

Review article
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The active collection of oat genetic resources at VIR, and its applications

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This article presents information on VIR's active oat collection that has served as a source of initial material for oat breeding in the Russian Federation for the past decades. The genetic collection is described, including alleles of identified genes for various morphological, biological, and biochemical traits. The results of a field study of the active oat collection conducted by VIR's experimental network in various ecogeographic zones of the country are highlighted, covering a wide range of valuable agronomic traits. In addition to describing the identified sources of such traits, this article provides an overview of a number of developed donors of semidwarfism and lodging resistance with various alleles of the semidwarfism gene, and donors with a neutral photoperiod. The results of fruitful collaboration with Russian breeding centers are summarized in the context of distributing source material for various trends in oat breeding, based on a comprehensive evaluation of the active oat collection. Thus, the active oat collection at VIR is comprehensively studied, safely preserved, and sustainably used for breeding purposes in the Russian Federation.

Keywords: oat, sources, donors, genetic collection, breeding, valuable agronomic traits, breeding centers

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Активная коллекция генетических ресурсов овса ВИР и ее использование

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В статье приводятся сведения об активной коллекции овса ВИР, которая на протяжении последних десятилетий является источником исходного материала для селекции овса в Российской Федерации. Приводится описание генетической коллекции с аллелями идентифицированных генов по различным морфологическим, биологическим и биохимическим признакам. Представлены результаты полевого изучения активной коллекции овса по широкому спектру хозяйственно ценных признаков, которое проводится опытной сетью ВИР в различных эколого-географических зонах нашей страны. Кроме описания выделенных источников хозяйственно ценных признаков, приводится обзор целого ряда созданных доноров короткостебельности и устойчивости к полеганию с различными аллелями гена короткостебельности и доноров с нейтральным фотопериодом. Подводится итог результативного сотрудничества с селекционными учреждениями РФ по рассылке исходного материала для различных направлений селекции этой культуры. Таким образом, активная коллекция овса ВИР комплексно изучается, надежно сохраняется и устойчиво используется для селекционных целей в РФ.

Ключевые слова: овес, источники, доноры, генетическая коллекция, селекция, хозяйственно ценные признаки, селекционные центры

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Oat is one of the most important cereal crops in the Russian Federation and worldwide. Oat grain is widely used for feed and food purposes. Oat products are an essential component of a healthy diet, and the demand for oats is constantly growing. A crucial aspect of the breeding process to improve this crop is the selection of source material based on comprehensive evaluation of useful biological and agronomic traits in plants of various ecogeographic origin. In the past decades, the global collection of the N.I. Vavilov All-Russian Institute of Plant Genetic Resources (VIR) has been supplying such source material for breeding.

Currently, VIR's active collection of oat genetic resources comprises over 12,000 accessions of various origin from all regions of oat cultivation worldwide. The methods used to evaluate this collection include botanical description, phenotypic (field), biochemical, physiological, phytopathological, and genetic approaches, used to identify or develop sources and donors of valuable agronomic traits and biological properties.

The history of the oat collection at VIR spans over 125 years. This collection is safely and securely stored on a long-term basis in the main building of VIR (St. Petersburg), and duplicated at the Kuban Gene Bank (Kuban Experiment Station – branch of VIR, Krasnodar Territory), using international seed storage standards. Furthermore, to maintain the germination rates of its accessions at the required level, the entire collection is periodically regenerated, strictly geographically, at leading experiment stations (branches) of VIR: Yekaterinino (Tambov Province), Kuban (Krasnodar Territory), Dagestan, and Maikop (Adygea) (Loskutov, 2025).

The collection preserves and maintains live germplasm accessions of all cultivated oat species: *A. sativa* L., *A. byzantina* K. Koch, *A. strigosa* Schreb., and *A. abyssinica* Hochst., including spring and winter oats, hulled and hullless accessions. A distinctive feature of the oat collection is the wide diversity of local varieties (landraces) collected in the 1900s–1930s by N. I. Vavilov and his colleagues from all continents (Loskutov et al., 2023).

VIR's global oat collection contains sources of diverse agronomic and biological traits. In recent years, extensive experience has been accumulated in the selection and development of source material through the evaluation of the oat collection, with the goal of maximizing the diversity of hybrid populations, from which valuable plant lines and genotypes are selected. Knowledge of genetic patterns and the nature of trait inheritance, combined with the results of studying the collection under various agroecological conditions, enables the selection of parent cultivars with the fewest negative traits. Proper selection of sources for breeding significantly increases the efficiency of breeding efforts. Compared to other cereals, oat has been understudied genetically, as it is an allohexaploid with three genomes (A, C, and D). The Oat, Rye, and Barley Genetic Resources Department at VIR has established a genetic collection of oats to address key breeding challenges at the current level of scientific advancement, as well as to identify and localize newly identified genes. This oat

collection includes oat cultivars, lines of cultivated species, and accessions of wild species with one or more identified genes controlling various morphological, agrobiological, biochemical, and other traits. The majority of the collection consists of accessions with identified genes for semidwarfism and photoperiodic response, and the most important genes for resistance to powdery mildew, crown and stem rust, and smut species. Currently, the genetic collection of oats at VIR includes more than 600 accessions classified into cultivated species—*A. sativa*, *A. byzantina*, *A. strigosa*, and *A. abyssinica*—and wild species—*A. sterilis*, *A. barbata*, and *A. magna*—based on identified genes controlling various morphological, physiological, biochemical, and other traits (Loskutov, 2005). The wide diversity of cultivars represented in the collection (catalogue), all containing identical genes, enables breeders from different regions of Russia to select appropriate source material for oat breeding (Loskutov, Merezko, 1997). Using the genetic collection significantly increases the efficiency of breeders, facilitates the selection of parental pairs for crossing, and reduces the time required to develop oat cultivars with specified parameters.

In addition to setting up the genetic collection, the Department's primary focus is on comprehensive evaluation of the entire species diversity of the genus *Avena* L. The development of new crop cultivars possessing a range of valuable traits, high yields, and product quality under diverse environmental conditions requires well-studied source material consisting of identified sources and developed donors of traits valuable for breeding. To study the diversity of the cultivated oat collection, experimental field studies are conducted at the research and production facilities of Pushkin and Pavlovsk Laboratories of VIR, as well as at VIR's branches. Comprehensive evaluation of the collection helps to select and provide breeders with sources based on the most important agronomic traits: earliness, high productivity, acidity tolerance, resistance to lodging, resistance to diseases and pests, high content of protein, starch, fat, etc., using the guidelines developed at VIR (Loskutov et al., 2024).

A comprehensive diversity of the *Avena* genus facilitates the identification and utilization of new sources through phytopathological assessment of the entire species, and donors of resistance to expand the genetic basis of newly developed oat cultivars. For all the most important oat diseases, including crown and stem rust, various types of leaf spots, smut, and *Fusarium* diseases, sources of resistance to pathogens and pests have been identified for various regions of the country (Loskutov, 2007; Loskutov, Rines, 2011; Gagkaeva et al., 2013; Radchenko et al., 2018).

To identify alleles of genes encoding resistance to crown and stem rust and smut species in various regions of the Russian Federation, researchers widely use the VIR oat genetic collection (Mishenkina, 2021; Bakulina et al., 2022; Zhuikova, Batalova, 2025). Lines with the *Pc14*, *Pc46*, *Pc49*, *Pc50*, *Pc50-2*, *Pc50-4*, *Pc58*, and *Pc59* gene alleles were resistant to the *Puccinia coronata* population in the northeast of the European part of Russia (Kirov Province) (Gradoboeva, Batalova, 2018; Zhuikova, 2025). Oat lines with the *Pc14*, *Pc38*, *Pc39*, *Pc48*, *Pc50*, *Pc50-2*, *Pc50-4*, *Pc58*, *Pc59*,

Pc60, *Pc61*, and *Pc68* genes were resistant to the population from Chelyabinsk Province. In Western Siberia (Novosibirsk and Omsk Provinces), the *Pc50*, *Pc58*, and *Pc59* genes were the most effective (Meshkova, Pyatkova, 2017).

Molecular markers have proved to be useful in identifying sources of resistance to biotic stress. Quantitative trait loci (QTLs) mapping has been used to select oat genotypes resistant to diseases, particularly *Fusarium* head blight (FHB) and the accumulation of the mycotoxin deoxynivalenol (DON) in grain. QTLs controlling resistance to mycotoxin accumulation have been identified, as well as QTLs that, with increasing the growing season duration and plant height, reduce the accumulation of the mycotoxin DON in oat grain. Sources of high resistance include numerous accessions of cultivated oat species (Gavrilova et al., 2011; Gagkaeva et al., 2013) and, in particular, wild species (Gagkaeva et al., 2017, 2018).

The most interesting indicators in terms of nutritional and feed value are the biochemical characteristics of oat grain. These include protein content and its amino acid composition, oil content, and its fatty acid composition. Recently, the most important biochemical components that enhance the nutritional value of oats have included β -glucans (Popov et al., 2022), tocopherols, sterols, avenanthramides, and other components. Currently, this area of studying the collection is the most promising, and we have isolated source material for all the studied characteristics (Leonova et al., 2020; Shelenga et al., 2021; Loskutov et al., 2022).

The results of a comprehensive evaluation of the oat collection are presented in 29 catalogues of the VIR global collection (1965–2023), which incorporate the data obtained during the study of over 30,000 duplicate accessions for key traits of breeding value under various soil and climate conditions of the Soviet Union and the Russian Federation (Loskutov et al., 2023). All of these catalogues have been sent to leading breeding centers throughout the country, and the source material listed in them is actively used by breeders in the Russian Federation (Batalova, 2013; Yusova et al., 2021, 2022; Tulyakova et al., 2022; Zhuikova, Batalova, 2022).

The development of donors of valuable agronomic traits for oats meets the pressing needs of breeders and accelerates the breeding of cereal crops. The problem of semidwarfism in oat is closely linked to its lodging resistance, which occupies a special niche in oat breeding and attracts considerable attention due to the distinctive features of the plant habit and the large wind-prone surface of the panicle. To solve this problem, oat lines with identified alleles of the dwarfism gene (*Dw4*, *Dw6*, *Dw7*, and *Dw8*) were engaged (Loskutov, 2006). Thirty-two oat genotypes, developed in the process of prebreeding between 1992 and 2024, are donors of dwarfism, including three with the *Dw4* gene, 23 with *Dw6*, one with *Dw7*, and five with *Dw8*. As a result of targeted selection, all hybrid populations are free of the negative traits that were present in the original lines. The resulting donors combine a strong shortened straw with a productive panicle and large grain and manifest an early growing season, high lodging resistance, moderate resistance

to stem and crown rust, and *Helminthosporium*, moderate tolerance to barley yellow dwarf virus (BYDV), increased grain productivity, and good grain quality. These donors are used in breeding programs in the Non-Black Earth and Central Black Earth regions of the Russian Federation (Donor Passports, 1992–2024) (Loskutov et al., 2023).

In addition to the large collection of semidwarf oat donors, over 30 oat donors have been developed through hybridization among diverse cultivars and lines with reliable trait expression, followed by multistage selection, based on resistance to crown rust, individual grain and panicle productivity factors, and a weak response to photoperiod length. Over the course of extensive evaluation of the collection, a large number of early-maturing local and improved oat cultivars originating from various oat-growing regions were identified among *A. sativa* and *A. byzantina* accessions. The most important factors influencing the length of a plant's growing season, particularly its first half, are daylength and temperature. The results of a long-term study revealed a variety of responses to photoperiod and vernalization (Loskutov, 2001; Koshkin et al., 2009, 2013), and also contributed to the development of sources and donors based on the studied traits (Koshkin et al., 2016; Loskutov et al., 2019). Four donors with a neutral photoperiod were produced, each exhibiting a weak response to photoperiod and good grain productivity comparable to standard oat cultivars.

All of these sources and donors, in addition to the traits listed above, demonstrate stable productivity comparable to standard oat cultivars. These donors are used in the Non-Black Earth and Central Black Earth regions of the Russian Federation, and genotypes with a weak response to the length of photoperiod are utilized in various regions of the country.

All of the abovementioned catalogues of the global collection, and all materials selected during the evaluation at VIR's experiment stations and breeding centers of the USSR and the Russian Federation are distributed to leading breeders for use as sources for obtaining new highly productive (Batalova, 2011; Eremin et al., 2023) and high-quality oat cultivars (Kozlova et al., 2009; Batalova, 2010, 2014; Nikolaev et al., 2021). The source material selected for breeding is also actively used by our colleagues from Belarus (Matys, 2013) and Kazakhstan (Abugaliyeva et al., 2013).

The VIR collection is an inexhaustible source of species and intraspecies diversity for plant breeding in the Russian Federation. Therefore, all identified and developed sources and donors of valuable agronomic traits are annually sent to leading breeding centers. Over the past five years, approximately 1,300 accessions from the oat collection, including 1,173 sources and 39 donors, have been sent to plant breeding centers across the Russian Federation in response to 47 requests.

Every year, a comprehensive study of newly acquired accessions in the VIR collection and their propagation within the oat group results in making a list of sources of valuable agronomic traits identified at VIR's experiment stations following a three-year evaluation, and donors developed and

tested in recent years. This list of sources and donors forms the basis for the targeted distribution of source material upon requests from plant breeding centers in the European (Batalova, 2025; Mishenkina, 2021) and Asian parts of the Russian Federation (Nikolaev et al., 2024). Recently, such sets of sources of valuable agronomic traits have been distributed upon requests from a majority of breeding centers (Ignatieva et al., 2023; Krotova, Batalova, 2023; Zhuikova, Batalova, 2023). Among the provided hulled and naked accessions, there were a large number of sources representing breeding lines with a neutral photoperiod, recently obtained from Brazil. The sets included sources of resistance to major oat diseases, including resistance to *Fusarium* head blight, with the lowest mycotoxin accumulation in grain, sources of earliness, sources with various productivity characteristics (Krotova, 2025; Vologzhanina, Batalova, 2025) and high biochemical component content, as well as donors of short stems, donors with a neutral photoperiod, and donors with resistance to crown rust.

Conclusion. The active oat collection at VIR is comprehensively evaluated in line with current breeding trends aimed at reducing human impact on the environment. As a result, source material is selected for shipment to plant breeding centers across the Russian Federation, where new high-yielding cultivars are being developed. This process includes studying the growing season and identifying sources with a neutral response to photoperiod duration, which would limit the use of herbicides, reduce fungal infections, and lessen mycotoxin accumulation in grain. The use of semidwarfism genes reduces culm length and increases lodging resistance, thus decreasing the application of retardants and lowering the incidence of *Fusarium* infection and mycotoxin accumulation. Identifying and using sources of pest resistance reduces the application of fungicides and insecticides to new cultivars, and decreases plant disease infestation, toxin accumulation, and pest damage. Studying various crop quality traits and identifying sources of such traits for the development of new cultivars cuts down the use of mineral fertilizers (especially N) and improves product quality; these cultivars may possess traits required for the production of functional foods. Thus, the active oat collection maintained at VIR is systematically expanded, comprehensively studied, safely preserved, and sustainably utilized in fundamental and exploratory research, thus contributing to the development of plant biotechnology, genetics and breeding in the Russian Federation.

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