
On the Rostrum of the RAS Presidium

Genetic Resources of Plants: The Conservation and Use Strategy in the 21st Century

E. K. Khlestkina^{a,*} and I. G. Chukhina^{a,***#}

^a Vavilov All-Russia Institute of Plant Genetic Resources, St. Petersburg, Russia

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

**e-mail: i.chukhina@vir.nw.ru

Received February 25, 2020; revised March 5, 2020; accepted March 19, 2020

Abstract—Problems of the conservation and use of plant resources in the context of climate change and socio-economic challenges are considered. Particular attention is paid to the conservation of crop wild relatives and traditional crop varieties as sources of genetic diversity, which had been lost by the modern gene pool of cultivated plants first in the process of domestication and then during the introduction of intensive varieties into production.

Keywords: genetic diversity, crop wild relatives, de novo domestication, landraces, climatic factors, food security, next generation selection, traditional crop varieties, phenomics, digital crop rotation.

DOI: 10.1134/S1019331620030089

Climate instability and, as a consequence, the increased impact of biotic and abiotic factors on production crops and valuable plant resources conserved in their habitats, as well as the need to reduce the load of chemical plant protection products on the environment and to provide the population with a sufficient amount of diverse and high-quality foods require a new strategy aimed at the coordinated functioning of the entire chain from the conservation of plant genetic resources and the construction of the genotypes of future varieties to agricultural production and the storage, transportation, and processing of agricultural products.

Today, the sustainable development of agriculture requires an integrated approach based on analysis of place- and time-specific big data on soil and climatic characteristics, crop productivity, crops under cultivation, and their diseases. Moreover, this information should be correlated with the taxonomic and genetic characteristics of plant varieties, soil microflora, pathogenic flora, pests, and weeds, as well as with the agricultural technologies applied. This will make it possible to provide long- and medium-term forecast scenarios important to choose a proper selection strategy; apply mathematical modeling methods to designing the genotypes of future varieties; select variety diversity; and choose agricultural technologies of cultivation and planning crop rotation, including digital,

to ensure stable agricultural production in a particular region of the Russian Federation. The collection of big data itself will also require significant digitalization and automation of valuation methods. It is closely associated with the development of high-performance phenotyping (phenomics) [1].

The potential shift of the borders of the cultivation of southern crops northward opens up a favorable prospect for expanding the range of cultivated plant species in Russia, which can contribute to the socio-economic development of rural areas through the production of highly profitable new crops, as well as to the development of crop production in the risk farming zone to provide the population in these regions with fresh and healthy foods.

However, the migration of southern crops to the north will inevitably be accompanied by the movement of pathogenic biota representatives in the same direction, which one should bear in mind when preparing and using forecast scenarios. In addition, recall that the key to success in the “northing” of southern crops is not only the increasing sum of positive temperatures during the growing season and the softening of conditions during dormancy but also adaptation to changes in other abiotic factors, especially the length of daylight hours. Representatives of the southern flora are, as a rule, “short-day” plants, unadapted to long photoperiod. Considering marker-assisted and genomic selection and next-generation breeding technologies, for example, genetic editing [2], this property can be used both to adapt southern crops to a long

Elena Konstantinovna Khlestkina, Dr. Sci. (Biol.), is Director of the Vavilov All-Russia Institute of Plant Genetic Resources. Irena Georgievna Chukhina, Cand. Sci. (Biol.), is a Leading Researcher at the same institute.

daytime and to limit the northward expansion of invasive plant species.

Note also technological challenges, which, most likely, will need consideration when new varieties are permitted for production. In view of the high complexity of controlling genetic changes introduced into a plant's genome using modern genetic editing technologies, it will be necessary to develop and implement specialized systems of intellectual analysis, forecasting, and identification of hidden "undesirable entries" in the genome of varieties proposed for production, as well as in the genome of the lineages conveyed to domestic breeding centers as part of technology transfer.

Obviously, stable yields under changeable environmental conditions will be based on the diversity, including varietal, of cultivated crops. To all appearances, the adaptive farming system developed at the Luk'yanenko National Grain Center, implying the so-called mosaic of varieties [3], will be widespread.

Until recently, the priority indicators evaluated during state variety trials were production characters. Today the situation is changing, and more attention is being paid to quality. Important tasks will be to improve the quality of consumer goods, primarily bread, which is still produced using improvers [4], and to create varieties for the production of specialized foods—functional, children's, sports, dietary, etc. [5].

Genetic resources are a tool that allows breeding to meet the challenges associated with climate change, the emergence of new pathogens, and the need to increase the volume of agricultural products and improve their quality. For example, the genetic diversity of the world cultural flora, concentrated in the oldest genetic bank of the planet, the Vavilov All-Russia Institute of Plant Genetic Resources, once made it possible to expand significantly the areas of cultivation of various crops, introduce new crops, and develop the risk farming zone.

According to the Convention on Biological Diversity [6], genetic resources are the genetic material of plant, animal, microbial, or other origin of actual or potential value that contains functional units of heredity. Both living and preserved materials, for example, herbarium samples, are meant.

Crop wild relatives (CWRs) and landraces (LRs, traditional crop varieties of traditional cultivated plants) are important components of plant genetic resources. They are of strategic importance at the national, regional, and international levels, primarily for ensuring food security and environmental sustainability in the 21st century. Crop wild relatives are population species systems of wild plants that are in evolutionary genetic kinship with cultivated plants belonging to the same genus [7, p. 3; 8]. The CWR gene pool contains the diversity lost by cultural forms when passing through the "bottleneck" of domestication.

Old local varieties of traditional crops are dynamic populations of cultivated plants that can be identified and, as a rule, have a local name, are devoid of formal varietal improvement, are adapted to local conditions in the cultivation area, and are associated with traditional agricultural systems [9]. Unlike CWRs, they are used in private gardening, horticulture, and, less often, agriculture.

Traditional crop varieties and landraces have useful properties that can be used on a targeted basis to breed varieties fit for changing environmental conditions and market requirements. However, the conservation of this biodiversity group was neglected and is now ignored by most organizations working in the field of environmental protection, as well as related to agriculture. CWR and LR diversity is threatened by the mismanagement of the environment and the loss of genetic diversity. While the crop wild relatives are threatened by degradation and fragmentation of the natural habitat, landraces suffered from replacement with modern varieties and changes in land use practices—the spread of monocultures, the use of pesticides, etc. Everything related to the study of the processes of depletion of the gene pool of cultivated plants and the problem of preserving traditional crop varieties belongs to the category of new problems both in our country and throughout the world. At the same time, under the onslaught of commercial, genetically homogeneous varieties, the areas occupied by traditional crop varieties are decreasing rapidly everywhere, and many of them have disappeared forever. Local wars and interethnic conflicts with subsequent humanitarian aid from the world community in the form of new breeding varieties also contribute to their disappearance [10].

It was shown that during the selection process, starting from the 1920–1930s, 14 unique alleles of the grain storage protein genes have disappeared from the gene pool of common wheat (*Triticum aestivum* L.) in Italian varieties, five in Serbian, seven in Saratov, and eight in the Krasnodar variety; 40 alleles have disappeared in winter varieties of the northern regions of Russia. The genotype of Bezostaya-1 and its descendants largely determines the gene pool of the Krasnodar, Serbian, and Italian varieties, and the genotypes of Mironovskaya-808 and Saratovskaya-29, respectively, of winter and spring varieties cultivated in the central part of the country and in Siberia [11–13]. Thus, we can talk about the erosion of the gene pool of common wheat and the loss of unique coadapted gene complexes that have formed over time.

The historical and political features of the development of our country radically affected the conservation of the gene pool of traditional crop varieties, leading to the loss of most domestic landraces in the places of their formation, but many were preserved in the collection of the Vavilov All-Russia Institute of Plant Genetic Resources.

The history of the study of the diversity of cultivated plants and their wild relatives in Russia covers more than a century, starting from the fundamental works of R.E. Regel', N.I. Vavilov, and their followers. At the first stages, the attention of researchers was focused on elucidating the origin of the domestic and global diversity of cultivated plants and studying their closest relatives that had directly given rise to certain crops or participated in their genesis. Vavilov believed that in-depth knowledge of the evolution of cultivated plants relied on the study of their wild relatives.

Vavilov noted the laboriousness of such work, which requires collecting many thousand samples from the same species—living forms and a complete herbarium [14]. Why so many? In this case, the maximum diversity of each species is of interest, and the most interesting may be not typical representatives but rare ones with allelic variants of genes that are valuable for selection. This is the specificity of collections of plant genetic resources in contrast to collections created with the aim of presenting taxonomic diversity and preserving some typical samples of each taxon. They are important for the process of learning and popularization but cannot replace collections of genetic resources—the basis for creating future varieties.

Research on the inventory of the CWR diversity was initiated by V.V. Nikitin and O.N. Bondarenko (Korovina), who published the first summary on their diversity in the Soviet Union [15]. Later Korovina laid the foundations of methodological approaches and developed some practical measures aimed at preserving the gene pool. She was the first in our country to propose preserving the CWR diversity both in places of their natural growth (in situ) and in collections (ex situ) [16]. This approach is now presented as a complementary ex situ/in situ conservation strategy [8; 17, p. 126]. Ex situ includes collection of samples and their transfer and storage outside the original habitats of populations of a given species—in genetic banks, collections of botanical gardens, and nurseries. in situ means the conservation, regulation, and monitoring of populations of individual species in their natural habitats or where they have acquired their distinctive characteristics. Conserving the gene pool of landraces in their habitats at farmers' places in traditional agriculture, horticulture, or rural forestry systems—*on farm* conservation—involves the sustainable management of the genetic diversity of local crop varieties and related wild and weed species and forms [8].

Despite the fact that the strategy of conserving the diversity of crop wild relatives and landraces has regional differences and depends on natural conditions, information on the modern diversity of plant genetic resources for food production and agriculture, financial and human resources, and the interest of various government agencies and public organizations, it implies the adoption of a number of general

measures aimed at preserving CWR and LR diversity. They include the following:

- inventorying the CWR and LR diversity and preparing national inventories;
- comparing the existing assessments of threats to the CWR and LR gene pool;
- determining CWR and LR taxa that are of priority importance for conservation;
- taxonomic and ecological—geographical analysis of priority CWRs and LRs;
- molecular genetic analysis of priority CWRs and LRs;
- gap analysis—determining gaps within in situ and ex situ preservation.

Today, associates of the Vavilov All-Russia Institute of Plant Genetic Resources continue to study the diversity of crop wild relatives, aiming at creating a unified national program for the conservation of their gene pool in situ, which will take into account the natural and economic characteristics of Russia. Its provisions will be based on the institute's experience over more than a century and on modern international practices. The proposed strategy consists of several interconnected blocks:

- inventorying the diversity of Russia's crop wild relatives;
- choosing objects (taxa or populations) that are of priority importance for conservation;
- choosing territories for in situ conservation;
- developing monitoring and management recommendations for various objects of in situ conservation.

Our institute is inventorying crop wild relatives used in the country's agriculture, namely grain, vegetable, fruit, and berry crops that ensure food security and are used as food and feed, as well as industrial plants—sources of vegetable oils, fibers, and rubber. The preliminary list of the CWRs of agricultural crops includes 1701 species from 49 families and 175 genera. Most species belong to the families Poaceae (491 species), Fabaceae (273), Rosaceae (177), and Alliaceae (106). Most CWRs belong to the genera *Allium* L. (106 species), *Poa* L. (103), *Festuca* L. (82), *Rosa* L. (65), and *Lathyrus* L. (62). Analysis of the CWR species by type of use shows that the undoubted leaders are fodder plants with 398 species, followed by food (fruit, berry, and vegetable) plants with 346 species.

Geographical analysis shows that the largest number of CWRs, 868 species, grows in the European part of Russia, of which 152 species typical of our country are limited only to its European part, and 18 are endemic to this territory (*Agropyron tanaiticum* Nevski, *Agrostis korczaginii* Senjan.-Korcz., *Avena aemulans* Nevski, *Rosa microdenia* Mironova, *Lotus zhegulensis* Klokov, etc.). In the Russian Caucasus, the area richest in flora, there are 766 CWR species. Crop wild relatives in the Russian Far East have their own distinctive features: out of the 606 species, more than



Fig. 1. Knowledge on the diversity of crop wild relatives in Russia: (A) the diversity of CWRs was inventoried and recommendations for the conservation of their gene pool were given; (B) only a preliminary list of CWRs was compiled; (C) CWR diversity was not inventoried.

a third (223) grow only there. Eastern Siberia has 564 CWR species. The smallest number of them are concentrated in Western Siberia (544). The review of the gene pool of crop wild relatives of Russia is still far from completion; the degree of its knowledge is presented on the schematic map (Fig. 1).

Analysis of the diversity of CWRs used in agricultural production by the degree of participation in the breeding process shows that 222 species are represented in a culture and another 72, as sources of genes or as rootstocks. Thus, a little more than 2% of the country's phytogenofond is in agricultural production. Modern genetic technologies [2] make it possible to accelerate domestication (de novo) of wild relatives [18, 19], which expands the possibilities to use CWRs in practical breeding and greatly increases the value of this gene pool.

Climate instability and new biotic and abiotic stress factors in the habitats of CWRs are unfavorable for the conservation of the gene pool. Continuous monitoring of it and well-timed decision making on the transfer from in situ to ex situ relative to endangered species are still another element of the conservation of genetic resources in Russia. A variety of ex situ conservation methods [20] and duplication, for which the efforts of the country's research universities may be united under the auspices of the national network collection of genetic resources of cultivated plants and their wild relatives, is a way to ensure the country's food security reliably.

FUNDING

This study was supported within the state budget, project no. 0662-2019-0005.

REFERENCES

1. D. A. Afonnikov, M. A. Genaev, A. V. Doroshkov, et al., "Methods of high-throughput plant phenotyping for large-scale breeding and genetic experiments," *Rus. J. Genet.* **52** (7), 688–701 (2016).
2. N. A. Kolchanov, A. V. Kochetov, E. A. Salina, L. A. Pershina, E. K. Khlestkina, and V. K. Shumny, "Status and prospects of marker-assisted and genomic plant breeding," *Herald Russ. Acad. Sci.* **87** (2), 125–131 (2017).
3. A. A. Romanenko, *New Varietal Policy and Varietal Agricultural Technology for Winter Wheat* (EDVI, Krasnodar, 2005) [in Russian].
4. E. K. Khlestkina, T. A. Pshenichnikova, N. I. Usenko, and Yu. S. Otmakhova, "Prospective applications of molecular genetic approaches to control technological properties of wheat grain in the context of the 'grain–flour–bread' chain," *Vavilov. Zh. Genet. Selek.* **20** (4) 511–527 (2016).
5. E. K. Khlestkina, N. I. Usenko, E. I. Gordeeva, O. I. Stabrovskaya, I. B. Sharfunova, and Y. S. Otmakhova, "Evaluation of wheat products with high flavonoid content: Justification of importance of marker-assisted development and production of flavonoid-rich wheat cultivars," *Vavilov. Zh. Genet. Selek.* **21** (5), 545–553 (2017).
6. *Convention on Biological Diversity, Rio de Janeiro, 1992, June 5* (United Nations, 1992).

7. *Crop Wild Relatives of Russia: VIR Global Collection Catalog*, Ed. by T. N. Smekalova and I. G. Chukhina (GNTs RF VIR im. N.I. Vavilova, St. Petersburg, 2005) [in Russian].
8. N. Maxted, B. V. Ford-Lloyd, and J. G. Hawkes, *Plant Genetic Conservation: The in situ Approach* (Chapman & Hall, London, 1997).
9. V. Negri, N. Maxted, and M. Veteläinen, “European landrace conservation: An introduction,” *Biodiversity Technical Bulletin*, No. 15, 1–22 (2009).
10. S. M. Aleksanyan, *Agrobiodiversity and Geopolitics (GNTs RF VIR im. N.I. Vavilova, St. Petersburg, 2002)* [in Russian].
11. A. Yu. Novoselskaya-Dragovich, V. A. Krupnov, R. A. Saifulin, and V. A. Pukhalskiy, “Dynamics of genetic variation at gliadin-coding loci in Saratov cultivars of common wheat *Triticum aestivum* L. over eight decades of scientific breeding,” *Russ. J. Genet.* **39** (10), 1330–1337 (2003).
12. A. Yu. Novoselskaya-Dragovich, A. V. Fisenko, A. G. Imasheva, and V. A. Pukhalskiy, “Comparative analysis of the genetic diversity dynamics at gliadin loci in the winter common wheat *Triticum aestivum* L. cultivars developed in Serbia and Italy over 40 years of scientific breeding,” *Russ. J. Genet.* **43** (11), 1236–1243 (2007).
13. E. K. Khlestkina, E. A. Salina, and V. K. Shumnyi, “Genotyping of the native varieties of soft wheat by the microsatellite (SSR) markers,” *Sel'skokhoz. Biol.*, No. 5, 44–52 (2004).
14. N. I. Vavilov, “Wild progenitors of the fruit trees of Turkestan and the Caucasus and the problem of the origin of fruit trees,” in *Report and Proceedings of the IX International Horticultural Congress, London, 1930* (London, 1931), pp. 271–286.
15. V. V. Nikitin and O. N. Bondarenko, *Wild Relatives of Cultured Plants and Their Dissemination in USSR Territory* (extended abstract) (VIR, Leningrad, 1975) [in Russian].
16. S. M. Aleksanyan, V. V. Ponomarenko, L. A. Burmistrov, et al., *Modern Methods and International Experience of Conservation of the Gene Pool of Wild Growing Plants (by the Example of Wild Fruit)* (Programma Razvitiya OON v Kazakhstane, Almaty, 2011) [in Russian].
17. *Natural Gene Pool of Wild-Growing Relatives of Cultivated Plants of the USSR Flora and Its Conservation* (Annotated List), Ed. by O. N. Korovina (VIR, Leningrad, 1986) [in Russian].
18. E. K. Khlestkina, “Genome editing as a time machine, or Domestication in a couple of years,” *Nauka Pervykh Ruk*, No. 5–6, 72–75 (2016).
19. M. Z. Khan, S. S. Zaidi, I. Amin, and S. Mansoor, “A CRISPR way for fast-forward crop domestication,” *Trends Plant Sci.* **24** (4), 293–296 (2019).
20. A. Börner and E. K. Khlestkina, “*Ex situ* genebanks—seed treasure chambers for the future,” *Russian J. Genet.* **55** (11), 1299–1305 (2019).

Translated by B. Alekseev