Dynamics of the genetic diversity of oat varieties in the Tyumen region at avenin-coding loci

A.V. Lyubimova[1,2] ✉, G.V. Tobolova[2], D.I. Eremin[2], I.G. Loskutov[3]

[1] 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, Moskowsky village, Tyumen district, Tyumen region, Russia
[2] Northern Trans-Ural State Agricultural University, Tyumen, Russia
[3] Federal Research Center the N.I. Vavilov All-Russian Institute of Plant Genetic Resources (VIR), St. Petersburg, Russia
✉ e-mail: ostapenkoav88@yandex.ru

Abstract. Molecular and biochemical markers are used to analyze the intraspecific genetic diversity of crops. Prolamin-coding loci are highly effective for assessing this indicator. On the basis of the Laboratory of Varietal Seed Identification of the State Agrarian University of the Northern Trans-Urals, 18 varieties of common oat included in the State Register of Selection Achievements in the Tyumen Region from the 1930s to 2019 were studied by electrophoresis in 2018–2019. The aim of the work was to study the dynamics of the genetic diversity of oat varieties at avenin-coding loci. For the analysis, 100 grains of each variety were used. Electrophoresis was carried out in vertical plates of 13.2 % polyacrylamide gel at a constant voltage of 500 V for 4.0–4.5 h. It was found that 44.4 % of the varieties are heterogeneous, each consisting of two biotypes. For three loci, 20 alleles were identified, 10 of which were detected for the first time. The allele frequency of avenin-coding loci varied with time. In the process of variety exchange, alleles that are characteristic of varieties of non-Russian origin were replaced by alleles present in domestic varieties and then in the varieties developed by local breeding institutions. The following alleles had the highest frequency in Tyumen varieties: *Avn A4* (50.0 %), *A2* (25.0 %), *Avn B4* (50.0 %), *Bnew6* (37.5 %), *Avn C1* (37.5 %), *C2* and *C5* (25.0 %). These alleles are of great value as markers of agronomically and adaptively important characters for the region in question. The amount of genetic diversity of oats varied with time from 0.33 in 1929–1950 to up to 0.75 in 2019. The high value of genetic diversity in modern breeding varieties of the Scientific Research Institute of Agriculture of the Northern Trans-Urals and an increase in this indicator over the past 20 years are associated with the use of genetically heterogeneous source material in the breeding process. This allowed obtaining varieties with high adaptive potentials in the natural climatic conditions of the region.

Key words: oat; variety; electrophoresis; storage proteins; avenin; avenin-coding loci; alleles; genetic diversity.

For citation: Lyubimova A.V., Tobolova G.V., Eremin D.I., Loskutov I.G. Dynamics of genetic diversity of oat varieties in the Tyumen region at avenin-coding loci. Vavilovskii Zhurnal Genetiki i Selektsii = Vavilov Journal of Genetics and Breeding. 2020;24(2):123-130. DOI 10.18699/VJ20.607

Динамика генетического разнообразия сортов овса в Тюменской области по авенин-кодирующим локусам

А.В. Любимова[1,2] ✉, Г.В. Тоболова[2], Д.И. Еремин[2], И.Г. Лоскутов[3]

[1] Научно-исследовательский институт сельского хозяйства Северного Зауралья – филиал Федерального исследовательского центра Тюменского научного центра Сибирского отделения Российской академии наук, пос. Московский, Тюменский район, Тюменская область, Россия
[2] Государственный аграрный университет Северного Зауралья, Тюмень, Россия
[3] Федеральный исследовательский центр Всероссийский институт генетических ресурсов растений им. Н.И. Вавилова (ВИР), Санкт-Петербург, Россия
✉ e-mail: ostapenkoav88@yandex.ru

Аннотация. Для анализа внутривидового генетического разнообразия сельскохозяйственных культур применяются разнообразные молекулярные и биохимические маркеры. Высокой эффективностью при оценке этого показателя обладают проламин-кодирующие локусы. На базе лаборатории сортовой идентификации семян Государственного аграрного университета Северного Зауралья в 2018–2019 гг. методом электрофореза исследованы 18 сортов овса посевного, включенных в Государственный реестр селекционных достижений по Тюменской области с 1930-х гг. до 2019 г. Целью работы было изучить динамику генетического разнообразия сортов по авенин-кодирующим локусам. Для анализа использовали по 100 зерновок каждого сорта. Электрофорез проводили в вертикальных пластинах 13.2 % полиакриламидного геля при постоянном напряжении 500 В в течение 4.0–4.5 ч. Установлено, что 44.4 % сортов гетерогенны и состоят из двух биотипов. Для трех локусов идентифицировано 20 аллелей, 10 из которых выявлены впервые. Частота встречаемости аллелей авенин-кодирующих локусов изменялась с течением времени.

Аллели, характерные для сортов иностранного происхождения, в процессе сортосмены заместились аллелями, присутствующими в отечественных сортах, а затем в сортах местных селекционных учреждений. Наибольшую частоту встречаемости в сортах тюменской селекции имели аллели *Avn A4* (50.0 %), *A2* (25.0 %), *Avn B4* (50.0 %), *Bnew6* (37.5 %), *Avn C1* (37.5 %), *C2* и *C5* (25.0 %). Эти аллели имеют большую ценность как маркеры хозяйственно ценных и адаптивно значимых признаков. Величина генетического разнообразия в сортах овса изменялась с течением времени от 0.33 в 1929–1950 гг. до 0.75 в 2019 г. Высокое значение генетического разнообразия в современных сортах селекции Научно-исследовательского института сельского хозяйства Северного Зауралья, а также увеличение этого показателя на протяжении последних 20 лет связаны с использованием в селекционном процессе генетически разнородного исходного материала. Это позволило получить сорта, обладающие высоким адаптивным потенциалом в природно-климатических условиях данного региона.

Ключевые слова: овес; сорт; электрофорез; запасные белки; авенин; авенин-кодирующие локусы; аллель; генетическое разнообразие.

Introduction

Common oat (*Avena sativa* L.) is a valuable agricultural crop used both for food and animal feed (Barsila, 2018). An important factor in increasing the production of oat is the creation of new intensive type varieties characterized by high productivity and environmental sustainability (Goncharenko, 2016). In the Tyumen region, breeding work with this culture is very active. From the first half of the twentieth century to the present, 18 varieties of spring oat have been included in the State Register of Selection Achievements in the region. In 1993, the first variety of local breeding, Megion, was regionalized. The proportion of varieties created by the Scientific Research Institute of Agriculture of the Northern Trans-Urals in the region's crops has since been constantly increasing. Nowadays, only varieties of local breeding are included in the State Register of Selection Achievements in the region.

However, active breeding can lead to a decrease in the genetic diversity of the species. This is due to the frequent involvement of the same genotypes in the breeding process to enhance specific agronomic characters. A decrease in genetic diversity negatively affects the resistance of populations to diseases and the populations' ability to adapt to changing environmental and climatic conditions (Novoselskaya-Dragovich et al., 2007; Afanasenko, Novozhilov, 2009; Goncharenko, 2016).

A variety of molecular and biochemical markers are used to analyze intraspecific genetic diversity (Konarev et al., 2000; Montilla-Bascón et al., 2013; Shavrukov, 2016; Scheben et al., 2017). Prolamin-coding loci are very effective for assessing this indicator (Che, Li, 2007; Melnikova et al., 2010; Kudryavtsev et al., 2014; Lyalina et al., 2016; Lyubimova, Eremin, 2018a; Zobova et al., 2018; Utebayev et al., 2019). Prolamins of oat (avenins) are inherited as blocks and are controlled by three independent loci: *Avn A*, *Avn B* and *Avn C*, located in three homeologous chromosomes of group A (Portyanko et al., 1987, 1998). Due to the high level of avenin polymorphism, almost every oat variety, biotype, or line is characterized by a unique component composition of storage proteins (Loscutov,

2007; Lyubimova, Eremin, 2018b). This allows analyzing the individual allele frequency of avenin-coding loci, the dynamics of changes in their occurrence in time and space, and also assessing the genetic transformations that occur under the influence of prolonged artificial selection.

The aim of the work is to study the dynamics of genetic diversity at avenin-coding loci in common oat varieties included in the State Register of Selection Achievements in the Tyumen region from the 1930s to the present for assessing the effectiveness of selection work carried out in the region.

Materials and methods

The studies were carried out in the Laboratory of Varietal Seed Identification of the Agrobiotechnological Center of the Northern Trans-Urals State Agrarian University in 2018–2019. Eighteen varieties of common oat included in the State Register of Selection Achievements in the Tyumen Region since 1929 were studied (Table 1).

Plant material was provided from the collection of the Federal Research Center N.I. Vavilov All-Russian Institute of Plant Genetic Resources and the institution-originator of varieties, the Scientific Research Institute of Agriculture of the Northern Trans-Urals, a Branch of the Tyumen Scientific Center of Siberian Branch of the Russian Academy of Sciences.

For laboratory analysis, 100 grains of each variety selected by random sampling were used. For one-dimensional electrophoresis of avenins, a published technique (Portyanko et al., 1998) with modifications was used. Proteins were extracted from individual crushed grains by adding 90 µl of 70 % ethanol. The obtained extract was centrifuged, and 300 µl of methylene green dye was added to it. Protein extract (22 µl) was added to the polyacrylamide gel. Gel composition: 13.17 g of acrylamide, 0.66 g of N,N′-methylene-bis-acrylamide, 7.17 g of urea, 2.0 mg of iron sulfate (III), 80.0 mg of ascorbic acid, and 0.26 g of aluminum lactate. All reagents were dissolved in 100 ml aluminum-lactate buffer (pH 3.1). Acrylamide polymerization was initiated by adding 25 µl of 15 % hydrogen peroxide to 75 ml of

А.В. Любимова, Г.В. Тоболова
Д.И. Еремин, И.Г. Лоскутов

Динамика генетического разнообразия сортов овса
в Тюменской области по авенин-кодирующим локусам

2020
24 • 2

Table 1. Varieties of common oat included in the State Register of Selection Achievements in the Tyumen region (1929–2019)

VIR catalog number	Variety	Origin	Year of regionalization	Year of removal from regionalization	Total in regionalization (years)
7965	Seger	Sweden	1929	1963	34
7947	Golden Rain		1929	1976	47
8494	Omhafer		1939	1982	43
8256	Udarnik 883	Krasnoyarsk region	1957	1960	3
2874	Nidar	Norway	1957	1963	6
11132	Severyanin	Arkhangelsk region	1966	1974	8
11717	Skorospelyj	Kirov region	1974	1981	7
11122	Narymskij 943	Tomsk region	1975	1996	21
12245	Tayozhnik		1977	2001	24
11379	Astor	Netherlands	1978	2000	22
11584	Selma	Sweden	1981	1993	12
13478	Perona	Netherlands	1985	2018	33
14039	Megion	Tyumen region	1993	–	26
14031	Novosibirskij 88	Novosibirsk region	1994	2004	10
14784	Tyumenskij golozyornyj	Tyumen region	2000	–	19
14785	Talisman		2002	–	17
15380	Otrada		2014	–	5
15451	Foma		2015	–	4

a gel solution. Electrophoresis was carried out in vertical electrophoretic chambers with dimensions of the formed plates of $17.8 \times 17.8 \times 0.15$ cm (VE-20, Helicon, Russia) for 4.0–4.5 h at a constant voltage of 500 V. To fix and stain the gel, a 10 % solution of trichloroacetic acid with the addition of 0.05 % Coomassie brilliant blue R-250 in ethanol was used. Identification of allelic variants of component blocks controlled by avenin-coding loci was carried out on the basis of a catalog developed by V.A. Portyanko et al. (1987). Astor common oat (*Avn A2 B4 C2*) were used as a standard. In case the detected block was not in the catalog, it was marked with a "new" mark.

In order to assess the dynamics of the change in the genetic diversity of oat varieties over time, all the studied samples were grouped. One group included varieties cultivated in the same ten-year period. The gene diversity at the locus (H) was calculated for each group of varieties separately according to the following formula:

$$H = \frac{n}{n-1} \times (1 - \Sigma_{i=1}^{k} p_i^2),$$

where p_i is the population frequency of the i-th allele; k is the number of locus alleles; n is the sample size (Nei, 1987). To calculate the average gene diversity ($\overline{H}$), the number of alleles per locus was averaged over all loci. The calculations were performed using the Arlequin Ver 3.5.2.2 program (Copyright 2015 L. Excoffier. CMPG, University of Berne).

Results

As a result of the studies, it was found that 8 (44.4 %) of the 18 analyzed varieties were heterogeneous in the composition of avenin. Seger, Golden Rain, Omhafer, Severyanin, Narymskij 943, Tayozhnik, Megion and Otrada varieties consisted of two biotypes. These varieties are characterized by the presence of several alleles at one or more avenin-coding loci. In the genetic formula, such states of loci were recorded with the "+" sign (Table 2). In subsequent calculations, each biotype was considered by us as a separate sample. A total of 26 samples were examined.

An analysis of the electrophoretic spectra of avenin allowed us to describe the genetic formulas for each of the studied varieties. Altogether, 8 alleles were detected for the *Avn A* locus; 7, for the *Avn B* locus; and 5, for the *Avn C* locus. It should be noted that some of the combinations of avenin components that we found were absent in the catalog of genetic nomenclature. To identify new blocks

Table 2. Alleles of avenin-coding loci of common oat varieties
included in the State Register of Selection Achievements in the Tyumen region (1929–2019)

Variety	Number of biotypes	Alleles of the avenin-coding locus		
		Avn A	*Avn B*	*Avn C*
Seger	2	*2 + new9*	*1*	*new8*
Golden Rain	2	*2*	*1*	*2 + new8*
Omhafer	2	*new9*	*1*	*2 + new8*
Udarnik 883	1	*new11*	*new9*	*3*
Nidar	1	*2*	*1*	*2*
Severyanin	2	*new11 + new12*	*new9 + new10*	*3*
Skorospelyj	1	*new12*	*new10*	*3*
Narymskij 943	2	*5 + 2*	*1 + 4*	*1 + 2*
Tayozhnik	2	*2 + 1*	*new8*	*2*
Astor	1	*2*	*4*	*2*
Selma	1	*new9*	*1*	*3*
Perona	1	*4*	*4*	*2*
Megion	2	*2 + new11*	*new6*	*5*
Novosibirskij 88	1	*2*	*4*	*2*
Tyumenskij golozyornyj	1	*2*	*new6*	*3*
Talisman	1	*4*	*4*	*2*
Otrada	2	*new10 + 4*	*4*	*1*
Foma	1	*4*	*new7*	*1*

Table 3. The allele frequency of avenin-coding loci of common oat varieties, %

Locus	Allele	Years								
		1929–1930	1940–1950	1950–1960	1960–1970	1970–1980	1980–1990	1990–2000	2000–2010	2010–2019
Avn A	*1*	0	0	0	0	8.3	12.5	10.0	12.5	0
	2	60.0	60.0	50.0	44.4	41.7	37.5	50.0	50.0	25.0
	4	0	0	0	0	0	12.5	10.0	25.0	50.0
	5	0	0	0	0	8.3	12.5	10.0	0	0
	new9	40.0	40.0	37.5	33.3	16.7	12.5	10.0	0	0
	new10	0	0	0	0	0	0	0	0	12.5
	new11	0	0	12.5	11.1	8.3	0	10.0	12.5	12.5
	new12	0	0	0	11.1	16.7	12.5	0	0	0
Avn B	*1*	100.0	100.0	87.5	77.8	41.7	25.0	20.0	0	0
	4	0	0	0	0	16.7	37.5	40.0	37.5	50.0
	new6	0	0	0	0	0	0	20.0	37.5	37.5
	new7	0	0	0	0	0	0	0	0	12.5
	new8	0	0	0	0	16.7	25.0	20.0	25.0	0
	new9	0	0	12.5	11.1	8.3	0	0	0	0
	new10	0	0	0	11.1	16.7	12.5	0	0	0
Avn C	*1*	0	0	0	0	8.3	12.5	10	0	37.5
	2	33.3	33.3	37.5	33.3	50.0	62.5	60.0	62.5	25.0
	3	0	0	12.5	22.2	25.0	25.0	10.0	12.5	12.5
	5	0	0	0	0	0	0	20.0	25.0	25.0
	new8	66.7	66.7	50.0	44.4	16.7	0	0	0	0

А.В. Любимова, Г.В. Тоболова
Д.И. Еремин, И.Г. Лоскутов

Динамика генетического разнообразия сортов овса
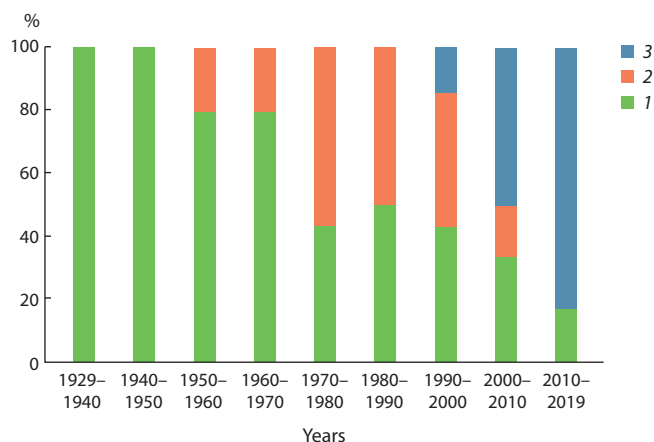в Тюменской области по авенин-кодирующим локусам

2020
24•2

Fig. 1. The dynamics of the regionalized assortment of common oat in the Tyumen region (1929–2019).

Varieties: *1* – of foreign breeding; *2* – of domestic breeding; *3* – of local breeding institutions.

of components, it is necessary to conduct a hybridological analysis and assess the nature of the inheritance of avenin components. However, we highlighted the alleged blocks of components, each of which was assigned a number following the blocks previously described in the catalog. A "new" mark was added before the number of each of the proposed blocks.

To assess genetic diversity at different time intervals, we calculated the allele frequency of avenin-coding loci (Table 3).

Different alleles predominate in different groups of varieties. For the *Avn A* locus, only alleles *2* and *new9* were found before 1950. However, the frequency of their occurrence began to decrease with the appearance of domestic varieties and then varieties of local breeding in the crops

of the region (Fig. 1). Alleles *1*, *5* and *new12* were characteristic of varieties cultivated from 1960 to 2010, and are no longer found today. Allele *4* (50.0 %) is currently the most widespread; allele *2* accounts for 25.0 %; *new11* and *new12*, for 12.5 % each.

For the *Avn B* locus of modern oat varieties, alleles *4* (50.0 %) and *new6* (37.5 %) predominate; *new7* is found with a frequency of 12.5 %. Alleles *1*, *new8*, *new9* and *new10*, which are characteristic of varieties of foreign and domestic breeding, but not found by us among the varieties of local breeding, are completely eliminated.

A similar situation is observed for the *Avn C* locus: allele *new8*, which occurred with a frequency of 66.7 % in 1929–1950, is currently replaced by alleles *1* (37.5 %), *5* (25.0 %) and *3* (12.5 %). It is necessary to pay attention to allele *2*, the presence of which in varieties has been noted at all periods of cultivation ever since 1929. This allele frequency ranged from 25.0 to 62.5 %. Nowadays, this allele is presented in 25.0 % of the varieties. The same feature was noted for allele *2* of the *Avn A* locus.

The value of genetic diversity, calculated on the basis of data on the allele frequency, also changed over time (Fig. 2).

This indicator was minimal before 1950 (0.38), when only three varieties of oat were cultivated in the region: Seger, Golden Rain and Omhafer. Subsequently, with the advent of new varieties in the region's crops, the value of genetic diversity increased, reaching its maximum in the period from 1970 to 1980 (0.78). During this period of time, an active variety exchange was carried out in the region – Seger, Udarnik 883 and Nidar were removed from regionalization, and they were replaced by Skorospelyj, Narymskij 943, Tayozhnik and Astor varieties bearing new alleles of avenin-coding loci. The period 1970–1980 was
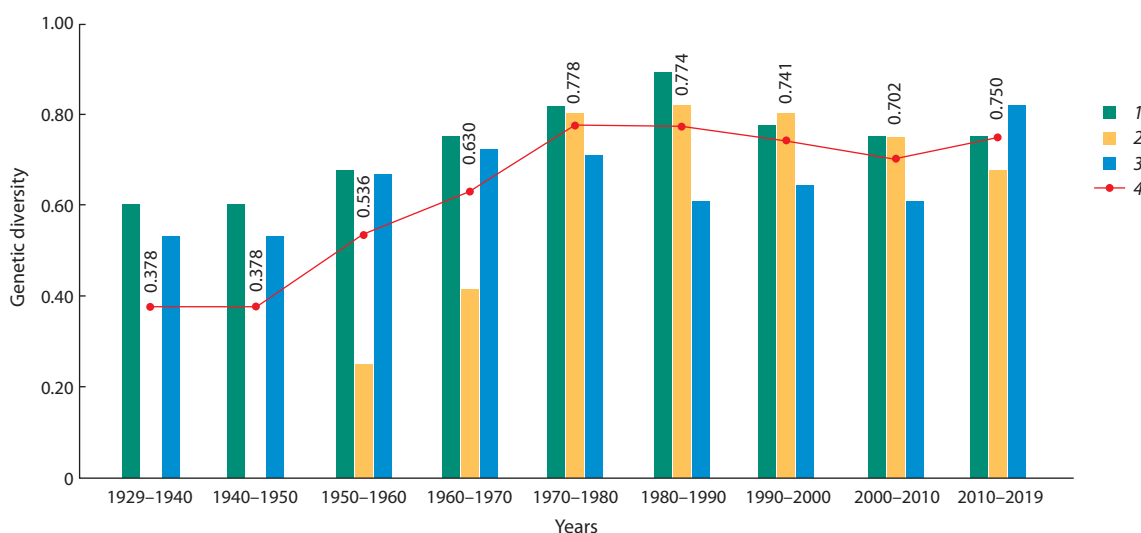

Fig. 2. Genetic diversity of oat varieties by avenin-coding loci.

Locuses: *1* – *Avn A*; *2* – *Avn B*; *3* – *Avn C*; *4* – average gene diversity.

characterized by the largest variety of allelic variants in varieties – 15 alleles were found at three *Avn* loci (Table 3). Subsequently, in the process of replacing foreign varieties with domestic ones, the indicator of genetic diversity decreased to 0.70 by 2010. A decrease in diversity was caused by the exclusion from regionalization of a large number of varieties bearing alleles not found in varieties of local breeding. However, to date, there has been an increase in average gene diversity to 0.75.

Discussion

As a result of our analysis using multiple alleles of avenin-coding loci, we described the genetic formulas for 18 varieties of common oat included in the State Register of Selection Achievements in the Tyumen region. It was established that the heterogeneity of varieties is 44.4 %. The presence of several biotypes increases the adaptive potential of the variety (Metakovsky, 1990; Novoselskaya-Dragovich et al., 2013), which is extremely important in the natural climatic conditions of the Tyumen region, which is a risky farming zone.

In some varieties, identical prolamin spectra were found. Thus, the first and second biotypes of Golden Rain are identical to Seger (I biotype) (*2.1.new8*) and Nidar (*2.1.2*), respectively. The second biotype of Seger coincided with the second biotype of Omhafer (*new9.1.new8*). The first and second biotypes of Severyanin coincide with Udarnik (*new11.new9.3*) and Skorospelyj (*new12.new10.3*). The same types of spectra are characteristic of the second biotype of Narymskij 943 as well as Astor and Novosibirskij 88 (*2.4.2*); the spectra of Perona and Talisman (*4.4.2*) coincide. As a result of the analysis, it was found that only 10 (38.5 %) of the 26 studied genotypes are variety-specific. This is a fairly low rate.

The identity of alleles of prolamin-coding loci in varieties is associated with the involvement of the same genotypes in breeding programs (Portyanko et al., 1998; Melnikova et al., 2010; Novoselskaya-Dragovich et al., 2013). For example, Seger and Golden Rain were bred from the same oat variety Milton (=Propsteier), and Omhafer, too, originated from it. The old oat variety Milton appeared in northern Germany and was widespread in northern Europe (Portyanko et al., 1998). Apparently, this variety possessed outstanding economic characteristics, which led to its frequent inclusion in the breeding process. This was reflected in the matching set of alleles of avenin-coding loci in its descendants. The presence of varieties with the same genetic formulas of prolamins reduces the efficiency of using the method of electrophoresis for their differentiation. A number of authors in their studies concluded that the use of avenin-coding loci as the only marker system for distinguishing a large number of oat varieties is insufficient, since the allelic diversity of oat prolamin loci is

characterized as low compared to wheat, barley and rye (Cliff, Cooke, 1984; Souza, Sorrels, 1990; Portyanko et al., 1998). In such cases, there is a need for an additional use of other marker systems (Wight et al., 2010). However, it should be noted that the modern varieties of oat created by the Scientific Research Institute of Agriculture of the Northern Trans-Urals have an individual allelic composition of avenin-encoding loci, which makes it possible to differentiate their genotypes with high accuracy.

An analysis of the frequencies of alleles of avenin-coding loci for all three loci allowed us to note the relationship between the frequency of alleles and a set of cultivated varieties, especially their origin. In the process of variety exchange, the alleles characteristic of varieties of foreign breeding were gradually replaced by alleles present in domestic varieties, and then in the varieties developed of local breeding istitutions. A similar replacement of one allele with another during breeding work was noted by many researchers in the study of prolamin-coding loci of wheat and barley (Novoselskaya-Dragovich et al., 2007; Lyalina et al., 2016). On a large number of examples, the adaptive nature of prolamin polymorphism has been proved. Their connection with adaptive gene complexes allows, based on the spectra of storage proteins, identifying genotypes that are most adapted to specific climatic conditions. A.Yu. Novoselskaya-Dragovich and the co-workers (2013) noted that genetic differences between varieties of different geographical origin are determined by natural selection. In this case, the reason for the rather rapid replacement of the "old" alleles with "new" ones is directed processes associated with new directions in breeding and the involvement of genetically different source material (Novoselskaya-Dragovich et al., 2007). Our data on the allele frequency of avenin-coding loci are in good agreement with this statement.

With the beginning of breeding work on oat in the Tyumen region, varieties appeared that possess a set of agronomically and adaptively significant characters for this region. This led to an increase in the frequency of certain alleles of avenin-coding loci, which can be considered markers of such genotypes or characters. At the same time, it caused a decrease in the frequency or even complete disappearance of alleles characteristic of foreign varieties. *A2* and *C2* alleles found in all groups of varieties, probably, mark highly competitive gene associations that give their carriers important advantages in the natural climatic conditions of the region.

Monitoring changes in the genetic diversity of varieties over time allows judging the presence or absence of genetic erosion. In the works devoted to the assessment of genetic diversity in varieties of other crops, its values were 0.62–0.76 for soft wheat varieties created in Serbia and Italy (Novoselskaya-Dragovich et al., 2007), 0.5–0.6 in soft

А.В. Любимова, Г.В. Тоболова
Д.И. Еремин, И.Г. Лоскутов

Динамика генетического разнообразия сортов овса
в Тюменской области по авенин-кодирующим локусам

2020
24 • 2

wheat varieties of Ukrainian selection (Zayka et al., 2014), and 0.42–0.64 in groups of durum wheat varieties originating from different countries of the world (Kudryavtsev et al., 2014). At the same time, a decrease in the value of this indicator in modern varieties is noted (Kudryavtsev et al., 2014; Lyalina et al., 2016).

The high values of genetic diversity identified as a result of our work and an increase in this indicator since 2000 indicate the absence of genetic erosion. It should be noted that, at different periods of time, the contribution of individual avenin-coding loci to the average gene diversity in varieties of oat in the region was not the same. In the period from 1970 to 2010, the *Avn A* and *Avn B* loci played an important role in the formation of genetic diversity. But currently, the maximum genetic diversity is observed at the *Avn C* locus. In our opinion, this suggests that the alleles of this locus may be important as markers of adaptively significant characters.

Conclusion

The allele frequency of avenin-coding loci in varieties of common oat included in the State Register of Selection Achievements in the Tyumen region from 1929 to 2019 changed over time. The alleles characteristic of the varieties of foreign selection were replaced by "new" ones, specific to the varieties of local selection: *Avn A4* (50.0 %), *A2* (25.0 %), *Avn B4* (50.0 %), *Bnew6* (37.5 %), *Avn C1* (37.5 %), *C2* and *C5* (25.0 %). These alleles are of great value as markers of agronomically and adaptively significant characters for the region in question.

Modern regionalized varieties of oat are characterized by high genetic diversity (0.75), which is associated with the use of heterogeneous source material in the breeding process. This allows obtaining varieties with high adaptive potentials in the climatic conditions of Western Siberia.

The high importance of genetic diversity in modern breeding varieties of the Scientific Research Institute of Agriculture of the Northern Trans-Urals and an increase in this indicator over the past 20 years indicate competently organized and effective breeding work with this crop in the Tyumen region.

References

Afanasenko O.S., Novozhilov K.V. Problems of rational use of genetic resources of plant resistance to diseases. Ekologicheskaya Genetika = Ecological Genetics. 2009;7(2):38-43. (in Russian)

Barsila S.R. The fodder oat (*Avena sativa*) mixed legume forage farming: Nutritional and ecological benefits. J. Agric. Nat. Resour. 2018;1(1):206-222. DOI 10.3126/janr.v1i1.22236.

Che Y.H., Li L.H. Genetic diversity of prolamines in *Agropyron mongolicum* Keng indigenous to northern China. Genet. Resour. Crop. Evol. 2007;54(5):1145-1151. DOI 10.1007/s10722-006-9006-7.

Cliff E.M., Cooke R.J. The characterisation of oat cultivars by electrophoresis. J. Natl. Inst. Agric. Bot. 1984;16:415-429.

Goncharenko A.A. Ecological stability of grain crop varieties and tasks of breedeng. Zernovoe Khozjaistvo Rossii = Grain Economy of Russia. 2016;3:31-37. (in Russian)

Konarev A.V., Konarev V.G., Gubareva N.K., Peneva T.I. Seed proteins as markers in solving problems of plant genetic resources, breeding, and seed production. Tsitologiya i Genetika = Cytology and Genetics. 2000;34(2):91-104. (in Russian)

Kudryavtsev A.M., Dedova L.V., Melnik V.A., Shishkina A.A., Upelniek V.P., Novoselskaya-Dragovich A.Yu. Genetic diversity of modern Russian durum wheat cultivars at the gliadin-coding loci. Russ. J. Genet. 2014;50(5):483-48. DOI 10.1134/S1022795414050093.

Loscutov I.G. Oat (*Avena* L.). Distribution, Taxonomy, Evolution and Breeding Value. Saint-Petersburg, 2007. (in Russian)

Lyalina E.V., Boldyrev S.V., Pomortsev A.A. Current state of the genetic polymorphism in spring barley (*Hordeum vulgare* L.) from Russia assessed by the alleles of hordein-coding loci. Russ. J. Genet. 2016;52(6):565-577. DOI 10.1134/S1022795416060077.

Lyubimova A.V., Eremin D.I. Peculiarities of the avenin component composition in oats cultivated in Western Siberia. Trudy po Prikladnoy Botanike, Genetike i Selektsii = Proceedings on Applied Botany, Genetics, and Breeding. 2018a;179(2):85-95. DOI 10.30901/ 2227-8834-2018-2-85-95. (in Russian)

Lyubimova A., Eremin D. Variety check as an element of precision farming in the modern agriculture. In: International Scientific and Practical Conference "AgroSMART – Smart Solutions for Agriculture" (AgroSMART 2018). 2018b. Vol. 151. DOI 10.2991/agrosmart-18.2018.91.

Melnikova N.V., Kudryavtsev A.M., Mitrofanova O.P., Liapunova O.A. Global diversity of durum wheat *Triticum durum* Desf. for alleles of gliadin-coding loci. Russ. J. Genet. 2010;46(1):43-49. DOI 10.1134/S1022795410010072.

Metakovsky E.V. The value of gliadin biotypes in commercial cultivars of wheat. In: Proc. 4th Int. Workshop on Gluten Proteins. Winnipeg, 1990.

Montilla-Bascón G., Sánchez-Martín J., Rispail N., Rubiales D., Mur L., Langdon T., Griffiths I., Howarth C., Prats E. Genetic diversity and population structure among oat cultivars and landraces. Plant Mol. Biol. Rep. 2013;31(1305):1305-1314. DOI 10.1007/s11105-013-0598-8.

Nei M. Molecular Evolutionary Genetics. New York: Columbia University Press, 1987.

Novoselskaya-Dragovich A.Yu., Fisenko A.V., Imasheva A.G., Pukhalskiy V.A. 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. 2007;43(11):1236-1242. DOI 10.1134/S1022795407110051.

Novoselskaya-Dragovich A.Y., Fisenko A.V., Puhal'skii V.A. Genetic differentiation of common wheat cultivars using multiple alleles of gliadin-coding loci. Russ. J. Genet. 2013;49(5):487-496. DOI 10.1134/S1022795413020087.

Portyanko V.A., Pomortsev A.A., Kalashnik N.A., Bogachkov V.I., Sozinov A.A. The genetic control of avenins and the principles of classification. Genetika = Genetics (Moscow). 1987;23(5):845-853. (in Russian)

Portyanko V.A., Sharopova N.R., Sozinov A.A. Characterization of European oat germ plasm: allelic variation at complex avenin loci detected by acid polyacrylamide gel electrophoresis. Euphytica. 1998;102:15-27. DOI 10.1023/A:1018399919953.

Scheben A., Batley J., Edwards D. Genotyping-by-sequencing approaches to characterize crop genomes: choosing the right tool for the right application. Plant Biotechnol. J. 2017;15(2):149-161. DOI 10.1111/pbi.12645.

Shavrukov Y. Comparison of SNP and CAPS markers application in genetic research in wheat and barley. BMC Plant Biol. 2016;16:11. DOI 10.1186/s12870-015-0689-9.

Souza E., Sorrels M. Inheritance and distribution of variation at four avenin loci in North American oat germplasm. Genome. 1990;33:416-424. DOI 10.1139/g90-063.

Utebayev M., Dashkevich S., Bome N., Bulatova K., Shavrukov Y. Genetic diversity of gliadin-coding alleles in bread wheat (*Triticum aestivum* L.) from Northen Kazakhstan. PeerJ. 2019; 7:e7082. DOI 10.7717/peerj.7082.

Wight C.P., Yan W., Fetch J.M., Deyl J., Tinker N.A. A set of new simple sequence repeat and avenin DNA markers suitable for mapping and fingerprinting studies in oat (*Avena* spp.). Crop Sci. 2010;50:1207-1218. DOI 10.2135/cropsci2009.09.0474.

Zayka E.V., Kozub N.A., Sozinov I.A., Sozinov A.A., Starichenko V.N. Analysis of genotypes of winter soft wheat varieties of the Institute of Farming of the National Academy of Agricultural Science according to alleles of storage protein loci. Vestnik Belorusskoy Gosudarstvennoy Selskohozyaystvennoy Akademii = Bulletin of the Belarussian State Agricultural Academy. 2014;4:53-57. (in Russian)

Zobova N.V., Surin N.A., Gerasimov S.A., Chuslin A.A., Onufrienok T.V. Spectra of prolamines in agroecological evaluation of the collection barley. Dostizheniya Nauki i Tekhniki APK = Achievements of Science and Technology of AIC. 2018; 32(5):45-47. DOI 10.24411/0235-2451-2018-10511. (in Russian)

ORCID ID
A.V. Lyubimova orcid.org/0000-0002-1570-9595
D.I. Eremin orcid.org/0000-0002-3672-6060
I.G. Loskutov orcid.org/0000-0002-9250-7225