Genetic evaluation of the breeding strategy effectiveness for horses of the New Altai breed

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Abstract. The purpose of the study was to study the dynamics of the main selected traits in horses of the New Altai breed and the genetic characteristics of the breed. In this paper, the indicators of the main measurements of the body and live weight of horses, depending on gender and region of birth, are analyzed. The main genetic and population parameters of the breed were calculated based on microsatellite DNA loci: the total number of alleles at 17 loci (Na), the average number of alleles per locus (Nv), the level of polymorphism (Ae), observed (Ho) and expected (He) heterozygosity, coefficients of intrapopulation inbreeding (Fis), genetic similarity (RXY) and genetic distances (DXY). It has been established that the horses of the New Altai breed are characterized by a relatively high level of polymorphism and genetic diversity, both in the breed as a whole and in the context of breeding regions. The high genetic similarity of the New Altai breed with the Russian Heavy Draft and Altai breeds has been revealed. The study of the genetic structure of the breed, the levels of its intra- and inter-population diversity in combination with classical zootechnical assessment methods showed the consistency of the chosen cultivation strategy of the New Altai breed.

1 Introduction

Currently, the process of actively improving the productive qualities of farm animals is underway all over the world based on the use of modern breeding methods, genetics and biotechnology.

In Russia, one of the promising specialized meat breeds is the New Altai [1]. As a result of breeding work, high meat productivity of horses of this breed has been achieved with good adaptation to year-round pasture maintenance. Given this fact, the prospects of its use in the development of domestic productive horse breeding become obvious [2].

The basis for the improvement of breeds is the phenotypic diversity of the selected traits, which have a continuous character of variability.

The most important breeding characteristics of the greatest practical interest in the New Altai horse breed are live weight, measurements and adaptive qualities.

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The study of the genetic characteristics of modern horses of the New Altai breed by 17-panel microsatellite loci showed that they are characterized by a relatively high level of genetic diversity [3-5].

Nevertheless, over time, under the effect of destabilizing natural and anthropogenic factors, a gradual depletion of genetic resources may occur. Therefore, monitoring the dynamics of genetic variability and genetic diversity of populations, as well as its preservation at an optimal level, is of great scientific interest for practical breeding.

The assessment of genetic and population parameters at the present stage is mainly carried out using molecular genetic methods.

Among the most informative methods of analyzing the allel-fund of horses of world breeds, modern publications consider the following: genome-wide and targeted genome sequencing on the Illumina platform [6-8], the use of SNP chips [9], microsatellite analysis [10-15], sequencing of the D-loop of mitochondrial DNA [16], Y-chromosome analysis [17-19].

Microsatellites belong to the first generation of DNA markers [20]. The highly polymorphic nature and Mendeleev type of inheritance make them ideal DNA markers of the genome of farm animals [21].

Currently, microsatellites are the most popular markers in studies of the genetic characteristics of horses, which is explained by the ease of use and high degree of information [22]. They serve as an effective means of studying the features of their gene pool, genetic polymorphism, phylogeny, and obtaining data on the breed formation and evolution of horse breeds [23].

The assessment of genetic diversity within individual breed groups and entire breeds makes it possible to create and improve both breeding programs and programs for the conservation of the gene pool of these breeds [9].

The purpose of the study was to analyze the results of breeding work with the New Altai horse breed.

2 Materials and Methods

The material for the study was sheets of the results of the valuation of breeding horses of the New Altai breed and documents of primary zootechnical accounting.

The object of the study was horses of the New Altai breed.

The main measurements of the horse were taken using a measuring stick and a measuring tape in the split. The live weight of the animal was determined by weighing.

The genetic and population analysis was performed according to generally accepted methods. The following indicators were determined: the total number of alleles at 17 loci (Na), the average number of alleles per locus (Nv), the level of polymorphism (Ae), observed (Ho) and expected (He) heterozygosity, coefficients of intrapopulation inbreeding (Fis), genetic similarity (RXY) and genetic distances (DXY).

The research results were processed biometrically using methods of variation statistics using the Microsoft Office Excel 2010 program.

3 Results and Discussion

Monitoring of indicators of selected traits of horses of the New Altai breed was carried out by gender and breeding regions for ten-year periods - 2010 and 2020. During the study period, data on 6,918 horses were analyzed, including 358 breeding stallions and 3,600 stallions of the New Altai breed.
Positive dynamics of live weight was established in horses of the analyzed breed at all ages, with the exception of mares aged 3.5 and 5.5 years and stallions aged 5.5 years (Figure 1). Stallions born on farms in the Altai Republic outperformed their peers from the Altai Territory in live weight over a life span of 6 months to 6.5 years. Nevertheless, mares from the Altai Territory turned out to be heavier than mares from the Altai Republic throughout their lives. Within the lines, the live weight index varied slightly, and there was no clear trend towards its increase or decrease. The highest value of live weight for the studied period among stallions was recorded in 2020 in the light bay stallion Anons 93-04 (Album 77-90 - 25-93-BO) at the age of 16 years - 807 kg; among mares – in the mare 47-14–A (Mercuriy 4-10 - 92-04–BO) at the age of 6 years - 818 kg. The stallion is a representative of the Arbas line, the mare is a representative of the Mech line.

![Graph showing dynamics of live weight in horses of the New Altai breed](image)

**Fig. 1.** Dynamics of live weight in horses of the New Altai breed.

There were no significant differences in body measurements in stallions of the New Altai breed during the analyzed period. Mares aged 2.5 years have positive dynamics of measurements of oblique body length and chest circumference. These measurements in 2020 increased by 1.37% and 4.07%, respectively, compared with 2010. No significant differences in body measurements were found in 5.5-year-old mares. At the same time, a comparative analysis of body measurements showed that stallions and mares born in the Altai Territory slightly surpassed their peers from the Altai Republic in all parameters, both at the age of 2.5 and 5.5 years.

Considering that over time, under the effect of various factors, the biodiversity and genetic potential of populations may decrease, the genetic characteristics of the New Altai horse breed were studied, both in the breed as a whole and in the context of its cultivation regions.

A comparative analysis of the genetic structure of horses from two breeding regions according to the main genetic and population characteristics showed that horses born in farms
of the Altai Republic slightly surpass animals from the Altai Territory in terms of genetic diversity and polymorphism (Table 1).

**Table 1.** Characteristics of the New Altai horse breed from different breeding regions by 17 loci of DNA microsatellites.

<table>
<thead>
<tr>
<th>Group of horses</th>
<th>n</th>
<th>Na</th>
<th>Nv</th>
<th>Ae</th>
<th>He</th>
<th>Ho</th>
<th>Fis</th>
</tr>
</thead>
<tbody>
<tr>
<td>whole selection</td>
<td>294</td>
<td>153</td>
<td>9.000</td>
<td>4.773</td>
<td>0.749</td>
<td>0.750</td>
<td>0.005</td>
</tr>
<tr>
<td>born in the Altai Territory</td>
<td>147</td>
<td>142</td>
<td>8.353</td>
<td>4.461</td>
<td>0.756</td>
<td>0.763</td>
<td>-0.005</td>
</tr>
<tr>
<td>born in the Altai Republic</td>
<td>147</td>
<td>143</td>
<td>8.412</td>
<td>4.471</td>
<td>0.750</td>
<td>0.734</td>
<td>-0.007</td>
</tr>
</tbody>
</table>

The data in Table 1 also reflect the absence of significant differences in the horses of the analyzed regions in terms of heterozygosity. Nevertheless, the highest degree of expected and observed heterozygosity was found in a group of horses from the Altai Territory. In the cohorts of both regions, the expected heterozygosity exceeded the observed one, which indicates the predominance of heterozygous genotypes and indicates the effectiveness of breeding measures to maintain genetic diversity in the studied subpopulations. At the same time, the Fis coefficient had a positive value for the breed as a whole, which indicates a slight shift in the genetic balance towards an excess of homozygotes. In this case, the observed deficiency of heterozygous individuals is a consequence of the Wahlund effect, manifested as a result of the presence of a geographical barrier to gene flow and gene drift in geographically separated subpopulations.

The results of the analysis of the genetic structure of the subpopulations of the New Altai breed demonstrate that each of them differs in the spectrum, frequency of occurrence of alleles and a set of alleles that are absent in horses of other breeding regions. Thus, horses born in the Altai Territory are characterized by the presence of the following alleles: HTG6 M, ASB23 R, ASB2 J, HTG10 T, HMS2 N, HMS2 S, ASB17 H, ASB17 K, HMS1 K, CA425 K, and for the group of horses from the Altai Republic – HTG4 Q, ATH4 R, HMS7 I, HMS7 K, AHT5 P, HTG10 I, HTG10 J, HTG10 Q, HNG7 P, ASB17 D, CA425 F. It should be noted that horses of both groups have the same set of alleles in 4 of 17 loci: VHL20, HMS6, HMS3, LEX3. The identical spectrum of LEX3 locus alleles in horses of both cohorts indicates their common maternal basis.

It was found that the genetic structure of the studied animals of both subpopulations of the New Altai breed is characterized by a high frequency of occurrence of the HTG6 O allele: 0.832 – horses born in the Altai Republic, 0.684 – horses born in the Altai Territory.

The coefficients of genetic similarity between the livestock of the experimental sample and the breeds involved in the creation of the New Altai breed varied in the range of 0.869-0.910 (Table 2). The horses of the New Altai breed had the highest coefficients of genetic similarity with the Russian Heavy Draft (0.910) and Altai (0.909) breeds. The Lithuanian Heavy Draught breed has the greatest genetic divergence in relation to the New Altai breed (0.709). The explanation for this fact is the less widespread use of stallions of the Lithuanian Heavy Draught breed (19 heads) compared to stallions of the Russian Heavy Draft breed (57 heads) when creating the New Altai breed [20], as well as the non-infusion of Lithuanian blood during further improvement of the new breed. At the same time, if the distribution of places by the value of the estimated parameter in the group of horses born in the Altai Republic coincides with the general picture according to the experimental sample, then the group of animals from the Altai Territory showed the highest degree of genetic similarity with the Altai breed (0.898), and then with the Russian Heavy Draft (0.878).
Table 2. Coefficients of genetic similarity ($R_{XY}$) and genetic distances ($D_{XY}$) in the New Altai horse breed with the breeds involved in its creation.

<table>
<thead>
<tr>
<th>Breed</th>
<th>Group of horses</th>
<th>whole selection</th>
<th>born in the Altai Territory</th>
<th>born in the Altai Republic</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>$R_{XY}$</td>
<td>$(D_{XY})$</td>
<td>$R_{XY}$</td>
</tr>
<tr>
<td>Altai</td>
<td></td>
<td>0.909</td>
<td>0.091</td>
<td>0.898</td>
</tr>
<tr>
<td>Russian Heavy Draft</td>
<td></td>
<td>0.910</td>
<td>0.090</td>
<td>0.878</td>
</tr>
<tr>
<td>Soviet Heavy Draft</td>
<td></td>
<td>0.879</td>
<td>0.121</td>
<td>0.857</td>
</tr>
<tr>
<td>Lithuanian Heavy Draught</td>
<td></td>
<td>0.869</td>
<td>0.131</td>
<td>0.845</td>
</tr>
</tbody>
</table>

4 Conclusions

The results of the study demonstrate a high level of polymorphism and genetic diversity of the horse population of the New Altai breed against the background of an emerging trend of increasing indicators of the main selected traits, which indicates the absence of inbred depression and indicates the viability of the implemented strategy for breeding horses of this breed. The results of the phylogenetic analysis demonstrated a high level of genetic similarity of the horses of the New Altai breed with the Russian Heavy Draft and Altai breeds and the greatest distance from the Lithuanian Heavy Draught breed. The data obtained are of significant importance for planning breeding work with the breed aimed at its further improvement, with options for implementation by both purebred and interbreed breeding with the infusion of blood of related breeds.

References

1. A.I. Nikonova, Horse breeding and equestrian sport, 4, 4-7 (2012).
2. A.V. Dubrovin, V.V. Kalashnikov, A.M. Zaitsev, Zootechny, 9, 12-16 (2023). DOI: 10.25708/ZT.2023.64.40.003.


