

Lebedeva T. V., Zuev E. V., Stetsyuk S. N. POWDERY MILDEW RESISTANCE IN WHEAT VARIETIES (*TRITICUM AESTIVUM* L.) FROM THE VIR COLLECTION. Proceedings on applied botany, genetics and breeding. Vol. 174. 2014. pp. 3–10.

Powdery mildew resistance of 533 spring wheat accessions (*Triticum aestivum* L.) was evaluated at the adult plant phase. Durable resistance to powdery mildew has been demonstrated by Omskaya 18 k-58220; Line IT-3 k-50849; Canon k-61222; Dragon k-61515; Dacke k-63479; Sunnan k-58177; Atson k-41993; Ask-34982; line I Sr5-Rb k-54868. Changes in the *Blumeria graminis* f. sp. *tritici* Golovin population in the Leningrad Province have been monitored from 1980 through 2012.

Key words: wheat, powdery mildew, virulence, population.

E. E. Radchenko CEREAL CROPS GENEPOOL AND BREEDING FOR APHID RESISTANCE. Proceedings on applied botany, genetics and breeding. Vol. 174. 2014. pp. 11–22.

The results of research on wheat and sorghum genetic resources resistance to cereal aphids are discussed. Both major and minor genes for aphid resistance in cereals differentially interact with insects. Therefore, the most rational grain crops breeding for aphid resistance provides for increasing genetic diversity of cultivated varieties. The share of either way of increasing the diversity depends on crop features. For wheat, it is primarily introgression of resistance from wild relatives, while for sorghum it is the search for resistance within the global collection of cultivated species. The newly identified genes for greenbug resistance in sorghum are offered for breeding practice.

Key words: wheat, sorghum, aphids, resistance.

E. V. Rogozina, E. E. Khavkin, E. A. Sokolova, M. A. Kuznetsova, T. A. Gavrilenko, L. A. Limantseva, V. A. Biryukova, N. A. Chalaja, R. W. Jones, K. L. Deahl CLONE COLLECTION OF WILD SPECIES AND INTERSPECIFIC HYBRIDS OF POTATO STUDIED PHYTOPATHOLOGICALLY AND BY MEANS OF DNA MARKERS. Proceedings on applied botany, genetics and breeding. Vol. 174. 2014. pp. 23–32.

Samples from the collection of wild tuber species *Solanum* and interspecific hybrids were evaluated in field and laboratory tests for resistance to most dangerous potato pathogens: *Phytophthora infestans* (Mont.) de Bary, Y-virus, *Globodera rostochiensis* (Woll.) Behrens. For the first time DNA markers for the *R*-genes for resistance to late blight (R1-1205, R3-1380, RB-629), potato virus Y (GP122/EcoRV-406, RYSC3-320), and nematode pathotype Ro1 (TG 689, Gro1-4) have been used to evaluate genetic variation in wild potato relatives and breeding material. New knowledge has been gained on the diversity of gene pools of wild potato species. Phenotypically and genotypically diverse material is maintained as clonal reproductions of potato genotypes. This collection of potato clones exhibits the range of variation of wild potato relatives and cultivated potato. It becomes a basis for further research in comparative and functional genomics and potato introgression breeding.

Key words: *Solanum*, potato breeding, late blight, potato virus Y, nematode pathotype Ro1, DNA markers, *R*-genes.

I. N. Anisimova, V. A. Gavrilova, N. V. Alpatieva, I. A. Malkov, A. G. Pinaev, V. T. Rozhkova MOLECULAR MARKING OF SUNFLOWER POLLEN FERTILITY RESTORATION GENES. Proceedings on applied botany, genetics and breeding. Vol. 174. 2014. pp. 33–43.

The genetic diversity of 132 sunflower inbred lines from the genetic collection was structured by components of the CMS-Rf genetic system using the SCAR-marker HRG02 linked with the nuclear gene *Rf1* and the STS-marker *orfH522* associated with CMS PET1. The majority of autofertile lines was shown to possess sterile cytoplasm and therefore can be used as reliable sources of the fertility restorer gene for breeding on the basis of CMS PET1. With the purpose of developing a functional marker of the *Rf1* gene polymorphism of the expressed sequence (EST QHL12D20) homologous to the restoration of pollen fertility gene of *Petunia × hybrida* was studied. The fragment contains 3 PPR-motives characteristic for plant *Rf* genes and includes intron of approximately 630 bp length. When the amplified fragment QHL12D20 was treated with the restrictase HaeIII, polymorphism of restriction patterns conditioned by single nucleotide substitution in the enzyme recognition site within the intron was revealed. Both CMS and maintainer lines (genotype *rf1rf1*) were characterized by the QHL12D20_2 variant whereas the QHL12D20_1 variant was found in the majority of restorer lines carrying dominant allele in the *Rf1* locus.

Key words: sunflower, lines, CMS, restoration of fertility, genes, EST, polymorphism.

A. I. Abugaliev, T. B. Azhgaliev, A. Zh. Zhumahanova, L. Dolgih GENETIC DIVERSITY OF OIL CROPS IN KAZAKHSTAN. Proceedings on applied botany, genetics and breeding. Vol. 174. 2014. pp. 44–52.

Varietal resources of oil crops in Kazakhstan are represented by 40 varieties and hybrids of sunflower, 6 varieties of safflower, 23 of rapeseed, 20 of soybean, 7 of flax, and 1 to 4 varieties of maize, castor bean, false flax and mustard. For rapeseed, varieties have been identified to contain at the average more than 46.5% of oil: Rusich, Gladiator, NPC 0607, Likolli, Jerry, DC 71-20, Zolotonivsky, Caviar, and Yubileyny. The analysis of integral oil quality evaluation [Dolgih, Abugaliev, 2010] made it possible to rank the studied varieties according to oil quality in the following order: Maibulak, Lipetsky, Safia, DK 71-2 Mayly, Yubileyny, Gladiator. Rapeseed is known to have increased oleic acid content: from 58.0% (Maibulak, Lipetsk) to 65.8% (Gladiator), and a high ratio of unsaturated/saturated fatty acids: from 6.70 (Lipetsky) to 7.80 (Yubileyny). Antinutrient erucic acid is within the range from 0.17% (Yubileyny) to 1.83% (Mayly). Authorized for cultivation in Kazakhstan are 32 hybrids and 13

varieties of sunflower. Oil content in sunflower seed broadly varies from 33.2% to 55.6%. Genotypes outstanding for oil harvest per hectare are Kandy, Brio, Kazakhstansky 1, Yubileyny 40, LG 5635, Printasol, Skorospely 87, PR 64, G-46, PR 63, and A62. Research results have shown that oil content in safflower seed varies within 20.0–43.3%. Safflower oil contains 76–82% of linoleic acid; it is the highest rate among the vegetable oils produced domestically. Seed oil content is 36%, as recalculated for absolutely dry matter. Linoleic acid content in Kazakhstan varieties ranges from 67.5% (Akmai) to 73.9% (Nurlan); the ratio of unsaturated/saturated fattyacids varies from 5.79 (Akkyzyl and Akmai) to 7.69 (Nurlan). With this, the content of erucic acid is minimal for Akmai (0.04%) and maximal for Akkyzyl (0.27%). Seed oil content in soybean varieties ranged from 18.0% to 26.9% in the SVT system, depending on the environmental conditions and the year of reproduction. The maximum oil content was observed in the varieties Annushka (22.2–25.4%) and Mavka (21.6–25.9%). The soybean variety Almaty is characterized by the highest content of oleic acid (35%), while the variety Zhalpaksay by high content of linoleic acid (47.5%) and Vitamin F (up to 58.4%).

Key words: rapeseed, sunflower, safflower, soybean, oil content.

V. I. Burenin, T. M. Piskunova DEVELOPMENT OF IDEAS OF N. I. VAVILOV CONCERNING EVALUATION AND USE OF GENETIC RESOURCES OF VEGETABLE AND CUCURBIT CROPS.

Proceedings on applied botany, genetics and breeding. Vol. 174. 2014. pp. 53–60.

The diversity of vegetable and cucurbit crop genetic resources, the main directions of their study and use, including modern aspects of research, are described. The results of research on interspecific hybridization of different species are summarized. Specificity of breeding vegetable crops for heterosis by using the phenomena of self-incompatibility, pollen sterility and polyploidy is demonstrated. The results of practical use of vegetable and cucurbit crop genetic resources by the leading breeding centers of the country are presented.

Key words: vegetable crops, collection, breeding, initial material, resistance to diseases, variety, hybrid.

N. I. Vorobyov, N. A. Provorov, O. V. Sviridova, V. N. Pishchik, N. V. Patyka, V. A. Dumova, Yu. V. Kruglov RANK OF GENETIC DESIGN AND ADAPTIVE POTENTIAL OF PLANT-MICROBIAL SYSTEMS.

Proceedings on applied botany, genetics and breeding. Vol. 174. 2014. pp. 61–67.

The fractal analysis of morphometric data on non-microbial components and structure of accompanying microbial communities made possible a comparison of genetic design ranks and adaptation potential of plant-microbial systems. An analysis has shown that accompanying microbial communities interact with non-microbial components, complicate bionetworks configuration and increase the adaptive potential of biosystems.

Key words: genetic design rank of plant-microbial system, fractal dimension of the space of morphometric data on non-microbial components and microbial bionetworks.

N. V. Zobova INFORMATION RETRIEVAL SYSTEMS ASSISTED RETROSPECTIVE AND CURRENT ANALYSIS OF BREEDING DATA.

Proceedings on applied botany, genetics and breeding. Vol. 174. 2014. pp. 68–78.

The analysis of software products created by Siberian scientists for the use in cereal crop breeding reflects both their information-evaluation and analytical orientation. Some examples and approaches to the analysis of long-term data using information retrieval systems, databases, criteria and algorithms for evaluating the effectiveness of breeding stages.

Key words: information technology, database, information storage and retrieval systems, breeding, cereals.

V. F. Krasavin, T. E. Aitbaev POTATO GENETIC RESOURCES AND THEIR USE IN BREEDING IN KAZAKHSTAN.

Proceedings on applied botany, genetics and breeding. Vol. 174. 2014. pp. 79–83. Fifteen hundred accessions from the global potato collection were studied in 2007–2011 in the Almaty Province of Kazakhstan. The research was carried out in two soil and climatic zones, namely in the foothills characterized by strong degeneration of potato and in the mountains favorable for potato cultivation.

Key words: potatoes, selection, biology, genetics, process.

T. V. Kulakouskaya ECOLOGICAL AND ECONOMIC ASPECTS OF CONSERVATION AND SUSTAINABLE USE OF PLANT BIOLOGICAL DIVERSITY FOR SOLVING GLOBAL PROBLEMS.

Proceedings on applied botany, genetics and breeding. Vol. 174. 2014. pp. 84–99.

The development of multifunctional agriculture promotes research that helps to make it both competitive and environmentally friendly, stimulates rural development and use of natural resources in a sustainable manner when producing sufficient quantities of safe and affordable feeds and biomass.

Key words: grassland farming, productivity, biodiversity, forage quality, fodder crops, ecological and economic aspects.

E. I. Mikhailova, A. V. Tolkacheva, S. P. Sosnikhina CONSERVATIVE AND SPECIFIC FEATURES OF MEIOSIS IN RYE (*SECALE CEREALE* L.) REVEALED BY MOLECULAR CYTOGENETIC METHODS.

Proceedings on applied botany, genetics and breeding. Vol. 174. 2014. pp. 100–106.

Key events of meiosis, namely clustering of telomeric and centromeric chromosome domains, recombination events and synaptonemal complex (SC) assembly were studied in rye. A hypothesis establishing hierarchy of links between them has been proposed: telomeres and centromeres clustering, as well as regular condensation of chromosomes in microsporocyte nuclei of rye at the pre-meiotic interphase-Prophase I stages ensure successful accomplishment of early events of recombination. The processes associated with the initiation and proper assembly of linear tracts of synaptonemal complex protein Asy1, are crucial for completion of recombination, though not for its initiation. The setting-up of a tripartite SC structure is also essential for completion of recombination and is implemented by a protein, which is different from Zyp1, the central region protein. The experimental data in support of this concept are presented.

Key words: rye, meiosis, recombination, bouquet, chromosome, SC proteins, Asy1, Zyp 1.

E. A Porokhovinova, C. Morvan, N. B. Brutch VIR FLAX GENETIC COLLECTION: FUNDAMENTAL AND APPLIED USE. Proceedings on applied botany, genetics and breeding, Vol. 174. 2014. pp. 107–116.

Inheritance of 30 genes controlling morphological characters' variability has been evaluated in flax by classical genetic analysis. The genetic control of dwarfness was analyzed. The *dwarf 1 (dw1)* gene is recessive for dwarfness and flower deformation. The discriminant analysis determined that it is semi dominant for plant height and internode length. A link (21cM) between the *dw1* gene and the *sfc1* gene of violet flower has been proved. A test for allelism has shown that the *dw1* gene and *curly stem 1 (cs1)* gene that controls the "curly" stem phenotype are not allelic, are inherited independently and act complementarily. It was found that the homozygotes recessive for *white flower 1 (wfl)* gene have a correlation with the short germination–flowering stage ($r_{bs} = 0,52$). The U Mann–Whitney rank test showed that the brown seeds have a significantly lower percent of pentosans and higher percent of pectins. Yellow seeds, in contrast, reliably contain much more of pentosans and less of pectins. It was found that the lines homozygous for the *star flower 1 (s1)* gene with yellow seeds had reliably more glucose and pentosans and less pectins.

Key words: *Linum usitatissimum*, genetic collection, genes, morphological characters, dwarfism, mucilage seeds.

E. A. Krylova, A. B. Ovchinnikova, L. Yu. Novikova, I. G. Chukhina, T. N. Smekalova, L. I. Kostina, T. A. Gavrilenko MORPHOMETRIC ANALYSIS OF AUTHENTIC HERBARIUM SPECIMENS FROM WIR AND LE COLLECTIONS OF CULTIVATED POTATO SPECIES OF THE SECTION PETOTA DUMORT. IN THE GENUS SOLANUM L. Proceedings on applied botany, genetics and breeding, Vol. 174. 2014. pp. 117–122.

Morphometric analysis of 28 morphological characters of vegetative and generative plant organs was made for 9 cultivated species from the section Petota, genus Solanum (*S. ajanhuiri*, *S. andigenum*, *S. chaucha*, *S. chilotanum*, *S. curtilobum*, *S. goniocalyx*, *S. juzepczukii*, *S. phureja*, *S. stenotomum*) presented by 185 authentic herbarium specimens from the Vavilov Institute of Plant Industry (WIR) and Komarov Botanical Institute (LE) herbaria. Taxonomic importance of some morphological characters has been re-examined on the basis of the obtained results.

Key words: morphological characters, herbarium specimens, cultivated potato species.

G. F. Safina, G. I. Filipenko LONGEVITY OF SEEDS AT STORAGE AND ITS PREDICTING BY THE ACCELERATED AGEING METHOD. Proceedings on applied botany, genetics and breeding, Vol. 174. 2014. pp. 123–130.

Accelerated ageing techniques applicable to the seed of winter wheat, common bean and peas, suitable have been elaborated for predicting seed longevity at storage. The mode with 37 °C and seed moisture content 2–3% below the critical one proved to be the most suitable for supervizing dynamics of ageing. In these conditions, viability decreased practically to zero within one-two months and the curves of viability change corresponded to those at long-term storage. The time of the studied samples ageing depended not only on initial viability and seed moisture content, but also on their genetic features.

Key words: wheat, common bean, peas, long-term storage of genetic resources of the plants, the accelerated ageing of seeds.

E. K. Khlestkina CYTOLOGICALLY AND GENETICALLY MARKED WHEAT LINES IN THE WORKS ON MOLECULAR AND FUNCTIONAL GENETICS OF CEREAL GRASSES. Proceedings on applied botany, genetics and breeding, Vol. 174. 2014. pp. 131–142.

Thanks to the allopolyploid nature of the common wheat genome (*Triticum aestivum* L., $2n=6x=42$, genome BBAADD), a wide range of cytologically marked lines such as nullitetrasonic, ditelosomic, deletion, addition, substitution, etc. has been created. Produced in recent decades for cytogenetic and genetic studies, today the cytologically marked lines as well as genetically marked isogenic lines find new application. The present paper reviews examples and prospects of the cytologically and genetically marked wheat lines application in molecular and functional genetic studies.

Key words: wheat, molecular genetics, functional genetics, deletion lines, ditelosomic lines, addition lines, substitution lines, nullitetrasonic lines, isogenic lines, introgression lines.

M. N. Fomina GENETIC RESOURCES FOR REALIZATION OF THE MAIN DIRECTIONS IN OAT BREEDING IN THE NORTHERN TRANS-URALS. Proceedings on applied botany, genetics and breeding, Vol. 174. 2014. pp. 143–148.

The results of a perennial study carried out in the Northern Trans-Urals on the main economically important traits in oats of different ecogeographic origin are presented. New sources for earliness, short stem, lodging resistance, resistance to common pathogens, productivity and high grain quality have been identified.

Key words: oatbreeding.