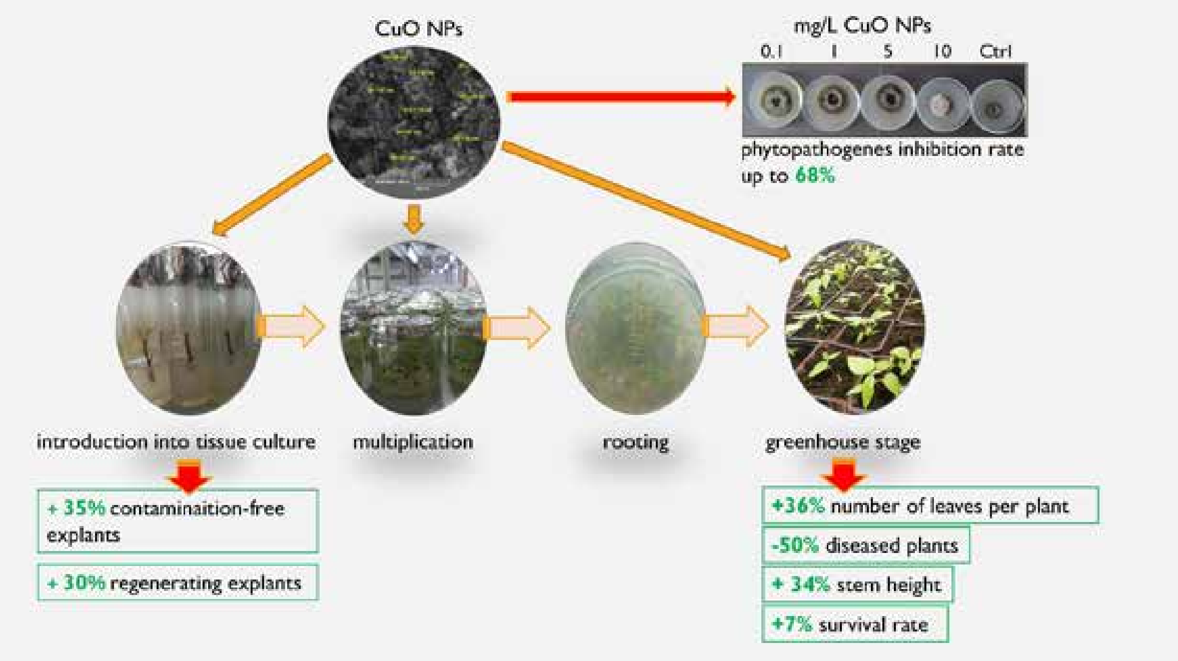
Возможность использования наночастиц в технологии клонального размножения продиктована их высокой антибактериальной и антифунгальной активностью в отношении многих представителей эпифитной микрофлоры растений. Было показано, что внесение наночастиц CuO в состав питательной среды WPM в 2 испытуемых концентрациях 5 и 10 мг/л на этапе введения в культуру *in vitro* молодых побегов тополя ПОК (Пирамидально-осокоревый Камышинский) позволяет получить до 90% стерильных эксплантов (в контроле 65%). При культивировании эксплантов на питательной среде WPM, содержащей 5 мг/л CuO, число растений с хорошо развитыми пазушными побегами составило 70% (в контроле 40%). Использование наночастиц при переводе растений тополя в условия *ex vitro* (теплица) способствовало улучшению показателей роста опытных растений тополя за счет снижения на 5% количества пораженных фитопатогенами растений и повышения их приживаемости. Установлен антифунгальных эффект наночастиц CuO, при этом действие на представителей полезной почвенной микрофлоры был минимальным.

The main publications of authors on the subject of the abstract:

Grodetskaya TA, Evlakov PM, Fedorova OA, Mikhin VI, Zakharova OV, Kolesnikov EA, Evtushenko NA, Gusev AA. Influence of Copper Oxide Nanoparticles on Gene Expression of Birch Clones In Vitro under Stress Caused by Phytopathogens. Nanomaterials. 2022. Vol. 12. No. 5. P. 864. doi: 10.3390/nano12050864 (Q1)

Take-home message:

Наночастицы оксида меди увеличивают процент стерильных и жизнеспособных эксплантов в условиях *in vitro* и при переводе микроклонов в закрытый грунт



Genetic diversity of oil crops of the Russian breeding for the development of new varieties and hybrids which is determined using molecular markers

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Golovatskaya A.V.

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Genetically diverse germplasm containing gens controlling valuable for breeding traits is necessary to develop new varieties of oil crops characterized with high productivity, resistance to biotic and abiotic stresses. The systems of DNA markers were developed to estimate the genetic diversity and the marking of appropriate gens of sunflower and oil flax in the VNIIMK. Sunflower and flax developed in the different ecological zones of cultivation, which were estimated using microsatellite markers are characterized with the genetic diversity. The results of estimation of AMOVA flax showed the most part of the total dispersion 71%, is conditioned by the differences between cultivars, 29% by the differences between individuals within cultivars. Concerning sunflower samples, the most part of the total dispersion 91%, is conditioned by the differences between lines within each collection, 3% by the differences between collections. Sunflower samples, which were estimated using markers of mutation of high oleic oil, resistance to the different races of the most dangerous pathogens, to herbicides, showed the wide diversity and have a potential for the development of promising hybrids.

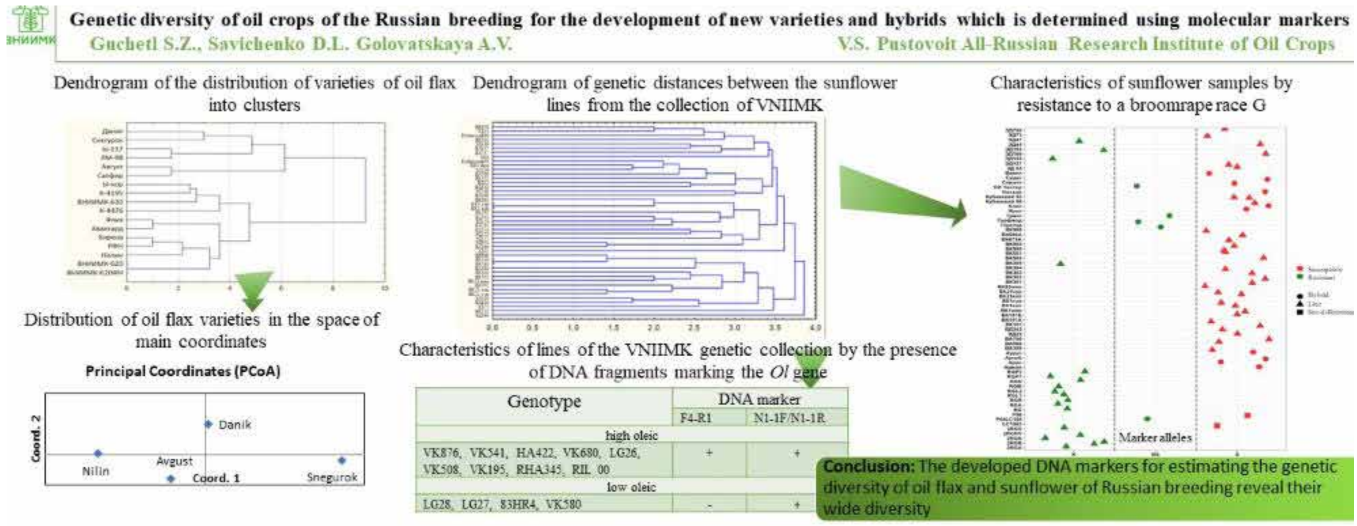
<u>The main publications of authors on the subject of the abstract:</u>

Guchetl S. Z. et al. Analysis of the structure of linseed flax varieties based on polymorphic microsatellite loci // Agricultural Science Euro-North-East (2022) 23: 184-193. doi: 10.30766/2072-9081.2022.23.2.184-193

Guchetl S.Z., Savichenko D.L. A linkage of gene of resistance to a broomrape race G with microsatellite loci of a sunflower line-donor RGP1 of VNIIMK'S breeding // Oil crops (2021) 2: 3-9. doi: 10.25230/2412-608X-2021-2-186-3-99

<u>Take-home message:</u>

Sunflower and flax were estimated using markers that reveal genetic diversity, high oleic oil mutations, resistance to different races of the most harmful pathogens, herbicides, showed the wide diversity for the development of varieties and hybrids



Genetic diversity of oil crops of the Russian breeding for the development of new varieties and hybrids which is determined using molecular markers

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Dendrogram of the distribution of varieties of oil flax into clusters

Distribution of oil flax varieties in the space of main coordinates

Dendrogram of genetic distances between the sunflower lines from the collection of VNIIMK

Characteristics of lines of the VNIIMK genetic collection by the presence of DNA fragments marking the *Ol* gene

Genotype	DNA marker	
	F4-R1	N1-1F/N1-1R
high oleic		
VK876, VK541, HA422, VK680, LG26, VK508, VK195, RHA345, RIL 00	+	+
low oleic		
LG28, LG27, 83HR4, VK580	-	+

Characteristics of sunflower samples by resistance to a broomrape race G

Conclusion: The developed DNA markers for estimating the genetic diversity of oil flax and sunflower of Russian breeding reveal their wide diversity

Molecular approaches in the study of the racial composition of the causative agent of wheat yellow rust

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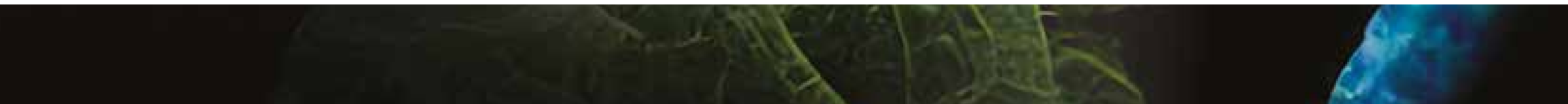
Yellow (stripe) rust is the damaging diseases world-wide on wheat. *Puccinia striiformis f.sp. tritici (Pst)* is a fungus caused this disease. The pathogen is highly mobile, either through the movement of people, trade intensification, or areal dispersion. The fungus has the capability to rapidly spread to new regions and crop varieties. Molecular markers, particularly microsatellites, have been reported to be important tools for deciphering pathogen population structure, invasion sources, and migration history (Ali et al., 2017). In these studies, microsatellite analysis was used for genotyping of Russian populations of the yellow rust pathogen. Twenty SSR markers were used. Eighty two isolates obtained from common and durum wheat and triticale in 2019-2020 from European, Asian and North Caucasuian regional (Pst) populations were tested. Most of the markers were polymorphic and revealed from 2 to 4 alleles. No significant differentiation beetwen regional pathogen populations was revealed, which is consistent with the results of virulence studies (Gultyaeva et al., 2022).

This study was funded by the Russian Science Foundation (project number 19-76-30005).

The main publications of authors on the subject of the abstract:

Gultyaeva E., Shaydayuk E., Kosman E. Virulence Diversity of Puccinia striiformis f. sp. tritici in common wheat in Russian regions in 2019–2021. Agriculture (2022) 12(11):1957. doi.org/10.3390/agriculture12111957

Shaydayuk E.L., Gultyaeva E.I. A highly aggressive invasive race group PstS2 in Russian populations of the wheat yellow rust pathogen. Mikologia I Fitopatogogia (2023) 57(1):60-66 DOI: 10.31857/S0026364823010129



Genetic regulation of seed shattering in *Fagopyrum esculentum*

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Seed shattering in buckwheat is almost unstudied, although his knowledge could be very useful for improving buckwheat as a crop. We studied the processes which happen in the pedicels during abscission and suggested a list of candidate genes which could be responsible for abscission breakage (non-shattering phenotype) in cultivars. Transcriprome analysis of shattering and non-shattering buckwheat allowed us to describe the dynamics of AZ development. In buds we see that ABA response genes are upregulated and its degradation is downregulated. In flowers and fruits we didn't observe the genes, which could directly affect ABA biosynthesis or degradation, but we see the genes providing stress response. Cell wall biosynthesis is intensified on the bud stage, when AZ is being build. Then cell wall biosynthesis reduces, providing evidence of meristem nature of AZ composing cells. In fruits we observed the activation of particular cell wall hydrolyzing enzymes, which are supposed to activate abscission. The most candidate to be a regulator of fruit abscission in buckwheat is JOINTLESS, which was previously described in tomato.

The main publications of authors on the subject of the abstract:

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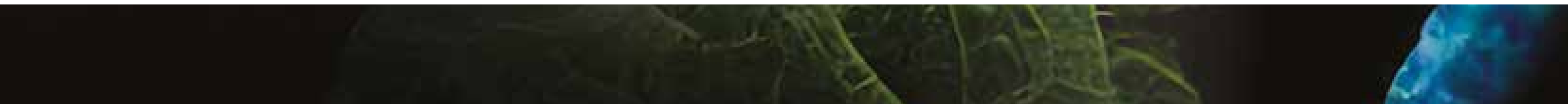
Take-home message:

Transcriprome analysis of shattering and non-shattering buckwheat allowed us to describe the dynamics of AZ development. The most plausible candidate responsible for seed shattering in buckwheat is JOINTLESS.



The role of symbiotic rhizobacteria in drought resistance of tomato plants (*Solanum lycopersicon*)

Gurina Anastasia, Frolova Nadezhda*, Lukasheva Elena, Kuznetsova Alena, Shumilina Julia*, Alhajje Katrina*, Bilova Tatiana, Orlova Anastasia*, Silinskaya Svetlana*, Cherevatsakya Maria, Shaposhnikov Alexander***, Syrova Daria***, Frolov Andrej*, Belimov Andrey*****

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Natural tolerance mechanisms bring new opportunities in agriculture due to its efficiency in growth promotion and enhanced stress tolerance. One of the natural mechanisms employing symbiosis of plants with Plant Growth Promoting Rhizobacteria, was shown to be able to reduce the negative effects of drought on plant biomass productivity. The observed protective effect could be attributed to the activity of ACC desaminase, the enzyme, which stimulates outflow of this 1-aminocyclopropane-1-carboxylate from plant roots, leading to decreased level of ethylene and it's hormonal inhibitory effect on plant biomass under stress conditions.

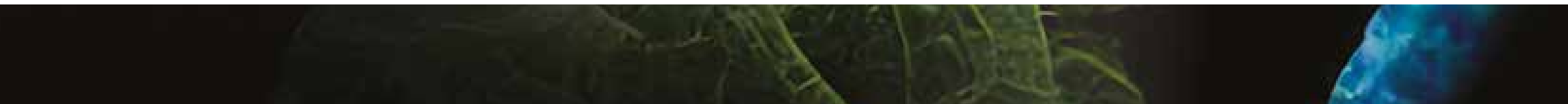
To address this problem, we investigated the effect of ACC deaminase expression in PGPRs on the dynamics of the tomato leaf proteome and metabolome in response to drought. The inoculation-specific plant responses to drought were comprehensively characterized at the levels of physiology and proteome. The obtained proteomics data were also integrated with the obtained data of identified metabolites and their dynamics.

Acknowledgment: Agreement No. 075-15-2922-320 dated 04/20/2022

The main publications of authors on the subject of the abstract:

Belimov A.A et al. Pseudomonas brassicacearum strain Am3 containing 1-aminocyclopropane-1-carboxylate deaminase can show both pathogenic and growth-promoting properties in its interaction with tomato. J. Exp. Bot., 2007, 58, 1485-1495.

Belimov A.A et al. ACC deaminase-containing rhizobacteria improve vegetative development and yield of potato plants grown under water-limited conditions. Aspects of Applied Biology, 2009, 98, 163-169.



Polimorphism of Rpi-vnt1 gene in landraces of genus Solanum sect. Petota

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Primitive potato cultivated species or landraces are early domisticated forms of potato. Accoding to some researcher, landraces are intermediate link between wild potatoes and *S. tuberosum* L. *Rpi-vnt1* - is late blight resistance gene discovered in South American wild species *S. venturii* Hawkes & Hjert. Possibly these gene is homologues of unsequenced gene *Rpi-phu1*, which was early founded in *S.phureja* Juz et Buk. - one of landraces species. But none of sequences homologues from landraces were functional, although previously positional markers showed correlation of late blight resistance with loci of *Rpi-phu1* gene. We research *Rpi-vnt1* polimorphism within group of landraces using in silico analysis of genomes and sequenced markers fragments of Rpi-vnt1 from samples contrasting in resistance to late blight from VIR collection. In landraces genomes we found several copies of *Rpi-vnt1* gene and analysing sequences of markers fragment in VIR collection we found different allelic variants. We suppose that one allelic variant is functional and preliminary genetic analysis of hybrid population confirmed correlation of developed CAPS marker wwith field resistance.

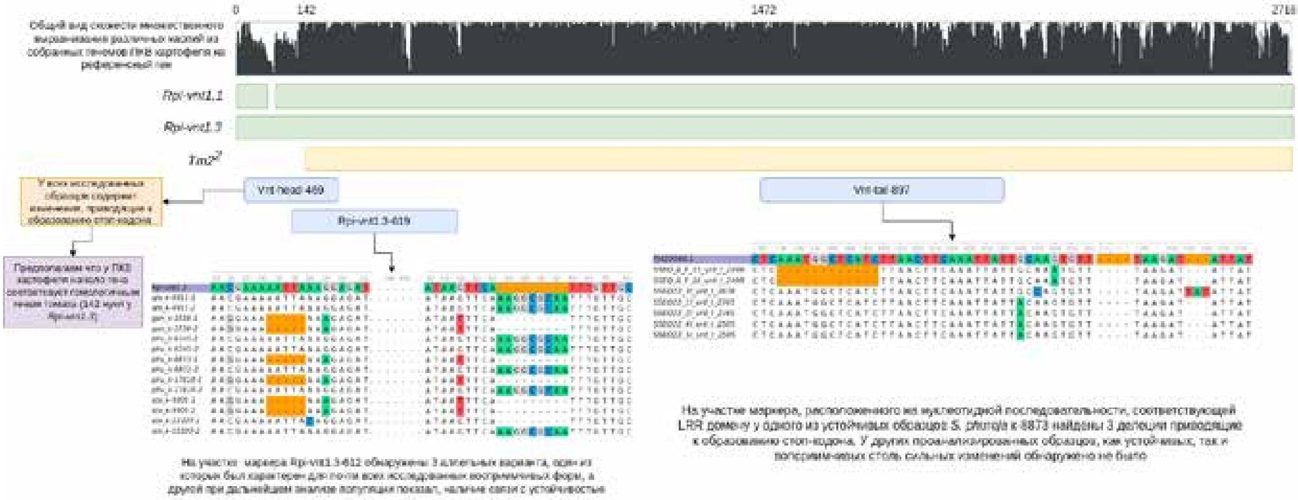
This research was supported by Russian Science Foundation, project No 22-26-00111

<u>The main publications of authors on the subject of the abstract:</u>

Gurina A.A., Alpatieva N.V., Chalaya N.A., Mironenko N.V., Khiutti A.V., Rogozina E.V. Homologs of Late Blight Resistance Genes in Representatives of Tuber-Bearing Species of the Genus Solanum L. // Russ J Genet. 2022; 58(12):1473–1484. DOI: 10.1134/S1022795422120043.

<u>Take-home message:</u>

Rpi-vnt1 is the most likely candidate late blight resistance genes among potatoes landraces
Several homologues of these gene were found in landraces genomes.
One of homologues have presumably functional allelic variant



На участке маркера Rpi-vnt1 3-612 обнаружены 3 аллельных варианта, один из которых был характерен для почти всех исследованных восприимчивых форм, а другой при дальнейшем анализе популяции показал наличие связи с устойчивостью

На участке маркера, расположенного на нуклеотидной последовательности, соответствующей LRR домену у одного из устойчивых образцов S. phureja к-8873 найдены 3 делеции приводящие к образованию стоп-кодона. У других проанализированных образцов, как устойчивых, так и восприимчивых столь сильных изменений обнаружено не было

Genomic and post-genomic technologies in the improvement of apricot assortment

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Industrial apricot production has recently faced serious economic problems due to the widespread spread of plum pox virus (PPV), which causes Sharka disease.

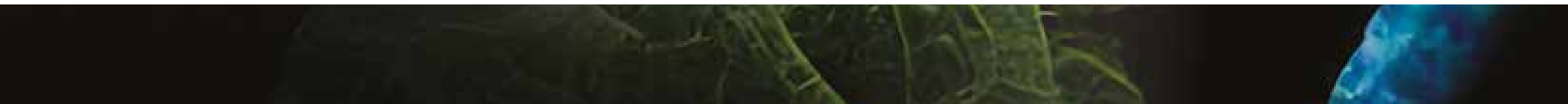
It is impossible to obtain completely tolerant forms of apricot to this disease by traditional breeding methods. The technology of integrating the RNA interference cassette to the virus envelope protein gene into the plant genome makes it possible to increase plant resistance to PPV.

Were obtained by genetic modification with transformation efficiencies of 32.2% for Kioto variety, 47.5% for Krokus, 13.8% for Spark Tavrida and 30.7% for Yuzhanin 75 independent transgenic lines of chimeric apricot plants by forming a rooting system expressing RNA interference sequences to the virus envelope protein gene of Sharka using pCam-PPV-rolB-dsRed vector.

Of the 75 chimeric lines obtained, 52 were analyzed by PCR. Of these, 7 lines were contaminated with agrobacterial vir - group genes, 46 lines contained a heterologous DNA insertion (hptll gene), and 41 lines contained the aPPV -pdk intron - sPPV target sequence. The research is supported by the Kurchatov Genomic Center of the NBG - NSC of the RAS (075-15-2019-1670).

Take-home message:

In the course of the studies, was developed a protocol to obtain chimeric apricot plants possessing a root system expressing RNA interference sequences to the plum pox virus envelope protein gene.



Gravity response and metabolism of flax fiber callose at the level of gene expression

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Двигательные реакции растений, относящимся к тропизмам, осуществляются с использованием механизмов роста растяжением. В данном исследовании при гравиответе изучались клетки, закончившие свой рост и формирующие третичную клеточную стенку (ТКС). Ранее нами было показано, что реабилитация пространственного положения стебля растения льна связана с модификацией волокон, формирующих конститутивно и индуцибельно ТКС, что предполагает важную роль таких клеток в гравиответе. Было показано, что волокна приобретали четкообразную форму - расширенные участки клетки чередовались перетяжками, в области которых обнаруживалась каллоза – 1,3-глюкан, роль которого не исследовалась. Здесь мы оценивали экспрессию генов каллозосинтаз (CALSs) и β-1,3-глюканаз (BGs), отвечающих за метаболизм каллозы. Анализ транскриптов, размещенных в базе данных FIBexDB, для волокон контрольных и гравистимулированных (8, 24, 96 ч) растений выявил незначительное количество генов CALSs и BGs, экспрессия которых изменялась. После 8 ч гравистимуляции примерно в 2 раза возрастала экспрессия генов Lus10042478 (AT3G14570, CALS8) и Lus10033689 (AT4G03550, CALS12), тогда как экспрессия генов Lus10002807 (AT3G57240, BG3) и Lus10027860 (AT3G57260, BG2) иногда (24ч) возрастала на порядок. Согласно литературным данным гомологичные гены проявляли повышенную экспрессию при патогенезе и/или регуляции функции плазмодесм.

Исследование выполнено при поддержке гранта РНФ № 23-24-00612

The main publications of authors on the subject of the abstract:

Ibragimova NN, Ageeva MV, Gorshkova TA. Development of gravitropic response: unusual behavior of flax phloem G-fibers // Protoplasma. 2017. V. 254. P.749–762.

Biogenic cilica in fruits of Boraginaceae

Ikkonen E.N., Chazhengina S.Y.*, Nikolaeva N.N., Teteryuk L.V.***, Sibelev O.S.*, Prokopovich P.F.*,**
Fedorov A.A*, Setin V.N.**, Vasjukov V.M.*****, Bondareva V.V.*****, Malov D.N.*****, Chuvashov A.V.*******

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***Institute of Biology of the Komi Research Centre, Russian Academy of Sciences, Syktyvkar, Russia,
****Scientific Research Institute of Medicinal and Aromatic Plants, Moscow, Russia,
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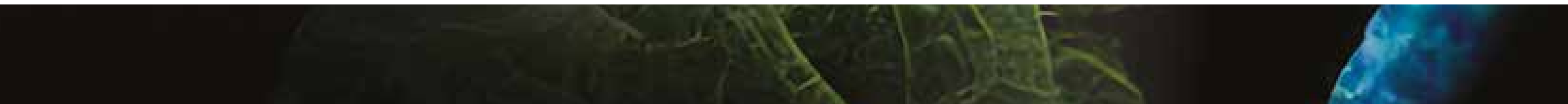
The understanding of biomineralization in plants is critical in designing new biomimetic materials for biomedical, optical and other applications. This study focused on Boraginaceae family, in some species of which mineralization of the pericarp cells of erem was noted. Scanning electron microscopy with energy-dispersive X-ray spectroscopy and Raman spectral studies were used to identify minerals for a wide range of species and to study their spatial distribution as well as co-location with organic substance and metal ions. Analytical studies showed that silicification ocurres in the pericarp of most but not all studied species. The silica was presented as a dense layer on the outer surface of erem with variation in the size of this layer depending of plant species. Elemental analysis of pericarp cross sections showed that structured silica deposits with a high specific area and porosity are located behind the surface layer. In each arrangement the silica particles are chemically pure and crystallographically amorphous. Biosilica present ordered hierarchical porous structures giving the material specific properties with possible application in industry including nanotechnologies.

The main publications of authors on the subject of the abstract:

Minerals in plants: case study of lithospermum arvense and celtis fruits Chazhengina S.Y., Ikkonen E.N., Prokopovich P.F., Nikolaeva N.N. Biogenic - abiogenic interactions in natural and anthropogenic systems. VII International Symposium. Saint-Petersburg State University. 2022. C. 96-97.

Take-home message:

Biosilica formed in erem pericarp sells of Boraginaceae family present ordered hierarchical porous structures giving the material specific properties with possible application in different types of industry including nanotechnologies.



Level of lipid-transporting protein and mRNA encoding it in pea plants inoculated with rhizosphere bacteria

Ivanov R.S., Martynenko E.V., Arkhipova T.N., Akhiyarova G.R., Sharipova G.V., Galin I.R., Seldimirova O.A., Nuzhnaya T.V., Finkina E.I.*, Ovchinnikova T.V.*, Kudoyarova G.R.

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The plant-growth-promoting (PGP) bacteria in the rhizosphere stimulate plant growth and increase their productivity. These bacteria induce changes in the formation of the apoplast barriers and thereby affect water transport in plants. Lipid transfer proteins (LTPs) are known to be involved in suberin deposition in the Casparian bands of pea roots thus reinforcing apoplast barriers. We investigated the effects of PGP bacteria *P. mandelii* IB-Ki14 on LTPs, formation of the Casparian bands, hydraulic conductance and activity of aquaporins (AQPs) in pea plants. Real time PCR showed a 1.6-1.9-fold up-regulation of the PsLTP-coding genes and an increase in the abundance of LTP proteins in the phloem of pea roots induced by the treatment with *P. mandelii* IB-Ki14. We also have shown that *P. mandelii* IB-Ki14 stimulates deposition of suberin, in the biosynthesis of which LTPs are involved, and increases aquaporin activity, which in turn prevents a decrease in hydraulic conductance due to formation of the apoplast barriers in pea roots.

This research was funded by the Russian Scientific Foundation (grant number 21-14-00070).

<u>The main publications of authors on the subject of the abstract:</u>

Martynenko E.V. et al. Effects of a pseudomonas strain on the lipid transfer proteins, appoplast barriers and activity of aquaporins associated with hydraulic conductance of pea plants // Membranes (2023) 13: 208. doi: 10.3390/membranes13020208

Akhiyarova G.R. et al. Effects of salinity and abscisic acid on lipid transfer protein accumulation, suberin deposition and hydraulic conductance in pea roots // Membranes (2021) 11: 762. doi: 10.3390/membranes11100762

<u>Take-home message:</u>

P. mandelii IB-Ki14 stimulates deposition of suberin, in the biosynthesis of which LTPs are involved, and increases aquaporin activity to compensate for decrease in hydraulic conductivity due to formation of the apoplast barriers in pea roots.

World collection of common hops (*Humulus lupulus* L.)

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The collection of the gene pool of ordinary hops (*Humulus lupulus* L.) is a source of valuable source material for the creation of new highly productive varieties in demand in agricultural production.

This collection consists of populations of female plants with a set of phenological, morphological and economically important features, has been preserved since 1981 and is maintained in the Chuvash Research Institute of Agricultural Sciences – a branch of the FGBNU FANC of the North-East. It is a living variety and consists of 244 varieties: 74 from various regions of Russia and 170 from foreign countries. This is a large gene pool of breeding, local and wild forms in the fourth tab, which is on a par with the collections of research institutions of foreign countries of the world.

Basic research:

- targeted introduction search and attraction of new samples from the Russian Federation and foreign countries;
- documentation of samples by creating and maintaining an information database using unified descriptors;
- comprehensive study of gene pool samples, identification of sources of economically valuable traits for breeding research;
- creation and maintenance of a collection of valuable ex situ samples.

The main publications of authors on the subject of the abstract:

Osipova Yu. S., Leontieva V. V., Ivanova I. Yu. Features of the hop breeding process //Gene pool and plant breeding. – 2020. – pp. 82-85.

Osipova Yu. S., Ivanova I. Yu., Leontieva V. V. Assessment of ecological sustainability of hop varieties // Siberian Bulletin of Agricultural Science. – 2020. – Vol. 50. – No. 1. – pp. 32-39.

Stress-resistance of plants as strategy and tactics: genomic super-molecular-proteomic nature of developmental biology

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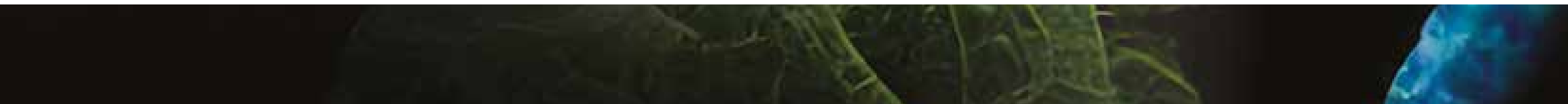
From the perspective of eco-genomic adaptation of plants, from the position of interdisciplinary science -supramolecular physical chemistry, the dynamics of topologically associated supra-blocks of the total chromatin matriciel (TChrM) is considered: nucleoplasm,(eu-, hetero-, chromatin) and nuclear matrix. On the interface of which, an analysis of the proteo-supermolecular reorganization of the ensembles: "linker", "core" histones and non-histones in the genetic subsystems of individual plant organs (root → mesocotyl → coleoptile) is presented, in the process of initiating a coordinated-regular growth, collection mature embryos of wheat seeds , when switching development routines. The original donor phenotype (spring) → transferred to the winter phenotype → transferred again to the spring phenotype. Based on the distribution of nucleosomal arginine-rich "core" histone (H3-H4)" on the interface of TChrM supra-blocks of genomic subsystems: donor (spring-mesocotyl) → winter donor (root) → again spring-phenotype (highly differentiated embryo), the combinatorial-barrier principle of the formation of proteomic ensembles is possible, in the role of potential epigenetic networks of the "histone code", in the conditions of the environmental ecosystem.

The main publications of authors on the subject of the abstract:

Ivanova E.A. Genetic-Proteomic Basis as a Morpho-Dynamic System, Strategies and Tactics of Plant Ecogenetic-Stress Resistance // Journal of Stress Physiology & Biochemistry, Иркутск – 2022 - 18, №4 - 73-88.

Иванова Э.А. Эко-генетическая стресс-устойчивость растений, как стратегия и тактика: супер-молекулярно-протеомного, морфодинамического дизайна физико-химической природы биологии развития //Научный журнал Актуальные вопросы биологической физики и химии. Севастополь. – 2022 – 7, №1 – 166-175.



DNA binding properties of *Nicotiana benthamiana* protein encoded by a methanol-inducible gene 21

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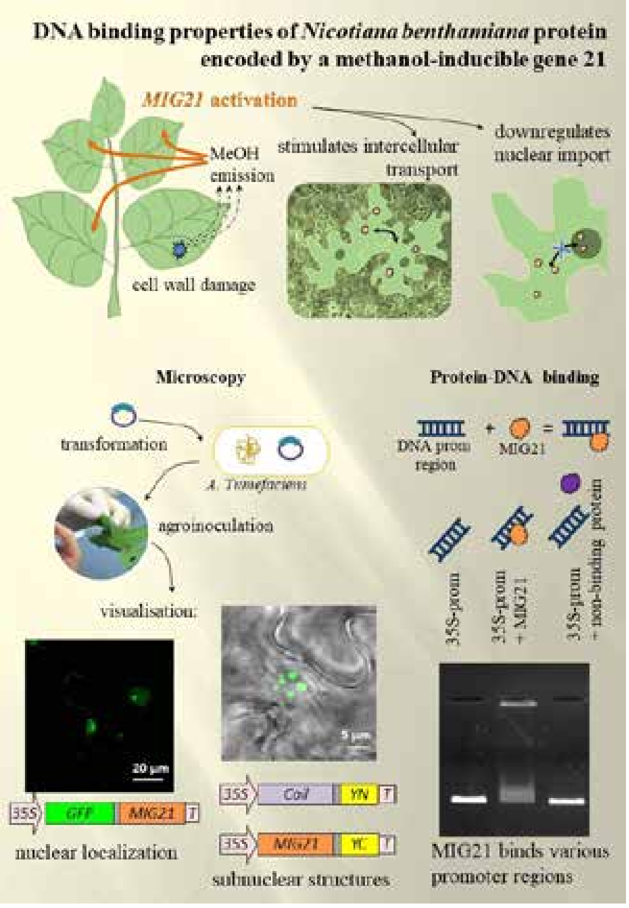
Plant cell wall damage results in the emission of multiple volatile organic compounds including gaseous methanol (MeOH). MeOH was demonstrated to be a signal molecule launching plant defense reactions. Although the mechanism of MeOH action is unknown it was shown that it activates the expression of methanol-inducible genes (MIGs) among which is *MIG21*. *MIG21* encodes MIG21 which does not share any homology with annotated proteins. MIG21p affects the intercellular and nucleocytoplasmic transport of macromolecules. Using transient expression in *Nicotiana benthamiana* and fluorescent microscopy we have demonstrated that MIG21p fused with fluorescent protein has nuclear localization predominantly occupying nucleolus and other subnuclear structures. To clarify MIG21p function we performed protein *in vitro* binding with several known promoter sequences followed by in-gel retardation assay. MIG21p was shown to bind various promoter regions including its own promoter. Taking into account MIG21p nuclear localization and its ability to interact with DNA we could speculate that it performs regulatory functions during plant defense reactions.

The study was supported by RSF grant №22-24-00895



The role of cytokinins and regulatory domains of the NIN transcription factor in the control of nodule morphogenesis in legumes

Kantsurova E.S., Ivanova A.N.*, Kozyulina P.Yu., Dolgikh A.V., Pavlova O.A., Dolgikh E.A.

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The development of legume-rhizobial symbiosis results in the formation of a special organ called a nodule. Previous studies revealed the nature of the infection process and early stages of organogenesis in nodulation. However, the later stages remain poorly understood. Our work was focused on elucidating the structural and molecular changes, occurring in the mature nodule.

It was suggested that nodule morphogenesis involves cytokinins and a complex of master regulators of legume-rhizobial symbiosis development, including the IPD3 and NIN transcription factors. Based on the comparative analysis, some specific structural motifs in NIN transcription regulator were found and analyzed. The role of *NIN* promoter elements regulated by cytokinins in the control of morphogenesis was also investigated.

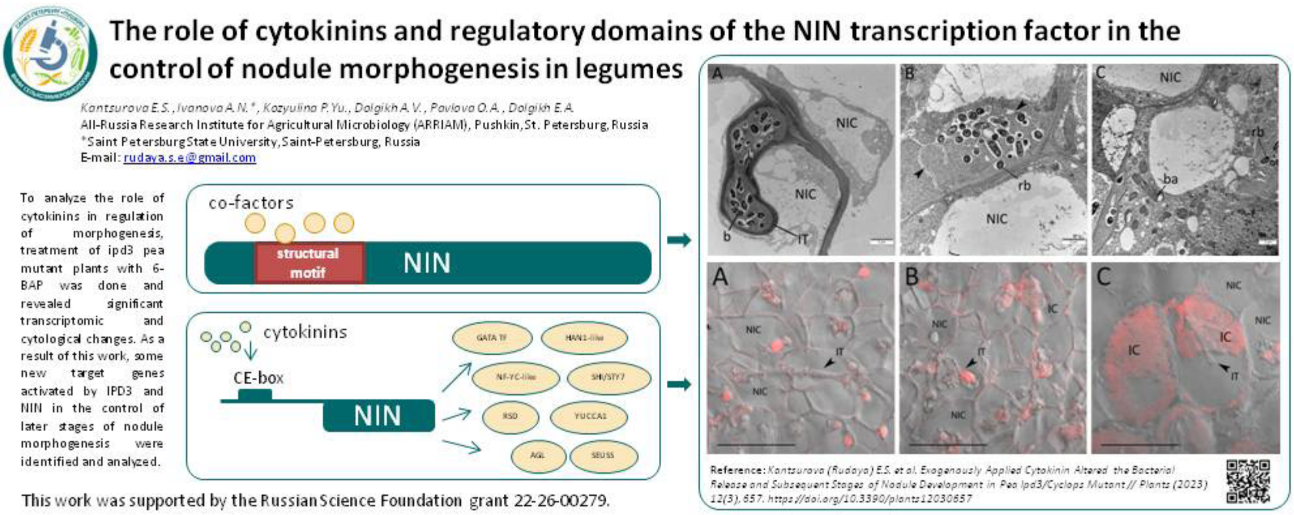
To analyse the role of cytokinins in regulation of morphogenesis, treatment of *ipd3* pea mutant plants with 6-BAP was done and revealed significant transcriptomic and cytological changes. As a result of this work, some new target genes activated by IPD3 and NIN in the control of later stages of nodule morphogenesis were identified and analyzed.

Was supported by the RSF grant 22-26-00279

<u>The main publications of authors on the subject of the abstract:</u>

Rudaya E.S. et al. Regulation of the Later Stages of Nodulation Stimulated by IPD3/CYCLOPS Transcription Factor and Cytokinin in Pea Pisum sativum L. // Plants (2022) 11(1), 56. https://doi.org/10.3390/plants11010056

Kantsurova (Rudaya) E.S. et al. Exogenously Applied Cytokinin Altered the Bacterial Release and Subsequent Stages of Nodule Development in Pea Ipd3/Cyclops Mutant // Plants (2023) 12(3), 657. https://doi.org/10.3390/plants12030657



The role of cytokinins and regulatory domains of the NIN transcription factor in the control of nodule morphogenesis in legumes

Kantsurova E.S., Ivanova A.N., Kozyulina P.Yu., Dolgikh A.V., Pavlova O.A., Dolgikh E.A.*
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To analyze the role of cytokinins in regulation of morphogenesis, treatment of ipd3 pea mutant plants with 6-BAP was done and revealed significant transcriptomic and cytological changes. As a result of this work, some new target genes activated by IPD3 and NIN in the control of later stages of nodule morphogenesis were identified and analyzed.

This work was supported by the Russian Science Foundation grant 22-26-00279.

Reference: *Kantsurova (Rudaya) E.S. et al. Exogenously Applied Cytokinin Altered the Bacterial Release and Subsequent Stages of Nodule Development in Pea Ipd3/Cyclops Mutant // Plants (2023) 12(3), 657. https://doi.org/10.3390/plants12030657*

Assessment of introduced species of *Miscanthus* in the conditions of the continental climate of the forest-steppe of Western Siberia

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Plants were planted in the Novosibirsk region in 2017. They showed resistance to a combination of local ecological factors. They were not affected by diseases and pests during 3 years of introduction. All introduced *Miscanthus* plants were found to be resistant to local winter temperatures during the study period. *M. sinensis, M. Sacchariflorus* differed in flowering rhythms (end of August - September), M. giganteus did not bloom during the years of observation. The productivity of *M. sinensis* and *M. Sacchariflorus* ranged from 210 to 332 g/m2 during biomass harvesting in the fall in the dying phase. The productivity of *M. giganteus* was within 168 g/m2 in the growing phase. This confirms the best adaptive function *of M. sinensis* and *M. Sacchariflorus* to growing conditions. Assessing the quality of the obtained raw materials, the following promising samples with the maximum content of cellulose (49-53%) and low content of lignin (17-19%) stand out - *M. sinensis* and *M. Sacchariflorus.* The biomass of *M. giganteus* contains 47% cellulose. *M. sinensis* and *M. sacchariflorus* are among the promising specimens with high productivity and for use in the pulp and paper industry.

This work was supported by the budget project № FVNR- 2022-0018 of the ICG SB RAS.

The main publications of authors on the subject of the abstract:

Kapustyanchik S.Yu., Burmakina N.V., Yakimenko V.N. Assessment of the ecological and agrochemical state of agrocenosis with long-term cultivation of miscanthus in Western Siberia // Agrochemistry. - 2020. - No. 9. - P. 65-73.

Yakimenko VN, Kapustyanchik S. Yu., Galitsyn G. Yu. Cultivation of miscanthus in the continental regions of Russia //Agriculture. -2021. - No. 2. - S. 27

Non-invasive whole-plant imaging of salicylic acid activity

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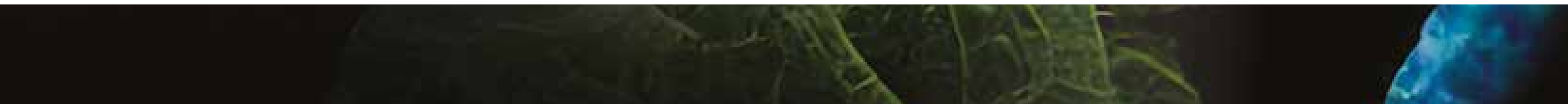
Plant hormone salicylic acid acts as a key player in the regulation of signalling networks involved in the reaction of plants to pathogens. Despite the utmost importance of this molecule for plant physiology, molecular tools for non-invasive visualisation of its activity in vivo are still lacking. Previously, we demonstrated that fungal bioluminescence pathway could be integrated into plant metabolism, creating plants with self-sustained luminescence (Mitiouchkina et al. 2020). In this study, we have developed a salicylic acid biosensor by controlling luciferase expression with the salicylic acid-responsive promoter pWRKY70 (Lehmann et al. 2020) while the rest of the fungal bioluminescence genes were constitutively expressed.We showed that luminescence response was activated by salicylic acid in transient expression assays. We then created Nicotiana benthamiana lines stably expressingthe sensor. We showed that transgenic pWRKY70-nnLuz plant lines began to glow in response to treatment with salicylic acid, proving that the luminescent biosensor was functional. The study was funded by RFBR and GACR, project number 20-54-26009.

The main publications of authors on the subject of the abstract:

Mitiouchkina T et al. Plants with genetically encoded autoluminescence// Nat Biotechnol (2020) Aug;38(8):944-946. doi: 10.1038/s41587-020-0500-9.



Analysis of the genome structure and its variations in potato cultivars grown in Russia

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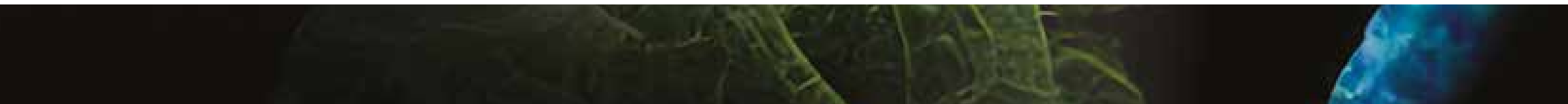
Solanum tuberosum L. is one of the most important agricultural crops grown almost all over the world. Potato genomic sequences pave the way for the study of molecular variation associated with diversification. We have assembled the genomic sequences of 15 tetraploid S. tuberosum potato varieties growing in Russia. We have identified protein-coding genes, identified orthologous groups, and characterized conserved and variable parts of the pangenome and the repertoire of NBS-LRR genes. We have identified copy number variations in the genomes of Russian varieties and South American varieties, conducted a comparative analysis, and identified genes associated with CNV. We have reconstructed complete assemblies of potato plastomes. Based on these assemblies, single nucleotide polymorphisms, insertions and deletions, microsatellites were identified, and the types of potato chloroplast DNA were determined.

The work was funded by the Kurchatov Genome Center of the Institute of Cytology and Genetics of Siberian Branch of the Russian Academy of Sciences, agreement with the Ministry of Education and Science of the Russian Federation, no. 075-15-2019-1662.

The main publications of authors on the subject of the abstract:

Karetnikov, D.I.; Vasiliev, G.V.; Toshchakov, S.V.; Shmakov, N.A.; Genaev, M.A.; Nesterov, M.A.; Ibragimova, S.M.; Rybakov, D.A.; Gavrilenko, T.A.; Salina, E.A.; Patrushev, M.V.; Kochetov, A.V.; Afonnikov, D.A. Analysis of Genome Structure and Its Variations in Potato Cultivars Grown in Russia // Int. J. Mol. Sci. 2023, 24, 5713. https://doi.org/10.3390/ijms24065713



Modification of eIF4E cap-binding pocket as a way to develop PVY-resistant potato plants

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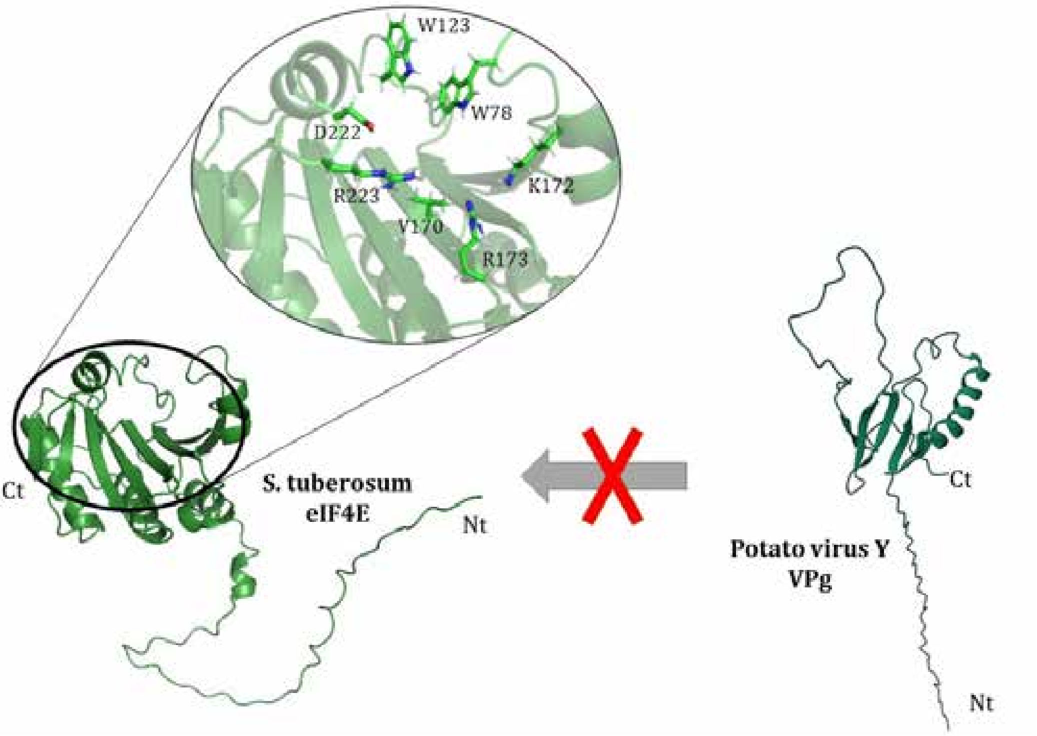
Potato virus Y is a member of the Potyvirus genus, which is considered as the most noxious pathogen for potato crops. PVY is a flexuous rod-like particle carrying a 10kb ssRNA(+) genome with covalently linked VPg protein at 5'-end. For successful infection PVY needs to recruit host translation machinery via interaction of VPg with eIF4E. There are cases of potyviral resistance driven by eIF4E mutations in different Solanaceae, except potato. Engineering of functional eIF4E mutants unable to bind VPg is considered a promising way to obtain resistant potato plants. To design eIF4E mutants incapable of binding VPg we referred to our spatial model of protein-protein interaction complemented with calculations of eIF4E molecular dynamics and picked some regions of cap-binding pocket for modification. A number of mutant eIF4E were produced by site-directed mutagenesis and tested for functionality. The ability to bind VPg was assessed by the Y2H assay. Obtained results provide a judgment on our eIF4E model performance and help us to confer PVY resistance in potato. The work was financially supported by the Comprehensive Research Program "Development of Potato Breeding and Seed Production".

The main publications of authors on the subject of the abstract:

Lebedeva M.V. et al. VPg of potato virus y and potato cap-binding eif4e factors: selective interaction and its supposed mechanism //Biochemistry (Moscow) (2021) 86: 1128-1138. doi: 10.1134/S000629792109008X



Evolution of expression patterns in Angiosperm

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In the course of evolution, many plant genomes have undergone polyploidization, which can lead to neofunctionalization or subfunctionalization of duplicated genes making it difficult to study gene function. Expression pattern of a gene can be considered as a proxy to its function at organism level. Thus, a comparison of expression profiles of orthologous genes can improve the understanding of the gene function. In this study, we analyzed the evolution of expression patterns in 16 species of angiosperms that represent main evolutionary lineages within this group (e.g., Arabidopsis thaliana, Vitis vinifera, Zea mays, etc.). We inferred gene orthogroups using OrthoFinder and collected publicly available RNA-seq data for these species. The expressogroups, which are parts of orthogroups with conservative expression profiles, were identified using the previously developed machine learning approach ISEEML. We analyzed expressogroups and identified orthologous genes with conservative expression profiles as well as system changes in gene expression patterns in Angiosperm evolution.

Studying expression of candidate radiation hormesis genes in irradiated barley cultivars for further genetic editing

Kazakova E.A., Gorbatova I.V., Shesterikova E.M., Prazyan A.A., Podlutskii M.S., Bitarishvili S.V., Blinova Ya.A., Pishenin I.A., Smirnova A.S., Volkova P.Yu.*

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The studying of the mechanisms of growth stimulation of agricultural crops after γ-irradiation of seeds is the promising approach for creating new cultivars with increased productivity and resistance to stressors. In the laboratory experiment we identified in several barley cultivars after low-dose irradiation of seeds three candidate radiation hormesis genes, homologous to *A. thaliana* genes *PM19L, CML39, AOS2.* Also, we conducted the greenhouse experiment and validated those genes at different stages of ontogeny. γ-irradiation of seeds of barley cultivars with the contrasting morphological sensitivity to irradiation was carried out at the dose of 20 Gy. The phenological phases of plants we monitored throughout ontogeny. Differential expression of candidate genes was assessed by RT-qPCR. We found that the shifts in the dynamics of plant growth phases may depend on the modulation of the expression of the studied genes. For subsequent genetic editing in order to obtain more productive barley lines, all three studied genes can be used.

Supported by Grant of Federal Scientific and Technical Programme for the Development of Genetic Technologies for 2019-2027 (No. 075-15-2021-1068).

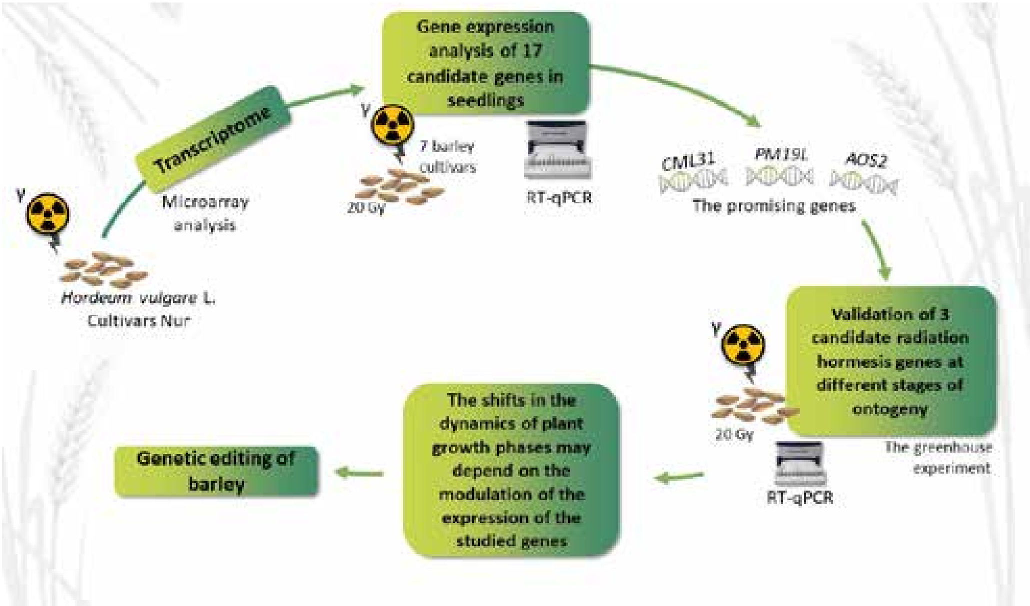
The main publications of authors on the subject of the abstract:

Gorbatova I.V., Kazakova E.A.*, Podlutskii M.S. et al. Studying gene expression in irradiated barley cultivars: PM19L-like and CML31-like expression as possible determinants of radiation hormesis effect // Agronomy. 2020. 10(11). 1837; doi:10.3390/agronomy10111837.*

** – These authors contributed equally*

Take-home message:

For subsequent genetic editing in order to obtain more productive and resistance barley lines homologues of *PM19L, CML31, AOS2* can be used as candidate genes.



Влияние предпосевной обработки семян ячменя салициловой кислотой на активность антиоксидантных ферментов и экспрессию кодирующих их генов при недостатке меди

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Поиск путей повышения устойчивости растений к недостатку микроэлементов является актуальной задачей современности. Для ее решения перспективным считается использование регуляторов роста, например, салициловой кислоты (СК). В настоящей работе изучено влияние предпосевной обработки семян ячменя сорта Нур СК (10 мкМ) на активность ферментов супероксиддисмутазы (СОД) и пероксидазы (ПО) и экспрессию кодирующих их генов (*HvSOD* и *HvPRX*) в листьях 28-дневных растений, при недостатке меди.

Обнаружено, что при недостатке меди у необработанных СК растений увеличивалась экспрессия изученных генов и активность ПО, активность СОД не изменялась. При этом повышалось содержание МДА. После обработки семян СК у растений в этих условиях экспрессия генов *HvSOD* и *HvPRX* и активность СОД и ПО не изменялась, но при этом содержание МДА возрастало меньше, чем у необработанных растений.

В целом, при недостатке меди предобработка семян ячменя СК обеспечивала сохранение окислительного баланса клеток без повышения активности антиоксидантных ферментов, что свидетельствует о ее возможном участии в повышении устойчивости растений к этому стресс-фактору.

Исследование выполнено за счет гранта РНФ №22-26-00168

The main publications of authors on the subject of the abstract:

Ignatenko et al. Influence of presowing treatment of seeds with salicylic acid on growth and photosynthetic apparatus of barley with different zinc contents in substrate // Russian Journal of Plant Physiology (2023) 70 (3): 251–258. doi: 10.1134/S1021443723700115

MASRUSplants: an online database of DNA markers associated with rust resistance genes of wheat

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Wheat is a valuable agricultural crop adapted for cultivation in various ecological and climatic conditions. During its life cycle, wheat is subject to various stresses that reduce yield and grain quality. One of these biotic stresses is rust fungi are the causal agents of plant diseases.

The identification of wheat resistance genes is the most accurate and fastest procedure when use of modern selection technologies, mainly Marker Assisted Selection (MAS).

For cataloging information on MAS we developed the MASRUSplants database (https://masrusplants.ru). The main goal of database is to increase the use of the genetic potential of wheat resistance to fungal diseases and to make the MAS technique widely available.

The developed database MASRUSplants provides a large list of protocols for more than 20 molecular markers of resistance genes in wheat. All molecular markers were verified on an expanded array of Russian germplasm. The database contains information on molecular markers for genes *Sr* (stem rust), *Lr* (stripe rust), *Yr* (leaf rust).

The study is supported by the Kurchatov Genomic Center of the Institute of Cytology and Genetics, SB RAS (075-15-2019-1662).

The main publications of authors on the subject of the abstract:

Kelbin V. N., et al. Diversity of stem rust resistance in modern Siberian bread wheat (Triticum aestivum) germplasm //Plant Breeding (2022) 141(2): 194-203 doi.org/10.1111/pbr.12999

Сколотнева Е. С., Кельбин В. Н., и др. Ген Sr38: значение для селекции мягкой пшеницы в условиях Западной Сибири // Вавиловский журнал генетики и селекции (2021) 25(7): 740–745 doi.org/10.18699/VJ21.084

Take-home message:

The developed database MASRUSplants provides a large list of protocols for more than 20 molecular markers of resistance genes (Sr, Lr, Yr) verified on an expanded array of Russian germplasm.

Difference of spring common wheat varieties according to the amino acid composition of grain

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The varieties of spring common wheat cultivated in the Republic of Tatarstan, according to the average test data in 2021 and 2022, are characterized by a similar content of essential amino acids in grain. The equalization coefficient (B) for the content of most essential amino acids is more than 90%, except for leucine and methionine, which have B = 85.8 and 87.9%. The highest content of lysine in protein is observed in the Yoldyz variety 3.54 g/100g of protein, and threonine in the 100letTASSR variety 3.31g/100g of protein, which is significantly higher, with a 99% probability, than in the Agata, Amir, Ekaterina, Idelle, Nadira, Nikon, Tulaykovskaya 10, Chernozemnouralskaya, Ester varieties by 15.7-20.5%. The conditions of arid 2021 are characterized by a higher content of the sum of amino acids in grain compared to a more moisture-rich 2022. When wheat growing conditions change, there is no total change in the amino acid content in the grain protein, and individual cases of changes in the amino acid composition require additional research. The research was performed within the frameworks of the state tasks according to the theme plan of: Tatar RIA-FRC KazRC RAS No.122011800138-7.

Selection of guide RNAs for modulating the expression of barley CML39 homologue

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The *HORVU.MOREX.r3.3HG0322130* gene (homologue of *CML39* gene in *A. thaliana*) is one of barley genes potentially associated with radiation hormesis. The calcium-binding protein encoded by this gene plays an important role in various plant development processes and is also involved in the response to various stress factors. To confirm the role of the target gene in stress tolerance, we decided to develop constructs for modulating the expression of barley homologue of *CML39* using the CRISPR activation system.

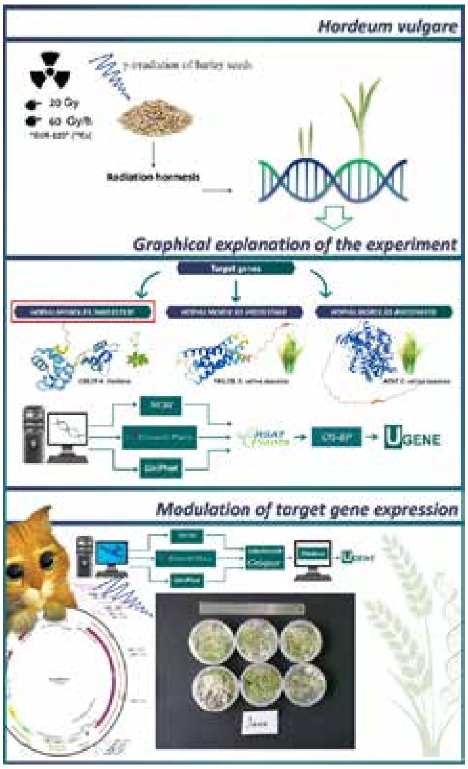
To analyze the target gene Ensembl Plants, UniProt, CATH, RSAT Plants, and CIS-BP were used. CRISPOR, CRISPR-P 2.0, UGENE, and RNAfold resources were applied for the selection and analysis of the secondary structures of guide RNAs (gRNAs).

gRNAs were evaluated and selected according to standard requirements. The following optimal gRNAs were chosen for further work: 5′- TGAATTTAACAACTGGGGT -3′(position 80-99 bp), 5′- ATCCGCTGCTTCGTTCGAAA -3′ (317-336 bp), and 5′- TATATACTCTGGGCGCGACG -3′ (459-478 bp).

The results were obtained with the financial support of the Ministry of Science and Higher Education of the Russian Federation (Agreement 075-15-2021-1068 of 09/28/2021).

The main publications of authors on the subject of the abstract:

I.V. Gorbatova, E.A. Kazakova, M.S. Podlutskii, et al. Studying Gene Expression in Irradiated Barley Cultivars: PM19L-like and CML31-like Expression as Possible Determinants of Radiation Hormesis Effect // Agronomy (2020). V10. №11. doi: 10.3390/agronomy10111837



Participants' Talks

Detection of genetic differentiation in small-leaved linden populations with the application of ISSR-markers on the territory republic of Bashkortostan

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Tilia cordata Mill. is a melliferous woody plant of the Republic of Bashkortostan. Analysis of DNA markers to determine the polymorphism of linden genomic DNA will reveal their intraspecific genetic diversity. Using DNA markers it is possible to create a genetic profile of linden populations with the ability to steadily secrete nectar under various climatic conditions. This will be promising for identifying populations of nectar-producing linden plantations. Genetic differentiation of *T. cordata* was investigated on the basis of DNA polymorphism analysis using the Inter Simple Sequence Repeats (ISSR) marker. A modified version of the classical CTAB method for linden was used for DNA isolation from herbarium samples. For ISSR-PCR analysis, a standard technique was used. For fractionation of isolated total DNA and analysis of amplicon size after PCR, 0.8% agarose gel was used and analysis was performed in 1xTAE buffer. The phylogenetic tree obtained in the Treecon program showed the expected genetic affinity and differences related to the geographical habitat of the small-leaved linden. Further researches were continued using SSR markers.

The main publications of authors on the subject of the abstract:

Khisamova R.R. et al. The research of populations of small-leaved Tilia cordata Mill. in the Republic of Bashkortostan, search, genotyping, in vitro propagation of limes with increased nectar production // Actual Biotechnology. C. 293-294

Application of ISSR-markers to detect and estimate the genetic differentiation of populations of small-leaved linden in the Republic of Bashkortostan // Modern Problems of Biochemistry, Genetics and Biotechnology. C. 222-226.

Take-home message:

The results of these researches will further identify populations of small-leaved linden that have a stable and high nectar-productive potential and use them in reforestation activities

Development of bioengineering methods for improving grapes

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The regeneration of individual transgenic plants from single transformed cells is a requisite for stable genetic transformation. In grapevine, a reliable method to accomplish this is through the induction of somatic embryogenesis. However, due to the high genetic diversity, the physiological aspects of the induction of somatic embryogenesis in different grape varieties can vary significantly. To date, most work on genetic transformation or CRISPR/Cas9 genome editing is based on a reliable and simple protocol for the regeneration of Thompson Seedless grape variety. With regard to vine grape varieties, most publications report about of transformation of the Chardonnay cultivar. Despite decades of work by scientists around the world, there is still no universal protocol or stably reproducible individual embryogenesis protocols even for the main commercial grape varieties. Our research team has made significant progress in the somatic embryogenesis and bioengineering of a number of commercial grape varieties of importance to the global wine industry. The described transformation system appears to be suitable for application to other *V. vinifera* cultivars.

The main publications of authors on the subject of the abstract:

Likhovskoi V. V., Zlenko V. A., Khvatkov P. A., Maletich G. K., Spotar G. Yu., Lushchay E. A., Klimenko V. P. Biotechnological and molecular genetic methods in grape breeding. Sadovodstvo i vinogradarstvo. 2022;6:5-15 doi: 10.31676/0235-2591-2022-6-5-15

Take-home message:

We have developed a protocol of callusogenesis, regeneration and genetic transformation of a number of grape cultivars.

Технологическая и питательная ценность сортов мягкой яровой пшеницы селекции ТатНИИСХ ФИЦ КазНЦ РАН

Кириллова Е.С., Пономарев С.Н.

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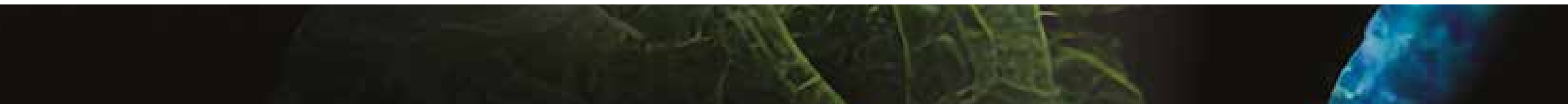
Селекция на качество в Татарском НИИСХ ведется в направлении улучшения хлебопекарных достоинств и мукомольных свойств зерна, повышения его технологической и питательной ценности. Наиболее важными технологическими свойствами зерна пшеницы являются водопоглотительная способность муки, устойчивость теста к замесу, упругость и растяжимость теста и их соотношение, способность давать ароматный хлеб большого объема с хорошей структурой мякиша. Стабильно высокие физические свойства теста и хлебопекарные качества зерна в условиях разной репродукции устойчиво сохраняют лишь немногие сорта пшеницы. Изучены физико-химические, химические и технологические показатели качества сортов мягкой яровой пшеницы Надира, Хазинэ, Сакара и Йолдыз за 2019-2022 гг. Сорта Хазинэ, Сакара и Йолдыз обладают способностью стабильно накапливать достаточное количество белка и клейковины хорошего качества, обуславливающие высокие физические качества теста и объемный выход хлеба, отличный вкус и хорошую структуру. Сорт Сакара показывает себя как сильный улучшитель зерна слабой пшеницы. Зерно сортов Надира и Хазинэ обладает высокой питательной ценностью за счет высокого содержания каротиноидов и фитоэкстрагенов.



Plant mobilome management: tools and approaches

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It was more than 70 years ago that Nobel Laureate Barbara McClintock uncovered mobile elements, or transposons, by studying cytogenetic abnormalities in maiz lines. With the advent of genome sequencing, it is clear that each plant species has a mobile element zoo consisting of hundreds or thousands non-identical copies. The transposition of mobile elements is a major driver of plant genome evolution, speciation and adaptation. Although transposons generate many different insertion sites in a genome, those insertions are rarely passed from one generation to the next. Some strategies are being developed to manage the plant mobilome to broaden the genetic diversity and add new alleles to modern cultivars. By creating genetic collections of plants, these approaches make it possible to conduct mobile element studies and open the door for plant breeding. These methods are coupled with advanced techniques for discovering new insertions and novel transpositionally active mobile elements in plant genomes. The latest approaches to manage plant mobilome activity will be discussed.

This work was supported by the Russian Scientific Foundation (grant №22-74-10055).

The main publications of authors on the subject of the abstract:

Kirov, Ilya, et al. "Epigenetic Stress and Long-Read cDNA Sequencing of Sunflower (Helianthus annuus L.) Revealed the Origin of the Plant Retrotranscriptome." Plants 11.24 (2022): 3579.

Kirov, Ilya, et al. "Illuminating the transposon insertion landscape in plants using Cas9-targeted Nanopore sequencing and a novel pipeline." bioRxiv (2022).

Take-home message:

Artificial induction of mobile element activity allows creating plant genetic collections and open the door for plant breeding and functional genomics studies.

Do DEEPER ROOTING 1 (DRO1) genes regulate the root system architecture formation of cucumber (*Cucumis sativus*)

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DRO1 gene is known as regulator of the rooting depth in rice and the gravitropic set point angle (GSA) in Arabidopsis lateral roots. This study focuses on whether cucumber *DRO1* regulates the GSA of lateral roots. Using phylogenetic analysis three putative orthologues, *CsDRO1a, CsDRO1b,* and *CsDRO1c*, were identified in cucumber. The auxin plays an important role in formation of root GSA. The quantitative real time PCR results showed that single gene, *CsDRO1a,* was auxin sensitive. Study of the promoter-reporter fusions using confocal laser scanning microscopy revealed that three *DRO1* genes show a partially overlapping expression pattern in cucumber roots. The CRISPR/Cas9-mediated knockout of single *CsDRO1* gene (*CsDRO1a, CsDRO1b* or *CsDRO1c*) did not change GSA of lateral roots. Our data suggest that single *CsDRO1* gene might not be sufficient to regulate the GSA of cucumber lateral roots. The study was supported by the Ministry of Science and Higher Education of the Russian Federation (075-15-2021-1056).

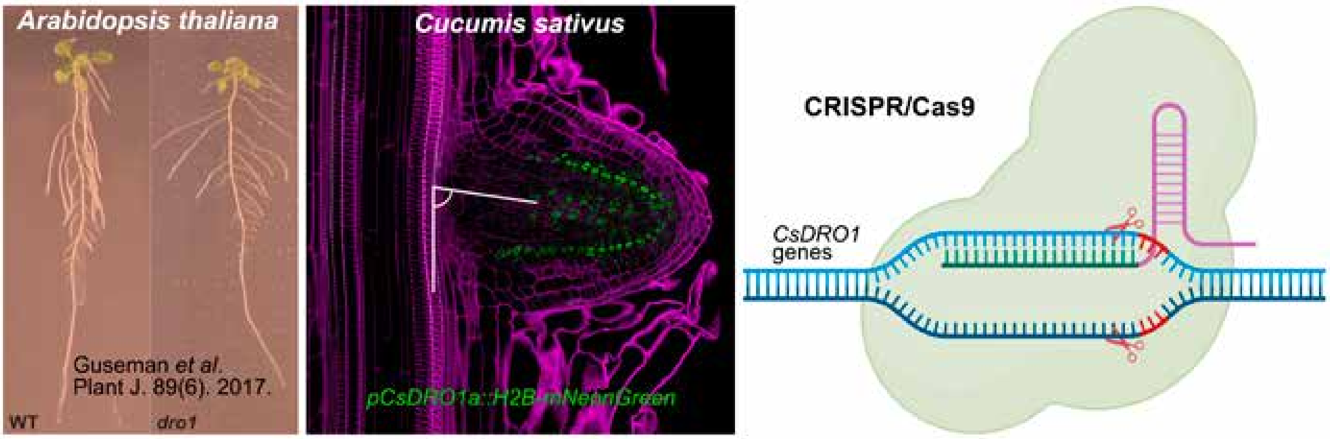
The main publications of authors on the subject of the abstract:

Kiryushkin A.S., Ilina E.L., Guseva E.D., Pawlowski K., Demchenko K.N. (2022). Hairy CRISPR: Genome editing in plants using hairy root transformation. Plants 11(1), 1-39. doi: 10.3390/plants11010051

Gogolev Y.V., Ahmar S., Akpinar B.A., Budak H., Kiryushkin A.S., Gorshkov V.Y., et al. (2021). OMICs, Epigenetics, and Genome Editing Techniques for Food and Nutritional Security. Plants 10(7), 1-44. doi: 10.3390/plants10071423

Take-home message:

A putative role of cucumber DRO1 genes in regulation of the lateral root gravitropic set point angle will be discussed in this report.



The effect of external treatment of *Arabidopsis thaliana* with plant-derived stilbene compounds on plant resistance to abiotic stresses

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Stilbenes are a group of plant phenolic secondary metabolites, where *trans*-resveratrol (3,5,4'-trihydroxy-trans-stilbene) is the most famous stilbene. Stilbenes possess a great potential for using in agriculture, since they possess considerable activities against plant microbial pathogens and have valuable beneficial effects on human health.

We studied the effects of direct application of stilbene solutions on the plant foliar surface for increasing *Arabidopsis* resistance to various abiotic stresses. We also analyzed the stress-protective effects of stilbene precursors and plant extracts reach in stilbenes.

It has been shown that the treatments improved plant resistance to drought, heat, and soil salinity. Plant cold resistance was not affected by the stilbene treatments. The present work provides new knowledge on stilbene applications for improvement of plant stress tolerance. This work was supported by a grant 22-16-00078 from the Russian Science Foundation.

The study and modification of wheat heading and maturity genes using genome approaches including CRISPR/Cas9 gene editing technology

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The key growth stages of wheat are heading and maturity. The dissection of genetic mechanisms and modification of these traits are important problems to improve plant adaptation and productivity.

In this work we used genome approaches to study genetics of heading and maturity which are to study allele variation and regulation of known genes and identification of novel loci and candidate genes for heading and maturity times. The most promising loci are on 4A, 5B, 6A, 6B, 7B chromosomes, where the most significant locus with highest effect is positioned on 7BL with *bZIP9* as best candidate gene.

Using the genome editing with CRISPR/Cas9 system we developed a collection of plants with different mutations in promoter of the *Ppd-1* genes, which is to study the regulation of their expression and effect on the vegetation period.

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

Take-home message:

- The collection of *Ppd-1* mutants obtained in this work will be used to study the heading time genetic mechanisms in common wheat.
- A number of novel loci for heading and maturity time are identified and candidate genes are proposed.

Design of a vector system for screening of plant morphogenic regulators

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In vitro regeneration is a critical step in the production of transgenic plants and an approach for studying gene functions. However, regeneration remains a highly genotype-dependent process. For plants with low regeneration potential, an increase in its frequency is possible by insertion constructs with morphogenic regulator genes. We designed a vector for more rapid cloning of genes potentially regulating *in vitro* morphogenesis. The work is based on the Golden Gate cloning method which enables assembly of the modules with DNA fragments using class IIS restriction enzymes in a given order into transcription units, and then form multigene constructs. To create a construct, we replaced the BpiI restriction sites on the pICH41308 plasmid with the Esp3I without inserting the PCR product with CDS. This leads to the preservation of the sites in the final vector intended for *Agrobacterium*-mediated transformation and allows the insertion of morphogenic regulator genes sequences directly into it. Currently we are constructing vectors. The work is supported by the Ministry of Science and Higher Education of the Russian Federation, (Agreement 075-10-2021-093, Project [PBB-RND-2243]).

Take-home message:

We designed a vector system for more rapid cloning of genes potentially regulating in vitro plant morphogenesis.

Two sides of Angiosperm transcriptome: ubiquitous and tissue-specific genes

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The coordinated expression of multiple genes underlies tissue differentiation of multicellular organisms. The evolutionary stability of gene expression patterns is a key to understanding both the essence of tissues and integrity of the organism. We have explored gene expression patterns of five Angiosperm species and identified tissue-specific genes and ubiquitously expressed (stable) genes. We inferred gene orthogroups for these species and identified genes with conservative across Angiosperm expression profiles. We found that stable genes tend to be single-copied, while many tissue-specific genes are unique for plant lineage. We explored structural and chromatin characteristics of studied genes as well as their regulatory elements, and described functions of both uniformly and strictly expressed genes.

The main publications of authors on the subject of the abstract:

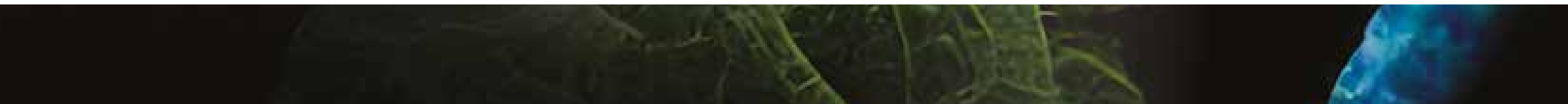
Kasianov AS, Klepikova AV, Mayorov AV, Buzanov GS, Logacheva MD, Penin AA. Interspecific comparison of gene expression profiles using machine learning. PLoS Comput Biol. 2023;19(1):e1010743

Penin AA, Kasianov AS, Klepikova AV, Kirov IV, Gerasimov ES, Fesenko AN, Logacheva MD. High-Resolution Transcriptome Atlas and Improved Genome Assembly of Common Buckwheat, Fagopyrum esculentum. Front Plant Sci. 2021 Mar 16;12:612382

Take-home message:

Angiosperm-scale stably expressed genes tend to be single-copied.

Plant tissue-specific genes are lineage-specific.



Breeding value of fasciated forms in buckwheat breeding for drought resistance

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В селекции крупноплодных сортов гречихи значимое место принадлежит таким наследственным новообразованиям как фасциации (деформациям побегов). Селекционная ценность фасциированных форм обусловлена наличием комплекса хозяйственно-ценных признаков. Наиболее важным является ограниченность ростовых процессов. Средняя высота таких растений 50-80 см, из-за меньшего числа междоузлий (8-9) и одновременного сокращения их длины в верхней части растения, что обуславливает более интенсивные процессы плоодообразования. Сорта, полученные на основе фасциаций являются более засухоустойчивыми. Средняя урожайность зерна популяции К-990 в засушливые годы была на уровне 0,81 т/га, у сорта Батыр, относящегося к морфотипу «Краснострелецкий», созданного на основе не фасциированных растений - 0,47 т/га. Плоды фасциированных растений имеют отчетливую крылатость. Масса тысячи плодов в среднем за три года исследования составила 31,3 г, что на 12% больше, чем у сорта Батыр. Однако крупность плодов достигается за счет увеличение доли пленки до 23% и одновременным снижение натуры в среднем на 20 г/л. Выравненность зерна достигает 95% и выше, содержание сырого протеина в зерне в 1,14 раза выше, чем у Батыра.

<u>The main publications of authors on the subject of the abstract:</u>

Klimova L.R., Kadyrova F.Z. Assessment of productivity and quality of yield of buckwheat varieties in the conditions of Pre-Kama zone of the Republic of Tatarstan // Vestnik of the Kazan State Agrarian University (2022) 4(68):5-10. doi 10.12737/2073-0462-2023-5-10.

Kadyrova F.Z. et al. New achievements in the buckwheat selection // Vestnik of the Kazan State Agrarian University (2018) 4(51): 35-39. doi 10.12737/article_5c3de480b68b41.05234576.

<u>Take-home message:</u>

1. Включение фасциированных форм в селекцию гречихи посевной повышает адаптивные свойства растений.
2. Фасциированные формы в засушливые годы формируют большую урожайность зерна по сравнению с морфотипом «Краснострелецким» в среднем на 45%.

СЕЛЕКЦИОННАЯ ЦЕННОСТЬ ФАСЦИИРОВАННЫХ ФОРМ В СЕЛЕКЦИИ ГРЕЧИХИ НА ЗАСУХОУСТОЙЧИВОСТЬ

Фасциированные формы диплоидной гречихи

Хозяйственно-ценные признаки фасциированных форм:

1. Ограниченность ростовых процессов (максимальная высота растений 50-80 см);
2. Более интенсивные процессы плодообразования;
3. Увеличение адаптивного потенциала растений;
4. Средняя урожайность зерна популяции К-990 в засушливые годы была на уровне 0,81 т/га, у сорта Батыр, созданного на основе обычных, не фасциированных растений - 0,47 т/га;
5. Плоды имеют отчетливую крылатость;
6. Увеличение крупности плодов на 12% и содержания белка в 1,14 раза в сравнении со сортом Батыр;
7. Выравненность плодов достигает 95% и выше.

Spatial transcription of wheat A-genome encoded circular RNA in triticale (x Triticosecale Wittmack)

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Circular RNAs are a class of endogenous single-stranded closed RNA molecules derived from mRNA precursor back-splicing and ubiquitously expressed in all eukaryotes and prokaryotic archaea. It is known that circular RNAs play important roles during plant growth and development and the responses to biotic and abiotic stress, although the functions of only a few circular RNAs have been reported. Circular RNAs exert their functions by forming R-loop structures, acting as miRNA sponges, interacting with RBPs, or being translated into proteins. The aim of our research was to identify circular RNAs in triticale. Using known databases (PlantCircBase, circFunBase, PlantcircNet), we selected wheat circular RNA that were located in the genes encoding transcription factors of A-genome. We evaluated the transcription of parental genes and circular RNAs in the leaves and roots of seedlings of some varieties of triticale by RT-PCR. In the present studies we discovered the spatial transcription of circular RNAs in several protein-coding genes in triticale. The function of circRNAs in plants still requires further study, which may provide new insights for improving the agronomic traits of crops.

The main publications of authors on the subject of the abstract:

Mamaeva A.S. et al. RALF Peptides Modulate Immune Response in the Moss Physcomitrium Patens // Frontiers in Plant Science (2023) 14. doi: 10.3389/fpls.2023.1077301

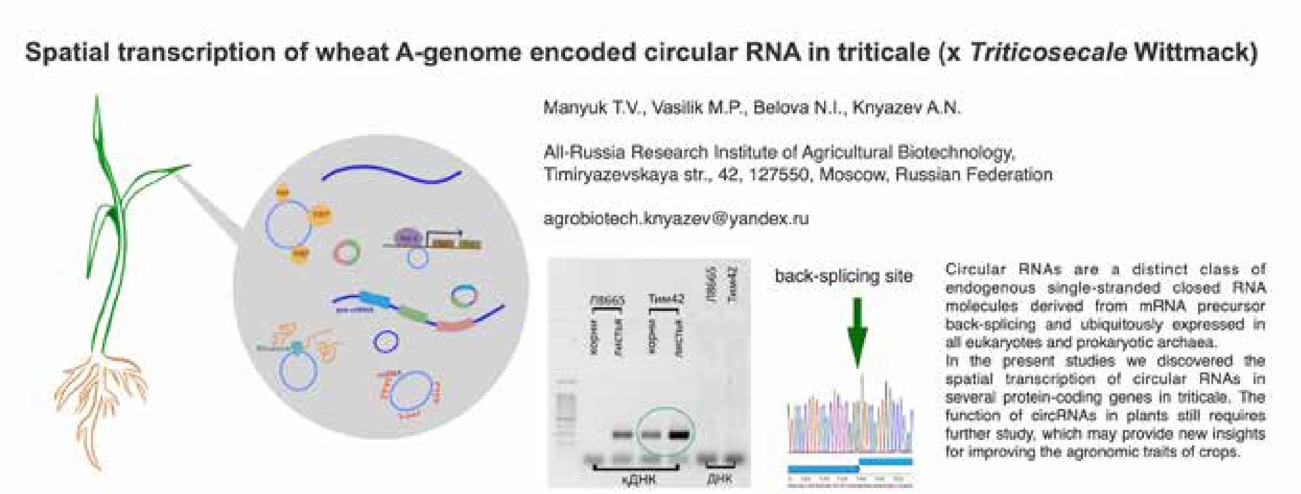
Fesenko I.A. et al. A vast pool of lineage-specific microproteins encoded by long non-coding RNAs in plants // Nucleic Acids Res. (2021) Oct 11;49(18):10328-10346. doi: 10.1093/nar/gkab816

Fesenko I.A. et al. Distinct types of short open reading frames are translated in plant cells // Genome Res. (2019). doi: 10.1101/gr.253302.119

Take-home message:

Several wheat A-genome encoded circular RNA transcribed in triticale (*x Triticosecale* Wittmack).

Transcription of wheat A-genome encoded circular RNA in triticale is spatial and temporal.



Spatial transcription of wheat A-genome encoded circular RNA in triticale (x *Triticosecale* Wittmack)

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Circular RNAs are a distinct class of endogenous single-stranded closed RNA molecules derived from mRNA precursor back-splicing and ubiquitously expressed in all eukaryotes and prokaryotic archaea.
In the present studies we discovered the spatial transcription of circular RNAs in several protein-coding genes in triticale. The function of circRNAs in plants still requires further study, which may provide new insights for improving the agronomic traits of crops.

Genetic basis of apetaly in *Capsella bursa-pastoris*

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Brassicaceae have a rigid floral ground plan that is robust to genetic and environmental changes. While some genera have variation in petal and stamen number, this variation is not present in Arabidopsis and its genetic basis is poorly understood. Petal loss is recurrent throughout populations of Capsella bursa-pastoris, a weed with a global distribution and well-adapted to lab conditions. Studies of apetaly in one of the lepidium-like lines, lel4 from Moscow, revealed that known petal development factors are not compromised, hinting at a previously undescribed developmental pathway.

We constructed the phylogeny of 63 lines from across Eurasia and North America, and discovered that apetalous lines belong to different clusters, which are concordant with geography. In lel4, we revealed several apetaly-linked loci through BSA and confirmed their association with the phenotype trough sequence-based genotyping. Analysis of F2 population grown from aged seeds revealed a correlation between apetaly and increased seed longevity, which could be the primary driver for positive selection at the corresponding loci.

The study is supported by RSF grant 21-74-20145

The main publications of authors on the subject of the abstract:

Klepikova A.V. et al. lepidium-like, a naturally occurring mutant of Capsella bursa-pastoris and its implications for the evolution of petal loss in Cruciferae // Frontiers in Plant Science 12 (2021): 714711. doi: Front Plant Sci. 2021 Nov 25;12:714711. doi: 10.3389/fpls.2021.714711.

CLE peptide hormones involved in symbiotic nodulation in pea (*Pisum sativum L.*) and possible mechanisms of their action

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CLE peptides (CLAVATA3/Embryo Surrounding Region) are important players of autoregulation of nodulation in legumes. Previously, we have identified four genes encoding PsCLE peptides that were activated in response to rhizobia inoculation in pea (Lebedeva et al., 2022).

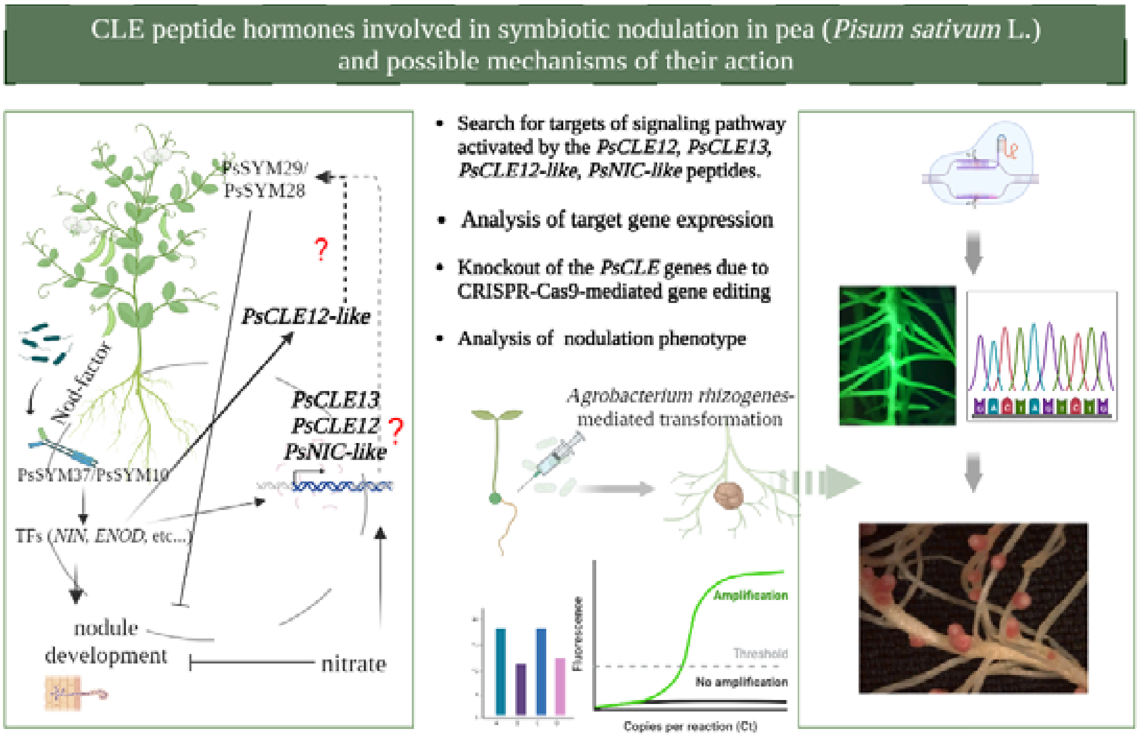
n this study, we constructed vectors for overexpression of the *PsCLE12-like* and *PsNIC-like* genes to study their possible role in nodulation. We found that overexpression of the *PsCLE12-like, PsCLE13* and *PsCLE12* genes resulted in increased expression level of two pea *TOO MUCH LOVE (PsTML)* genes. The effect of *PsCLE* overexpression on the activity of other possible target genes in the root will be assessed in our study.

Furthermore, we constructed vectors for CRISPR-Cas9-mediated gene editing of two *PsCLE* genes, *PsCLE12* and *PsCLE13*, based on the pKSE401 plasmid (Xing et al., 2014). We modified pKSE401 plasmid by the addition of a GFP-encoding reporter cassette. We are going to analyze nodulation phenotype and symbiotic effectivity of nodules formed on *PsCLE12* and P*sCLE13*-knockout roots.

This research was funded by the Sirius University of Science and Technology project: PBB-RND-2243.

Take-home message:

PsCLE12 and PsCLE13 are negative regulators of symbiotic nodule development in pea and could mediate nitrate-dependent systemic inhibition of nodulation. Knock-out of the PsCLE genes due to gene editing could have positive effect on nodulation.



CLE peptide hormones involved in symbiotic nodulation in pea (*Pisum sativum* L.)
and possible mechanisms of their action

- Search for targets of signaling pathway activated by the *PsCLE12, PsCLE13, PsCLE12-like, PsNIC-like* peptides.
- Analysis of target gene expression
- Knockout of the *PsCLE* genes due to CRISPR-Cas9-mediated gene editing
- Analysis of nodulation phenotype

PsCLE13, PsCLE12 and *PsNIC-like* could mediate nitrate-dependent inhibitory effect on symbiotic nodulation

Genetic model of a variety of agronomically important traits of oat varieties for the Tyumen region

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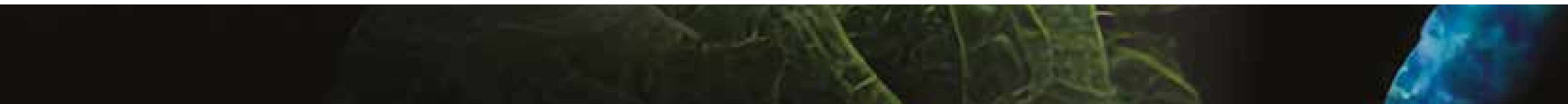
The breeding work of oats in Western Siberia is aimed at creating varieties with high yields and grain quality. But at the same time, these varieties should have high resistance to diseases and lodging.

For the genetic diversity of new varieties, hybridization often uses local varieties and varieties from another ecological-geographical zone as parental forms.

One of the priorities is the development of varieties resistant to crown rust, the effectiveness of Pc-genes of which is associated with the racial composition of the pathogen. On the territory of Western Siberia (Omsk and Novosibirsk regions), varieties containing the *Pc50, Pc58, Pc59* genes may have resistance to crown rust. The introduction of the PC 58 variety (*Pc58* gene) into the breeding process can ensure efficient gene transfer while maintaining economically valuable properties for the Tyumen region.

The problem of lodging of oats is solved by introducing into the breeding process short-stemmed varieties (Pennline 6571, OT 207, Echidna) with the Dw6 gene, while does not adversely affect such elements of the crop structure as panicle grain size and grain size.



Haploids and Doubled Haploids in *Beta vulgaris* L. breeding

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Приоритетной задачей селекции Beta *vulgaris* L. является создание качественных гибридов на линейной основе. Важна при этом оптимизация процессов создания гомозиготных линий, на получение которых уходит 12 лет при использовании традиционных методов. Для этой цели широко применяются DH-технологии, что позволяет ускорить селекцию примерно в 2 раза. Целью работы явилось изучение факторов, обуславливающих эффективное получение гомозиготных форм Beta *vulgaris*. Исследования были выполнены в ООО «СоюзСемСвекла» с применением методов культуры тканей. В работе использовали МС-формы, О-типы, ОП. Плоидность контролировали посредством проточной цитометрии. Показано, что наиболее регенерационно способными являлись экспланты, расположенные на центральном стебле. Неоплодотворенные семязачатки лучше регенерировали после 5 дней холодовой обработки бутонов. Был установлен оптимальный состав питательной среды MS для получения гаплоидов. Выявлены концентрации агар-агара, гормонов и мутагена для получения максимального числа DH-растений при частоте диплоидизации более 50 %, выживаемости – 82%. На основании полученных данных была разработана технология получения удвоенных гаплоидов Beta *vulgaris in vitro.*

The main publications of authors on the subject of the abstract:

Kolesnikova E.O. et al. Haploid biotechnology as a tool for creating a selection material for sugar beets // Vavilovskii Zhurnal Genetiki i Selektsii. 2021. Vol. 25. No. 8. P. 812-821. DOI: 10.18699/VJ21.094

Колесникова Е.О. и др. Биотехнологии удвоенных гаплоидов в селекции Beta vulgaris L. // Проблемы селекции - 2022: тезисы докладов междунар. научной конф., г. Москва, 12-15 октября 2022 г. М.: Изд-во РГАУ – МСХА, 2022 г., С. 102. https://www.elibrary.ru/item.asp?id=4960668

Take-home message:

В селекции Beta vulgaris актуально применение DH-технологий, позволяющих оптимизировать создание гомозиготных линий. На основании полученных в ходе исследований данных была разработана технология получения удвоенных гаплоидов Beta vulgaris in vitro.

Application of SeedCounter app in genetic research

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Grain morphometry is an important step in the wheat breeding to develop new high-yielding cultivars. Counting grains by hand is labor-intensive and time-consuming, while measuring parameters such as grain length, width, roundness, and color is significantly difficult. For high-throughput phenotyping of wheat grains, we implemented the Android-based SeedCounter mobile app. The app allows to takeimage of wheat grains located on a white sheet of standard-sized paper. The program recognizes the sheet of paper, performs perspective correction, identify grains in the image, and measures their morphological characteristics (size, area, roundness, etc.). The app uses OpenCV library [1] to process images obtained from the mobile device camera. Measurement results are stored on the device and can be used further for statistical analysis.

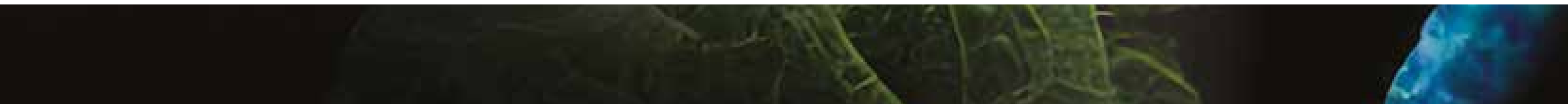
The workshop is devoted to the practical use of the developed SeedCounter application for data acquisition and analysis.

The app is available at https://play.google.com/store/apps/details?id=org.wheatdb.seedcounter

TheSeedCounter app developing was supported by the Russian Science Foundation, the project 22-74-00122.

References:

[1] OpenCV (OpenSourceComputerVisionLibrary): software library of algorithms for computer vision, image processing and general-purpose numerical algorithms with an open source code.



The role of exogenous auxin in the regulation of growth and development of seedlings of *Arabidopsis thaliana* mutants *tir-1* and *axr1-3*

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Exploring the mechanisms of auxin regulation is still relevant for deciphering the fundamental processes occurring in the plant organism.

In research used mutants of *Arabidopsis thaliana tir-1* and *axr1-3*, defective in TIR1 and AXR1 respectively. AXR1 is a component of the E1 ligase, while TIR1 is a component of the E3 ligase. Both proteins are participants in the transduction cascade of the phytohormone auxin. These proteins are involved in the process of ubiquitination, which, in the presence of auxin, leads to proteasomal degradation of Aux/IAA repressor proteins, which induces the expression of early auxin-dependent genes. Therefore, disruption of the coding of these proteins leads to a decrease in sensitivity to the phytohormone and may mediate changes in the growth and development of seedlings.

The data obtained indicate that the presence of exogenous auxin (IAA) inhibited development of mutants and appear morphological defects. To identify the cause of that differences in the manifestation of the action of the exogenous hormone, we analyzed the expression of genes encoding enzymes for the synthesis and breakdown of IAA, as well as auxin transporters.

The search for inhibitors of somatic embryogenesis in *Medicago truncatula*

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The genetic transformation of legumes is limited due to their low regeneration capacity. Plant regeneration can take place both along the path of shoot regeneration and their further rooting, and along the path of somatic embryogenesis (SE). SE is a method of asexual reproduction, determined by the totipotency of plant cells, in which embryos are formed from the somatic cells.

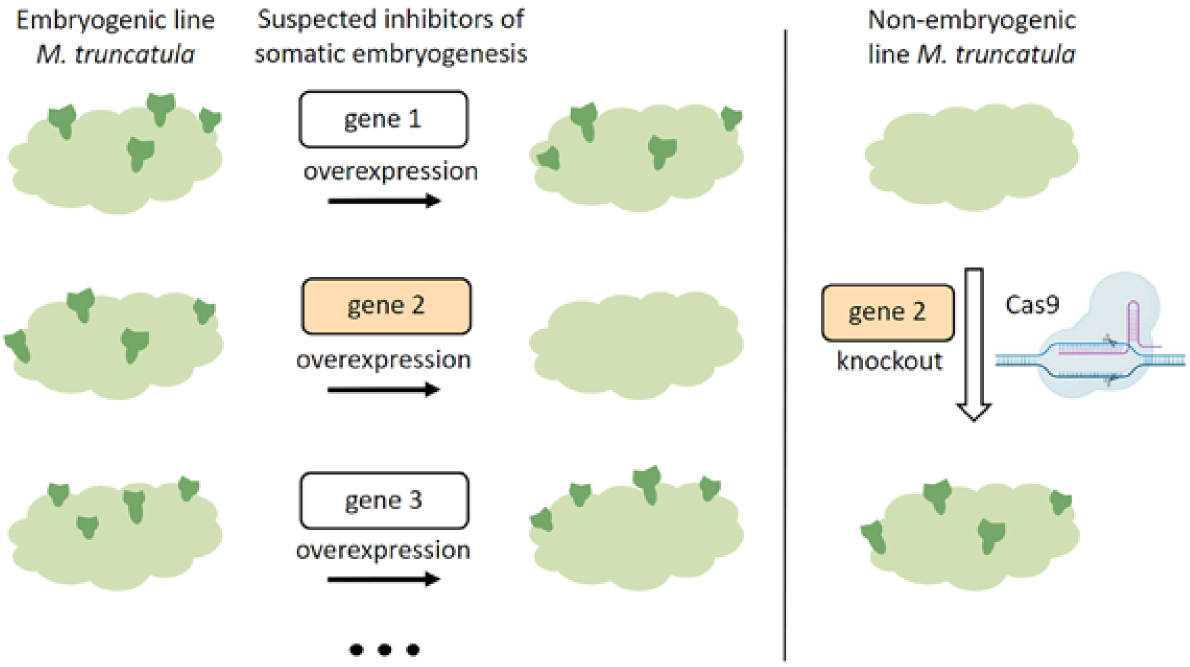
SE has some similarities with zygotic embryogenesis, since these developmental pathways involve common participants in transcriptional, hormonal, and epigenetic control. Like many processes in the plant organism, SE is determined by the activity of various genes: stimulators or repressors.

As a result of the analysis of transcriptomes of *Medicago truncatula* embryogenic and non-embryogenic calli at different stages of development, putative genes-inhibitors of somatic embryogenesis were found. Using the Golden Gate system, vectors for agrobacterial transformation were created to overexpress genes of interest in embryogenic calli and to assess their effect on SE.

Supported by the Ministry of Science and Higher Education of the Russian Federation, (Agreement 075-10-2021-093, Project [PBB-RND-2243]).

Take-home message:

We are studying the effect of somatic embryogenesis inhibitors in *Medicago truncatula* in order to find targets for knockout with CRISPR/Cas9.



Identification of eIF4E isoforms in the multisubunit translation initiation complex of the potato virus Y (PVY)

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Potato virus Y (PVY) is an economically important pathogen for the *Solanaceaes.* A key role in the reproduction of this virus is played by the VPg protein associated with the 5' end of the viral RNA. Interaction of VPg with translation initiation factor 4E (eIF4E) leads to recruitment of the host cell's translation complex. For potato plants, it was not established *in planta* which eIF4E isoforms the Y virus uses. The aim of our study is to identify the proteins that make up the viral translation complex, since this will facilitate understanding of the mechanisms of infection and resistance formation.

Recently, mass spectrometry-based proteomics has become a powerful approach to characterize viral interactomes. Therefore, in our study, tandem mass spectrometry combined with pull-down methods were used, which made it possible to characterize proteins interacting with viral VPg. As a result of the work done, the content of eIF4E isoforms in various fractions of potato cells was quantified and the proteins that make up the potato virus Y translation initiation complex were identified.

This work was supported by the Russian Science Foundation under grant No. 21-76-10050.

New approaches to increasing the efficiency of strawberry micropropagation

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Наиболее актуальной проблемой клонального микроразмножения является адаптация микрорастений *ex vitro*. Целью изучения была технологическая адаптация метода in vitro для массового микроразмножения земляники, позволяющая стабилизировать выход адаптированных растений. Эффективность адаптации микрорастений земляники на уровне 100% получили в ходе массовой высадки, которая производилась непосредственно в теплице при благоприятной солнечной активности в период с апреля по июль месяц. До этого момента жизнеспособность микрорастений в период с августа по март поддерживали в лаборатории в виде вегетирующих почек. Их получали в процессе удаления у уже сформировавшихся стерильных микрорастений корней и листьев, что периодически повторяли с интервалом 1-1,5 месяца. После этого материал подвергали реабилитации на питательной среде Мурасиге-Скуга с бензиламинопурином (0,05 мг/л) до восстановления корней и листьев. Это позволило сохранить в полном объеме микрорастения в течение указанного периода и исключить необходимость адаптации их при искусственном освещении, а также автоклавирование субстрата для этого, что обычно сопряжено с большими трудозатратами и дает слабо предсказуемый результат.

The main publications of authors on the subject of the abstract:

Корнацкий С.А. Вопросы фенотипической стабильности и физиологического статуса растений земляники садовой (Fragaria × ananassa duch.) при длительном культивировании in vitro // Плодоводство и ягодоводство России (2019)59:25-32 https://doi.org/10.31676/2073-4948-2019-59-25-32
Корнацкий С.А., Кузьмина М.В., Голощапова Л.С. Способ выращивания растений земляники с использованием метода in vitro. Патент на изобретение 2762979 С1, 24.12.2021

Take-home message:

- Данный подход позволит по-новому оценить возможности и перспективы клонального микроразмножения.
- Представленная информация может быть использована для реализации промышленных схем получения исходного материала методом *in vitro.*

Screening of spring durum wheat collection for the allelic state of *Glu-A1* and *Glu-B1* genes using KASP-analysis and SDS-PAGE

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Durum wheat grain, which is used in the pasta and cereal industry, must have high gluten quality. The quality of gluten depends on many factors, including the allelic state of the genes of high molecular weight glutenins, which encode various subunits of wheat storage proteins. Therefore, the study of allelic diversity of HMW-GS genes is an important step for durum wheat breeding.

We assessed the allelic diversity of the HMW-GS genes in collection of spring durum wheat collected in the National Grain Center named after P.P. Lukyanenko, consisting of 198 varieties and breeding lines, using SDS-PAGE and KASP molecular markers.

Based on the results of the studies, we identified 3 allele variants of *Glu-A1* locus: the predominant allele *Glu-A1c* (98%) and alleles *Glu-A1b* (1.5%) and *Glu-A1a* (0.5%). 8 allele variants were identified for the *Glu-B1* locus: *Glu-B1al* (60%), *Glu-B1d* (17%), *Glu-B1e* (12%), *Glu-B1b* (3%), rare alleles *Glu-B1h* (1%), *Glu-B1i* (1%) and *Glu-B1z* (1%), as well as a new allele designated by us as *Glu-B1z** (5%).

The research was supported by the Russian Science Foundation grant No. 21-16-00121.

The main publications of authors on the subject of the abstract:

Kroupina, A.Y.; Yanovsky, A.S.; Korobkova, V.A.; Bespalova, L.A.; Arkhipov, A.V.; Bukreeva, G.I.; Voropaeva, A.D.; Kroupin, P.Y.; Litvinov, D.Y.; Mudrova, A.A.; et al. Allelic Variation of Glu-A1 and Glu-B1 Genes in Winter Durum Wheat and Its Effect on Quality Parameters. Foods 2023, 12, 1436. https://doi.org/10.3390/foods12071436

Production of *Hordeum vulgare* doubled haploids by anther culture

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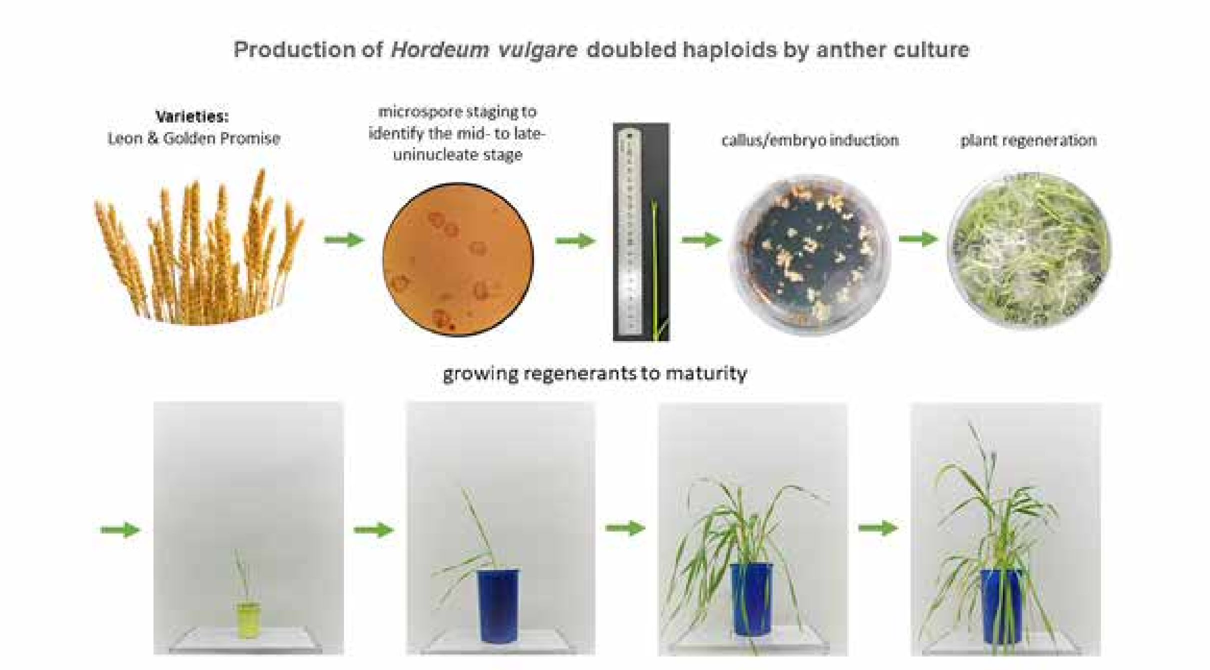
Barley is a widely used and valuable cereal crop. *Hordeum vulgare* has many varieties destined for different growth conditions and new genotypes are still required for seed supply and malt quality improvement. Doubled haploid (DH) is an important tool for molecular breeding and genetic editing of barley.

In this study we used Russian commercial variety Leon and a model variety Golden Promise for DH generation. We modified and optimized known protocols for production of green DH plants. In pretreatment phase mannitol was used.

Spikes with optimal stage of microspores were selected based on 4 morphological indicators. Each spike was revised under a microscope by staining with acetocarmine.

Leon matured first and required an average of 76 days to reach the optimal microspore stage, followed by Golden Promise (81.5 days). For both varieties amount of albino plants was approximately 50% and the frequency of deaths following transplanting was less than 20%.

The results were obtained with the financial support of the Russian Federation represented by the Ministry of Science and Higher Education of the Russian Federation (Agreement No. 075-15-2021-1068 of 09/28/2021)



Heterosis effect in flax hybrids (*Linum usitatissimum* L.) in the system of diallel crosses

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Diallel analysis provides information on the nature and importance of gene effects affecting quantitative traits; Valuable forms of fiber flax in early generations can be identified by the influence of ACS and SCS. The value of flax (Yarok, Grant, Alize, Bertelsdorfer) was determined in the system of diallel crosses according to Griffing at the biological station of the Tyumen State University "Lake Kuchak" (Niznetavdinsky district of the Tyumen region). Based on the analysis of variance, differences ($p>0.05$) were revealed for the studied traits. In F1 hybrids (Yarok, Grant), the effect of heterosis (relative to the best parental form) was obtained by plant height (G=103.8%), technical stem length (G=102.1%), stem weight (G=101.1). %). Combinations with heterosis effect in F3 were classified according to technical stem length (♀ Grant× ♂ Bertelsdorfer, ♀ Alize× ♂ Yarok, ♀ Grant× ♂ Yarok, ♀ Yarok× ♂ Grant), stem weight Bertelsdorfer× ♂ Yarok, ♀ Grant× ♂ Yarok, ♀ Alize × ♂ Yarok, ♀ Grant× ♂ Bertelsdorfer), fiber (♀ Yarok× ♂ Grant, ♀ Grant×♂Yarok, ♀Alize×♂Grant, ♀Bertelsdorfer×♂Yarok). Jarock, Grant and Bertelsdorfer were selected for general (GDR q) specific (SCS σ2s) ability.

Работа выполнена в рамках Государственного задания Министерства науки и высшего образования РФ «Адаптивная способность сельскохозяйственных растений в экстремальных условиях Северного Зауралья» (№ FEWZ-2021-0007).

The work was carried out within the framework of the State task of the Ministry of Science and Higher Education of the Russian Federation "Adaptive ability of agricultural plants in the extreme conditions of the Northern Trans-Urals" (No. FEWZ-2021-0007).

Take-home message:

A tool for increasing the genetic diversity of fiber flax in difficult soil and climatic conditions of the Northern Trans-Urals.

Investigation of the formation mechanism of hulled barley trait on the model of isogenic lines obtained by genome editing

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The sign of nakedness is a valuable breeding trait in barley. Naked barley has advantages over hulled barley for consumption, as it is cheaper to process and contains more valuable nutritional components. The Nud gene encodes a transcription factor presumably involved in the formation of the lipid layer on the surface of grain. In the recent study, we generated lines with a disrupted nud gene by site-directed mutagenesis using guide RNA and Cas9 endonuclease in the Golden promise cultivar [1].

The lines were analyzed of different agronomically significant properties [2] and one was selected for transcriptomic analysis to identify a set of genes involved in the nudity formation. For the experiment, two isogenic lines were taken: the control line and the nud mutant line. The seed coats of the grains were collected at two stages of spike development: early milk development and dough development.

RNA was isolated from samples of aleurons and pericarp and was subjected to transcriptomic analysis. A group of genes with expression upregulation and downregulation were identified in the mutant line.

The work was supported by the Russian Science Foundation № 21-66-00012.

The main publications of authors on the subject of the abstract:

1. Gerasimova, S.V., Hertig, C., Korotkova, A.M. et al. Conversion of hulled into naked barley by Cas endonuclease-mediated knockout of the NUD gene // BMC PLANT BIOL –2020 – 20, 255.

2. Antonova, E.V.; Shimalina, N.S.; Korotkova, A.M. et al. Seedling Biometry of nud Knockout and win1 Knockout Barley Lines under Ionizing Radiation // Plants 2022, 11, 2474. https://doi.org/10.3390/plants11192474

Take-home message:

The nakedness of barley is a valuable agricultural trait. However, how the Nud gene is involved in its suppression remains to be explored. Naked mutants have been obtained. They appear a good model for studying the nakedness trait.

Betula pendula Roth sugar transporters genes identification and characterization *in silico*

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Sugars are the main assimilates obtained by sink tissues of higher plants play an important role in xylogenesis. They are distributed through the plant via sugar transporters. This work is dedicated to sugar transporters genes of *Betula pendula. B. pendula* was chosen as the object of study because of the different xylogenesis scenarios in various birch forms. Blastp search of the *B. pendula* genome, using the amino acid sequences of the sugar transporters from *Arabidopsis thaliana* and *Populus trichocarpa* as query, allowed the identification more than a hundred sequences encoding putative sugar transporters in *B. pendula*. These sequences were checked for the presence of conserved domains and transmembrane domains. As a result, 65 sequences of putative *B. pendula* sugar transporters belonging to three families were obtained. For all families, phylogenetic relationships and exon-intron structure were established. A 2 kb promoter region was identified for all 65 sequences found. Based on a transcriptome published in 2019, genes putatively involved in xylogenesis were selected.

The work is supported by the grant from the Russian Scientific Foundation (project No. 22-74-00096).

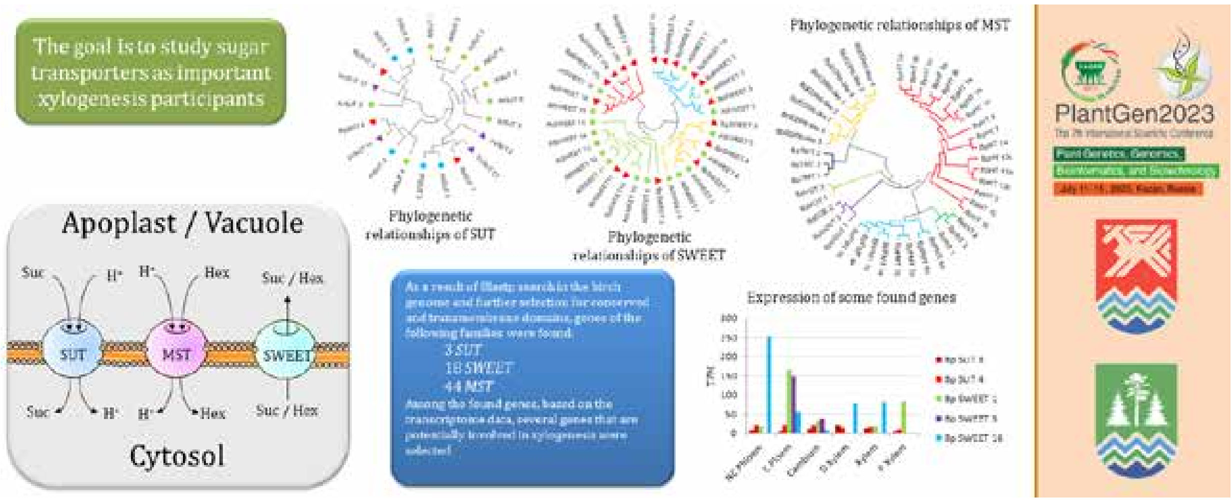
<u>The main publications of authors on the subject of the abstract:</u>

Moshchenskaya et al. The Role of Sucrose Synthase in Sink Organs of Woody // Russian Journal of Plant Physiology. 2019. Vol. 66. No. 1. P. 10-21. DOI: 10.1134/S1021443719010114

Tarelkina et al. In Silico Analysis of Regulatory cis-Elements in the Promoters of Genes Encoding Apoplastic Invertase and Sucrose Synthase in Silver Birch // Russian Journal of Developmental Biology 51(5). 2020. Pp. 323-335. DOI: 10.1134/S1062360420050082

<u>Take-home message:</u>

65 sequences of putative B. pendula sugar transporters belonging to three families were obtained.
Phylogenetic relationships and exon-intron structure were established.
A 2 kb promoter region was identified for all sequences found.


The goal is to study sugar transporters as important xylogenesis participants

As a result of Blastp search in the birch genome and further selection for conserved and transmembrane domains, genes of the following families were found.
3 SUT
18 SWEET
44 MST
Among the found genes, based on the transcriptome data, several genes that are potentially involved in xylogenesis were selected.

RUBISCO activity of agricultural crops

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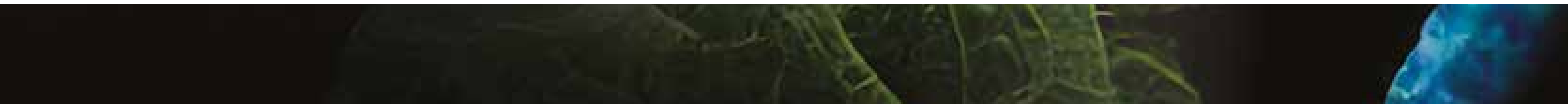
Фотосинтез – один из основных процессов, который влияет на продуктивность растений и зависит от ряда факторов. Так, процесс фиксации СО2 регулируется прежде всего светом, который активирует ряд ферментов цикла Кальвина, среди которых – *RUBISCO* (К.Ф. .4.1.1.39). Формирование *RUBISCO* , включая сборку субъединиц (8 больших и 8 малых), которые кодируются в разных клеточных геномах. Объектом исследования были проростки С3–растений (ячмень, тритикале, редис) и С4–растения (кукуруза). Карбоксилазную активность *RUBISCO* определяли радиометрическим методом при 30^{O}C по скорости включения $^{14}CO_2$ из Na $H^{14}CO_3$ в кислотоустойчивые продукты реакции при наличии рибулозо–1,5–бисфосфата. Выяснили, активность *RUBISCO* (ед./мг суммарного растворимого белка, включая *RUBISCO*) проростков ячменя и тритикале при освещенности 0,12 Вт/м^2 в 2 раза превышала активность фермента проростков кукурузы и редиса.

The main publications of authors on the subject of the abstract:

Kosogova T., Rusinova N., Karapetyan N. Effects of norflurazon on CO2 fixation and Rubisco activity in some C3 and C4 plants under different light intensity // Botanica Pacifica, 2016. 5(1): 87–90. DOI: 10.17581/bp.2016.05110

Kosogova T., Rusinova N., Karapetyan N. Fixation of CO2 and RUBISCO activity of plants under the carotenoids biosynthesis blocked by norflurazone // Int. scientific conference "Genetic and Physiological fundamentals of plant growth. Abstracts. – Vilnius, 2006. 31–32.



Study of the influence of various genes of rice breeding samples on resistance to prolonged flooding

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The resistance of rice varieties to prolonged flooding allows you to fight weeds that cannot overcome a deep layer of water. In Russia there are no resistant varieties, so the problem of their creation is relevant, as it will reduce the loss of grain, the cost of its production and the pesticide load on the ecosystem. We studied 180 rice samples obtained by crossing our varieties with donors of resistance genes Sub1A, AG, Sk. To assess the growth energy during flooding, rice seeds were germinated and the length of plants was measured in dynamics in test tubes and cylinders. As a result of the morphological assessment, some rice accessions revealed the potential to quickly lengthen the first leaves, overcome a large layer of water and accumulate vegetative mass. PCR analysis showed the presence of AG, Sk genes in them. Other accessions had the Sub1A flood resistance gene, which stops plants from growing under water. This allows you to wait out the period of flooding, being at rest, and then resume vegetation when the water layer decreases. Both rice survival strategies can be used in breeding. Received the source material, which is of practical importance for improving the breeding.

The materials were prepared within the framework of the competition of the Russian Science Foundation in 2021 "Conducting fundamental scientific research and exploratory scientific research by small individual scientific groups" (Agreement No. 22-26-00246 of 12/21/2022).

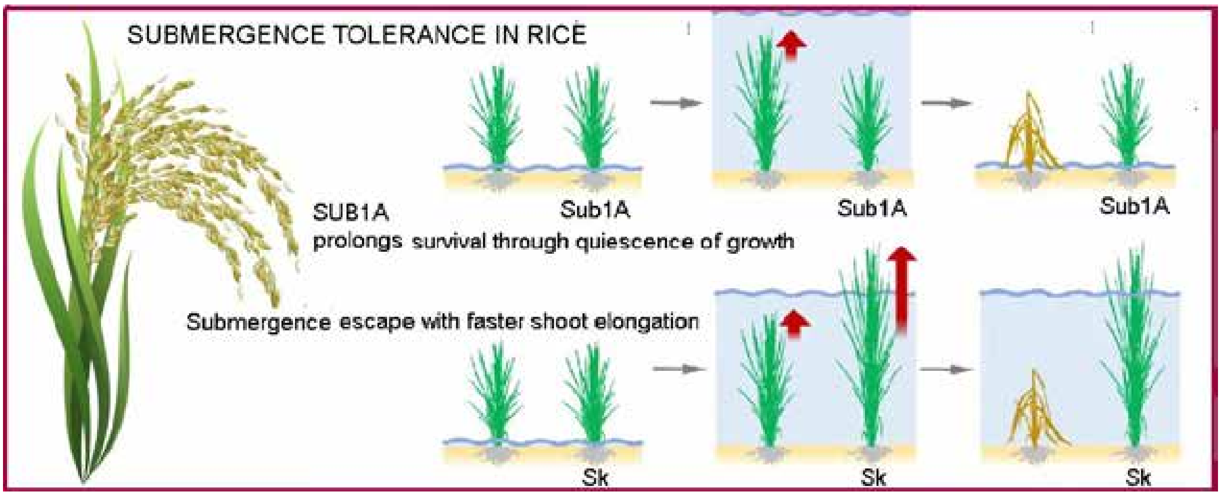
The main publications of authors on the subject of the abstract:

Kostylev P.I., Golubova V.A., Vozhzhova N.N., Kalinina N.V. A new method of protecting rice from weeds by prolonged immersion in water // Biosphere. 2022. V. 14. No. 4. S. 343-346. DOI: 10.24855/biosfera.v14i4.696

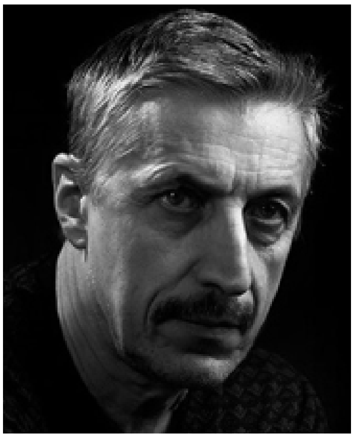
Kostylev P.I., Golubova V.A., Kalinina N.V., Vozhzhova N.N. Study of the energy of initial growth of rice plants in laboratory conditions // Grain Economy of Russia. 2022. V. 14. No. 5. S. 77-83. DOI: 10.31367/2079-8725-2022-82-5-77-83

Take-home message:

Rice can fight weeds with a layer of water. Flooding resistance is determined by genes: rapid growth and emergence to the surface (AG, Sk), temporary dormancy (Sub1A). We have created forms of rice suitable for Russian conditions with these genes.



Laboratory phenotyping of plants



Koval V.S.

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Modern technologies can assist in the precise and rapid assessment of plant phenotypic characteristics. This study presents approaches to plant phenotyping based on photography in laboratory condition. Digital cameras were used for plant photography, capturing both visible spectrum (RGB) and hyperspectral images using the CUBERT camera. To ensure uniform shooting conditions, artificial LED-lighting with diffusing octaboxes was used in the studio. The cameras were mounted on tripods to avoid blurred photos. The shooting was done under the control of software compatible with the corresponding cameras. This allowed for high-quality, high-resolution two-dimensional images to be obtained for subsequent analysis using computer vision and deep learning methods. This method can be used for phenotyping various biological objects, which can improve the efficiency of selection processes and accelerate the development of new varieties.

The work was funded by the Kurchatov Genome Center of the Institute of Cytology and Genetics of Siberian Branch of the Russian Academy of Sciences, agreement with the Ministry of Education and Science of the Russian Federation, no. 075-15-2019-1662.

Wheat yield estimation based on analysis of UAV images at low altitude

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In the last years many papers were published in order to automate labor intensive manual wheat heads counting. Recently we proposed a software package WDS (Wheat Detection System) for ears counting in wheat crops based on RGB images obtained from UAVs. WDS creates the flight plan, for the acquired images carries out automatic georeferencing to the appropriate fragment of the field, counts ears using the neural network models, reconstructs the density of ears in the crop and visualizes it as a heat map in the interactive web application. Based on the field experiment the accuracy of ears counting in plots was assessed: Spearman and Pearson correlation coefficients between the ears density counted manually and using WDS were 0.618 and 0.541, respectively (p-value < 0.05). WDS available at https://github.com/Sl07h/wheat_detection. Further accuracy improvement can be achieved with the use of rotated bounding boxes detection models.

The work was funded by the Kurchatov Genome Center of the Institute of Cytology and Genetics of Siberian Branch of the Russian Academy of Sciences, agreement with the Ministry of Education and Science of the Russian Federation, no. 075-15-2019-1662.

The main publications of authors on the subject of the abstract:

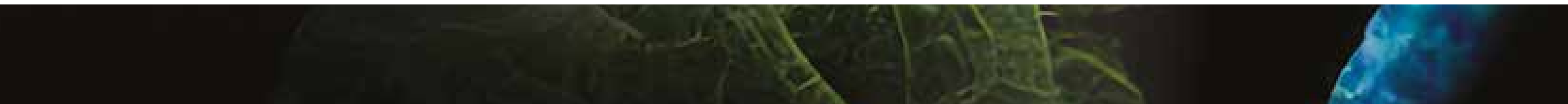
Кожекин М. В. Система компьютерного зрения для анализа урожайности посевов пшеницы // МНСК-2021. –2021. – С. 89-89.

Kozhekin M. et al. Wheat yield estimation based on analysis of UAV images at low altitude //BIO Web of Conferences. – EDP Sciences, 2022. – T. 47. – C. 05006.

Kozhekin M., et al. Wheat yield estimation based on analysis of UAV images at low altitude. //In Bioinformatics of Genome Regulation and Structure\Systems Biology (BGRS\SB-2022). – 2022 – pp. 617-618.

Take-home message:

With the use of UAV's and object detection models tedious procedure of manual wheat spikes count can be automated. We proposed software package that allows to form a flight mission, detect wheat heads, link them to map, and visualize the result.



Colour view on plant transgenic tissue

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In plant biotechnology, various gene engineering approaches are often used. One of such approaches is genetic transformation. For the purposes of control of the genetic transformation process, as well as for further selection of transgenic organisms, and also for tracking of the the transgene fate in a genetically modified transformant, various screening platforms are used. These platforms can include blue-white GUS staining and visualization using fluorescent proteins (e.g. GFP, DsRED) or vital dyes (e.g. anthocyanins, betalains). Our research group is involved in the adaptation of such coloring platforms for early transgenic tissue detection in our model objects from the Fabaceae family and their implementation for studying the somatic embryogenesis process.

This work was supported by the Ministry of Science and Higher Education of the Russian Federation in accordance with agreement № 075-15-2022-322 date 22.04.2022 on providing a grant in the form of subsidies from the Federal budget of Russian Federation. The grant was provided for state support for the creation and development of a World-class Scientific Center “Agrotechnology for the Future”.

On the evolution of plastid sequences in the genus *Lotus* (Fabaceae): from markers to whole plastomes

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The phylogeny of *Lotus* by plastid markers shows partial incongruence with the phylogeny by nuclear markers. Plastid data show the division of the genus into two large clades: the "northern" and "southern" branches, having a Mediterranean origin, but different centers of diversity, Europe and N Asia for the "northern" branch, Africa and S Asia for the "southern". Nuclear markers (ITS, ETS) revealed the disintegration of the "northern" branch into two or more clades (Kramina et al., 2016).

In the *Lotus* section, *L. corniculatus* complex is isolated by all studied markers, and *L. angustissimus* complex does not form a monophyletic clade by any marker. Plastid data show the separation of *L. parviflorus* from other species of *L. angustissimus* group. Various phylogenetic relationships of *L. subbiflorus* may indicate its hybrid origin. Molecular data confirm some geographical patterns in the *L. angustissimus* group.

For further study of plastid evolution, plastome sequences of *Lotus* species (*L. herbaceus, L. hirsutus*) were produced and combined with plastomes of other genera of Loteae (*Anthyllis, Hippocrepis* and *Ornithopus*). The study is supported by Russian Science Foundation grant 23-24-00052.

The main publications of authors on the subject of the abstract:

Kramina T. E., Degtjareva G. V., Samigullin T. H., Valiejo-Roman C. M., Kirkbride Jr, J. H., Volis S., Deng T. & Sokoloff D. D. Phylogeny of Lotus (Leguminosae: Loteae): Partial incongruence between nrITS, nrETS and plastid markers and biogeographic implications // Taxon (2016) 65(5): 997-1018. doi: 10.12705/655.4

Take-home message:

1. The plastid phylogeny of Lotus is partially inconsistent with the nuclear phylogeny.
2. The *L. angustissimus* complex is not a natural group.
3. Studies of complete plastomes will clarify controversial aspects of the evolution of Loteae tribe.

The study of the spectral characteristics of winter wheat varieties with different development of economically significant diseases

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Применения методов ДЗЗ для мониторинга уровней развития листовых болезней сельскохозяйственных растений, должен учитывать биометрические и физиологические особенности растений, которые могут оказывать влияние на спектральные характеристики растений при воздействии болезней.

Целью исследований являлось изучение спектральных характеристик генетически разнородных сортов озимой пшеницы, пораженных возбудителями болезней в разной степени. Методика исследований была основана на сравнительном анализе данных наземной спектрометрии с результатами воздушной спектральной съемки, осуществленной с помощью БПЛА. Сопоставление спектральных характеристик посевов исследуемых сортов выявило, что показатели отражательной способности сортов в значительной степени определялись их биометрическими особенностями и различным характером происходящих в них физиологических процессов. Установлено, что данные наземной спектрометрии и результаты дистанционной съемки с помощью БПЛА позволяют детектировать схожий характер изменений спектральных характеристик исследуемых посевов озимой пшеницы.

Исследование выполнено за счет средств гранта Российского научного фонда и Кубанского научного фонда № 22-26-20119

The main publications of authors on the subject of the abstract:

Resistance of winter wheat varieties to tan spot in the North Caucasus region of Russia. Saudi Journal of Biological Sciences. 2021. 28. 3:1787-1794. Spore-Trapping Device: An Efficient Tool to Manage Fungal Diseases in Winter Wheat Crops. Plants 2023,12,391. Spectral characteristics of winter wheat varieties depending on the development degree of Pyrenophora tritici-repentis. Precision Agriculture, 2022. https://doi.org/10.1007/s11119-022-09976-2

Take-home message:

Данные наземной спектрометрии и результаты дистанционной съемки с помощью БПЛА позволяют детектировать схожий характер изменений спектральных характеристик посевов озимой пшеницы, в разной степени пораженной возбудителями болезней

Copy number analysis of satellite repeats in Triticeae by quantitative PCR

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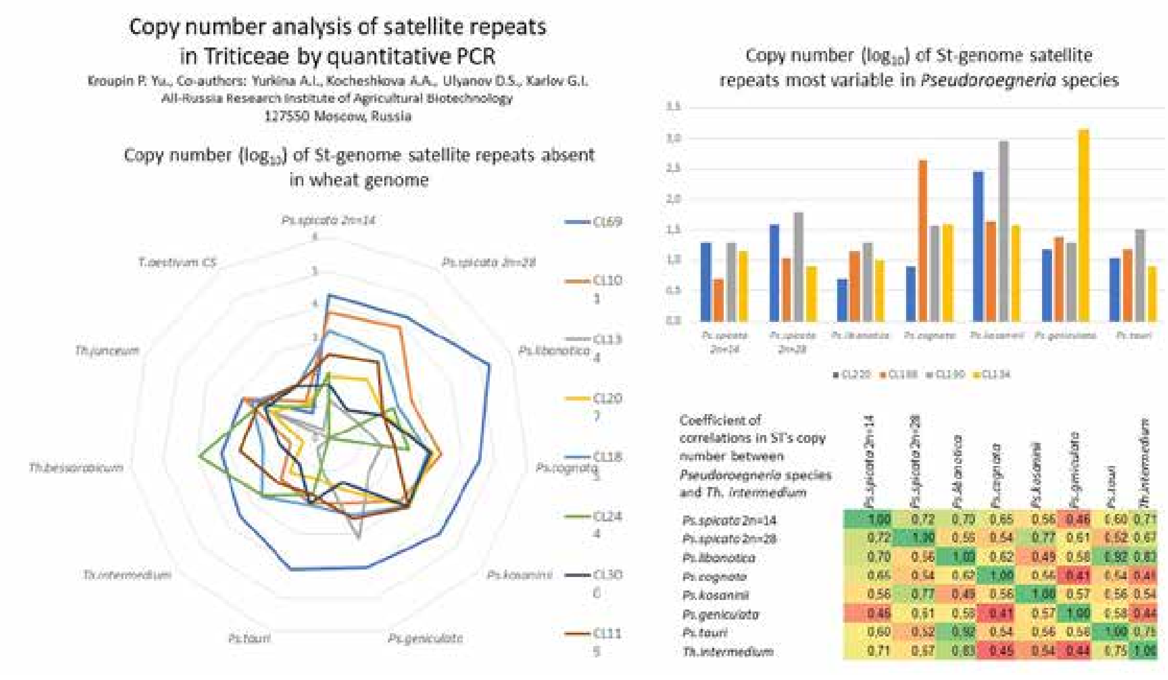
Based on whole-genome sequencing data of *Pseudoroegneria* species using RepeatExplorer2, 23 new satellite repeats (SRs) were identified, their abundance were estimated in *Pseudoroegneria, Thinopyrum, Elymus, Secale, Triticum,* and *Aegilops* species using qPCR. CL69, CL101, CL134, CL207, CL185, CL244, CL300, and CL119 showed high abundance in all or individual studied *Pseudoroegneria* and *Thinopyrum* species, and were almost absent in wheat. CL184 showed specificity for S. cereale, while CL82 was highly abundant in all studied species. Among *Pseudoroegneria* species, CL220, CL186, CL190, and CL134 showed high coefficient of variation, while among *Thinopyrum* species, CL101, CL244, and CL134 showed high variability. Two groups of SRs showed similar copy number profiles: 1) CL220, CL190, CL186, and CL3; 2) CL168, CL207, and CL300. High similarity in copy number was found in *Pseudoroegneria* species (>0.9), as well as between *Pseudoroegneria* and *Th. intermedium* (>0.6) due to the presence of a common St genome. The identified variable and specific SRs can be used in studying the evolution of grasses and wide hybrids. The work was supported by the Russian Science Foundation grant 21-16-00123.

<u>**The main publications of authors on the subject of the abstract:**</u>

Kroupin et al. Aegilops crassa Boiss. repeatome characterized using low-coverage NGS as a source of new FISH markers: Application in phylogenetic studies of the Triticeae // Front Plant Sci. 2022; 13: 980764. doi: 10.3389/fpls.2022.980764

Divashuk et al. qPCR as a Selective Tool for Cytogenetics // Plants 2023, 12(1), 80; doi: 10.3390/plants12010080



Copy number analysis of satellite repeats in Triticeae by quantitative PCR

Kroupin P. Yu., Co-authors: Yurkina A.I., Kocheshkova A.A., Ulyanov D.S., Karlov G.I.
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Copy number ($\log_{10}$) of St-genome satellite repeats absent in wheat genome

Copy number ($\log_{10}$) of St-genome satellite repeats most variable in *Pseudoroegneria* species

Coefficient of correlations in ST's copy number between *Pseudoroegneria* species and *Th. intermedium*

	Ps.spicata 2n=14	*Ps.spicata 2n=28*	*Ps.libanotica*	*Ps.cognata*	*Ps.kosaninii*	*Ps.geniculata*	*Ps.tauri*	*Th.intermedium*
Ps.spicata 2n=14	1,00	0,72	0,70	0,65	0,56	0,46	0,60	0,71
Ps.spicata 2n=28	0,72	1,00	0,56	0,54	0,77	0,61	0,52	0,67
Ps.libanotica	0,70	0,56	1,00	0,62	0,49	0,58	0,92	0,83
Ps.cognata	0,65	0,54	0,62	1,00	0,56	0,41	0,54	0,45
Ps.kosaninii	0,56	0,77	0,49	0,56	1,00	0,57	0,56	0,54
Ps.geniculata	0,46	0,61	0,58	0,41	0,57	1,00	0,58	0,44
Ps.tauri	0,60	0,52	0,92	0,54	0,56	0,56	1,00	0,75
Th.intermedium	0,71	0,67	0,83	0,45	0,54	0,44	0,75	1,00

Study of species-specific traits and earliness in wheat of different levels of ploidy

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The efficiency of automated phenotyping of wheat species based on the morphology of spike can be improved by introduction of IT technologies for digital image analysis.

The purpose of study is to identify the inheritance of taxonomically significant (classification) traits in di-, tetra- and hexaploid wheat species for a build database (DB).

Materials and methods. As a material were taken 26 wheat species of different ploidy levels. Hybridization of tetraploid wheat species was carried out and hybrid forms F_1 and F_2 were obtained.

Results. The following signs of the studied species were introduced into the DB: speltoidness, compactness, roundness and branchiness, presence of awns, earliness. Most interest are also signs of tetraploid wheat species that require further study. As a result of the conducted research, algorithm has been compiled that allows predicting the type of ploidy. Then information was entered into DB and was be basis for development of a neural network.

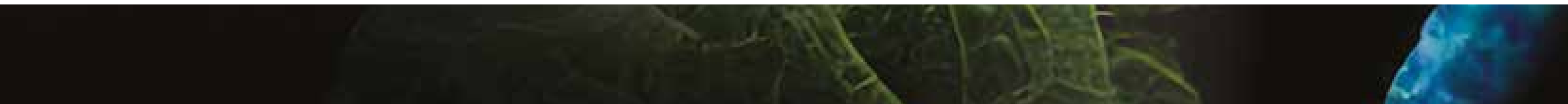
Conclusions. By use designed DB, in plans to create a classifier based on the species-specific characteristics of wheat plants.

Work was supported by the RNF 22-16-20026 and Government of Novosibirsk region.

The main publications of authors on the subject of the abstract:

1. Genaev M.A., Komyshev E.G., Kruchinina Y.V. et al. Morphometry of the wheat spike by analyzing 2D images //Agronomy ISSN: 2073-4395 2019г (Q1)

2. Komyshev E., Kruchinina Y., Genaev M. et al. Spikes morphometric characteristics analysis of five species of wheat // Bioinformatics of genome regulation and structure / Systems Biology (BGRS/SB-2020) The Twelfth International Multiconference Abstracts. 2020 : Institute of Cytology and Genetics, SB RAS – 324



Identification of molecular mechanisms related to determinate growth habit of *Vigna unguiculata* (L.) Walp. at high relative air humidity

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The expansion of crop production diversity in Russia can be achieved through the successful introduction of various crops. Cowpea (*V. unguiculata*) is among such important crops. Many signs (the type of growth habit, the plant length) depend on the growing conditions.

We studied the variability of 14 morphological features in vegetable varieties of cowpea with different types of stem growth habit in contrast air humidity conditions. Their comparative transcriptomic analysis was performed. The search for differentially expressed genes was carried out within the framework of group comparisons of same sample but in contrast humidity conditions.

It was shown significant influence of air humidity on the variability of the length, width of the first leaf, the formation of a curly shoot. The results of RNA-seq analysis revealed significant changes in gene expression level at high air humidity.

Further search and characterization of genes involved in the genetic control of the determinate type of stem growth in humid conditions will be as the basis for marker-oriented selection of vegetable varieties of cowpea.

The work was supported by the Russian Science Foundation (№ 21-66-00012).

The main publications of authors on the subject of the abstract:

Krylova EA, Khlestkina EK, Burlyaeva MO. Influence of air humidity on variability of morphological features of Vigna unguiculata (L.) Walp. in artificial conditions. Ecological genetics. 2022;20(3):215-229. DOI: https://doi.org/10.17816/ecogen108877

Optimizing soil sample preparation for Illumina MiSeq microbiome analysis

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All-Russia Research Institute for Agricultural Microbiology, St.-Petersburg, Russia,
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The analysis of the soil microbiome by the Illumina MiSeq method is a common procedure in the study of biodiversity. In addition to the presence of PCR inhibiting agents in soils, the sorption of nucleic acids on soil particles is also a problem. The first problem is more significant in chernozem, the second — in sandy soils. The problem with inhibitors is solved by cleaning samples on columns, using magnetic particles, DNA dilution before PCR. The problem of DNA sorption on clay components of the soil is solved either by the procedure of additional flushing with water from the soil or by using blocking agents of organic or inorganic origin (phosphate ions, proteins, modified nucleotides, etc.), at the binding centers of clay particles. In our work, the modified CTAB method using phosphate ions showed the greatest efficiency. This may be especially important for the detection of rare DNA sequences, for example, when analyzing arbuscular mycorrhiza fungi, the proportion of which does not exceed 2-3%of other microorganisms in the soil.

This work was supported by the Russian Science Foundation under grant no. 22-16-00064 and the state task No. FGEW-2021-0004.

The main publications of authors on the subject of the abstract:

Kryukov A.A., Gorbunova A.O., Machs E.M., Mikhaylova Y.V., Rodionov A.V., Zhurbenko P.M., Yurkov A.P. Perspectives of using Illumina MiSeq for identification of arbuscular mycorrhizal fungi. // Vavilovskii Zhurnal Genet Selektsii 2020, 24(2), 158-167. https://doi.org/10.18699/VJ19.38-o.

Intoduction *Lilium pilosiuculum* (Freyn) Miscz. in vitro culture

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An alternative common species is in vitro plant biotechnology. The aim of the work is to introduce a rare species *Lilium pilosiusculum into in vitro* culture. The initial explants were bulb scales of a wild plant growing in Northwestern Yakutia. For cultivation, various ratios and concentrations of auxins and cytokinins were tested. Cultivation was carried out under phytorack conditions during a light period of 18/6 at 26°C. Murashige-Skoog (MS) nutrient medium supplemented with benzylaminopurine at a concentration of 0.5 mg/L was the optimal application for shoot initiation. The resulting microshoots were divided and transplanted for root formation by adding naphthylacetic acid (NAA) in various concentrations. Active root formation was observed on the nutrient medium MS with the presence of NAA at a concentration of 1 mg/L. The formed microclones of *Lilium pilosiusculum* were adapted to the soil substrate (peat, sand) and were transferred for adaptation in open ground conditions.

The study was carried out at the NEFU at the expense of the Russian Science Foundation Grant No. 22-14-20031, https://rscf.ru/en/project/22-14-20031.

Phenotypic diversity of the North Caucasian *P. triticina* population from 2010 to 2020

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Leaf rust (pathogen *Puccinia triticina* Erikss.) is a harmful wheat disease that is common in all grain-producing regions of the world. In the North Caucasian region of Russia, which has favorable climatic conditions, the pathogen is recorded annually. An annual analysis of the virulence of the P. triticina population is essential for effective leaf rust control. In this paper, we analyzed the phenotypic composition of the North Caucasian *P. triticina* population from 2010 to 2020. Phenotypes were determined according to the North American nomenclature, isolation and differentiation of mono uredinial isolates were carried out according to generally accepted methods. A total of 1190 isolates were analyzed, of which 877 phenotypes were isolated. 769 *P. triticina* phenotypes are unique. In 2010, phenotypes PHTS and THTS dominated, In 2011 - FHRQ and KHTQ. In 2012, due to unfavorable conditions, the dominance of avirulent phenotypes was noted - out of 106 P. triticina isolates, 47 phenotypes from group B were identified. In other years, highly virulent phenotypes such as THTS, THRQ, PHTT, PHRS, PHTT, and THTT dominated in the population.

The main publications of authors on the subject of the abstract:

Volkova G.V., Kudinova O.A., Vaganova O.F. Diversity of virulence phenotypes of the Puccinia triticina population in different agro-climatic zones of the North Caucasus // Russian Agricultural Science. No. 6. 2019. P. 23-26.

Take-home message:

The virulence of 1190 isolates of the North Caucasian population of P. triticina was analyzed from 2010 to 2020. 877 phenotypes were identified, of which 769 are unique.

In all years except 2012, virulent phenotypes prevailed in the population.

Marker-assisted selection of new barley genotypes accumulating anthocyanins in grain

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Marker-assisted selection (MAS) is becoming increasingly important in breeding and genetic studies. It allows selecting valuable genotypes from hybrid populations precisely. Here, barley lines based on *cvs.* Tanay, Aley, Vorsinsky2, Biom, Krasnoyarsky1 accumulating anthocyanins in grain were created by MAS. The Bowman near-isogenic lines (NILs) PLP (or P18) and BA carrying dominant alleles *Ant1/Ant2* (or *Ant2* only) and *HvMyc2* controlling purple pericarp and blue aleurone, respectively, were used as donors. The selection of homozygote purple- and blue-grained plants by primers specific to *Ant1/Ant2* or *HvMyc2* was conducted in the F_2 hybrid populations obtained by crossing the parental forms. The purple- and blue-grained F_{11} lines and BC_6F_6NILs were obtained on Aley, Tanay, Vorsinsky2, while on Biom and Krasnoyarsky1 purple-grained BC_1F_4 lines were obtained. Black-grained lines homozygous for three genes *Ant1/Ant2, HvMyc2* were developed by crossing purple- and blue-grained NILs. The yield-related traits and content of anthocyanins and antioxidants in grain were evaluated in the lines developed. The study was supported by Kurchatov Genomic Center of ICG SB RAS (No. 075-15-2019-1662).

The main publications of authors on the subject of the abstract:

Gordeeva E.I., Glagoleva A.Y., Kukoeva T.V., Khlestkina E.K., Shoeva O.Y. 2019. Purple-grained barley (Hordeum vulgare L.): marker-assisted development of NILs for investigating peculiarities of the anthocyanin biosynthesis regulatory network // BMC Plant Biology (2019). 19(Suppl 1):52. doi: 10.1186/s12870-019-1638-9.

Take-home message:

For the first time in Russia, a set of the lines, accumulating anthocyanins in pericarp, aleurone and in both these tissues were developed based on barley cultivars of Siberian breeding.

Characterization of microRNAs involved in formation of nitrogen-fixing nodules and arbuscular mycorrhiza in pea

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*Saint-Petersburg State University, Saint-Petersburg, Russia
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Pea (*Pisum sativum L.*) is one of the main valuable agricultural crops; however, the molecular genetic mechanisms underlying the development of pea mutualistic symbioses, in particular, the role of microRNAs in symbioses, is insufficiently studied. In this study, using Illumina sequencing of small RNA and degradome libraries, we identified and characterized the conserved and novel pea microRNAs and their targets in roots inoculated with nodule bacteria and arbuscular mycorrhizal fungi. We identified microRNAs that were differentially expressed during the formation of arbuscular mycorrhiza in different environmental conditions (in closed and open growth boxes). Mycorrhization changed the expression of several pea microRNAs, including miR156, miR395, and miR405, and growth conditions influenced the expression of novel and conserved pea microRNAs, including miR164, miR395, miR156, miR160 and miR166. For differentially expressed microRNAs the target genes were predicted; large number of them were involved in sulfate metabolism, ethylene and auxin signaling during development of symbiosis with arbuscular mycorrhiza fungi in pea. This work was supported by RSF 22-16-00109.

The main publications of authors on the subject of the abstract:

Zhukov, V.A. et al. Association Study of Symbiotic Genes in Pea (Pisum sativum L.) Cultivars Grown in Symbiotic Conditions // Agronomy (2021) 11, 2368.

Зорин Е.А. с соавт. микроРНК растений: методы изучения и роль в развитии симбиозов с полезными микроорганизмами // Биомика (2021) 13(2): 166-175.

Zorin, E.A. et al. Transcriptome Analysis of Alternative Splicing Events Induced by Arbuscular Mycorrhizal Fungi (Rhizophagus irregularis) in Pea (Pisum sativum L.) Roots// Plants (2020) 9, 1700.

Take-home message:

Pea (*Pisum sativum L.*) is one of the main valuable agricultural crops. In this study, we identified the conserved and novel pea microRNAs and their targets in roots inoculated with nodule bacteria and arbuscular mycorrhizal fungi.

Dynamics of changes in the expression of carbohydrate metabolism genes and carbohydrate content in potato tubers during long-term low-temperature storage

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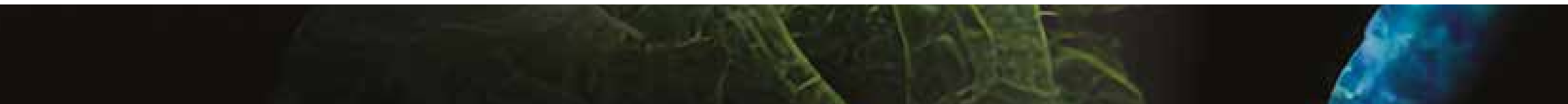
Potato (*Solanum tuberosum* L.) is the most important food, industrial and fodder crop. Low temperature storage of tubers leads to the degradation of starch and, as a result, the accumulation of reducing sugars. The response of tubers of cultivars Barin, Utro, Krasavchik, Severnoe siyanie, and Nadezhda, differing in starch and sugar content, to long-term storage at low temperature (+3°C) was studied. In September, February and April, the expression of α- and β-amylase (*Amy23, StBAM1, StBAM9*), amylase inhibitor (*StAI*), α-glucan-water-dikinase (*GWD*) and vacuolar invertase (*Pain-1*) genes, which degrade starch and sucrose, was determined. Biochemical testing showed that from September to April, the starch content decreases (all cultivars) and the amount of hexoses increases (Nadezhda, Utro). qRT-PCR analysis revealed an increase in the *Amy23* and *GWD* expression (except for Severnoe siyanie) and a decrease in the *StBAM1, StBAM9, StAI* and *Pain-1* expression. Differences in the expression profile of the studied genes and the content of starch/sugars in the dynamics of cold response can be used to assess the sensitivity of potato genotypes to low-temperature stress.



Electrogenic properties of a new small radish cultivar bred for growing in a controlled environment with artificial light

Kuleshova T.E., Zhelnacheva P.V., Ezerina E.M., Vertebny V.E., Khomyakov Yu.V., Kochetov A.A., Sinyavina N.G.

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Bioelectrochemical systems (BES) based on electroactive processes in the root environment are a promising direction for the combined of green electricity generation and plant production. The use of root crops in BES has not been previously described. The purpose of this work was to study the electrogenic properties of small radish which has been breed specifically for growing in a controlled environment with artificial light (CEAL).

Plants were grown under controlled conditions with the use of developed LED lamps simulating sunlight. It was shown that the small radish (*Raphanus sativus L.*) cultivar Petersburgskiy fioletovyy has the best complex of economically valuable traits in CEAL.

In the developed BES based on radish the generation of electric potential difference in the first 7 days was 406±36 mV, then it increased to 438±27 mV and after 14 days decreased to stationary 354±40 mV until the end of the growing season. The power density was 50 μW per m^2 with an external load of 51 kOhm. The total weight of the plant was 33.8±3.1 g, the mass of the root crop was 22.5±1.5 g.

The reported study was funded by St.Petersburg Science Foundation and RSF, grant №23-26-10050.

The main publications of authors on the subject of the abstract:

Sinyavina N.G. et al. Genetic-biochemical studies and morphobiological assessment of small radish (Raphanus sativus L.) under artificial light culture conditions // Russian Journal of Genetics (2022) 6: 662-670. doi: 10.1134/S1022795422060102

Kuleshova T.E. et al. Bioelectrochemical systems based on the electroactivity of plants and microorganisms in the root environment (review) // Agricultural Biology (2022) 3: 425-440. doi: 10.15389/agrobiology.2022.3.425eng

Take-home message:

Radish cultivar Petersburgskiy fioletovyy was bred specifically for high yield and high quality cultivation under controlled environment with artificial light and has a potential for use in bioelectrochemical systems.

Potential of plant growth promoting rhizobacteria for enhancing lignocellulosic biomass and its utilization for biochar and biofuel production

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Soil nutrient deficiency results in limited formation of lignocellulosic biomass and thus becomes a constraint for production of beneficial biochar and biofuel. The *P.koreensis* SA 10b isolated from rhizosphere soil of Sinapsis alba, identified by 16S rRNA gene sequencing improved biomass of *Amaranthus caudatus* L. gibbosus alba by producing different PGP attributes (phosphate solubilization, IAA and siderophore production). SA10b improved pigments and biometric growth parameters(shoot biomass and length and leaf area) compared to control plant. Obtained biomass was pyrolyzed in a self-designed biochar retort at 470 °C for 2h by novel indirect heating method. The biochar was alkaline, high in EC and water holding capacity with micro- and macronutrients. SEM-EDS study showed microporous structure of the biochar with high carbon and presence of K, Ca and Mg. Availability of multiple functional groups for absorption of impurities was confirmed by FTIR study. High lignocellulosic content further classifies *A. caudatus* as putative plant for biofuel production.

Funding:*The work was funded by the Russian Science Foundation Grant No. 23-26-00292, https://rscf.ru/project/23-26-00292.*

<u>The main publications of authors on the subject of the abstract:</u>

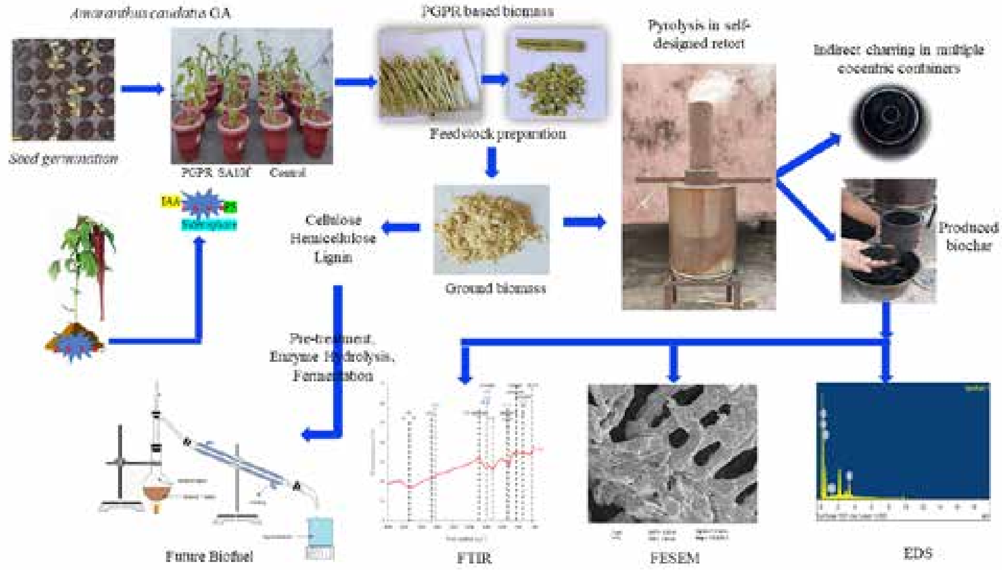
Tripti, Kumar A., Maleva M., Borisova G., Rajkumar M. (2023) Amaranthus Biochar-Based Microbial Cell Composites for Alleviation of Drought and Cadmium Stress: A Novel Bioremediation Approach. Plants 12(10), 1973. https://www.mdpi.com/2223-7747/12/10/1973

Kumar A., Tripti, Maleva M., Borisova G. (2022) Amaranthus caudatus as a putative bioenergy plant for preparation of biochar to enhance biomass production. Agrofor Int J 7(2). http://agrofor.ues.rs.ba/data/20221122-09_Kumar_et_al.pdf

<u>Take-home message:</u>

PGPR P. koreensis helps in enhancing lignocellulosic biomassin *A. caudatus.*

A. caudatus gibbosus alba is a potential plant for biochar and future biofuel production.



Biochemical patterns of B. rapa resistance to diamondback moth (*Plutella xylostella*) and cabbage moth *(Mamestra brassicae*)

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The widespread expansion of damage by leaf-eating pests of brassicas crops determines the need to obtain fundamental knowledge about the patterns of accumulation of biologically active substances with protective properties by plants, the features of their regulation in plant-insect interaction, and the development of a strategy for creating new Brassica cultivars with complex resistance to insects. The purpose of our study was to assess the relationship between the damage to plants by diamondback moth (*Plutella xylostella*) and cabbage moth (*Mamestra brassicae*), and the accumulation of pigments and phenolic compounds during artificial infection. The material was 29 accessions of four *B. rapa* crops (Chinese cabbage, pakchoi, wutacai and root turnip) grown on an artificial infectious background. Biochemical analysis was carried out using the spectrophotometric method (pigments) and the GC-MS method. As a result of biochemical analysis, six pigment compounds and 17 phenolic compounds of various classes were identified. A number of positive correlations were found between the degree of resistance to diamondback moth and the total content of chlorophylls, xanthophylls, benzoic acid, querticin and chlorogenic acid. Positive correlations were also found between the degree of resistance to cabbage moth and the content of lutein, violoxanthin, hydroxyquinone, shikimic acid, and kaempeferol.

Acknowledgements: The reported study was funded by RFBR and DFG, project number 21-516-12001.

Comparison of the rhizobiomes of wheat (*Triticum aestivum* L.) and its closely related species couch grass *(Elymus repens*)

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The microbial communities of the plant rhizosphere play an important role in the efficient functioning of the ecosystem, including influencing the morphology, physiology, growth, development, and health of plants. At the same time, it is known that the soil microbiome diversity is affected by the type of soil, the cultivated crop, and the tillage. In this study, the diversity of rhizosphere bacteria of wheat (*Triticum aestivum* L.) and its closely related species, couch grass (Elymus repens), was assessed. Rhizosphere soil samples were taken during the summer of 2022 in fields with 5 different types of soils in Tatarstan (Russia). According to sequencing data, the wheat rhizobiome included 948 strains (301 families), couch grass - 1241 strains (349 families). The dominant families were the same for both plants. The plant had a greater influence on the rhizobiome than the soil type. 209 strains were found only in the wheat rhizobiome, 509 - only in the couch grass rhizobiome, 739 - in both cases. The data obtained will form the basis for the development of a complex biological product to increase wheat yields and soil fertility by maintaining the microbial diversity of soils.

The main publications of authors on the subject of the abstract:

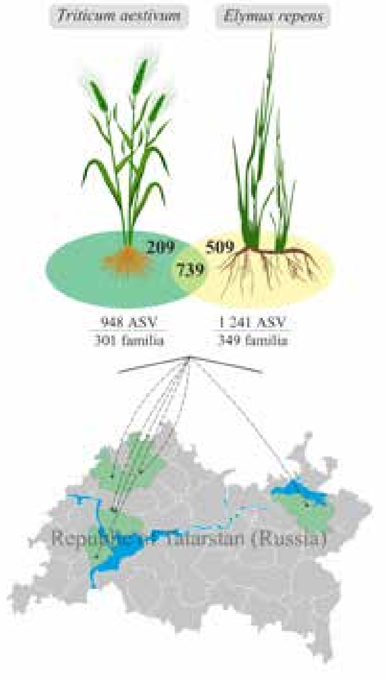
Glazunova D. et al. Assessment of the diversity of rhizospheric cultivated bacteria in wheat plants grown on different soil types // SGEM 2022 (2022) DOI: 10.5593/sgem2022V/6.2/s25.11

Galieva, G. et al. Influence of chiken manure biochar on microorganisms and plants // Uchenye Zapiski Kazanskogo Universiteta. Seriya Estestvennye Nauki (2021) DOI: 10.26907/2542-064X.2021.2.221-237

Karamova, K. et al. Biological agents to control plant wilt // SGEM 2019 (2019) DOI: 10.5593/sgem2019/5.2/S20.025

Take-home message:

Wheat rhizobiome is less diverse compared to couch grass rhizobiome growing on the same soil types. The type of plant more determines the rhizobiome. Fundamental data obtained in this research will be the basis for complex biological agent.



Meristem regulators during root development in radish *(Raphanus sativus* L.)

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Radish (*Raphanus sativus L.*) is an agronomically important root crop of the Brassicaceae family. Under the lateral meristem cambium activity, radish develops a xylem-type storage root. Some radish genotypes can besides evolve other structures of cambial origin called spontaneous tumors. It is well known that components of the WOX-CLAVATA system govern the cambial development. Despite this, the role of individual cambial regulators in the root development in radish is still unclear.

In this work, we have assembled the genomes of tumor-forming and non-tumor lines of the St. Petersburg State University radish genetic collection. We have found differences in SNPs and indels between these contrasting radish lines. Based on the results of quantitative analysis of roots with overexpression and silencing of cambium regulator genes as well as transcriptome analysis, we have identified probable targets of RsWOX4-2 and RsCLE41-1. This work contributes to the understanding of the storage root and spontaneous tumors genetic control.

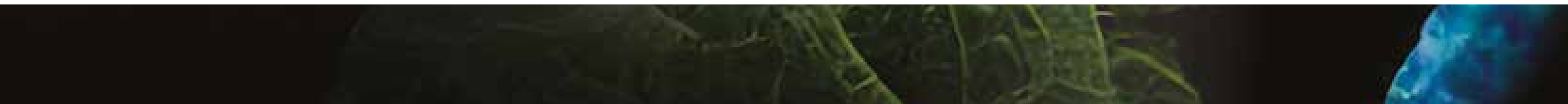
This work was supported by the Ministry of Science and Higher Education of the Russian Federation in accordance with agreement № 075-15-2022-322 date 22.04.2022.

<u>The main publications of authors on the subject of the abstract:</u>

Dodueva et al. Plant tumors: a hundred years of study. Planta. 2020 Mar 18;251(4):82. doi: 10.1007/s00425-020-03375-5.

Kuznetsova et al. Transcriptomic Analysis of Radish (Raphanus sativus L.) Roots with CLE41 Overexpression. Plants (Basel). 2022 Aug 20;11(16):2163. doi: 10.3390/plants11162163.

Kuznetsova et al. Genetic control of storage root development. Russian Journal of plant physiology. 2020. V. 67, P. 589-605. doi: 10.1134/S102144372004010X.



The first appearance of a virulence to the wheat gene *Sr24* among stem rust samples from Kemerovo

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The stem rust resistance *Sr24* gene is very important for agriculture, since it has been providing effective protection against stem rust for many years in the Russian Federation and throughout the world (with the exception of some races in South Africa and India). The *Sr24* gene is located on the 3DL chromosome, within a spontaneous translocation from the 3Ag chromosome of *Agropyron elongatum.*

Despite this, for the first time we recorded a race fungus *Puccinia graminis f.* sp. *tritici* from Kemerovo virulent to the *Sr24* gene.

The main purpose of the work was to confirm the virulence of the Kemerovo race of the fungus to the *Sr24* gene and to conduct an extended analysis. For this, series of inoculation of wheat lines carrying the *Sr24* gene with monopustular isolates of this race were carried out. To postulate the presence of the gene, each plant was genotyped (before the inoculation with the fungus) using specific molecular marker (Sr24#12).

The study was funded by the RSF grant № 23-16-00119.

Developing plasmid vectors with cultivar specific U6 promoter to enhance CRISPR/Cas9 genome editing efficiency in potato (*Solanum tuberosum*)

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Genetic engineering could bypass complications associated with potato breeding. Our goal was to develop a plasmid vector for efficient potato CRISPR/Cas9 genome editing via utilizing potato small nuclear U6 RNA promoter for single guide RNA (sgRNA) expression. Cultivar-specific StU6 promoter sequences were acquired from genome assemblies of Nevsky and Udacha using BLASTn algorithm and GenBank potato U6 promoter reference sequences Z17290, Z17292, Z17293, Z17301. Identified promoter variants (regions 400 bp upstream of U6 gene) were generated by PCR-amplification. The sgRNA was previously used to knockout potato GBSS gene by another group. We generated several sgRNA expression cassettes with various U6 promoters from potato cultivars Nevsky and Udacha. These cassettes were ligated into a plasmid vector which encodes Cas9 protein (pHDE-35S-Cas9-mCherry). Next, generated vectors will be introduced into protoplasts of Nevsky and Udacha to evaluate frequency of target sequence editing events.

The study is supported by the Kurchatov Genomic Centre of the Institute of Cytology and Genetics, SB RAS (075-15-2019-1662)

Take-home message:

We develop a plasmid-vector for efficient potato genome editing by utilizing potato U6 RNA promoter for sgRNA expression.

Transcriptomic analysis of N-glycosylation process genes

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of Sciences, Kazan, Russia
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N-glycosylation is a process assembly of glycans attached to a protein each stage of which is carried out by a specific set of enzymes that create sets of glycocoproteins characteristic of certain types of cells and tissues, as well as specific for various functional states of plants. The changes in the expression of genes related to certain stages of the process of N-glycosylation of proteins were characterized for maize root tissues selected at the stage division and elongation. A total of 92 genes were identified, the expression of which had a significant difference between the analyzed growth stages. The group of genes encoding subunits of the OST-complex was more numerous. The highest levels of expression were observed in genes encoding proteins involved in the folding of protein and quality control process. In almost all groups, gene expression was higher in the root meristem; however, in the genes encoding ER α-mannosidase and trans-Golgi galactosyltransferase, gene expression was higher in the elongation zone.

Take-home message:

Differences in gene expression in different part of the root may indicate differential regulation of structural modifications of glycans in cells in different functional states.

CisCross web server: a gene set enrichment analysis to predict the upstream regulators in *Arabidopsis thaliana*

Lavrekha V.V., Levitsky V., Tsukanov A.V., Bogomolov A.G., Omelyanchuk N., Zemlyanskaya E.V., Mironova V.*

Federal Research Center Institute of Cytology and Genetics, Siberian Branch of Russian Academy of Sciences, Novosibirsk, Russia,

*Radboud University, Nijmegen, Netherlands

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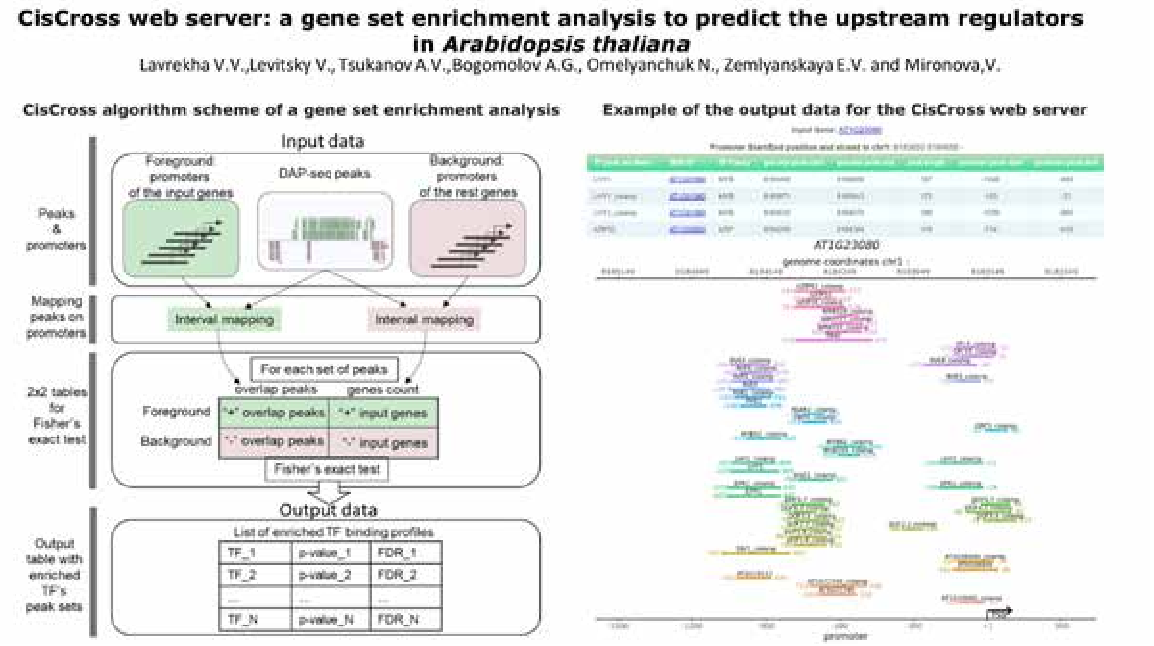
It is supposed that co-expressed genes are controlled by common transcription factors (TFs), which could be predicted by the enrichment analysis of their binding loci in promoters of these genes. Recently, a high-throughput DNA affinity purification followed by sequencing (DAP-Seq) method was used to generate the collection of the binding profiles for 387 *Arabidopsis thaliana* TFs (Plant Cistrome). In our work, we aim to improve the results of the gene set enrichment analysis by creating alternative collections of peak sets via reprocessing of raw DAP-Seq data and getting a better quality of peak sets. We implemented gene set enrichment analysis using new collections of peak sets as CisCross web server. CisCross is capable of defining potential target genes of TFs with respect to upstream regions of different length and visualizing the corresponding TF binding loci. Using several different gene expression profiles, we demonstrated that CisCross flexibility ensures accurate data analysis and potentiates a deeper insight into the mechanisms of gene transcription regulation compared with other web-applications. This work was supported by the RSF 21-14-00240.

The main publications of authors on the subject of the abstract:

Lavrekha, V.V., Levitsky, V., Tsukanov, A.V., Bogomolov, A.G., Grigorovich, D.A., Omelyanchuk, N., Zemlyanskaya, E.V. and Mironova, V. (2022). CisCross: A gene list enrichment analysis to predict upstream regulators in Arabidopsis thaliana // Front. Plant Sci. 13, 942710. doi: 10.3389/fpls.2022.942710.

Take-home message:

The CisCross (https://plamorph.sysbio.ru/ciscross/) is a flexible tool for prediction of the upstream transcriptional regulators in A. thaliana gene sets, which provides a whole spectrum of settings, including alternative collections of peak sets.



CisCross web server: a gene set enrichment analysis to predict the upstream regulators in *Arabidopsis thaliana*

Lavrekha V.V.,Levitsky V., Tsukanov A.V.,Bogomolov A.G., Omelyanchuk N., Zemlyanskaya E.V. and Mironova,V.

CisCross algorithm scheme of a gene set enrichment analysis

Example of the output data for the CisCross web server

Genetic analysis of birch and oak populations for tolerance to drought stress

Lebedev V.G., Evlakov P.M.*, Grodetskaya T.A.*, Isakov I.Yu.*, Popova A.A.*, Romashkina I.V., Shestibratov K.A.

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*Voronezh State University of Forestry and Technologies Named after G.F. Morozov, Voronezh, Russia
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Trees from the genera Quercus and Betula are very important species in Russian forestry, but they have proven to be sensitive to water deficit caused by climate change. This problem is especially urgent in the forest-steppe zone, and for reforestation it is necessary to select drought-resistant genotypes of oak and birch. We genotyped about 300 plants for each tree species: geographical cultures of Q.robur from territory of the former USSR, half-sibs of plus oak trees from the Voronezh region, and two generations of B.pendula, B.pubescens and birch hybrids. Population genetic diversity was assessed using published SSR markers (20 for each species). In addition, markers were developed from SSR loci in the structural and regulatory oak and birch genes associated with drought tolerance. In the work, the most polymorphic markers were identified, the genetic structure of the offspring was assessed, and dendrograms of genetic relationships were constructed. The results can be used to study molecular mechanisms of drought tolerance in woody plants and to select genotypes with the highest adaptive potential. The work was supported by the Russian Science Foundation (grant 22-64-00036).

Development of potato (*Solanum tuberosum* L.) plants with StLEAFY knockout

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*Institute for Information, Transmission Problems of the RAS, Moscow, Russia
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The tetraploid potato (*Solanum tuberosum* L.) is an important agricultural crop worldwide. In this study, we used CRISPR/Cas9 to inactivate the potato homolog (*StLFY*) of the *LEAFY* gene-a key regulator of the transition to flowering and floral meristem identity-in a tetraploid potato cultivar Vector. Independent potato lines were developed using two different sgRNAs. For genome editing events detection we used target NGS-sequencing, which allows to reveal all variants and assess their proportion in individual tetraploid plant. Thus, it was shown, that we achieved high rates of all-allelic knockouts even in a T0 plant generation. Then, next vegetative generation for the best T0 plants were developed and re-sequenced with target NGS approach in order to confirm frameshift mutations in *StLFY* gene. *StLFY* knockout led to phenotypic alterations, including indeterminate inflorescence development and the replacement of flowers with the leafy-like structures.

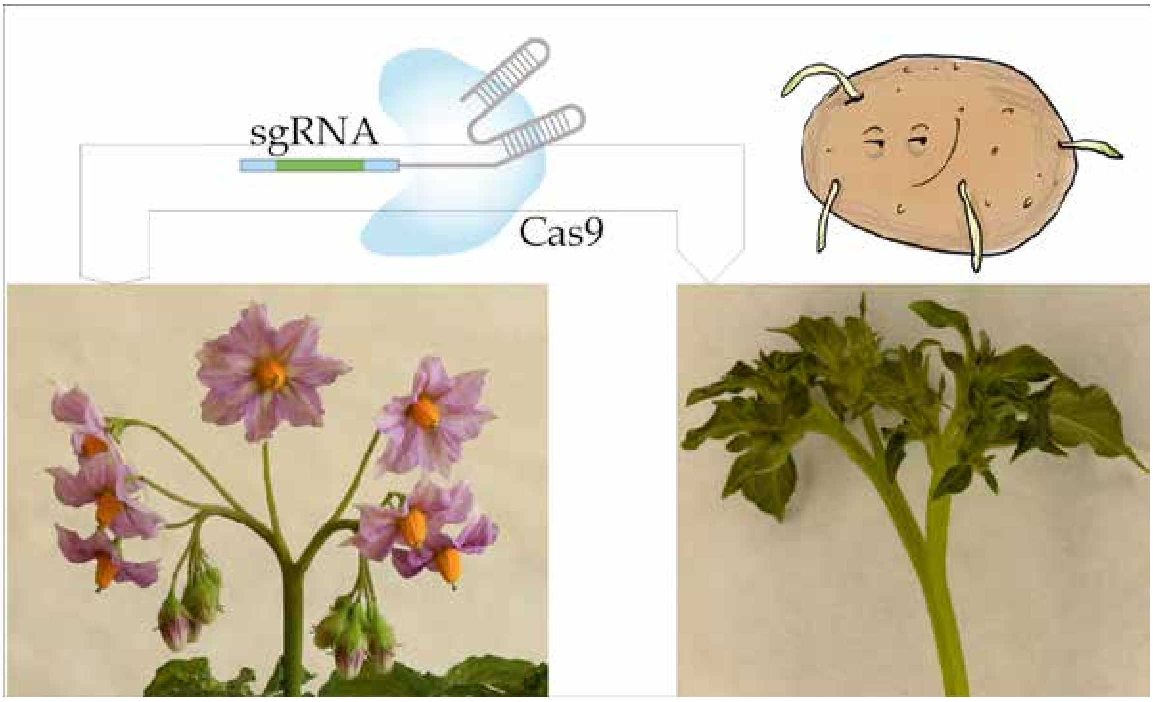
The work was supported by the Comprehensive Research Program “Development of Potato Breeding and Seed Production”.

The main publications of authors on the subject of the abstract:

Lebedeva, M., Komakhin, R., Konovalova, L. et al. Development of potato (Solanum tuberosum L.) plants with StLEAFY knockout // Planta 256, 116 (2022). https://doi.org/10.1007/s00425-022-04032-9

Take-home message:

StLFY-knockout potato plants were developed using CRISPR/Cas9 system. Inflorescences of edited plants transited to flowering, but inflorescence structures lacked flowers and were indeterminate, producing multiple shoot meristems.



Root exudation of plants under conditions of stress caused by exposure to toxic metals and phytopathogens

Lebedinskii M.I., Shaposhnikov A.I., Azarova T.S., Vishnevskaya N.A., Shakhnazarova V.Yu., Borodina E.V., Strunnikova O.K., Yuzikhin O.S., Belimov A.A.

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To create effective plant-microbial systems, it is necessary to study the mechanisms that determine the regulation of the processes of joint adaptation of plants and rhizosphere microbiomes to adverse environmental factors. Our studies were devoted to the investigation of root exudation of various plant genotypes under toxic metals and phytopathogenic stresses, including their interaction with PGPR. The study was carried out in gnotobiotic hydroponic systems using various methods of chromatographic analysis.

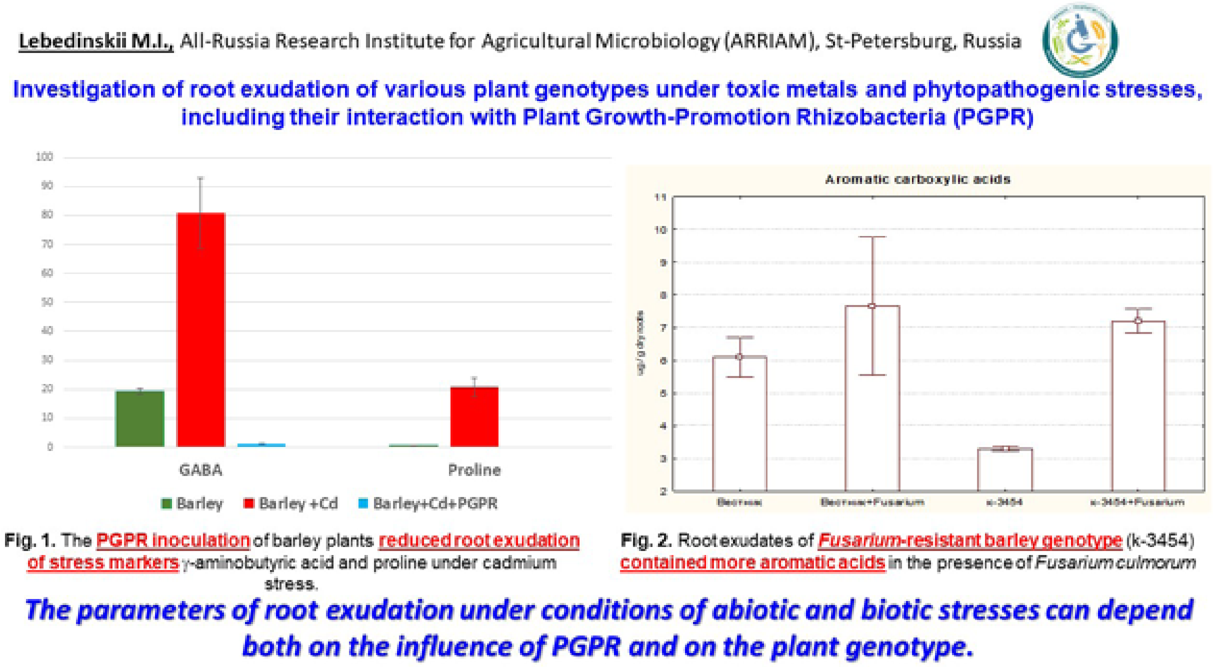
Treatment of pea plants with Cd and Al induced root exudation of organic acids, amino acids and sugars. PGPR modulated root exudation via utilization and/or stimulation processes and effects of toxic metals and bacteria on plants varied depending on pea genotype. The PGPR inoculation of barley plants reduced root exudation of stress markers g-aminobutyric acid and proline under cadmium stress. Root exudates of *Fusarium-resistant* barley genotype contained more of some aromatic acids than exudates of sensitive genotype in the presence of *Fusarium culmorum*.

The study was supported by grants from the Russian Science Foundation (19-16-00097, 22-26-00341).

The main publications of authors on the subject of the abstract:

Vishnevskaya N., Shakhnazarova V., Shaposhnikov A., Strunnikova O. The role of root exudates of barley colonized by Pseudomonas fluorescens in enhancing root colonization by Fusarium culmorum // Plants (2020) 9: 366. doi: 10.3390/plants9030366.

Belimov A.A., Shaposhnikov A.I., Azarova T.S. et al. Rhizobacteria mitigate the negative effect of aluminum on pea growth by immobilizing the toxicant and modulating root exudation // Plants (2022) 11: 2416. doi: 10.3390/plants11182416.



Lebedinskii M.I., All-Russia Research Institute for Agricultural Microbiology (ARRIAM), St-Petersburg, Russia

Investigation of root exudation of various plant genotypes under toxic metals and phytopathogenic stresses, including their interaction with Plant Growth-Promotion Rhizobacteria (PGPR)

Fig. 1. The PGPR inoculation of barley plants reduced root exudation of stress markers γ-aminobutyric acid and proline under cadmium stress.

Fig. 2. Root exudates of *Fusarium*-resistant barley genotype (k-3454) contained more aromatic acids in the presence of *Fusarium culmorum*

The parameters of root exudation under conditions of abiotic and biotic stresses can depend both on the influence of PGPR and on the plant genotype.

Transcriptome profiling of lichen myco- and photobionts during desiccation and rehydration

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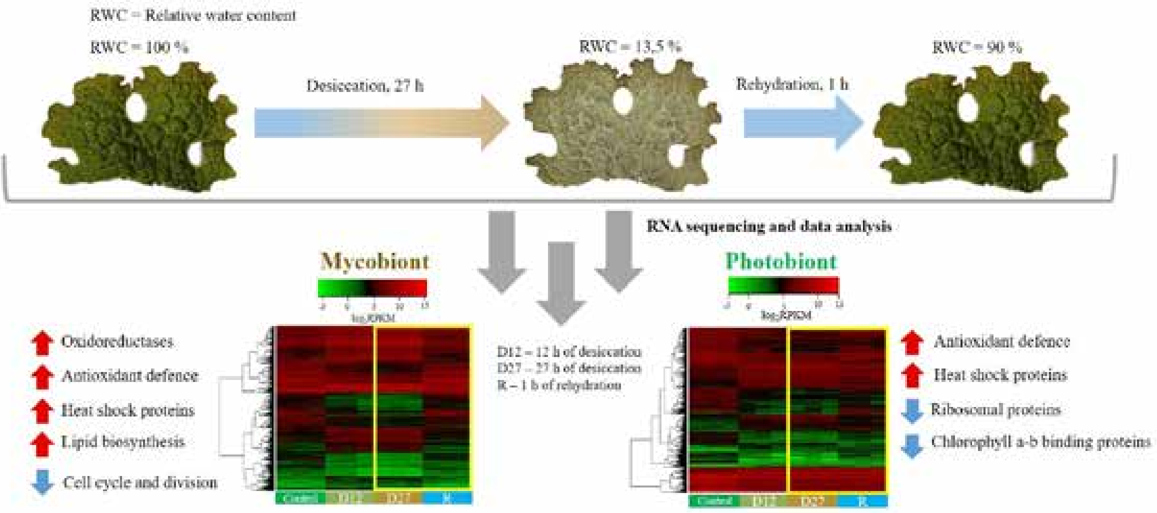
Lichens belong to extremophilic organisms, which survive in adverse environments. Mechanisms of their high stress tolerance include upregulation of genes encoding defence proteins. Information on transcriptome changes in stressed lichens is scarce. Here we analyzed differentially expressed genes (DEGs) in the myco- and photobionts of the lichen Lobaria *pulmonaria i*n response to desiccation and rehydration. Analysis of gene expression of photo- and mycobionts performed by RNA-seq data and RT-qPCR demonstrated upregulation of genes encoding defence proteins such as antioxidant enzymes and chaperones from Hsp70 and DnaJ superfamilies for both bionts after 27 h desiccation. Following 1 h rehydration, the patterns of gene expression differed between myco- and photobionts. Compared with the dehydration for 27 h, fewer mycobiont's genes were diferentially regulated upon rehydration (937 vs 140), whereas in photobiont, the number of DEGs (1275 vs 643) changed less abrupt. This work was supported by RSF (grant № 23-14-00327).

Take-home message:

Desiccation causes upregulation of defence genes in lichen photo- and mycobionts. Our results suggest different susceptibility of lichen bionts to desiccation, when photobiont is more sensitive to water deficit than mycobiont.



Common wheat introgression lines with genetic material of the tribe Triticeae as a source of diversity for quality traits

Leonova I.N., Kiseleva A.A., Berezhnaya A.A., Potapova N.A., Tsepilov Ya.A., Vinichenko N.A., Salina E.A.

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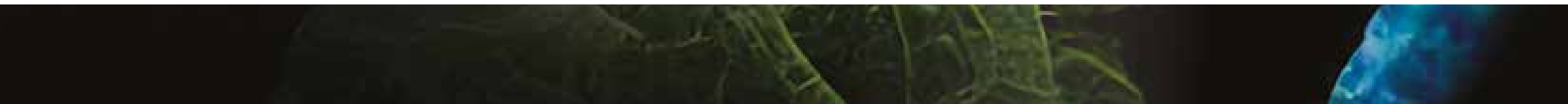
Wild and cultivated wheat relatives have a high potential for expanding the genetic diversity of common wheat for grain quality traits. The aim of the study was identification and chromosomal localization of loci associated with gluten and mineral element contents. A wheat panel consisted of cultivars and introgression lines developed on the base wild relatives was characterized by gluten content, glutenin alleles and seven mineral elements. Phenotypic evaluation showed that introgression lines exceeded commercial wheat varieties in gluten content and concentration of Ca, Fe, K, Mn and Zn. Genome wide association study revealed 13 significant QTNs contributed to the gluten content on chromosomes 1D, 2A, 2B, 5A, 6A, 6D, and 7B. Among them, the locus on chromosome 2A inherited from Triticum timopheevii is of the greatest importance. Four QTLs located on the 5B, 6A, and 7A chromosomes were associated with the mineral elements, of which two loci have a significant effect on the content of both Fe and Mn. Genotypes containing putative QTLs can be used as prospective material for breeding.

Acknowledgments: The work was supported by Russian Science Foundation (project no. 23-16-00041)

The main publications of authors on the subject of the abstract:

Leonova I.N. et al. Identification of QTLs for grain protein content in Russian spring wheat varieties (2022) Plants 11, 437. doi:10.3390/plants11030437

Leonova et al. Detection of genomic regions associated with resistance to stem rust in Russian spring wheat varieties and breeding germplasm (2020) Int. J. Mol. Sci. 21, 4706; doi:10.3390/ijms21134706



The role of the PAS-domain of the sensory histidine kinase Hik33 in the regulation of stress responses in *Synechocystis sp. PCC 6803 GT-L*

Leusenko A.V., Mironov K.S., Los D.A.

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The PAS domain is a widespread functional part of the protein structure. The proteins with this domain include histidine and serine/threonine kinases, photoreceptors, and others. The PAS domain is responsible for the sensory and signaling functions of these proteins and is involved in the formation of their tertiary structure. Hik33 is a sensory histidine kinase, which, together with the corresponding response regulator, constitutes a two-component signaling system. Hik33 is involved in regulating the expression of a large number of genes in response to cold, salt, and hyperosmotic stresses. The structure of Hik33 includes three transmembrane domains, HAMP-, PAS-, and kinase domains. Previously, it was shown that simultaneous exposure of *Synechocystis* cells to cold and darkness critically reduced the expression of Hik33-dependent genes, indicating an apparent light-dependent nature of signal transmission. To study the functional role of individual domains of Hik33 in signal transduction, we obtained independent mutants of *Synechocystis* carrying this histidine kinase with partially and completely deleted transmembrane domains, as well as a mutant with a deletion of the PAS domain.

Design of synthetic operons to study the regulation of stress responses in the cyanobacteria

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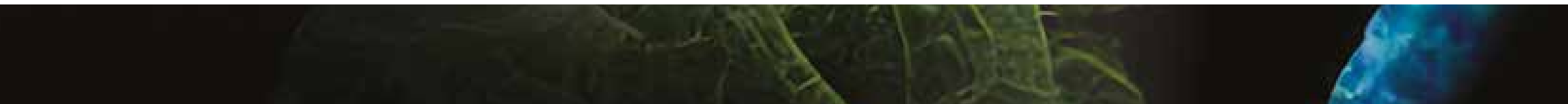
The fatty acid desaturases (FA) are enzymes that catalyze the conversion of single bonds between carbon atoms in acyl chains into double bonds at a specific position, thereby increasing the unsaturation of FA. The degree of FA unsaturation determines the cytoplasmic membrane fluidity, which in turn determines the resistance of cells to stress factors. Studies in this area have bio- and agrotechnological importance since they allow the obtaining of plants which more resistant to adverse environmental factors. To study the effect of the FA-profile on stress tolerance, we created a vector pLPA7 with the Bio-Bricks operon assembly system for integration into the *Synechococcus elongatus* PCC 7942 chromosome. The desA, desB, and desD genes from the cyanobacterium *Synechocystis sp.* PCC 6803 were used for construction of different operons . The presence of mRNA desaturases was confirmed by RT-PCR, and the fatty acid profiles were verified by gas chromatography.



Refinement of the values of spectral indices determined in plants, depending on the angle of inclination of the leaves

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Spectral indices (SIs) such as the NDVI (Normalized Differential Vegetation Index) are widely used for remote monitoring of plant state. SIs are used for determining abiotic and biotic stress in plants, predicting the yield and quality parameters of crops. SIs use reflectance values of light at specific wavelengths. The reflection of light by plants depends on the content of various pigments in the leaves, as well as the surface properties and microstructure of the internal tissues of the foliage. When light falls on leaves at different angles, the light beam travels a different path through the pigments and light-scattering inhomogeneities in the tissue.

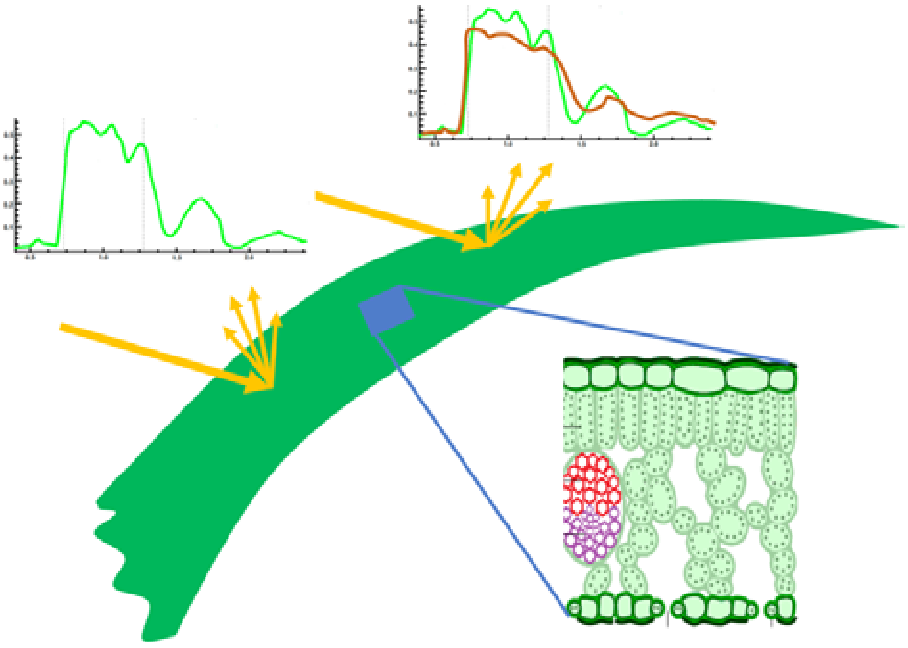
We hypothesized that the spectrum of the reflected light and SIs depend on the angle of incidence of the light. To test the hypothesis, we used hyperspectral imaging. The data obtained indicate that the reflection spectrum and SIs depend on the angle of inclination of the foliage. Thus, the SIs are not parameters that are completely independent of morphometric parameters (leaf angle), however, the spectral component can be extracted from the measured SI to compare SI values in plants despite different leaf angles.

The main publications of authors on the subject of the abstract:

Mirgorodskaya, A.B. et al. Enhanced Herbicidal Action of Clopyralid in the Form of a Supramolecular Complex with a Gemini Surfactant. Agronomy 2023, 13, 973. doi: 10.3390/agronomy13040973

Take-home message:

NDVI and other spectral indices based on reflected light are affected by the position of plant parts and the position (inclination) of the light source relative to the plants.



Construction and analysis of pansecretome for flax infected ascomycete *Fusarium oxysporum f. sp. lini*

Logachev A.A., Samsonova A.A.*, Kanapin A.A.*,
Samsonova M.G.

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Interaction of fungal organism with plant immunity as well as digestion of plant cells to get nutrients are provided by secretion of specific proteins, that totally constituted an individual secretome. We studied 13 isolates from different strains of *Fusarium oxysporum f.sp. lini (Folini)*. This secretome in our dataset varied in size in range between 799 genes in MI39 and 855 in different isolates. We defined Folini pansecretome and revealed that it composed of 1233 protein clusters that was 6,95% of the constructed pangenome. Core and non-core secreted proteins were distributed almost equally in the pansecretome and comprised 49,1% (605 clusters) and 50,9% (628 clusters), respectively. Among non-core, accessory genes fraction reached 29,4% (362 clusters), while singletons proportion constituted only 21,6% (266 clusters). Further, we analysed Folini pansecretome and defined three significant functional groups of secreted proteins: CAZYmes, proteases and effectors. Their ratio in the pansecretome was following: 29,1% (359 clusters) for effector proteins, 20,8% (257 clusters) for CAZYmes and 11,3% (139 clusters) for proteases.

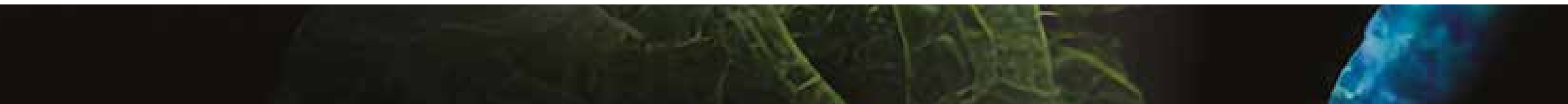
The main publications of authors on the subject of the abstract:

Kanapin A.A. et al. The genome sequence of five highly pathogenic isolates of Fusarium oxysporum f.sp. lini // MPMI (2020) 33(9): 1112-1115

Samsonova A.A. et al. A genomic blueprint of flax fungal parasite Fusarium oxysporum f.sp. lini // Int. J. of Mol. Sci. (2021) 22(05): 2665

Take-home message:

Analysis of pansecretome of F. oxysporum f.sp. linii revealed higly plastic genome



De novo assembly and annotation of plant genomes: problems and prospects

Logacheva M.

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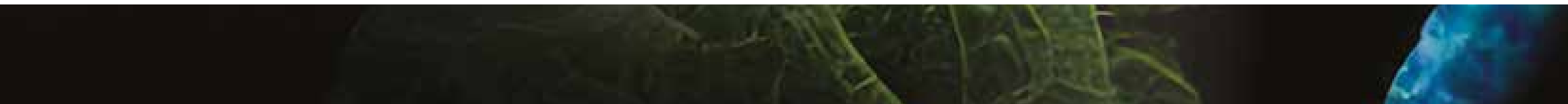
Развитие технологий секвенирования дало огромный импульс геномике. Из масштабной самостоятельной задачи, посильной только крупным межинститутским, а иногда межнациональным, консорциумам, де ново сборка геномов становится отправной точкой для исследований в области генетики, физиологии, эволюционной биологии. Тем не менее, сборка геномов растений до сих представляет большую сложность. Так, всего несколько лет назад был собран и аннотирован геном первого модельного объекта генетики –гороха. Это связано с двумя особенностями строения геномов растений – для них характерны многочисленные раунды полногеномных дупликаций и большое количество повторов, возникших за счет активности мобильных элементов. Именно растениям принадлежит абсолютный рекорд по размеру генома –150 миллиардов п.н., в 50 раз больше генома человека. Тем не менее, исследователи в области геномики растений продолжают двигаться вперед, переходя от геномов к пангеномам. В своем докладе я расскажу о том, как современные технологии секвенирования и анализа данных позволяют решить эти проблемы, какие сложности ещё остаются и какие открытия были сделаны в области геномики растений в последние годы.

The main publications of authors on the subject of the abstract:

1. The genome of the toxic invasive species Heracleum sosnowskyi carries an increased number of genes despite absence of recent whole-genome duplications: https://www.biorxiv.org/content/10.1101/2023.02.14.528432v3

2. Comparative analysis of plastid genomes in the non-photosynthetic genus Thismia reveals ongoing gene set reduction. https://www.frontiersin.org/articles/10.3389/fpls.2021.602598/full



The role of StBAM and StTDR genes in *Solanum tuberosum* L. development

Losev M.R., Gancheva M.S., Poliushkevich L.O., Lutova L.A.

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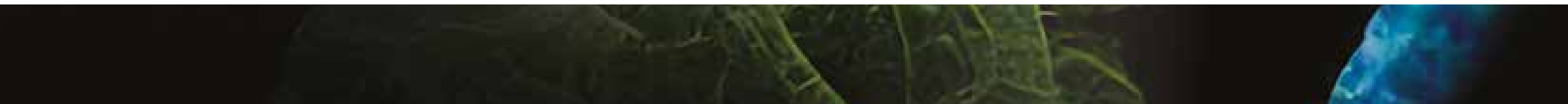
Potato is an important agricultural crop – potato tubers are actively used for food all over the world, however, the regulation of potato development is poorly understood.

In many plants signaling of CLE hormones with the participation of their TDR receptors activates cell division in lateral meristems and regulates xylem differentiation, and BAM receptors are involved in the regulation of phloem development. Thus, we suggest that *TDR* and *BAM* genes may also participate in potato development.

We found accumulation of transcripts of *StTDR* and *StBAM* genes in the potato stem. We managed to localize the activity of promoters of *StTDR1* and *StBAM3* genes in the potato stem and tuber in the cells of the vascular system. Work is also underway to localize the activity of promoters of other *TDR* and *BAM* genes in potato.

To clarify the function of *StBAM* and *StTDR* genes in potato development, we are working on editing these genes using the CRISPR/Cas9 system.

This work was supported by the Ministry of Science and Higher Education of the Russian Federation in accordance with agreement No. 075-15-2022-322 date 22.04.2022 (World-class Scientific Center “Agrotechnologies for the Future”).



Plants proteomics: sample preparation for a best results

Lukasheva E.M., Danko K.V., Soloveva M.A., Frolov A.A.*

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*K.A. Timiryazev Institute of Plant Physiology, Russian Academy of Sciences, Moscow, Russia
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Протеомика является одним из важнейших инструментов пост-геномного подхода к изучению жизни. При изучении протеома растений, ключевыми являются вопросы о количестве, функциях и локализации индивидуальных белков, синтезируемых в конкретный момент времени в ходе экспрессии отдельных генов. Основой методологической базой современной протеомики является масс-пектрометрия. Хромато-масс-спектрометрический подход (LC-MS/MS) в рамках стратегии bottom-up позволяет использовать высокое аналитическое разрешение и производительность обратнофазовой жидкостной хроматографии для получения наиболее полного покрытия протеома, а также охарактеризовать максимально полный спектр пост-трансляционных модификаций белков. При этом, стадия пробоподготовки играет в растительной протеомике важную роль в связи с такими особенностями объектов как наличие жесткой клеточной стенки, пигментов, развитых мембранных систем, сахаров и вторичных метаболитов.

В нашей группе накоплен большой опыт работы с различными растительными объектами с использованием спектра техник изоляции отдельных частей растительного организма или клетки, выделения и гидролиза белка, в том числе лабильных детергентов или фильтров (FASP).

The main publications of authors on the subject of the abstract:

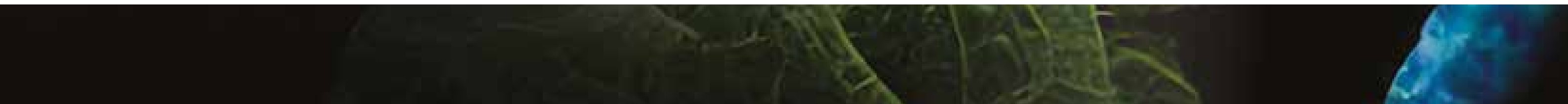
Danko, K., Lukasheva, E., Zhukov, V.A., et al, 2022. Detergent-Assisted Protein Digestion—On the Way to Avoid the Key Bottleneck of Shotgun Bottom-Up Proteomics. Int. J. Mol. Sci. 23, 13903. https://doi.org/10.3390/ijms232213903

Mamontova, T., Lukasheva, E., Mavropolo-Stolyarenko, G., et al, 2018. Proteome Map of Pea (Pisum sativum L.) Embryos Containing Different Amounts of Residual Chlorophylls. Int. J. Mol. Sci. 19, 4066. https://doi.org/10.3390/ijms19124066

Take-home message:

Протеомика-методология постгеномных исследований.

Пробоподготовка-ключевой момент протеомики.



Identification of genetic factors of *Betula pendula var. carelica* “wood patterning” using genome-wide association study

Lytkin K.F., Gubaev R.F., Karzhaev D.S., Safronycheva E.D., Volkov V.A., Vetchinnikova L.V., Zhigunov A.V., Potokina E.K.*

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*Skolkovo Institute of Science and Technology, Moscow, Russia
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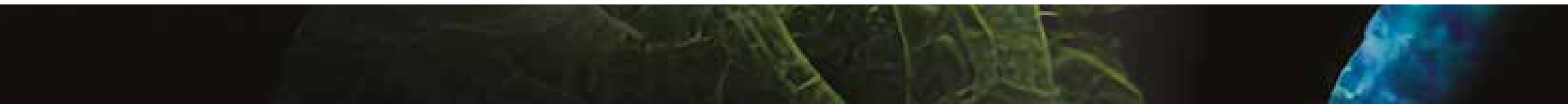
Curly birch is native to the northern countries of Europe, its “patterned” wood is highly valued in the woodworking industry. Some recent studies suggested that swirling wood pattern could be a monogenic trait, inherited according to the classical Mendelian laws. Using RADseq-based high-throughput genotyping and subsequent association analysis, we searched for novel genetic polymorphisms associated with this trait. Two pairs of parents and 188 full-sibs and half-sibs progeny were genotyped by RADseq method, resulting in 145,000 SNPs identified after the alignment of Illumina NovaSeq reads to Betula pendula reference genome using GATK4 pipeline. As a result, we were able to identify SNPs linked to the putative candidate genes that may be responsible for the “curly” wood patterning. The genes could potentially be used in future breeding programs to enhance the quality of the wood.

Acknowledgements: This work was funded by Russian Science Foundation grant No. 22-16-00096.



Identification of new blocks of avenin components in oat varieties

Lyubimova A.V., Akhtyamova A.A.

Scientific Research Institute of Agriculture of the Northern Trans-Ural Region - Branch of the Tyumen Scientific Center of Siberian Branch of the Russian Academy of Sciences, Tyumen, Russia
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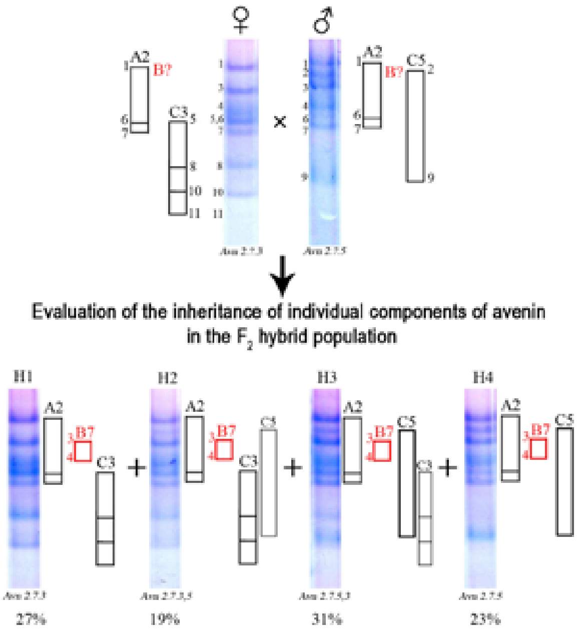
Avenins are oat prolamins. They are used to determine the genetic diversity of populations, certification of varieties, and are also promising for study as markers of hypoallergenic genotypes. But the genetic control of these proteins is not well understood. The method of native electrophoresis was used to study avenins of 8 populations F_1 -F_2 from monohybrid crossing of oat varieties. The spectra of F_1 grains were the total spectrum of proteins of parental genotypes. The dose effect of the maternal endosperm gene was noted. In the second generation in all populations, splitting into four phenotypic classes was noted: 21-27% of genotypes had a spectrum identical to the spectrum of the first parent, 22-24% – to the spectrum of the second parent, the remaining genotypes were heterozygotes with the effect of a gene dose from one of the parental varieties and combined into one class. The observed grain number ratio was in line with that theoretically expected for codominant monohybrid inheritance. It was confirmed that avenins are inherited in linked blocks, and their synthesis is controlled by 3 independent clusters of genes. Nine new blocks of avenin components have been described.

<u>The main publications of authors on the subject of the abstract:</u>

Lyubimova A. V. Studying the nature of inheritance of avenin components in F2 hybrids from crossing oat varieties of Siberian selection // Agrarian Bulletin of the Urals (2022) 02: 48-59. DOI: https://doi.org/10.32417/1997-4868-2022-217-02-48-59 A. V. Lyubimova et al. Dynamics of the genetic diversity of oat varieties in the Tyumen region at avenin-coding loci // Vavilov Journal of Genetics and Breeding (2020) Vol. 24, No. 2. – P. 123-130. – DOI 10.18699/VJ20.607.

Hybridization of oat varieties with a new block of components for the *Avn B* locus



The observed ratio of the number of grains that make up the phenotypic classes H1, H2 + H3 and H4 corresponds to the theoretically expected ratio of 25:50:25 for codominant monohybrid inheritance.
($\chi 2 = 0{,}32$; the critical value of $\chi 2=5{,}99$; d.f. = 2; p = 0,95)

Suspension cell cultures as a model for investigation of mitochondria participant in extreme temperatures plant response

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Siberian institute of plant physiology and biochemistry of SB RAS, Irkutsk, Russia,
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E-mail: ostrov1873@yandex.ru

Study of the functioning of intracellular structures using suspension cell cultures allows you to analyze cell response simultaneously at the biochemical, molecular and cytological levels. To date, it is not known whether the mitochondria functioning can influence the choice of a cell stress strategy between an adaptive response and activation of the death process. We used the method of polarographic, fluorescence microscopic and Western blot analysis. With Arabidopsis, Winter wheat and Sugar cane cell cultures we revealed that co-operative functioning of complex I and alternative cyanide-resistant oxidase (AOX) provided gradual realizing of cell death process and adaptive plant cell response to temperature stress. At the early death stage cells maintained a high electrochemical potential on the inner mitochondrial membrane, which was a consequence of a disruption of the ATP-synthase function. High rates of respiration were supported by stable AOX activity. If cells could not provide timely detoxification of ROS formed due to high mitochondrial functioning, then it led to the cytochrome c release from mitochondria to the cytosol and further collaps of cell metabolism.

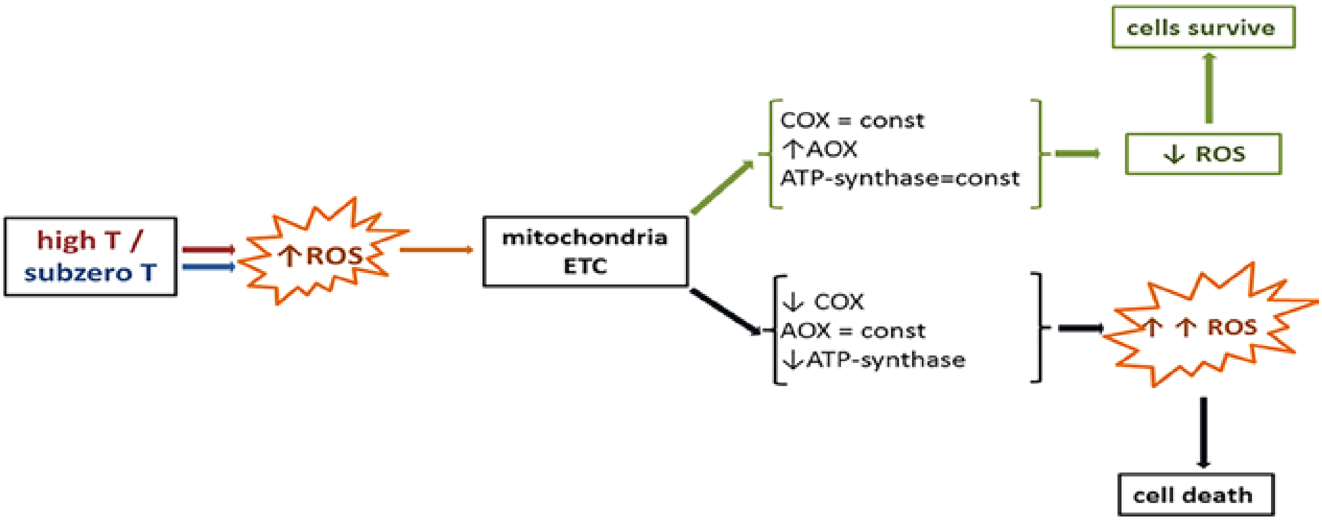
The main publications of authors on the subject of the abstract:

Lyubushkina I.V. et al. Temperatures induces ROS generation and damage to respiratory activity in Saccharum officinarum suspension cells // J. of Siberian Federal University. Biology (2021) 14: 354-369. doi:10.17516/1997-1389-0355

Lyubushkina I.V. et al. Mitochondria and cell death in suspension culture of Saccharum officinarum L. under subzero temperature treatment // Rus. J. Plant Physiol. (2022) 69: 113. doi: 10.1134/S1021443722060188

Take-home message:

Maintaining a balance between the energy supply of cellular metabolism and the processes of ROS detoxification is one of the key switching points between the ways of adaptation and death of a plant cell under conditions of temperature stress.



Computer simulations of complex biomolecular systems

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The rapid growth of genome and proteome data, together with the fast development of computer power, paves the way to a detailed in silico analysis of protein functions. In the current report, the state-of-the art of computational approaches will be overviewed followed by some case studies exemplified by glycosyltransferases (GT). One GT, monogalactosyldiacylglycerol synthase 1 *Arabidopsis Thaliana,* functions in the chloroplast and synthesizes the bulk of glycolipids, monogalactosyldiacylglycerol, needed for the rapid and massive expansion of thylakoid membranes in response to light. Despite the major importance of this process in plant growth and bioenergy conversion, there still remain many aspects of the protein action to be unraveled. Another example will illustrate how GTs can be used for in situ adding a sugar to glycolipids. The results of Coarse-Grained and All-Atom molecular dynamics simulations will unveil molecular details of catalytic complex assembly on the membrane surface and among them the modes of carbohydrate presentation and the protein-induced transient lipid domain formation.

The study was funded by RFBR & CNRS according to the research project № 21-54-15008.

The main publications of authors on the subject of the abstract:

Perez S. & Makshakova O. Multifaceted Computational Modelling in Glycoscience // Chemical Reviews (2022) 22: 15914–15970.

Makshakova O. et al. Unraveling the complex enzymatic machinery making a key galactolipid in chloroplast membrane: a multiscale computer simulation // Scientific Reports (2020) 10: 13514.

RALF peptides modulate immune response in the moss Physcomitrium patens

Mamaeva A.S., Lyapina I.S., Knyazev A.N., Golub N.O., Mollaev T., Chudinova E.*, Elansky S.*, Babenko V.V., Veselovsky V.A.**, Klimina K.M.**, Gribova T.N.**, Kharlampieva D.**, Lazarev V.N.**, Fesenko I.A.**

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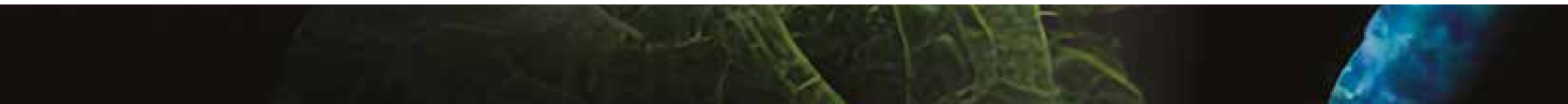
RAPID ALKALINIZATION FACTOR (RALFs) are cysteine-rich peptides that regulate many physiological processes in plants. This peptide family has considerably expanded during land plant evolution, but the role of ancient RALFs in modulating stress responses is unknown. Here, we used the moss Physcomitrium patens as a model to gain insight into the role of RALF peptides in the coordination of plant growth and stress response in non-vascular plants. The quantitative proteomic analysis revealed concerted downregulation of M6 metalloprotease and some membrane proteins, including those involved in stress response, in PpRALF1, 2 and 3 knockout lines. The subsequent analysis revealed the role of PpRALF3 in growth regulation under abiotic and biotic stress conditions. We found that knockout of the PpRALF2 and PpRALF3 genes resulted in increased resistance to phytopathogens, Pectobacterium carotovorum and Fusarium solani, suggesting the role of these peptides in negative regulation of the immune response in P. patens. Thus, our study sheds light on the function of the previously uncharacterized PpRALF3 peptide and gives a clue to the ancestral functions of RALF peptides in plant stress response.

The main publications of authors on the subject of the abstract:

Mamaeva et al., RALF peptides modulate immune response in the moss Physcomitrium patens // Front. Plant Sci., (2023) DOI: 10.3389/fpls.2023.1077301



Генофонд озимой ржи для селекции на устойчивость к снежной плесени

Маннапова Г.С., Пономарева М.Л., Пономарев С.Н., Сайфутдинова Д.Д., Гараева Н.Ш., Иванова И.О., Павлова С.Ю.

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Снежная плесень относится к прогрессирующим заболеваниям озимой ржи с явной тенденцией к нарастанию эпифитотийных ситуаций. Сложноустроенный патокомплекс возбудителей снежной плесени, включающий таксономически разнообразные грибы *Microdochium nivale, Typhula ishikariensis/T.incarnata,* сильно вариабелен и практически не исследован. Обновление генофонда за счет привлечения новых исходных форм весьма ограничено, хотя именно это является базисом селекции любой сельскохозяйственной культуры. Поэтому необходимым условием эффективного подавления снежной плесени является использование качественно нового селекционного материала для создания перспективных сортов. В связи с этим, нами проведен анализ устойчивости генофонда озимой ржи из коллекции ВНИИР им. Н.И.Вавилова и собственной селекции к снежной плесени. Исследования проведены на естественном фоне развития заболевания и на специально созданном искусственном фоне с дополнительным внесением отдельных возбудителей и комплекса снежноплесневых грибов. В результате работы выявлены более 20 источников устойчивости озимой ржи к этому заболеванию, создан селекционный генофонд, не имеющий мировых аналогов по уровню устойчивости к снежной плесени.

The main publications of authors on the subject of the abstract:

Ponomareva M., Gorshkov V., Ponomarev S., Mannapova G., Askhadullin D., Askhadullin D., Gogoleva O., Meshcherov A., Korzun V. Resistance to Snow Mold as a Target Trait for Rye Breeding // Plants (2022) 11: 2516. doi: 10.3390/plants11192516

Ponomareva M.L., Gorskov V.Y., Ponomarev S.N., Korzun V., Miedaner Th. Snow mold of winter cereals – a complex disease and a challenge for resistance breeding // Theoretical and Applied Genetics (2021) 134: 419-433. doi: 10.1007/s00122-020-03725-7

Take-home message:

Проведен обширный анализ генофонда озимой ржи на естественном и искусственном инфекционных фонах на устойчивость к снежной плесени. Выявлены источники устойчивости и получен новый селекционный материал для выведения сорта с повышенной устойчивостью.

Genome-scale insights into the virulence of the snow mold causal fungus *Microdochium nivale*

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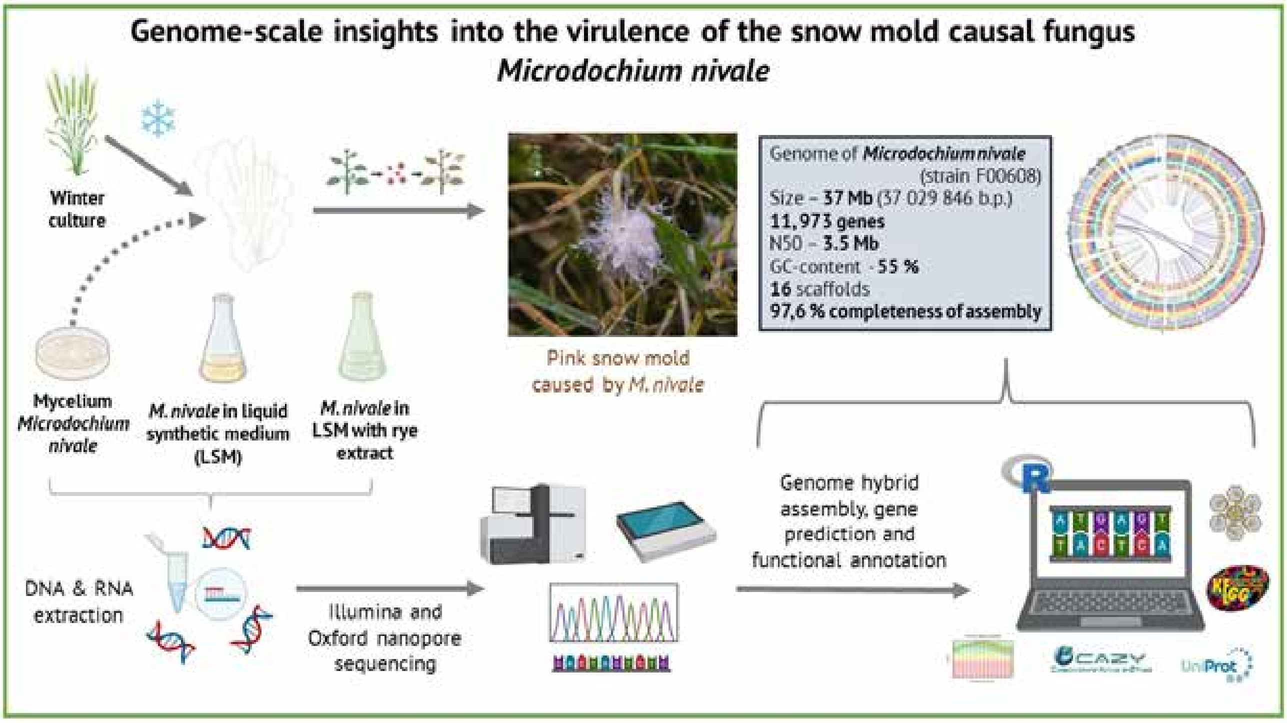
Microdochium nivale causes the harmful disease pink snow mold of winter cereal crops. In our study, we applied a hybrid assembly based on Oxford Nanopore and Illumina reads to decipher and annotate the first sequence of the *M. nivale* genome. The gene products of this fungus were classified into metabolic pathways to elucidate the genetic potential of *M. nivale* to synthesize virulence factors and mycotoxins hazardous to humans. Using PHI-base in the *M. nivale* genome, the gene products that best fit the criteria for virulence factors were identified. This category included secreted proteins and mycotoxins such as fumonisin, ochratoxin B, aflatoxin, and gliotoxin. The work resulted in the assembly and annotation of the *M. nivale* genome sequence. The genes whose products most likely determine the virulence of the phytopathogen under study were identified. The metabolic pathways of *M. nivale* responsible for the synthesis of mycotoxins hazardous to humans were discovered.

The main publications of authors on the subject of the abstract:

Tsers I.D. et al. IMA Fungus (2023) 14(1): 1-20. doi.org/10.1186/s43008-022-00107-0



Physiological and biochemical mechanisms of effective and ineffective interaction of *Bacillus subtilis* with different varieties of beans

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Plant growth promoting bacteria do not always effectively interact with some plant varieties. The aim of the work is to identify indicators that reflect the specific reactions of bean plants to inoculation with different strains both in normal conditions and under stress. Elsa seeds were inoculated with B. subtilis 26D and 10-4. 21-day plants were exposed to 1% NaCl for 48 h. The content of proline (Pro), malondialdehyde (MDA), and photosynthetic pigments (PSP) in plant leaves were determined spectrophotometrically, water-retaining capacity (WHC) by weight method. Without stress both strains promoted the root and shoot growth of 7-day-old seedlings, 26D activated the formation of adventitious roots. In 3-week-old plants, the strains reversed the ratio of Pro/MDA in roots and PSP in the leaves, and 10-4 increased WHC more strongly. Under stress, inoculation with both strains equally reduced the level of Pro, MDA, and moisture content in roots compared to the stressed control, but had a different effect on shoot watering. The revealed differences in plant response to inoculation serve as a basis for further analysis of effective/ineffective variety-strain combinations.

The main publications of authors on the subject of the abstract:

Markova O.V., Garipova S.R. Effect of bean inoculation by endophytic bacteria isolated from nodules // Agrarian Scientific Journal (2022) 4: 32–36. doi:10.28983/asj.y2022i4pp32-36

Markova O.V., Garipova S.R. Adaptive potential of bean (Phaseolus vulgaris L.) varieties cultivated in the conditions of southern Urals // Problems of agrochemistry and ecology (2020) 4: 40-43. doi:10.26178/AE.2020.78.87.007

Take-home message:

The study of plant-microbe interaction mechanisms allows for targeted selection of variety-strain combinations

To select a microbiome, it is necessary to search for physiological and biochemical markers of effective symbiosis

Analysis of changes in cucumber (*Cucumis sativus*) roots proteome under overexpression of small signal peptide RALF34

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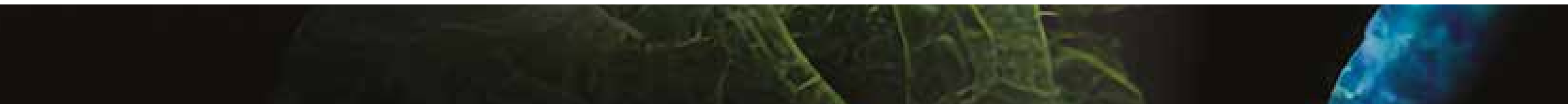
Until recent times, it was believed that orthologs of the small signal peptide RAPID ALKALINIZATION FACTOR 34 (RALF34) in different plants have similar effects, inhibiting the growth of lateral roots. To clarify the functional role of small signaling peptide RALF34, we have analyzed proteome changes of representative of the agriculturally valuable *Cucurbitaceae* family cucumber (*Cucumis sativus*) roots with overexpression of *CsRALF34* via shotgun bottom-up proteomics method. Transgenic root systems harbouring overexpression construction p*35S::CsRALF34*, as well as the control containing the β-glucuronidase gene, were used. Based on chromato-mass-spectrometric data processed by PEAKS Studio software (v.10.6) in the *Cucumis sativus* protein sequence database constructed by our group, several main effects of RALF34 were established. RALF34 blocks the transition of root cells from the G2-stage to mitosis. This peptide is involved in the suppression of ROS production and activation of cellular antioxidant systems, too. Under the influence of RALF34, the adaptability of plants to the action of abiotic stressors rises due to increase in the sensitivity of ABA receptors to the ligand.

The main publications of authors on the subject of the abstract:

Shumilina, J.; Kiryushkin, A.S.; Frolova, N.; Mashkina, V.; Ilina, E.L.; Puchkova, V.A.; Danko, K.; Silinskaya, S.; Serebryakov, E.B.; Soboleva, A.; Bilova, T.; Orlova, A.; Guseva, E.D.; Repkin, E.; Pawlowski, K.; Frolov, A.; Demchenko, K.N. Integrative Proteomics and Metabolomics Analysis Reveals the Role of Small Signaling Peptide Rapid Alkalinization Factor 34 (RALF34) in Cucumber Roots. Int. J. Mol. Sci. 2023, 24, 7654. https://doi.org/10.3390/ijms24087654



Genotyping of tea collection *Camellia sinensis* (L). based on SCoT-and chloroplast markers

Matskiv A.O., Samarina L.S.*, Malyarovskaya V.I.

Federal Research Centre the Subtropical Scientific Centre of the Russian Academy of Sciences, Sochi, Russia,
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Генотипирование коллекции чая на основе SCoT- и хлоропластных маркеров

Особенностью коллекции является наличие сортов с высокой устойчивостью к низким температурам. Генетические механизмы доместикации, внутри- и межвидовое разнообразие не изучены.

В исследовании применены мультилокусные SCoT- и хлоропластные ДНК маркеры.

Из 36 SCoT праймеров – 11 генерировали результаты с четким полиморфизмом. Всего получено 194 бэнда, средний уровень полиморфизма-55%. У 56 генотипов мутантных форм обнаружены уникальные фрагменты SCoT. Для анализа генетических дистанций коллекцию ранжировали по площади листа. В коллекции обнаружены 3 кластера. Результаты проверки 50 пар хлоропластных праймеров in silico показали амплификацию фрагментов одинаковой длины у *C.sinensis* var *sinensis* и *C.sinensis* var. *assamica.*

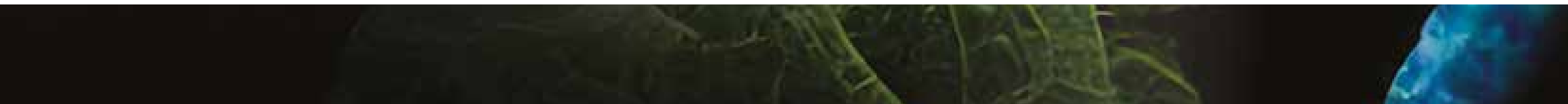
Выявлены различия по кривым плавления амплифицированных фрагментов по 4 из 50-ти праймеров.Наличие двух гаплотипов выявлено 3 маркерами, ампликоны которых различаются по температуре плавления, тепловые карты отражают присутствие 2 различных групп.

Исследования выполнены при финансовой поддержке РНФ № 18-76-10001

The main publications of authors on the subject of the abstract:

Samarina, Lidiia S. and Matskiv, Alexandra O. and Shkhalakhova, Ruset M. and Koninskaya, Natalia G.et al. Genetic Diversity and Genome Size Variability in the Russian Genebank Collection of Tea Plant [Camellia sinensis (L). O. Kuntze // Frontiers in Plant Science (2022) 12. doi:10.3389/fpls.2021.800141.

https://www.frontiersin.org/articles/10.3389/fpls.2021.800141



Natural GMOs as models for studying the role of Agrobacterium genes in plant evolution

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Plants containing homologs of “Agrobacterium” T-DNA in their genomes are called natural GMOs (nGMOs). Such T-DNA was named cellular (cT-DNA). NGS data shows, that about 6% of dicots are nGMOs. The extended cT-DNAs in their genomes are usually organized as imperfect inverted repeats. Based on the analysis of the divergence of these repeats, it was proposed that nGMOs began to appear about 15 mya and have been appearing till present time. They have been used by humans throughout their history as food, drinks and drugs. Natural GMOs differ in the composition of intact and expressed genes within cT-DNAs. Accordingly, these genes perform different functions. T-DNA in toadflax enhances their regenerative capacity and activates secondary metabolism, the *rol*B/C-like gene of sweet potato leads to the early flowering in transgenic *Arabidopsis,* and the genes of tobacco, dodder, peanut, and hop opine synthase lead to the synthesis of opines, which can be used for microbes feed, changing the biological environment of plants. These plant species are used to study different functions of cT-DNA and their evolutionary role.

Supported by RSF 21-14-00050

The main publications of authors on the subject of the abstract:

Matveeva, T. V., Otten, L. Widespread occurrence of natural genetic transformation of plants by Agrobacterium// Plant molecular biology, 2019. 101(4-5): 415–437.

Matveeva T, Otten L. Opine biosynthesis in naturally transgenic plants: Genes and products// Phytochemistry. 2021 Sep;189:112813.

Matveeva, T. New naturally transgenic plants: 2020 update. Biological Communications, 2021. 66(1), 36–46.

Take-home message:

Natural GMOs appeared without human intervention millions of years ago and continue to appear till nowdays. Different species maintain intact and expressed different sets of “Agrobacterium” genes, which play different evolutionary roles

S-nitrosylation of proteins during stress-induced autophagy in *Triticum aestivum*

Mazina A.B., Gazizova N.I., Daminova A.G., Soloveva M.A.*, Schumilina U.S.*, Gorbach D.P.*, Lukasheva E.M.*, Frolov A.A.*, Minibayeva F.V.

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Autophagy is a highly conserved, catabolic process in eukaryotic cells. Reactive nitrogen species are play roles as inductors and signaling molecules of autophagy. A key mechanism of NO-mediated signaling is a posttranslational modification of proteins by S-nitrosylation. For plants, information about the role for S-nitrosylation of proteins in autophagy processes is very scarce. The aim of this work is to analyze S-nitrosylation of proteins involved in the autophagy in the cells of wheat (Triticum aestivum) roots. Incubation of roots in the solutions of NO-donors or antimycin A led to accumulation of autophagosomes and increased expression of autophagic (ATG) genes. Bioinformatic analysis revealed the presence of S-nitrosylation sites in the structure of ATG proteins involved in different stages of autophagosome formation. The accumulation of S-nitrosylated proteins in the root cells during autophagy induction were visualized by immunocytochemical and Western blot analysis. S-nitrosylated proteins identified by Shotgun sequencing suggest that S-nitrosylation is a key posttranslational modification regulating the activity of various proteins involved in autophagy in plants.

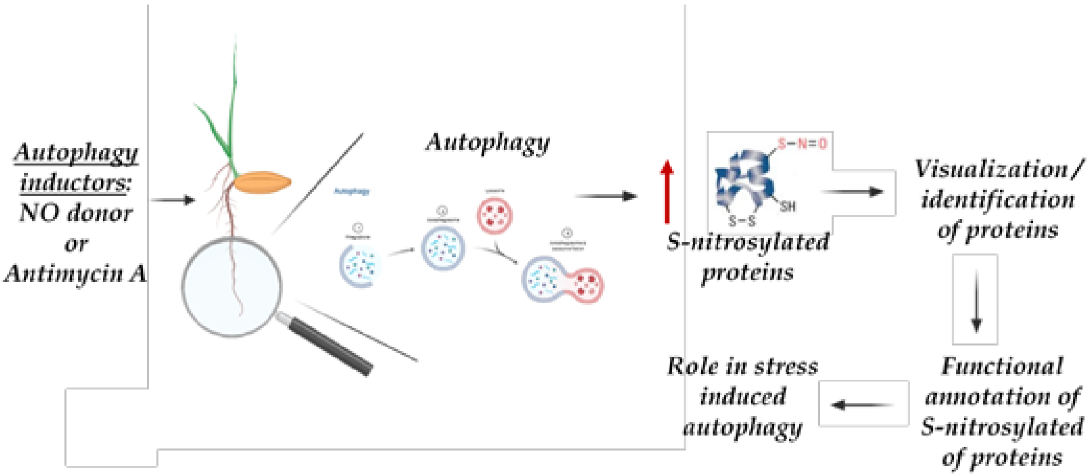
The main publications of authors on the subject of the abstract:

Mazina A.B. et al. Protein S-nitrosylation during induced autophagy in Triticum aestivum // AIP Conference Proceedings (2021) 2388: 030023. doi: 10.1063/5.0069510

Minibayeva F.V. et al. Oxidative stress-induced autophagy in plants: the role of mitochondria // Plant Physiology and Biochemistry (2012) 59: 11-19. doi: 10.1016/j.plaphy.2012.02.013

Take-home message:

Stress-induced autophagy in wheat roots is accompanied with an increase in the level of S-nitrosylated proteins. S-nitrosylation of proteins is a fine mechanism regulating autophagy in plants.



Seed-to-seedling transition in *Pisum sativum* L.: an omics approach

Medvedev S.S., Krylova E.A.*, Strygina K.V., Vilis P.S., Bilova T.E., Frolov A.A.***, Khlestkina E.K.*, Smolikova G.N.**

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Higher plants reduce productivity even with slight dehydration. However, their genome includes genes whose products allow plant seeds to remain viable under significant water loss. We studied the embryo axes of *Pisum sativum* L. during the transition from germinated seeds to seedlings. Massive reprogramming of the transcriptome, proteome, metabolome, and attendant signaling pathways resulted in silencing seed-maturation genes and activating vegetative growth. Seedlings lost desiccation tolerance but improved their ability to respond to biotic stressors. The latter was accompanied by suppressing ABA-related transcription factors ABI3, ABI4, and ABI5. We analyzed the methylation profiles of promoters of *PsABI3, PsABI4,* and *PsABI5* genes as potential master regulators during seed germination. Surprisingly, their methylation level was high already before root growth initiation. At that, the promotor of the PsABI5 showed many potential binding sites for proteins of the LAFL network (LEC1, ABI3, FUS3 и LEC2). The research was funded by the Russian Science Foundation, project N 20-16-00086 (https://rscf.ru/project/20-16-00086).

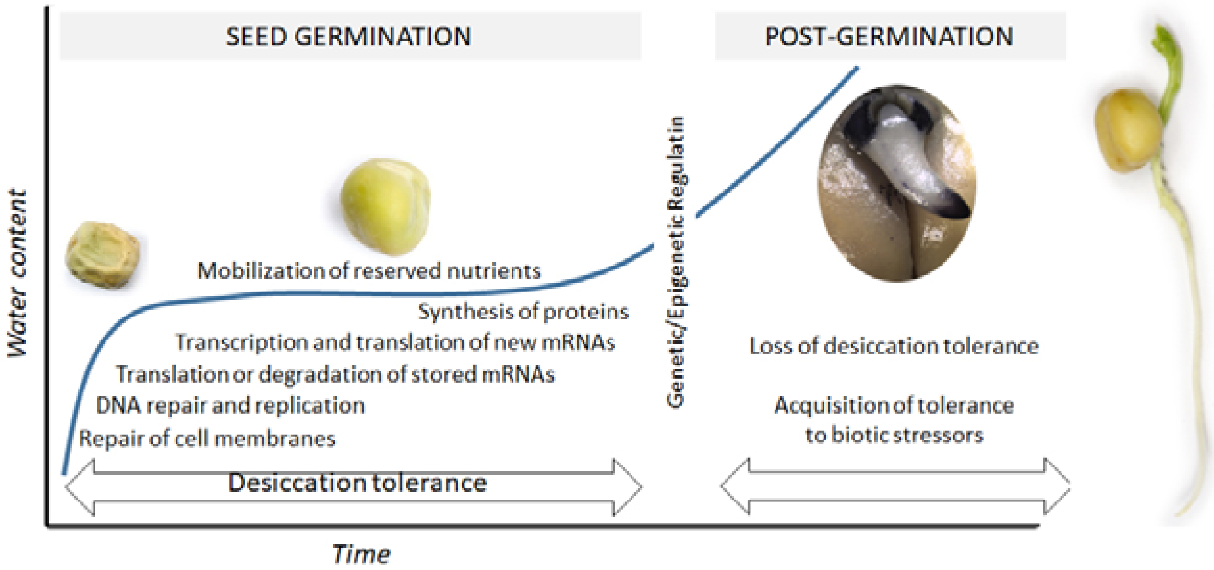
The main publications of authors on the subject of the abstract:

1) Smolikova et al. Seed-to-seedling transition in Pisum sativum L.: a transcriptomic approach // Plants (2022) 11: 1686. doi:10.3390/plants11131686.

2) Smolikova et al. Transition from seeds to seedlings: hormonal and epigenetic aspects // Plants (2021) 10: 1884. doi:10.3390/plants10091884.

Take-home message:

The seed-to-seedling transition occurs during seed germination and corresponds to embryonic root growth. It requires reprogramming of the transcriptome, proteome, and metabolome, resulting in the switching of stress tolerance mechanisms.



Peroxidases in peach: identification, structure and phylogeny

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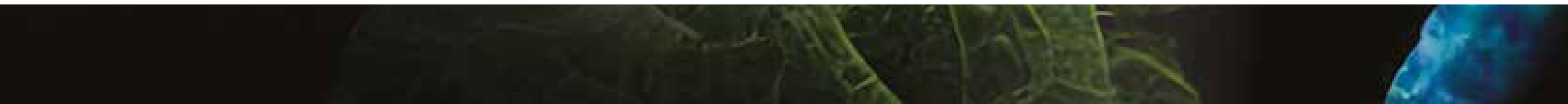
Peroxidase (POD) is a protein superfamily which play two important roles in plants: development and growth and stress responses and resistance to abiotic and biotic factors. It is lack of research about PODs in peach. The localization of POD genes through chromosomes of Lovell cultivar genome and exon-intron genes structure were analysed. Sixty annotated peroxidase genes revealed high nucleotide and amino acid variability and widely distributed over eighth chromosomes. all chromosomes as well as their regions had a different density of PpPODs. The highest density of PpPOD genes was observed at the chromosome 6. The exon-intron structure also varies greatly: some genes are intron-less, while others have several long introns. The number of exons was 1-5, most peroxidases had 4 exons. To investigate the evolutionary relationship of PpPODs, a phylogenetic tree was constructed with the 60 amino acid sequences of P. persica and 73 of A. thaliana. The evolutionary relationship and the motif analyses of POD family shown the high diversity and six phylogenetic subgroups were described. The study is supported by the Kurchatov Genomic Centre of the NBG–NSC (075-15-2019-1670).

Take-home message:

The genes encoding peroxidase in peach were described for the first time. Analysis of genetic variability and evolutionary relationships revealed suggest that considerable diversity for the PODs that can be connect with different gene subfunctions



Nanopore sequencing as tool for investigation of transposon-derived eccDNA in plants

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Extrachromosomal circular DNA (eccDNA) is a type of double-stranded DNA and can be observed in cells of a wide list of organisms, including humans, animals and plants. The development of high-throughput sequencing made it possible to get a first insight into the landscape of plant circulome. Thus an eccDNA derived from transposable elements (TEs) has been shown to make up a significant part of plant eccDNA. Although short read sequencing is widely used to identify eccDNA generated by TEs, the structure of individual circular molecules is still poorly studied. In our research we applied Nanopore sequencing of eccDNA of *Arabidopsis* wild-type stressed plants and DNA hypomethylation mutant *ddm1*. The obtained data made it possible to compare the structure of the eccDNA of active mobile elements *ONSEN* and *EVD* in different stress and epigenetic backgrounds. Thus a shift in *ONSEN* eccDNA profile to truncated eccDNA compared to predominance in full-length eccDNA in *ddm1* mutant was revealed. Overall, our work demonstrates the great potential of Nanopore sequencing for the study of plant eccDNA. This work was supported by the Russian Science Foundation (grant no. 22-74-10055).

Plant responses associated with the snow mold disease

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Pink snow mold is a dangerous plant infectious disease of winter grain crop plants. The causative agent of pink snow mold is psychorotolerant fungi Microdochium nivale. Despite the serious damage caused by this pathogen to the yield of winter grain crops it is little known about the aspects of interaction between M. nivale and plant hosts. We provided transcriptomic profiling of winter rye plants infected with highly virulent strain of M. nivale. In obtained transcriptomic dataset we revealed that a lot of differentially expressed genes (DEGs) encoding enzymes associated with protein and lipid degradation processes, terpenoid and alkaloid biosynthesis and ABA-signaling. Results of transcriptomic profiling were verified using biochemical assays (estimation of total terpenoid amount and protease/lipase assay) and physiological experiments (exogenic treatment with plant ABA). Based on obtained results we hypothesized about physiological determinants of plant resistance/susceptibility to the studied pathogen.

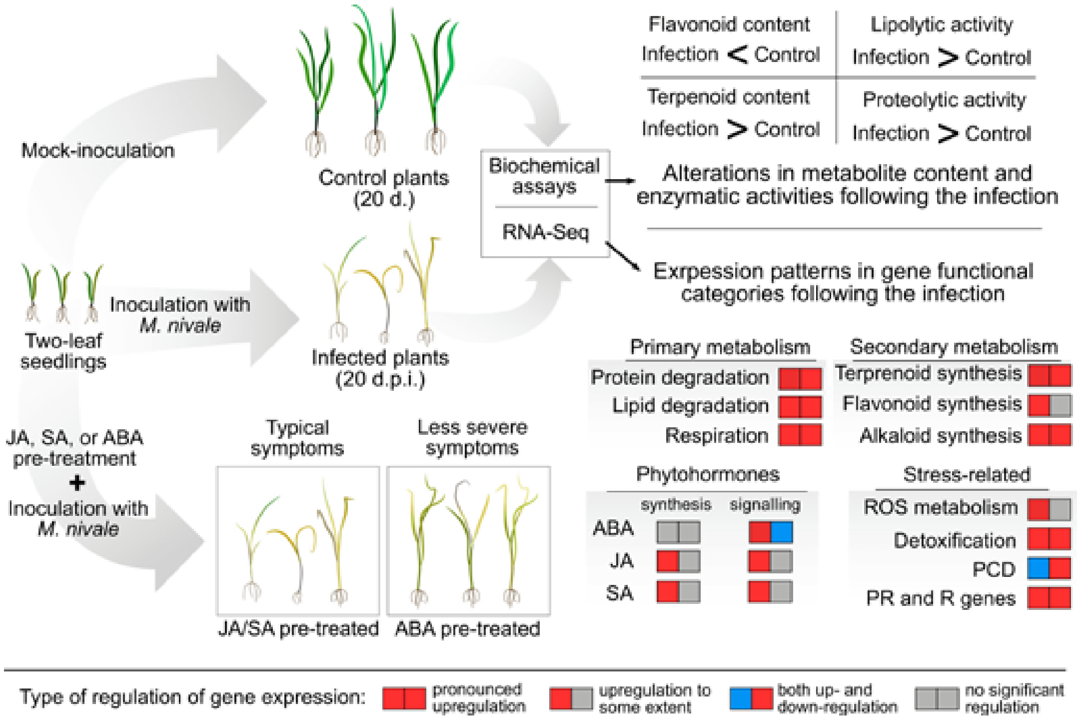
The main publications of authors on the subject of the abstract:

Tsers I. et al. Alterations in the transcriptome of rye plants following the Microdochium nivale infection: Identification of resistance/susceptibility-related reactions based on RNA-Seq analysis //Plants. – 2021. – T. 10. – №. 12. – C. 2723. doi.org/10.3390/plants10122723

Take-home message:

Aspects of interaction between M. nivale and plant hosts.

Transcriptomic profiling of winter rye plants infected with highly virulent strain of M. nivale.



Genome editing of Table Beet (*Beta vulgaris* L.) to increase the betalain content

Mikhailova A.S., Sokolova D.V., Popov V.S., Shvachko N.A., Khlestkina E.K.

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Table beet (*Beta vulgaris* L.) is valued as a source of the red-colored food dye (E162). The genes in loci R and Y are responsible for betalain accumulation in the pulp and determined its red, yellow or white color. We resequenced identified earlier the *CYP76AD1 (R), BvMYB1 (Y), BvDODA* genes to reveal their allelic diversity among contrast table beet genotype and choose the target gene for editing. We consider the CRISPR/Cas9 system as an approach to knockout the genes coding enzymes of the yellow pigment biosynthesis pathway. The *BvMYB1* product activates *BvDODA* through binding with the promotor region that leading to yellow betaxanthins accumulation. It is supposed that cutting in the promotor and in the end of the first exon will be more effective. We designed vector containing gRNA and target sequence to transformate table beet and receive the forms with increased red-colored pigments content in the pulp. This research was supported by the Russian Science Foundation under Project No. 21-66-00012 "The development with genetic technologies and the study of new plant lines adapted to changing environmental conditions, with increased productivity and dietary value"

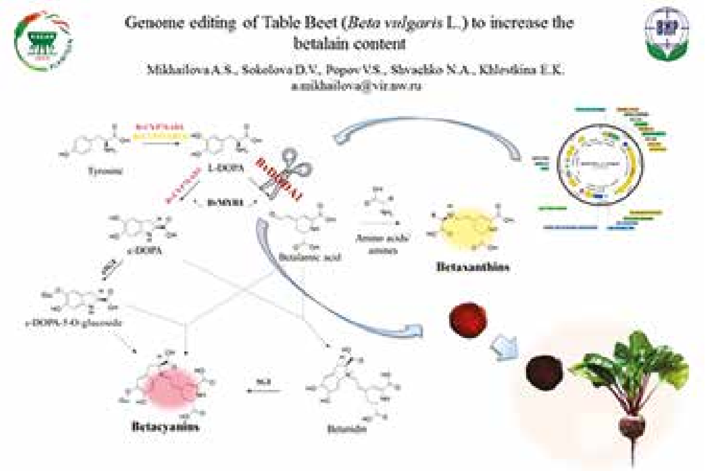
The main publications of authors on the subject of the abstract:

Sokolova D.V., Shvachko N.A., Mikhailova A.S. et.al. Betalain Content and Morphological Characteristics of Table Beet Accessions: Their Interplay with Abiotic Factors // Agronomy 2022:10.3390/agronomy12051033; Михайлова А.С., Соколова Д.В. и др. Ресеквенирование аллелей ключевых генов биосинтеза беталаинов у свеклы столовой (Beta vulgaris L.) коллекции ВИР // ВИР

Михайлова А.С., Соколова Д.В. Введение свеклы столовой в культуру in vitro //V Вавиловская международная конференция «Поколение F3»

Take-home message:

We consider the CRISPR/Cas9 system as an approach to knockout the genes coding enzymes of the yellow pigment biosynthesis pathway. It will allow to receive the forms of table beet with increased red-colored betalain pigments content in the pulp.



Genome editing of Table Beet (*Beta vulgaris* L.) to increase the betalain content

Mikhailova A.S., Sokolova D.V., Popov V.S., Shvachko N.A., Khlestkina E.K.
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Induction of precise deletions in negative regulators of anthocyanin biosynthesis genes in *A. thaliana* using CRISPR

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The most common method of gene editing with a single guide RNA does not allow to predict mutations that are to be induced. In *A. thaliana* and other *Brassicaceae* species frequently used 35S promoter also contributes to the formation of chimeric plants. Therefore, the use of new approaches, such as tissue-specific promoters and more precise mutations, is highly relevant. It is known that the use of multiple guide RNAs at once most often results in easily identifiable deletions between editing sites. Thus, induction of pre-designed large deletions in the coding gene sequence will lead to its knockout or loss-of-function of the protein.

Negative regulators of anthocyanin biosynthesis genes in A. thaliana AtMYBL2, At60MYB and AtCPC were used as targets. Multiple gRNAs (3, 4 and 3, respectively) controlled by an egg-specific promoter were delivered in a single construct with *Cas* gene under CmYLCV promoter. Deletions were successfully induced between the outermost gRNAs, and target gene expression in the edited plants decreased to almost zero.

This research was funded by Russian Science Foundation, grant number 20-74-10053, https://rscf.ru/en/project/20-74-10053/

The main publications of authors on the subject of the abstract:

1. *https://doi.org/10.21203/rs.3.rs-2805928/v1*
2. *https://doi.org/10.3390/ijms231911865*
3. *https://doi.org/10.3390/ijms22168752*
4. *https://doi.org/10.3390/ijms24043939*
5. *https://doi.org/10.1007/s11240-020-01963-7*
6. *https://doi.org/10.1134/S0026893320010069*
7. *https://doi.org/10.1134/S1021443722010137*
8. *https://doi.org/10.1134/S102144371905011X*

Take-home message:

Large deletions are easily programmable and efficient in achieving gene knockout.

Cellulose synthase gene superfamily and their cofactors in collenchyma cell wall

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The biosynthesis of cell wall polysaccharides is one of the most exciting problems in plant science. Despite the fact that the main participants in the machinery for cellulose biosynthesis have been identified, there are still a lot of gaps in our understanding of these processes. The cells of collenchyma have a thicker primary cell wall and can elongate. This capacity distinguishes it from the thickened cell wall of another mechanical tissue, sclerenchyma, formed by fibers. So, collenchyma is a convenient model not only for studying the formation of primary cell walls but also for searching for factors that ensure the elongation of cells with a thickened cell wall. We revealed in collenchyma increased expression of genes encoding the central components of cellulose biosynthesis (CESAs, COBRA, CTL, etc.) and specific gene activation of AgrCMU, AgrCC, and AgrGH9B. Also, genes for CSL proteins were analyzed. Collenchyma is characterized by an increased expression of CESA1, 3, and 6, which is inherent in primary cell walls. We suggest that this may serve as a marker of thickened primary cell walls of collenchyma, distinguishing it from thickened tertiary cell walls of fibers.

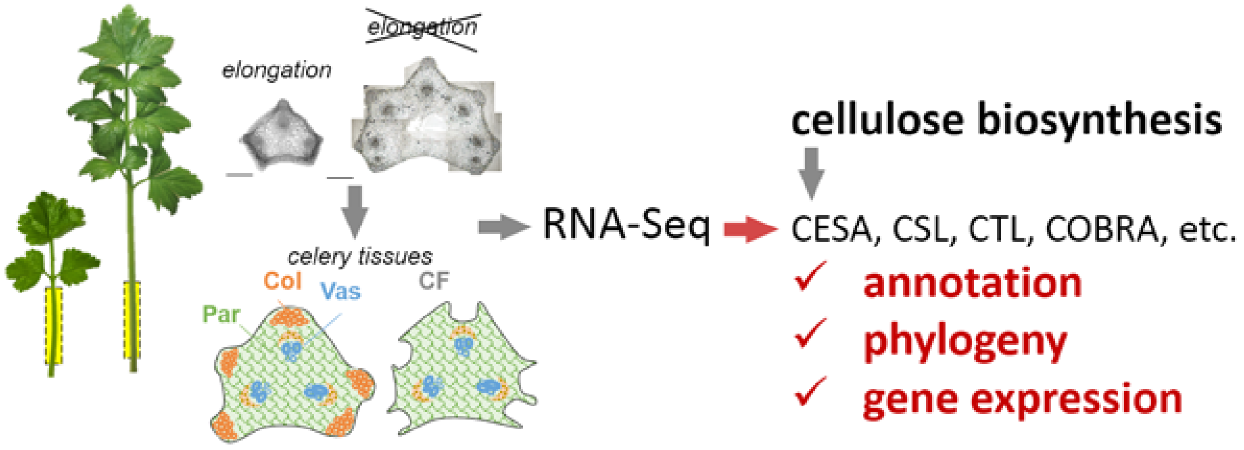
The main publications of authors on the subject of the abstract:

The work was partially supported by the RSF project 20-14-00335 (RNA-seq).

Mokshina, N. et al. Transcriptome profiling of celery petiole tissues reveals peculiarities of the collenchyma cell wall formation // Planta (2023) 257(1): 18. doi: 10.1007/s00425-022-04042-7

Take-home message:

The revealed features of cellulose biosynthesis demonstrate that collenchyma is a convenient model for studying the mechanisms of the formation of the primary cell wall. A criterion that distinguishes collenchyma from fibers has been found.



Changes in the fatty acid composition of tomato leaves (*Solanum lycopersicum*) due to the expression of the heterologous Δ9-desaturase gene in various cellular compartments

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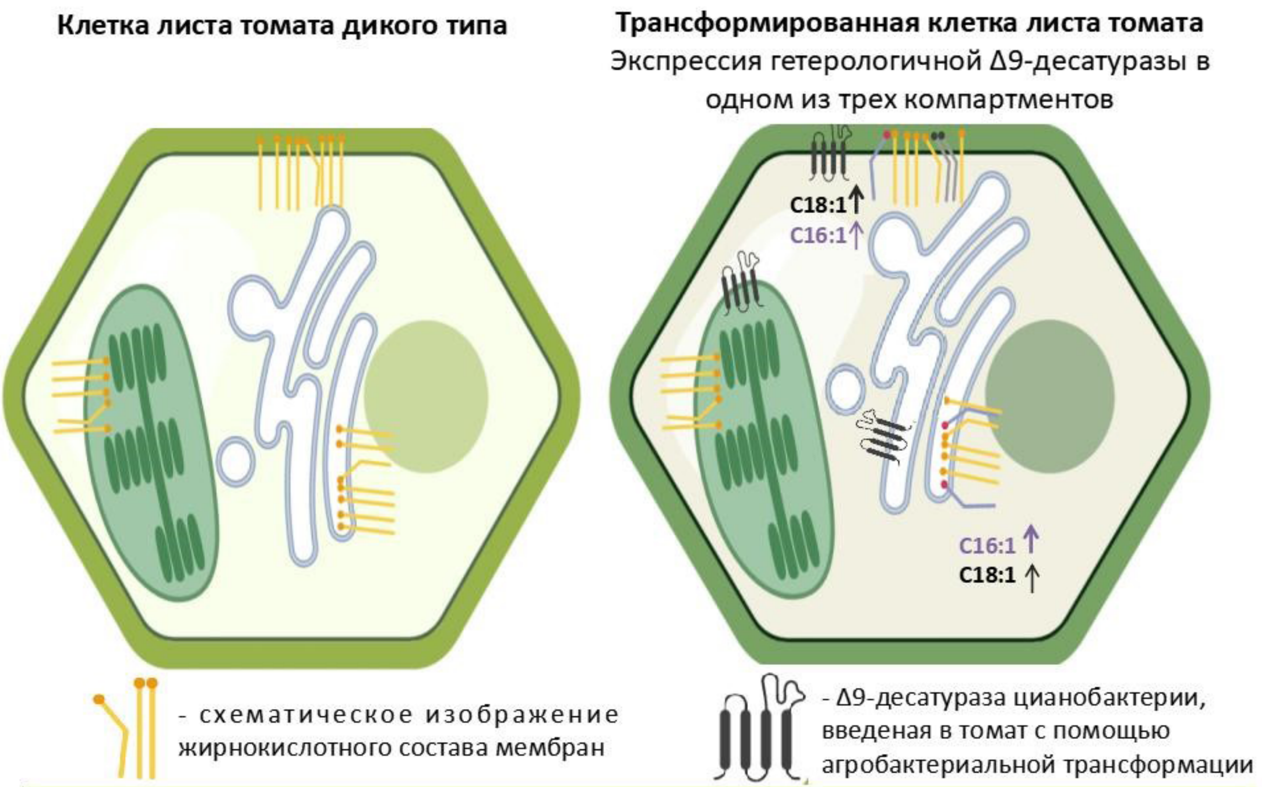
To obtain transgenic tomato plants (*Solanum lycopersicum*) expressing gene for Δ9 acyl-lipid desaturase (*desC*) of cyanobacteria and to evaluate the effect of heterologous desaturase expression on the fatty acid (FA) composition of total lipids, vectors carrying the *desC* gene were constructed. The gene sequence was fused with the leader sequences providing localization of the protein product in chloroplasts, ER or cytoplasmic membrane. FA analysis of transgenic plants showed that when Δ9 acyl-lipid desaturase is localized in the cytoplasmic membrane and ER, the content of Δ9-monounsaturated fatty acids is increased. In the case of localization in the cytoplasmic membrane, an increase in both C18:1- and C16:1-acids were noted. In the case of ER localization, the observed changes in the FA content are more pronounced for C16:1-acid, which is due to the peculiarity of the distribution of substrates for desC protein, namely, the predominance of the content of C16:0-acid over C18:0-acid in ER. The obtained data can be used to develop strategies for directed modification of the FA content of tomato plants.



Локализация гетерологичной Δ9-десатуразы desC (изображена черным) в цитоплазматической мембране или мембране ЭПР приводит к увеличению содержания C18:1- и C16:1-кислот в листьях томатов. При локализации desC в мембране хлоропластов изменение ЖК-состава листьев не происходит.

Analysis of tomato breeding samples of alleles of resistance genes to meloidoginosis and tomato mosaic virus

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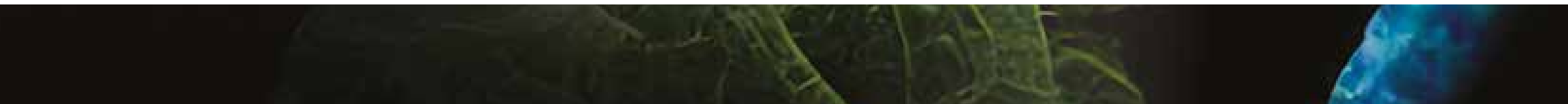
The tomato has a range of infectious diseases. Resistance to pathogens is an important characteristic of a variety or hybrid. The development of molecular genetic analysis methods provides for the possibility to select genotypes with desirable characteristics at the initial stages of breeding work to reduce significantly the time to commercialize tomato hybrids. The systems for simultaneous identification of alleles of resistance genes to several diseases is one of the currently important aims of agricultural biology. In this investigation the multiplex PCR system was developed to identify alleles of the *Mi 1.2* and *$Tm2^2$* genes that determine resistance to meloidoginosis and tomato mosaic virus, respectively. The primers Mi23Fnew:GAATATTCTGGCAAAATTTGAGC/Rnew:TCGTCTACTTAATAGTTCCGTCG and Tm2 SenF: TTTTTTGAACCTTTAGCGCCTTTG/R: GTTTCTGATGCCTCATTCAACTTCC make it possible to amplify fragments of different lengths to make a conclusion about the genotype. Among the analyzed 89 samples, 27 were identified as resistant to two diseases simultaneously, among them 2 samples are heterozygous for the *Mi 1.2* gene. These studies have a high degree of agreement with the results of field tests.

The main publications of authors on the subject of the abstract:

Milyukova et al. MOLECULAR GENETIC ANALYSIS OF F1 TOMATO HYBRIDS FOR RESISTANCE TO FUSARIUM WILT// POTATO AND VEGETABLES (2021) 5:37-40. doi: 10.25630/PAV.2021.44.34.006

Take-home message:

The multiplex PCR system was developed for simultaneous identification of alleles alleles of the *Mi 1.2* and *$Tm2^2$* genes that determine resistance to meloidoginosis and tomato mosaic virus, respectively.



Sun-tanning in lichens: key drivers by transcriptome and metabolome profiling

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Kazan Institute of Biochemistry and Biophysics, Federal Research Center "Kazan Scientific Center of RAS", Kazan, Russia,

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Lichens are unique extremophilic organisms with phenomenal resistance to adverse environmental factors, including UV irradiation. Dark-brown pigment melanin plays a special role in the protection of lichens from UV-B stress; however, the key drivers of melanization in lichens remain unstudied. Melanins are hydrophobic heterogeneous polymers formed by sequential oxidative polymerization of phenolic or indole compounds. Transcriptional profiling by RNA-seq and qPCR identified the differentially expressed genes in melanized lichen *Lobaria pulmonaria*. UV-B irradiation significantly upregulates genes of biosynthesis of several types of melanins and other secondary metabolites. Genes involved in the biosynthesis of specific secondary metabolites are organized into biosynthetic gene clusters. Metabolome profiling identified, along with melanins, lichen substances, including depsidons, depsides, bianthraquinones, xanthones, and some carbohydrates being highly elevated in melanized thalli. Melanization of lichens is a complex, finely regulated process directed to protect thalli from UV, oxidative stress, desiccation. This work was supported by RSF (grant № 23-14-00327).

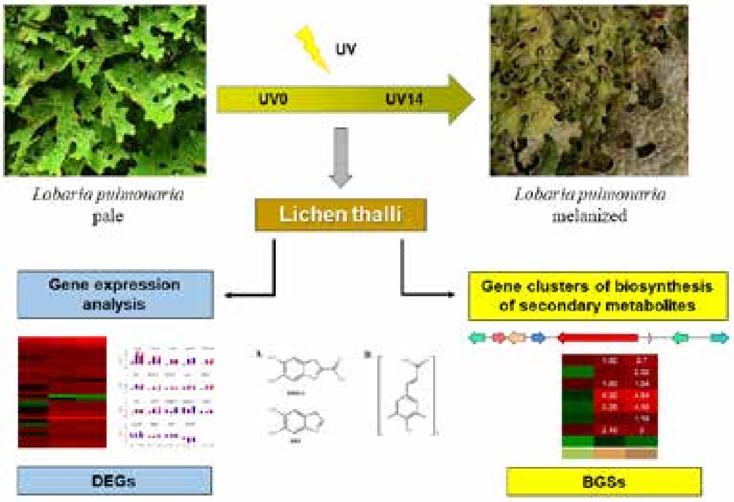
<u>The main publications of authors on the subject of the abstract:</u>

Mafole T.C. et al. Occurrence and possible roles of melanic pigments in lichenized ascomycetes // Fungal Biology Reviews (2019) 33: 159-165. doi:10.1016/j.fbr.2018.10.002

Rassabina A.E. et al. Melanins from the lichens Lobaria pulmonaria and Lobaria retigera as eco-friendly adsorbents of synthetic dyes // International Journal of Molecular Sciences (2022) 23, 15605. doi:10.3390/ijms232415605

<u>Take-home message:</u>

UV-B irradiation of lichen *Lobaria pulmonaria* significantly upregulates genes of biosynthesis of melanins and other secondary metabolites. Genes are organized into biosynthetic gene clusters. Melanization protects lichens from UV, ROS, desiccation.



Phytopathological and molecular screening of wheat cultivars for resistance to tan spot

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The search for new sources of resistance to tan spot caused by the fungus *Pyrenophora tritici-repentis* (Ptr) remains relevant, due to the high variability of the pathogen, which is the cause of the emergence of new races and overcoming the resistance of cultivars. We assessed the resistance of 68 landraces of wheat to isolates from three Ptr populations and 25 cultivars from new arrivals in the VIR collection to isolates from four Ptr populations of different geographical origin. As a result, 17 sources of resistance were selected from landraces and three from modern ones, which showed a resistance to all tested pathogen populations. In parallel, molecular screening for the presence of *Tsn1* and *Tsc2* sensitivity genes to toxins that induce necrosis and chlorosis in susceptible cultivars was carried out. In almost 50% of samples, resistance to toxins is not associated with the presence of recessive alleles *tsn1* and *tsc2*. Dominant alleles of *Tsn1* and *Tsc2* in resistant samples can be suppressed by non-specific resistance genes or quantitative resistance loci (QTLs).The question of the expediency of removing both susceptibility genes from the breeding material is still debatable.

Investigating the microbiome of Siberian larch trees (*Larix sibirica* Ledeb.) affected by *Porodaedalea niemelaei* in the Arctic

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Porodaedalea niemelaei M. Fischer is a fungal pathogen that can cause white rot root of conifer trees and has the ability to remain its high phytopathogenicity in permafrost conditions. The larch tree is especially susceptible to this disease, which is concerning given their importance for forest formation in the Arctic permafrost condition. While larch trees live in symbiosis with diverse microorganisms that influence their growth and adaptation, little is known about the fungal communities in the rhizosphere during *P. niemelaei* infection, as well as the characteristics of fungal and bacterial communities in the affected tree needles.

We analyzed soil and tree needle samples at each stage of infection using ITS and 16S rRNA amplicons to identify fungal and bacterial communities. Fungal communities in the soil consisted mostly of members of *Ascomycota, Basidiomycota, Mucoromycota,* and *Mortierellomycota phyla.* Ascomycota was consistently the most prevalent phylum across all samples. The fungal community in the tree needles had only members of Ascomycota and Basidiomycota. The bacterial community had a high diversity and abundance of *Actinobacteriota, Proteobacteria,* and *Firmicutes.*

Take-home message:

It has been established that *P. niemelaei* infection, even at early stages, is accompanied by changes in the fungal and bacterial microbiomes of the rhizosphere and needles, and an increased susceptibility of larch trees to other pathogens.

Impact of plant growth-promoting rhizobacteria inoculation on the physiological response and productivity traits of early-maturing spring wheat (*Triticum aestivum* L.)

Mirskaya G.V., Pishchik V.N.*, Khomyakov Yu.V., Vertebny V.E., Dubovitskaya V.I., Chesnokov Yu.V.

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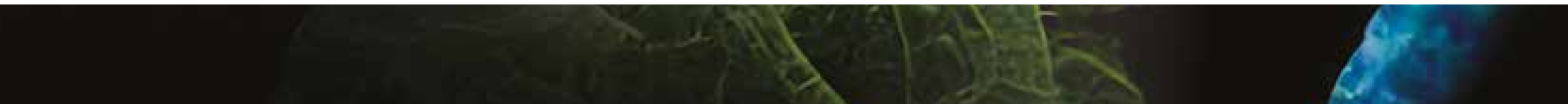
*All-Russia Research Institute for Agricultural Microbiology, Saint Petersburg, Russia
E-mail: galinanm@gmail.com

The current study aimed to study the effect of a plant growth-promoting bacterium (PGPB) *Bacillus sp.* V2026, was isolated from wheat seeds, on the ontogenesis and productivity of four genotypes of early-maturing spring wheat. Using allele-specific primers the presence of alleles of the *VRN-1* and *PPD-D1* loci in early-maturing wheat cultivars Sonora 64 and Leningradskaya rannyaya and ultra-early-maturing lines AFI177 and AFI91 was determined. The inoculation of wheat plants with *Bacillus sp. V2026* increased the levels of chlorophylls and carotenoids and reduced lipid peroxidation in leaves of all genotypes. The inoculation resulted in a significant increase in grain yield (by 33–62%), a reduction in the time for passing the stages of ontogenesis (by 2–3 days), and an increase in the content of macro- and microelements and protein in the grain. It was found differences in the response of wheat genotypes with different allele combinations plants of *VRN-1* and *PPD-D1* genes to inoculation with PGPB *Bacillus sp. V2026.* This means that further studies are necessary to select the most effective association for growing high-yielding early-ripening wheat plants.

The main publications of authors on the subject of the abstract:

Mirskaya, Galina V., Yuriy V. Khomyakov, Nataliya A. Rushina, Vitaliy E. Vertebny, Elena P. Chizhevskaya, Vladimir K. Chebotar, Yuriy V. Chesnokov, and Veronika N. Pishchik. 2022. "Plant Development of Early-Maturing Spring Wheat (Triticum aestivum L.) under Inoculation with Bacillus sp. V2026" Plants 11, no. 14: 1817. https://doi.org/10.3390/plants11141817



Diversity of the collection of cultivated oat species by the growing season in the conditions of Western Siberia

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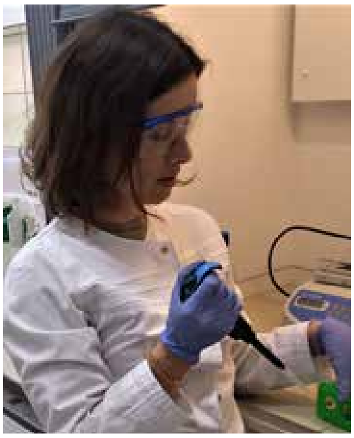
Animal husbandry in Western Siberia requires the creation of a stable feed base, in which oats occupies a leading position. The most in demand are precocious and medium-ripened varieties. A collection of 310 samples of cultivated oat species according to the duration of the growing season was analyzed in the Research Institute of the Northern Trans-Urals. Samples of Avena sativa L., A. byzantina C.Koch, A. abyssinica Hochst., A. strigosa Schreb. and interspecific hybrids of *A. sativa* × *A. byzantina* were studied. A group of 16 ultra-ripe genotypes (5% of the collection) related to sown oats was isolated. The precocious group included 159 genotypes, which made up half of the collection. 94 and 28 genotypes, respectively, were assigned to the mid-ripe and mid-late ones. The group of medium-ripened included 11 interspecific hybrids and 6 specimens of the species *A. byzantina.* The mid-late group is represented by 9 hybrids of *A. sativa* × *A. byzantina*. Thus, the studied collection contains all groups of ripeness, which makes it possible to effectively create varieties for Western Siberia using the genetic diversity of genotypes from different regions.

Take-home message:

A collection of 310 samples of cultivated oat species according to the duration of the growing season was analyzed. Five groups of ripeness were identified, which made up the genotypes of five different species, whose distribution was uneven.

Antioxidant system in pear leaves



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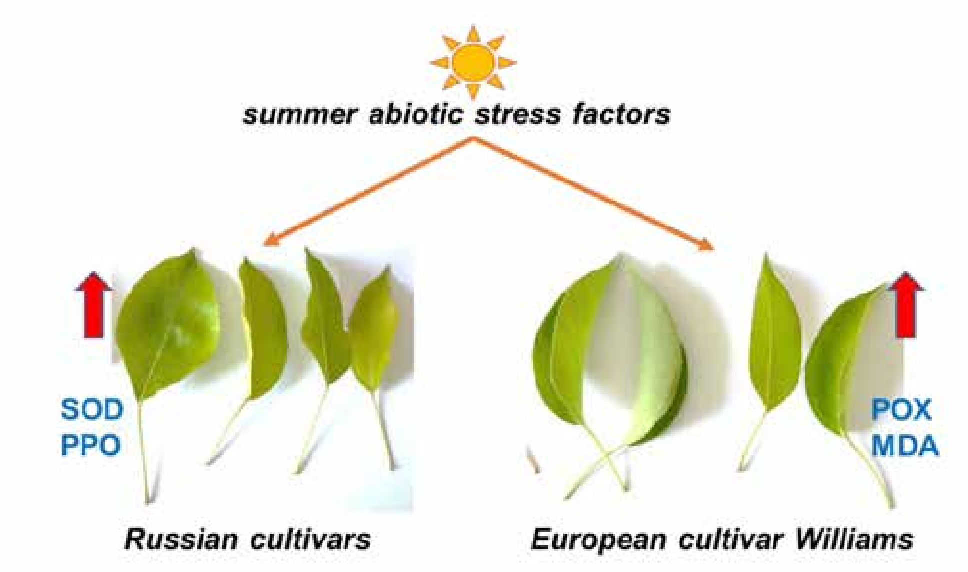
A comparative analysis of the antioxidant activities (superoxide dismutase SOD, peroxidase POX, catalase CAT) and its gene expression levels, including polyphenol oxidase PPO, in the leaves of 4 pear cultivars (*Pyrus communis*) in summer was performed.The materials were collected from orchards in Krasnodar. It's found that Russian cv.Samorodok is characterized by the highest level of PPO activity and gene expression. PPO increase indicates the processes of phenols oxidation.A high level of POX ctivity and expression of Williams was observed.POX eliminates H_2O_2 , which is formed during oxidative processes. The Russian cultivars had slightly higher values of SOD activity and gene expression compared to foreign cultivars. SOD is a marker of the initial stage of oxidative stress, as it is involved in the neutralization of O_2^-.Thus, it can be assumed that the Russian and American cultivars didn't experience significant stress during the summer or suppressed its development at the initial stages. The European cultivar Williams most likely had a more unstable state, which contributed to the increase in POX activity.The study has been supported by a grant from RSF and KSF No 22-26-20072.

Take-home message:

Two Russian pear cultivars showed greater resistance to summer stressors in terms of the antioxidant enzyme activity than the widespread European cultivar Williams.



Bio- and Genomic Technology for Plant Propagation and Biodiversity Conservation

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*M.V. Lomonosov Moscow State University, Moscow, Russia,
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World experience demonstrates the high efficiency of complex investigation in plant biotechnology and genomic. The usage of biotechnological approaches open the ways of plant morphogenetic capacity realization and develop effective *in vitro* plant propagation and conservation protocols. In leading Botanical Gardens and Horticultural Institutes of the Russian Federation an *in vitro* plant gene pool collections of horticultural crops, rare and endangered species are created. The viral phytopathogen monitoring in collection plots of ornamental, essential oil and fruit plants is a key question. More than eight viruses were detected for the first time on the territory of the Russian Federation. The development of technologies for high-throughput next generation sequencing (NGS) opens up completely new perspectives in the field of plant bioresource investigation, as a basis for the development of molecular selection methods, studying the fundamental bases of plant morphogenesis and adaptation to the effects of stress factors of various etiologies.

The research was supported by assignments 122042700002-6 of the Ministry of Science and Higher Education (Russia) and RSF grant No.23-16-00032.

The main publications of authors on the subject of the abstract:

Chirkov S. et al. Characterization of Divergent Grapevine Badnavirus 1 Isolates Found on Different Fig Species (Ficus spp.) // Plants (2022) 11 (19): 2532. https://doi.org/10.3390/plants11192532

Mitrofanova I.V. et al. The effect of plant growth regulators on the in vitro regeneration capacity in some horticultural crops and rare endangered plant species // Acta Hortic. (2022) 1339: 182-189. doi: 10.17660/ActaHortic.2022.1339.24

Take-home message:

The usage of biotechnological approaches for horticultural crops and wild species propagation and conservation, viral pathogen detection and charecterisation, NGS application open a new perspectives in the field of plant bioresource investigation.

Genotyping, biochemical and yield component analysis of barley lines with anthocyanin grain pigmentation

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In the current study, the effect of genomic regions inherited by barley near-isogenic lines (NILs) by introducing dominant alleles of *Ant1/Ant2* and *HvMyc2* genes responsible for anthocyanin grain pigmentation into local varieties Aley, Tanay and Vorsinsky2 was investigated.

Genotyping-by-sequencing (GBS) was used to search for genomic regions inherited from donors. The GBS data were processed using a pipeline created at ICG SB RAS, which includes alignment of sequenced reads, variants calling, clustering and phylogram building. Hordeum vulgare IBSC_v2 (rel. 51) was used as a reference genome. Relatedness analysis showed that NILs formed clusters with the corresponding recurrent variety, demonstrating their genetic similarity, while donors formed an outgroup.

Antioxidant activity, total phenolic and anthocyanin content in grains, as well as yield-related traits were measured to compare NILs to the parent varieties. All investigated traits were changed in barley NILs with anthocyanin-pigmented grain. Further analysis of genomic regions inherited from donors is expected to reveal the genetic basis of the observed differences.

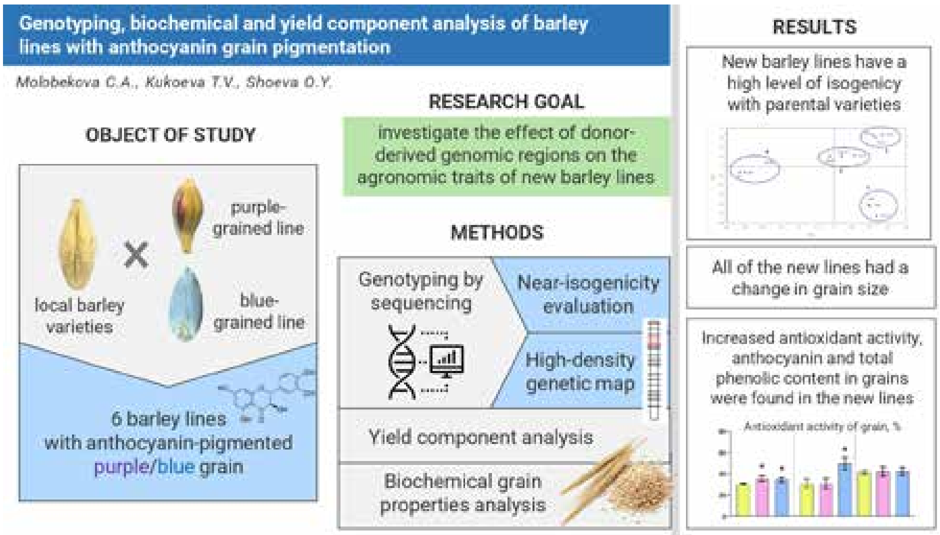
The study was supported by RSF 21-76-10024.

The main publications of authors on the subject of the abstract:

Кукоева Т.В. и др. Разработка генетико-селекционного подхода для получения новых сортов ячменя с повышенным содержанием антоцианов в зерне // Генофонд и селекция растений: тезисы V международной конференции 327 (2020): 165-168.

Take-home message:

The introduction of genes responsible for anthocyanin pigmentation of grain affects its biochemical properties and yield-related traits of barley near-isogenic lines. Genotyping by sequencing will allow characterizing donor-derived genomic regions.



Genotyping, biochemical and yield component analysis of barley lines with anthocyanin grain pigmentation

Molobekova C.A., Kukoeva T.V., Shoeva O.Y.

OBJECT OF STUDY

local barley varieties × purple-grained line, blue-grained line

6 barley lines with anthocyanin-pigmented purple/blue grain

RESEARCH GOAL

investigate the effect of donor-derived genomic regions on the agronomic traits of new barley lines

METHODS

Genotyping by sequencing

Near-isogenicity evaluation

High-density genetic map

Yield component analysis

Biochemical grain properties analysis

RESULTS

New barley lines have a high level of isogenicity with parental varieties

All of the new lines had a change in grain size

Increased antioxidant activity, anthocyanin and total phenolic content in grains were found in the new lines

Macro-, microelements and trace metals in spring wheat grain in Kazakhstan and Russia: variation, G x E interaction and genetic control

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Kazakh Agrotechnical Univ./Omsk State Agrarian Univ., Almaty, Kazakhstan,
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Grain content for 23 elements (Ca, K, Mg, P, S; B, Fe, Cu, Na, Mn, Zn; As, Cd, Co, Cr, Ni, Pb, Se; Li, Mo, Rb, Sr) from Kazakhstan and Russia was analyzed for 2200 samples. The analysis of grain from production fields showed very low concentration of toxic metals (As, Cd, Cr, Li and Pb) and grain is safe.

Grain analysis of KASIB trial from six sites in Kazakhstan and Russia in 2017-2018 demonstrated that for P, S, Cu, Mn, Mo the site effect was 2-3 times higher compared to genotype effect. The genotype and site effects were similar for Ca, Mg, Fe, Cd, Sr concentration. Protein content had positive genotypic correlations with Mg (0.57), P (0.60), S (0.68), Fe (0.64), Cu (0.50), Mn (0.50) and Zn (0.53).

Study of genetic resources at Omsk in 2017-18 showed that primary synthetics had high concentrations of Ca, K, S, Cd and Mo. US cultivars had high concentrations of Ca, Mg and Fe. KASIB germplasm had average values for most elements. GWAS analysis of the trial identified 47 marker-element associations including 20 with validated effects using multilocational KASIB trials.

Supported by Min. of Sci. & High Educ. of the Russian Federation (Agreement No. 075-15-2021-534 of 28.5.2021)

The main publications of authors on the subject of the abstract:

Abugalieva A et al. 2021 Ionomics of Grain from Kazakhstan and Russia. Com Soil Sci Plant An, 52(7):704-711.

Morgunov A et al. 2022 Effects of env. and cultivars on grain ionome of wheat in Kazakhstan and Russia. Crop and Pasture Sci, 73(5):515-527.

Shepelev S et al. 2022 Variation of Macro-and Microelements, and Trace Metals in Spring Wheat GR in Siberia. Plants, 11(2):149.

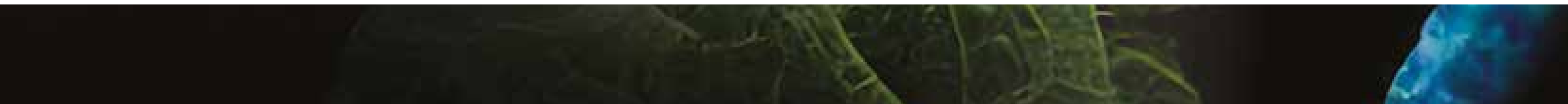
Morgunov A et al. 2022 Gen. Character. of Spring Wheat for Macro-, Microelements and Trace Metals. Plants, 11(16):2173.

Take-home message:

Grain from production is safe with low content of toxic elements.

G x E interaction is important for grain elemental composition.

Genetic variation for most elements allows to make breeding progress.



Satellite DNAs in the genome of *Salvia officinalis* L

Muravenko O.V., Semenov A.R., Dvorianinova E.M.,
Kalnyuk J.V., Melnikova N.V., Zoshchuk S.A., Amosova A.V.

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The genus *Salvia* L. (Lamiaceae) comprises economically valuable *Salvia officinalis* L. which widely distributed in the Mediterranean and cultivated throughout the world. It is very important for pharmaceutical, culinary and ornamental purposes. *S. officinalis* contains a large amount of essential oil, flavonoids, terpenes and tannins. Our previous study demonstrated FISH-based unique chromosome patterns of tandem DNA repeats. It was found that most of the satellite DNAs identified in the genome of *S. officinalis* were localized in the distal region of one pair of chromosomes and on one of the B chromosomes. To clarify the structural organization of the satellite DNAs in this region, the genome sequencing of this species has been performed using nanopore sequencing technique with MinION flow cell. It is shown that the four repeats identified earlier are modifications of the main sequence motif. Among them, two repeats are complex, consisting of several motifs. Most of the revealed clusters of satellite DNAs intersperse with each other and are localized together in the genome of *S. officinalis.*

This research was funded by the Russian Science Foundation (project No. 22-26-00222).

The main publications of authors on the subject of the abstract:

Muravenko O. V. et al. Integration of Repeatomic and Cytogenetic Data on Satellite DNA for the Genome Analysis in the Genus Salvia (Lamiaceae) //Plants. – 2022. – T. 11. – №. 17. – C. 2244.

Kirov I. et al. A Pipeline NanoTRF as a New Tool for De Novo Satellite DNA Identification in the Raw Nanopore Sequencing Reads of Plant Genomes //Plants. – 2022. – T. 11. – №. 16. – C. 2103.

Constitutive expression of the AtGSTF11 gene increases the survival rate of hairy roots during storage under stress conditions

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Kuluev B.R.

Institute of Biochemistry and Genetics â€“ Subdivision of the Ufa Federal Research Centre of the Russian Academy of Sciences, Ufa, Russia
E-mail: mg@khalit.ru

Long-term storage of cultures of hairy roots in biotechnology is an actual task. Because hairy roots cannot feed in an autotrophic way, they need to be constantly fed, which in turn leads to a constant renewal of the environment in which they grow. Traditionally, valuable cultures of hairy roots are usually stored in liquid nitrogen, which requires special equipment in the form of special refrigeration units, and expensive reagents. Hairy root cultures of tobacco with constitutive expression of the AtGST gene were obtained by agrobacterial transformation of transgenic tobacco plants (T2) with Agrobacterium rhizogenes strain A4. We managed to keep tobacco HRs alive for 240 days (8 months) at low positive temperatures (+3⁰). At a sucrose concentration of 1.8 g/l, the survival rate of transgenic hairy roots was 200 days. Methods for storing hairy roots at high concentrations of sodium chloride (250 mM) and mannitol (50 mM) were also tested, which did not give the expected results. The introduction of the AtGSTF11 gene into the HRs culture really helped to increase the survival rate of cultures after long-term storage.

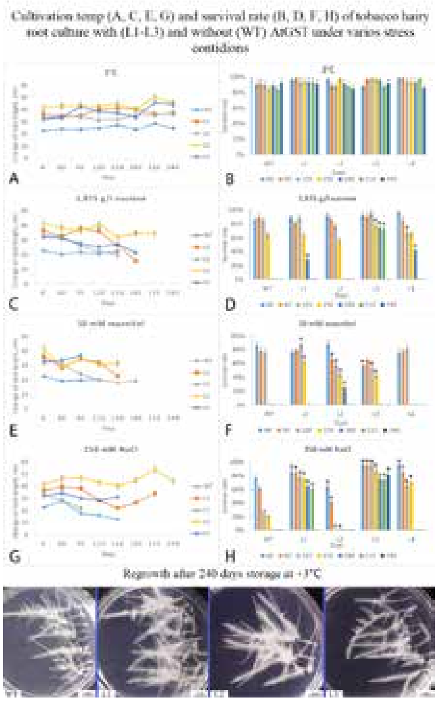
The main publications of authors on the subject of the abstract:

Musin K.G., Fedyaev V.V., & Kuluev B.R. State of Antioxidant System and Long-Term Storage of Tobacco Hairy Roots with Constitutive Expression of Glutathione-S-Transferase Gene ATGSTF11 // Russian Journal of Plant Physiology (2021), 68, 641-651.

DOI: 10.1134/S1021443721040105

Take-home message:

Hairy roots of tobacco can be stored at low positive temperatures (+3⁰) and with a deficiency of sucrose. Constitutive expression of the AtHST gene increases the survival rate of hairy roots.



Molecular genetic markers in *Beta vulgaris* L. breeding

Nalbandyan A., Fedulova T., Cherepukhina I., Rudenko T.

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In Federal State Budgetary Scientific Institution “The A.L. Mazlumov All-Russian Research Institute of Sugar Beet and Sugar”, new polymorphisms in BTC1gene controlling bolting had been revealed that made it possible to select sources of resistance to bolting. Screening of sugar beet regenerants for presence of genes of resistance to heavy metals, and drought/salinization allowed selection of forms with resistance to these abiotic stresses. Molecular testing of sugar beet samples with specific primers for loci of resistance to fusariose (SE2, SP2) promoted selection of valuable genes’ sources of resistance to this disease. Study of single nucleotide polymorphisms (SNPs) in the gene of resistance to root-knot nematodes (R6m-1) allowed revealing genotypes resistant to this pest. To produce perspective hybrids, 250 genotypes were differentiated and clustered using 50 SSR-markers that allowed selection of the most valuable parental forms for hybridization. Based on the genetical homogeneous lines selected using SSR-markers, there were developed the highly productive hybrids of RMS-133 and RMS-137 put in the State registry of Russian Federation

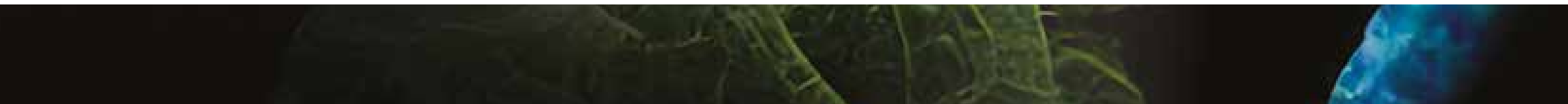
The main publications of authors on the subject of the abstract:

Nalbandyan A.A,Fedulova T.P.,ryukova T.I.,Cherepukhina I.V.,Kulikova N.V.Polymorphic Microsatellite Markers to Study Sugar Beet’s (Beta vulgaris L.)Genetic Diversity//Russian Agricultural Sciences,2023,Vol.49,No.1,pp.1–7.DOI: 10.3103/S1068367423010123

Hussein A.S., Nalbandyan A.A., Fedulova T.P.,Cherepukhina I.V.,Kryukova T.I.,Mikheeva N.R.,Rudenko T.S.New nucleotide polymorphisms in the btc1 gene of sugar beet//Biotechnology,2020,Vol.36,No.6,pp.49-54.DOI:10.21519/0234-2758-2020-36-6-49-54

Take-home message:

Based on the genetical homogeneous lines selected using SSR-markers, there were developed the highly productive hybrids of RMS-133 and RMS-137 put in the State registry of Russian Federation.



The prospects of current molecular approaches associated with resistance in crop plants through transcriptome-proteomic and markers co-profiling offers

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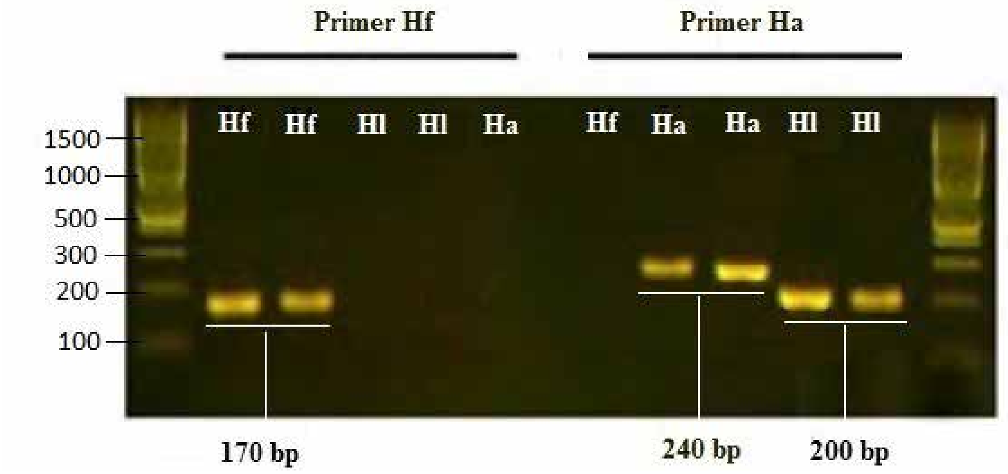
Improvement of disease resistance in crops has great potential to increase productivity by preventing the huge losses caused by the plant pathogens. In addition, new pathogen variants often cause greater threat to crops. Success stories like the production and commercialization of resistant plants, and today's availability of powerful molecular techniques, such as genomics and proteomics, have elicited studies that pursue their final objective of increasing plant stress resistance by investigating the plant stress response. While very little work has been done on the dual role of particular genes covering resistance to more than a disease at a time. However, the stress control methods which have been postulated to date are, in most cases, of general significance and could be readily applied to commercial plants in the near future. This talk briefly reviews some of the most interesting molecular approaches to controlling biotic stresses, with particular attention to the interaction of soil borne fungal pathogens and nematodes with vegetables and wheat crops, with special reference to cereal cyst nematodes, including genomic regions, molecular markers, and flanking genes tolerance.

The main publications of authors on the subject of the abstract:

Moghaddam G.A. et al. 2020. Bio-genetic. Phytochem. 179, 112486.
Bagheri L.M. et al. 2021. Genetic diversity. Phytochem. 190, 112884.
Qalavand, F. et al. 2022. Enzyme activity. Phytochem. 200, 113208.
Qalavand, F. et al. 2023. Transcriptome based. Plant Biol.
Soheili-Moghaddam B. 2022. Identification of novel. Int. J. Biol. Macromol. 215, 321-333.
Soheili-Moghaddam B. 2023. Biochemical defense. Planta 257(1), 13.

Take-home message:

This talk briefly reviews some of the most interesting molecular approaches to controlling biotic stresses, with particular attention to fungal pathogens and nematodes including genomic regions, molecular markers, and flanking genes tolerance.



Development of sterile aspen clones with gene editing technology

Nesterchuk V.V., Karzhaev D.S, Safronycheva E.D., Volkov V.A., Potokina E.K.*

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With the CRISPR/Cas9 technology it has become possible to create sterile trees and prevent the spread gametes carrying edited genes. Aspen is a perfect subject both for biotechnology and forestry due to its rapid growth and easy in vitro cultivation. We report the results of experiments on editing the LEAFY and AGAMOUS genes in aspen to obtain sterile clones. Thirty spacers targeting the first exons of the genes have been created. Editing was conducted by bio ballistics using RNP complexes synthesized based on the pUC57-sgRNA vector. Success of the delivery methods was proven with GFPGUSPlus reporter vector as control. After bombardment, shoot formation was successfully initiated and more than 500 regenerants were obtained. Root formation of regenerants was stimulated by adding to the medium indole-3-butyric acid. Rooted plants were transplanted into peat soil in a growth room. Illumina MiSeq was employed for targeted sequencing of PCR products of a pooled sample DNA of the leaves obtained plants, to detect CRISPR editing events.

The research was performed within the state assignment to the FSBI SPbFRI № 053-00011-23-00 from December 29, 2022

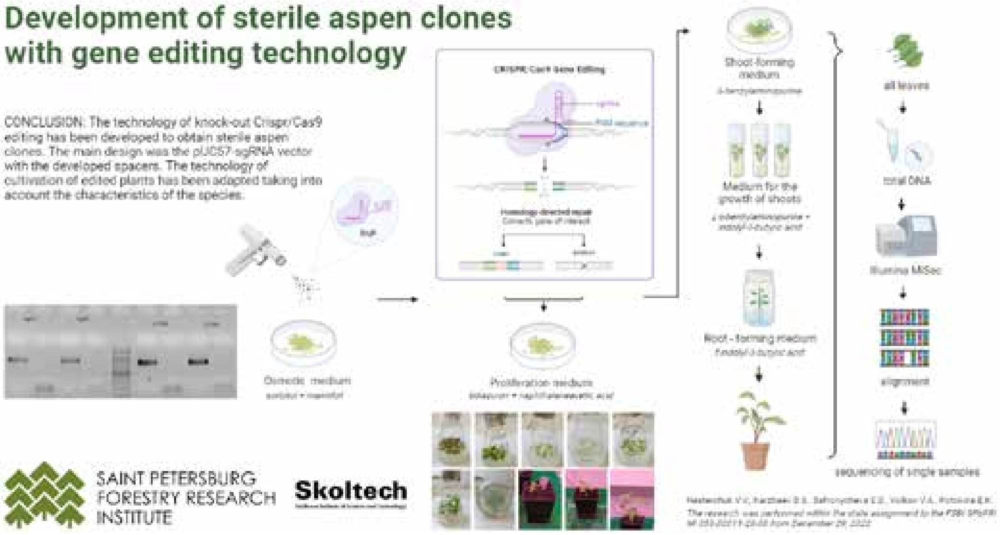
<u>The main publications of authors on the subject of the abstract:</u>

Karzhaev D.S. Employing of CRISPR/Cas9 technology to knockout genes associated with flowering in aspen //PlantGen2021. – 2021. – C. 88. doi: 10.18699/PlantGen2021-088

Karzhaev D.S. et al. Methods of obtaining sterile clones of poplar and aspen (Populus ssp.) using genetic engineering // Proceedings of the St. Petersburg Scientific Research Institute of Forestry. -2022. - C.4-17. doi: 10.21178/2079-6080.2022.4.4

<u>Take-home message:</u>

CRISPR/Cas9 gene editing allows it has become possible to create sterile trees and prevent the spread plants carrying edited genes. We report the results of experiments on editing the LEAFY and AGAMOUS genes in aspen to obtain sterile clones.



Development of sterile aspen clones with gene editing technology

CONCLUSION: The technology of knock-out Crispr/Cas9 editing has been developed to obtain sterile aspen clones. The main design was the pUC57-sgRNA vector with the developed spacers. The technology of cultivation of edited plants has been adapted taking into account the characteristics of the species.

Comparative and phylogenetic analysis of the complete chloroplast genomes of seven *Peliosanthes* and *Aspidistra* species (Asparagaceae)

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Peliosanthes and Aspidistra are large genus of Asparagaceae family, growing in South-East Asia. Many of them are local endemics and deserve environmental protection due to the rapid destruction of tropical ecosystems. However, the phylogenetic relationship of species remains unclear. The molecular barcoding such as nrITS does not allow to construct resolved phylogenetic trees and that is why chloroplast DNA sequences are useful. Nowadays there are only 6 species cpDNA sequences in public databases which is not enough for analysis. We studied one more *Aspidistra* species (*A. subrotata*) and seven more *Peliosanthes* species (*P. cambodiana, P. densiflora, P. grandiflora, P. micrantha, P. inaperta, P. irinae, P. teta*). Libraries for high-throughput sequencing were conducted on DNBseq-400 using 150-bp paired-end condition. Sequences were assembled *de novo* using GetOrganelle, which demonstrated the best assembly quality metrics. Analysis of the sequences revealed high level of similarity among genus and some differences in intergenic spacers. We did not reveal any significant large genome rearrangements. Supported by RSCF, project 19-14-00055-П.

Take-home message:

Peliosanthes is a monophyletic genus.

The best approach in *Peliosanthes* and *Aspidistra* cpDNA assembly is GetOrganelle.

Genetics of potato resistance to Pectobacterium spp.

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The lack of potato cultivars resistant to soft rot and blackleg is at least partly due to poor understanding of *Pectobacterium* spp. recognition mechanisms in the host plant. These pathogens have long been considered as necrotrophs massively producing exoenzymes to destroy plant cells and overcome immunity. Through mutagenesis, silencing, protein-protein interactions screening and transcriptome studies, we have revealed the complex dynamic nature of molecular communications between pectobacteria and host plants. The key points of such communications in the context of providing resistance to a pathogen are the recognition of the main effector protein DspE and hormone signalling reorganization upon plant contact with the pathogen. RNA-seq based correction of potato reference genome annotation allowed us to identify non-annotated genes for abscisic acid biosynthesis and establish the central role of this hormone in providing resistance to pectobacteria. Among the receptor-like kinases of *Solanaceae* plants, including wild potato species with recently published genome, we have identified four specific DspE receptors with a potential for use as R genes in resistance breeding.

The main publications of authors on the subject of the abstract:

Kravchenko U. et al. The PhoPQ two-component system is the major regulator of cell surface properties, stress responses and plant-derived substrate utilisation...//Frontiers Microbiol(2021)11:3596 doi:10.3389/fmicb.2020

Gorshkov V. et al. Transcriptome profiling helps to identify potential and true molecular switches of stealth to brute force behavior in Pectobacterium atrosepticum during systemic colonization of tobacco plants // Eur J Plant
Pathol(2018)152:957-76 doi:10.1007/s10658-018-1496-6

Take-home message:

Potato resistance to Pectobacterium spp. could be achieved with DspE-specific receptor kinases and control of abscisic acid levels.

Amyloid proteins of plants and symbiotic bacteria: biological functions and structural similarity

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*Institute of Cytology of the Russian Academy of Sciences, Saint-Petersburg, Russia
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Amyloids are protein fibrils with a highly ordered spatial structure. Recently, our group identified functional amyloids in plants and demonstrated their role in protein storage in seeds. Evolutionary conserved β-barrel domain CUPIN which is a characteristic feature of various seed storage globulins was identified as a crucial amyloid-forming region of such proteins. Besides, functional amyloids were identified in root nodules bacterium *Rhizobium leguminosarum,* where they are formed by outer membrane proteins with a predicted β-barrel structure. Amyloids produced by *R. leguminosarum* are formed in the plant root nodules and participate in the interaction between the symbiont and the host plant. Moreover, root nodules also contain plant globulin amyloids affecting the aggregation of bacterial amyloids. Intriguingly, plant and bacterial amyloid-forming proteins share similar β-barrel domains suggesting the involvement of these structures in the amyloidogenesis and host-symbiont interactions.

This work is supported by the Ministry of Science and Higher Education of the Russian Federation, agreement № 075-15-2020-920, World-class Scientific Center "Agrotechnologies for the Future".

The main publications of authors on the subject of the abstract:

Antonets K.S. et al. Accumulation of storage proteins in plant seeds is mediated by amyloid formation // PLOS Biol. (2020) 18(7): e3000564.

Kosolapova A.O. et al. RopB protein of Rhizobium leguminosarum bv. viciae adopts amyloid state during symbiotic interactions with pea (Pisum sativum L.) // Front. Plant Sci. (2022) 13: e1014699.

Sulatskaya A.I. et al. β-Barrels and Amyloids: Structural Transitions, Biological Functions, and Pathogenesis // Int. J. Mol. Sci. (2021) 22(21):11316.

Take-home message:

Recent discovery of amyloid proteins in plants and their symbionts revealed functional roles of amyloids in protein storage in plant seeds and host-symbiont interactions.

Study of the genetic mechanisms of adaptation of Siberian larch based on dendrogenomic analysis

Novikova S.V., Oreshkova N.V.*, Sharov V.V.*, Zhirnova D.F., Belokopytova L.V.**, Babushkina E.A.**, Krutovsky K.V.*****

Laboratory of Forest Genomics, Institute of Fundamental Biology and Biotechnology, Siberian Federal University, 660041, Krasnoyarsk, Russia,
*Laboratory of Genomic Research and Biotechnology, Federal Research Center “Krasnoyarsk Science Center of the Siberian Branch of the Russian Academy of Sciences”, 660036, Krasnoyarsk, Russia,
**Laboratory of Dendroecology and Ecological Monitoring, Khakass Technical Institute, Siberian Federal University, 655017, Abakan, Russia,
***Department of Forest Genetics and Forest Tree Breeding, Georg-August University of Göttingen, 37077, Göttingen, Germany
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The Siberian larch is one of the key conifer species of Eurasia that has an important ecological and economic value, but could be greatly affected by global climate change. It has a high level of phenotypic variation and plasticity, the genetic mechanisms of which are still poorly understood. We analyzed the genetic basis of the individual reactions of Siberian larch trees in the forest-steppe zone of Khakassia to the repeated droughts that severely inhibited their growth. Based on the genotyping by sequencing (GBS) approach using double digest restriction-site-associated DNA (ddRAD-seq), 11,095 SNPs were genotyped in 136 individual trees sampled from five natural populations and used to study their genetic variation, structure, and differentiation. The impact of environmental factors and tree age on the width of annual rings was assessed for each tree. We evaluated the correlation between SNP variation and variation of dendrophenotypes that reflect individual tree response to the environmental stresses such as severe droughts, including resistance (Rt), recovery (Rc), and resilience (Rs) indices, to find underlying adaptive genetic variation related to drought tolerance.

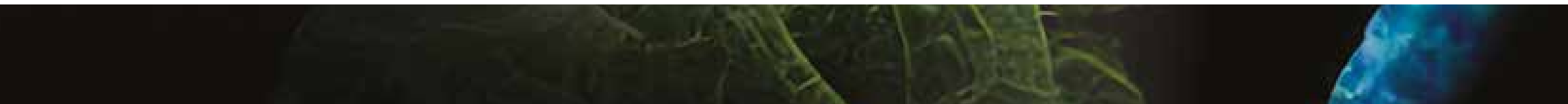
The main publications of authors on the subject of the abstract:

Krutovsky K.V. Dendrogenomics is a new interdisciplinary field of research of the adaptive genetic potential of forest tree populations integrating dendrochronology, dendroecology, dendroclimatology and genomics // Russ. J. Genetics (2022) 58. N 11: 1273–1286.

Novikova S.V., Sharov V.V., Oreshkova N.V., Simonov E.P., Krutovsky K.V. Genetic Adaptation of Siberian Larch (Larix sibirica Ledeb.) to High Altitudes // Int. J. Mol. Sci. (2023) 24. N 5: Article number 4530.

Take-home message:

Dendrogenomic analysis was carried out in the Siberian larch using ddRADseq (GBS) data. Sets of dendrochronological, environmental, and genomic data were analyzed to find signatures of local adaptation and genetic mechanisms of adaptation to drought.



Search Novel Sources of Resistance to *Stagonospora nodorum* in Wheat

Nuzhnaia T.V., Veselova S.V., Maksimov I.V.

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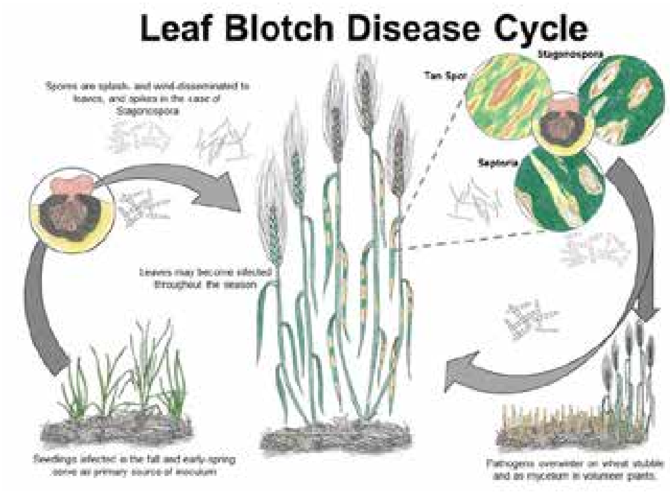
Virulence factors of the pathogen Stagonospora nodorum Berk. are numerous necrotrophic effectors (NEs) (SnTox), which interact with the products of host susceptibility genes (Snn), causing the development of the disease. In this study, 55 accessions of bread spring and winter wheat were screened for sensitivity to NEs SnToxA, SnTox1, and SnTox3 using different isolates of S. nodorum. In general, our wheat panel differed from other wheat collections with available data in that it was less sensitive to SnToxA and SnTox3, and more sensitive to SnTox1. Six sources of strong SNB resistance were identified in our wheat panel. In addition, during the study, wheat cultivars were identified as appropriate objects in which to study the different effects of SnTox-Snn interactions, which is important for marker-assisted selection for SNB resistance. The current study has shown, for the first time, that the expression level of Snn1 and Tsn1 susceptibility genes and the disease severity of the different wheat cultivars are interconnected. Future work should focus on the deep characterization of SnTox-Snn interactions at the molecular level.

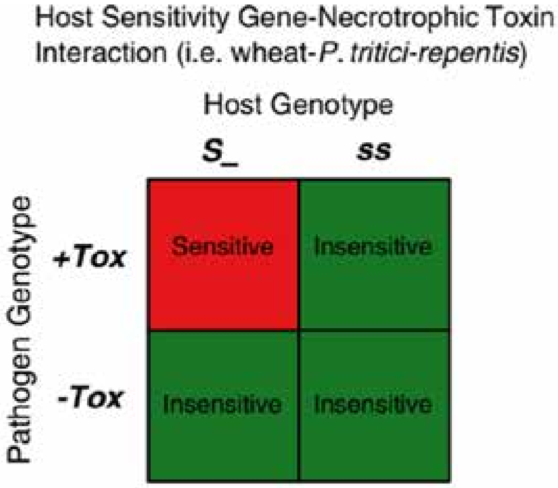
The reported study was funded by a grant from the Russian Science Foundation, No. 22-76-00055.

<u>The main publications of authors on the subject of the abstract:</u>

Nuzhnaya T.V. et al. Novel Sources of Resistance to Stagonospora nodorum and Role of Effector-Susceptibility Gene Interactions in Wheat of Russian Breeding. Int. J. Plant Biol. 2023, 14, 377–396. https://doi.org/10.3390/ijpb14020031

Nuzhnaya T.V et al. Primary search for new sources of effective resistance in representatives of the genus Triticum L. against Stagonospora nodorum Berk. Biomics. 2022. T.14(3). P. 227-233. DOI: 10.31301/2221-6197.bmcs.2022-17





Host Sensitivity Gene-Necrotrophic Toxin Interaction (i.e. wheat-*P. tritici-repentis*)

Host Genotype

Pathogen Genotype	*S_*	*ss*
+Tox	Sensitive	Insensitive
-Tox	Insensitive	Insensitive

New RT-PCR tests for identification *Rathayibacter tritici*

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The Federal State Budgetary Institution All-Russian Plant Quarantine Center, Bykovo, Russ
E-mail: 7812romalist@mail.ru

Возбудитель желтого слизистого бактериоза пшеницы Rathayibacter tritici регулируется Единым Перечнем карантинных организмов ЕАЭС. Идентификация методом ПЦР-РВ наиболее оптимальна при проведении лабораторной диагностики. В настоящий момент существует два теста ПЦР-РВ на одну генетическую мишень *Rathayibacter tritici.* Целью исследования стала разработка дополнительных тестов для идентификации *Rathayibacter tritici* обеспечивающих высокую достоверность результата диагностики.

Для подбора зондов использовали мишени, кодирующие гипотетические белки A6122_2866 и A6122_2790. Для ПЦР in silico использовали программу Ugene46. Подбор зондов проводили с использованием программы Олиго Кальк. Синтез олигонуклеотидов осуществляли в компании ЗАО «Евроген». Испытания праймерных систем проводили с ДНК штамма *Rathayibacter tritici* CFBP 1385 на детектирующем амплификаторе CFX96.

В результате исследования подобраны новые зонды и обратные праймеры и разработаны три новые праймерные системы (Rt-3F/3Rnew/3P.1, Rt-3F/3Rnew/3P.2 и Rt-5F/5Rnew/5P), показатель аналитической чувствительности которых составил 10^3 КОЕ/мл. Разработанные тесты могут быть использованы при диагностике *Rathayibacter tritici.*

Take-home message:

Идентификация *Rathayibacter tritici* методом ПЦР-РВ наиболее оптимальна при проведении лабораторной диагностики. В дополнение к двум существующим, нами разработаны три новых теста ПЦР-РВ для более точной идентификации *R.tritici*

Разработка ПЦР-теста в режиме «реального времени» для диагностики желтого слизистого бактериоза пшеницы

Идентификация *Rathayibacter tritici* методом ПЦР-РВ наиболее оптимальна при проведении лабораторной диагностики. В дополнение к двум существующим, нами разработаны три новых теста ПЦР-РВ для более точной идентификации *R. tritici*

Influence of the 135 bp intron on stilbene synthase VaSTS11 transgene expression in cell cultures of grapevine and different plant generations of *Arabidopsis thaliana*

Ogneva Z.V., Kiselev K.V., Dubdovina A.S., Aleynova O.A., Suprun A.R., Ananev A.A., Nityagovsky N.N.

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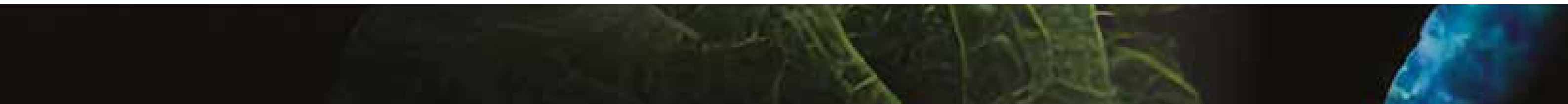
Modern plant biotechnology often faces the problem of obtaining a stable and powerful vector for gene overexpression. It is known that introns carry different regulatory elements whose effects on transgene expression have been poorly studied. To study the effect of an intron on transgene expression, the *VaSTS11* gene of grapevine *Vitis amurensis* was selected and overexpressed in several plant generations of Arabidopsis thaliana as two forms, intronless *VaSTS11*c and intron-containing *VaSTS11d*. The STS genes play an important role in the biosynthesis of stilbenes, valuable plant secondary metabolites. *VaSTS11d* contained two exons and one intron, while *VaSTS11c* contained only two exons. It has been shown that the intron-containing *VaSTS11d* was better expressed in several generations of transgenic A. thaliana than *VaSTS11c* and also exhibited a lower level of cytosine methylation. As a result, the content of stilbenes in the *VaSTS11d*-transgenic plants was much higher than in the *VaSTS11c*-transgenic plants. The results indicate that an intron sequence with regulatory elements can have a strong positive effect on both transgene expression level and its biological functions in plants.

This work was supported by a grant 22-16-00078 from the Russian Science Foundation.



Problems and possibilities of micropropagation of rare and endangered plants of Yakutia

Okhlopkova Zh.M., Kucharova E.V., Antonova E.E., Rozhina Z.G., Terentieva S.G., Eliseeva I.T.

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The creation of specially protected natural areas partially addresses the task of preserving rare and endangered plant species. Possibilities of *in vitro* plant biotechnology are proposed. The goal of this work is to develop a technology for the micropropagation of rare plants of Yakutia. The objects of research are *Dracocephalum jacutense, Lilium pilosiusculum, Artemisia martjanovii, Polygala sibirica.* Low seed productivity, various requirements for the pH value of nutrient media and soil substrates, and other, required an individual approach. Based on experiments, protocols for the processing of seed material and explants were developed, different variants of the ratio and concentrations of phytohormones for introducing the research objects into *in vitro* culture were tested. A phytohormonal composition of the nutrient medium was selected for optimal initiation of indirect morphogenesis and rhizogenesis. The obtained microclones were adapted to corresponding soil substrates and prepared for adaptation in open-ground conditions.

The study was carried out at the NEFU at the expense of the Russian Science Foundation Grant No. 22-14-20031, https://rscf.ru/en/project/22-14-20031.

<u>The main publications of authors on the subject of the abstract:</u>

Razgonova M.P., Okhlopkova Z.M. et al. Comparison of Wild and Introduced Dracocephalum jacutense P.: Significant Differences of Multicomponent Composition // Horticulturae 2022, 8, 1211. https://doi.org/10.3390/horticulturae8121211.

Охлопкова Ж.М., Разгонова М.П., Егорова П.С., Голохваст К.С. Характеристика комплекса полифенольных соединений эндемика Якутии Dracocephalum jacutense Peschkova с использованием метода тандемной масс-спектрометрии // Физиология растений. 2023. Т.70. №3. С.327-336.

Agrobacterium-mediated transformation of non-model plants *Fagopyrum esculentum* and *Capsella bursa-pastoris*

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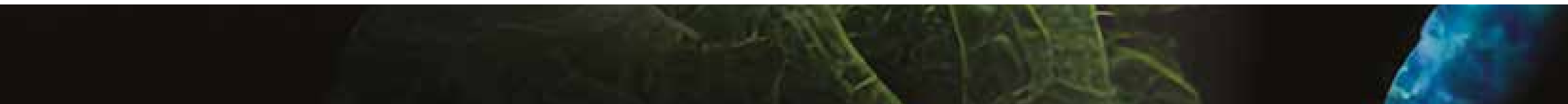
Efficient transformation is an essential step in gene function and genome editing studies. In this work, we tested the Agrobacterium-mediated transformation of two non-model plants: C. bursa-pastoris is a young allopolyploid and a promising object for studying the evolution and functionalization of homoeologous genes; F. esculentum is an important agricultural object, the successful transformation of which will make it possible to obtain improved varieties faster. *A. tumefaciens* strains GV3101 and EHA105 and *A. rhizogenes* strains A4 and R1000 were used for transformation. Vectors carrying GFP or OLE1-tagRFP were designed to assess transformation efficiency. Floral-dip transformation of C. *bursa-pastoris* from the Middle East, Europe, and Asia genetic clusters showed that the ecotype from China has the highest transformation efficiency of ~1%. The transformation of *F. esculentum* varieties showed that *A. rhizogenes* strains successfully induce hairy root culture in hypocotyl explants; *A. tumefaciens* strains efficiently transform cotyledon explants to regenerate into stably transformed plants.

Supported by the Ministry of Science and Higher Education, project #075-15-2021-1064



Temperature-induced expression of ergosterol biosynthetic genes (ERGs) in the lichen *Lobaria pulmonaria*

Onele A., Swid M., Leksin I., Valitova J., Minibayeva F.

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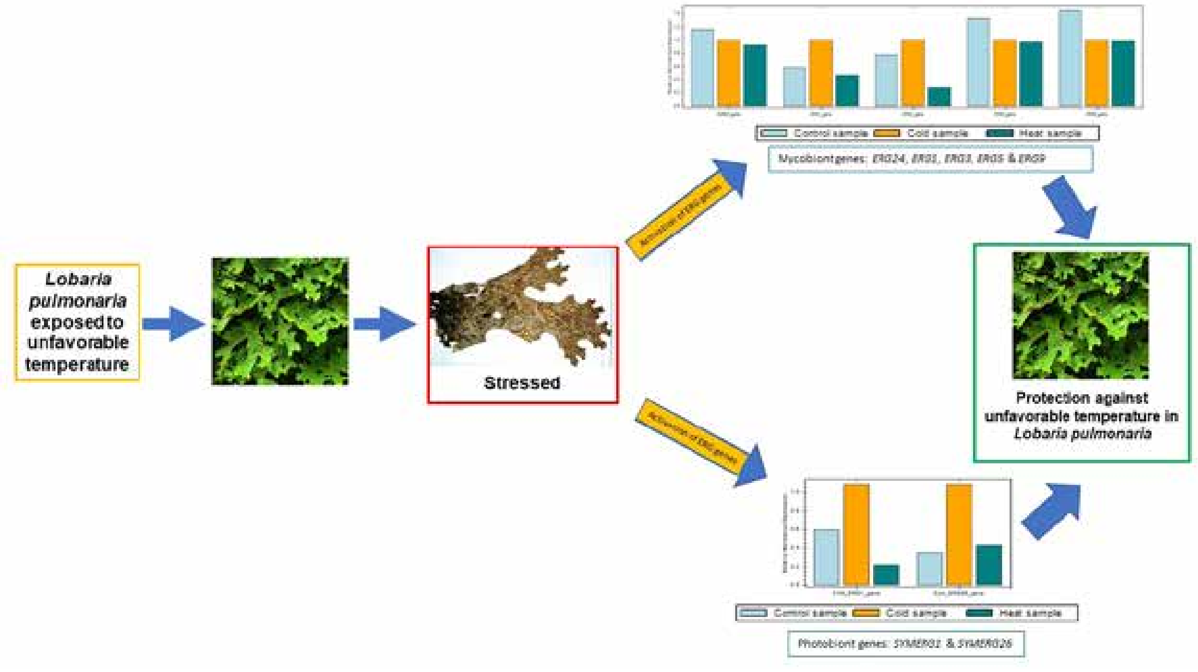
Sterols are important components of the cell membrane and lipid rafts that play a critical role in various physiological and biochemical processes during development and stress tolerance in living organisms. Depending on their different sources, sterols can be divided into animal sterols, plant sterols, and fungal sterols, although lichens have a unique and diverse sterol composition that differs from that of fungi and algae, and may also determine high stress tolerance of these symbiotic organisms. In recent years, many studies in vascular plants and some fungi on the biosynthetic pathway of sterols have been reported, whereas the knowledge of the regulation and accumulation of sterols in lichens is not well understood. Here, genes involved in the biosynthesis of sterols in *Lobaria pulmonaria,* particularly ergosterol (ERG) genes, were identified *in silico.* RT-qPCR analysis showed that ERG genes were upregulated in response to freezing temperature in *L. pulmonaria* and its photobiont. Activation and expression of genes involved in ERG biosynthesis in *L. pulmonaria* suggest that ERGs could play an important role in lichen stress tolerance. Fund: RFBR: 22-14-00362

Take-home message:

This study provides a better knowledge of the synthesis and regulation of sterols in the lichen *Lobaria pulmonaria* and the role of ERGs involved in ergosterol biosynthesis, in development and abiotic stress tolerance in lichens.



Development of genome-wide SSR markers in three fir species by next generation sequencing

Oreshkova N.V., Bondar E.I., Sharov V.V., Dhungana S.P.*, Gailing O.*, Krutovsky K.V.*

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The results of the search for microsatellite or simple sequence repeat (SSR) loci with tri-, tetra-, penta- and hexanucleotide tandem repeat motifs in the draft *de novo* assembly of the Siberian fir (*Abies sibirica Ledeb.*) genome and the development of convenient highly polymorphic markers that can be easily genotyped even by simple gel electrophoresis will be presented. In total, 64 pairs of oligonucleotide PCR primers for 32 detected microsatellite loci were designed and tested. Based on whole genome sequencing data, 10 polymorphic microsatellite markers were developed for *A. sibirica*, 14 for *A. alba* and 13 for *A. nordmanniana* including common markers that can be used in all three species. The markers were tested on samples from eight natural populations of *A. sibirica* and four populations of *A. alba,* and preliminary data on the level of population genetic variation and differentiation were obtained. These markers can be potentially used also in other species in genus *Abies* with the ability to use simple gel electrophoresis, which is very convenient in field research. We have developed also multiplex panels of 14 loci for capillary gel electrophoresis.

The main publications of authors on the subject of the abstract:

Oreshkova N., Bondar E., Putintseva Yu., Sharov V., Kuzmin D., Krutovsky K. Development of nuclear microsatellite markers with long (three -, four -, five-and six-nucleotide) motives for Siberian larch // Russ. J. Genet. 2019. 55 (4): 444-450.

Oreshkova N., Putintseva Yu., Sharov V., Kuzmin D., Krutovsky K. Development of microsatellite genetic markers in Siberian larch (Larix sibirica Ledeb.) based on the de novo whole genome sequencing // Russ. J. Genet. 2017. 53 (11): 1194–1199.

Oreshkova N., Bondar E., Sharov V., Dhungana S., Gailing O., Krutovsky K. Population genetic variation of microsatellite markers developed for Siberian fir (Abies sibirica Ledeb.) and European silver fir (A. alba Mill.) using whole genome sequencing data // Plant Genet. Resour. 2023 (in press)

Take-home message:

The proposed nuclear microsatellite loci will be very useful for studying variation of different fir species helping to address different problems and questions related to conservation, restoration and reproduction of fir forests.

Genomic clusters of transcription factor binding sites in plants

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Crop breeding has entered a new era using high-throughput technologies, such as transcriptomics, genomics, and metabolomics. Integration of omics data provides a comprehensive understanding of the biological processes underlying plant traits and their interactions. We have studied regulatory transcription networks in model plants. The distribution of the number of links in the network of protein-protein interactions follows certain statistical patterns. The distribution of the number of hub genes in such a network for transcription factors also has an exponentially decreasing character. We discuss the hypothesis about the general nature of the distribution of clusters of binding sites in the genome according to the number of different transcription factors, which is determined by the structure of the regulatory gene network. A method and computer tool for searching for regulatory regions based on the statistics of the distribution of binding sites in plant genomes were presented (Dergilev et al., 2021). The existence of nonrandom clusters of binding sites in all studied plant genomes has been shown.

The work was supported by RSF (23-44-00030).

The main publications of authors on the subject of the abstract:

Dergilev A.I., Orlova N.G., Dobrovolskay O.B., Orlov Y.L. Statistical estimates of transcription factor binding site clusters in plant genomes based on genome-wide data. Journal of Integrative Bioinformatics. 2022; 18, 20200036 doi: 10.1515/jib-2020-0036

Perspective methods for increasing the productivity of transgenic plants-producers of recombinant proteins

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A key trend in modern pharmacology is the shift from low-molecular-weight drugs to protein drugs (antibodies, antigens, cytokines, enzymes). Their production has become profitable with the appearance of transgenic producer organisms. Bacteria, yeasts or animal cell cultures are most often used.

A high potential as a producer is found in plants. They have a eukaryotic expression system and the lowest cost per biomass unit. However, their use is limited by a number of challenges, particularly the low and often unstable level of transgene expression.

A widely known way of enhancing transcription is combining two or more promoters. However, according to the literature, the use of two terminators in a transgene also provides a significant increase in the production of the target protein.

Another known method is to optimize the codon composition of transgene coding sequence in favour of codons that are more frequently used by the producer organism.
To refine the methods for optimizing codons and dual terminators, we have created plant transformation vectors based on previously tested constructs for the synthesis of bovine gamma interferon in plants.

The main publications of authors on the subject of the abstract:

Burlakovskiy, M. et al.//The Structure of T-DNA Insertions in Transgenic Toba co Plants Producing Bovine Interferon-Gamma. Appl. Sci. 2022, 12, 761.doi:10.3390/app12020761 Beyene, G. et.//Unprecedented enhancement of transient gene expression from minimal cassettes using a double terminator. Plant Cell Rep 30, 13–25 (2011). doi:10.1007/s00299-010-0936-3

Take-home message:

The use of two terminators in a transgene and codon optimization provides a significant increase in the production of the target protein.

To refine the methods we have created plant transformation vectors based on previously tested constructs.

Structure and expression of the NAM-B1 gene in bread wheat lines with *Triticum dicoccoides* and *T. kiharae* genetic material introgressions

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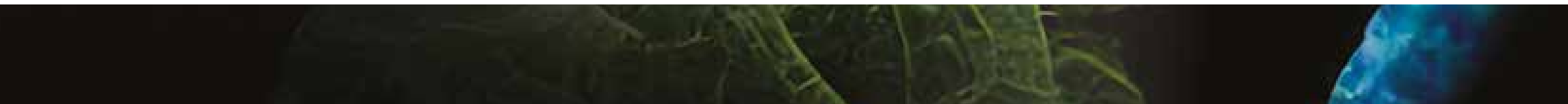
The identification of functional (wild-type) *NAM-B1* allele associated with high grain protein and essential microelements content in wheat relatives enhanced the significance of distant hybridization for bread wheat nutritional value increase. The allelic polymorphism of the *NAM-B1* and gene expression in 13 wheat lines with genetic material of *T. dicoccoides* and *T. kiharae* and their parental forms were evaluated. The functional *NAM-B1* allele was identified only in samples of wheat relatives among the parental forms. All parental varieties and most of introgressive lines (69,2%) had non-functional (mutant) allele. A statistically significant difference was found in the level of *NAM-B1* gene exspression between the group of genotypes with mutant and wild-type alleles ($p<0,002$). It has been shown that genotypes with functional allele have a higher level of expression. A close significant association was established between the level of expression and protein content ($r = 0,77$). The obtained results showed that differences in grain protein content can be due to both the structural features of the *NAM-B1* gene (wild-type and mutant alleles) and the level of their expression.

The main publications of authors on the subject of the abstract:

Orlovskaya Olga et al. Molecular cytological analysis of alien introgressions in common wheat lines derived from the cross of Triticum aestivum with T. kiharae // BMC Plant Biology (2020) 20 (Suppl. 1):201. doi:10.1186/s12870-020-02407-2

Орловская О. А. и др. Показатели продуктивности и питательной ценности зерна у генотипов пшеницы с различными аллелями гена NAM-B1 // Доклады Национальной академии наук Беларуси (2022) 66, № 5:517-524. doi: 10.29235/1561-8323-2022-66-5-517-524



Hydroponic technologies in the regulation of crop quality

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Hydroponic culture is still undervalued as a promising biotechnology for obtaining high-quality environmentally friendly crop products. Essentially, that it provides an opportunity to ensure the supply of mineral elements to plants in the mode of selective or forced absorption by means of high- or low-affinity ion transport systems functioning adaptively in open and closed hydroponics. In addition, hydroponics technologies create the possibility of targeted impact on the formation of mineral and biochemical composition of plants, accelerating the development and increasing the yield and quality of the crops. For a number of plants (cabbage, beets, carrots) we have demonstrated the effectiveness of the nutrient stress strategy (impossible under soil cultivation), for initiating and enhancing the outflow and reallocation of assimilates from donor (leaves) to acceptor (commercial parts of plants) with increase in their carbohydrate content. Equally important is the established possibility to reduce nitrates accumulation in various parts of plants by means of operational changes in nutrient solution composition at different stages of plant cultivation without decrease in their productivity.

The main publications of authors on the subject of the abstract:

Osmolovskaya N.G. et al. Ion homeostasis response to nutrient- deficiency stress in plants //Cell Growth. Ed. by Biba Vikas and Michael Fasullo (2019). IntechOpen. 23 pp. DOI: 10.5772/intechopen.73916

Take-home message:

Nutrient stress provoked by temporary decrease of macronutrients concentrations in the supplied solution becomes a trigger for the redistribution of assimilates within the whole plant providing increase in the crop yield and improving its quality.

Opportunities of a regulated agroecosystem in the management of the plant production process

Panova G.G., Udalova O.R., Kanash E.V., Kochetov A.A., Artemyeva A.M.*, Priyatkin N.S., Sinyavina N.G., Mirskaya G.V., Galushko A.S., Kuleshova T.E., Khomyakov Yu.V., Zhuravleva A.S., Chesnokov Yu.V.

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The report is devoted to the description of the strategy and the main results of the research carried out by the Agrophysical Research Institute in recent years in the regulated agroecosystem and demonstrating its opportunities in managing the plants production process. The key role of a regulated agroecosystem in elucidating the production and adaptive potential of agricultural crops, the mechanisms of their interaction with the environment and response to agrotechnological impacts under simulated conditions while minimizing the effect of environmental noise, and in creating a system of effective resource-saving, environmentally safe management of the plants production process through multidimensional optimization of plant growing conditions, the development of non-invasive methods for express assessment of the seed materials quality characteristics and of the vegetating plants physiological state, as also genetic breeding approaches and methods, accelerating and increasing the breeding's efficiency, as well as through agrotechnological highly effective means and methods of operational impact on crops.

The main publications of authors on the subject of the abstract:

Panova G.G. et al. Scientific basis for large year-round yields of high-quality crop products under artificial lighting //Russian Agricultural Sciences (2015) 41 (5): 335-339. doi: 10.3103/S1068367415050158.

Panova, G.G. et al. Fundamentals of Physical Modeling of "Ideal" Agroecosystems // Technical Physics (2020) 65(10): 1563–1569. doi:10.1134/s1063784220100163.

Take-home message:

A regulated agroecosystem and its possibilities is the basis for obtaining knowledge about the mechanisms of plants interaction with the environment and creating a system of effective management of their production process.

Agrophysical Research Institute

Opportunities of a regulated agroecosystem in the management of the plants production process

REGULATED AGROECOSYSTEM

Strategies for research activities using the regulated agroecosystem's possibilities in Agrophysical Research Institute

Diversity of cultivated crops in a regulated agroecosystem at the agro-biopolygon of the Agrophysical Research Institute

The role of extracellular phosphonates of *Pectobacteria* in plant-microbial interaction

Parfirova O.I., Petrova O.E., Mikshina P.V., Syromyatnikova E.D., Smolobochkin A.V.*, Gorshkov V.Y.

Kazan Institute of Biochemistry and Biophysics of Kazan Scientific Center of Russian Academy of Sciences, Kazan, Russia, *Arbuzov Institute of Organic and Physical Chemistry, Federal Research Center Kazan Scientific Center of Russian Academy of Sciences, Kazan, Russia
E-mail: parfirovaolga.i@gmail.com

Phytopathogenic bacteria, including *Pectobacterium atrosepticum (Pba)*, not only cause plant disease but also interact with plants asymptomatically. Except for coronofacic acid, no low molecular weight metabolites that determine the strategy of *Pba* interaction with plants were characterized. Based on our RNA-Seq results, we proposed that low-molecular-weight extracellular phosphonates—the metabolites that have not been previously described for *Pba*—influence plant-*Pba* interactions, and our aim was to test this hypothesis.

By 31P NMR spectroscopy and knockout of the candidate phosphonate-biosynthetic gene, we specified that Pba synthesizes extracellular phosphonates, whose production is induced by plant metabolites. By mass spectrometry, we determined the basal elements of the structure of these compounds. Using a number of test systems and plant infection tests, we showed that phosphonates serve as quenchers of *Pba* virulence. Thus, *Pba* produces phosphonates to reduce the manifestation of their pathogenic potential in order to prolong interaction with the host plant, which is of great importance for both the host plant and the pathogen. The work was supported by the RSF (19-14-00194)

<u>The main publications of authors on the subject of the abstract:</u>

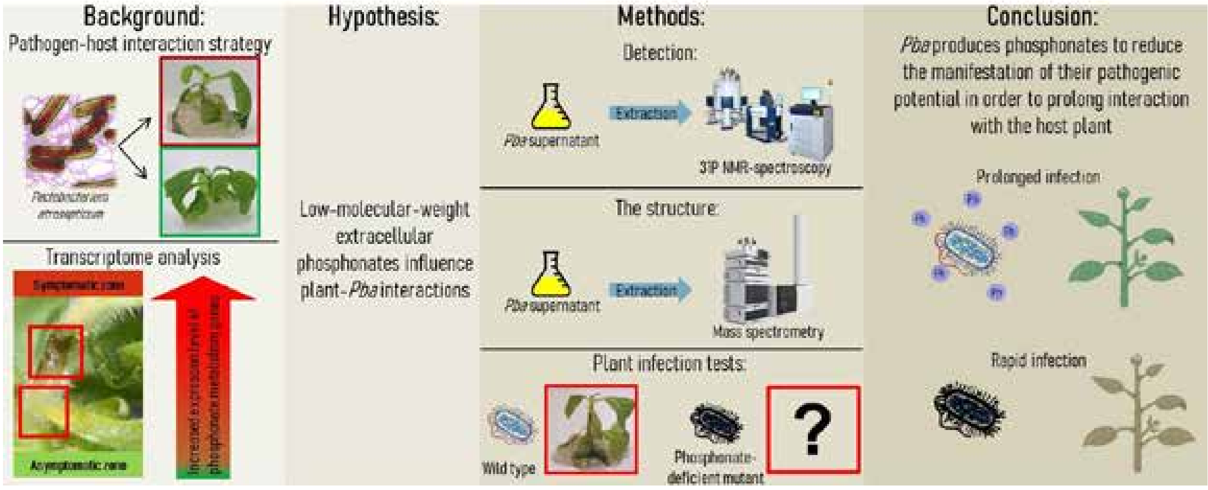
Gorshkov V. et al. Host plant physiological transformation and microbial population heterogeneity as important determinants of the Soft Rot Pectobacteriaceae–plant interactions //Seminars in Cell & Developmental Biology (2023).

Gorshkov V. et al. Transcriptome profiling helps to identify potential and true molecular switches of stealth to brute force behavior in Pectobacterium atrosepticum during systemic colonization of tobacco plants //European Journal of Plant Pathology (2018) 152: 957-976.

<u>Take-home message:</u>

Phytopathogenic pectobacteria produce low-molecular-weight phosphonates with a specific structure.

Phosphonates restrain the manifestation of pathogenic potential in pectobacteria in order to prolong their interaction with the host plants.



Cytogenetic stability of collection embryogenic cultures of *Larix sibirica* Ledeb.

Park M.E., Goryachkina O.V., Tretyakova I.N.

V. N. Sukachev Institute of Forest Russian Academy of Sciences, Siberian Branch - Separate division of FRC KSC SB RAS, Krasnoyarsk, Russia
E-mail: mtavi@bk.ru, culture@ksc.krasn.ru

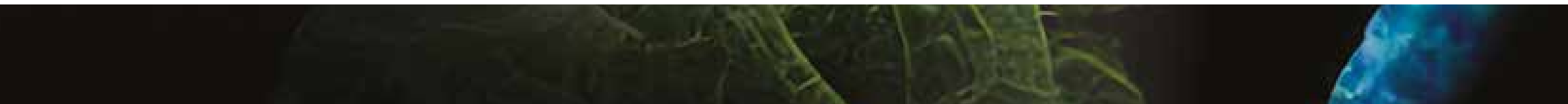
In vitro embryogenic culture collection of Pinaceae family species was created at the IF SB RAS (Krasnoyarsk). The *Larix sibirica* collection consists of 22 actively proliferating cell lines (CL, 54 CL in total) obtained from explants (immature zygotic embryos) of open and controlled pollination. The duration of proliferation of individual cell lines reached 14 years. CL differed in growth intensity, embryonic productivity, hormonal balance and genetic stability, as well as regenerative ability. Cytogenetic studies revealed the genetic stability of young CLs (up to 1 year), in which the karyotype consisted of a diploid number of chromosomes ($2n$=24). Genomic and chromosomal mutations were observed in a number of the studied cells, which could be present in the initial explant, or appear during cultivation. The long-term proliferating CL, from which viable clones producing seeds and pollen were obtained, retains a diploid number of chromosomes for 11 years of cultivation and remains genetically stable.

This research was funded by a grant from the Russian Science Foundation and the Krasnoyarsk Regional Fund for Support of Scientific and Technical Activities, grant number 22-14-20008.

The main publications of authors on the subject of the abstract:

Goryachkina O.V., Park M.E., Tretyakova I.N., Badaeva E.D., Muratova E.N. Cytogenetic stability of young and long-term embryogenic cultures of Larix sibirica // Cytologia (2018) 83(3): 323–329. doi: 10.1508/cytologia.83.323

Tret'yakova I.N., Park M.E., Oreshkova N.V., Padutov V. E. The Regenerative capacity of Siberian larch cell lines in vitro // Biology Bulletin (2022) 49(6): 609–619. doi: 10.1134/S1062359022050193



Species of the genus Exobasidium on plants in the park "Dendrarium" Sochi

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The novelty of the study lies in obtaining information about the species of the genus Exobasidium (department Basidiomycota) found on plants in the park, the of degree of lesion and assessment of their distribution in the conditions of the park "Dendrarium".

The collection of the material was carried out from April to June 2021-2022 in the Arboretum Park. The material was the the organs of a living plant affected by the fungus, mostly y the buds, leaves and stems of plants from the families *(Ericaceae, Theaceae)*.

The percentage of plant infection and the intensity of disease development (IRB) were determined in accordance with the generally accepted phytopathological methodology.The total degree of lesion was estimated in points: 1 point – up to 5%; II – 5-25; III – 25-50; IV – 50-75; V – 75-100%.

As a result of our work, 3 species of the genus Exobasidium were identified on the plants: *Exobasidium japonicum* Shir, *Exobasidium discoideum* Ell. et Ev., *Exobasidium camelliae* Shirai var. graelis.

Kinds *Exobasidium japonicum* Shir, *Exobasidium discoideum* Ell. et Ev.n a strong degree they amaze and spread in the park on plants *rhododendrona* and its varieties.

The main publications of authors on the subject of the abstract:

Diseases and pests of flower plants of the open ground of the Arboretum Park in Sochi // Floriculture: theoretical and practical aspects, theses of the second International Scientific Conference. 2020, Yalta, November 09-13, 2020 P-59.

Take-home message:

The article presents information about the species of the genus Exobasidium (department Basidiom cota) found on plants in the park, the degree of degree of lesion and evaluations of their distribution in the conditions of the park "Dendrarium".

Transcriptomic analysis of *Euonymus europaeus* fruit at different stages of development

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*Azerbaijan National Academy of Sciences, Baku, Azerbaijan
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DGAT family enzymes catalyze a third acylation leading to the formation of triacylglycerols (TAGs). Five types of DGAT enzymes have been found in plant cells, differing from each other in structural organization, substrate specificity and localization in the cell. While in some plants different types of DGAT play overlapping roles in others they may play a unique role. For example, in *Euonymus alatus* EaDAcT showed specificity for very short chain organic acid radicals. Euonymus accumulates TAGs and acetylated diacylglycerols (AcDAGs), in which the third carbon atom is esterified with an acetic acid residue. The presence of AcDAG gives *Euonymus* oil special properties, which makes it a promising raw material for the chemical and food industries. It was shown that the ratio of TAG and AcDAG fractions changes during fruit maturation. However, until now, nothing has been known about the contribution of each individual DGAT gene. To identify the role of various DGATs in the accumulation of storage lipids during fetal development, a transcriptomic analysis was performed at the stages when the maximum, minimum, and average values of TAG levels and AcDAG accumulation were observed.

The main publications of authors on the subject of the abstract:

Pavlenko, O.S., Akashkina, Y.V., Suhorukova, A.V. et al. Diversity of Types of Plant Diacylglycerol Acyltransferases, Peculiarities of Their Functioning, and How Many DGATs are Required for Plants // Russ J Plant Physiol 69, 2 (2022). https://doi.org/10.1134/S1021443722010162

Take-home message:

DGATs are key regulatory enzymes of lipid homeostasis and combine carbon and energy fluxes for TAG production in eukaryotic cells.

Fast growing transgenic poplar: main features and perspectives of use

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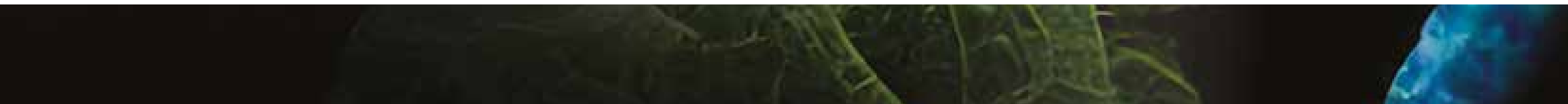
Genes encoding key enzymes of gibberellins biosynthesis were shown as an effective tool for transgenesis aiming at fast-growing plant development. Here we show a successful genetic transformation of Populus berolinensis K. Koch by gibberellin-20-oxidase gene resulting in a fast growing phenotype. We used *GA20ox1* CDS from *Arabidopsis thaliana* cDNA for agrobacterium mediated transformation of poplar using pBI121 binary vector system. Only one type nutrient media supplemented with BAP (0.2 mg L^{-1}), TDZ (0.02 mg L^{-1}), NAA (0.01 mg L^{-1}), kanamycin (50 mg L^{-1}) and cefotaxime (250 mg L^{-1}) was used for the selection and regeneration of transgenic plants. Transgenesis was proved by rooting in the presence of kanamycin in the nutrient media and by PCR for both *nptII* and *AtGA20ox1* genes. Obtained transgenic plants were characterized by narrow leaves, long internodes and 3 times faster growing rate in comparison to control plants. Fast growing transgenic poplars have perspectives in phytoremediation, soil reclaiming and biorefining including biofuel production.

The study was financed by RSF grant № 22-24-01113, https://rscf.ru/project/22-24-01113/.



Nanobiocomposites of chalcogens and metals in natural polymer matrices: stimulation of plant growth and development and antibacterial effect

Perfileva A., Sukhov B.*

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Most of the pesticides currently used are unsafe and are aimed at regulating the number of phytopathogenic fungi, and there are practically no agents against bacteria. In order to search for new environmentally friendly agents for regulating the number of microbes pathogenic for cultivated plants, it is interesting to study nanosubstances. In this work, we studied the biological activity of a number of chemically synthesized nanocomposites (NCs) consisting of nanoparticles (NPs) of selenium or metal compounds (copper oxide, manganese hydroxide) densely packed into natural polymer matrices (arabinogalactan, starch, and carrageenan).

The results showed that some of the studied NCs had both an antibacterial effect and a growth stimulating effect for plants. At the same time, NC increased the immune status of the infected plant, which affected its interaction with the pathogen. In addition, NPs from these NCs did not accumulate in the tissues of the treated plants and did not kill the soil microflora. The presented results will contribute to the development of scientific bases for obtaining new information about the effect of nanosubstances on the interaction of plants and pathogens.

The main publications of authors on the subject of the abstract:

Perfileva A.I., et al. Effect of nanopriming with selenium nanocomposites on potato productivity in a field experiment, soybean germination and viability of Pectobacterium carotovorum// Horticulturae. 2023. https:// doi.org/10.3390/horticulturae9040458.

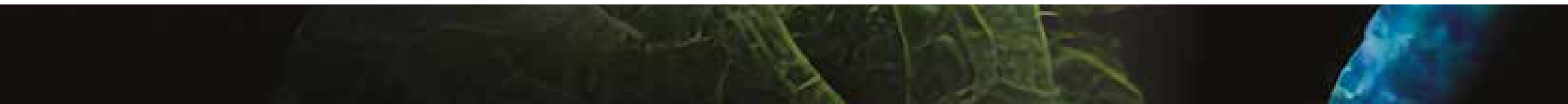
Perfileva A.I., et al. Effect of selenium nanocomposites based on natural polymer matrices on the biomass and storage of potato tubers in a field experiment// Agronomy. 2022. https://doi.org/10.3390/agronomy12061281.

Take-home message:

Nanobiocomposites (NCs) have antibacterial and fungicidal effects.

NCs are able to stimulate the germination of seeds of cultivated plants.

NCs increase plant resistance to phytopathogens and in field experiments increase plant productivity.



Site-specific insertion of genes into the *Arabidopsis thaliana* genome using Cas9 endonuclease

Permyakova N.V., Marenkova T.V., Belavin P.A., Zagorskaya A.A., Sidorchuk Yu.V., Uvarova E.A., Kuznetsov V.V., Rozov S.M., Deineko E.V.

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Сайт-специфическое встраивание целевых генов в такой район генома, который характеризуется стабильно высоким уровнем экспрессии может решить проблему низкого уровня экспрессии рекомбинантных белков. В нашей лаборатории был проведен ряд экспериментов, позволивших разработать эффективный протокол сайт-специфического встраивания генов с помощью эндонуклеазы Cas9. Нами был экспериментально выявлен оптимальный состав трансгенной конструкции для встраивания. Целевые гены должны быть окружены участками ДНК гомологичными сайту встраивания в геномной ДНК дополненными сайтами узнавания эндонуклеазы Cas9. Эксперимент с различными способами доставки позволил выяснить, что доставка при помощью генной пушки более эффективна, чем агробактериальная трансформация. При этом при доставке конструкций с помощью генной пушки сайт-специфическое встраивание проходит эффективнее, если используются две плазмиды, одна из которых несет гены системы редактирования, а другая конструкцию с целевыми генами, так как для успешной гомологичной рекомбинации матрица для гомологичной рекомбинации должна быть представлена в клетке в достаточном количестве. Работа поддержана грантом РНФ 21-14-00091.

The main publications of authors on the subject of the abstract:

1. Permyakova, N. V. et al. Assessment of the Level of Accumulation of the dIFN Protein Integrated by the Knock-In Method into the Region. Cells 2021, 10, 2137, doi:https://doi.org/10.3390/cells10082137.

2 Permyakova, N. V. et al. CRISPR/Cas9-Mediated Targeted DNA Integration: Rearrangements at the Junction of Plant and Plasmid DNA. Int. J. Mol. Sci. 2022, 23, doi:10.3390/ijms23158636.

Take-home message:

Для эффективного *knock-in* в геном растительной клетки матрица для гомологичной рекомбинации дожна быть окружена плечами гомологии и сайтами узнавания Cas9

Для доставки конструкций в клетки лучше использовать генную пушку.

Influence of allelic variability of photoperiod genes on soybean maturity time in central Russia and West Siberian

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Kurchatov Center for Genome Research, Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia,
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Soybean is a short day crop with a strong sensitivity to photoperiod. Under the long daylight, the flowering and maturity time of soybean is greatly delayed. The *E1-E4* genes have the strongest effect on photoperiod sensitivity. Recessive alleles of the *E1-E4* genes reduce sensitivity to photoperiod, resulting in early flowering and maturity. How these genes affect the growing season of soybeans in field conditions of Russia is still unknown. To clarify this issue, we studied the flowering and maturity time of 180 soybean accessions under natural daylight in the Novosibirsk and Orel regions. Also, for all accessions the *E1-E4* genotype was established. As a result, accessions with genotypes *e1-as/e2/e3/e4* and *e1-nl/e2/e3/e4* had the shortest flowering and maturity time in both regions.

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

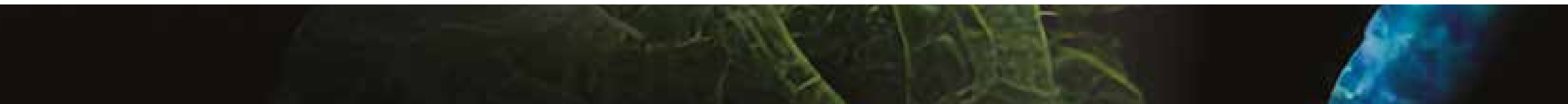
The main publications of authors on the subject of the abstract:

Perfil'ev, R.N.; Shcherban, A.B.; Salina, E.A. Development of a Marker Panel for Genotyping of Domestic Soybean Cultivars for Genes Controlling the Duration of Vegetation and Response to Photoperiod. Vavilov J. Genet. Breed. 2021, 25, 761–769, doi:10.18699/VJ21.087.

Take-home message:

1) Recessive alleles *E1-E4* provide adaptation of soybean to northern latitudes.

2) The *E4* gene has a different effect on the flowering time in the Novosibirsk and Orel regions.



Doubled haploid technology as accelerate of the breeding programs

Petrash N.V., Piskarev V.V., Sovetov V.V.

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The production of doubled haploids (DH) from hybrids allows breeders to significantly speed up the breeding process. In addition, DH-lines can be used as constant sources of target genes. The effect of genotype is the main limiting factor of androgenesis *in vitro*. Therefore, one of the propos approaches is to use AC only with responsive genotypes. The study of the breeding material will make it possible to identify genotypes that are responsive in AC. In our study, varieties and hybrids F_1 and F_2 were studied to androgenesis response. Sources of a high degree of responsiveness and a poor response have been identified. More than 100 DH-lines from 17 combinations have been created. The use of doubled haploid technology made it possible to quickly create lines with resistance to powdery mildew, lines with short-stemming. The best lines are included in the further selection process. Three-year study of 7 DH lines (*L* Velut×Tulun 15) in the field conditions allowed us to identify promising lines, which exceeds the parental forms in terms of yield.

Acknowledgements: This work was supported by IC&G budget project FWNR-2022-0037

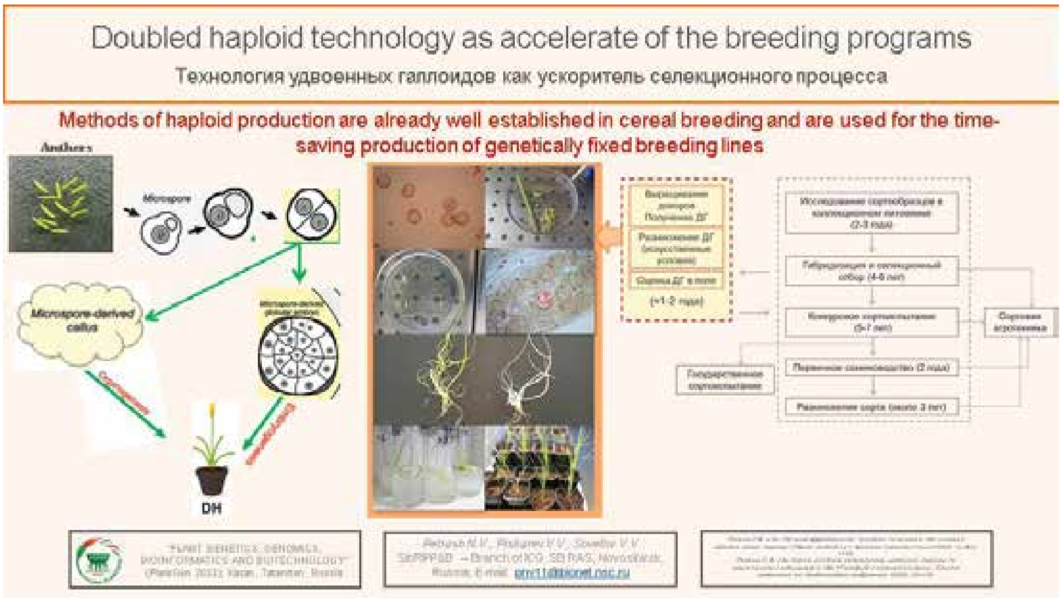
<u>The main publications of authors on the subject of the abstract:</u>

Петраш Н.В. и др. Изучение эффективности культуры пыльников in vitro сортов и гибридов мягкой пшеницы (Triticum aestivum L.) // Зерновое хозяйство России (2022) 14, № 6: 17-22

Петраш Н. В. и др. Оценка исходного селекционного материала пшеницы по отзывчивости к андрогенезу in vitro // Генофонд и селекция растений : Сборник материалов 6-й Международной конференции (2022): 126-130.

<u>Take-home message:</u>

DH-technique is a promising direction in the modern breeding process
More than 100 DH-lines from 17 combinations have been created
Sources of a high degree of responsiveness and a poor response have been identified



Doubled haploid technology as accelerate of the breeding programs

Технология удвоенных галлоидов как ускоритель селекционного процесса

Methods of haploid production are already well established in cereal breeding and are used for the time-saving production of genetically fixed breeding lines

"PLANT GENETICS, GENOMICS, BIOINFORMATICS AND BIOTECHNOLOGY" (PlantGen 2023) Kazan, Tatarstan, Russia

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Does a plastid stringent response modulate plant defense systems?

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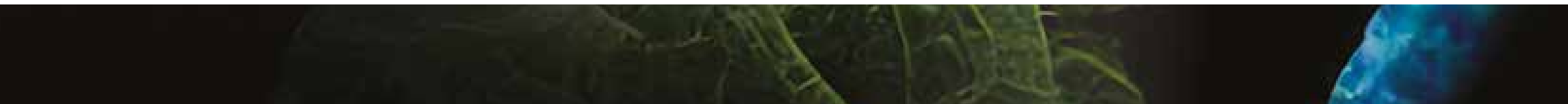
Stringent response (SR), a primary stress reaction in bacteria and plant chloroplasts, is a molecular switch that provides operational stress-induced reprogramming of transcription under conditions of abiotic and biotic stress. Because the infection is a stressful situation for both partners (the host plant and the pathogen), we analyzed the expression of bacteria land plastid SR-related genes during plant–microbial interaction. In the phytopathogenic bacterium *Pectobacterium atrosepticum,* SpoT-dependent SR was induced after contact with potato or tobacco plants. In plants, two different scenarios of molecular events developed under bacterial infection. Plastid SR was not induced in the host plant potato *Solanum tuberosum*, which co-evolved with the pathogen for a long time. In this case, the salicylic acid defense pathway was activated and plants were more resistant to bacterial infection. SR was activated in the tobacco *Nicotiana tabacum* (experimental host) along with activation of jasmonic acid-related genes *AOS, LOX2, JAZ*, resulting in plant death. These results are important to more fully understand the evolutionary interactions between plants and symbionts/pathogens.

The main publications of authors on the subject of the abstract:

Petrova, O., Parfirova, O., Gogolev, Y., & Gorshkov, V. (2021). Stringent Response in Bacteria and Plants with Infection. Phytopathology, 111(10), 1811-1817.



Selection of plant expression systems for production of recombinant flax lectins

Petrova N.V., Mokshina N.E., Gorshkova T.A.

Kazan Institute of Biochemistry and Biophysics, Federal Research Center Kazan Scientific Center of Russian Academy of Sciences, Kazan, Russia
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Lectins are a large group of plant proteins that remain poorly characterized at the level of individual proteins, many of which were discovered by the genome analysis and cannot be detected by methods of proteomics.

Previously, we have shown the stage- and tissue-specific expression of lectin genes by transcriptomic analysis of flax stem samples. To reveal the substrate specificity of these proteins, which can give insight into their functions, it is necessary to obtain them in preparative amounts.

For the production of recombinant lectins, *N. benthamiana* and the culture of *Chlorella vulgaris* were tested. The use of plant systems is associated with the requirement to obtain glycosylated proteins since this modification may affect the implementation of lectin functions.

Lectin genes (*Lus10016109, Lus10031473,Lus10024290*) belonging to the amaranthin, Nictaba and jacalin families and activated in tissues with different cell wall types were chosen and successfully cloned into the vector p35SHSPG and then sub-cloned into the pBCKB expression vector. A protein product of *Lus10016109* was obtained in tabacco leaves.

The study was partially supported by RSF grant #20-64-47036.

The main publications of authors on the subject of the abstract:

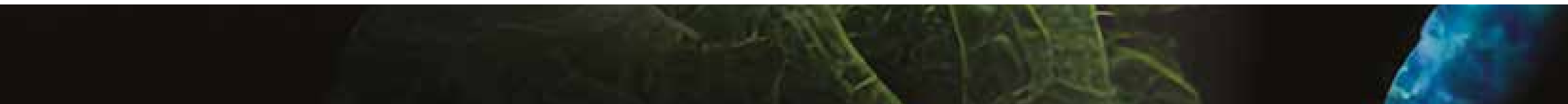
Petrova N.V. et al. Using FIBexDB for in-depth analysis of flax lectin gene expression in response to Fusarium oxysporum infection // Plants (2022) 11: 163. doi: 10.3390/plants11020163

Petrova N. et al. Gene Expression patterns for proteins with lectin domains in flax stem tissues are related to deposition of distinct cell wall types // Front Plant Sci (2021) 12: 634594. doi: 10.3389/fpls.2021.634594

Take-home message:

Lectins are proteins capable of recognizing and binding specifically and reversibly to carbohydrate structures without changing the carbohydrate moiety

Glycosylation of the lectins may affect the implementation of their functions



Search for links between the allelic composition of glutenin genes and the feed qualities of triticale grain

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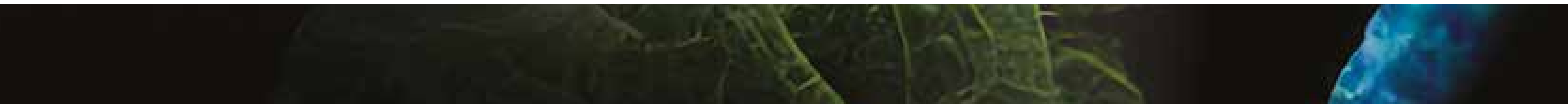
The search of new allelic glutenin encoding variants opens up a vast range of potentialities for working with new markers of these genes and establishing relationships between them and grain quality. The protein content determines the nutritional and feed value of grain, its processed products and technological properties of the grain. Triticale proteins are characterized by a well-balanced amino acid composition, occupying an intermediate position between wheat and rye proteins by content of aspartic acid, threonine, alanine, valine and tyrosine. To identify the genes encoding certain subunits of high molecular weight glutenins (alleles of the *Glu-A1* and *Glu-B1 loci*) in triticale cultivars, the following primers were developed: F: CAACCTCTCCACAG-CAGC, R: CTTGTCCTGACTGTTGCGG. Twenty six samples of the studied collection were analyzed with these primers. According to the analysis, the majority of varietal samples were heterogeneous. Combinations of alleles are different in the investigated samples and have different frequency of occurrence. Among the studied triticale samples, five of the most promising were identified, namely Grebeshok, C95, 08844, P1-13-5-13 and P1-13-5-2.

<u>The main publications of authors on the subject of the abstract:</u>

1. Pirsikov et al. Development of molecular markers for the identification of prolamins genes and their correlation with baking qualities of grain // PLANTGEN (2021): 173. doi: 10.18699/PlantGen2021-157

2. Pirsikov et al.Correlation analyses between the allelic composition of glutenin genes and the quality of triticale grain via new molecular marker and sds-page // Kormoproizvodstvo (2022) 9: 27-33. eLIBRARY ID: 50173291



Comparative analysis of stress metabolites concentrations in barley seeds of inhibited and stimulated varieties in response to low-dose gamma irradiation

Pishenin I.A., Smirnova A.S., Gorbatova I.V., Khanova A.S., Podobed M.Yu., Kazakova E.A., Shesterikova E.M., Babina D.D., Podlutsky M.S., Blinova Ya.A., Volkova P.Yu.*, Bondarenko E.V.

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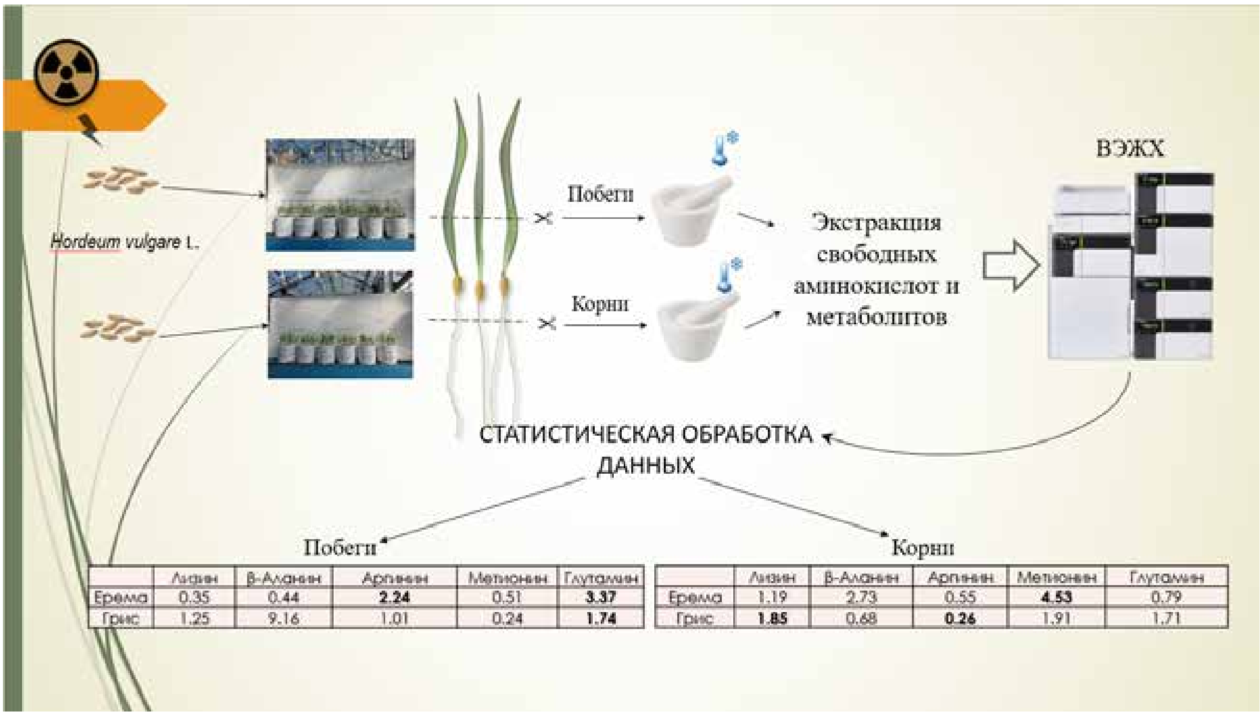
Exposure to low doses of γ-radiation on agricultural seeds in some cases leads to the stimulation of plant growth and development. Improving the overall tolerance of plants to environmental stressors is a major focus of agrobiology, while the study of changes in metabolic pathways in response to stress may be the key to developing resistant plants. The active development of omics-technologies opened up many opportunities for finding determinants of the tolerance of living organisms to the harmful effects of the environment and allowing the analysis of large arrays of biological data. These technologies are indispensable for finding the determinants of molecular tolerance to a variety of stressors. To determine the metabolic pathways involved in the occurrence of the effect of radiation hormesis, we studied changes in the concentrations of five proteinogenic amino acids. A method, determining the concentration of target metabolites was developed using an HPLC system. A correlation was found between the mass of shoots of the studied barley varieties and the change in the concentration of free glutamine, which presumably plays an important role in establishing the hormesis effect.

The main publications of authors on the subject of the abstract:

Volkova, P.Y. et al. Early response of barley embryos to low- and high-dose gamma irradiation of seeds triggers changes in the transcriptional profile and an increase in hydrogen peroxide content in seedlings. J Agro Crop Sci 2020, P. 206, P. 277–295, doi:10.1111/jac.12381.

Pishenin, I.; Free Amino Acids and Methylglyoxal as Players in the Radiation Hormesis Effect after Low-Dose γ-Irradiation of Barley Seeds. Agriculture 2021, 11, 918. https://doi.org/10.3390/agriculture11100918



Побеги

	Лизин	β-Аланин	Аргинин	Метионин	Глутамин
Ерема	0.35	0.44	**2.24**	0.51	**3.37**
Грис	1.25	9.16	1.01	0.24	**1.74**

Корни

	Лизин	β-Аланин	Аргинин	Метионин	Глутамин
Ерема	1.19	2.73	0.55	**4.53**	0.79
Грис	**1.85**	0.68	**0.26**	1.91	1.71

Genetic and agronomic characteristics of donors of valuable wheat traits

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Siberian reserch institute of Plant Production and Breeding - Branch of Federal State Budget Scientific Institution "The Federal Research Center Institute of Cytology and Genetics of siberian Branch of the Russian Academy of Sciences", Novosibirsk, Russia,

*Federal Research Center the N.I. Vavilov All-Russian Institute of Plant Genetic Resources, Saint-Petersburg, Russia

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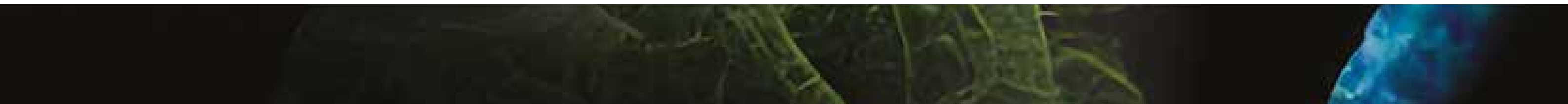
The main factors that reduce yields are the interaction of the variety genotype with growing conditions and disease damage, so it is necessary to identify donors of resistance and high expression of valuable traits that have a different genetic nature. Infection of 49 wheat samples with soft leaf rust population, two monopustular isolates with virulence p9, p24 and in the field was assessed. The experimental data of field observations and the structure of the yield of lines were obtained using the VIR method. Varieties (carrying the Lr24 gene) KWS Buran, KW 340-3-13 and Etyud, which form the yield at the level of the best standard Sibirskaya 17 (417.2-514.1 g/m²) can be used in breeding. Variety Omskaya 44 (yield 440.8 g/m²) can be used as a donor of resistance gene Lr19 and partially effective Lr26. The breeding value of CS2A/2M (Lr28) and Pavon (Lr47) varieties under the conditions of Western Siberia is low. Varieties Doka (plant height 66.5 cm, yield 589.2 g/m2) and Cheshskaya 17 (80.0 cm, 547.7 g/m2) can be used in breeding for resistance and short stems, without reducing winter hardiness and yield in conditions of Western Siberia.

Study was supported by FWNR-2022-0037.

The main publications of authors on the subject of the abstract:

Skolotneva E.S. et al. Effectiveness of leaf rust resistance genes against Puccinia triticina populations in Western Siberia during 2008-2017 // Journal of Plant Diseases and Protection (2018) 125:549-555.

Piskarev V.V. et al. Sources for the breeding of soft spring wheat in the conditions of Novosibirsk region // Vavilovskii Zhurnal Genetiki i Selektsii = Vavilov Journal of Genetics and Breeding. 2018;22(7):784-794. DoI10.18699/VJ18.422 (in Russian).



Identification of Single Nucleotide Polymorphisms in the genomes of *A. thaliana* from the area contaminated due to the accident at the Chernobyl Nuclear Power Plant

Podlutskii M.S., Voronezhskaya V.S., Shesterikova E.M., Babina D.D., Korol M.Yu., Kazakova E.A., Volkova P.Yu.*

Russian Institute of Radiology and Agroecology, Obninsk, Russia,
*Independent Researcher, Geel, Belgium
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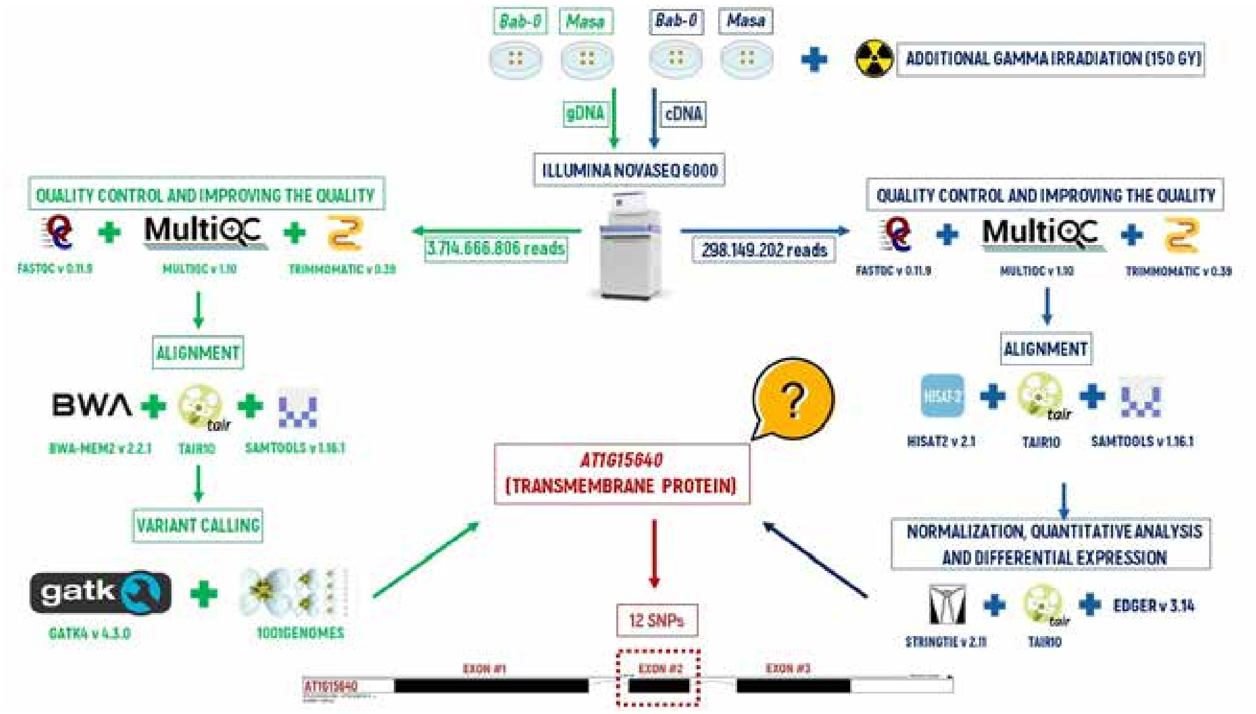
Seeds of A. thaliana plants were collected at two experimental plots in the Polesye State Radiation-Ecological Reserve (Republic of Belarus) with different levels of radioactive pollution: Babchin (*Bab-0*, 0.3 μGy/h) and Masany (*Masa*, 8.0 μGy/h).

A total of 310.240 single nucleotide polymorphisms (SNPs) were identified for *A. thaliana* seedlings obtained from *Bab-0*, while 439.783 SNPs were identified for seedlings obtained from *Masa.* For each accession, a shared set of 12.368 SNPs was identified among non-annotated SNPs in "1001Genomes", as well as 3.744 SNPs (*Bab-0*) and 20.849 SNPs (*Masa*) with the greatest potential to elucidate plant adaptation to radiation exposure.

Through a transcriptome analysis of seedlings obtained from *Masa*, 46 genes were identified as differentially expressed in response to acute additional gamma irradiation, including a candidate resistance gene – *AT1G15640* (a transmembrane protein). Within the exon region of the *AT1G15640*, 12 SNPs were identified that may have the potential to alter the transformation and corresponding functional characteristics of the protein, potentially promoting resistance to chronic radiation exposure in *A. thaliana* plants.

<u>The main publications of authors on the subject of the abstract:</u>

Podlutskii M.S. et al. Arabidopsis thaliana Accessions from the Chernobyl Exclusion Zone Show Decreased Sensitivity to Additional Acute Irradiation // Plants (2022) 11:3142. doi:10.3390/plants11223142



Genetic diversity of Ledum species on Sakhalin Island: data from chloroplast DNA markers

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The Labrador Teas (subsection Ledum, genus Rhododednron) are a group of highly polymorphic evergreen shrubs common in the Northern Hemisphere. Their nomenclature and taxonomy are still not clarified. The problem of delimiting these species is associated with the gradual transition of morphological features and with adaptive plasticity. There are four species distinguished in Russia: R. tomentosum, R. subarcticum, R. tolmachevii and R. hypoleucum. The ranges of the species overlap on Sakhalin. We evaluated the effectiveness of cpDNA markers for the estimation of the genetic diversity level and the elucidation of the relationships within subsection. A high genetic variability was revealed. The haplotype diversity of five chloroplast intergenic spacers (trnH-psbA, petB-petD, trnV-ndhC, K2R-K707, atpB-rbcL) was quite high.

There were 16 haplotypes identified; no species-specific ones were found. AMOVA indicate that about 37% of the genetic diversity is due to among population differences. Molecular phylogenetic analysis didn't reveal a clear species structure, but revealed a trend towards the isolation of two genetic groups: a group from the southern and the middle parts of Sakhalin.

This research was financially supported by a grant from the Russian Science Foundation, No 23-24-00173, https://rscf.ru/project/23-24-00173/

Take-home message:

The complex of the sympatric Ledum subsect. species on Sakhalin is extremely genetically diverse. Phylogenetic analysis based on cpDNA revealed a trend towards the isolation of two genetic groups from the southern and the middle parts of Sakhalin.

Identification of non-annotated genes involved in the grain development

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Transcriptomics refers to the search for a connection between the abundance of identified transcripts with changes at certain stages of plant development, including the formation of the ear, which tends to change rapidly. Understanding how each stage of development is controlled, both of the ear as a whole and of the grain, is complicated by the presence of multigenic families encoding many enzymes in various biochemical pathways and their interactions.

Here, a comprehensive transcriptomic analysis was carried out using long cDNA readings and direct RNA sequencing at different stages of development of triticale grains (10, 15, 20 days after flowering). The results showed that 17%(7128) of the expressed genes were in the A, B and R genomes of triticale, which were not annotated in the wheat and rye genomes as transcriptionally active, and lncRNAs make up more than 10% of the transcriptome, which emphasizes their involvement in many biological processes.

This research was funded by the Ministry of Education and Science of Russian Federation (goszadanie No. FGUM-2022-0005).

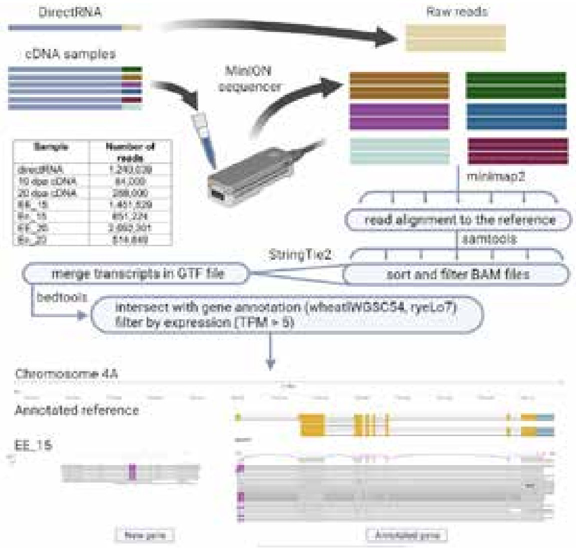
The main publications of authors on the subject of the abstract:

Polkhovskaya E. et al. Long-Read cDNA Sequencing Revealed Novel Expressed Genes and Dynamic Transcriptome Landscape of Triticale (x Triticosecale Wittmack) Seed at Different Developing Stages //Agronomy (2023) 13(2): 292.

Polkhovskaya E. S. et al. Identification of unannoted genes of grain development using Nanopore sequencing //Genetic and radiation technologies in agriculture (2022): 35-37.

Take-home message:

Modern sequencing technologies make it possible to obtain the distribution of genes that are expressed differently during the ear development, and to identify new genes, which can lead to the emergence of new genes with valuable functions for humans.



The cellular localization and plant transcriptome response to the overexpression of the virus-like particle protein GAG

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LTR retrotransposons (LTR-RTs) are mobile elements that occupy a significant portion of the genome in most plant species. The LTR-RT life cycle is very similar to that of retroviruses and involves the assembly of a virus-like particle from GAG proteins, which interact and encapsulate LTR-RT RNA. In animal cells, this process takes place in special organelles, retrosomes. Whether retrosomes are present in plant cells remains unclear. To study the cellular localization of the GAG LTR-RT protein, we performed transient expression in the cells of several plant species. We showed that in all the studied species, GAG as well as the dGAG (domesticated GAG) protein form protein aggregates with extranuclear localization. RNAseq analysis of transgenic Arabidopsis thaliana plants with GAG overexpression was performed to assess the effect of GAG on the cell transcriptome. Significant changes of genes expression involved in the plant response to biotic stimuli (more than 200 genes) and a decrease in the expression of genes responsible for photosynthesis and cell division were observed.

This work was supported by grant no. 22-74-10055 from the Russian Science Foundation.

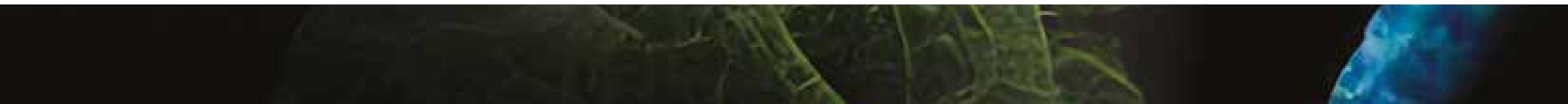
The main publications of authors on the subject of the abstract:

Kirov I.V. et al. Epigenetic Stress and Long-Read cDNA Sequencing of Sunflower (Helianthus annuus L.) Revealed the Origin of the Plant Retrotranscriptome // Plants 2022, 11, 3579. https://doi.org/10.3390/plants11243579

Take-home message:

GAG as well as the dGAG (domesticated GAG) protein form protein aggregates with extranuclear localization.

GAG overexpression leads to significant changes in plant transcriptome.



In vivo localization of whole *Arabidopsis thaliana* gyrase subunits and their transcription changes in response to phytohormone application

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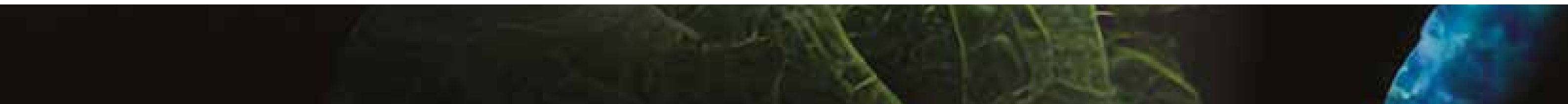
Plant gyrase plays a crucial role in DNA replication and transcription in plant cells. Similar to bacterial gyrase, it is a type II topoisomerase that catalyzes cleavage and rejoining of double-stranded DNA to relieve topological stress during DNA replication and transcription. Moreover, it can be inhibited and trapped on DNA by certain antibiotics such as ciprofloxacin. Plant gyrase consists of two GyrA and two GyrB subunits, which interact to form a heterotetrameric complexes. It is believed that gyrase complex localization depends on its composition, since there are three different genes coding Gyrase B and only one gene encoding Gyrase A, in case of *Arabidopsis thaliana* genome.

In this study we performed transient expression of whole *Arabidopsis thaliana* gyrase subunits fused with GFP to analyze their localization in *Arabidopsis thaliana in vivo.* We were able to observe strong correlation of Gyrase A subunit localization with chloroplasts and Gyrase B3 with nucleus. We also analyzed changes of gyrase genes transcription due to various phytohormone applications. Cytokinin application caused increase in Gyrase A, Gyrase B1 and Gyrase B2 transcription rate.

<u>The main publications of authors on the subject of the abstract:</u>

Sutormin DA, Galivondzhyan AK, Polkhovskiy AV, Kamalyan SO, Severinov KV, Dubiley SA. Diversity and Functions of Type II Topoisomerases // Acta Naturae. 2021 Jan-Mar;13(1):59-75. doi: 10.32607/actanaturae.11058. PMID: 33959387; PMCID: PMC8084294.



Кластеризация генетических ресурсов для использования в селекции озимой тритикале

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В коллекциях разных стран хранится около 16000 образцов тритикале, из которых более 11700 сосредоточены в 23 генбанках 18 стран Европы. Поскольку у тритикале нет диких предков, а гибридное происхождение образцов часто неизвестно, сохранение уникальных комбинаций генов необходимо для дальнейшего использования в селекции. В последнее десятилетие результаты российской селекции тритикале впечатляют. Создание и выявление селекционно-ценного исходного материала тритикале для условий Поволжского региона предполагает оценку свыше 250 образцов озимой тритикале по более чем 30 хозяйственно-полезным показателям. Использование в нашей работе кластерного анализа позволяет учесть всю совокупность оцениваемых признаков и определить генетическую структуру исходного материала. На основе кластерного анализа отобраны группы высокоурожайных образцов и генотипы с отдельными улучшенными характеристиками. Путем внутривидовой гибридизации выделенных источников хозяйственно-ценных признаков из разных кластеров создан качественно новый материал озимой тритикале для успешной селекции.

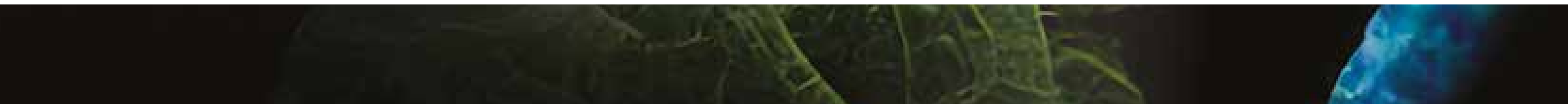
The main publications of authors on the subject of the abstract:

Пономарев С.Н. и др. Урожайность и содержание белка в зерне коллекционных образцов озимой тритикале//Аграрная наука Евро-Северо-Востока (2021).22(4):495-506 DOI: 10/30766/2072-9081.2021.22.4.495-506

Пономарев С.Н. и др. Кормовая ценность сортов озимой тритикале в Средневолжском регионе// Достижения науки и техники АПК. (2018). т.32. №7:47-51. DOI: 10.24411/0235-2451-2018-10711

Take-home message:

Кластерный анализ является перспективным методом прогнозирования селекционной ценности значительного количества коллекционных образцов озимой тритикале при создании нового исходного материала.



Genetic resources of winter rye for fundamental and applied breeding purposes

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Rye is a clearly underappreciated cereal crop used for food and feed purposes, as well as raw material for energy production. According to the FAO declaration (2020), the world genetic resources of rye currently include only 26100 accessions. This germplasm is largely unevaluated for potentially useful traits. Research goals for winter rye genetic resources include the following:1) fundamental knowledge of processes in plants, including gene structure, function, and expression;2) methodologies for application in product development; 3) a gene pool for research and breeding; and 4) varieties for direct use in agriculture. The development of population and hybrid breeding in winter rye is conceptually similar: find the gene resource; introduce it into the plant population; select plants with desirable combinations of traits; evaluate the material for economic and adaptive traits; and release a new variety for general use. Marker-assisted selection (MAS) and genomic (GWAS, GS) selection in general do not change this sequential process, but they provide new opportunities for the breeder and greatly accelerate the selection of individual steps and the breeding process as a whole.

The main publications of authors on the subject of the abstract:

Ponomareva M. et al. Resistance to Snow Mold as a Target Trait for Rye Breeding //Plants (2022). 11: 2516. DOI: 10.3390/plants11192516

Ponomareva M. et al. Snow mold of winter cereals – a complex disease and a challenge for resistance breeding //Theoretical and Applied Genetics (2021) 134:419-433 DOI: 10.1007/s00122-020-03725-7

Take-home message:

Characterization of winter rye genetic resources is necessary for breeding new target varieties. Assessment of rye gene pool is the first step to enhance genetic diversity and should be effectively included in fundamental and application research.

Определение содержания биологически активных соединений в каллусных культурах *Hyssopus officinalis* L.

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Соединения, содержащиеся в иссопе лекарственном (*Hyssopus officinalis* L.), обладают рядом важных фармакологических эффектов. Каллусные культуры могут стать перспективным биотехнологическим методом для получения ценных биологически активных веществ. Определение содержания фенольных соединений, флавоноидов, гидроксикоричных кислот проводилось по стандартным методикам. Антиоксидантная активность оценивалась методом DPPH. Высокое содержание фенольных соединений и гидроксикоричных кислот показали экстракты каллусных культур, культивируемых на средах MS-6 (35,5 ± 1,2 мг экв. галловой кислоты/г сухой массы (СМ) и 82,5 ± 2,6 мг экв. розмариновой кислоты/г СМ соответственно) и MS-1 (29,3 ± 1,2 мг экв. галловой кислоты/г СМ и 62,1± 0,6 мг экв. розмариновой кислоты/г СМ соответственно). Наибольшее количество флавоноидов наблюдалось в каллусных культурах, выращенных на среде MS-1 (2,4 ± 0,2 мг экв. рутина/г СМ) и MS-3 (2,4 ± 0,4 мг экв. рутина/г СМ). Высокая антиоксидантная активность наблюдалась в каллусных культурах, выращенных на среде MS-6 (127,9 ± 5,6 мг экв. аскорбиновой кислоты/г СМ) и MS-5 (74,1 ± 6,3 мг экв. аскорбиновой кислоты/г СМ).

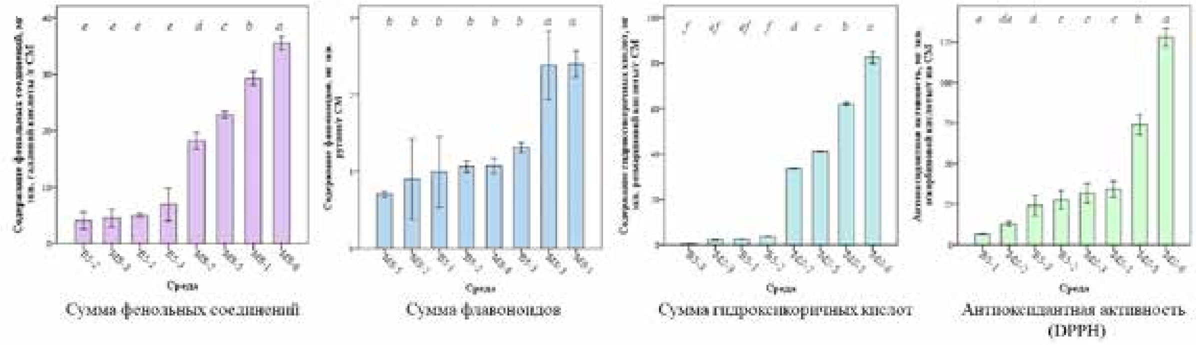
The main publications of authors on the subject of the abstract:

Пунгин А.В., Попова Е.А., Ларцева Л.О. Повышение синтеза вторичных метаболитов в культуре бородатых корней Hyssopus officinalis L. // Вестник балтийского федерального университета им. И. Канта. Серия: естественные и медицинские науки. – 2022. – №. 1. – С. 98-107.

Попова Е.А. Влияние аминокислот на содержание биологически активных веществ культуры бородатых корней Hyssopus officinalis L. // ХимБиоSeasons 2022 : Сборник тезисов докладов Форума молодых исследователей (2022) – С. 33.

Take-home message:

Наибольшее содержание биологически активных веществ отмечено в каллусной культуре, выращенной на средах MS-1 и MS-6. Высокая антиоксидантная активность отмечена в экстракте каллусной культуры, культивируемой на среде MS-6.



Сумма фенольных соединений

Сумма флавоноидов

Сумма гидроксикоричных кислот

Антиоксидантная активность (DPPH)

(разными буквами отмечены достоверно различающиеся значения, ANOVA с критерием Тьюки: $p \leq 0{,}05$)

Analysis of immune Vitis ssp. genome introgressions into Russian grapevine germplasm to promote breeding of resistant varieties

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Intraspecific diversity of the immune grape Muscadinia rotundifolia can serve as a source of resistance loci to the most widespread pathogens and pests of grapevine. We report results of the project focused on identifying genomic introgressions of Muscadinia into Russian grapevine breeding germplasm. 12,734 SNPs were revealed as the result of RADseq-based genotyping of 144 grapevines. 52 of the SNPs were significantly associated with 21 chromosome intervals conferring resistance of grapes to pests and mildew pathogens. 10 identified intervals contain the previously reported resistance loci. Two SNPs on LGs 14 and 18 were found in the exons of putative candidate genes, making these genes a perfect target for editing.To facilitate the further discovery of valuable loci in Muscadinia, we constructed a high-density linkage map using a mapping population obtained from the self-pollination of M. rotundifolia cv. Dixie – the only Muscadine variety maintained alive in Russia. 3730 SNPs were ordered across 20 linkage groups. QTLs were discovered on LG14 and LG18, affecting the morphological traits associated with the adaptability of young Muscadinia vines in the conditions of Crimea.

The main publications of authors on the subject of the abstract:

Lytkin K. et al. Development of a High-Density Genetic Map for Muscadine Grape Using a Mapping Population from Selfing of the Perfect-Flowered Vine ‘Dixie’ // Plants (2022), 11:3231. https://doi.org/10.3390/plants11233231

Vasylyk I. et al. SNPs Associated with Foliar Phylloxera Tolerance in Hybrid Grape Populations Carrying Introgression from Muscadinia // Horticulturae (2022) 8:16 https://doi.org/10.3390/horticulturae8010016

Take-home message:

The Crimean grape breeding genepool was characterized in terms of chromosomal localization of introgressions from Muscadinia rotundifolia, carrying genes of resistance to phylloxera, downy and powdery mildew.

Use of perennial wheat accessions in the winter wheat breeding under conditions of the southern forest-steppe of Western Siberia

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The untapped potential of perennial wheat as a starting material for expanding genetic diversity when creating new varieties of winter wheat is an important direction in winter wheat breeding. On the experimental field of Omsk SAU in 2019–2022 a study of perennial wheat samples was performed. These accessions were obtained by crossing of the common wheat varieties with wheatgrass species *Th. ponticum, Th. elongatum,* and *Th. intermedium*. It was found that accessions A 235 and Otrastayutsaya 38, obtained on the basis of wheatgrass *Th. elongatum* and wheatgrass *Th. intermedium,* were characterized by increased winter hardiness (78–90%). Depending on the meteorological conditions of the year, accessions 11955, TAF46, and Otrastayutsaya 38 are capable of producing an acceptable yield level (in average 239–289 g/m^2). Under conditions of dry years, a significant correlation of the thousand kernel weight with the upper internode length (r = 0.54), the flag leaf length (r = 0.55 to 0.71), and productive tillering (r = 0.55 to 0.70) was noted.

This study was conducted with financial support from the Russian Science Foundation (project No. 23-16-20006, dated April 20, 2023).

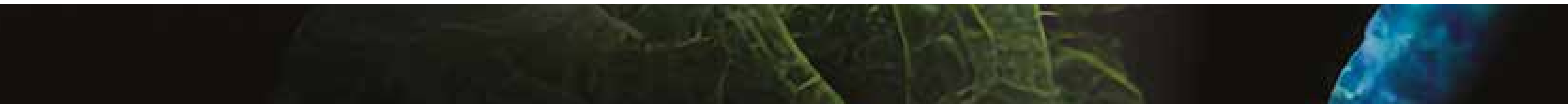
The main publications of authors on the subject of the abstract:

1. Shamanin V.P. et al. Large-grained wheatgrass variety Sova (Thinopyrum intermedium) as an alternative to perennial wheat // Sel'skokhozyaistvennaya Biologiya (2021) 56(3): 450-464.

2. Pototskaya I.V. et al. The usage of wheatgrass (Thinopyrom intermedium) in the breeding (Review). Vavilov Journal of Genetics and Breeding. 2022; 26 (5): 413-421. doi: 10.18699/VJGB-22-51.

Take-home message:

Varieties of perennial wheat, primarily forage, can provide a public demand for the greening of the crop industry and the formation of a global trend - multifunctional agriculture.



How do MtLEC1 and MtL1L work in *Medicago truncatula* during somatic embryogenesis

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Somatic embryogenesis (SE) is widely used in biotechnology as a regeneration process conditioning many plant transformation methods, artificial seeds obtaining and zygotic embryogenesis studying. We are exploring the functions of main SE regulators - LEC1 and LEC1-like - in *Medicago truncatula* via analyzing their overexpression and loss-of-function effect on embryo formation. MtLEC1 loss of function plants were obtained by using CRISPR/Cas9 technology. MtLEC1 and MtL1L, which belong to the NF-YB family, are able to interact with proteins NF-YA and NF-YC, and the resulting complex can bind a specific DNA motif. Using a yeast two-hybrid system, we identified potential partners of MtLEC1 and MtL1L in the NF-Y family, whose genes demonstrated high levels of expression during SE. We confirmed our choice by transcriptome analysis of contrasting embryogenic R108 and non-embryogenic 108-1 M.truncatula lines. These results enabled us to initiate coexpression experiment on the selected NF-YA, B and C genes.

The research was supported by the Ministry of Science and Higher Education of the Russian Federation Agreement 075-10-2021-093, Project PBB-RND-2243.

The main publications of authors on the subject of the abstract:

Potsenkovskaia E.A. et al. Novel NF-Y genes expressed during somatic embryogenesis in Medicago truncatula //Plant Gene (2022) 31:100364. doi:10.1016/j.plgene.2022.100364

Take-home message:

MtLEC1 loss of function plants were obtained by using CRISPR/Cas9 technology.

Potential partners of MtLEC1 and MtL1L were identified in the NF-YA and NF-YC families and coexpression experiment was initiated.

Barley growth rate and gene expression after different types of irradiation

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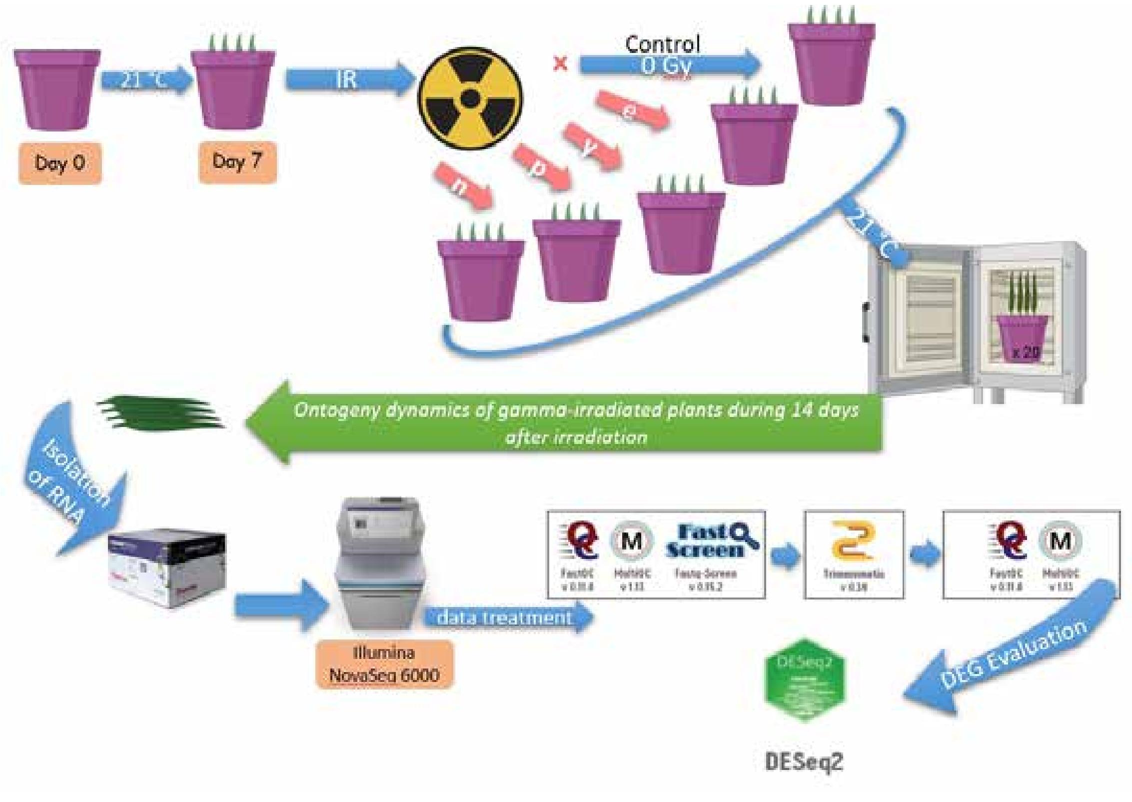
The object of the study was winter barley (cultivar Fox 1). On the 7th day of germination, the plants were irradiated with different types of ionizing radiation (IR) (gamma, electron, proton, neutron). Every day for 14 days, the rate of development of each plant was assessed. In a subsequent experiment under the same conditions, RNA was isolated after 24 hours for subsequent evaluation of differential gene expression.

Plants that were exposed to any kind of IR significantly slowed down the rate of germination. On the 14th, last, day of observation, it was noted that the plants of the control group not only developed faster within one stage, but also moved to the next one, which was not achieved by any of the irradiated groups. However, the neutron irradiated group has several plants several stages higher than the other irradiated groups.

When studying the response reactions of barley after exposure to various types of ionizing radiation, common differentially expressed genes were elucidated; the total number was 47. Common genes with negative DEG (decreased expression) were not found.

<u>Take-home message:</u>

Investigation of the influence of various types of ionizing radiation for search for common adaptive response genes



The genetic diversity of buckwheat with a focus on self-compatible lineages

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Common buckwheat is an obligate cross-pollinated plant. It prevents self-pollination through heterostyly, which means it has two types of flowers: short-styled and long-styled. The self-incompatibility mechanism is controlled by the S-locus. However, the mutants with break of self-incompatibility are known. The study of such mutants helps to uncover the mechanisms of self-incompatibility; they are also a prospective material for buckwheat breeding. Here we report results of analysis of three self-compatible lines: short-styled KK5 and KK8, and Shinano-SC using whole-genome sequencing. We reconstructed phylogenetic tree that includes multiple cultivars and accessions of common buckwheat. It shows that all self-compatible lines arose independently. Also we analyzed the sequences of S-ELF3, a gene that is known to play a role in self-incompatibility and which is disrupted in self-compatible species and long-styled plants. A frameshift deletion was found in the Shinano-SC. However, no high effect mutations were found in KK5 and KK8, what may indicate that S-ELF3 is functional in this species.

The study is supported by the project №075-15-2021-1064.

The ICAnnoLncRNA pipeline for a Long-Non-coding-RNA identification and Annotation in Transcriptomic Data

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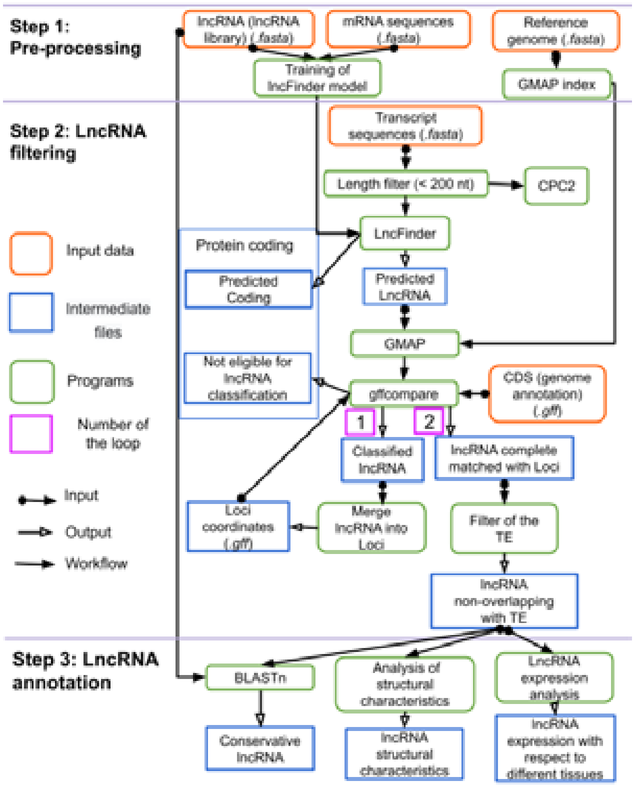
Long non-coding RNAs (lncRNAs) are molecules of more than 200 nucleotides in length that do not encode proteins. LncRNAs play essential roles in different regulatory processes in animals and plants. Existing pipelines often develop lncRNA recognition models using well-annotated data from a limited number of model organisms. This makes it difficult to apply this pipelines forgrowing transcriptomic data. In the present work, we developed automatic bioinformatics pipeline ICAnnoLncRNA for identification and analysis of lncRNA sequences in assembled transcriptomic sequences. The pipeline includes: Pre-processing, LncRNA filtering and LncRNA annotation. We analysed 15 maize transcriptome libraries from different plant tissues/organs. We identified 61,004 (9%) lncRNAs. Homologous search for lncRNAs identified in study among sequences from databases revealed - 643 maize lncRNA transcripts similar with lncRNAs in other plants. The largest numbers of homologues found in O.sativa. Analysis of the expression of newly detected lncRNAs points to high expression of them in the tassels of maize. The work was funded by the Kurchatov Genome Center of the FRC-IC&G SB RAS, № 075-15-2019-1662.

<u>Take-home message:</u>

The proposed automatic pipeline made it possible to identify 61,004 new lncRNAs in maize genome, classified into classes depending on their localization in the genome, annotate them and evaluate their structural features.



A collection of genes for high protein and gluten content in grain introgressed into bread wheat from relative species: intra-chromosomal localization, molecular markers and agronomic effects

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Protein and gluten content in wheat grain are the most important indicators in determining the grain class in accordance with Russian and international trade standards. They are also one of the most difficult to predict under genotype selection in breeding and in marketable grain production. This is because the genetic control of protein and gluten content is poorly understood and the number of donors for this trait are limited. The results of a long-term work will be presented on the transfer of introgressions from the five relative species from genus *Triticum* and *Aegilops* into the bread wheat chromosomes that carry genetic factors increasing the target traits. A collection of lines carrying the introgressions was created on the same genetic background of the Saratovskaya 29 variety. It makes it possible to compare their effects on both target and other agronomic traits. Introgressions are studied and marked with microsatellite markers within a particular chromosome. The lines were studied in terms of protein and gluten content and yield components both in greenhouse and field conditions. Financial support: Russian Science Foundation (23-26-10046) and Novosibirsk Region (p-59).

Take-home message:

The genes that increase protein and gluten content in grain were extracted from the bread wheat relative species *T. timopheevii, T. durum, Ae. speltoides, Ae. markgrafii* and *Ae. tauschii.* Molecular markers designate their intra-chromosomal positions.

Genetic diversity of invasive plant *Heracleum sosnowskyi*

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Geltman D.V.**, Penin A.A., Logacheva M.D.*****

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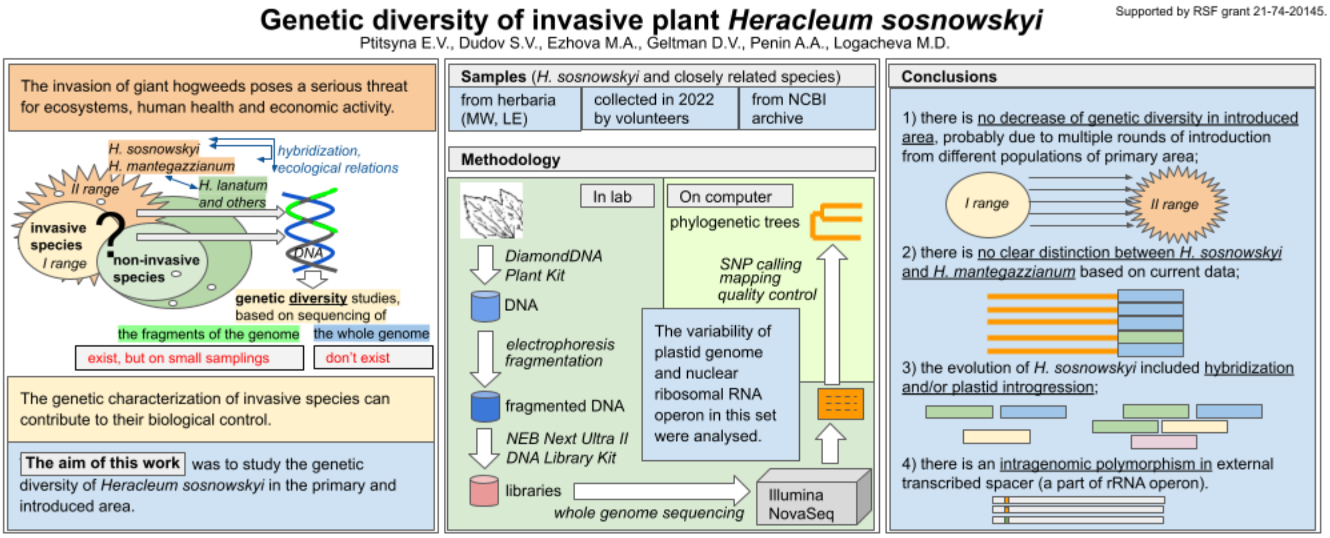
The invasion of giant hogweeds poses a serious threat for ecosystems, human health and economic activity. The genetic characterization of invasive species can contribute to their biological control. The aim of this work was to study the genetic diversity of Heracleum sosnowskyi in the primary and introduced area. We investigated a set of Heracleum samples obtained from herbaria (MW, LE) and collected in 2022 by volunteers using whole genome sequencing, complemented with sample from NCBI archive. Our data included closely related species such as H. mantegazzianum, also with high invasive potential. We analyzed the variability of plastid genome and nuclear ribosomal RNA operon in this set. Our results show that: 1) there is no decrease of genetic diversity in introduced area, probably due to multiple rounds of introduction from different populations of primary area; 2) there is no clear distinction between H. sosnowskyi and H. mantegazzianum based on current data; 3) the evolution of H. sosnowskyi included hybridization and/or plastid introgression; 4) there is an intragenomic polymorphism in external transcribed spacer (a part of rRNA operon).

Supported by RSF grant 21-74-20145.



Genetic diversity of invasive plant *Heracleum sosnowskyi*

Ptitsyna E.V., Dudov S.V., Ezhova M.A., Geltman D.V., Penin A.A., Logacheva M.D.

Supported by RSF grant 21-74-20145.

The invasion of giant hogweeds poses a serious threat for ecosystems, human health and economic activity.

The genetic characterization of invasive species can contribute to their biological control.

The aim of this work was to study the genetic diversity of *Heracleum sosnowskyi* in the primary and introduced area.

Samples (*H. sosnowskyi* and closely related species)

from herbaria (MW, LE)	collected in 2022 by volunteers	from NCBI archive

Methodology

The variability of plastid genome and nuclear ribosomal RNA operon in this set were analysed.

Conclusions

1) there is no decrease of genetic diversity in introduced area, probably due to multiple rounds of introduction from different populations of primary area;

2) there is no clear distinction between *H. sosnowskyi* and *H. mantegazzianum* based on current data;

3) the evolution of *H. sosnowskyi* included hybridization and/or plastid introgression;

4) there is an intragenomic polymorphism in external transcribed spacer (a part of rRNA operon).

Regulation of the Respiration Process in Potato Plants Transformed with the Bt-Gene

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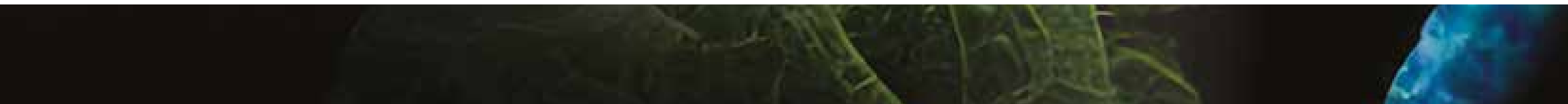
Research on insecticidal Bt-crops is mainly concerned with their effects on the environment. Physiological processes remain poorly understood. The purpose was to study the effect of zinc and boron trace elements on the respiration intensity of germinating tubers of potato with the Bt-gene. Options included soaking tubers in 10-3 M solutions of $ZnSO_4$ or H_3BO_3. The intensity of respiration was determined by the amount of CO_2 released, the content of IAA and ABA - by the ELISA method. After 72 hours from the beginning of germination, the eyes of the transgene tubers had a 25% lower respiration intensity against the background of a higher content of ABA, but a lower IAA. Trace elements increased breathing. A greater effect was noted in transformants with zinc. After 30 days, respiration in the shoots decreased by 24% in plants with the Bt-gene and by 11% in the original plants. The transgenes contained 20% less IAA. In shoots, boron was more effective than zinc against the background of a higher IAA/ABA ratio. A conclusion is made about the participation of boron and zinc in the regulation of the respiration process through a change in the hormonal status of plants with the Bt-gene.

<u>The main publications of authors on the subject of the abstract:</u>

Puzina, T. I. Changes in the Hormonal Status and Photosynthesis of Potato Plants Transformed by the Bt Gene / T. I. Puzina, V. V. Korol, I. Y. Makeeva // Biology Bulletin. – 2021. – Vol. 48. – No 5. – P. 555-560. – DOI 10.1134/S1062359021050137. – EDN CJTGIY.



Melanization of the lichen *Lobaria pulmonaria* (L.) Hoffm. as a stress response to UV-B irradiation

Rassabina A.E., Daminova A.G., Khabibrakhmanova V.R., Minibayeva F.V.

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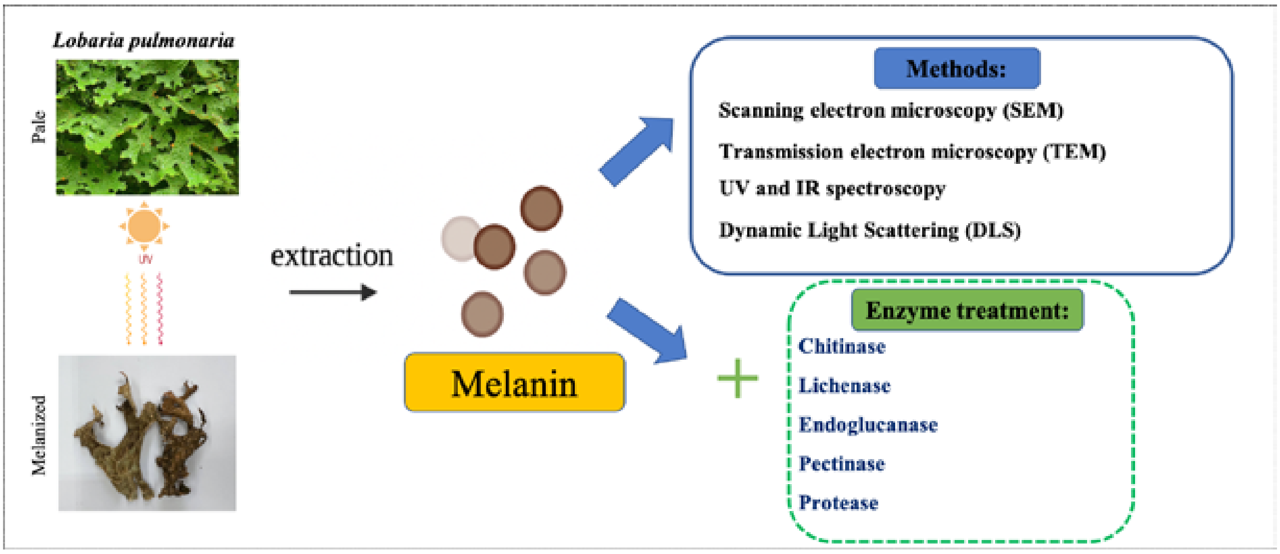
In the study of the mechanisms of stress tolerance, special attention is given to symbiotic organisms - lichens. The high stress tolerance of lichens is due to the presence of a number of secondary metabolites, including a dark pigment melanin. Among melanins, lichen melanin is the least studied. The lichen *Lobaria pulmonaria* (L.) Hoffm. accumulates melanin in the upper cortex in response to intense UV irradiation. Using scanning electron microscopy (SEM) and transmission electron microscopy (TEM), it was found that melanization changes the morphology of the lichen thallus. The treatment of thalli with hydrolytic enzymes increased the yield of melanin and caused the release of carbohydrates and phenols from melanized thalli. These results suggest that in lichen thalli, melanin can form associations with carbohydrates, and thereby can strengthen the melanized upper cortex and contribute to the survival of lichens under UV-B stress. Lichen melanins possess high photoprotective, antioxidant and adsorption activities due to the presence of hydroxyl and carboxyl groups.

This work was supported by RSF (grant № 23-14-00327).

<u>The main publications of authors on the subject of the abstract:</u>

Daminova A.G. et al. Effect of melanization on thallus microstructure in the lichen Lobaria pulmonaria // Journal of Fungi (2022) 8: 791. doi: 10.3390/jof8080791.



Fungal and microbiome communities of soils in Chernevaya taiga of Western Siberia

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Kulemzina A.I.**, Lapidus A.L.**

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**Institute of Molecular and Cellular Biology SB RAN, Novosibirsk, Russia
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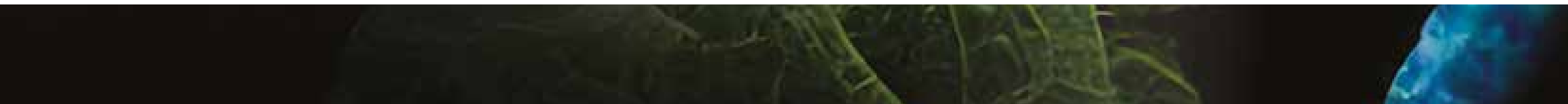
Chernevaya taiga of Western Siberia is a unique ecosystem characterised by gigantism of perennial grasses and shrubs. While the phenomenon of gigantism has been previously studied from the perspective of climate and soil studies, the microbiota of the soil has not been deeply investigated. In our previous works, we performed a metagenomic analysis based on 16S rRNA amplicons for bacterial and ITS for fungal communities, determining their taxonomic composition.

The current study is dedicated to the analysis of the seasonal dynamics of changes in these communities. We analysed the rhizosphere of model plants (*Crepis sibirica* and *Aconitum septentrionale*) and used correlation analysis to identify keystone taxa, common to the rhizosphere of different plants at different time points. We also traced the correlation between bacteria and fungi in samples from Chernevaya taiga and control soils with dynamics across seasons. Comparison with previously obtained data from a laboratory vegetation experiment allowed us to determine which of the found taxa can be used to improve soil fertility.

The main publications of authors on the subject of the abstract:

Kravchenko I, Rayko M, Tikhonova E, Konopkin A, Abakumov E, Lapidus A. Agricultural Crops Grown in Laboratory Conditions on Chernevaya Taiga Soil Demonstrate Unique Composition of the Rhizosphere Microbiota. Microorganisms. 2022 Oct 31;10(11):2171.

Rayko M, Sokornova S, Lapidus A. Fungal metagenome of Chernevaya Taiga soils: taxonomic composition, differential abundance and factors related to plant gigantism. Journal of Fungi. 2021 Oct 27;7(11):908.



Analysis of interaction between potato eIF4E translation initiation factors and natural PVY VPgs

Razhina O.L., Lebedeva M.V., Kolesnikova V.A.

All Russia Research Institute of Agricultural Biotechnology, Moscow, Russia
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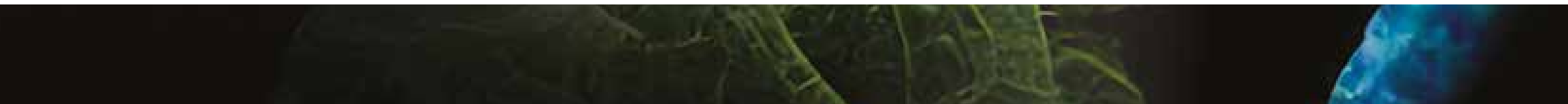
Potato virus Y (PVY) is a worldwide distributed pathogen which affects the number of plants from family Solanaceae. One of the mechanisms of PVY resistance is disrupting interaction between plant translation initiation factor elF4E and the viral protein VPg. Moreover, single mutations in the susceptibility eIF4E factor could be enough to stop the infection spreading. However, it was shown that some mutations in VPg can break plant resistance via interaction with another translation initiation factor of eIF4E multigene family.

Solanum tuberosum multigene family contains 3 translation initiation factors, elF4E-1, elF4E-2 and elF(iso)4E. Thus, we analyzed all available VPg-NTNs (the most spread and harmful PVY strain) from the NCBI database. VPg variants found in potatoes were developed in vitro conditions and tested for interaction with potato eIF4E translation initiation factors in a two-hybrid yeast system.



Comparative analysis of repeatomes sheds light on the evolution of the sex of *Elaeagnaceae*

Razumova O., Bone K., Ulyanov D., Divashuk M., Karlov G.

All-Russia Research Institute of Agricultural Biotechnology, Moscow, Russia
E-mail: razumovao@gmail.com

Dioeciousness is a rare phenomenon in the plant world. It arose repeatedly, in different ways, even in closely related species. In our work, for the first time, we performed DNA sequencing of the male and female plants of the buffalo berry (Shepherdia argentea Nutt.) and compared the resulting repeatomes with each other, as well as with repeatomes of plants of other genera of the Elaeagnaceae family - sea buckthorn and sucker. The results obtained demonstrated an independent evolution of dioeciousness in Shepherdia, apparently formed after the transition of this group to North America.

The main publications of authors on the subject of the abstract:

Razumova O.V. et al. GISH painting of the Y chromosomes suggests advanced phases of sex chromosome evolution in three dioecious Cannabaceae species (Humulus lupulus, H. japonicus, and Cannabis sativa). Protoplasma 260, 249–256 (2023). https://doi.org/10.1007/s00709-022-01774-x

Razumova O.V. et al. Sex Chromosomes and Sex Determination in Dioecious Agricultural Plants. Agronomy 2023, 13, 540. https://doi.org/10.3390/agronomy13020540

The development of oral therapeutic vaccine against cancer using "early" proteins of high-risk HPV16 on the basis of transgenic tomato plant expression system

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Siberian institute of plant physiology and biochemistry of SB RAS, Irkutsk, Russia
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Онколитическую активность "ранних" белков HPV16 E2, E6 и E7 изучали на клетках HeLa и на опухолях семенников и легких мышей, инокулированных с HeLa. E2 вызывал быстрое разрушение клеток HeLa в суспензии. E6 и E7 в сочетании с CRISPR/Cas9 разрушали клетки HeLa. Инфицирование мышей клетками HeLa приводило к опухолевому разрастанию во внутренних органах и особенно опухолей семенников. Пероральное вакцинирование мышей HPV16 E2, обуславливало регрессию опухолей семенников уже на 2-5 сутки. Инфицирование самцов и самок мышей HeLa, а также инокуляция легких приводила к быстрому развитию опухолей. Вакцинация мышей с E2 устраняла опухолевый морфогенез в легких. После вакцинации в Т лимфоцитах, выделенных из периферической крови инфицированных HeLa мышей и из спленоцитов, обнаружили значительное возрастание количества интерферона (INF), Т клеточного рецептора (TCR), CD4/CD8 лигандов, а также ферментов апоптоза: гранзима B, перфорина и гранулизина, определяемое по Элиспот.В Т лимфоцитах из легких в присутствии IgG к чекпойнту PD-1 и E2 определяли увеличение INF, TCR и CD4/CD8, а в присутствии IgG к чекпойнту PD-L1 вакцинный белок E2 увеличивал до 10 раз синтез INF, генерацию TCR и CD4/CD8.

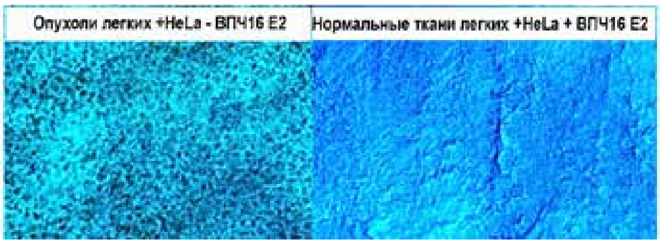
The main publications of authors on the subject of the abstract:

1. Саляев Р.К.,. Действие "ранних" белков E2, E6 и E7 папилломавируса высококанцерогенного типа ВПЧ16 на раковые клетки HeLa, вызывающие опухолевые разрастания в легких у мышей // Acta Biomedica Scientifica (2022) 7; 260-276. Doi:10.29413/ABS.2022-7.3.26

2. Саляев Р. К., . Индукция синтеза интерферона, CD4 и CD8 Т лимфоцитов в крови и в селезенке мышей, перорально вакцинированных "ранним" белком ВПЧ16 E2 // Доклады Академии Наук (2019) 488; 333-337. DOI:10.31857/S0869-56524883333-337

Take-home message:

Установлена онколитическая активность антигенных "ранних" белков HPV16 E2, E6 и E7 на модели опухолей мышей в легких и семенниках после инокуляции с раковыми клетками HeLa. Вакцинирование E2 активировало генерацию INF,TCR,CD4/CD8 в Т лимфоцитах.



Identification, characterization, and expression analysis of carotenoid biosynthesis genes in the moss *Hylocomium splendens*

Renkova A.G., Koulintchenko M.V., Mazina A.B., Leksin I.Y., Minibayeva F.V.

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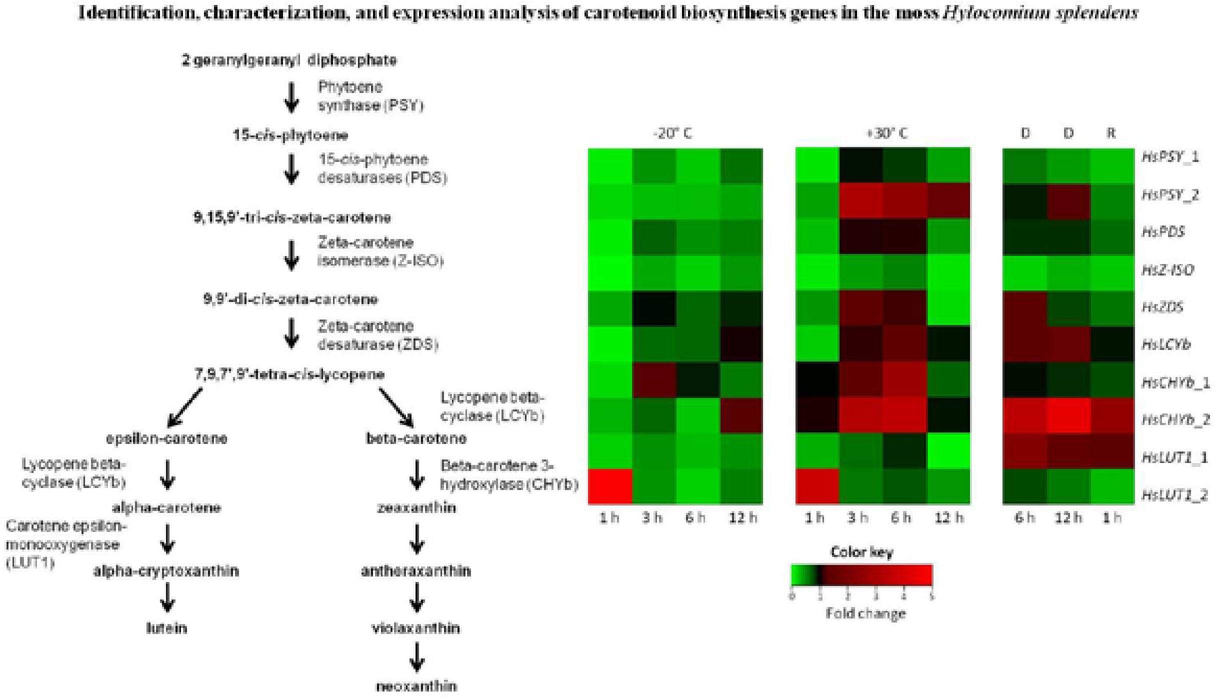
E-mail: renkova@kibb.knc.ru

Hylocomium splendens is one of the most common and widespread mosses of the circumboreal forest and tundra; however, genomic information regarding this species is limited. In this study, we performed the first comprehensive analysis of the key 10 genes of CBP in H. splendens, which were found from Metatranscriptome data deposited to the SRA in the NCBI. Multiple alignments of CBP gene sequences revealed several conserved motifs characteristic of each distinct gene. Expression analysis revealed that some of CBP genes were sensitive in response to freezing, high temperatures and desiccation/rehydration. In particular, results showed that the expression levels of *HsPSY_2, HsZDS, HsLCYb, HsCHYb* were upregulated during exposure to 30°C and desiccation. Transcript of *HsCHYb_1* was sensitive only to temperature stresses. Transcript level of *HsLUT1_2* was highest after 1 h during exposure to extreme temperatures. *HsLUT1_1* was upregulated during only desiccation/rehydration. Taken together, differential regulation of transcript levels of CBP genes during abiotic stresses was more evident in the middle and downstream genes of CBP.

This work was supported by a grant from the RSF № 22-24-00595.

The main publications of authors on the subject of the abstract:

A.G. Renkova, V.R. Khabibrakhmanova, A.V. Chasov, J.N. Valitova, E.I. Galeeva, and F.V. Minibayeva (2023) Changes in Composition and Content of Lipophilic Compounds in the Seedlings of Triticum aestivum L. Treated with Stress Phytohormones. Russian Journal of Plant Physiology, Vol. 70:6. DOI: 10.1134/S1021443722602415



Genetic resources of VIR potato collection and their use for accelerated potato breeding

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VIR holds one of the largest collections of potato and its relatives. A total 8400 accessions represent germplasm diversity including varieties (28%), landraces (42%), wild species (23%) and breeding lines (7%). Potato is the important non-cereal food crop threatened many pathogens. Late blight (LB) caused by the oomycete *Phytophthora infestans* Mont. de Bary affects potato production worldwide. The most effective way to reduce this damage is stacking several Rpi genes into varieties to provide durable resistance to LB. In this regard the study of potato germplasm in VIR collection is an urgent task. The set of accessions representing wild species, potato breeding lines and varieties was subjected to phenotypical evaluation of LB resistance and the molecular screening with well-validated SCAR markers. The structural homologs of the *Rpi-R2, Rpi-R3a, Rpi-R3b, Rpi-R8, Rpi-blb1/Rpisto1* and *Rpi-vnt1* genes were found in various species of the section Petota. Some accessions of wild species and several multiparental potato hybrids combined the markers for three even five *Rpi* genes. New germplasm and new knowledge about *Rpi* gene polymorphisms will promote development of potato breeding.

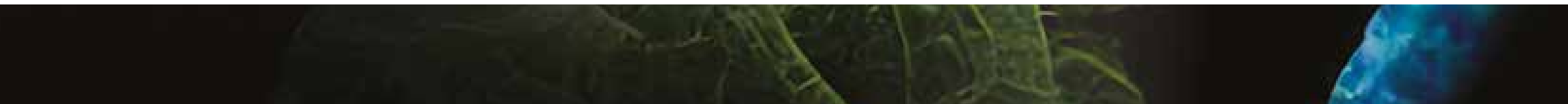
This research was supported by Russian Science Foundation, project No 22-26-00111

The main publications of authors on the subject of the abstract:

Rogozina, E.V.;Gurina,A.A.; Chalaya, N.A.; Zoteyeva, N.M.; Kuznetsova, M.A.; Beketova, M.P.; Muratova, O.A.; Sokolova, E.A.; Drobyazina, P.E.; Khavkin, E.E. Diversity of Late Blight Resistance Genes in the VIR Potato Collection. Plants 2023, 12, 273. https://doi.org/10.3390/plants12020273.

Take-home message:

Diversity of potato and related tuber-bearing species are maintained at VIR collection. Study of potato germplasm and new advanced hybrid clones will contribute to the development of genetic technologies in practical breeding program.



Antibacterial, fungicidal and insecticidal properties of novel *Bacillus* isolates suitable for crop protection

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Plant diseases and pests cause losses in crop production and storage. To decrease the ecological burden of agriculture, biological control agents including *Bacillus*-based are developed. Isolating new *Bacillus* strains and identifying their diversity are crucial for creating effective control agents and overcome pests' resistance. In the search for antibacterial, fungicidal and insecticidal activities, new 150 *Bacillus* isolates have been isolated from the soil from different regions of Eurasia. Sixty-two isolates produced inclusions, similar to those formed by insecticidal proteins. Genomes of four strains harbored genes encoding insecticidal proteins (*cry, spp, vpb*). Moreover, we observed from 25 to 40 gene clusters and 1 cluster putatively encoding antibacterial compounds and fungicidal proteins, respectively. Twenty-three isolates had antibacterial activity against crop pathogens. Hence, these isolates have a promising role in agricultural field due to discovered properties.

This work was made with the support of the Ministry of Science and Higher Education of the Russian Federation in accordance with agreement № 075-15-2021-1055 date September 28, 2021.

Take-home message:

Study of *Bacillus* isolates revealed a promising role in agricultural field due to their antibacterial, fungicidal and insecticidal properties.

Resistance of spring bread wheat varieties to stem rust in Western Siberia

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*Institute of Cytology and Genetics, Novosibirsk, Russia
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Breeders pay great attention to the search for sources of resistance among collection samples and breeding lines to involve them in the breeding when creating varieties resistant to leaf pathogens. In recent years, the State Register of the Russian Federation has included more and more varieties resistant to stem rust. A deep analysis of the genealogy of varieties shows that they have from 30 to 90 genotypes, among which >30% are resistant to fungal pathogens.Varieties Tarskaya 12 and Ishimskaya 14 were created directly with the participation of the collection samples Aranka and Augustina, respectively, in Omsk Agricultural Research Center. Most varieties resistant to stem rust were created by crossing resistant breeding lines Omskaya 37, 38, 42, 44, Uralosibirskaya, Omskaya krepost, etc. Together with scientists from the Institute of Cytology and Genetics using alloplasmic introgression wheat lines with the cytoplasm of cultivated barley Hordeum vulgare, varieties Sigma and Uralosibirskaya 2 were created, which have a high level of resistance to stem rust. In 2022 resistant varieties occupied more than 40% of the sown areas of bread spring wheatin the Omsk region.

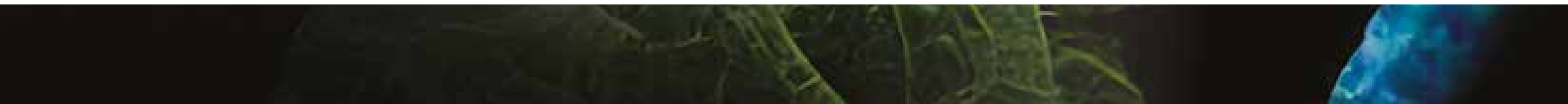
The main publications of authors on the subject of the abstract:

Resource potential of bread spring wheat varieties for the conditions of Western Siberia and the Omsk region (analytical review)/ I.A. Belan, L.P. Rosseeva, N.P. Blokhina [and others] // Agrarian science of the Euro-North-East. 2021. DOI 10.30766/2072-9081.2021.22.4.449-465.

Early maturing variety of spring bread wheat Tarskaya 12 for the northern regions of the Omsk region / Yu.P. Grigoriev, I. A. Belan, L.P. Rosseeva, I.V. Pakhotina // Agrarian Russia, 2020. DOI 10.30906/1999-5636-2020-3-3-7.

Take-home message:

Большинство сортов, устойчивых к стеблевой ржавчине, созданы путем скрещиваний селекционных линий и коллекционных образцов. Сорта Сигма и Уралосибирская 2 созданы благодаря использованию аллоплазматических линии пшеницы, несущих цитоплазму ячменя.



Comparison of methods for genotyping peach cultivars

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Nikita Botanical Gardens–National Scientific Centre, Yalta, Russia
E-mail: i.rozanova@vir.nw.ru

Peach (Prunus persica L.) is one of the most important stone fruit crops in the world. Currently, much research is devoted to genotyping of stone fruit crops cultivars, including peach.

Nowadays there are many genetic markers that can be used to identify cultivars. The aim of this work was to genotype peach cultivars based on SNPs and compare with the data obtained using SSR markers. A sample of 87 peach cultivars and forms from the Nikitsky Botanical Garden collection was analyzed by GBS using the restriction endonuclease pair MspI/PstI. Clustering based on the obtained 7086 SNPs of the studied peach cultivars was carried out and the formation of two clusters was revealed. The obtained data do not coincide with the results of clustering based on SSR markers, that raises the question of the impossibility of using SSR markers in the analysis of peach cultivars origin.

The study was supported by the Kurchatov Genomic Center of Nikitsky Botanical Garden - National Scientific Center of RAS (075-15-2019-1670).

Take-home message:

A comparative analysis of genetic similarity of peach cultivars based on 12 SSR markers and 7086 SNPs obtained by GBS was performed. We revealed inconsistencies in the clustering of cultivars.

Genetic analysis of barley productivity traits in Siberian collection

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*Federal Research Center Institute of Cytology and Genetics, Siberian Branch of Russian Academy of Sciences, St. Petersburg, Russia
E-mail: i.rozanova@vir.nw.ru

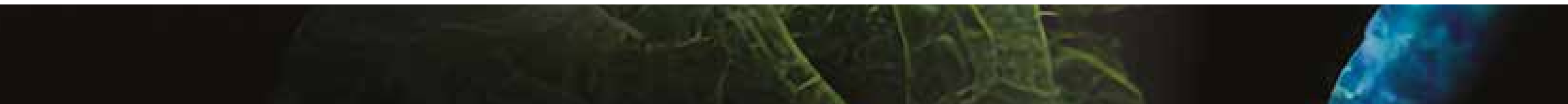
Barley (*Hordeum vulgare* L.) is one of the most commonly cultivated cereals worldwide.

Its local varieties may represent a valuable source of unique genetic variants useful for crop improvement. The aim of the present study is to identify the loci associated with grain productivity traits using GWAS and assess the influence of genes that control spike row-type in the studied phenotypes.

In present study, such traits “spike length”, “grain number per main spike”, “1000 grain weight”, “grain weight of main spike” were investigated. These traits are economically important as they are primary determinants of barley yield.

Take-home message:

A genome-wide association analysis using a panel of 94 barley varieties was performed. It turns out that all markers identified by GWAS will be correlated with genes that affect row-type.



Prognostic of yield of potatoes of promising domestic varieties under the impact of stress abiotic factors

Rozentsvet O.A., Bogdanova E.S., Rubtsov S.L., Lomakina E.E.

Samara Federal Research Scientific Center RAS, Institute of Ecology of the Volga Basin RAS, Togliatty, Russia,
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Potato (Solanum tuberosum L.) is a valuable crop for human nutrition and food security in many countries. Cultural potatoes are sensitive to moisture deficiency and high temperatures. The purpose of this study was to identify the contribution of morphophysiological parameters of leaves to the formation of potato yields of various genetic origins under conditions of high temperature and lack of moisture. Plant height, linear dimensions, the number of stomata per unit area of the leaf, as well as the content of pigments, proline, membrane lipids and proteins, the level of lipid peroxidation in the leaves of 24 potato varieties for 3 years were studied. The 3D modeling method showed: (I) a negative correlation between the yield of early varieties and temperature (II); positive correlation between the yield of mid-early varieties and soil moisture; (iii) negative correlation between the number of tubers of mid-ripening varieties and soil moisture. Experimental models can be used in the selection and forecast of potato's yield depending on the weather conditions in the growing region.

This work was supported by a grant from the Russian Science Foundation, N. 23-26-10020.

The main publications of authors on the subject of the abstract:

1. Rozentsvet O.A. et al. // Doklady Biological Sciences (2021) 497: 65–68. doi: 10.1134/S0012496621020095.

2. Rozentsvet O.A. et al. // Doklady Biochemistry and Biophysics (2022) 507: 371–374. doi: 10.1134/S1607672922340129.

3. Rozentsvet O.A. et al. Physiological and Biochemical Parameters of Leaves for Evaluation of the Potato Yield //Agriculture (2022) 12: 757. doi:10.3390/agriculture12060757.

Search for microRNAs involved in the resistance of wheat plants against cereal aphids

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The mechanism of RNA interference (RNAi) and small RNAs are currently being intensively studied and considered as important regulators of gene expression reprogramming in plant immune responses and pathogen or pest virulence. At the same time, the problem is the lack of knowledge about the mechanisms of RNAi functioning in insect and plant cells during their interaction. The object of the study was the bird cherry aphid (*Rhopalosiphum padi*) and Salavat Yulaev, a variety of soft spring wheat *T. aestivum*. Some miRNA targets have been shown to include genes involved in the regulation of hormonal signaling pathways. Our results showed that the treatment of plants with phytohormones led to a decrease in the fertility of aphids feeding on these plants. Treatment with CK led to a decrease in the number of individuals by 19%. And treatment with ABA or ET led to a decrease in fertility by more than 50%. Therefore, in our work, we studied the transcription of nine microRNAs (miR156, miR159, miR160, miR164, miR166a, miR393, miR396b, miR398 and miR408) involved in the regulation of signaling pathways of various hormones. The study was funded by a grant from the RSF № 22-76-00056.

The main publications of authors on the subject of the abstract:

Rumyantsev, S.D.; Alekseev, V.Y.; Sorokan, A.V.; Burkhanova, G.F.; Cherepanova, E.A.; Garafutdinov, R.R.; Maksimov, I.V.; Veselova, S.V. Additive Effect of the Composition of Endophytic Bacteria Bacillus subtilis on Systemic Resistance of Wheat against Greenbug Aphid Schizaphis graminum Due to Lipopeptides. Life. 2023,13,214. https://doi.org/ 10.3390/life13010214

Take-home message:

Recent studies have shown that small RNAs are important regulators of the plant immune response.

JetGene - online resource for an analysis of regulatory regions or nucleotide contexts at differently translated plants transcript

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We have created JetGene (https://jetgene.bioset.org/) that includes cDNA, CDS, 5'/3'-UTR sequences from six different groups of organisms. Information about CDS and cDNA is downloaded and updated from Ensembl. We have developed JetGene with the aim of searching regulatory codes in mRNA and studying their correlation with the efficiency of translational. It allows to do a comparative analysis of sequences, namely: (1) to estimate the length variation, nucleotide composition, codon usage frequency, to analyze GC-content, CpG-islands, to study nucleotides surrounding of the start codon and far more; (2) to identify and define the statistically significant representation of potential regulatory contexts at mRNA with different translation efficiency. A user can make *in silico* analysis for coding/non-coding regions, or for full-length transcripts, or for a fragment of transcripts. In addition, the beta-version of JetGene (https://beta.bioset.org, under construction) allows to compare two datasets of mRNA.

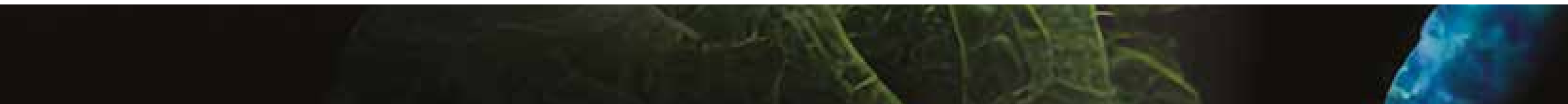
The research was carried out within the state assignment of Ministry of Science and Higher Education of the Russian Federation (theme No. 122042700043-9).

The main publications of authors on the subject of the abstract:

Sadovskaya N.S. et al. JetGene: Internet Resource for Analysis of Regulatory Regions or Nucleotide Contexts in Differentially Translated Plant Transcripts // Russian Journal of Plant Physiology (2021) 68: 633-640. https://doi.org/10.1134/S1021443721040142

Take-home message:

A friendly interface and numerous sets of untrivial tools of JetGene allow to make a comprehensive in silico analysis of cDNA, CDS, 5'/3'-UTR from six groups of living organisms: Bacteria, Fungi, Metazoa, Plants, Protists and Vertebrates.



Study of spring triticale resistance to stem rust, *Puccinia graminis f. sp. Tritici*

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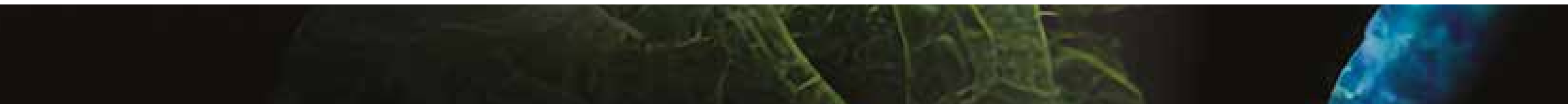
Climate change and saturation of crop rotations with grains has led to an increase in the infectious load on plants. In particular, in the south and in the center of Russia, Puccinia graminis f. sp. tritici is increasingly affected by stem rust. Spring triticale, relative to others, is a fairly young and little-spread crop that can be used for grain, as an insurance crop and a donor of resistance genes obtained from parent species. The paper presents the results of PCR analysis of the spring triticale collection for the presence of wheat resistance genes: *Sr9a, Sr13, Sr23, Sr24, Sr25, Sr26, Sr32, Sr33, Sr38* effective against the causative agent of stem rust, including against the highly pathogenic Ug99 race. The results of the analysis of the collection for the *Sr31* and *Sr50* genes, of which the rye genome is a donor, are also presented.

The main publications of authors on the subject of the abstract:

Sayenko, K. Yu. Molecular genetic screening of spring triticale cultivars by genes of resistance to the pathogen of stem rust Puccinia graminis Pers. f. sp. tritici / K. Yu. Sayenko, M. V. Dudnikov // Biological protection of plants - the basis of stabilization of agroecosystems : Materials of the International scientific and practical Conference, Krasnodar, September 13-15, 2022. Volume Issue 11. – Krasnodar: EDVI Publishing House, 2022. – pp. 333-337. – EDN RKIGBT.



Towards the discovery of genetic determinants of curly birch wood features based on high-throughput genotyping

**Safronycheva E.D., Karzhaev D.S., Volkov V.A.,
Vetchinnikova L.V., Zhigunov A.V.**

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The patterned wood of Karelian birch (*Betula pendula var. carelica*) has valuable decorative properties. The presence of this trait can be established by the morphological features, but not earlier than 8-10 years of age. Identification of genetic loci that determine the valuable trait would make it possible to create plantations of Karelian birch without admixture of the trees of silver birch, which would increase the economic efficiency of such plantations.

The aim of the research is to find genetic loci of "patterned" wood, based on genotyping by RADseq method. At this stage of the project, we report the results of the preparation of sequencing libraries for 192 samples, as well as the results of the quality analysis of the reads obtained. A protocol using *NlaIII* and *HindIII* endonucleases was used to prepare RADseq libraries. Sequencing of the libraries was performed on an Illumina NovaSeq 6000. The quality of the reads was assessed using FastQC and MultiQC, all key statistics showed positive results. A total of 2 059 269 798 reads will be used to align to a reference genome and search for SNP.

The research was funded by the Russian Science Foundation (project no. 22-16-00096).

The main publications of authors on the subject of the abstract:

Zhigunov A. V. et al. Development of F1 hybrid population and the high-density linkage map for European aspen (Populus tremula L.) using RADseq technology //BMC plant biology. – 2017. – T. 17. – №. 1. – C. 1-12.

Vetchinnikova L.V. Karelian birch and other rare representatives of the genus Betula L. /; [ed. by A.F. Titov]; Forest institute of the Karelian Scientific Center of the Russian Academy of Sciences. - Moscow: Nauka, 2005 - 269 p.

Analysis of the potato virus S populations in different regions of the Russian Federation

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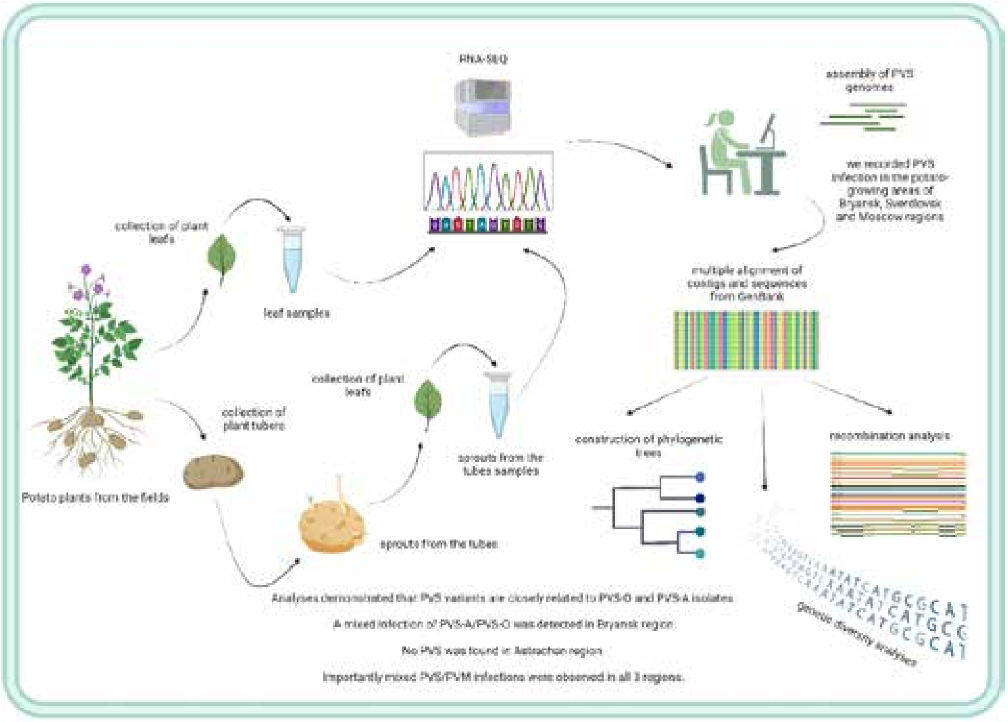
Potato virus S (PVS, genus Carlavirus) is considered the fourth most important viral pathogen affecting potato (*Solanum tuberosum*) production worldwide. Tuber yield losses can reach 20% in the case of infection with severe PVS strains or even more in the case of mixed infections with other common potato viruses.

In this work, we recorded PVS infection in the potato-growing areas of Bryansk, Sverdlovsk, Moscow and Astrachan regions. We used high-throughput sequencing RNA-Seq to characterize PVS variants. We analyzed RNA-seq libraries from RNA samples of the leaves and sprouts from the tubers collected during season 2021 and generated full length PVS contigs. Sequence identity matrix and phylogenetic analyses demonstrated that PVS variants are closely related to PVS-O and PVS-A isolates. A mixed infection of PVS-A/PVS-O was detected in Bryansk region. No PVS was found in Astrachan region. Importantly mixed PVS/PVM infections were observed in all 3 regions. Data obtained will be discussed in the context of the PVS diversity and evolution in a range of geographic zones with distinct climate.

This work was supported by the grant of the Russian Science Foundation No. 23-74-30003.



Intraspecies polymorphism of *Calendula officinalis* L.

Samatadze T., Yurkevich O., Khazieva F.*, Savchenko O.*, Basalaeva I.*, Amosova A., Muravenko O.

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*All-Russian Scientific Research Institute of Medicinal and Aromatic Plants, Moscow, Russia
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The aim of this study was a comparative analysis of the intraspecific chromosomal polymorphism of *C. officinalis* in karyotypes of four samples from different habitats and four varieties of Russian selection: 'Ryzhik', 'Kalta', 'Rajskij sad', and 'Zolotoe more'. A morphometric analysis showed that all studied karyotypes contained 16 pairs of chromosomes (3.5–5.0 μm). FISH analysis revealed 45S rDNA signals of varying intensity on satellite chromosome pairs 1 and 9. In one variety ('Rajskij sad') and the accessions from Yaroslavl (K-212) and from Minsk, Belarus (K-22-364), a minor polymorphic 45S rDNA site was found in the median position of the short arm of chromosome pair 5. In all studied samples a large 5S rDNA site was found in the long arm of chromosome 10. In one *C. officinalis* sample from the Crimea (K-214/02), a 5S rDNA site co-localized with a minor 45S rDNA locus, was observed on chromosome 10. In other studied samples, the minor 45S rDNA locus on chromosome 10 was not revealed.

This work was supported by the Russian Science Foundation grant No. 22-26-00221

<u>The main publications of authors on the subject of the abstract:</u>

Samatadze T.E. et al. Phenotypic and molecular cytogenetic variability in calendula (Calendula officinalis L.) cultivars and mutant lines obtained via chemical mutagenesis. Scientific Reports. 2019. DOI: 10.1038/s41598-019-45738-3

Samatadze T.E. et al. Agro-Morphologicaland Cytogenetic Characterization of Colchicine-Induced Tetraploid Plants of Polemonium caeruleum L. (Polemoniaceae). Plants 2022, 11, 2585. https://doi.org/10.3390/plants11192585

<u>Take-home message:</u>

Thus, intraspecific polymorphism on the chromosomal localization of 45S rDNA was revealed in the *C. officinalis* samples from different habitats, which can be related with both recombinational variability and adaptive mechanisms of plant genomes/

Toward an integrative view of *Fusarium* wilt infection in flax

Samsonova M., Kanapin A., Samsonova A., Logachev A., Bankin M., Rozhmina T.*

Peter the Great St. Petersburg Polytechnic University, St.Petersburg, Russia,
*Federal Research Center for Bast Fiber Crops, Torzhok, Russia
E-mail: m.samsonova@spbstu.ru

One of the most economically damaging flax diseases is Fusarium wilt caused by the fungus *Fusarium oxysporum f. sp. lini*. The mechanisms of flax resistance to Fusarium wilt have never been fully understood, although resistance to the disease was developed by selection. Here we applied the analysis of genomics, transcriptomics and methylomics data, as well as innovative breeding methods (GWAS and bulk segregant analysis) to 1) perform chromosme-level assembly of the fungus genome and reveal its complex multi-compartmentalized organization, 2) construct the pangenome of the pathogene and map to reference flax genome several resistance genes identified previously by classical genetics methods. We found that flax varieties start to respond to infection earlier that the sensitive ones and that fungus expression *in planta* parallels plant response. A significant proportion of plant genes with differential expression upon infection is also differentially methylated indicating the involvement of epigenetic mechanisms in the control of plant resistance. Our results provide novel insights into plant-pathogen interactions and pinpoint potential candidate genes for further in-depth studies.

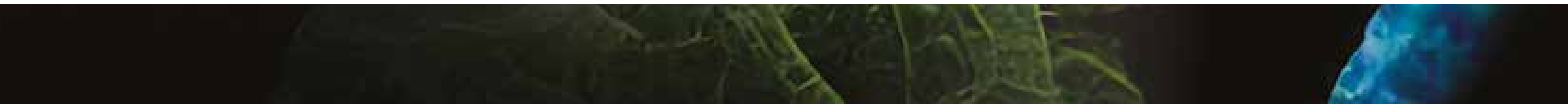
<u>The main publications of authors on the subject of the abstract:</u>

Kanapin A, Bankin M, Rozhmina T, Samsonova A, Samsonova M. Genomic Regions Associated with Fusarium Wilt Resistance in Flax. Int J Mol Sci. 2021 Nov 17;22(22):12383. doi: 10.3390/ijms222212383.

Samsonova A, Kanapin A, Bankin M, Logachev A, Gretsova M, Rozhmina T, Samsonova M. A Genomic Blueprint of Flax Fungal Parasite Fusarium oxysporum f. sp. lini. Int J Mol Sci. 2021 Mar 6;22(5):2665. doi: 10.3390/ijms22052665.

<u>Take-home message:</u>

Plants are inolved in a continuous co-evolutionary fight with their pathogens. Its outcomes have a profound impact on agricultural systems. The current synthesis of plant–pathogen interactions boosts our efforts to control pathogen infections.



Relationships between three species of *Fritillaria* Tourn. ex L. from the South Siberia

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Institute of General and Experimental Biology of SB RAS, Tunkinsky National Park, Ulan-Ude, Russia,
*Siberian institute of plant physiology and biochemistry of SB RAS, Irkutsk, Russia
E-mail: denis.sandanov@gmail.com

Fritillaria Tourn. ex L. is one of the taxonomically complex groups of Liliaceae. *Fritillaria* species have diverse morphology and phylogenetic relationships between many of them are still remained unclear. We combined morphological survey with analysis based on nuclear (ITS) and plastid (matK+rps16+trnH-psbA) DNA of three Siberian *Fritillaria* (*F. dagana* Turcz., *F. maximowiczii* Freyn, and *F. sonnikovae* Shaulo & Erst). We found a close affinity between *F. sonnikovae* and *F. maximowiczii* based on morphological features and DNA data, while F. dagana was a sister to *F. maximowiczii*+*F. sonnikovae. Fritillaria* sonnikovae and *F. maximowiczii* having similar morphology differed in perianth color with colorless pattern in the first mentioned. Colorless perianth is known for other *Fritillaria* and such morphs are genetically similar to the common ones. The light-yellow *F. dagana* included in analysis and showing no differences in the nucleotide sequences with common morph can be an example. We suggest considering *F. sonnikovae* as a synonym for *F. maximowiczii.*

The study was financed by RSF grant No 23-24-00501, https://rscf.ru/project/23-24-00501/

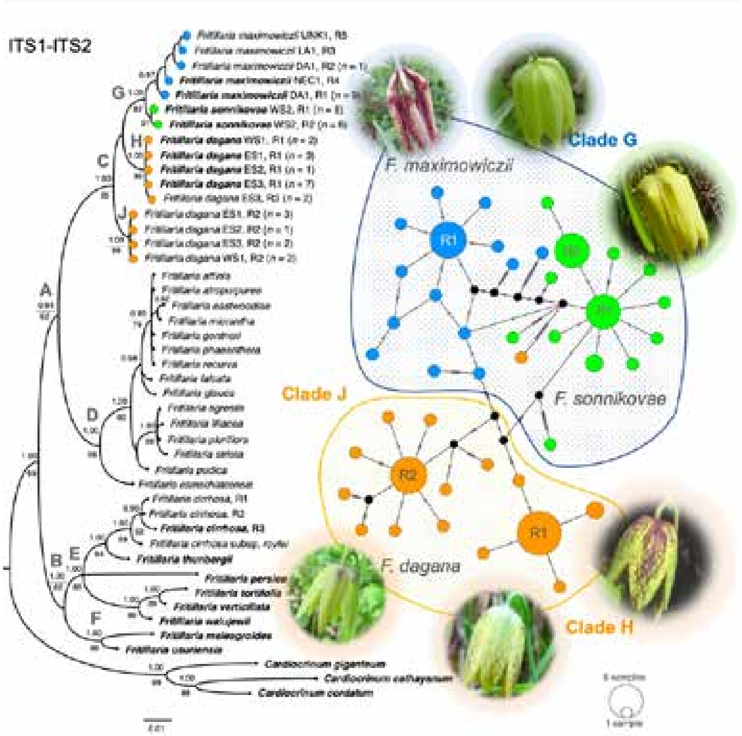
The main publications of authors on the subject of the abstract:

Protopopova M et al. The Curious Case of Fritillaria sonnikovae (Liliaceae) in South Siberia: New Insights into Its Origin and Phylogeny. Diversity (2023) 15:193. https://doi.org/10.3390/d15020193

Take-home message:

Fritillaria sonnikovae is a synonym for Fritillaria maximowiczii.

Fritillaria sonnikovae may be considered as narrow endemic of the Western Sayan mountains and tertiary remnant of F. maximowiczii.



The role of conserved TRFL genes in the regulation of *Marchantia polymorpha* telomere length

Sannikova A., Sharipova M., Shakirov E.*, Valeeva L.

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*Department of Biological Sciences, College of Science, Marshall University, Huntington, USA
E-mail: anastasya.sannikova@bk.ru

Telomeres are the most important structures at the physical ends of eukaryotic chromosomes involved in DNA protection from disintegration and shortening. A number of specific proteins play a crucial role in the functioning and maintenance of telomeres. Herein, we analyzed the role of the telomeric TRFL proteins in the regulation of *Marchantia polymorpha* telomere length.

Telomere length analysis was performed by TRF coupled with Southern blot analysis. The average telomere length was calculated using the TeloTool software. Bioinformatic analysis showed the presence of 3 TRFL gene paralogs in *M. polymorpha* genome (TRB1, TBP, TRFL6). Using the CRISPR/Cas9 genome editing technique, 10 TRFL6-knockout and 3 TBP1-knockout individual plants of *M. polymorpha* were developed. It was shown that TRFL6 mutant plants are characterized by a shorter telomere length compared to the wild type and had thallus tissue growth defects. Thus, TRFL6 of *M. polymorpha* is a positive regulator of telomere length and presumably has additional functions.

This work was part of Kazan Federal University Strategic Academic Leadership Program (PRIORITY-2030) and funded by grant No.21-14-00147.

The plastid genome of the non-photosynthetic plant *Rhopalocnemis phalloides* is the most polymorphic genome ever reported

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*Department of Higher Plants, Biological Faculty, M.V. Lomonosov Moscow State University, Moscow, Russia,
**Skolkovo Institute of Science and Technology, Moscow, Russia
E-mail: shelkmike@gmail.com

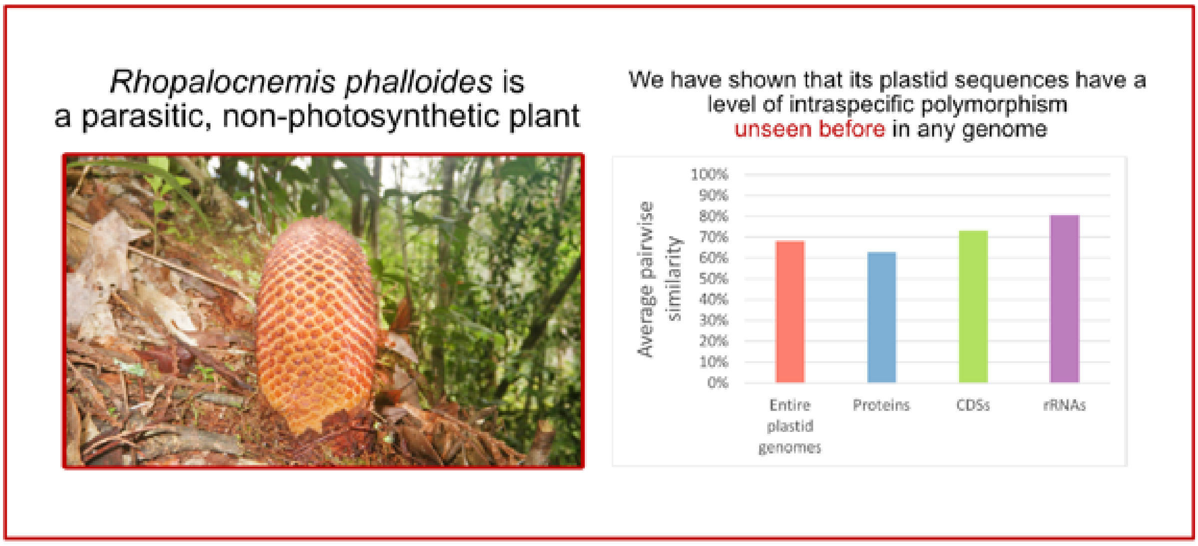
The plant family Balanophoraceae consists entirely of non-photosynthetic species. Their ancestors lost the ability to photosynthesize and instead started to rely entirely on parasitizing other plants. Previously we showed that the plastid genome of *Rhopalocnemis phalloides,* a plant from Balanophoraceae, possesses a number of unusual features, including a very high AT content (approximately 85%) and a highly elevated mutation accumulation rate. These peculiarities are a consequence of a loss of plastid genome repair genes encoded in the nuclear genome.

We hypothesized that the very high mutation accumulation rate may have led to a very high intraspecific polymorphism in *Rhopalocnemis phalloides.* To test this hypothesis, we studied plastid genomes of five samples of this species. The analysis showed that the average similarity between protein-coding genes in this species is 73.2%and the average similarity between rRNA-coding genes in this species is 80.6%. This makes the plastid genome of *Rhopalocnemis phalloides* the most polymorphic genome ever reported.

The work was supported by the Russian Science Foundation (project 21-74-10006) and by IITP RAS FFNU-2022-0037.

Take-home message:

The plastid genome of the non-photosynthetic plant *Rhopalocnemis phalloides* is the most polymorphic genome ever reported



Rhopalocnemis phalloides is
a parasitic, non-photosynthetic plant

We have shown that its plastid sequences have a
level of intraspecific polymorphism
unseen before in any genome

The functions of novel plant transmembrane microprotein FAMOSS in *Physcomitrium patens*

Sedlov I.A., Kniazev A.N.*, Golub N.O., Kharlampieva D.D., Lazarev V.N.**, Ptushenko V.V.***, Mamaeva A.S.**

Shemyakin-Ovchinnikov Institute of Bioorganic Chemistry of the Russian Academy of Sciences, Moscow, Russia,
*All-Russian Research Institute of Agricultural Biotechnology, Moscow, Russia,
**Lopukhin Federal Research and Clinical Center of Physical-Chemical Medicine of Federal Medical Biological Agency, Moscow, Russia,
***Belozersky Institute of Physico-Chemical Biology, Lomonosov Moscow State University, Moscow, Russia
E-mail: sedlov8@yandex.ru

Microproteins encoded by small open reading frames (smORFs) located on long non-coding RNAs (lncRNAs) constitute a significant but insufficiently studied part of the plant cell proteome.

Previously, we confirmed translation of an sORF encoding a conserved 41 a.a. microprotein located on a transcript annotated as lncRNA in the moss Physcomitrium patens. Because of the characteristic phenotype of the mutant lines, the microprotein was named FAMOSS (FAst-growing MOSS).

We showed that this microprotein is localized in the thylakoid membrane of chloroplasts. The analysis of the microprotein interactome suggested its interaction with the light harvesting-like proteins. Plants overexpressing the microprotein have increased sensitivity to high light due to reduced non-photochemical quenching (NPQ). In addition, we observed changes in vesicular trafficking in mutant lines, which may be associated with the regulation of photosynthesis.

Thus, we consider that the FAMOSS microprotein has role in NPQ regulation and influences vesicular trafficking in apical protonema cells.

This study was supported by the Russian Science Foundation grant no. 23-66-10013.

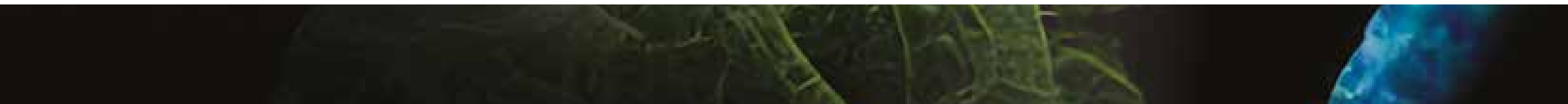
The main publications of authors on the subject of the abstract:

Fesenko I. et al. Distinct types of short open reading frames are translated in plant cells //Genome research (2019) 29.9: 1464-1477. doi: 10.1101/gr.253302.119

Mamaeva A. et al. FAMOSS, a conserved 41-aa peptide involved in plant tip growth regulation //bioRxiv. (2021) 2021.11. 24.469821. doi: 10.1101/2021.11.24.469821

Take-home message:

Novel plant transmembrane thylakoid microprotein FAMOSS regulates photosynthetic performance and NPQ after interaction with LHC-like proteins.



Architectonics the spike of ancient barley from the Usvyatsky settlement of the XII century

Semilet T.V., Shipilina L.Yu, Smirnova N.V., Shvachko N.A.

Federal Research Center N. I. Vavilov All-Russian Institute of Plant Genetic Resources (VIR),
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Archaeologists find the remains of humans, animals and plants, which can shed light on the formation of ancestral culture, domestication processes and identify phylogenetic outliers between modern and ancient organisms. At the same time, scientists use paleogenetic methods. There are studies with ancient DNA of animals and humans in Russia and abroad, but works with a genetic material of plant fossils remain unique. The identification of phylogenetic relationships between cultivated plants and their wild ancestors provides valuable information on the historical geography of flora and the role of autochthonous and allochthonous elements in this process. Our research was carried out on grains of the XII century, obtained during excavations of the Usvyaty settlement. Isolation of DNA fragments was carried out under conditions precluding contamination with foreign DNA. The genes associated with the architectonics of cereal spike (*Nud, Btr, Vrs*) were selected for the study. The sequencing of gene fragments suggested that the ancient farmers grew filmy two-row barley with a brittle rachis.

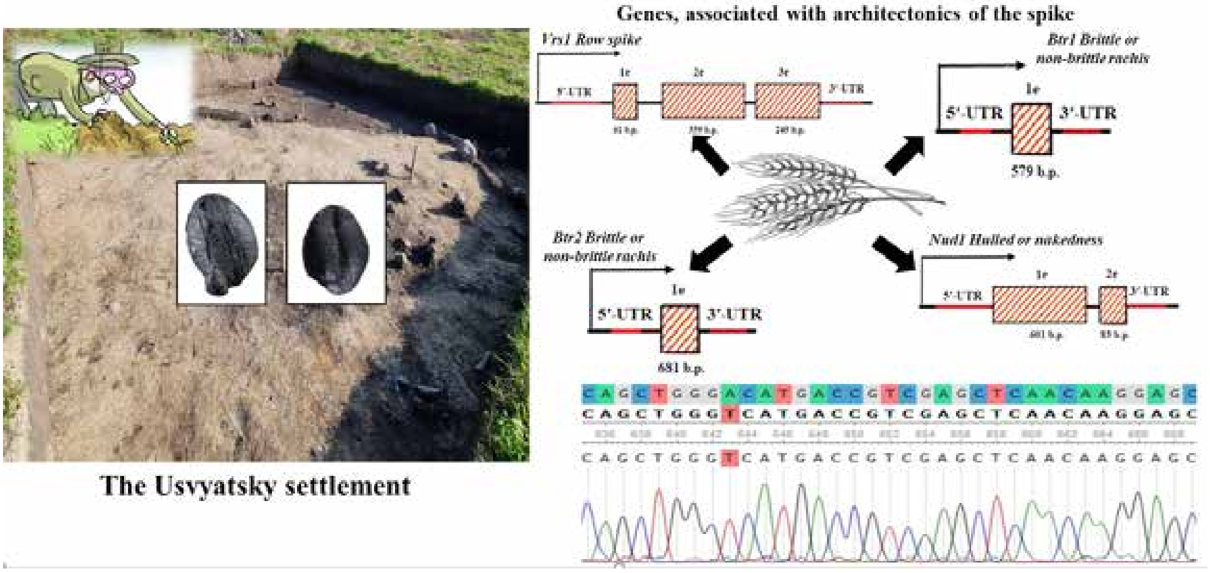
The work was carried out within the framework of the state assignment № 15H 0481-2022-0007.

<u>The main publications of authors on the subject of the abstract:</u>

Semilet T.V., Shvachko N.A., Smirnova N.V., Shipilina L.Yu., Khlestkina E.K. Using DNA markers to reconstruct the lifetime morphology of barley grains from carbonized cereal crop remains unearthed at Usvyaty Settlement /BIOLOGICAL COMMUNICATIONS, vol. 68, issue 1, p 3-9 2023. https://doi.org/10.21638/spbu03.2023.101

<u>Take-home message:</u>

1. Extraction of ancient DNA was carried out from material found on the territory of Russia
2. The work was carried out under conditions excluding contamination with foreign DNA, which made it possible to obtain reliable about ancient cereals.



Preparation of recombinant plant rhamnogalacturonan lyase (LusRGL6) by transient expression in tobacco leaves

Serdyukova M.V., Mokshina N.E.

Kazan Institute of Biochemistry and Biophysics, FRC Kazan Scientific Center of RAS, Kazan, Russia
E-mail: m.serdyukova5@gmail.com

The cell wall is the key structure of a plant cell. Understanding the activity of enzymes that modify its components sheds light on the processes of regulation and functioning of the cell wall.

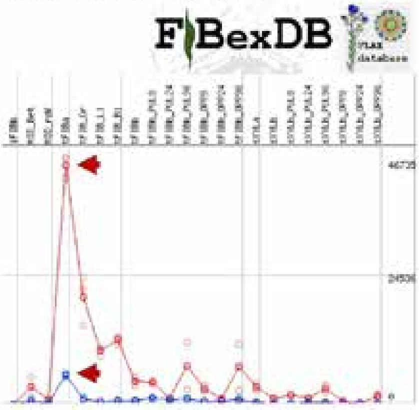
Special associates of rhamnogalacturonan I (RG-I) play an essential role in the formation of the "muscular" properties of the cellulosic tertiary cell wall, which is formed by plant fibers. In addition to galactosidase, which «shortens» the long galactan chains of RG-I after its deposition in the tertiary wall, rhamnogalacturonan lyase genes (LusRGL6) are activated in flax phloem fibers and are capable of degrading the RG-I backbone. Although the mechanism of action of RGL is known, for a long time there has been no clear biochemical evidence of the presence of endogenous activity of rhamnogalaturonan lyase in plant cells, and information about its effect on plant physiology is limited.

We have cloned the rhamnogalacturonan lyase gene (LusRGL6-A), whose expression is specifically increased in fibers at the stage of tertiary cell wall formation. During temporary expression in tobacco leaves, a recombinant LusRGL6-A protein without a signal peptide was obtained.

Take-home message:

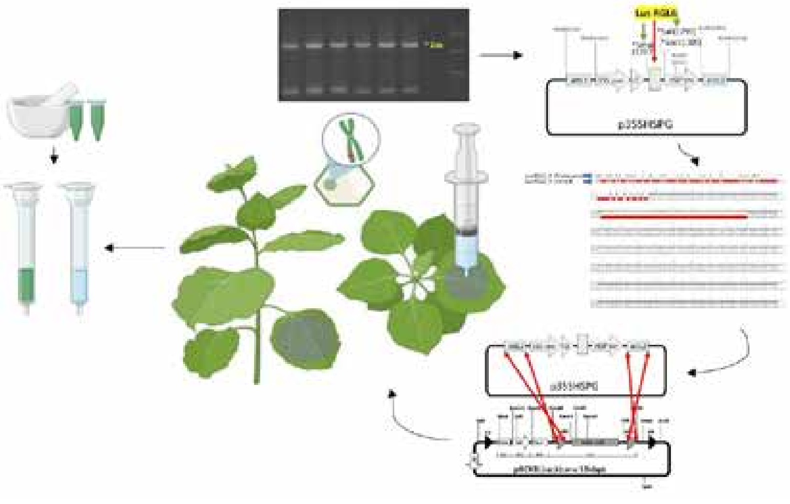
The analysis of plant RGLs will expand our understanding of plant enzymes, methods of specific recognition of substrates, and mechanisms of catalysis in the plant organism.

Expression profile of two paralog genes (LusRGL6-A/B) in flax tissues.



The arrows mark the samples of fibers forming the tertiary cell wall.

The general scheme of the strategy for obtaining a recombinant protein of plant rhamnogalacturonan lyase is given.



Structural analysis of genes affecting the tuber starch content and properties in Russian potato varieties

Sergeeva E.M., Karetnikov D.I., Afonnikov D.A., Larichev K.T., Salina E.A., Kochetov A.V.

Kurchatov Genomic Center of the Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia
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The potato *Solanum tuberosum* is the fourth agronomically important crop and starch producer in the world. The large number of genes involved in carbohydrate turnover and starch metabolism described to date. However, the data for allelic combinations of genes associated with increased starch content remain unknown. In this work, we analyzed the nucleotide sequences of 21 genes coding for starch synthases, starch phosphorylases, AGPase, beta-amylase, sucrose synthases, in 7 Russian potato varieties with different starch content (Fritella, Grand, Krasa Meschery, Krasavchik, Krepysh, Kolobok, Severnoe Siyanie). Gene sequences were obtained with *Illumina* platform and MUSCLE multiple alignments performed. The SNP density in the coding regions ranged from 1/22 bp to 1/89 bp, average was 1/43. From them the proportion of nonsynonymous substitution sites ranged from 3 to 58%. The sequence comparison by phylogenetic analysis showed that for 10 genes the candidate variants characteristic to high and low starch content could be identified.

This research was funded by the *Kurchatov* Genomic Centre of the Institute of Cytology and Genetics, SB RAS (075-15-2019-1662).

Features of in vitro regeneration of valuable Norway maple trees

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All-Russian Research Institute of forest genetics, breeding and biotechnology, Voronezh, Russia
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Norway maple (*Acer platanoides* L.) is one of the most common and valuable species of maple. Maple is stable in mixed stands, widely used in landscaping, has numerous forms and varieties that differ in leaf color, crown shape and other features.

Optimization of maple clonal micropropagation technology will accelerate the production of high-quality Norway maple planting material for reforestation and landscaping. Conditions for the effective production of aseptic viable cultures, shoot formation and rooting of maple *in vitro* were selected for adult productive, stable and decorative Norway maple trees.

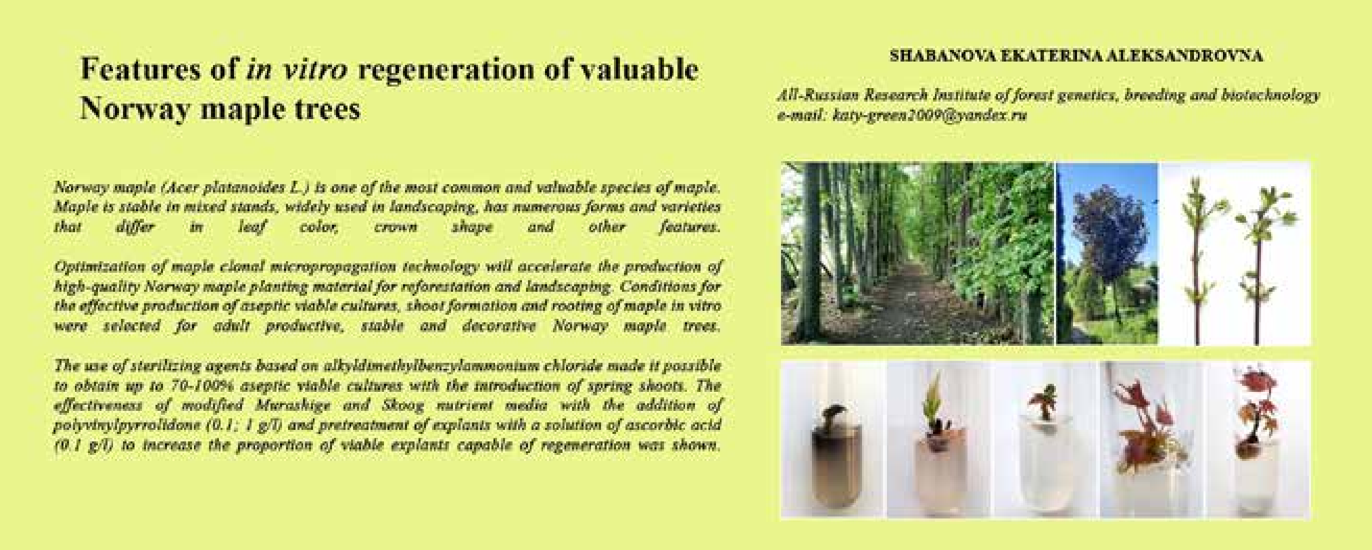
The use of sterilizing agents based on alkyldimethylbenzylammonium chloride made it possible to obtain up to 70-100% aseptic viable cultures with the introduction of spring shoots. The effectiveness of modified Murashige and Skoog nutrient media with the addition of polyvinylpyrrolidone (0.1; 1 g/l) and pretreatment of explants with a solution of ascorbic acid (0.1 g/l) to increase the proportion of viable explants capable of regeneration was shown.

The main publications of authors on the subject of the abstract:

Mashkina O.S., Shabanova E.A., Varivodina I.N., Grodetskaia T.A. Field Trials of in vitro Propagated Aspen Clones (Populus tremula L.): Growth, Productivity, Wood Quality, and Genetic Stability // Lesnoy Zhurnal (Forestry Journal). –No. 6. P. 25-38. – DOI 10.17238/issn0536-1036.2019.6.25

Take-home message:

Conditions for the effective production of aseptic viable cultures, shoot formation and rooting of maple in vitro were selected for adult productive, stable and decorative Norway maple trees.



Features of *in vitro* regeneration of valuable Norway maple trees

SHABANOVA EKATERINA ALEKSANDROVNA

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Norway maple (Acer platanoides L.) is one of the most common and valuable species of maple. Maple is stable in mixed stands, widely used in landscaping, has numerous forms and varieties that differ in leaf color, crown shape and other features.

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Wheat breeding for yield and grain quality in Western Siberia

Shamanin V.P., Shepelev S.S., Chursin A.S., Pototskaya I.V., Gordeeva E.I.*, Morgunov A.I., Koksel H.**

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In the nurseries of the breeding process of the Omsk State Agrarian University, a genetic collection with identified genes has been formed that has a significant effect on increasing the traits of plant productivity, adaptability and quality of wheat grain. Marker-controlled selection has created a valuable source material for wheat breeding for yield and grain quality. The state register includes spring soft wheat varieties with a yield potential of 6.5-7.0 t/ha -Stolypinskaya 2, Silantiy, Niva 55, etc., valuable and strong in terms of grain quality. By marker-controlled selection together with the geneticists of the Institute of Cytology and Genetics high-yielding variety EF 22 with purple grain color was created in six years, which successfully passes the state variety testing.

Keywords: wheat; productivity; grain quality; marker - controlled selection

Field studies were carried out with the support of the Ministry of Agriculture of the Russian Federation; determination of grain quality - with the support of the Ministry of Science and Higher Education of the Russian Federation (agreement No. 075-15-2021-534 dated May 28, 2021).

The main publications of authors on the subject of the abstract:

V. Shamanin, Z.H. Tekin-Cakmak E.I. Gordeeva, S. Karasu, I.Pototskaya, A. Chursin, V. Pozherukova, G. Ozulku, A. Morgounov, O. Sagdic, H. Koksel, Antioxidant Capacity and Profiles of Phenolic Acids in Various Genotypes of Purple Wheat // Foods, 2022, 11(16), 2515

SRAP marker system for analysis of mutant inflorescence types in alfalfa

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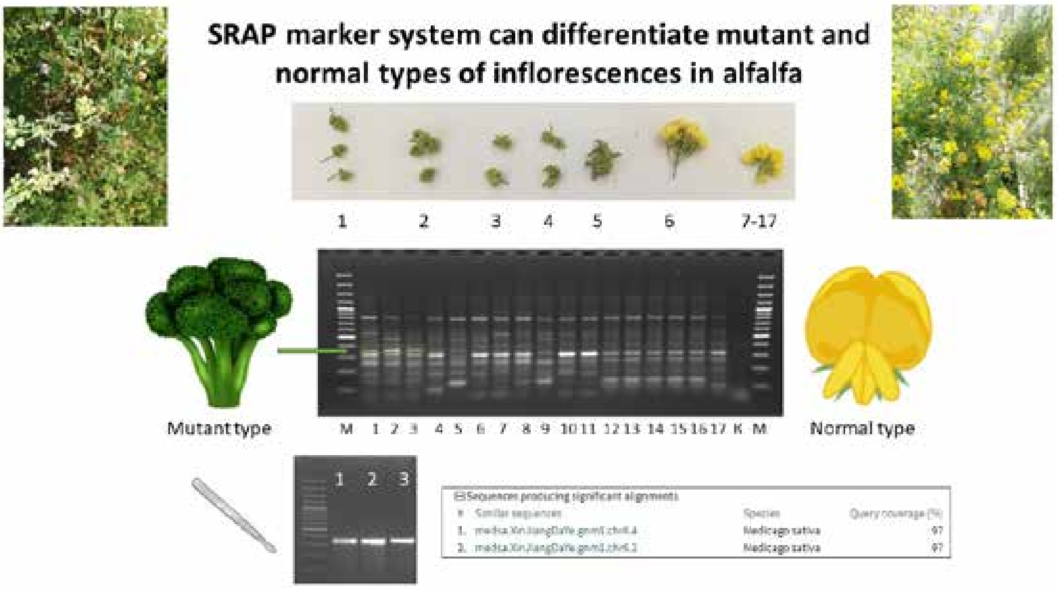
Люцерна (*Medicago L.*) - одна из самых ценных и широко распространенных в мире высокобелковых многолетних культур. Для селекционно-семеноводческой работы большое значение имеют морфологические и биологические особенности ее цветения, оплодотворения и плодообразования. Типичное соцветие люцерны – открытая брактеозная кисть, но в процессе многократного самоопыления отмечаются и мутантные формы. Цель данной работы состояла в выявлении на генетическом уровне отличий растений со стерильными метёлковидными соцветиями («цветная капуста») от имеющих типичную форму цветка.

Анализ генетического полиморфизма проводили на образцах геномной ДНК, выделенной из листовой ткани 11 растений с обычной формой цветения и 6 – с измененным типом соцветий. Использовали 10 комбинаций SRAP-маркеров, основанных на амплификации интрон-экзонных областей генома.

С помощью комбинации праймеров F9-R8 получен уникальный бэнд (357 п.н.), характерный для трёх растений с соцветием «цветная капуста», но отсутствующий у остальных образцов. Секвенированием установлено, что фрагменты картируются на один участок хромосомы, расположенный в кодирующей области гена.

<u>The main publications of authors on the subject of the abstract:</u>

Шамустакимова, А. О., Мавлютов, Ю. М., & Клименко, И. А. (2021). Применение SRAP-маркеров для ДНК-идентификации российских сортов люцерны. Генетика, 57(5), 536-543.



Root exudation and activation of defense reactions in barley genotypes with different susceptibility to root rot caused by *Fusarium culmorum*

Shaposhnikov A.I., Shakhnazarova V.Yu., Lebedinskii M.I., Vishnevskaya N.A., Borodina E.V., Kovaleva O.N.*, Strunnikova O.K.

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In sterile experiments (without influence of soil microbiomes) the root exudation and expression levels of the plant defense genes (such as *PAL, LOX, PR1*) under relationship between *Fusarium culmorum* (FC) and barley plants of susceptible (SG) and resistant (RG) genotypes were studied. The root exudation of sugars, organic acids, amino acids and aromatic carboxylic acids will be determined by the methods of high-performance liquid chromatography. The genes expression was assessed by RT-PCR.

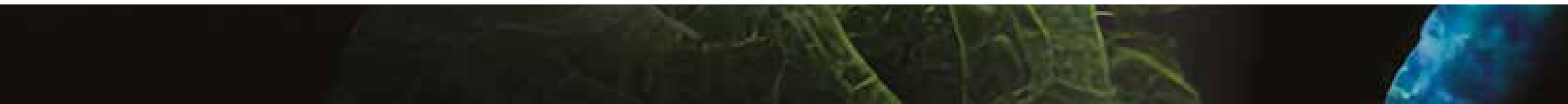
It was found that barley root exudates of the SG contained a much larger amount of organic acids, sugars, amino acids and aromatic acids than exudates of RG. Colonization of roots by *FC* of both SG and RG led to an increase of root exudation of much components in exudates. Root exudates of the RG stimulated the growth of FC to a greater extent than exudates of the SG. All studied protective genes were induced in both SG and RG in response to F. culmorum infection on different days of analysis. However, only PR genes were expressed in roots of SG. In roots of RG, in addition to *PR* genes, the *LOX* gene was induced.

The study was supported by grant from the Russian Science Foundation 22-26-00341.

<u>The main publications of authors on the subject of the abstract:</u>

Vishnevskaya N., Shakhnazarova V., Shaposhnikov A., et al. The role of root exudates of barley colonized by Pseudomonas fluorescens in enhancing root colonization by Fusarium culmorum. Plants, 2020, 9:366. doi:10.3390/plants9030366

Shaposhnikov A., Shakhnazarova V., Vishnevskaya N. et al. Aromatic carboxylic acids in barley-root exudates and their influence on the growth of Fusarium culmorum and Pseudomonas fluorescens. Appl. Biochem. Microbiol. 2020, 56:343–50. doi:10.1134/S0003683820030138



Racial composition of Russian populations of the yellow rust pathogen and effective *Yr* genes for wheat resistance breeding

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Yellow (stripe) rust, caused by *Puccinia striiformis* (Pst) have been frequent and destructive mostly in the Russian North Caucasus. Over the last 5 years, the significance of Pst has markedly increased in other Russian regions. Race composition of Pst was investigated in North Caucasus, North-West, Low Volga, Central Black Earth region, Volga-Vyatka, West Siberia. Virulence pathotypes (races) were identified using the 12 Avocet *Yr* gene lines (*Yr:1,5,6,7,8,9,10,15,17,24,27,Sp*) and eight wheat differentials (Heines VII, Vilmorin 23, Hybrid 46, Strubes Dickkopf, Carstens V, Suwon 92/Omar, Nord Desprez, Heines Peko). High variability in races composition was detected. All isolates were avirulent on *Yr5, Yr10, Yr15,* and *Yr24*, i.e., these genes were effective against the Russian Pst populations. Virulence to *Yr17* was detected for several isolates from the North-West and Low Volga. High resistance to yellow rust in the field was noted in lines with genes *Yr5, Yr8, Yr10, Yr15,Yr24* and varieties Moro, Compare, Carstens and Spaldings Prolific. These effective resistance genes can be proposed for wheat resistance breeding in Russia.

This study was funded by by RSF grant No. 23-26-00042.

The main publications of authors on the subject of the abstract:

Gultyaeva E., Shaydayuk E., Kosman E. Virulence Diversity of Puccinia striiformis f. sp. tritici in common wheat in Russian regions in 2019–2021. Agriculture. 2022;12(11):1957. https://doi.org/10.3390/agriculture12111957

Differences in co-expression of transcription factor genes of the R2R3-MYB and bHLH families determine the specialties in the regulation of anthocyanin biosynthesis in pepper (*Capsicum annuum* L.) and eggplant (*Solanum melongena* L.)

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Federal State Institution «Federal Research Centre «Fundamentals of Biotechnology» of the Russian Academy of Sciences», Moscow, Russia
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The co-expression of TF genes of the R2R3-MYB (*CaMYB113, CaMYB1, CaMYB1-like; SmMYB1, SmMYB2, SmMYB75*) and bHLH (*CaMYC, Ca/SmbHLH137, Ca/SmbHLH143, SmGL3*) families was determined in various organs of pepper and eggplant cultivars differed by the anthocyanin content in leaves, flowers and fruit peel. It was found that in pepper, the purple color of all organs correlates with the *CaMYB113* and *CaMYC* expression. In eggplant, the petal purple color is associated with the expression of *SmMYB2, SmMYB75, SmbHLH137,* and *SmTT8*, while the fruit purple color – with the *SmMYB1, SmGL3,* and *SmTT8* expression. Thus, in two related Solanaceae species, pepper and eggplant, MYB113, a key regulator of the expression of the flavonoid pathway structural genes, functions differently: pepper homolog CaMYB113 controls the anthocyanin biosynthesis in all organs, while eggplant homolog SmMYB2 regulates it only in petals. In the eggplant peel, the anthocyanin biosynthesis is associated with the *SmMYB1* gene, while in pepper, homologous genes (*CaMYB1* and *CaMYB1-like*) are not expressed.

The work was supported by the RSF grant No. 19-16-00016.

Optimization of the intensive cultivation modes for *Chlorella sorokiniana* IPPAS C-1 in the laboratory flat-panel photobioreactors

Shcherbakova N.V., Gabrielyan D.A, Sinetova M.A, Gabel B.V., Gabrielian A.K., Markelova A.G., Los D.A.

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Microalgae are photoautotrophic organisms that have high growth rates and photosynthesis efficiency and may be cultivated indoors in large-scale photobioreactors (PBRs) that allow for the production of high-quality and -purity biomass under controlled conditions of illumination, temperature, pH, etc. The final productivity depends on the choice of the cultivation technology - batch or continuous - which is determined by the tasks, environmental conditions, and other reasons. It is known that semi-continuous mode is more appropriate for biomass production. Here we estimated the productivity of *Chlorella sorokiniana* IPPAS C-1 in laboratory flat-panel PBRs depending on period of harvest and dilution of the suspension. The determined cultivation parameters resulted in a high specific productivity (1.3-1.5 g dw L^{-1} d^{-1}) for a batch mode and were used for biomass accumulation on a first stage of semi-continuous cultivation. The duration of each experiment with three biological repeats was 14-15 days. The discussed principles of intensive cultivation are relevant for the development of technological regimes for the industrial production of Chlorella in flat-panel PBRs of various sizes.

The main publications of authors on the subject of the abstract:

David A. Gabrielyan et al. Cultivation of Chlorella sorokiniana IPPAS C-1 in Flat-Panel Photobioreactors: From a Laboratory to a Pilot Scale // Life, 2022, V. 12(9), p. 1309

David A. Gabrielyan et al. Optimization of CO2 Supply for the Intensive Cultivation of Chlorella sorokiniana IPPAS C-1 in the Laboratory and Pilot-Scale Flat-Panel Photobioreactors // Life, 2022, V. 12(10), p. 1469

Influence of innovative biological plant protection products on the resistance of common wheat to fungal diseases

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Due to climate change, over the past 10-15 years there has been an intensive development of various fungal diseases of the main crops. Chitosan, obtained by means of deacetylation of chitin, has got great potential as safe plant protection product. Novochisol, an innovative derivative of chitosan, has recently been obtained, which has a number of advantages: chemical stability, higher solubility and adhesion, the ability to form very effective complexes with active substances of various action. However, the properties of novochisol have not yet been sufficiently tested on plant objects in vivo. We tested the effectiveness of chitosan and novohizol on seedlings and plants of common wheat T. aestivum. Stem rust Puccinia graminis, a very harmful pathogen of this crop, was used as the causative agent. The preparations were applied to different plant organs (leaf, stem, spikes) at different times before pathogen infection. As a result, novochizol at a concentration of 2.5% showed the greatest effectiveness against stem rust damage when it was applied to the organs of an adult plant 6 days before the fungus attack.

This research was funded by the Russian Science Foundation (RSF project No. 23-16-00119).

The main publications of authors on the subject of the abstract:

Teplyakova O.I., Fomenko V.V, Salakhutdinov N.F. Novochizol™ Seed Treatment: Effects on Germination, Growth and Development in Soft Spring Wheat // Natural Products Chemistry & Research (2022) 10(5): 1-4. doi 10.35248/naturalproducts.10.5.1-04

Take-home message:

Novochisol is very effective and safe innovative preparation for plant protection against fungal diseases

Introgressions into 2A chromosome of bread wheat from relative species as a source of genetic diversity of protein and gluten content in grain

Shchukina L.V., Shamanin V.P.*, Klykov A.G., Lepekhov S.B.***, Börner A.****, Pshenichnikova T.A.**

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The gene pool of wild relatives is a source of genes for improving grain quality. Fragments of 2A chromosome of the relative species *Triticum timopheevii* and *T. militinae* that carry a new genetic factor responsible for the protein content in the grain were transferred into the genome of Saratovskaya 29 (S29). The line S29 (821 2A) with introgression from *T. timopheevii* showed an increase in gluten content in the grain by 3-4% and in protein content by 1-2% when studied in different climatic zones (Shchukina et al. 2022). The yield of the line remained at the level of the parent variety S29. The line S29 (8/1 2A) with the introgression from *T. militinae* (Jakobson et al. 2006) showed an increase in protein by 5% and gluten content by 10% in the grain of different backcrosses grown in greenhouse conditions. Comparison of the introgression regions of the both lines was carried out using molecular markers. It is possible that the identified genetic factor in chromosome 2A belongs to the Gps-2 homoeoallelic series, which controls the high protein content in grain of wheat. Financial support: Russian Science Foundation (№ 23-26-10046) and Novosibirsk Region (№ p-59).

The main publications of authors on the subject of the abstract:

Shchukina L.V. et al. Increased grain protein and gluten contents of bread wheat caused by introgression of a T. timopheevii segment into chromosome 2A // Euphytica (2022) 218:170. doi: 10.1007/s10681-022-03121-w

Jakobson I. et al. Adult plant and seedling resistance to powdery mildew in a Triticum aestivum × Triticum militinae hybrid line // Theor Appl Genet (2006) 112:760–769. doi: 10.1007/s00122-005-0181-2

Take-home message:

Introgressions in 2A chromosome from *T. timopheevii* and *T. militinae* increase protein and gluten content in bread wheat grain.

The impact of salicylic and jasmonic acids on SnDCL1 gene activity of pathogenic fungus *Stagonospora nodorum* in culture *in vitro* and during infection of wheat plants

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Maksimov I.V.

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Stagonospora nodorum is one the most dangerous fungal pathogens, which can affect up to 30-40% of the common wheat crop. For effective protection of wheat, it is necessary to know the physiology of the relationship between the fungus and its host. In this work, we performed a phylogenetic analysis of the *SnDCL1* gene and its expression potential in culture *in vitro* and during infection of wheat plants with varying degrees of resistance to the pathogen under conditions of seed immunization with salicylic and jasmonic acids. It was found that in the pathogenic system the level of *SnDCL1* gene transcripts during the development of the disease steadily accumulated throughout the entire period in both susceptible and resistant cultivars. On a nutrient medium, during cultivation, the level of gene transcripts decreased both in control and experimental conditions, in comparison with the initial fixation point. Thus, our data suggest that the RNA-interfering system of the fungus effectively reacts when interacting with the affected plant, and this interaction depends on the degree of resistance of the host.

Acknowledgements: This work was supported by the RFBR project No. 20-34-90004.

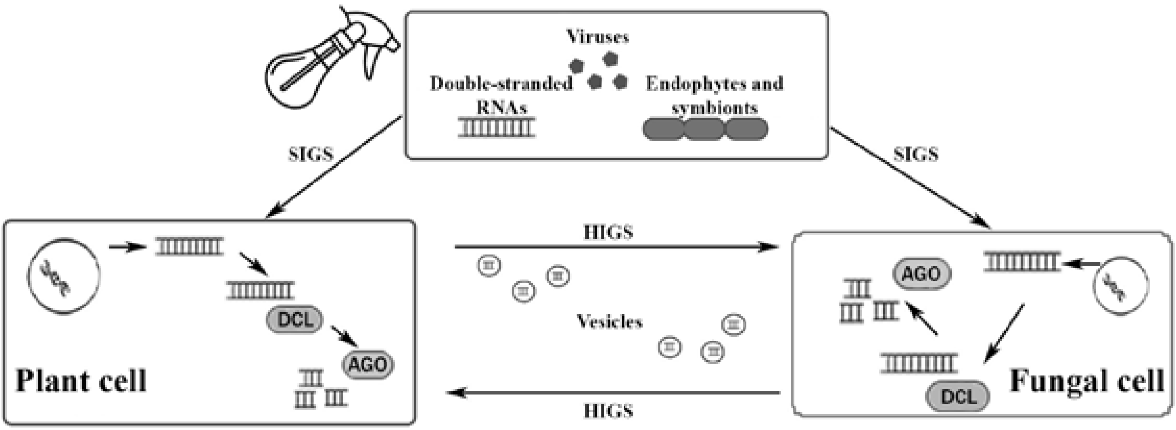
The main publications of authors on the subject of the abstract:

Maksimov I. V., Shein M. Y., Burkhanova G. F. RNA Interference in Plant Protection from Fungal and Oomycete Infection //Applied Biochemistry and Microbiology. 2022. T. 58. №. Suppl 1. C. S16-S31. DOI: 10.1134/S0003683822100106

M.Yu. Shein, et al. Changes in transcriptional activity of TaAgo2 and TaAgo4 genes in wheat plants at infection with Stagonospora nodorum Berk// Труды Кубанского государственного аграрного университета. 2021. 5 (92). C. 196-200. DOI: 10.21515/1999-1703-92-196-200

Take-home message:

RNA-interfering system of the fungus effectively reacts when interacting with the affected plant. The level of SnDCL1 gene transcripts in the pathogenic system steadily accumulated throughout the entire period of the disease.



Genetic diversity of Scots pine (*Pinus sylvestris* L.) populations in the south of Middle Siberia

Sheller M.A., Tóth E.G.*, Ciocîrlan E., Mikhaylov P.V., Tatarintsev A.I., Kulakov S.S., Kulakova N.N., Melnichenko N.P., Ibe A.A.***, Sukhikh T.V.***, Curtu A.L.****

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*Forest Research Institute (FRI), University of Sopron (UOS), Sárvár, Hungary,
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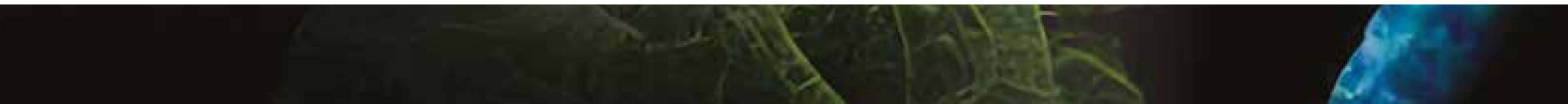
Scots pine (*Pinus sylvistris* L.) is one of the most widespread conifer trees in Eurasia. In the south of Siberia, Scots pine forests are considered as especially valuable natural objects. Here, we evaluated the genetic diversity of three Scots pine populations located in southern Middle Siberia. A total of 80 samples were genotyped with eight nuclear microsatellite markers: Psyl16, Psyl42, Psyl44, Psyl57, PtTX2146, PtTX4001, lw_isotig04306, lw_isotig07383. The results showed high genetic diversity in the studied Scots pine populations, with an average expected heterozygosity of 0.585. Analysis of molecular variance (AMOVA) showed that only 6% of genetic variation existed among populations. The obtained results can be used in monitoring of the state of Scots pine genetic resources in Middle Siberia.

Funding: The research was carried out within the State Assignment (theme «Fundamental principles of forest protection from entomo- and phyto- pests in Siberia» No. FEFE 2020-0014) supported by the Ministry of Education and Science of the Russian Federation.



Inheritance of ear productivity in early-ripening hybrids of soft spring wheat

Shelomentseva T.V., Novohatin V.V., Aitbaeva R.N.

The Research Institute of Agriculture of the Northern Trans-Urals is a branch of the Federal State Budgetary Institution of Science of the Federal Research Center of the Tyumen Scientific Center of the Siberian Branch of the Russian Academy of Sciences, Tyumen, Russia
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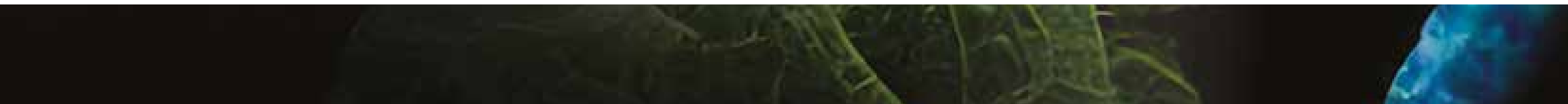
Генетика продуктивности колоса изучена у норвежских сортов: Demonstrant, Laban, Berserk, Krabat, GN 06600, GN 04526. Тестеры - Тюменская 25, Аделина, Лютесценс 70 и АВИАДа. Масса признака. в F_1=0,92г (0,8-1,3г), у тестеров – 0,9г. ОКС лучше выражена у АВИАДы и Лютесценс 70 (gi=0,17;0,14), и Krabat, GN 04526, Demonstrant (gi=0,28;0,18). Тестеры имеют средние значения СКС (δS^2i=0,0303-0,0372), более значима у GN 04526 и GN 06600, (δS2i=0,0312). Berserk, с низкими значениями ОКС и СКС бесперспективен. Laban и Тюменская 25 с низким ОКС (gi=0,13) и выраженной СКС (δS^2i=0,0309-0,0452) дают продуктивные колосья. GN 04526 с низкой СКС (δS^2i=0,018) и выраженной ОКС (gi=0,18), использовать в синтетической селекции. У 75%комбинаций гетерозис, из них у 12 он выражен на 20-55%, более значим: Demonstrant×АВИАДа (1,4г), GN 06600×Лютесценс 70 (1,3) и GN 06600×АВИАДа и GN 04526×Лютесценс 70 (1,2г)-возможны положительные трансгрессии. Полное доминирование у 5 комбинаций (0,9г). В комбинациях GN 04526×Аделина и Laban×Аделина, родители с выраженными ОКС и СКС-отбор возможен после F_3. Неполное доминирование у Laban×Лютесценс 70 и невысокие величины ОКС и СКС родителей ограничивают отбор.



The lichen *Peltigera aphthosa* symbionts functioning under UV-B stress

Shelyakin M.A., Silina E.V., Zakhozhiy I.G., Malyshev R.V., Golovko T.K.

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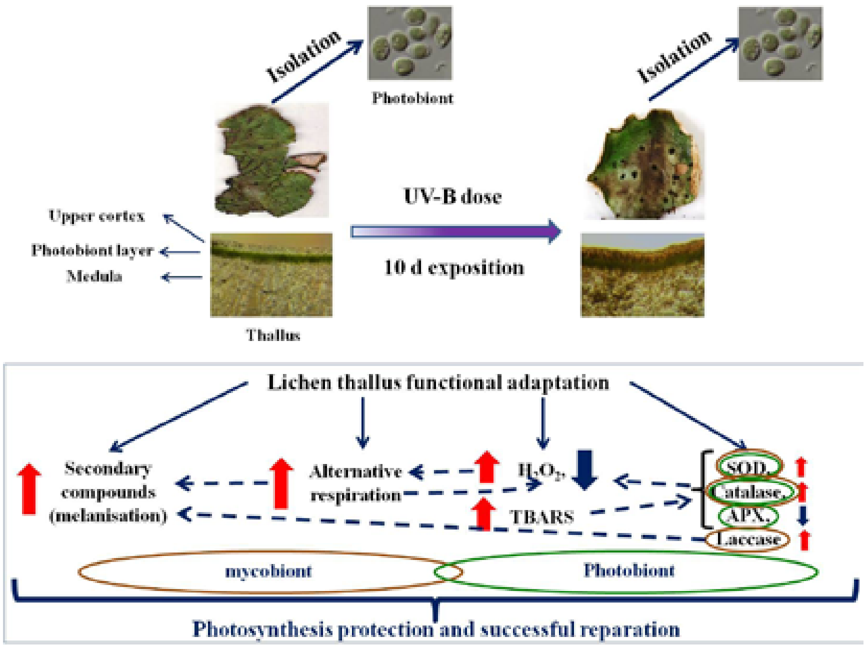
Lichens are an association of a fungus (mycobiont) with green algae and/or cyanobacteria (photobiont) resistant to adverse factors. The physiological and biochemical parameters of *P. aphthosa* thalli and isolated from them green algae *Pseudococcomyxa* cells after exposure to UV-B radiation were studied. UV induced the thallus upper cortex darkening due to the synthesis of secondary metabolites (melanins) by the mycobiont. Accumulation of ROS, an increase in the alternative oxidase content and alternative respiratory pathway were noted in the UV exposed thalli. However, stressed thalli and isolated algae had similar photosynthetic activity parameters to the control ones. At the same time, differences between stressed thalli and isolated algae in the content of ROS, the antioxidant enzymes and their isoforms activity were revealed, which indicates the effect of UV on the redox balance of lichen components. The obtained results reflect the coordinated reaction of the photo- and mycobiont to stress and open up prospects for studying the molecular and genetic interaction between the lichens components.

The work was carried out within the framework of the R&D topic No. 122040600021-4.

<u>**The main publications of authors on the subject of the abstract:**</u>

Shelyakin, M. A. et al. The effect of UV-B radiation on the antioxidant system in the Peltigera aphthosa and Peltigera rufescens lichens // Journal of Siberian Federal University. Biology (2021) 14: 328–338. doi: 10.17516/1997-1389-0359.

Shelyakin, M. A. et al. UV-B induced changes in respiration and antioxidant enzyme activity in the foliose lichen Peltigera aphthosa (L.) Willd. // Acta Physiologiae Plantarum (2022) 44: 116. doi.org/10.1007/s11738-022-03457-9.



Pangenome analysis to reveal phytopathogenic and insecticidal properties of *Serratia marcescens*

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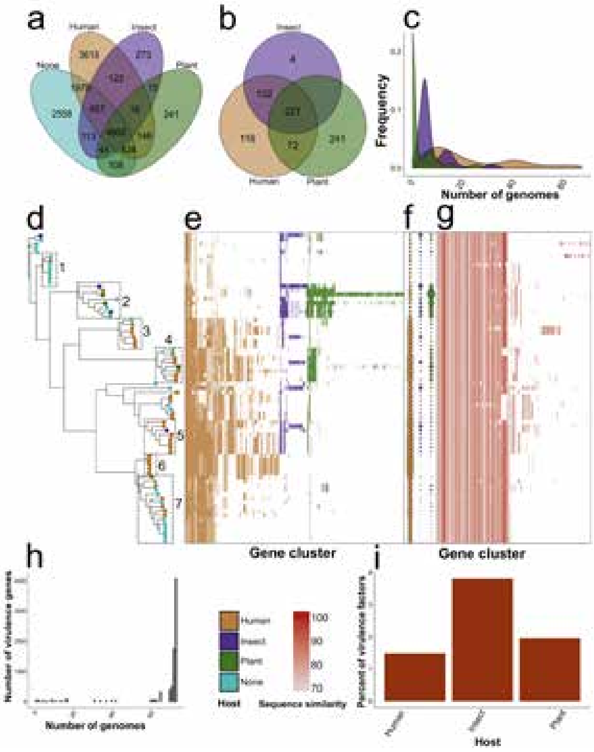
Being commonly known as an opportunistic pathogen, the gram-negative bacterium *Serratia marcescens* exhibits a wide range of activities, namely insecticidal, plant growth-promoting or phytopathogenic. It was shown that environmental isolates may possess these kinds of properties. However, molecular mechanisms delineating host preference remain understudied. A suitable approach for finding specific determinants lies in pangenome reconstruction. To archive this, we analyzed 73 genome assemblies of *S. marcescens* attributed to different hosts, namely, humans, insects, and plants. We found that affecting insects is linked with enzymes, including isochorismatase, hydrolases, and Gcn5-related N-acetyltransferase, which is notable due to putative neurotoxic effects impairing synthesis of neuromediators. Assemblies isolated from plants, were enriched with type VI secretion systems and modulators of cell wall synthesis. Functional annotation revealed that identified gene sets form distinct clusters. This work was made with the support of the Ministry of Science and Higher Education of the Russian Federation in accordance with agreement № 075-15-2021-1055 date September 28, 2021.

<u>Take-home message:</u>

Pangenome analyses of *Serratia marcescens* provided molecular determinants of host preference towards plants and insects.

Identified host adaptation factors represent diverse functional pathways.



Bioinformatics from genome to optimal diet

**Shlikht A.G., Kramorenko N.V.,
Tamkovich S.N.*, Shtam T.A.****

Far Eastern Federal University, Vladivostok, Russia,
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The aim of the study is to create an integrated intelligent bioinformatics system that allows you to trace the entire chain of omics biochemical processes, including: genomics, epigenomics, transcriptomics, exomics, proteomics, metabolomics, reactomics, genomic mutations and genetic diseases related to nutrition, nutrigenetics, nutrigenomics, nutriciology, and finally to analyze and optimally synthesize diets based on an expanded a linear programming model that allows taking into account a wide variety of norms and restrictions in the diet. For these purposes, highly structured relational models of omics data, databases and knowledge bases, algorithms and programs were created that made it possible to formalize omics interactions and transformations. The basis for the practical implementation of diets is a system-cybernetic model, in the direct chain of which lies the traditional analysis of the diet, and in the feedback of control the optimal synthesis of an additional diet to ensure a balance of physiological norms and restrictions. The AI is built on the basis of deep classical production expert systems, which makes it possible to give a full explanation of the solutions

The main publications of authors on the subject of the abstract:

A.Shlikht, N. Kramorenko. (2020) Genome-centered integrated instrumental information system modeling and interpretation of human and virus omics, Bioinformatics of Genome Regulation and Structure/Systems Biology (BGRS/SB-2020): 114-115.

Шлихт А.Г., Краморенко Н.В. Геном-центрированная интеллектуальная системно кибернетическая структурированная модель в задачах оптимального синтеза рационов человека. // Актуальные вопросы биологической физики и химии, т.5, №2, 2020, - С.301-305

Take-home message:

Creation of a digital model "Genotype-Habitat-Phenotype"

Artificial intelligence (AI) in the problem of analysis and interpretation of omics data

From quantitative computer BigData to qualitative human SmallData

Transcriptomic response of *Solanum tuberosum* L. to potato spindle tuber viroid infection

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Potato spindle tuber viroid (PSTVd) causes diseases of *Solanaceae* crops, including tomato and potato, negatively affecting yields. Mechanisms underlying development of desease phenotypes remain elusive. PSTVd strain NicTr-3 causes severe desease symptoms in *S. tuberosum* cv Colomba. After three cycles of propagation in tomato, however, viroid caused very mild symptoms in potato. Analysis of potato leaves transcriptome at three time points showed significant changes of gene expression at 14 dpi and 30 dpi. Genes with decreased expression at 30 dpi are associated with DNA replication, regulation of cell cycle and cell wall-associated and microtubule-based processes, indicating supression of growth and cell division. Additionally, genes associated with general metabolism lower their expression. Thus, transcriptomic changes point to plant dormancy in responce to viroid inoculation.

The work was funded by the Kurchatov Genome Center of the Institute of Cytology and Genetics of Siberian Branch of the Russian Academy of Sciences, agreement with the Ministry of Education and Science of the Russian Federation, no. 075-15-2019-1662

The main publications of authors on the subject of the abstract:

Kochetov, A.V.; Shmakov, N.; Afonnikov, D.A.; Vasiliev, G.V.; Shatskaya, N.V.; Egorova, A.A.; Mironenko, N.V.; Lashina, N.M.; Khiutti, A.V.; Afanasenko, O.S. Three Cycles of Continuous Propagation of a Severe PSTVd Strain NicTr-3 in Solanum lycopersicum cv. Rutgers Resulted in Its Attenuation and Very Mild Disease Symptoms in Potato //Agronomy (2023) 13: 684. https://doi.org/10.3390/agronomy13030684

Take-home message:

Transcriptomic changes in potato inoculated with PSTVd after three cycles of propagation in tomato are associated with negative regulation of cell cycle, metabolism retardation and general dormancy of leaves

Determining molecular functions of the loci controlling synthesis of flavonoids in barley (*Hordeum vulgare* L.)

Shoeva O.Y., Mukhanova M.A.*, Zedgenizova V.D., Kukoeva T.V., Totsky I.V., Li R.*, Denisov A.A.*, Shmakov N.A., Zakhrabekova S.***, Stuard D.***, Hansson M.***, Khlestkina E.K.******

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**Institute of Cytology and Genetics, Siberian Branch of Russian Academy of Sciences,
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Flavonoid compounds are secondary metabolites, having important functions in plant physiology. In barley, they are synthesized in grain envelopes and in addition to important role in seed dormancy and in protection of seeds against adverse environments they have a significant impact on the quality characteristics of grain, determining its intended use. Thirty *Anthocyanin-less (Ant)* loci that control synthesis of flavonoids in barley have been revealed, but molecular functions have been determined only for some of them. In the current study, the molecular functions of *Ant1, Ant2, Ant5, Ant13, Ant25,* and *Ant27* participating in genetic control of anthocyanins and proanthocyanidins synthesis in vegetative tissues and grain were revealed. The natural and induced allelic diversity of the candidate genes of these loci was studied as well. The results obtained are of fundamental importance and also contribute to the solution of practical problems related to efficient breeding new barley cultivars with given profiles of flavonoid compounds in grain. The study was supported by Kurchatov Genomic Center of ICG SB RAS (No. 075-15-2019-1662).

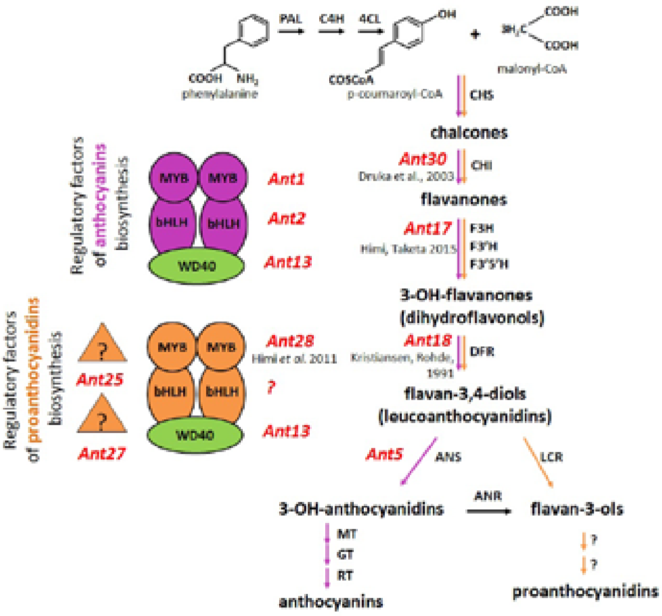
The main publications of authors on the subject of the abstract:

Shoeva O.Yu., et al. Genes determining the synthesis of flavonoid and melanin pigments in barley // Vavilovskii Zhurnal Genetiki i Selektsii = Vavilov Journal of Genetics and Breeding (2018) 22(3):333-342. doi 10.18699/VJ18.369

Shoeva O.Yu., et al. Ant13 encodes regulatory factor WD40 controlling anthocyanin and proanthocyanidin synthesis in barley (Hordeum vulgare L.) // J Agri Food Chem (2023) doi: 10.1021/acs.jafc.2c09051

Take-home message:

Molecular functions and allelic diversity of some loci controlling flavonoid compounds biosynthesis in barley were studied. It is a basis for further identification of genes and breeding new cultivars with given profiles of flavonoids in grain.



Receptor-like kinases of the LRR-RLKIII subfamily as potential resistance genes in plants of the *Solanaceae* family to *Pectobacterium* spp.

Shrub E.V., Vychyk P.V., Badalyan O.A., Nikolaichik Y.A.

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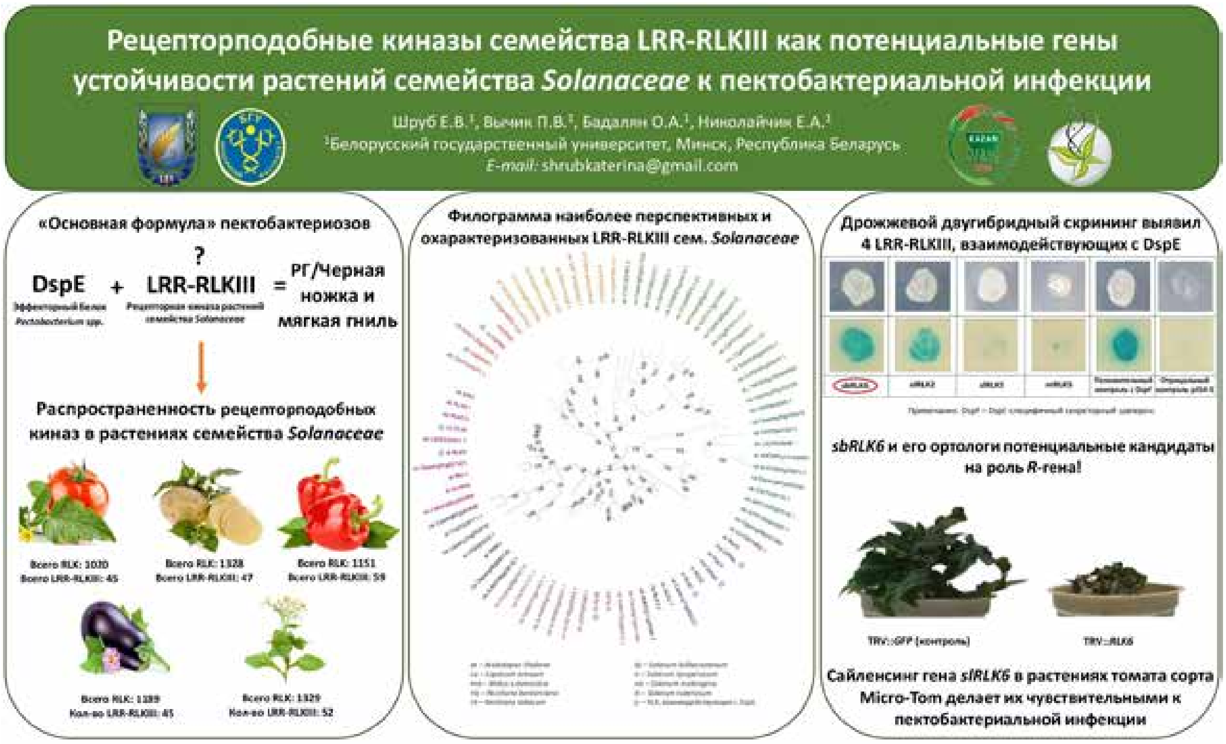
Геномы растений семейства пасленовых содержат 600+ генов рецепторных протеинкиназ с лейцин-богатыми повторами (LRR-RLK), из них большинство вероятно связано с детекцией патогенов, но функционально не охарактеризовано. Для актуальных патогенов картофеля из рода *Pectobacterium* специфические иммунные рецепторы не описаны. Однако у *Malus x domestica* охарактеризованы 4 LRR-RLK из подсемейства LRRIII (DIPM1-4), специфически взаимодействующие с эффекторным белком DspE и участвующие в распознавании *Erwinia amylovora.* Поскольку ортолог DspE является основным эффектором и у *Pectobacterium* spp., мы выполнили филогенетический анализ рецепторов подсемейства LRRIII из четырех видов пасленовых–потенциальных доноров генов устойчивости и выделили 8 кластеров родственных RLK. Проверка киназных доменов репрезентативных представителей кластеров в дрожжевой двухгибридной системе выявила четыре RLK, взаимодействующих с DspE. Вирус-индуцированный сайленсинг этих RLK показал, что они участвуют в распознавании пектобактерий. Наиболее перспективным в качестве потенциального гена устойчивости оказался ген RLK6 из *Solanum bulbocastanum,* не ортологичный DIPM-белкам яблони.

Take-home message:

Впервые выявленные потенциальные рецепторы основного эффектора *Pectobacterium* spp. имеют хороший потенциал как гены устойчивости к бактериозам.



Рецепторподобные киназы семейства LRR-RLKIII как потенциальные гены устойчивости растений семейства *Solanaceae* к пектобактериальной инфекции

Шруб Е.В.[1], Вычик П.В.[1], Бадалян О.А.[1], Николайчик Е.А.[1]
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«Основная формула» пектобактериозов

DspE + ? LRR-RLKIII = РГ/Черная ножка и мягкая гниль

Распространенность рецепторподобных киназ в растениях семейства *Solanaceae*

Всего RLK: 1020
Всего LRR-RLKIII: 45

Всего RLK: 1328
Всего LRR-RLKIII: 47

Всего RLK: 1151
Всего LRR-RLKIII: 59

Всего RLK: 1189
Кол-во LRR-RLKIII: 45

Всего RLK: 1329
Кол-во LRR-RLKIII: 52

Филограмма наиболее перспективных и охарактеризованных LRR-RLKIII сем. *Solanaceae*

Дрожжевой двугибридный скрининг выявил 4 LRR-RLKIII, взаимодействующих с DspE

sbRLK6 и его ортологи потенциальные кандидаты на роль *R*-гена!

TRV::GFP (контроль)

TRV::RLK6

Сайленсинг гена *slRLK6* в растениях томата сорта Micro-Tom делает их чувствительными к пектобактериальной инфекции

Transcriptomic markers of the effectiveness of pea symbioses associated with the duration of seed maturation

Shtark O.Y., Zorin E.A., Kulaeva O.A., Romanyuk D.A., Sulima A.S., Kichigina N.E., Zhernakov A.I., Akhtemova G.A., Zhukov V.A.

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E-mail: oshtark@yandex.ru

Symbioses of legumes with nodule bacteria (NB) and arbuscular mycorrhizal (AM) fungi improve the biomass and quality of seeds. In this work, we sought for transcriptomic markers of prolongation of the seed maturation and consequent increase in seed biomass in pea (*Pisum sativum* L.). Pea genotypes k-8274 and k-3358 (responsive and nonresponsive to inoculation) were grown under inoculation with AM fungi, NB, AM + NB, and in the absence of inoculation, and the seed transcriptome was analyzed at four stages of maturation by 3-MACE-RNAseq. The genes with gradually increasing expression (from timepoint I to IV, no inoculation) were considered as potential seed maturation markers. The analysis of expression of these genes indicated that NB contributed to acceleration of seed maturation, whereas AM (alone, or in combination with NB) contributed to prolongation of seed maturation in the responsive genotype k-8274. For the non-responsive genotype k-3358 this effect was much less pronounced. Thus, the genes of k-8274, which were down-regulated upon AM inoculation, can be considered as potential seed markers of symbiotic responsivity. This work was supported by the RSF grant #22-16-00109.

The main publications of authors on the subject of the abstract:

Shtark O.Y. et al. Metabolic alterations in pea leaves during arbuscular mycorrhiza development // PeerJ (2019) 7: e7495. doi:10.7717/peerj.7495

Mamontova T. et al. Profiling of seed proteome in pea (Pisum sativum L.) lines characterized with high and low responsivity to combined inoculation with nodule bacteria and arbuscular mycorrhizal fungi. // Molecules (2019) 24(8): 1603. doi:10.3390/molecules24081603

Take-home message:

Mycorrhiza prolongs the process of seed maturation of the pea k-8274 genotype (highly responsive to inoculation). Using seed transcriptome analysis, we have identified a number of genes that can be considered as markers of symbiotic responsivity.

Features of the formation of generative parts of plants in pea genotypes with recessive alleles affecting productivity

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Изучение динамики формирования потенциала продуктивности генотипов с усатым типом листа, лигнифицированными бобами и деформированным синтезом лигнина, устойчивых к полеганию и раскрыванию бобов, позволило определить генотипические особенности развития репродуктивных органов под воздействием экстремальных условий. Среди генотипов с лущильными бобами у новых сортов Салават и Нарат сформировалось большее число завязей 7,2-8,2. Полноценные семена были получены от 60,7-68,2 %заложенных семязачатков с максимальным показателем у сорта Нарат. У сортов с беспергаментными бобами число завязей насчитывалось в среднем на растение 8,2, максимальное их число (9,7) формировал перспективный сорт Купидон. Для генотипов с беспергаментными бобами характерным является большее число семязачатков и семян на растении. В процессе совершенствования селекции сорта данной группы удалось постепенно увеличить продуктивность семяобразующей способности до 72,6-81,1%. У сортов с беспергаментными бобами основная масса семян приходилась на два нижних продуктивных узлах со смещением 30 % на второй и небольшой части в зависимости от генотипа 4,7-13,6 % – на третий верхний.

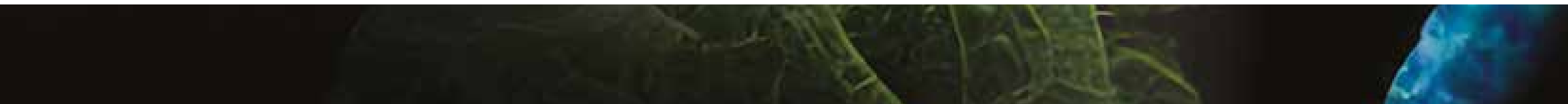
The main publications of authors on the subject of the abstract:

Фадеева А.Н., Шурхаева К.Д., Фадеев Е.А. Особенности продуктивности плодо- и семяобразования у сортов гороха с различным типом листа. Нива Татарстана. 2014. №2-3. с. 37-39.

Фадеева А.Н., Шурхаева К.Д. Эффективность использования продуктивности семяобразования в селекции Pisum sativum L. Вестник Казанского государственного аграрного университета. 2018. т.13. №2 (49). с. 52-56.

Take-home message:

У сорта Нарат полноценные семена были получены от 68,2% заложенных семязачатков. В процессе совершенствования селекции у сортов с деформированным синтезом лигнина удалось постепенно увеличить продуктивность семяобразующей способности до 72,6-81,1%.



Peculiarities of recombinant GFP accumulation in leaves of transplastomic tobacco plants *Nicotiana tabacum* L. cv. Petit Havana

Sidorchuk Y.V., Zagorskaya A.A., Belavin P.A., Khajrulina E.S., Samodurov D.E., Deineko E.V.

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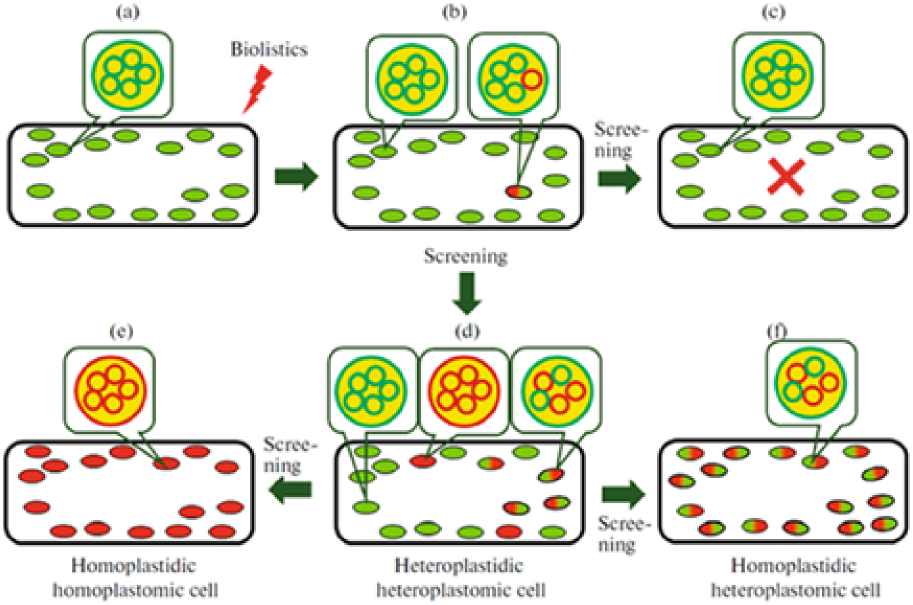
E-mail: sidorch@bionet.nsc.ru

Транспластомные растения обладают способностью достигать высоких значений выхода рекомбинантных белков по сравнению с ядерными трансформантами, что обеспечивается чрезвычайно высокой копийностью пластома в клетках. Однако на пути их создания существует ряд трудностей, основными из которых являются крайне низкая эффективность трансформации и сложность отбора высокопродуктивных гомопластидных форм. В лаборатории биоинженерии растений методом биобаллистики была создана серия транспластомных растений, экспрессирующих репортерный ген *gfp* и селективный маркер aadA, обеспечивающий устойчивость к антибиотикам спектиномицину и стрептомицину. Одновременно для контроля были получены ядерные трансформанты, экспрессирующие тот же самый ген *gfp.* Согласно полученным данным количество рекомбинантного GFP белка в листьях транспластомных растений было в 4 раза ниже, чем в листьях обычных ядерных трансформантов, и составило в среднем 0,12±0,01% от ОРБ. Особо следует отметить полное отсутствие вариабельности по данному признаку. Вероятно, это связано с тем, что при использованных методах отбора не был достигнут уровень полной гомопластомности хлоропластов.

Работа поддержана грантом РНФ № 23-24-00545.

The main publications of authors on the subject of the abstract:

Rozov S.M., Sidorchuk Yu.V., Deineko E.V. Transplastomic Plants: Problems of Production and Their Solution //Russian Journal of Plant Physiology (2022) 69 (2): 132-141. DOI: 10.1134/S1021443722020157



Genome assemblies of *Colletotrichum lini* strains of different virulence

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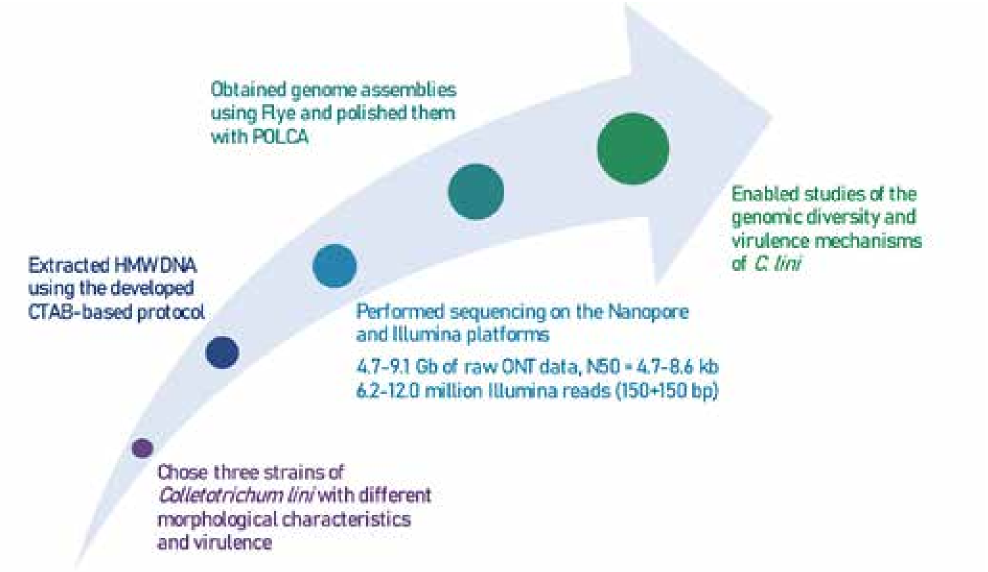
Colletotrichum lini is known as a fungal pathogen of flax which causes anthracnose and leads to yield and product quality losses. To study the diversity of strains and establish the mechanisms of virulence, we chose three strains of C. *lini*. The selection of strains was based on a number of features, including pathogenicity degree, form and size of conidia, and growth rate. The chosen strains had the following characteristics: #771 – low virulence, moderate sporulation, dark-grey mycelium; #778-1 – medium virulence, copious sporulation, light-grey mycelium; #751-1 – high virulence, copious sporulation, grey-rose mycelium. Sequencing was performed on the Oxford Nanopore Technologies (ONT) and Illumina platforms. We obtained 4.7-9.1 Gb of raw ONT data with an N50 of 4.7-8.6 kb, 6.2-12.0 million Illumina reads (150+150 bp). Genome assemblies were obtained using Flye, polished with POLCA. The lengths of produced assemblies were in the range of 52.0-52.6 Mb, N50 laid in the range of 1.0-1.5 Mb, the BUSCO completeness was 95.6-96.7%. The obtained assemblies will help in studying the genomic diversity and virulence mechanisms of C. *lini*. This work was funded by RSF, grant 22-16-00169.



Ascorbate metabolism in *Arabidopsis* plants with knockout of genes encoding enzymes of the L-galactose pathway for ascorbate synthesis

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Ascorbate (Asc) is an important low molecular antioxidant in the plant cell, a substrate of ascorbate peroxidase in the ascorbate–glutathione cycle (AGC). Asc synthesis via the L-galactose pathway is connected with the mitochondrial electron transport chain (mETC). We studied the role of the L-galactose pathway of Asc synthesis in the activity of AGC enzymes, as well as in the mETC response to the suppression of Asc synthesis in *Arabidopsis thaliana* plants with a knockout of VTC2 and GLDH – genes encoding key enzymes of the L-galactose pathway, under high light (400 µmol/m² s). Knockout lines, especially *vtc2*, responded to high light by activation of alternative oxidase in mETC (AOX) reflected in the higher level of *AOX1a* expression and the enzyme activity, as well as increased Asc synthesis, in *vtc2* line – due to GLDH activation. Based on the gene expression and activity of APX and DHAR, the Asc pool was insufficient for effective functioning of AGC. This indicated a weakening of the ability of Asc to be included in defense reactions at its stable deficiency in tissues and the participation of AOX in maintaining Asc synthesis.

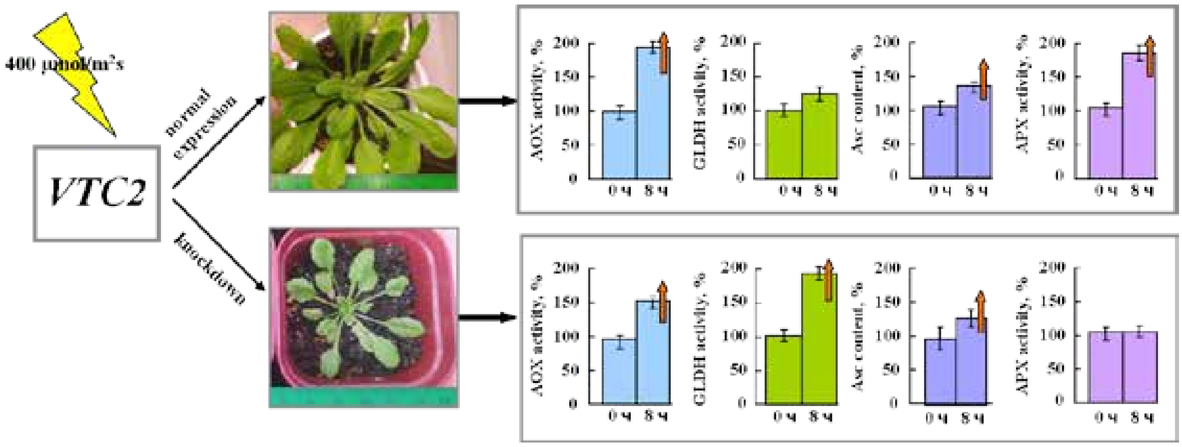
This research was funded by the RSF (22-24-01082).

The main publications of authors on the subject of the abstract:

Garmash, E.V.; Dymova, O.V.; Silina, E.V.; Malyshev, R.V.; ,Belykh E.S.; Shelyakin, M.A.; Velegzhaninov, I.O. AOX1a expression in Arabidopsis thaliana affects the state of chloroplast photoprotective systems under moderately high light conditions // Plants. 2022, 11, 3030. https://doi.org/10.3390/plants11223030

Take-home message:

Ascorbate synthesis depends on activity of mitochondrial alternative oxidase.



Enrichment of the bread wheat genome with new leaf pubescence genes from related species

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Leaf hairiness is an important adaptive trait as affects the leaf surface microclimate. Variability for this trait is found in common wheat. Three genes are known for today. The *Hl1* gene located on 4B chromosome provides a dense layer of trichomes up to 150 µm. The *Hl2* gene located on 7B chromosome forms rare long trichomes more than 400 µm. The predicted *Hl3* gene forms a rare layer of short trichomes, mainly on the underside of the leaf. The wheat genome has been enriched with hairiness genes from various sources. Homologous to the *Hl2* gene, the $Hl2^{aesp}$ gene was transferred to chromosome 7B from *Aegilops speltoides.* The Hltt gene with the phenotypic effect similar to *Hl2* was transferred to 5A chromosome from T*riticum timopheevii,* The replacement of chromosome 4B by 4Th from wheatgrass changes the dense hairiness into rare long trichomes. In 4D/4Th substitution, rare long trichomes are combined with a canopy of short trichomes. Some of these genes affect the intensity of transpiration and photosynthesis and may be relevant to adaptation to diverse environment including the droughty ones. Financial support: Russian Science Foundation (23-24-10029) and Novosibirsk Region (p-63).

The main publications of authors on the subject of the abstract:

Simonov et al. The identification of a new gene for leaf pubescence introgressed into bread wheat from Triticum timopheevii Zhuk. and its manifestation in a different genotypic background // Plant Genetic Rerources: Characterization and Utilization (2021) 19(3): 238-244. doi:10.1017/S1479262121000277

Pshenichnikova et al. Diversity of leaf pubescence in bread wheat and relative species // Genetic Resources and Crop Evolution (2017) 64(7):1761-1773. doi: 10.1007/s10722-016-0471-3

Development of a system for the search of regeneration regulators in pea

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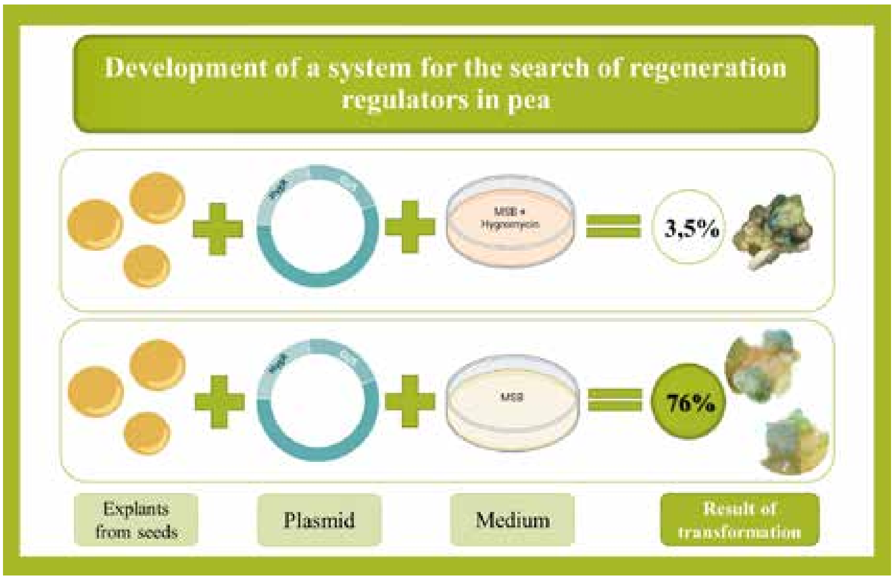
Breeding of *Pisum sativum* L. *in vitro* is laborious to achieve. For pea the main type of regeneration is shoot formation, but their rooting can be difficult. Only limited success has been reported for in vitro regeneration of seed legumes by somatic embryogenesis. To search for morphogenetic regulators of somatic embryogenesis, it is necessary to develop a system which will allow obtaining of transgenic pea calli. To achieve this goal, we have selected protocols for in vitro cultivation of pea, which in combination with the transformation of explants make it possible to obtain calli with transgenic tissue. Under certain conditions, transgenic tissue was observed in 76% of transformed calli. We also assessed the possibility of using hygromycin as a selective marker for these protocols. Sensitivity to hygromycin was different in different cultivation systems. Supported by the Ministry of Science and Higher Education of the Russian Federation, (Agreement 075-10-2021-093, Project [PBB-RND-2243]).

The main publications of authors on the subject of the abstract:

Simonova V. Y. Development of a testing system for regeneration regulators in Pisum sativum L. // Ecological genetics (2022) 21. DOI: 10.17816/ecogen112419



Identification and characterization of SP5G-like genes in genus *Prunus*

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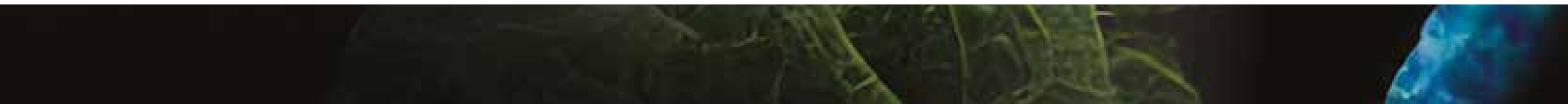
The regulation of flowering time is the most important factor affecting the fruit yield in many crop species. There are several genes containing the PEBP domain that are involved in the regulation of flowering: CEN, TFL1, FT, SP and MTF. For the self pruning 5G (SP5G) gene in tomato, a mechanism dependent of photoperiod has been established. Currently, this gene was studied in Solanaceae plants (potato, tomato). However, few people know about SP5G homologous genes in stone fruit crops. In this study, we found SP5G-like genes in apricot, almond and peach based on complete genomes. PEBP family genes, including putative SP5G homologs, were identified in genus Prunus. Phylogenetic analysis based on genes containing the PEBP domain in Solanaceae plants and stone fruit crops was performed, revealing strong clustering within this family. MTF and FT genes form separate clusters with high booster support, the SP5G genes of Solanaceae are in the same cluster as FT and CEN genes and are diverged from the genus Prunus. The study is supported by the Kurchatov Genomic Centre of the Nikita Botanical Garden – National Scientific Center of RAS (075-15-2019-1670).

Take-home message:

Through a phylogenetic analysis of homologous genes in tomato, potato, apricot, almond and peach, we have identified potential gene-candidates for regulating flowering time in genus Prunus by genetic engineering.



Carbon partitioning between neutral lipids and starch in green microalga *Neochlorella semenenkoi* strain IPPAS C-1210.

Sinetova M.A., Bobrovnikova L.A., Starikov A.Yu., Sidorov R.A., Gabrielyan D.A., Mironov K.S.

K.A. Timiryazev Institute of Plant Physiology, Russian Academy of Sciences, Moscow, Russia
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The object of the study was a unicellular green microalga *Neochlorella semenenkoi* strain IPPAS C-1210. The effect of N and Mg starvation on growth and general biochemical composition of microalgal cells was studied. Both types of starvation resulted in growth inhibition, a significant decrease in chlorophyll and carotenoid content, impairment of photosynthesis, and in starch accumulation. N starvation also induced TAG accumulation. Cycloheximide inhibitor analysis showed that translation of proteins responsible for TAG biosynthesis was induced already at 3-4 h of N starvation.

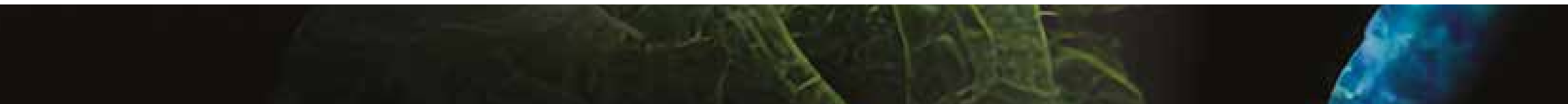
The study of the dynamics of total lipid fatty acid (FA) composition showed that the greatest variability was observed in the content of oleic and alpha-linolenic acids. The study of FA composition of TAG in late stages of growth and under N and P starvations showed that it is possible to obtain TAGs with a large range of unsaturated index.

The addition of organic compounds mainly stimulated lipid accumulation especially in -N cells, both in the light and in the dark. In some cases, starch accumulation was enhanced.

Sequencing and assembly of de-novo transcriptome of the studied strain was performed.

<u>The main publications of authors on the subject of the abstract:</u>

Krivina, E.S., Bobrovnikova, L.A., Temraleeva, A.D., Markelova, A.G., Gabrielyan, D.A., & Sinetova, M.A. (2023). Description of Neochlorella semenenkoi gen. et. sp. nov.(Chlorophyta, Trebouxiophyceae), a Novel Chlorella-like Alga with High Biotechnological Potential. Diversity, 15(4), 513. https://doi.org/10.3390/d15040513



Pathways of selenium effect on the secondary metabolism of *Lamiaceae* plants

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Maslennikov P.V., Golovin A.V.**

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The most important groups of secondary metabolites of *Lamiaceae* plants are components of essential oils (mono- and sesquiterpenes, alcohols, aldehydes, etc.) and phenylpropanoids (hydroxycinnamic acids, flavonoids). A number of studies have shown that the treatment of plants with selenium (in the form of selenate, selenite, nano-Se, Se-containing amino acids) leads to changes in the qualitative and quantitative content of these metabolites. The following aspects were identified as possible ways of regulating plant secondary metabolism by Se-supplementation: changes occurring in primary metabolism (especially in metabolism of sulphur and nitrogen), hormonal regulation (changes in the expression of genes sensitive to auxin, cytokinin, ethylene and/or jasmonic acid), changes in redox-metabolism (selenium compounds can act as antioxidants, pro-oxidants, affect the level of glutathione and the activity of antioxidant enzymes), as well as changes at the transcriptomic level of the biosynthesis of secondary metabolites (for example, changes in the expression of *PAL, CHS, FLS, FOMT, MYB1, MYB2*).

This research was funded by Russian Science Foundation, grant number 22-14-00106.

The main publications of authors on the subject of the abstract:

Skrypnik L. et al. The Integral Boosting Effect of Selenium on the Secondary Metabolism of Higher Plants // Plants (2022) 11(24):3432. doi: 10.3390/plants11243432.

Skrypnik L. et al. Biomass, Phenolic Compounds, Essential Oil Content, and Antioxidant Properties of Hyssop (Hyssopus officinalis L.) Grown in Hydroponics as Affected by Treatment Type and Selenium Concentration // Horticulturae (2022) 8(11):1037. doi: 10.3390/horticulturae8111037.

Take-home message:

The study of "Se-sensitive" metabolic pathways, including pathways for the biosynthesis of secondary metabolites, will provide a deeper understanding of the actual role of selenium in plant organisms.

Research of doubled *Cucurbita pepo* L. haploids obtained by in vitro culture of unsullied ovules for resistance to real powdery mildew

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Federal State Budgetary Scientific Institution Federal Scientific Vegetable Center Moscow Region, Odintsovo, Russia
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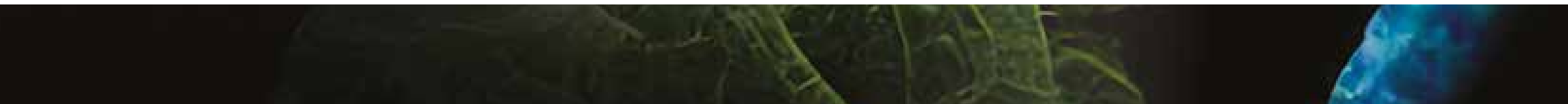
Obtaining stable homozygous lines opens up opportunities for the selection of valuable genotypes, including those with resistance to economically significant diseases of crops. The improved technology of obtaining doubled haploids on the squash culture by the method of culture of unsullied ovules *in vitro* makes it possible to obtain valuable material for solving the problems of breeding this popular culture. The F1 Gold Rush hybrid of Seminis Vegetable Seeds, Inc. selection was used as a donor material for the squash. In the conditions of the Non-Chernozem region, the most harmful pathogens on representatives of the Cucurbitaceae family L. the pathogens of this powdery mildew include: Podosphaera xanthii and Erysiphe cichoracearum. As a result of the evaluation, valuable samples were selected.

The main publications of authors on the subject of the abstract:

Sletova M.E. Species composition and identification of pathogens of real powdery mildew of pumpkin crops. Vegetable crops of Russia. 2022;(4):91-97. (In Russ.) https://doi.org/10.18619/2072-9146-2022-4-91-97

Ermolaev A.S., Domblides E.A. Optimization of steps in the technology of obtaining doubled haploids of summer squash (Cucurbita pepo L.) in the culture of unpollinated ovules in vitro. Vegetable crops of Russia. 2022;(5):5-14. (In Russ.) https://doi.org/10.18619/2072-146-2022-5-5-14



Identification of quantitative trait loci based on a comprehensive phenotypic assessment of the genotyped population of winter rye

Smirnova N.V., Semilet T.V., Khlestkina E.K.

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This study is aimed at the main problem in the field of modern crop genetics - the identification of quantitative trait loci associated with economically valuable traits and the analysis of genomic regions significantly associated with such traits. The purpose of this work is to identify and label QTLs that control economically valuable traits of winter rye under the conditions of VIR Pushkin Laboratories. Rye (*Secale cereale L.*) is one of the main food and fodder crops with the largest sown areas in Russia, Poland and Germany (FAO). As a plant material in this study, a splitting population based on the «New Era» variety created by Professor V.D. Kobylyansky, will be served. At this stage, a comprehensive phenotypic assessment of individual plants in the splitting population in the offspring from free pollination of selected broad-leaved accessions of the «New Era» variety population was carried out. And also carried out genotyping of the studied individual plants using SNP-markers. In the near future, QTL analysis will be carried out based on the obtained pheno- and genotypic data, the identification of loci with the greatest contribution to phenotypic variability.

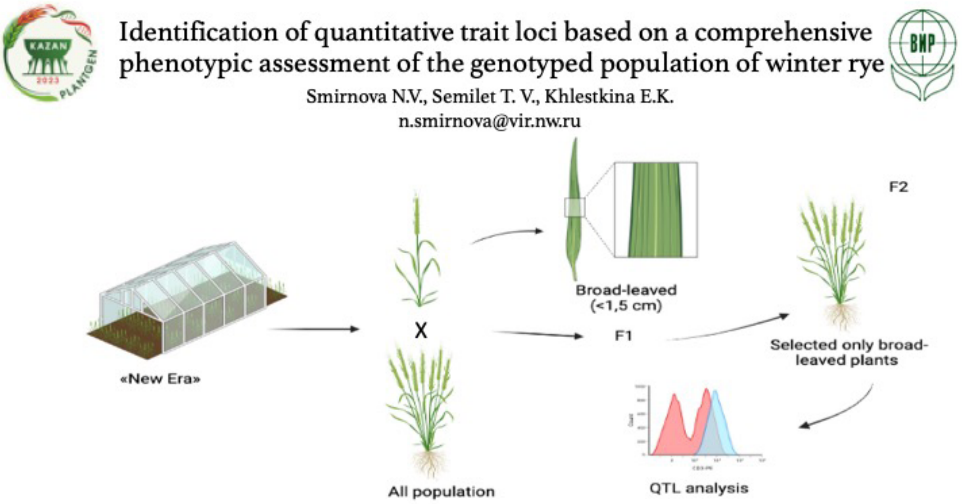
The work was carried out at a support of the research program «Bread of Russia» agreement № 075-15-2021-1066 from 28.09.2021

The main publications of authors on the subject of the abstract:

Semilet T, Shvachko N, Smirnova N, Shipilina L, Khlestkina L. Using DNA markers to reconstruct the lifetime morphology of barley grains from carbonized cereal crop remains unearthed at Usvyaty Settlement. Biol Commun. In press

Take-home message:

The purpose of this work is to identify and label QTLs that control economically valuable traits of winter rye under the conditions of VIR Pushkin Laboratories.



Identification of quantitative trait loci based on a comprehensive phenotypic assessment of the genotyped population of winter rye
Smirnova N.V., Semilet T. V., Khlestkina E.K.
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Detection Of Allene Oxide Synthase Genes In The Genome Of Rye (*Secale cereale*)

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Oxylipins are bioactive compounds that take part in the plant defense formation against phytopathogens and other stressors. There are several ways of the oxylipins biosynthesis. One of them is lipoxygenase cascade. The "key players" of this process are lipoxygenases and CYP74 enzymes. The most "famous" CYP74s are allene oxide synthases (AOS), the product of their activity is jasmonic acid (JA).

Rye (Secale cereale) is one of the most important agricultural crops. It is considered as one of the most resistant to phytopathogens. Despite this, rye is often affected by pink snow mold. This rye disease is caused by the fungus Microdochium nivale.

There were shown that infection of rye with a weakly virulent strain of M.nivale 499 led to a great increase in the content of JA, which may indicate activation of the AOS pathway of the lipoxygenase cascade. However, none of the rye AOS has been previously described. Moreover, in 2021 rye genome was annotated. These facts formed the basis of this research. Transcriptomic analysis of rye showed the presence of four genes that could encode AOSs.

The work is supported by the Russian Science Foundation (Project No. 23-14-00350).

The main publications of authors on the subject of the abstract:

Gorshkov V.Y. et al. Differential modulation of the lipoxygenase cascade during typical and latent Pectobacterium atrosepticum infections // Annals of Botany (2022) 129(3):271-286. doi: 10.1093/aob/mcab108.

Take-home message:

As a result of transcriptome analysis of rye, four genes encoding potential allene oxide synthases were found.

Green seed photosynthesis: What do we know about?

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Photosynthesis can occur not only in leaves but in other green plant organs (petioles, stems, fruits, seeds, etc.). While leaves serve as primary photosynthetic organs, reproductive organs could provide themselves with 60% of their total carbon requirement. However, the mechanisms of non-foliar photosynthesis are poorly understood. We studied the green embryos of developing *Pisum sativum* L. seeds. The developing embryos have chlorophylls (Chl) a and b, carotenoids, and chloroplasts. The primary function of embryonic Chl is to provide photochemical processes, contributing to a more efficient accumulation of reserve nutrients. The synthesized in the light reactions NADPH and ATP are involved in metabolizing maternal sucrose to acetyl-CoA and then to fatty acids. At late maturation, against the seed desiccation background, the thylakoid system of plastids is destroyed, and Chl degraded. The gene expression of Chl degradation enzymes is controlled by the transcription factors ABI3 and ABI5. The stay-green mutation or blocking of the SGR genes leads to non-efficient Chl degradation. The research was funded by the Russian Science Foundation № 22-26-00273 (https://rscf.ru/project/22-26-00273).

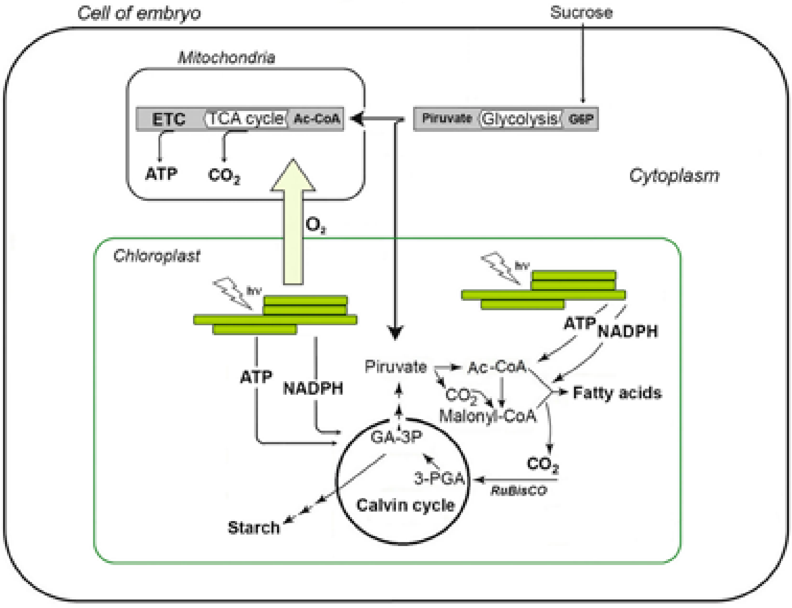
The main publications of authors on the subject of the abstract:

1) Smolikova G. et al. Genetic and hormonal regulation of chlorophyll degradation during maturation of seeds with green embryos // IJMS (2017) 18(9): 1993. doi:10.3390/ijms18091993

2) Smolikova G. et al. Comparative analysis of the plastid conversion, photochemical activity and chlorophyll degradation in developing embryos of green-seeded and yellow-seeded pea (Pisum sativum L.) cultivars // Funct. Plant Biol. (2020) 47(5): 409-424. doi:10.1071/FP19270

Take-home message:

Primary function of embryonic chlorophylls is to provide photochemical processes, contributing to a more efficient accumulation of reserve nutrients. Green seed photosynthesis has been a target for improving crop yield.



Study the dynamics of the *Nicotiana benthamiana* chloroplasts proteome in response to drought stress

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*Institute of Bioengineering, Federal Research Center of Biotechnology of the Russian Academy of Sciences, Moscow, Russia,
**Laboratory of Analytical Biochemistry and Biotechnology, Timiryazev Institute of Plant Physiology, Russian Academy of Sciences, Moscow, Russia
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Studying the dynamics of the proteome of *Nicotiana benthamiana* chloroplasts in response to drought stress is a relevant topic in plant biology. To effectively conduct such research, it is necessary to ensure compatibility between chloroplast isolation methods and proteomic analysis methods. One of the most effective approaches is isolation in a percoll gradient. This method allows obtaining a fraction of chloroplasts with the lowest amount of contamination from other cellular organelles. We adapted this method for leaves of mature, 50-day-old *Nicotiana benthamiana* plants grown under normal controlled conditions and under drought stress. The isolated chloroplasts were further analyzed using the bottom-up LC-MS/MS proteomic approach. This method is based on the trypsin digestion of proteins, with the FASP technology, and subsequent purification of the hydrolysate with solid-phase liquid chromatography. The purified peptides were analyzed by nanoflow liquid chromatography-mass-spectrometry, it is allowing us to characterize the dynamics of the proteome of N. benthamiana chloroplasts in response to drought stress.

Plant PARP1 can act as a mediator in a functional link between nucleolar protein activities and SA-mediated antivirus defense

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Shemyakin-Ovchinnikov Institute of Bioorganic Chemistry of the Russian Academy of Sciences, Moscow, Russia,
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This study uncovers a previously unrecognized mechanism by which Cajal bodies (CBs) and their components regulate host defenses against pathogen attack. Our previous results demonstrated that the tobacco rattle virus (TRV) 16K protein interacts with and relocalizes coilin from CBs to the nucleolus and these events are accompanied by activation of salicylic acid (SA)-responsive gene expression and restriction of TRV systemic infection.

In this work we have found that poly(ADP-ribose) polymerase 1 (PARP1) modulates this antiviral response. We reveal that coilin in turn traps PARP1 within this sub-nuclear domain, preventing it trafficking from the nucleolus for PAR cleavage and recycling. This leads to over-accumulation of PAR/PARylated proteins and may enhance accumulation of SA and increase elicitation of SA-mediated defense responses. The SA treatment subverted a negative effect of 3AB PARP inhibitor on plant recovery from TRV infection, implicating PARP1 as a key component of a regulatory network integrating CB functions, SA signalling pathways and plant antiviral defense.

This work was supported by the grant of the Russian Science Foundation No. 22-14-00049.

The main publications of authors on the subject of the abstract:

Spechenkova, N. et al. ADP-Ribosylation and Antiviral Resistance in Plants // Viruses (2023) 15: 241, doi:10.3390/v15010241

Shaw, J. et al. Interaction of a Plant Virus Protein with the Signature Cajal Body Protein Coilin Facilitates Salicylic Acid-Mediated Plant Defence Responses // New Phytologist (2019) 224: 439–453. doi:10.1111/nph.15994.

Multi-omics profiling of flax in response to *Fusarium* wilt disease

Stanin V.A.*, Samsonova A.A., Kanapin A.A.**, Bankin M.P.*, Logachev A.A.*, Rozhmina T.A.***, Samsonova M.G.***

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Flax wilt is an aggressive disease caused by soil-borne pathogen *Fusarium oxysporum* f. sp. *lini*. The fungus poses a major threat to flax production worldwide, as occasionally yield losses reach 70%. Here, we present first insights into regulatory mechanisms involved in response to the infection.

The susceptible LM98 and resistant Atalante flax varieties have been infected with MI39 *Fusarium* isolate, harvested on the 3rd and the 5th day post inoculation. The roots were subjected to omics profiling to gain mechanistic insights into the induced systemic resistance in flax.

The in-depth molecular profiling revealed distinct response modes in the studied flax varieties. Specifically, Atalante exhibited sharp response to infection and activation of mechanisms of ROS reduction, cell wall modification and phytoalexins synthesis. In contrast, the LM98 failed to show any specific reaction to pathogen, thus highlighting the difference in defense response dynamics between the two studied varieties.

A rich molecular dataset generated in the framework of this study paves the way for further in-depth studies of mechanisms of resistance to flax wilt within the host-pathogen paradigm.

<u>The main publications of authors on the subject of the abstract:</u>

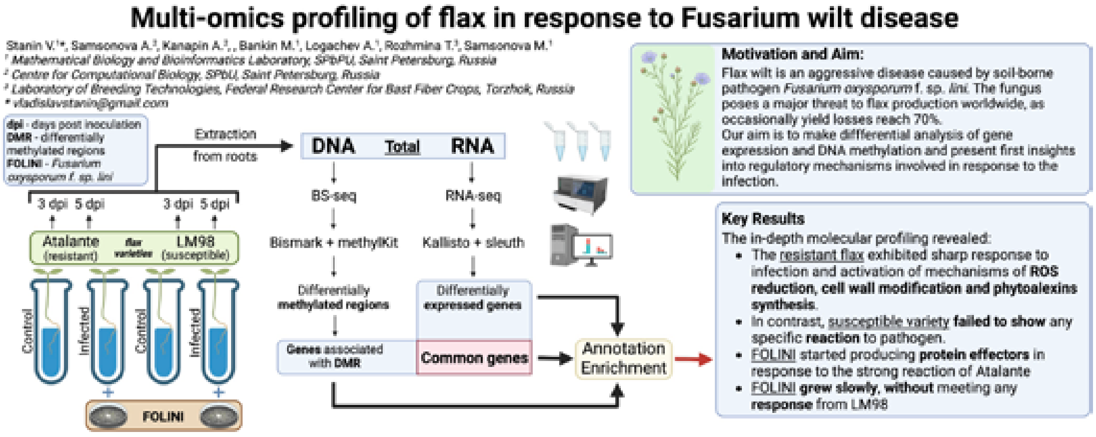
Duk M. et al. The Genetic Landscape of Fiber Flax // Front Plant Sci. (2021) vol.12. doi: 10.3389/fpls.2021.764612

Kanapin A. et al. The Genome Sequence of Five Highly Pathogenic Isolates of Fusarium oxysporum f. sp. lini // MPMI. Scientific Societies (2020) vol.33, №9:1112–1115. doi: 10.1094/MPMI-05-20-0130-SC

Kanapin A. et al. Genomic Regions Associated with Fusarium Wilt Resistance in Flax // International Journal of Molecular Sciences. MDPI (2021) vol.22, №22. doi:10.3390/ijms222212383

<u>Take-home message:</u>

The study of molecular mechanisms of response to Fusarium infection lays the foundation for further research of resistance to flax wilt in host-pathogen paradigm.



Multi-omics profiling of flax in response to Fusarium wilt disease

Stanin V.[1]*, Samsonova A.[2], Kanapin A.[2], , Bankin M.[1], Logachev A.[1], Rozhmina T.[3], Samsonova M.[1]
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dpi - days post inoculation
DMR - differentially methylated regions
FOLINI - *Fusarium oxysporum f. sp. lini*

Motivation and Aim:

Flax wilt is an aggressive disease caused by soil-borne pathogen *Fusarium oxysporum* f. sp. *lini*. The fungus poses a major threat to flax production worldwide, as occasionally yield losses reach 70%.
Our aim is to make differential analysis of gene expression and DNA methylation and present first insights into regulatory mechanisms involved in response to the infection.

Key Results

The in-depth molecular profiling revealed:
- The <u>resistant flax</u> exhibited sharp response to infection and activation of mechanisms of **ROS reduction, cell wall modification and phytoalexins synthesis**.
- In contrast, <u>susceptible variety</u> **failed to show** any specific **reaction** to pathogen.
- <u>FOLINI</u> started producing **protein effectors** in response to the strong reaction of Atalante
- <u>FOLINI</u> **grew slowly, without** meeting any **response** from LM98

Effects of alleles of *Ppd-D1* and *Vrn-B3* genes on heading time and yield-related traits in spring common wheat

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The heading time in wheat is of great importance for adaptation to environmental conditions and grain yield. The spring common wheat varieties Tulun 15 and Obskaya 2 were selected for hybridization. Both varieties had the same alleles of the Vrn-1 genes, however, the Tulun 15 variety had dominant *Ppd-D1*a and *Vrn-B3a* alleles, while the Obskaya 2 variety had recessive *Ppd-D1b* and *Vrn-B3b* alleles. Using allele-specific primers F_2 generation plants with different combinations of *VRN* and *PPD1* alleles were detected. The F3-4 generation plants were sown in the field to study the alleles' effect of the *Ppd-D1* and *Vrn-B3* genes on the heading time and yield traits. The estimate showed that the heading time from early to late was distributed in plants containing the alleles: *Ppd-D1a and Vrn-B3a → Ppd-D1a and Vrn-B3b → Ppd-D1b and Vrn-B3a → Ppd-D1b* and *Vrn-B3b.* The yield-related traits were also evaluated: the number of grains per plant, the weight of grains per plant, the weight of 1000 grains, etc.

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

Take-home message:

It was shown that the dominant allele Ppd-D1a has a stronger effect on the heading time of wheat than the dominant allele Vrn-B3a. The results obtained in this work can be used in the breeding of common wheat for heading time.

Gaining Aspen Protoplasts and Their Regeneration Protocol Development

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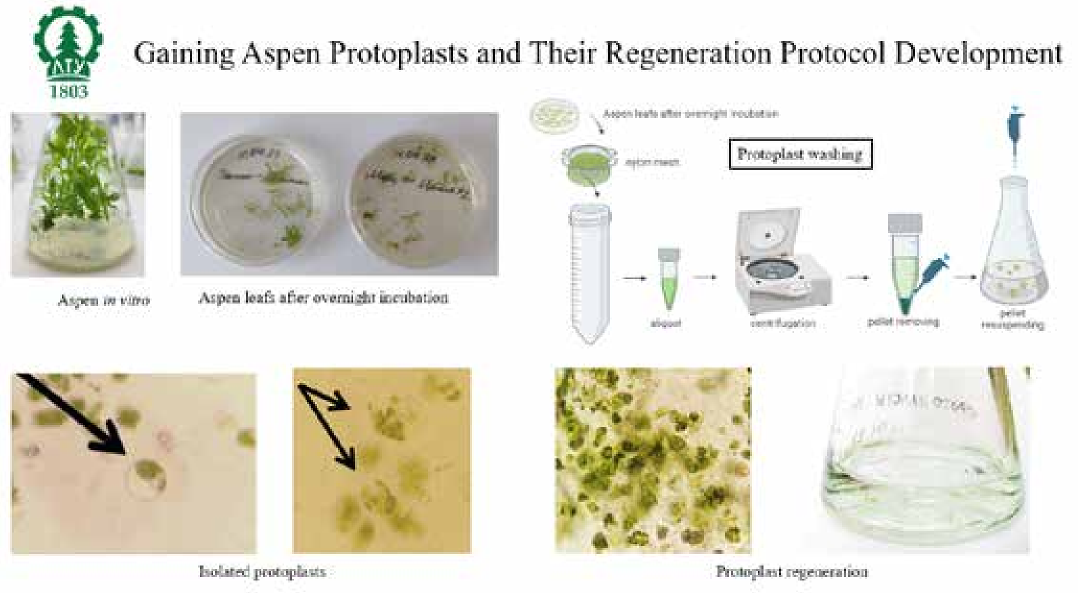
Development of methods for obtaining and regenerating aspen protoplasts enables the expansion of genome editing capabilities in woody plants. Protoplasts lack cell walls, which considerably enhances transfection efficiency. However, plant regeneration from single cells is challenging. A series of experiments were conducted to obtain protoplasts from aspen leaves using a combination of mechanical and enzymatic cell wall degradation methods, followed by regeneration in nutrient media. The most effective enzyme ratios were determined as macerozyme:cellulase - 1:3.75 and pectinase:cellulase - 1:2. The enzymatic cell wall degradation efficiency of the first composition was higher than that of the second. Protoplast cell wall regeneration was carried out in a suspension medium containing ½ MS with the addition of mannitol (0.6M) to maintain the osmotic environment. The proliferation medium contained 0.1 mg/L 6-benzylaminopurine (BAP) and 0.22 mg/L naphthaleneacetic acid.

Take-home message:

We have experimentally obtained protoplasts from aspen leaves using a combination of mechanical and enzymatic methods for breaking down cell walls and their regeneration to expand the possibilities of genetic engineering in woody plants.



Gaining Aspen Protoplasts and Their Regeneration Protocol Development

Aspen *in vitro*

Aspen leafs after overnight incubation

Protoplast washing

Isolated protoplasts

Protoplast regeneration

Data monitoring system for crop production tasks

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The modern scientific community is increasingly uniting to jointly solve many issues related to crop production. Currently, IT technologies are tightly connected with every aspect of our life, but the share of digitalization of the experimental base for research centers remains insufficient. Scientists need more and more modern equipment with feedback on the parameters of lighting, temperature, humidity, composition of cultivation media, gas composition, air movement and others. But even if the researcher has at least some of the equipment that allows reading these parameters, then when writing an article, the question arises of how to process this data at the modern level and display them in it. This can be helped by the use of a cloud storage system for the received data, which also allows the exchange of information, including the results of experiments in real time, with other scientific teams. Also, such a system allows you to follow the progress of research, which can simplify the writing of joint papers with colleagues from other countries.

Take-home message:

Scientists need more and more modern equipment and more digitalization of their research.

How to store and process the data received by the researcher at the modern level and display them in the future article.

Phytopathogenic fungi in forest nurseries of Krasnoyarsk region and the Republic of Khakassia

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Грибные фитопатогены являются одной из основных причин гибели посадочного материала в лесных питомниках, что отражается на эффективности ведения лесовосстановления. В 2022 году в рамках работ по оценке фитосанитарного состояния посадочного материала и насаждений было проведено обследование шести лесных питомников, расположенных в Красноярском крае и Республике Хакасия. Объектами исследования служили сеянцы сосны обыкновенной, сосны кедровой сибирской) и ели сибирской 1-5-летнего возраста. Идентификация видового состава патогенных организмов проводилась молекулярно-генетическими методами. Секвенирование фрагментов ДНК проведено на генетическом анализаторе ABI PRISM 310. В результате диагностики были обнаружены представители 15 родов патогенных и условно-патогенных грибов, вызывающих болезни посадочного материала: *Alternaria, Botrytis, Herpotrichia, Cladosporium, Lophodermium, Coleosporium, Phoma, Darkera, Aspergillus, Rhizoctonia, Sclerotinia, Gremmenia, Fusarium, Sydowia, Cenangium*. По частоте встречаемости доминировали такие фитопатогенные грибы как *Rhizoctonia sp., Gremmenia sp., Sydowia polyspora, Cenangium acuum, Darkera parca, Herpotrichia sp., Sclerotinia nivalis.*

Exogenous double-stranded RNAs for regulation of anthocyanin accumulation in tomato *Solanum lycopersicum*

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RNA interference (RNAi) is a natural post-transcriptional regulatory mechanism that can be artificially induced by exogenous application of double-stranded RNAs (dsRNAs) to the plant surfaces. Recent studies show that it is possible to silence plant genes and change plant properties using plant RNA spraying and other approaches for dsRNA delivery. In this study, we investigated the effect of exogenous gene-specific dsRNAs on tomato leaves for silencing tomato *Solanum lycopersicum* genes encoding MYB-family transcription repressors of anthocyanin biosynthesis. We found that exogenous application of dsRNAs encoding MYB-family transcription factors led to the silencing of endogenous genes *SlMybATV, SlMyb32, SlMyb76,* and *SlTry* encoding MYB transcriptional repressor of anthocyanin biosynthesis and up-regulated anthocyanin levels. We demonstrated that exogenous gene-specific dsRNAs can induce post-transcriptional gene silencing in tomato by direct foliar application of dsRNA. This approach may be used for plant secondary metabolism induction and as a silencing tool for gene function studies.

This work was supported by the grant 23-26-00253 from the Russian Science Foundation.

The main publications of authors on the subject of the abstract:

Kiselev K.V., Suprun A.R., Aleynova O.A., Ogneva Z.V., Kalachev A.V., Dubrovina A.S. External dsRNA downregulates anthocyanin biosynthesis-related genes and affects anthocyanin accumulation in Arabidopsis thaliana // International Journal of Molecular Sciences. — 2021— V. 22. — P. 6749. doi: 10.3390/ijms22136749.

Take-home message:

We demonstrated that exogenous gene-specific dsRNAs can induce post-transcriptional gene silencing in tomato leaves by direct foliar application of dsRNA.

The role of vernalization in flowering transition of wild and cultivated *Cicer*

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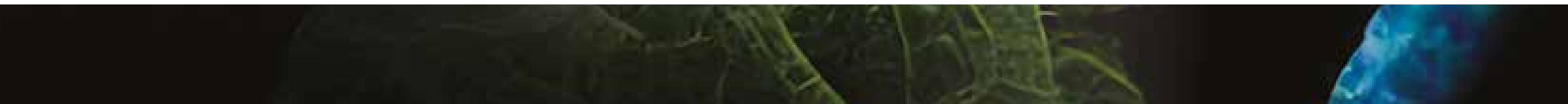
The vernalization treatment significantly promotes flowering in wild legume species. However, domestication led to the development of early flowering varieties that lost their response to vernalization. Nevertheless, the late flowering accessions of cultivated *Cicer* have been shown to be vernalization sensitive. To understand the molecular mechanisms of the vernalization response in wild and cultivated *Cicer,* we apply an intergative approach, which combines mathematical modeling and experiment. The data on flowering time gene expression in plants after vernalization and without vernalization treatment is used as an input for the dynamical mathematical model. The model evaluates regulatory interactions within the core gene network based on the RT qPCR data. We aim to identify the regulatory modules responsible for the differences in vernalization-induced flowering between wild and cultivated Cicer.

This research is funded by Russian Science Foundation (RSF), grant № 23-26-00203.

The main publications of authors on the subject of the abstract:

Surkova S.Yu. and Samsonova M.G. Mechanisms of Vernalization-Induced Flowering in Legumes // International journal of molecular sciences (2022) 23(17): 9889. doi:10.3390/ijms23179889

Surkova S.Yu. et al. Transcriptomic Analysis of Flowering Time Genes in Cultivated Chickpea and Wild Cicer. International journal of molecular sciences (2023) 24(3): 2692. doi:10.3390/ijms24032692



Identification of mutations introduced by the CRISPR-Cas9 system in the genome of polyploid plants

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Mannans and shoot gravitropism in *Arabidopsis thaliana*

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Gravitropism is bending of a plant organ in response to gravity. It is controlled by cell wall extensibility, flexibility and compression resistance, and can be used to decipher cell wall polymer functions. We have recently demonstrated that brassinazol (BRZ), an inhibitor of brassinosteroid hormone biosynthesis, stimulated Arabidopsis hypocotyl gravitropism, which was accompanied by a decrease in mannans, minor cell wall polysaccharides with unknown functions. Now we tried to establish if mannans actually mediated the BRZ effect by comparing the wall biomechanics and metabolomics of hypocotyls in gravistimulated/unstimulated BRZ-treated Col-0 Arabidopsis plants and *csla2csla3csla9* (*csla2,3,9*) triple mutants, which are devoid of cell wall mannans. The wall biomechanics and metabolomics were studied by the creep method and GC-MS, respectively. We found that BRZ modified the biomechanics via cell wall loosening proteins, while *csla2,3,9* affected it by changing the basic cell wall polymer structure. The BRZ- and *csla2,3,9*-induced changes in the metabolome were also very different. We thus conclude that the BRZ effect on shoot gravitropism is not mediated by mannans.

The main publications of authors on the subject of the abstract:

Somssich M. et al. Brassinosteroids Influence Arabidopsis Hypocotyl Graviresponses through Changes in Mannans and Cellulose // Plant & Cell Physiology (2021) 62: 678-692. doi: https://doi.org/10.1093/pcp/pcab024

This study was supported by the RSF grant № 23-24-00379, https://rscf.ru/project/23-24-00379/

Dynamics of root water transport and transpiration in intact maize plants during adaptation to water stress: the role of aquaporins

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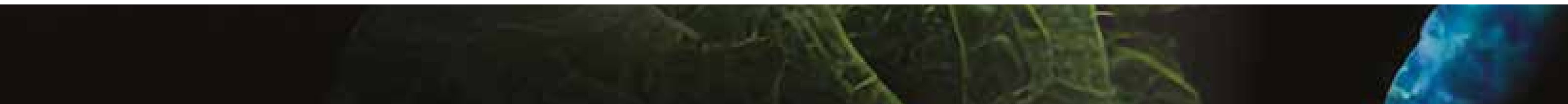
Using an original methodological and technical approach, we studied the dynamics of radial water transfer in roots and the rate of transpiration in intact maize plants in response to water stress. It was shown that the response of maize plants to water stress is accompanied by changes in the intensity and redistribution of water transfer along different pathways of radial water transport in the roots. During the first minutes after the onset of water stress, the intensity of symplastic and transmembrane water transport in roots decreases with a parallel, short-term increase in the rate of transpiration in leaves and apoplastic transfer in roots. Then, the intensity of transmembrane and symplastic water transfer is restored to initial values and is accompanied by increase in the expression of aquaporin genes and changes in aquaporins localization in root tissues. Under conditions of water stress cell-to-cell water transport in roots becomes dominant. The important role and relationship of aquaporins in roots and leaves in the process of adaptation of the plant hydraulic system to water stress is shown.

This study was supported by the RSF (project number 22-74-10087).



Interspecific Hybridization in Lentil Breeding

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Lentil *Lens culinaris* Medik. is a valuable legume crop with annual world production about 6 million tons and average yield of 1 t/ha. The relatively low yield depends on biological features of lentil plant. Hybridization with wild relatives can increase biological potential of the crop.

Among the seven taxa of the genus *Lens* Mill. only *L. culinaris* is cultivated one. Wild lentil species are characterized by small brown mottled seeds, small dehiscent pods and strong seed dormancy. We crossed L. *culinaris* with two species L. *orientalis* [Boiss.] Hand.-Mazz. and L. *tomentosus* Ladiz. In cross with L. *orientalis* the F_1 seeds were germinated *in vitro* to get out of dormancy. Embryo rescue technique was used to overcome the postzygotic barrier in cross with L. *tomentosus*. All pod-dehiscent plants were eliminated in F_2 generation. The breeding lines recombinant in cotyledon color and seed coat color were obtained after some cycles of selection.

Variety Vostochnaya was released in 2017 as a result of interspecific hybridization of cultivated lentil with wild relative L. *orientalis.* Variety Flamenco created with use of germplasm of wild species L. t*omentosus* was released in 2021.

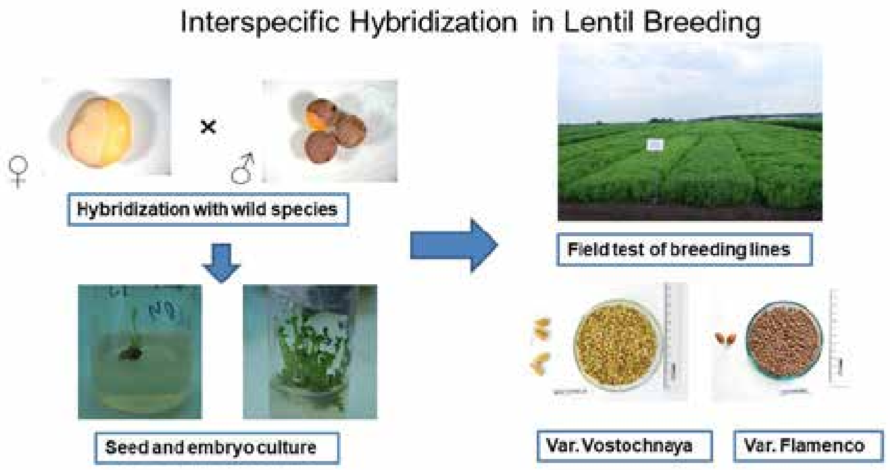
<u>The main publications of authors on the subject of the abstract:</u>

Suvorova G. N. at. al. The yield of new varieties of lentil Lens culinaris Medik. // Sustainable and Innovative Development in the Digital Age IOP Conf. Series: Earth and Environmental Science 650(2021) 012094 IOP Publishing doi:10.1088/1755-1315/650/1/012094

Suvorova G. N. at. al. New Lentil variety Flamenco // Legume and Groat Crops (2020) 4(36): 42-46 DOI: 10.24411/2309-348X-2020-11203 (in Russian)

<u>Take-home message:</u>

Lentil varieties Vostochnaya and Flamenco released in 2017 and 2021 have been created by means of interspecific hybridization with wild relatives *Lens* orientalis and L. *tomentosus* respectively.



Search of target genes of ERFs by their transient gene expression in isolated celery protoplasts

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Cell walls largely determine plant biology: cell growth and shape, differentiation into tissues, interaction with the environment, etc. Plant cell walls are composed mainly of polysaccharides, which are the most common organic materials on earth.

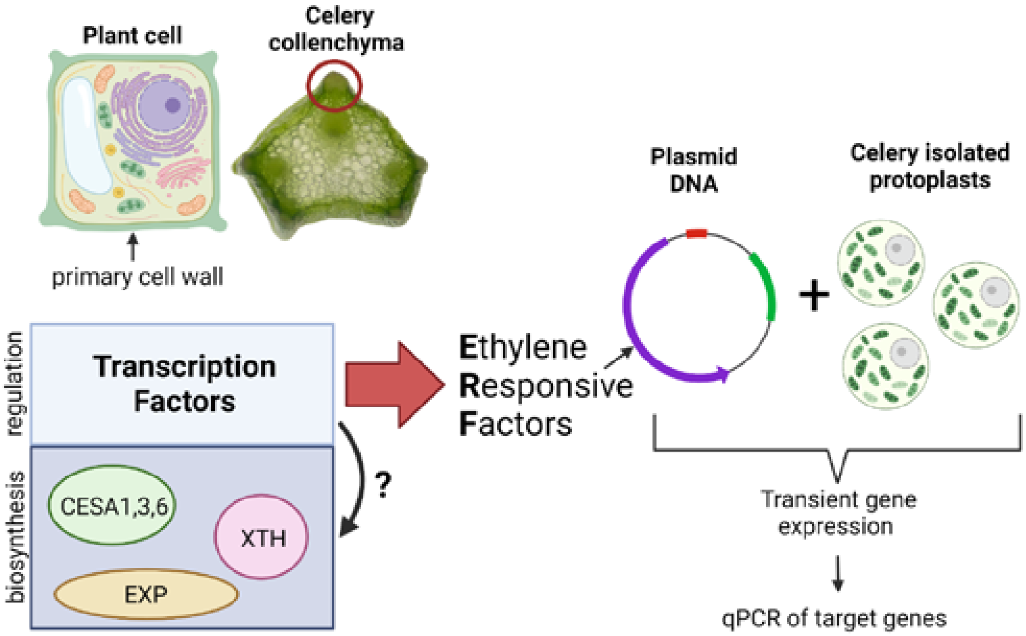
There are three types of cell walls that differ in biochemical and physical features: primary, secondary, and tertiary. But only the primary cell wall is present in all types of plant cells.

There are plenty of genes in plant genomes involved in the biosynthesis of cell walls and their regulation. So far, only a few regulators are known to be involved in primary cell wall formation: Ethylene Responsive Factors (ERFs) of the IIId/e groups showed an effect on primary cell wall biosynthesis.

We offered to use celery collenchyma with a thickened primary cell wall as the model to search for unknown regulators of primary cell wall development. We optimized a system of isolated celery protoplasts and used this for transient expression of several celery *ERF* genes. Then, using qPCR, we analyzed the expression of potential target genes for selected ERFs. Thus, an effective tool for investigating the function of transcription factors was developed.

Take-home message:

We used transient gene expression of ERFs in a system of isolated celery protoplasts and analyzed the expression of their potential target genes by qPCR to determine ERFs' functions in regulating plant primary cell wall biosynthesis.



Hydrophobins of the phytopathogenic fungus *Microdochium nivale* – putative weapons for host plant colonization

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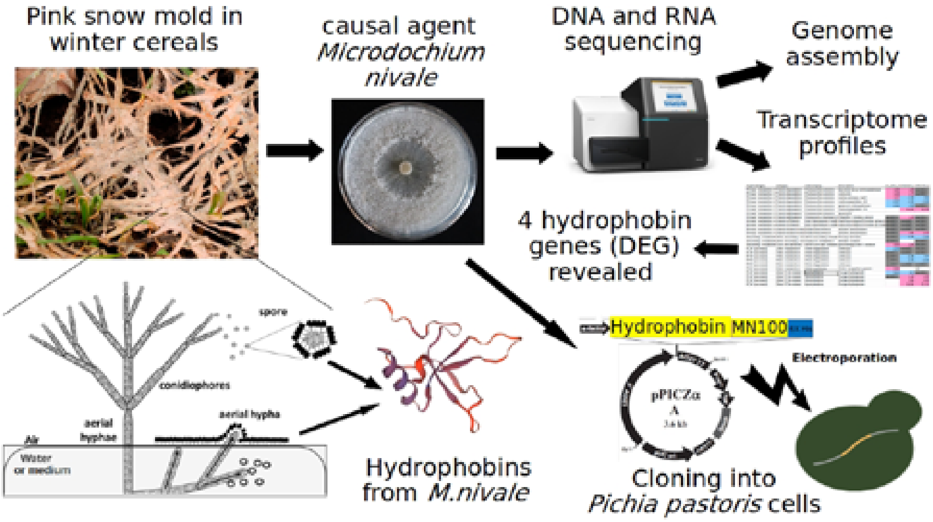
Hydrophobins are small surface-active proteins found only in the fungal kingdom that can self-assemble into amphipathic monolayers at a hydrophobic-hydrophilic interface. These proteins promote the formation of aerial hyphae, protect spores from the external environment, and participate in host plant colonization. Hydrophobins have not been previously investigated in fungi that cause snow mold in winter cereals — the disease that progresses under the snow cover. Recently assembled and annotated genome of the snow mold causal agent, the psychrotolerant fungus *Microdochium nivale*, enabled us to search for genes encoding hydrophobins in this psychrotolerant fungus. We revealed four genes encoding these proteins, all of which belong to class II hydrophobins. We demonstrated that the expression of hydrophobin-encoding genes is differentially regulated under different culture conditions and during host plant colonization. To get better insight into the role of the most in planta upregulated *M. nivale* hydrophobin in plant colonization, we created a genetic construct to obtain the corresponding recombinant protein in *Pichia pastoris* cells.

Take-home message:

1. Four genes encoding hydrophobins are present in the *Microdochium nivale* genome.
2. The expression of genes encoding *M. nivale* hydrophobins is differentially regulated during host plant colonization.



Molecular phylogeny of *Junipers of Sabina* section and *Juniperus* section in Crimea

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22 samples of 5 Crimean species of the genus*Juniperus* L. were selected: J. *sommipis* L., *J.* J. *deltoides* R.P. Adams, *J. excelsa* M.-Bieb., *J. foetidissima* Willd., *J. sabina* L. from different localities of the Crimean Peninsula for phylogenetic analysis.

DNA was isolated from needles using the DNeasy Plant Mini Kit (Quagen, Germany). Chloroplast (petN-psbM, trnD-trnT, trnL-trnF, tRNS-trnG) non-coding regions of the genome were used for analysis. The obtained sequences were compared with those available in the database of the National Center for Biotechnological Information (NCBI).

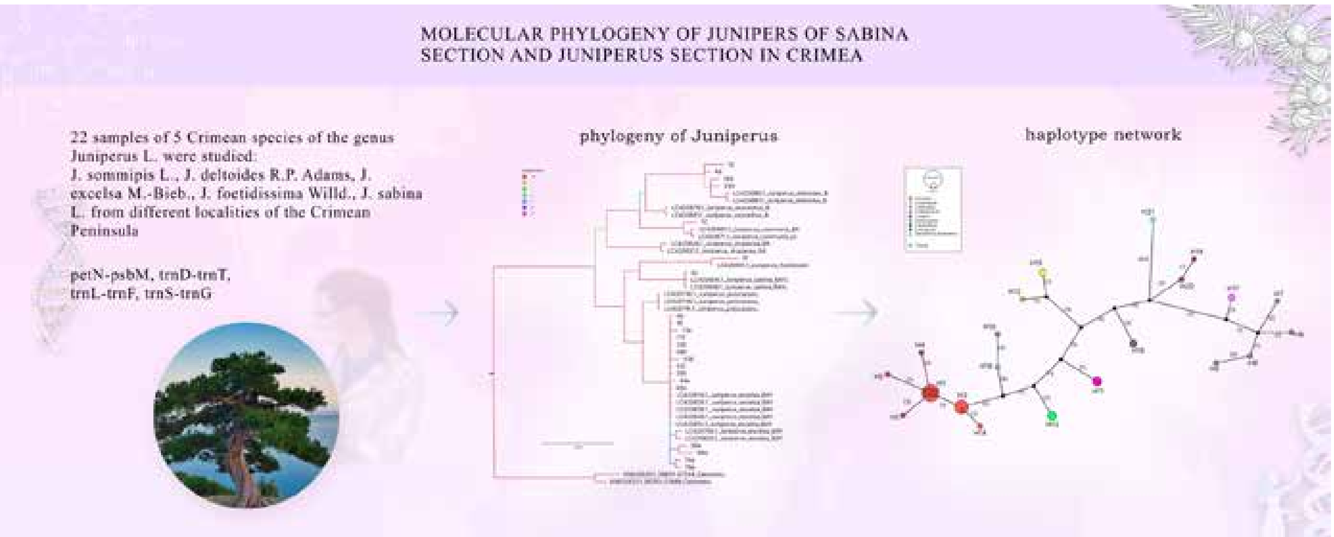
For all the studied samples, their species belonging was confirmed, while a comparison of the most common populations of *J. excelsa* and *J. deltoides* showed a large variability in the genetic parameters of *J. excelsa.*

Based on the analysis, it can be assumed that the divergence of the Crimean individuals of the *Juniperus* section (*J. communis*, *J. deltoides*) occurred somewhat earlier than the junipers growing in Turkey. For the rest of the studied species, the divergence times of the Crimean and Turkish populations are approximately the same.

The work was made within the program 'Prioritet-2030' of Sevastopol State University (strategic project № 3, №121121700318-1).

<u>Take-home message:</u>

A phylogenetic analysis of 5 species of the Crimean population of the genus Juniperus was carried out. It can be concluded that the divergence of the Crimean populations of Juniperus section (*J. communis, J. deltoides*) was earlier than in Turkey.



MOLECULAR PHYLOGENY OF JUNIPERS OF SABINA
SECTION AND JUNIPERUS SECTION IN CRIMEA

22 samples of 5 Crimean species of the genus Juniperus L. were studied:
J. sommipis L., J. deltoides R.P. Adams, J. excelsa M.-Bieb., J. foetidissima Willd., J. sabina L. from different localities of the Crimean Peninsula

petN-psbM, trnD-trnT,
trnL-trnF, trnS-trnG

Inactivation of the TOM-TIM complex components leads to a decrease in the level of DNA import into *Arabidopsis* mitochondria

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The phenomenon of DNA import into mitochondria has been shown for all major groups of eukaryotes. Apparently, DNA import occurs in plants and mammals in different ways, but the mechanism of this process remains poorly understood. Remarkably, components of the protein import machinery are involved in tRNA import in plants. This indicates the possibility of crossing the pathways for the import of DNA and other macromolecules into mitochondria. In our work, we studied the role of distinct components of the TOM and TIM complexes in the process of DNA import into isolated Arabidopsis mitochondria. Using knockout mutants for the genes encoding the Tim17, Tim23, or Tom20 proteins, we showed varying extent of their involvement in the import of DNA fragments of different lengths. Inhibition of transport channels with specific antibodies to the channel-forming proteins Tom40, Tom9, or VDAC led to a decrease in the level of DNA import into mitochondria. However, only the import into Tim17-1 mutant was further reduced in the presence of anti-VDAC antibodies. Thus, the Tim17-1, Tim23-2, and Tom20-2 proteins are important participants in the machinery for DNA translocation into mitochondria.

The study was supported by the Russian Science Foundation grant No. 22-74-00114, https://rscf.ru/project/22-74-00114/.

The main publications of authors on the subject of the abstract:

Tarasenko T.A.et al. DNA import into plant mitochondria: complex approach for in organello and in vivo studies //Biochem.(M).(2019)84:817-828.doi:10.1134/S0006297919070113

Tarasenko T.A.et al. Plant mitochondrial subfractions have different ability to import DNA // TxPP.(2020)32 5-18.doi:10.1007/s40626-020-00167-w

Tarasenko T.A.et al. Plant mitochondria import DNA via alternative membrane complexes involving various VDAC isoforms // Mitochondrion (2021) 60:43-58.doi: 10.1016/J.MITO.2021.07.006

Take-home message:

Tim23-2 and Tom20-2 proteins are specifically involved in the small size DNA import.

Tim17-1 protein, together with VDAC1, is involved in the transfer of DNA across the mitochondrial membrane.

The natural ability of mitochondria to import DNA makes it possible to study the functioning of regulatory elements of *Arabidopsis* mitochondrial genome

Tarasenko V.I., Tarasenko T.A., Gorbenko I.V., Konstantinov Yu.M., Koulintchenko M.V.

Siberian institute of plant physiology and biochemistry of SB RAS, Irkutsk, Russia
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It is known that mitochondria have a natural ability to import DNA from the cytoplasm. This work is aimed at studying the effectiveness of regulatory elements of mitochondrial genes flanking exogenous DNA using the phenomenon of natural competence of plant mitochondria. For this purpose, genetic constructs carrying the GFP gene under the control of the promoter regions of the mitochondrial RRN26 or COX1 genes and one of the two 3'-untranslated regions (3'-UTR) of mitochondrial genes were imported into isolated Arabidopsis mitochondria, followed by transcription *in organello.* It was shown that the level of GFP expression under the control of promoters of the RRN26 or COX1 genes *in organello* correlates with the level of transcription of these genes observed *in vivo.* At the same time, the presence of the tRNA(trp) sequence in the 3'-UTR leads to a higher level of the GFP transcript than the presence in this region of the binding site of the MTSF1 protein from the 3'-UTR of the NAD4 gene. The results obtained open up prospects for creating a system for efficient transformation of the mitochondrial genome.

The main publications of authors on the subject of the abstract:

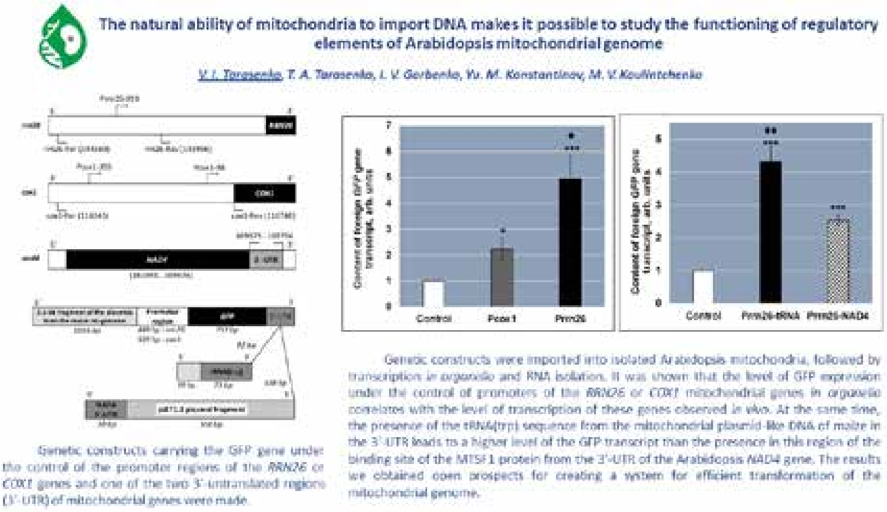
Tarasenko V.I. et al. Differential expression of a foreign gene in Arabidopsis mitochondria in organello // Mol Biol (2023) 57:3,447–456. doi:10.1134/S0026893323030123

Tarasenko T.A. et al. Plant mitochondria import DNA via alternative membrane complexes involving various VDAC isoforms // Mitochondrion (2021) 60:43-58. doi: 10.1016/J.MITO.2021.07.006

Take-home message:

The tRNA sequence located at the 3'-end stabilize the transcript more effective than the 3'-UTR of NAD4 gene.

The GFP expression level under the control of RRN26 or COX1 promoters *in organello* correlates with the level of transcription *in vivo.*



The natural ability of mitochondria to import DNA makes it possible to study the functioning of regulatory elements of Arabidopsis mitochondrial genome

V. I. Tarasenko, T. A. Tarasenko, I. V. Gorbenko, Yu. M. Konstantinov, M. V. Koulintchenko

Genetic constructs carrying the GFP gene under the control of the promoter regions of the *RRN26* or *COX1* genes and one of the two 3'-untranslated regions (3'-UTR) of mitochondrial genes were made.

Genetic constructs were imported into isolated Arabidopsis mitochondria, followed by transcription *in organello* and RNA isolation. It was shown that the level of GFP expression under the control of promoters of the *RRN26* or *COX1* mitochondrial genes *in organello* correlates with the level of transcription of these genes observed *in vivo*. At the same time, the presence of the tRNA(trp) sequence from the mitochondrial plasmid-like DNA of maize in the 3'-UTR leads to a higher level of the GFP transcript than the presence in this region of the binding site of the MTSF1 protein from the 3'-UTR of the Arabidopsis *NAD4* gene. The results we obtained open prospects for creating a system for efficient transformation of the mitochondrial genome.

Evaluation of the oat collection for resistance to crown rust in the conditions of the Northern Trans-Urals

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Scientific Research Institute of Agriculture of the Northern Trans-Ural Region - Branch of the Tyumen Scientific Center of Siberian Branch of the Russian Academy of Sciences, Tyumen, Russia
E-mail: atautekenova@gmail.com

In Western Siberia, crown rust is considered one of the most harmful diseases, the causative agent of which is *Puccinia coronata Corda* – a macrocyclic basidiomycete.

The purpose of this work is to assess the damage of oat varieties in favorable conditions for Western Siberia. The research material was 380 varieties and lines. In 2022, favorable conditions were created for the development of oats, but for the pathogen of crown rust, optimal conditions developed only during the ripening phase of oats. Therefore, crown rust appeared mainly on the fitting or late-ripening varieties. It was found that in the conditions of Western Siberia, the following varieties were affected: local (k-4483), Moola, Pollard, Aurom, R0ABDH, C.I.9271, Marshal, Dogoy, Express, Phobos, Horizon, Vilensky, Silver, local (k-4075), Precocious and Hein. The late-maturing varieties Ordinary (k-6529), Mutika 556, Riby A were most affected.

Structure-functional characteristics of Svx protein of *Pectobacterium atrosepticum* and its role in plant-microbial interactions

Tendiuk N.V., Konnova T.A., Petrova O.E., Osipova E.V., Mukhametzyanov T.A.*, Makshakova O.N., Gorshkov V.Y.

Kazan Institute of Biochemistry and Biophysics of Kazan Scientific Center of the Russian Academy of Science, Kazan, Russia,

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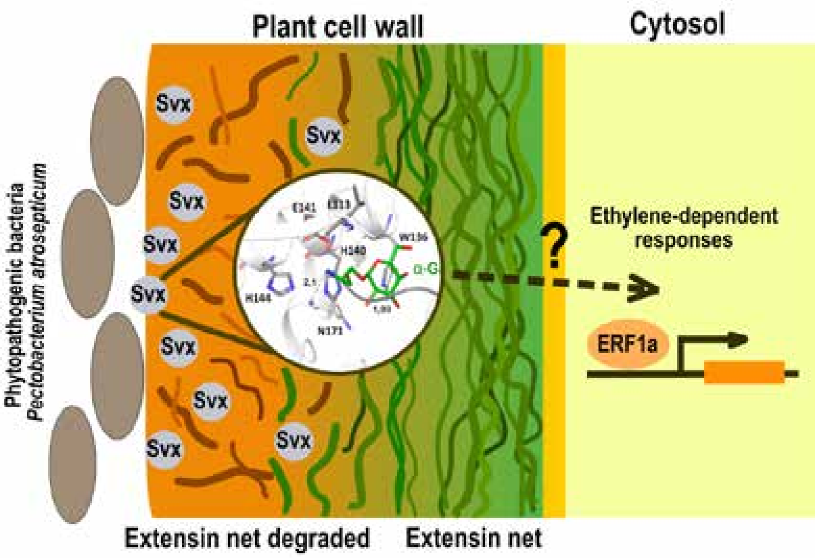
Phytopathogenic bacteria of the *Pectobacterium* genus cause soft rot disease, leading to large crop losses. *Pectobacterium* species have a wide range of virulence determinants, including those for which the function and role in pathogenesis still remain unclear. One such virulence factor is the extracellular Svx protein. As a result of the conducted experiments, two functional domains (possible glycopeptidase and acyltransferase-like) were revealed in the Svx protein. HEXXHX(8,28)E motif with additional carbohydrate-binding residues, forms the active site of the protease domain. The purified recombinant protein was shown to have protease activity, which was reduced 3 times in the mutant protein that had a single amino acid substitution in the protease domain. Protein-ligand docking revealed that extensins (plant cell wall proteins) could be the possible substrates of the Svx protein. The experiments with the infiltration of Svx protein into plant leaves revealed that this protein induces the ethylene-mediated susceptible response of the host. Based on the obtained results, the role of Svx protein in pathogenesis has been hypothesized. This study was supported by RSF (19-14-00194).

The main publications of authors on the subject of the abstract:

Tendiuk, N. V. et al. Structure-Functional Characteristics of the Svx Protein-The Virulence Factor of the Phytopathogenic Bacterium Pectobacterium atrosepticum // International journal of molecular sciences (2022) 23(13): 6914. doi 10.3390/ijms23136914

Take-home message:

Svx protein of *Pectobacterium atrosepticum* is an extracellular metallopeptidase, that triggers suspectible response in the host-plant, that contributes to the development of the pectobacterial infection



Effect of inoculation of a barley plants with a *Pseudomonas* strain on the level of aquaporins and their encoding mRNA

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Insufficient attention has been paid to the effects of plant growth promoting rhizobacteria on expression of the genes encoding aquaporins (AQP), although they control water flow into the cells thereby regulating cell extension. Barley was chosen as a model species due to availability of antibodies against the N-region of plasma membrane HvPIP2 AQP. PCR revealed up-regulation of HvPIP2;3, HvPIP2;4 and HvPIP2;5 gene expression by inoculation of plants with *Pseudomonas mandelii.* However, since antibodies against the N-region of HvPIP2;3 showed cross-reactivity with HvPIP2;4, we focused on immunolocalization of PIP2;5 aquaporins with specific antibodies. Up-regulation of PIP2;5 gene correlated with increased level of corresponding AQP proteins especially in the endoderm and exoderm, where the formation of apoplastic barriers was strengthened by bacterial treatment. The high content of aquaporins apparently increased water flow across membranes thereby compensating for the decrease in the hydraulic conductivity of the apoplastic pathway caused by the strengthening of apoplastic barriers.

The main publications of authors on the subject of the abstract:

Arkhipova, T.; Sharipova, G.; Akhiyarova, G.; Kuzmina, L.; Galin, I.; Martynenko, E.; Seldimirova, O.; Nuzhnaya, T.; Feoktistova, A.; Timergalin, M.; et al. The Effects of Rhizosphere Inoculation with Pseudomonas mandelii on Formation of Apoplast Barriers, HvPIP2 Aquaporins and Hydraulic Conductance of Barley. Microorganisms 2022, 10, 935. ttps://doi.org/10.3390/microorganisms10050935

Take-home message:

Pseudomonas mandelli increased the expression of the aquaporin gene PIP2;5. This could compensate for the decrease in hydraulic conductivity caused by the strengthening of apoplastic barriers as a result of bacterial treatment.

This research was funded by the Russian Scientific Foundation № 21-14-00070.

The use of microclonal propagation to create a genetic pool of *Quercus robur* L. for breeding and seed production.

Timina O.O., Timin O.Y.*, Plugar O.V.*

Taras Shevchenko Transdnistrian State University, Tiraspol, Moldova, Republic of,
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В Приднестровье принята Государственная программа на период с 2021 по 2041 годы «Восстановление высокоствольных дубрав на землях Гослесфонда Приднестровья». Для ее выполнения необходима разработка соответствующих методик по изучению, использованию, селекции и сохранению естественных популяций дубрав в варьирующих условиях произрастания. Очевидна актуальность и необходимость разработок не только традиционных методик по селекции и сохранению естественных популяций дубрав, но и наработка инновационных биотехнологий для создания генетического пула породы в виде объектов семеноводства. В Приднестовье подобные работы проводятся впервые. С учетом долгосрочных исследований определяются: наиболее отзывчивый для культивирования *in vitro* эксплант; время изъятия экспланта у деревьев различного календарного возраста и онтогенетического состояния; регенерационная способность различных климатипов, эдафотипов и внутрипопуляционных формовых разнообразий дуба (фенотипов и морфотипов).). Получен полный цикл развития растений из зрелых зиготических зародышей плюсовых деревьев пойменных и лесостепных форм дуба черешчатого.

<u>The main publications of authors on the subject of the abstract:</u>

Тимин О.Ю., Тимина О.О., Усенко А.И.Таксационные характеристики плюсовых и нормально-лучших деревьев Quercus robur L. и Populus tremula L. на территории Гослесфонда Приднестровья/ Международная конференция "Управление трансграничным бассейном Днестра и Евроинтеграция - шаг за шагом". Материалы Международной конференции Eco-Tiras, Кишинев, 2022. с. 215-218

Efficient CRISPR/Cas9-based genomic editing technique for *Nud* gene mutagenesis in commercial barley cultivar mediated by particle bombardment

Timonova E.M., Kiseleva A.A., Nesterov M.A., Sergeeva E.M., Filipenko E.A., Adonina I.G., Kochetov A.V., Salina E.A.

The Federal State Budgetary Institution of Science Federal Research Center Institute of Cytology and Genetics, Siberian Branch of the Russian Academy of Sciences (ICG SB RAS) and Kurchatov Genomics Center, Novosibirsk, Russia
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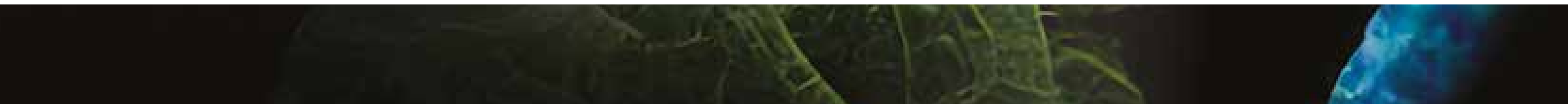
Barley is one of the economically important cereal crops after wheat, rice, and maize. Barley biotechnology requires effective genetic engineering tools for selective mutation of defined genes. Agrobacterium-mediated genetic transformation is a basic technique for delivering CRISPR/Cas9 system into barley cells, but mostly effective with the model cv. 'Golden promise'. Particle bombardment could be an alternative transformation method for commercial barley varieties. In this study we demonstrate the efficient CRISPR/Cas9-based editing of *Nud* gene of barley cv 'Tselinny 5' mediated by particle bombardment. Mutations in *Nud* gene result in a phenotype with naked grains. The JD633 binary DNA vector with two effective gRNA sequences targeting the first exon of *Nud* gene was used. The regeneration of plants was carried out according to the modified protocol for wheat particle bombardment using callus. As a result, the five T0 plants of barley cv 'Tselinny 5' carry the several mono- and biallelic mutations in *Nud* gene, and two of them represent transgene-free plants.

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



Alteration in expression level of some growth and stress-related genes of potato microplants after rhizobacteria inoculation

Tkachenko O., Kulikov A.

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The aim of the research is to study the mechanisms of the influence of rhizobacteria on the adaptive ability of potato microplants.

Earlier, we conducted a comprehensive morphometric and biochemical evaluation of the effectiveness of *in vitro* co-inoculation of potato microplants of Nevsky and Condor varieties with rhizobacteria A*zospirillum baldaniorum* Sp245 and *Ochrobactrum cytisi* IPA7.2, as well as *Azospirillum baldaniorum* Sp245 and *Kocuria rosea* T1Ks19. The positive effect of rhizobacteria in the process of adaptation of potato microplants in aeroponics conditions has been established.

At this stage of the studies, data on the level of relative expression of potato genes *AMI, TIR1, GH3.1, IPAM, GH3, StERF, StLOX*, associated with hormone biosynthesis and stress response, on the 30th day of *in vitro* cultivation and in the process of adaptation to aeroponics conditions on the 10th and 20th days of cultivation, were obtained by qRT-PCR.

The research was carried out at the expense of a grant from the Russian Science Foundation № 22-26-00087, https://rscf.ru/en/project/22-26-00087

The main publications of authors on the subject of the abstract:

Tkachenko O. V. et al. Increased activity of the pro/antioxidant system of potato microplants by rhizospheric bacterias in aeroponics conditions // Agrarian Scientifi c Journal (2023) 3: 65–72. (In Russ.). doi: 10.28983/asj.y2023i3pp65-72

Take-home message:

The increase adaptive capacity of potato microplants inoculated *in vitro* by rhizospheric bacteria is due to the expression of genes associated with hormone biosynthesis and stress response.

The diversity of lipoxygenase genes in plant genomes: first explanations

Toporkova Y.Y., Smirnova E.O., Egorova A.M., Iljina T.M., Lantsova N.V., Gorina S.S., Grechkin A.N.

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Plant lipoxygenase cascade is a source of various bioregulators, oxylipins. The lipoxygenase cascade is initiated from the formation of hydroperoxides by the lipoxygenases (LOXs). LOXs are traditionally divided into 9S-, 13S- or 9S/13S-specific, and at the same time, many plant species have more than twenty LOXs. The significance of this apparently non-random multiplicity of lipoxygenases has not yet been explained. LOXs are not new objects of research. However, until now, researchers have limited themselves to the study of individual LOXs, while describing similar data on LOXs of different organisms. An integrated approach, including the methods of biochemistry, biophysics, bioinformatics, and molecular biology (including transcriptomic and proteomic analysis), will make it possible to approach the answer to the question of the significance of the multiplicity of LOXs in plants.

Bioinformatics analysis was carried out with financial support from the state assignment of the Federal Research Center "Kazan Scientific Center of the Russian Academy of Sciences". Catalytic studies of LOXs were performed under support of grant 21-14-00397 from Russian Science Foundation.

Spring wheat varieties generative organs resistance to soil borne pathogens

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The purpose of the research was to identify spring wheat varieties, which generative organs are resistant to a complex of soil borne pathogens - *Helminthosporium sativum* Sacc. and *Fusarium spp.* Link. Spring wheat varieties from the collection of the Institute of Cytology and Genetics were taken for investigations. The studies were carried out in 2020-2022 in the northern forest-steppe of the Ob region (West Siberia) using generally accepted methods. Among 20 varieties of spring wheat collection from different regions of Russia and countries of the world, no varieties were found, that not absolutely affected by the soil borne pathogens. By the way, significant differences between spring wheat varieties by résistance to pathogenic species were found. H. sativum affected wheat varieties grains with the difference 9-17 times, and this phenomenon took place every year. On wheat spike rods differences between varieties were 3.8-10 times. Similar results were obtained for *F.oxysporum* Schltdl. and *F. poae* (Peck.) Wollenw.

Acknowledgment: The reported study was funded by RSCF, project number 22-26-00066.

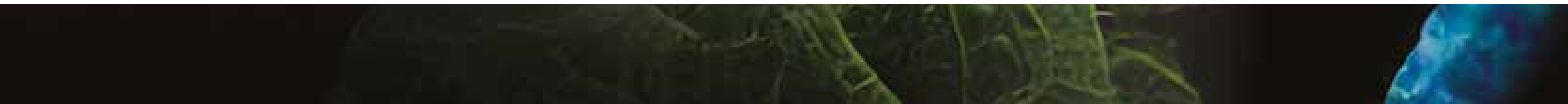
The main publications of authors on the subject of the abstract:

1. Торопова Е. Ю., Воробьева И. Г., Казакова О. А. и др. Инфицированность органов зерновок сортов яровой пшеницы почвенными фитопатогенами // Труды Кубанского государственного аграрного университета. № 7(100). 2022. С. 185-192. DOI: 10.21515/1999-1703-100-185-192

2. Vorob’evaa I. G., and Toropova E. Yu. Ecological Niches of Fusarium poae (Peck) Wollenw. in Western Siberia // 5, Contemporary Problems of Ecology, 2022, Vol. 15, No. 4, pp. 393–399. DOI: 10.1134/S1995425522040114

Take-home message:

This results show perspective direction for practical breeding of spring wheat varieties resistant to *Helminthosporium* and *Fusarium* ear blight, widespread throughout the world.



Comparative Analysis of Productivity Traits in Proanthocyanidin-free Barley Mutants and Their Parental Varieties

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Federal Research Center Institute of Cytology and Genetics, Siberian Branch of Russian Academy of Sciences, Novosibirsk, Russia,

*Novosibirsk State University, Novosibirsk, Russia

E-mail: totsky@bionet.nsc.ru

One of the main problems in the production of beer is colloidal haze, which leads to reduced storage stability of the beer. It is caused by binding proteins by proanthocyanidins . Chemical stabilizers and beer filtering are used to prevent colloidal haze. Breeding barley varieties that lack proanthocyanidins can also be used to overcome this problem. The aim of our work was to study a number of proanthocyanidin-free mutants with impairments at the *Ant25, Ant26, Ant27* loci and to identify promising donors for breeding proanthocyanidin-free malting barley with high economically valuable traits. The weight of grain, root and shoot, “harvest index”, length of the main stem, number of secondary stems were measured. During study, it was found that the *ant26.486* mutant is the most promising sample for use in breeding, because it is proanthocyanidin-free and does not differ from the parent variety Grit in all traits, including surpassing the original variety in mass of roots.

This work was supported by the Russian Science Foundation grant no. 21-76-10024.

Deciphering zinc solubilizing and siderophore producing plant growth promoting rhizobacteria for biofortification of microgreens

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Zinc and iron are essential micronutrients for the proper growth and development of crops and its dietary deficiency causing multiple health issues in human being. The study focussed on the identification of Zn-solubilizing and Fe-chelating plant growth promoting (PGP) rhizobacteria for biofortification of microgreens. Rhizosphere soils of two plant species were analysed from the territory of Chelyabinsk region (Russia) and 90 rhizospheric strains tolerant to Zn and Fe were isolated. A total of 26 isolates showed significant resistance to multiple metals (Zn, Fe, Cu, Ni) and antibiotics. Among them, 31% produced siderophores and 65% solubilized different forms of insoluble Zn. In total, 7 strains showed ZnO, $ZnCO_3$ and $Zn_3(PO_4)2$ solubilization, Fe-chelation properties along with moderate to high drought resistance (-0.73 MPa). Two best Zn, Fe and PGP exhibitors were identified as *Bacillus* sp. and *Pseudomonas* sp. by 16S rRNA sequencing using Oxford Nanopore Technologies whose efficiency study is under investigation for biofortification of multiple microgreens.

Funding: *The work was funded by the Russian Science Foundation Grant No. 23-26-00292, https://rscf.ru/project/23-26-00292.*

<u>The main publications of authors on the subject of the abstract:</u>

Kumar A, Tripti et al. (2021) Synergistic effect of ACC deaminase producing Pseudomonas sp. TR15a and siderophore producing Bacillus aerophilus TR15c for enhanced growth and copper accumulation in Helianthusannuus L. // Chemosphere 276. doi:10.1016/j.chemosphere.2021.130038

Jiang Y, El Mehdawi, Tripti et al. (2018) Characterization of selenium accumulation, localization and speciation in buckwheat–implications for biofortification. // Frontiers Plant Sci 9:1583. doi:10.3389/fpls.2018.01583

<u>Take-home message:</u>

Zn solubilizing and Fe-chelating PGPR can replace use of chemical fertilizer for biofortification of microgreens.

Healthy microgreens can fulfil the demand of Zn and Fe dietary supplements.

Effects of cytoplasm and chromosomes of wild barley *H. marinum* ssp. *gussoneanum* on characteristics of wheat-alien introgression lines

Trubacheeva N.V., Pershina L.A.

Federal Research Center Institute of Cytology and Genetics, Siberian Branch of Russian Academy of Sciences, Novosibirsk, Russia
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H. marinum ssp. gussoneanum Hudson is a source of new genes for wheat. Euplasmic wheat-barley substitution lines $7H^{m}$(7D), 4H (4B) and alloplasmic substitution lines $7H^{m}$(7D), $7H^{m}$(7B) with cytoplasm of wild barley, as well as reciprocal hybrids 7H (7B) × variety Omskaya 37 (with translocation 1RS.1BL) and their progenies were studied. A combination of genomic situ probing and marker genotyping have identified barley chromosomes in the genome of studied lines. It was found that the cytoplasm of *H. marinum* in the presence of chromosome $7H^{m}$, regardless of the type of barley-wheat chromosome substitution, negatively affects the manifestation of morphobiological traits and yield. Among the progenies of hybrids $7H^{m}$ (7B) × Omskya 37 alloplasmic lines carrying 1RS.1BL with heterosis for some traits were identified. These lines are used in crosses with promising wheat genotypes to create a new breeding material. The values of morphobiological traits and yield in wheat-barley lines $7H^{m}$ (7D) and 4H (4B) are either at the control level or exceed it.

Acknowledgements: This work was supported by the Kurchatov Genomic Center of the Institute of Cytology and Genetics, SB RAS (075-15-2019-1662).

The main publications of authors on the subject of the abstract:

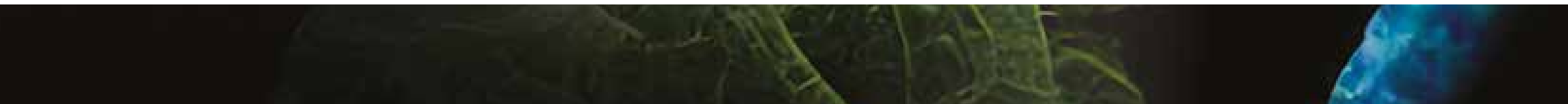
Trubacheeva N.V., Badaeva E.D., Osadchaya T.S., Pershina L.A. Use of H. vulgare EST markers, GISH and C-banding to study bread wheat-H. marinum subsp. gussoneanum (2n=28) introgression lines. Cereal Res Comm. 2019. 47(4):593-603.

Trubacheeva N.V., Divashuk M.G., Chernook A.G., Belan I.A., Rosseeva L.P., Pershina L.A. The effect of chromosome arm 1BS on the fertility of alloplasmic recombinant lines in bread wheat with the Hordeum vulgare cytoplasm. Plants (Basel). 2021; 10(6):1120

Take-home message:

H. marinum cytoplasm in the presence of chromosome $7H^{m}$ negatively affects the morphobiological traits and yield.

Alloplasmic lines with translocation 1RS.1BL are used in crosses with promising wheat genotypes to create new breeding material.



LTR retrotransposon survey in *Avena* L. species based on clade-specific k-mers

Tsalkovsky I.A., Zhurbenko P.M.*, Solomennikova Y.N.

ITMO University, Saint-Petersburg, Russia,
*Komarov Botanical Institute, Russian Academy of Sciences, Saint-Petersburg, Russia
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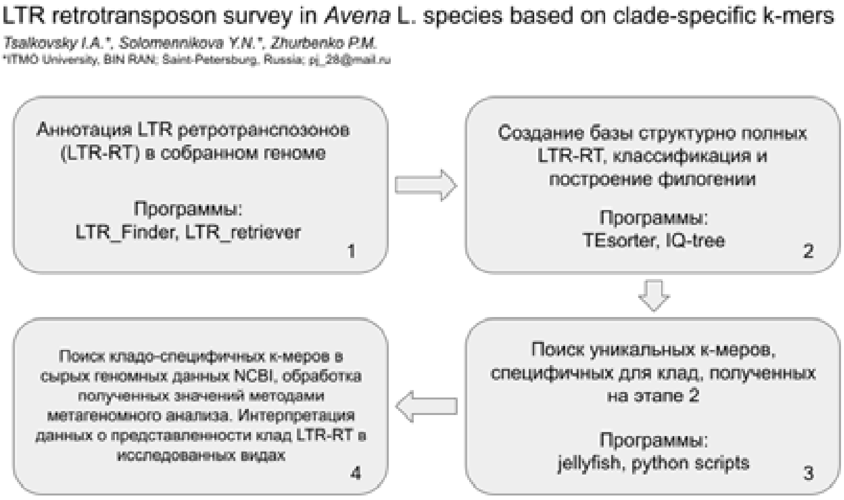
Мобильные элементы занимают значительную часть генома растений. Многие современные подходы для их поиска в сырых геномных данных основаны на частичной сборке коротких ридов с последующей таксономической аннотацией. Однако, такие подходы могут нести искажения, вызванные сложностью сборки повторенных последовательностей. В данной работе мы предлагаем альтернативный путь изучения мобилома на примере LTR ретротранспозонов (LTR RT) видов рода Avena L., пользуясь наличием качественных геномных сборок нескольких видов рода.

В геноме A. longiglumis Durieu и субгеномах A. insularis Ladiz. был проведен поиск LTR RT с помощью программ LTR Finder и LTR retriver. Полученные последовательности структурно интактных LTR RT были аннотированы в TE sorter. Далее, с помощью построения филогении по последовательностям генов, была выполнена более точная кластеризация LTR RT и для каждого кластера были найдены уникальные к-меры. Подсчет числа данных к-меров в собранных геномах и доступных в базе NCBI сырых геномных данных видов Avena позволил оценить представленность каждого кластера и сделать выводы о динамике LTR RT в пределах рода. Работа выполнена при финансовой поддержке гранта РНФ № 22-24-01117.

Take-home message:

Наличие геномной сборки позволяет провести аннотацию и кластеризацию мобильных элементов генома. Уникальные для кластеров к-меры могут быть успешно использованы для оценки представленности кластеров в сырых геномных данных без дополнительной сборки.



LTR retrotransposon survey in *Avena* L. species based on clade-specific k-mers

Tsalkovsky I.A., Solomennikova Y.N.*, Zhurbenko P.M.*

*ITMO University, BIN RAN; Saint-Petersburg, Russia; pj_28@mail.ru

Аннотация LTR ретротранспозонов (LTR-RT) в собранном геноме

Программы:
LTR_Finder, LTR_retriever

1

Создание базы структурно полных LTR-RT, классификация и построение филогении

Программы:
TEsorter, IQ-tree

2

Поиск уникальных к-меров, специфичных для клад, полученных на этапе 2

Программы:
jellyfish, python scripts

3

Поиск кладо-специфичных к-меров в сырых геномных данных NCBI, обработка полученных значений методами метагеномного анализа. Интерпретация данных о представленности клад LTR-RT в исследованных видах

4

Апробация SSR-праймеров для выявления генетического разнообразия в коллекциях сортов фундука *Corylus* L.

Tsaturyan G.A., Malyarovskaya V.I., Tutberidze T.V.

Федеральное государственное бюджетное учреждение науки «Федеральный исследовательский центр «Субтропический научный центр Российской академии наук», Сочи и Россия
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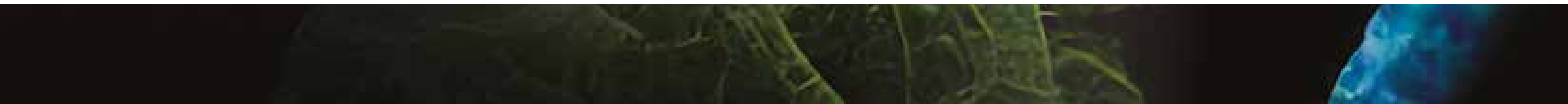
Одной из перспективных культур для Краснодарского края и России, является фундук (Corylus avellana (L.) H. Karst.). Разработка и применение молекулярных маркеров для коллекции фундука станет важным инструментом для совершенствования сортимента, позволит выявить пробелы и пополнить их донорами новых признаков и дистантными генотипами.Для выявления эффективных наборов маркеров необходима их апробация на коллекции фундука Кавказа.Апробация ядерных SSR-праймеров проходила на первичной выборке из 7 сортов фундука. У данных генотипов выявлены редкие и уникальные аллели. На основе данных полиморфизма изучаемых микросателлитов построена дендрограмма, отражающая филогенетические отношения между изучаемыми сортами фундука. Исследуемые генотипы разделились на три кластера с наибольшими генетическими дистанциями между ними. Выявлены новые микросателлитные маркеры с высоким полиморфизмом, которые могут быть использованы для генотипирования биоразнообразия *C. avellana*. Полученные результаты будут полезны для характеристики биоразнообразия коллекций фундука на Кавказе.

Публикация подготовлена в рамках реализации ГЗ ФИЦ СНЦ РАН № FGWR-2021-0006.



Peterhof genetic collection of rye: history of creation and prospects of use

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Rye varieties are sources of genetic diversity maintained through a stringent system of self-incompatibility. The use of self-compatible mutants made it possible to reveal a high level of heterozygosity and heterogeneity in rye populations and to create on this basis the Peterhof genetic collection of rye (Smirnov, Sosnikhina, 1984). Based on the inbred lines of the collection, genes responsible for self-compatibility, numerous morphological and biochemical traits, chromosome behavior in meiosis, mutations of post-zygotic incompatibility with common wheat, and quantitative trait loci have been identified and mapped. The domestication as a weed plant in wheat and barley crops led to some features in rye secondary metabolism. These features explain the high resistance of rye to biotic and abiotic stresses, and they can be associated with the health promoting effects of rye grain products. The prospect of research in this direction is related to the study of the pleiotropic effects of identified structural and regulatory genes of anthocyanin biosynthesis in caryopsis tissues.

The main publications of authors on the subject of the abstract:

Tsvetkova N.V. et al. Two Rye Genes Responsible for Abnormal Development of Wheat–Rye Hybrids Are Linked in the Vicinity of an Evolutionary Translocation on Chromosome 6R// Plants (2018) 7(3): 55. https://doi.org/10.3390/plants7030055

Braun E.M. et al. Gene expression profiling and fine mapping identifies a gibberellin 2-oxidase gene co-segregating with the dominant dwarfing gene Ddw1 in rye (Secale cereale L.) // Fronties in Plant Science (2019). doi.org/10.3389/fpls.2019.00857

Take-home message:

Creating of genetic collections to study latent genetic diversity in cross-pollinated species opens up opportunities for expanding fundamental knowledge of the implementation of traits and understanding their molecular nature.

Regulators of somatic embryogenesis in legumes

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Regeneration is an important step in the majority of protocols for plant transformation. During regeneration, a new plant can develop through shoot regeneration and further rooting or through somatic embryogenesis pathway. In our study, we search for inhibitors and stimulators of somatic embryogenesis in *Fabaceae*. Using *Medicago truncatula* as a model object, we found several genes from the *WOX* family, which are able to stimulate somatic embryogenesis, as well as a *CLE* gene inhibiting this process. Now we are checking if somatic embryogenesis stimulators which we found can alleviate transformation in pea and lentil. To do that, we are developing systems to obtain transgenic calli and choosing suitable markers for transgenic tissues visualization in these species.

This work was supported by the Ministry of Science and Higher Education of the Russian Federation in accordance with agreement № 075-15-2022-322 date 22.04.2022 on providing a grant in the form of subsidies from the Federal budget of Russian Federation. The grant was provided for state support for the creation and development of a World-class Scientific Center "Agrotechnologies for the Future".

The main publications of authors on the subject of the abstract:

Tvorogova, V.E. et al. The WUSCHEL-related homeobox transcription factor MtWOX9-1 stimulates somatic embryogenesis in Medicago truncatula // Plant Cell, Tissue and Organ Culture (PCTOC) (2019) 138: 517-527. doi: 10.1007/s11240-019-01648-w

The assess expression of duplicated genes by RT-PCR: problems and recommendations

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Gene duplications are one of the evolutionary mechanisms that can lead to paralogization and the emergence of new functions. This process is very often not taken into account when assessing the gene expression by RT-PCR and the designed primers could be complementary to only one gene. It could lead to incorrect results. The aim of this study was to compare the relative expression of catalase in Prunus persica (it has two duplications) with different primers to demonstrate the necessity to check gene duplications before the experiment. It was shown that the relative expression values when using primers complementary to CAT1 only and primers complementary to both genes (CAT1 and CAT2) differ by 100 times. Thus, when estimating the total expression of catalase, it is necessary to use primers complementary to all the genes encoding the target protein. Otherwise, it is necessary to use transcriptomics approach. The study is supported by the Kurchatov Genomic Centre of the Nikita Botanical Garden – Nationa Scientific Center of RAS (075-15-2019-1670).

Take-home message:

During this work, primers were developed to estimate the total expression of catalase in the Prunus persica genome. The difference in gene expression was shown when using primers complementary to a single gene duplication and to two copies.

The role of protein prenylation in multicellular organization of the thallus in *Marchantia polymorpha*

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Protein prenylation is one of the main posttranslational modifications played a crucial role in the regulatory processes in multicellular organisms. Multicellularity transition is one of the major evolutionary acquisitions of living organisms. Herein, we study the role of protein prenyltransferases in the regulation of multicellularity development of a liverwort Marchantia polymorpha. Knockout lines of M. polymorpha protein prenyltransferases' genes plp, ggb, era, rggta, and rggtb were obtained via CRISPR/Cas9 technology. Δplp and Δggb lines demonstrated callus-like phenotype with undifferentiated cells, whereas Δera1 plants formed wild type phenotype. Mutations in Rab-GGT genes were lethal. Protein and RNA expression analysis in Δplp and Δggb lines allowed us to find out the differential expression of phytocyanin and lectin proteins genes. Therefore, the influence of protein prenylation on the development of the multicellular thallus of M. polymorpha was shown and two candidate genes were determined for the further study.The work was supported by the Russian Federation Presidential Scholarship № СП-3391.2021.4 and PRIORITY-2030 Program of Kazan Federal University.

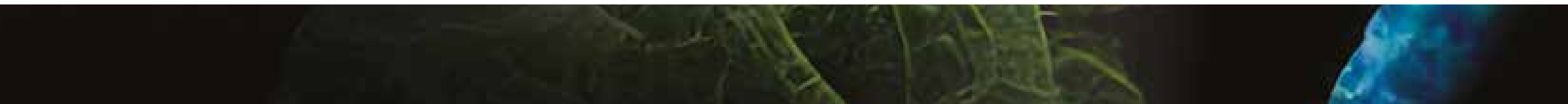
The main publications of authors on the subject of the abstract:

Valeeva L.R. et al. Cis-prenyltransferases of Marchantia polymorpha: phylogenetic analysis and determination of research prospects in the regulation of synthesis of antimicrobial agents // Molecular biology (Russian) (2022) 56(5):1-14.

Montgomery S.A. et al. Chromatin organization in early land plants reveals an ancestral association between 3K27me3, transposons, and constitutive heterochromatin // Current Biology. (2020) 30:1-16. doi.org/10.1016/j.cub.2019.12.015

Take-home message:

Protein prenylation plays an important role in the development of plant multicellular tissue formation. Phytocyanin- and lectin-domain containing proteins genes were identified as a candidates in the prenylation-associated regulatory pathway.



Lichen sterols under temperature stress: genes and metabolites

Valitova J.N., Khabibrahmanova V.R., Uvaeva V.L., Rakhmatullina D.F., Galeeva E.I., Leksin I.Y., Minibayeva F.V.

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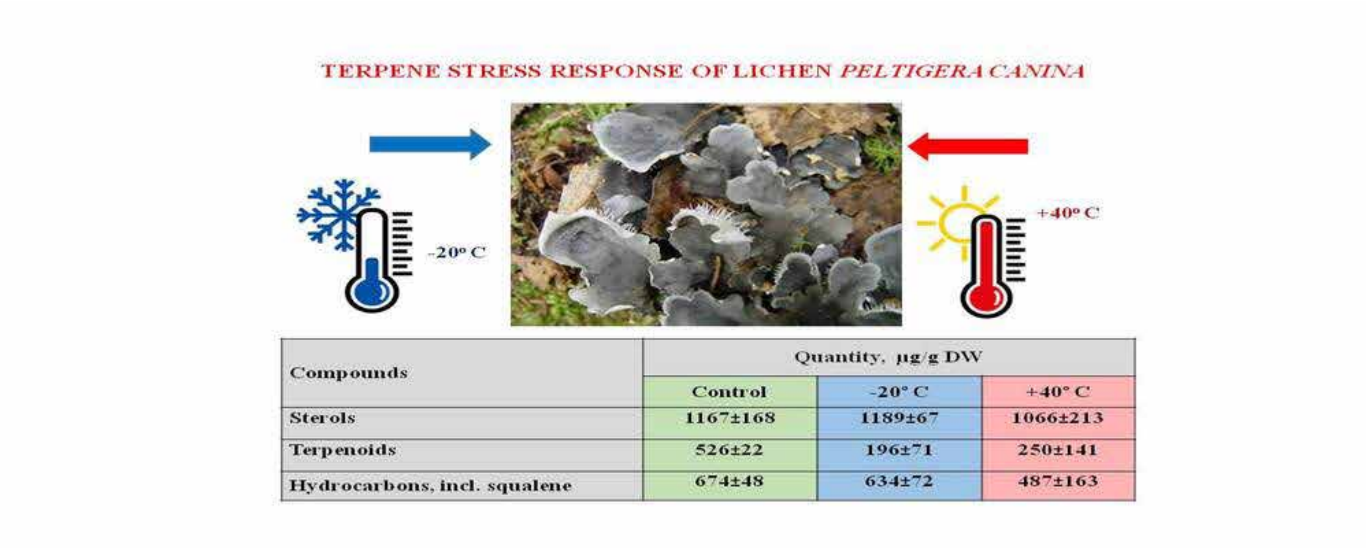
The study of the mechanisms of stress resistance of extremophilic organisms is the subject of close attention of researchers. In particular, the biochemical mechanisms of resistance of lichens to thermal stress mediated by compounds of isoprenoid nature, which include terpenes and sterols, are of interest. In this study, it was shown that the effect of unfavorable temperatures on thalli of the lichen *Peltigera canina* led to a significant decrease in the absolute content of triterpenes and did not change the content of sterols and squalene. It is known that lichens have a very rich spectrum of triterpene compounds, which can play an important role in the formation of their stress response. Bioinformatic analysis of the genes involved in the biosynthesis of sterols in the lichen mycobiont *P. canina* using sequences from *Saccharomyces cerevisiae* as references showed the presence of almost all genes of synthesis of ergosterol, base sterol of lichen mycobiont. For a clearer understanding of the mechanisms of involvement of sterols and triterpenes in the formation of the stress response of lichens, further studies are needed.

This work was supported by a grant from the RSF № 22-14-00362



TERPENE STRESS RESPONSE OF LICHEN *PELTIGERA CANINA*

Compounds	Quantity, µg/g DW		
	Control	-20° C	+40° C
Sterols	1167±168	1189±67	1066±213
Terpenoids	526±22	196±71	250±141
Hydrocarbons, incl. squalene	674±48	634±72	487±163

Is all centromeric DNA functionally competent for centromere identity?

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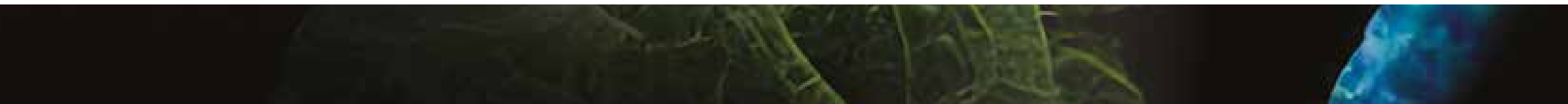
Centromeres are essential chromosomal regions that mediate the accurate inheritance of genetic information. Until now, centromeres have remained largely underexplored, especially in Triticeae genomes being difficult to completely assemble due to the highly repetitive DNA sequences and complex structure, so the functional contribution of centromeric DNA to centromere identity remains elusive. New approaches in genome sequencing have enabled the gap-less reconstructing of the sequences of entire eukaryotic chromosomes. However, the complete composition of centromeric DNA of such species as wheat, barley, rye remains unknown. Using a datasets of molecular markers, we conduct an in-depth analysis of gaps between contigs in individual chromosomes that were recently annotated as so-called pseudomolecules in genomic assemblies of rye, *S cereale.* We estimated the centromere positions and determined the molecular nature of the DNA sequences in these loci. The report will present the composition and abundance of different DNA sequences in the centromeres of each rye chromosome and this comparison will be extended to other cereal species. This work is supported by RSF (No. 19-14-00051-P).

The main publications of authors on the subject of the abstract:

Elisafenko EA, Evtushenko EV, Vershinin AV. The origin and evolution of a two-component system of paralogous genes encoding the centromeric histone CENH3 in cereals//BMC Plant Biol (2021) 21: 541. doi: 10.1186/s12870-021-03264-3

Vershinin AV, Lux T, Gundlach H, Elisafenko EA, Keilwagen J, Mayer KFX, Spannagl M. The gene and repetitive element landscape of the rye genome. In: "The Rye Genome" (Rabanus-Wallace MT, Stein N, Eds), Springer, pp 117-133, 2021. doi: 10.1007/978-3-030-83383-1_8



Effectors of pathogens - targets for new agricultural technologies in plant defense based on the RNA-interference mechanism

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Effectors have been found in practically all harmful organisms, including bacteria, fungi, viruses, and insects. Effectors are responsible for pathogen virulence and seek to suppress the plant immune system by influencing components of the redox system and manipulating plant hormonal signaling pathways. We have shown that the treatment of wheat plants with phytohormones (salicylic acid, abscisic acid, and cytokinins) suppressed the expression of the SnToxA and SnTox3 effector genes of the Stagonospora nodorum pathogen and led to a decrease in the damage areas. The transcription of nine wheat miRNAs during the initial period of infection with S. nodorum was also studied. In resistant and susceptible cultivars of bread spring wheat, the miRNA expression pattern during infection differed. The highest induction of miR156, miR160, miR166 and miR408 transcription was observed in resistant cultivar Omskaya35 24 hours after infection. Treatment of plants with phytohormones increased the level of transcripts of some miRNAs. The role of miRNAs in the regulation of hormonal signaling pathways is discussed. The work was supported by grant MK-2293.2022.1.4.

The main publications of authors on the subject of the abstract:

Veselova, S.V. et al., Ethylene-Cytokinin Interaction Determines Early Defense Response of Wheat against Stagonospora nodorum Berk. Biomolecules 2021, 11, 174. https://doi.org/10.3390/biom11020174

Take-home message:

Research of pathogens effectors is cutting edge as it will lead to the development of new level strategies in plant protection against pathogens. Plant protection will become targeted and safe for non-target organisms.

GATA family transcription factors in algae: features of ZnF-domain structure and classification

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GATA family transcription factors (GATA-TFs) are evolutionarily conserved proteins with zinc finger domain (ZnF) that perform important biological functions in all eukaryotes. In angiosperms, GATA-TFs most often regulate the metabolic pathways of nitrogen and carbon, as well as light-inducing processes. Based on structure of DNA-binding ZnF and presence of additional HAN and LLM domains in *Arabidopsis thaliana* and *Oryza sativa* plant GATA-TFs were divided into four main classes A–D and several subclasses. Phylogenetic studies show some commonality of these classes among angiosperms, but the algal GATA-TFs appears to be different.

We analyzed the genome of unicellular green alga *Chlamydomonas reinhardtii* and found 12 genes encoding GATA-TFs. Based on bioinformatic and phylogenetic analysis, we showed that all GATAs of C. *reinhardtii* do not contain HAN and LLM domains and can be subdivided into 3 groups according to the structure of the ZnF. These classes were also found in another lineages of algae. Unlike land plants, the biological functions of GATA-TFs in algae are not investigated sufficiently. We propose that algal GATA-TFs diverged during water-to-land transition in evolution.

The main publications of authors on the subject of the abstract:

Virolainen P.A., Chekunova E.M. Optimization of CRISPR/Cas9 method for transgenesis of model microalgae Chlamydomonas reinhardtii // Ecological Genetics (2022) 20(1S): 42-43. doi: 10.17816/ecogen112332

Chekunova E.M., Savelieva N.V. LTS3 gene controls light-independent chlorophyll biosynthesis in green algae Chlamydomonas reinhardtii // Ecological Genetics (2010) 8(2): 35-44. [In Russian, with English summary]

Take-home message:

1. Based on bioinformatic and phylogenetic analysis, algal GATA-TFs can be subdivided into three classes, which differs from land plants GATAs classification.
2. Presumably, GATA-TFs diversity in land plants arose as a result of terrestrialization.

Virus- induced modification of plant DNA methylation

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*Moscow Institute of Physics and Technology, Dolgoprudny, Russia
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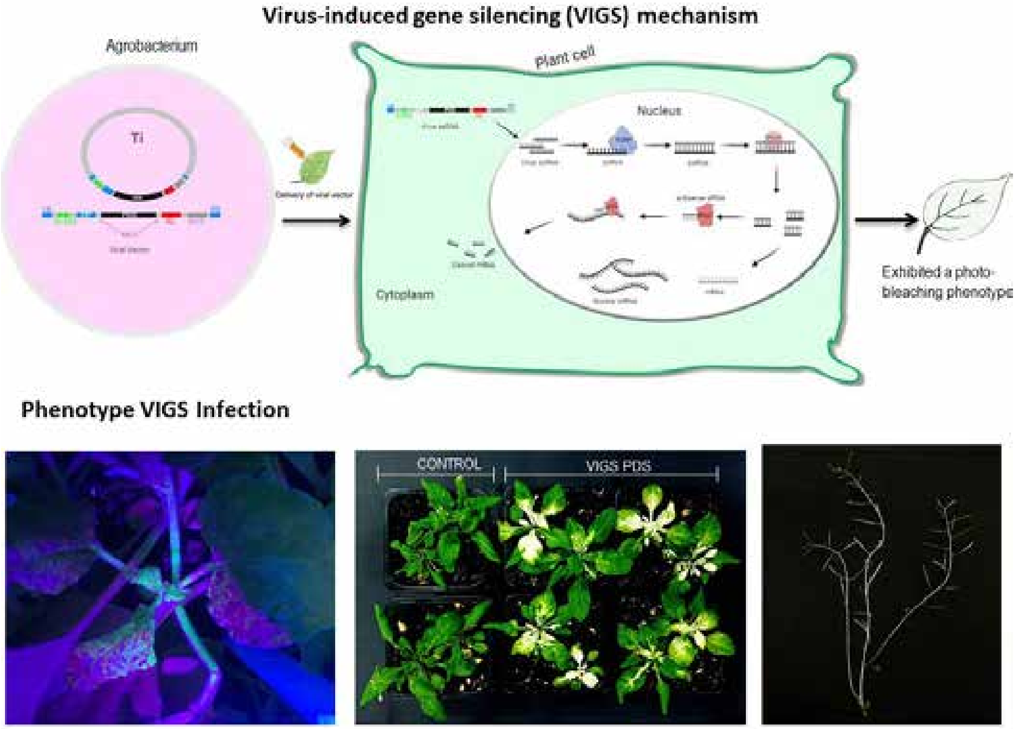
DNA methylation (5mC) is considered one of the main resources for creating phenotypic diversity in agricultural plants. It plays an important role in controlling mobile genome elements, the activity of which usually leads to genetic changes. To study 5mC-mediated phenotypic and genomic changes in agricultural plants, new tools for modifying the plant epigenome are needed. In our lab, we are developing a virus-induced gene silencing (VIGS) approach involved in DNA methylation. We optimized VIGS infection conditions for *Arabidopsis thaliana*. 90%of VIGS efficiency was achieved for the model phytoene desaturase gene (PDS). Various vector constructs were used to enhance the effect of VIGS as well as GFP tracking of viral infection spread. Using VIGS, the Arabidopsis *ddm1* gene, involved in the methylation pathway of mobile elements in heterochromatin, was silenced and its expression was detected by qPCR.

This research was funded by the Russian Science Foundation (grant № 22-64-00076).

<u>Take-home message:</u>

Our study is about to develop a new approach for plant epigenome modification by targeting DNA methylation through the means of virus-induced gene silencing. This new approach will provide insights for new possibilities of studying DNA methylation.



Peroxidases in peach: gene duplication as one of the evolution adaptation mechanism

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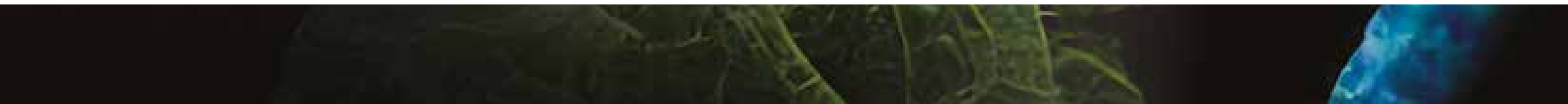
Duplications of genes and genomes, which are observed quite often in plants, can be rightfully considered as the evolutionary adaptation mechanism. As a result of the process of duplication of individual genes, the loss of functionalization, subfunctionalization and neofunctionalization in duplicated genes can be observed.

This study aims to investigate gene duplication and subsequent paralogization in peaches using peroxidase, an enzyme of the antioxidant complex involved in most stress responses. Based on genomic analysis, 60 genes were found in peach that encode this enzyme, differing in structure and conserved motifs. Based on the transcriptomic data and the laboratory experiment performed, it was found that the expression of different genes encoding peroxidase is switched during exposure to different stress factors (watering, fungus infection, cold stress); tissue specificity of gene expression is observed as well as differences in expression in different varieties. The data obtained suggest subfunctionalization of these POD duplications. The study is supported by the Kurchatov Genomic Centre of the NBG–NSC (075-15-2019-1670).

Take-home message:

The study is devoted to the analysis of peroxidase gene duplications in peach and their expression patterns under different conditions. The results suggest that paralogization of these genes during evolution led to their subfunctionalization.



Efficiency of Rph genes against *Puccinia hordei* in Southern Russia

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Barley leaf rust (*Puccinia hordei* Otth.) is considered a harmful disease that occurs in barley-growing regions worldwide. In Russia, the disease is among the most prevalent in the Krasnodar region, which is the leader in the production of barley grain and has a favorable climate for disease development. In this paper, we studied the efficiency of 17 varieties and lines of barley from the International and Australian sets containing currently known Rph resistance genes or their combinations to *P. hordei* in the field, and 15 varieties and lines in the seedling phase in greenhouse conditions during 2019–2021. We concluded that the lines carrying the *Rph7* and *Rph13* genes remained immune throughout the three years of studies in the seedling and adult plant stages. The *Rph1* and *Rph23* genes showed moderate efficiency during the three years. The *Rph2, Rph3, Rph4, Rph5, Rph6+2, Rph8, Rph12, Rph19,* and *Rph21+2* genes showed low efficiency over the three years. This was also confirmed by the results of their assessment in the seedling phase: the number of monopustular isolates virulent to lines with the majority of the studied genes for three years was above 90%. Fluctuations in the virulence of the P. hordei population were observed under sufficiently unfavorable weather for disease development in 2019, 2020, and 2021. This proves the ability of the fungus to adapt to changing conditions. Therefore, annual monitoring of the response of lines and varieties carrying resistance genes and studying the virulence of the pathogen are crucial for the selection of rust-resistant varieties, and, hence, the prevention of barley leaf rust epidemics in all grain-producing regions worldwide.

WOX transcription factors and their partners in the regulation of somatic embryogenesis in *Medicago truncatula*

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Somatic embryogenesis (SE) is the process of non-zygotic cells transformation into embryogenic cells, which then form embryo-like structures and can eventually form a new plant. The genetic regulation of SE has not yet been clearly understood. The identification of the regulators of this process is important for improving the methods of obtaining somatic embryos.

Previously in our studies, it was found that overexpression of *MtWOX9-1* and *STENOFOLIA* genes from the *WUSCHEL-RELATED HOMEOBOX* family of transcription factors leads to an increase in the capacity for SE in Medicago truncatula. Moreover, transcription factors interacting with *MtWOX9-1* were discovered and the importance of a homeodomain for their interaction was shown.

The aim of this study is to search for new *WOX* genes which can be involved in SE regulation in M. truncatula and to search for *MtWOX9-1* homeodomain structures necessary for interaction with other transcription factors. We evaluated the *SE* capacity of calli with overexpression of *MtWOX11-1* and *MtWOX11-2* genes. Meanwhile, using a yeast two-hybrid system, we found amino acids significant for the interaction of *MtWOX9-1* with its partners.

The main publications of authors on the subject of the abstract:

Elina Potsenkovskaia et.al. Novel NF-Y genes expressed during somatic embryogenesis in Medicago truncatula//Plant Gene, Volume 31, 2022, 100364, ISSN 2352-4073. https://doi.org/10.1016/j.plgene.2022.100364.

Take-home message:

The WOX9-1 homeodomain is necessary for interaction with other transcription factors - regulators of embryogenesis.

Features of introduction into *in vitro* culture of industrial varieties and wild species of grapes cultivated in Uzbekistan

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Возделывание винограда требует некоторых технологических особенностей. При введении эксплантов in vitro верхушки побегов винограда стерилизовали водным раствором нитрата серебра, и коллоидного серебра, стабилизированного полигексаметиленбигуанидином гидрохлоридом в концентрациях 0,1, 0,05, 0,01 и 0,001 мг/л в сочетании с водными растворами тимеросала в тех же концентрациях. Результаты показали для стерилизации побегов 0,1 мг/л. Побегообразование проводили на средах без добавления фитогормонов, а для укоренения использовали в-индолилуксусную кислоту или а-нафтилуксусная кислоту в концентрации 0,2 мг/л. Среди двух протестированных базальных сред MS и WPM без каких-либо регуляторов роста индуцировали 90 и 84% распускания почек соответственно. Индукция двух или более побегов у максимального количества эксплантов (80%) наблюдалась в среде MS. WPM питательной среде индукция побегообразования пошел очень медленно, и побегообразование была очень низкой. МС привел к получению сравнительно лучших побегов с нормальным междоузлием и светло-зелеными листьями. Из протестированных сред было установлено, что MS является наиболее подходящей средой, приводящей к появлению сильных всходов.

The main publications of authors on the subject of the abstract:

1. *Yakubov M.D., Dalimova D.A. Study of the ACTN3 gene polymorphism to assess the physical performance of athletes \\ International Engineering Journal for Research & Development, India, Vol. 7, Issue 1, 2022, P. 1-3. CJIF 7.1*

2. *Yakubov M.D., Dalimova D.A. Distribution Of PPARG Gene Pro12Ala Polymorphism // The American Journal of Applied sciences, USA, 2021, Volume 3, Issue 12-01, P. 1-11. CJIF 5,6*

Take-home message:

Для микроразмножения использовали питательную среду МС, с сахарозой в концентрации 20 г/л, иннозитол 100 мг/л, а побегообразование проводили на средах без фитогормонов, а для укоренения использовали β-НУК или α-НУК 0,2 мг/л.

Features of the formation of defense reactions in potato plants when treated with *Bacillus subtilis* bacteria and conjugates chitosan

Yarullina L.G., Cherepanova E.A., Sorokan A.V., Zaikina E.A., Burkhanova G.F., Tsvetkov V.O.*, Kalatskaya Zh.N., Nikolaichuk V.V.***, Mardanshin I.S.******

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Chitosan and its derivatives are active elicitors of plant immunity, which are used to increase the biological activity of biological products. The effect of *B. subtilis* (strains 26D and 11VM) and chitosan nanocomposites with caffeic (ChCA) and ferulic (ChFA) acids on the resistance of potato to *Phytophthora infestans* was researched. On 15th day after germination, plants were sprayed with 5 ml per 1 plant of *B. subtilis* (108 cells/ml), ChCA and ChFA (0.3 mg/ml), and its mixture. On the 3rd day after treatment, the plants were sprayed with of P. infestans zoospore.

We revealed a decrease in damage of leaves, most significantly – under the ChCA. The maximum protective effect was with B. subtilis 26D with ChFA. Resistance was mediated by catalase, peroxidase, hydrogen peroxide, and transcripts of PR proteins genes. Identified activation of expression of PR-1 (marker of SAR) and PR-6 (ISR induced) under influence of bacteria with conjugates indicates that various signaling pathways are involved in defense reactions.

The work was financially supported by the Russian Science Foundation (grant no. 23-16-00139) using the equipment of the Center for Collective Use "Biomika".

The main publications of authors on the subject of the abstract:

Yarullina L.G., et al. Impact of Bsubtilis bacteria in combination with SA and JA on changing the proteome of potato leaves when infected by P. infestans with a moisture deficit. Rus J Plant Phys. 2022. DOI: 10.1134/S1021443722040215

Yarullina L.G., et al. Stimulation of the protective mechanisms of Solanum tuberosum by the bacteria Bacillus subtilis and chitooligosaccharides upon infection with Phytophthora infestans. Appl Biochem Microbiol. 2022. DOI: 10.1134/S0003683822020168

Take-home message:

Identified activation of the expression of PR-1 and PR-6 under the influence of a complex of bacteria with chitosan nanocomposites indicates that various signaling pathways are involved in the development of defense reactions with their participation

Plastome structure and evolution in *Burmannia* (*Burmanniaceae, Dioscoreales*)

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Mycoheterotrophic plants are those that obtain nutrients from fungi and do not fix carbon using photosynthesis. They are known to have a tendency to plastid genome reduction. *Burmannia*, the largest genus of Burmanniaceae, is a demonstrative model of plastome reduction as it comprises both photosynthetic and mycoheterotrophic species.

We performed genome skimming for 7 *Burmannia* species using Illumina NGS platform. We assembled complete plastomes and performed their comparative analysis. We also reconstructed phylogeny using nuclear and mitochondrial markers.

Burmannia plastomes uniformly retain quadripartite structure. Their sizes vary within the genus from 39 kb in *B. oblonga* (fully mycoheterotrophic) to 157 kb in *B. disticha* (fully autotrophic). All studied mycoheterotrophic species completely lost or have as pseudogenes the photosynthesis-related genes (*rbcL, psa, psb*) and most of the transfer RNA genes. Most of the retained genes in their plastomes are represented by ribosomal protein genes and other housekeeping genes.

Supported by the Russian Science Foundation (project 21-74-10006) and by IITP RAS FFNU-2022-0037.

Take-home message:

The genus *Burmannia* is a descriptive model of the plastome evolution in non-photosynthetic plants. Plastid genomes of *Burmannia* demonstrate a large range in size and number of genes.

Allelic variation at the vernalization response (VRN-1) genes of spring soft wheat varieties of different ecotypes from Bashkir selection

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The allelic composition of the vernalization gene VRN-1 of 7 varieties of spring soft wheat (Triticum aestivum L.) developed with the participation of Bashkir breeders over the past 30 years was studied. From the 7 varieties of Bashkir selection 3 varieties (Bashkirskaya 24, Zauralskaya Zhemchuzhina and Ekada-113) have the Vrn-A1a/vrn-B1/vrn-D1 haplotype. These wheat varieties belong to forest-steppe West Siberian ecotype of wheat and possessed recessive allele vrn-B1. Interestingly, another 2 varieties of forest-steppe West Siberian ecotype from Bashkir selection – Bashkirskaya 26 and Salavat Yulaev – have the Vrn-A1a/Vrn-B1a/vrn-D1 haplotype possessing dominant allele Vrn-B1a. Meanwhile remaining 2 varieties of Bashkir selection, Ekada-70 and Ekada-109, which are representatives of the steppe Volga ecotype have another dominant allele Vrn-B1c. Thus, it was shown that the main difference between the wheat varieties of the Bashkir selection from different ecotypes is observed in the Vrn-B1 gene.

The work was supported by the Russian Science Foundation grant No. 23-26-00246,
https://rscf.ru/project/23-26-00246/

Comparative bioinformatics of repeatomes of three *Hedysarum* species based on NGS technologies

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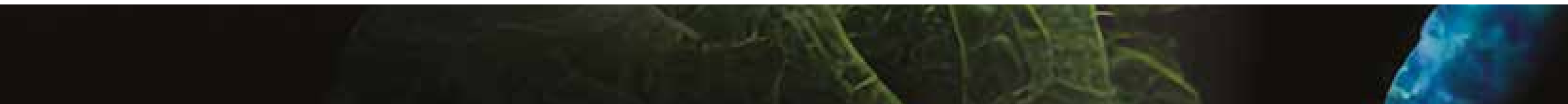
The genus *Hedysarum* L. comprises up to 200 species, which are widely distributed throughout the world. Based on taxonomic studies, the genus *Hedysarum* was subdivided into two sections: *Hedysarum* and *Multicaulia,* which was confirmed by comparative molecular (plastid and nuclear ITS data) and cytogenetic (chromosome numbers) studies. In the present study, for the first time, repetitive DNA sequences of *H. theinum* Krasnob., *H. neglectum* Ledeb., and *H. alpinum* L. were investigated using high-throughput sequencing technologies and a subsequent bioinformatic analysis of repeat elements with the RepeatExplorer2 and Tandem Repeat Analyzer (TAREAN) software. The comparison of repeatomes of these species showed that mobile elements made up 42-45.44 % (Class 1) and about 5.8-7.44%(Class 2) of their repetitive DNAs. The amount of ribosomal DNA varied from 0.95 to 1.99%, the content of satellite DNA families (satDNAs) ranged from 0.89 to 1.33%. For each species, six high confident putative satDNAs and 3-4 (depending on species) low confident putative satDNAs were identified.

This research was funded by the Russian Science Foundation (project No. 23-26-00037).

The main publications of authors on the subject of the abstract:

Yurkevich O.Y. et al. Molecular Cytogenetics of Eurasian Species of the Genus Hedysarum L. (Fabaceae)// Plants (Basel). (2021), 10(1):89. doi: 10.3390/plants10010089

Yurkevich O.Y. et al. Integration of Genomic and Cytogenetic Data on Tandem DNAs for Analyzing the Genome Diversity Within the Genus Hedysarum L. (Fabaceae)// Front Plant Sci. (2022), 13:865958. doi: 10.3389/fpls.2022.865958



Study of localization of satellite repeats decaploid *Thinopyrum bessarabicum*

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Nine satellite repeats (SRs) were localized to the chromosomes of decaploid *Thinopyrum bessarabicum* PI 21890 (2n=70) using fluorescent *in situ* hybridization (FISH). The SRs were identified using RepeatExplorer2 based on whole-genome sequencing data of the target accession and *Th. bessarabicum* PI 531711 (2n=14).

The SRs were localized to the following chromosomes: CL170, pericentromerically on the short arm of two chromosomes; CL149, terminally on 28 chromosomes; CL198, centromeric and subtelomeric signals on 32 chromosomes; CL193, terminally on the short arm of two chromosomes; CL192, terminally on the short arm of one pair and proximally on the long arm of another pair of chromosomes; CL148, pericentromerically on four chromosomes and terminally on short or long arms of eight chromosomes; CL16 and CL44, dispersed, with CL44 showing bright centromeric signals on 22 chromosomes. No localization was observed for CL2.

The localization pattern suggests non-equivalence of the subgenomes in the studied accession. The identified SRs can be used in evolutionary and population studies of Triticeae.

The work was supported by the Russian Science Foundation grant 21-16-00123.

The main publications of authors on the subject of the abstract:

Kroupin P.Y. et al. Aegilops crassa Boiss. repeatome characterized using low-coverage ngs as a source of new FISH markers: Application in phylogenetic studies of the Triticeae // Frontiers in Plant Science (2022) 13: 980764. doi: 10.3389/fpls.2022.980764

Mechanisms controlling symbiotic efficiency of arbuscular mycorrhiza: role of plant genotype and fungal biodiversity

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The development of effective arbuscular mycorrhiza (AM) depends both on host plant symbiotic potential and AM fungi ability to form an effective AM. We selected *Medicago lupulina* MlS-1 line with high mycorrhizal growth response (MGR) under condition of inoculation with different AM fungi. Analysis of root metabolic profile including 317 metabolites already at the early stages of host plant development showed that compounds supporting AM fungus growth (especially amino acids, specific lipids and carbohydrates) were accumulated and coincided with intensive developments of AM structures.

The high AM fungi biodiversity, shown in natural ecosystems (river valleys), determined the possibility to select AM fungi with different MGR. *M. lupulina* genes with differential expression during inoculation with isolates contrasting in MGR was tested. The use of this model system has shown that, despite strong control for AM efficiency by the host plant, many genes specifically expressed during AM development are not markers of symbiotic efficiency. The results revealed a number of genes involved in the development of effective AM. The study was supported by RSF 22-16-00064.

Evaluation of the differentiating ability of ecological points of the Ekada program

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В селекционной работе создание сортов обладающих высокой и стабильной продуктивностью при широком варьировании условий возделывания невозможно без комплексной оценки среды, как фона для отбора желаемого идеатипа.

Целью исследования являлась оценка с помощью GGE biplot анализа дифференцирующей способности сред пяти экологических точек программы «Экада», их сходство и репрезентативность. Объектом исследований была модельная популяция из 20 сортов яровой пшеницы. Дисперсионный анализ урожайности выявил значимые различия между генотипами, средами и их взаимодействием. В среднем за два контрастных года, наибольшая урожайность получена в точке Курган – 3,54 т/га, далее Ульяновск – 3,49 т/га, Пенза – 3,38 т/га, Казань – 2,99 т/га и Безенчук – 2,60 т/га. В результате визуализации результатов biplot анализа выявлено, что наибольшей дифференцирующей способностью и репрезентативностью характеризуются точки Безенчук, Ульяновск и Казань, которые позволяют выделять адаптированные генотипы. Высокая дифференцирующая способность, но низкая репрезентативность присуща также пунктам Пенза и Курган, следовательно, в них возможен отбор узкоадаптированных сортов и браковка нестабильных генотипов.

The main publications of authors on the subject of the abstract:

В.Г. Захаров, О.Г. Мишенькина. Адаптивные свойства новых сортов овса в условиях Средневолжского региона // Вестник Ульяновской государственной сельскохозяйственной академии № 4 (52). – С. 100-107. 10.18286/1816-4501-2020-4-100-107

GWAS of soybean breeding collection for resistance to charcoal rot in the condition of South-East Kazakhstan

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Soybean (*Glycine max* (L.) Merr) is an essential food, feed, and technical crop. One of the main problems of soybean production is root diseases that cause yield losses of up to 30%. Modern genomic studies can be applied to facilitate efficient breeding research for the improvement of soybean fungal disease tolerance. The objective of this genome-wide association study (GWAS) was the analysis of the world soybean collection consisting of 252 accessions in relation to resistances to charcoal rot (*Macrophomina phaseolina*). GWAS using 44385 SNP markers of resequencing data identified 177 SNPs for twenty-four QTLs for the resistance to charcoal rot (CR). Comparison with previously reported QTLs showed that twelve out of twenty-four presumably novel was genetically mapped on eight chromosomes. The results can be used to improve local breeding projects based on a marker-assisted selection approach.

The authors would like to acknowledge the funding from the MSHE RK in the framework of grant AP13068118 and Program O.001B "Biological safety of the Republic of Kazakhstan: assessment of threats, scientific and technical basis for their prevention and elimination".

The main publications of authors on the subject of the abstract:

Zatybekov A. et al. GWAS of agronomic traits in soybean collection included in breeding pool in Kazakhstan // BMC Plant Biology (2017) 17:179. doi:10.1186/s12870-017-1125-0.

Zatybekov A. et al. GWAS of soybean breeding collection for resistance to fungal diseases in condition of South-East and South Kazakhstan // Vavilov Journal of Genetics and Breeding (2018) 22:536-543. doi:10.18699/VJ18.392.

Take-home message:

First research using resequencing technology for genotyping of perspective cultivars and lines of local soybean breeding programs.

Computational reconstruction of transcriptional cascades induced by plant hormones

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Reconstruction of hierarchical transcriptional cascades (TCs) orchestrated by plant hormones is the key for understanding the molecular mechanisms underlying different plant traits. Despite recent progress in methods for automatic inference of gene regulatory networks (GRNs), there is still a shortage of computational approaches for the large-scale reconstruction of TCs, which define GRN architecture. Here, we introduce an original three-step procedure to reconstruct hormone-induced TCs based on the integrated analysis of differentially expressed gene lists and a representative collection of transcription factor binding profiles. We applied this procedure to reconstruct TCs induced by auxin and ethylene in *Arabidopsis thaliana*. We identified transcriptional subnetworks, which operated before hormone treatment and were switched off upon hormone application, and the ones, which were switched on by the hormone. Moreover, we illustrated the functioning of the auxin-induced TC in regulation of chlorophyll biosynthesis. Our results demonstrate a promising outlook of using a new approach for computational reconstruction of TCs. This work was supported by the RSF grant no. 20-14-00140.

Take-home message:

A new three-step procedure based on the integrated analysis of differentially expressed gene lists and a representative collection of transcription factor binding profiles enables automatic reconstruction of transcriptional cascades.

Sex-determining region in studying the phylogeny of sections *Aigeiros* Dubi and *Tacamahaca* Spach of the genus *Populus L.* (*Salicaceae*)

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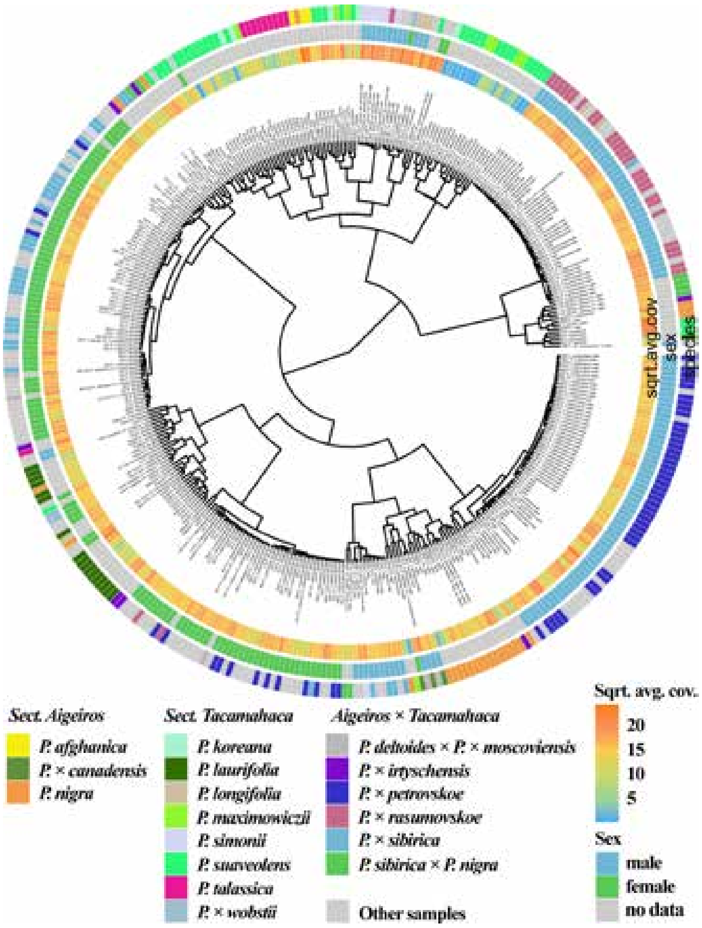
The genus Populus L. plays an important role in the formation of forests in the northern hemisphere and is also used in urban landscaping and for timber production. Species of the genus *Populus* are characterized by extensive hybridization between closely related sections. Therefore, the microsystematics of the taxon is confusing and non-obvious in many cases, especially for poplars of hybrid origin. We evaluated the efficacy of using the sex-determining region (SDR) in addition to the nuclear and chloroplast genome sequences traditionally used in phylogenetic studies to establish the relationships between poplars of sections *Aigeiros* Dubi and *Tacamahaca* Spach. Targeted deep sequencing of NTS 5S rDNA, ITS, nuclear and chloroplast genes, and the SDR and *ARR17* gene was performed for 379 poplar accessions. The SDR and *ARR17* gene, together with the traditionally used multicopy and single-copy nuclear and chloroplast DNA sequences, allowed us to obtain a clustering best consistent with poplar systematics based on morphological data and shed light on several controversial hypotheses about the origin of the studied taxa.



RrolB/C-like natural transgene for phylogenetic studies of genus *Vaccinium* L.

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Various wild plant species have agrobacterial T-DNAs in their genomes, that they transmit in a series of sexual generations. That T-DNAs are called cellular T-DNAs (cT-DNAs). cT-DNAs have been found in dozens of plant genera.

In our previous work we found untypical cT-DNAs in the genome data of two *Vaccinium* L. species. These cT-DNAs contain the *rolB/C*-like gene. Here, we present a larger study of these sequences in *Vaccinium* genus. We applied molecular-genetic and bioinformatics methods for sequencing, assembly, and analysis of the *rolB/C*-like gene. We discovered *rolB/C*-like gene in 26 new *Vaccinium* species and *Agapetes serpens* (Wight) Sleumer. Most samples of these species were found to contain full-size genes. It allowed us to develop approaches for the phasing of cT-DNA alleles and reconstruct a *Vaccinium* phylogenetic relationship.

Our data demonstrate that levels of intra- and interspecific polymorphism of the *rolB/C*-like gene allow to use it as a convenient molecular marker for phylogenetic and phylogeographic studies of *Vaccinium* genus.

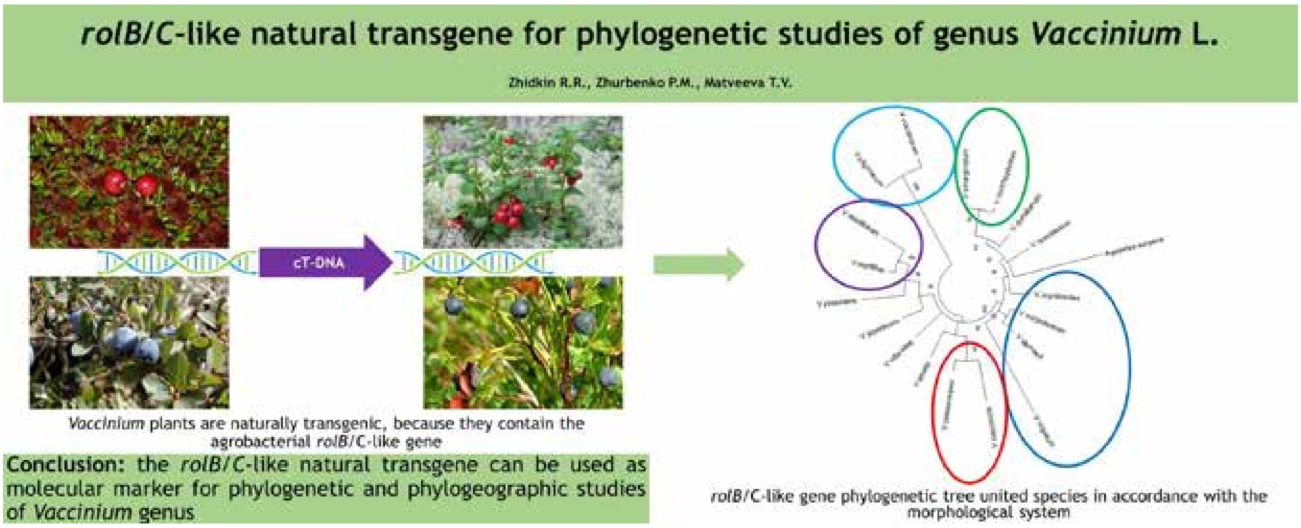
<u>The main publications of authors on the subject of the abstract:</u>

Matveeva T. New naturally transgenic plants: 2020 update // Biological Communications (66) 1: 36-46. doi: 10.21638/spbu03.2021.105

Zhidkin R. et al. Biodiversity of rolB/C-like Natural Transgene in the Genus Vaccinium L. and Its Application for Phylogenetic Studies // International Journal of Molecular Sciences (24) 8: 6932. doi: 10.3390/ijms24086932

<u>Take-home message:</u>

Vaccinium species are naturally transgenic, containing *rolB/C*-like gene. This gene can be used as convenient molecular marker for phylogenetic and phylogeographic studies.



rolB/C-like natural transgene for phylogenetic studies of genus *Vaccinium* L.

Zhidkin R.R., Zhurbenko P.M., Matveeva T.V.

Vaccinium plants are naturally transgenic, because they contain the agrobacterial *rolB/C*-like gene

Conclusion: the *rolB/C*-like natural transgene can be used as molecular marker for phylogenetic and phylogeographic studies of *Vaccinium* genus

rolB/C-like gene phylogenetic tree united species in accordance with the morphological system

Functional genomics of pea (*Pisum sativum* L.): focus on plant-microbe interactions

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Pea (*Pisum sativum* L.) is an important crop plant and a model object for studying the interactions of legume plants with nodule bacteria (NB) and arbuscular mycorrhizal (AM) fungi. Different pea cultivars have high or low responsiveness to inoculation with NB and AM. Here, we present the results of comprehensive genomic and transcriptomic analysis of the response of pea plants to inoculation with NB and AM fungi in different combinations. First, we show that the highly responsive genotype k-8274 is able to suppress the development of nodules locally (but not systemically) when inoculated with both NB and AM fungi. Second, we demonstrate that the response to inoculation in k-8274 and its descendant cv. Triumph (which inherited the high responsivity to inoculation from k-8274) involves gibberellin signaling, which leads to suppression of AM spreading in the root tissues. Last, the genome sequencing showed that cv. Triumph inherited certain genomic regions that carry some candidate genes possibly determining the high responsiveness to inoculation with NB and AM fungi. The results of the analysis will be used in breeding programs. This work is supported by the RSF grant #22-16-00109.

Take-home message:

Whole-genome and whole-transcriptome analysis reveals that in pea, the responsiveness to inoculation with nodule bacteria and arbuscular mycorrhizal fungi relies on strict control of plant over its microsymbionts in roots.

Changing the specificity of the symbiosis of pea (*Pisum sativum* L.) with nodule bacteria using genetic engineering technologies

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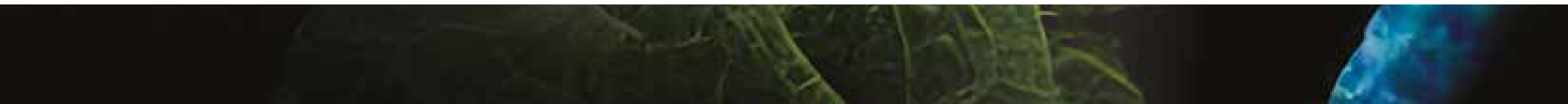
Pisum sativum L., commonly known as pea, represents a crucial source of plant protein in the human diet. In modern pea farming practices, bio-preparations that include rhizobia strains capable of efficiently fixing atmospheric nitrogen are vital. The improvement of specificity in the interaction between pea and rhizobia can help to prevent competition with less effective strains of nodule bacteria present in the soil. This presentation outlines the creation of highly effective symbiotic pairs through the modification of the specificity of the pea-rhizobia symbiosis. Specifically, we have successfully deactivated the *NodX* symbiotic gene of nodule bacteria, resulting in a wider range of interaction specificity. Also, report will present plans to utilize CRISPR/Cas9 genomic editing technology to enhance the specificity of interaction between pea and particular strains of nodule bacteria. The resulting genome-edited pea plants are expected to exhibit high specificity of interaction with nodule bacteria, leading to an increase in nitrogen fixation efficiency and improved yield. This research project was funded by the Sirius University of Science and Technology project PBB-RND-2243.



New mechanisms of systemic regulation of the development of arbuscular mycorrhiza in garden pea (*Pisum sativum* L.)

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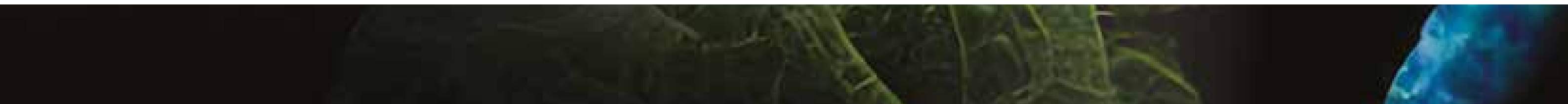
Pisum sativum L. forms mutually beneficial symbioses with nitrogen-fixing nodule bacteria and arbuscular mycorrhiza (AM) fungi. For the first time in the world, we observed that in closed containers for growing plants (SacO2 Microboxes), pea plants developed normal nodules, but did not form AM. We hypothesized that the absence of AM under these conditions was due to the systemic regulation mechanisms, which were also involved in the formation of the cuticle in the aerial parts of plants. Pea plants of cv. Frisson were grown in containers either completely closed (Conditions 1, C1), or with open lids (C2). Analysis of the transcriptome and metabolome of roots and aerial parts of plants showed that cultivation in C1 led to significant changes in the expression profiles of genes involved in cutin biosynthesis, and in the composition of lipophilic primary metabolites in both plant parts. In C1, as compared with C2, the content of precursors of cutin monomers was significantly reduced both in the roots and in the shoots. This result supported our hypothesis. The work was made within the framework of the World-class Scientific Center "Agrotechnologies for the Future".

The main publications of authors on the subject of the abstract:

Zorin E.A. et al. Transcriptome Analysis of Alternative Splicing Events Induced by Arbuscular Mycorrhizal Fungi (Rhizophagus irregularis) in Pea (Pisum sativum L.) Roots // Plants (2020) 9: 1700. https://doi.org/10.3390/plants9121700

Zorin E.A. et al., The effect of microbox conditions on the expression of pea genes involved in the pathway of cutin biosynthesis during inoculation of plants with arbuscular mycorrhizal fungi and nodule bacteria // Modern mycology in Russia (2022) 5: 229-231



Unraveling the Intricacies of Water Flow in Conductive Systems of Maize Leaves Using Multi-Level Data

Zubairova U.S., Doroshkov A.V.*, Romashchenko A.V.*, Pushkareva A.A., Nikolaev S.V.***, Penenko A.V.******

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The plant organism is formed through coordinated self-organizing mechanisms, in which water flows play a key role at the level of organs, tissues, and cells. Therefore, it is important to investigate how transport processes depend on the xylem architecture resulting from phenotypic plasticity of the plant regulated by environmental factors within a given genotype that determines the plant's internal developmental factors. This study used a comprehensive approach, including physiological measurements, multi-view, microscopy, contrast-enhanced magnetic resonance imaging, and modeling of water flows in porous media to study the transport processes in maize leaves growth zone under contrasting environmental conditions. Experimental data were obtained from young maize seedlings exposed to high light during 4-8 leaf development. The results of inverse modeling made it possible to establish quantitative dependences between the parameters of water flows and the parameters of growth and transpiration processes in leaves.

The main publications of authors on the subject of the abstract:

Zubairova, U. S., Kravtsova, A. Y., Romashchenko, A. V., Pushkareva, A. A., Doroshkov, A. V. (2022). Particle-based imaging tools revealing water flows in maize nodal vascular plexus. Plants, 11(12), 1533. https://doi.org/10.3390/plants11121533

Nikolaev, S. V., Zubairova, U. S. (2021). A computational model of the cereal leaves hydraulics. In Journal of Physics: Conference Series (Vol. 2099, No. 1, p. 012039). IOP Publishing. https://doi.org/10.1088/1742-6596/2099/1/012039

Take-home message:

Modeling of water flows in porous media based on data from multi-view, microscopy, and contrast-enhanced magnetic resonance imaging revealed quantitative dependences between water flows, growth, and transpiration processes in young maize leaves.

Metabolomic diversity of rye (*Secale cereale* L.) grains

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Plant secondary metabolites are a diverse group of natural compounds. Domestication of modern crops has lead to their lower diversity and content in modern varieties. Many secondary metabolites have a prominent effect on human health, both beneficial and detrimental, depending on concentration and preexisting health conditions. One of the ubiquitous and actively studied group are flavonoids. Since we use many plants, especially cereals, for food production, it is tempting to create a set of lines with qualitatively and quantitatively modified content of these compounds. Rye still have high genetic heterogeneity and also high flavonoid content second only to sorghum. We have analyzed lines from 'Peterhof' rye genetic collection and found lines with low flavonoid content as well as lines with high content of peonidin, quercetin, luteolin, syringetin glucosides; dihydroquercetin, tricetin, chrysoeriol C-glucoside.

The work was supported by the Ministry of Science and Higher Education of the Russian Federation in accordance with agreement No. 075-15-2022-322 date 22.04.2022 on providing a grant in the form of subsidies from the Federal budget of Russian Federation.

The main publications of authors on the subject of the abstract:

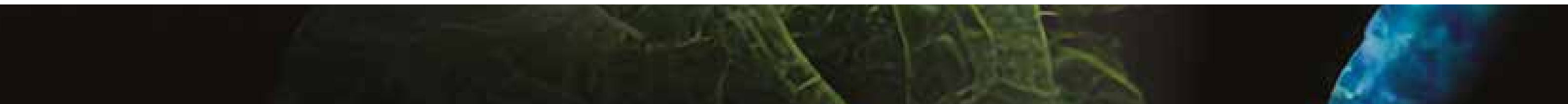
Zykin, P.A.; Andreeva, E.A.; Lykholay, A.N.; Tsvetkova, N.V.; Voylokov, A.V. Anthocyanin Composition and Content in Rye Plants with Different Grain Color. Molecules 2018, 23, 948. https://doi.org/10.3390/molecules23040948

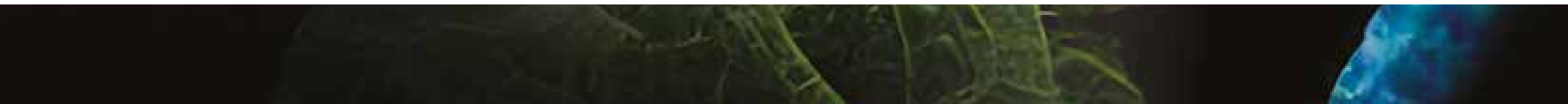
Zykin, P.A.; Andreeva, E..A.; Tsvetkova, N.V.; Voylokov, A.V. Anatomical and Image Analysis of Grain Coloration in Rye. Preprints.org 2020, 2020110530. https://doi.org/10.20944/preprints202011.0530.v1.

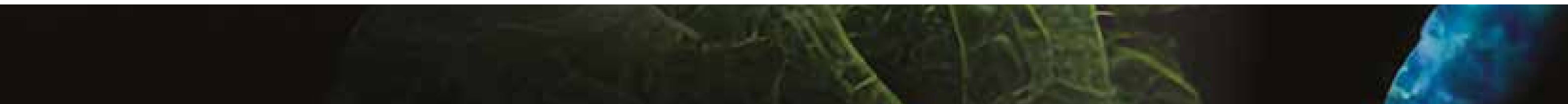
Take-home message:

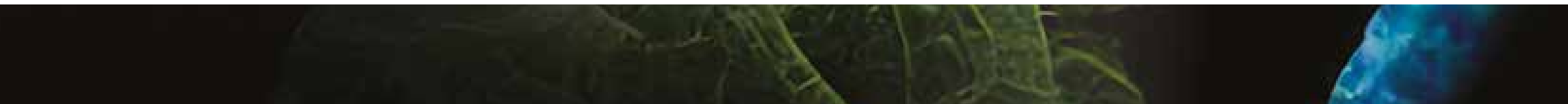
Rye lines in Petergof rye mutant collection have diverse flavonoid content and can be used as a donor for creating a specialized flavonoid-rich varieties

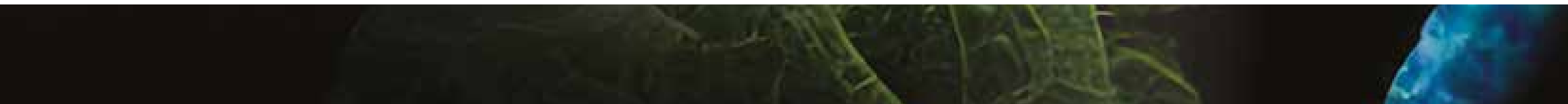
CONTENT

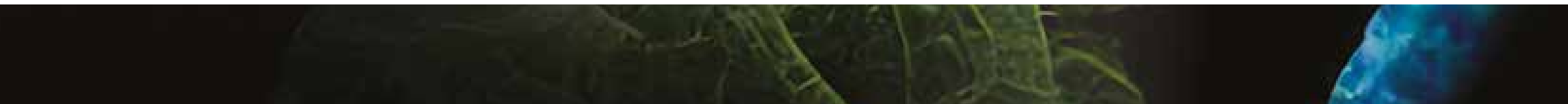


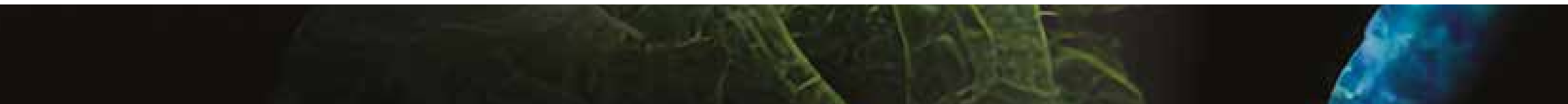


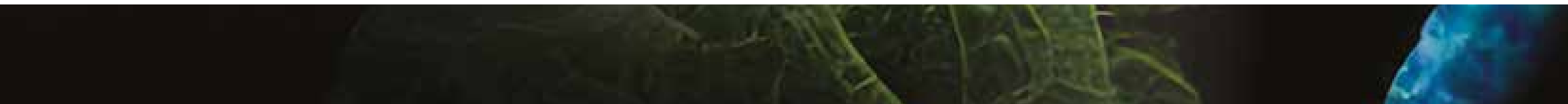


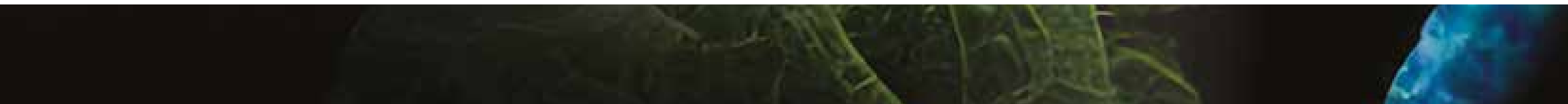


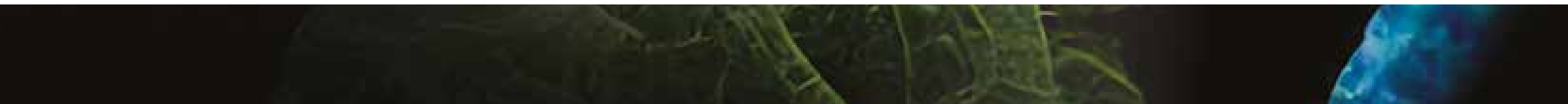


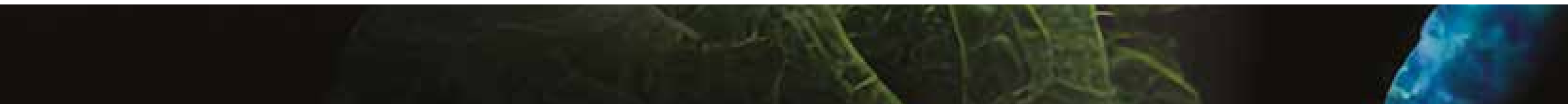


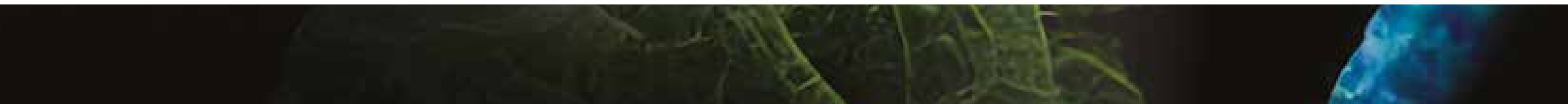


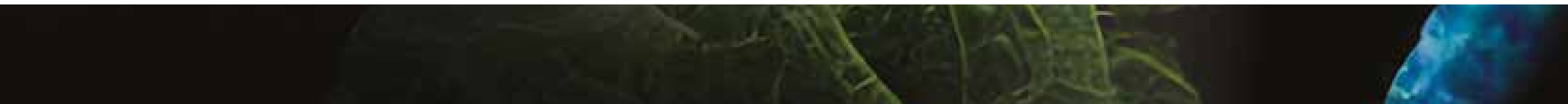


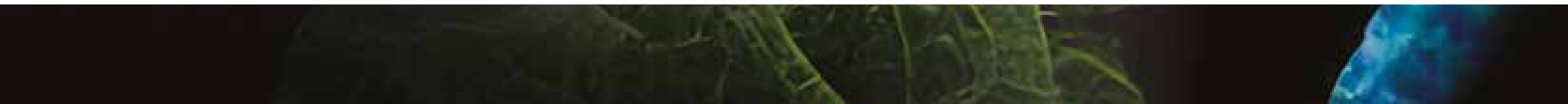


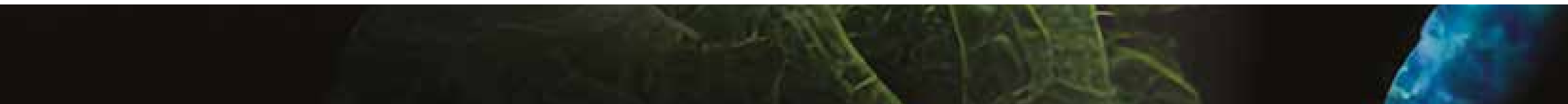












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