Most relations predict a value in the right order of magnitude, although differences between various relations are large, as might be expected [3].

In conclusion: the available relations give an indication of scour to be expected in coarse non-cohesive material or fissured rock. For scour problems related to the construction of high-head dams, detailed studies including model studies, should be performed for each case.

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УДК 636

GENETIC DIVERSITY OF THOROUGHBRED HORSES BREEDS IN RUSSIA

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Abstract: The aim of the study is to assess and compare the genetic diversity between 9 lines of Thoroughbred horses in Russia, which originated from three eastern ancestors - Godolphin Barb, Burleigh Turk, and Darley Arabian, based on microsatellite markers.

Key words: Allele, Thoroughbred Horses(TB), Microsatellite DNA, Horse genetics.

Introduction. Thoroughbred (TB) horses have greatly influenced the development of horse breeding around the world. In Russia, the Thoroughbred horse breed has been bred since the second half of the eighteenth century [1]. Detailed information about levels of genetic diversity and patterns of Thoroughbred breed gene structure is very important to meet the requirements of future breeding programs and to formulate effective conservation strategies for Thoroughbred horses.

In recent years, several studies have been conducted to investigate the genetic characteristics of Thoroughbred horses using DNA markers. The aim of our study was to characterize the genetic diversity of Thoroughbred lines based on 17 microsatellite markers (AHT4, AHT5, ASB2, HMS2, HMS3, HMS6, HMS7, HTG10, HTG4, HTG6, HTG7, VHL20, ASB17, ASB23, CA425, HMS1, LEX3), recommended by the International Society for Animal Genetics (ISAG) for identification and pedigree analysis in Thoroughbred horses.

Materials and methods. The genetic diversity of thoroughbred horses was evaluated in the laboratory of the Russian innovative biotechnological company "GORDIZ", by isolating the DNA with the commercial set " Extra Gene TM DNA Prep 200 " (Isogene Laboratory, Moscow, Russia), by conducting a polymerase chain reaction. The results of the studies were processed using generally accepted statistical standard methods [2, 3] and using the POPGENE 1.31 program.

Results. A comparative analysis of representations of different lines of Thoroughbred breeds with genetic and population parameters shows that there are small differences between representatives of different lines in the number of alleles (Na), the level of polymorphic information content (PIC), and the degree of observed heterozygosity (Ho). The number of alleles in stallions of different lines varied within 12-15, and the largest number of alleles -15-was found in representatives of the Douglas line, the smallest -12-in the group of stallions of the Ribot line.

The effective number of alleles (Ae) varied in the range - 2.496-3.120, and the highest effective number of alleles was 3.120 in the Nasrullah line, the lowest-in the Douglas line, this indicator is slightly higher in the Ribot line, and the stallions of the other lines are characterized by almost the same values of this indicator.

The highest degree of observed heterozygosity (Ho) was 0.671 in the Native Dancer line, and the lowest in the Mr.Prospector line (0.600), the highest degree of expected heterozygosity (He) was 0.652 in the Nasrullah line, and the lowest in the Man o'War line (0.559) (Table 1).

Table 1

Lines	Ν	N_a	A _e	PIC	Ho	H _e
Northern Dancer	5	14	2.792	0.541	0.635	0.598
Native Dancer	5	13	2.778	0.515	0.671	0.604
Mr. Prospector	5	13	2.748	0.528	0.600	0.594
Tourbillon	5	13	2.789	0.557	0.637	0.616
Douglas	5	15	2.496	0.503	0.600	0.565
Ribot	6	12	2.649	0.526	0.627	0.581
Nasrullah	7	14	3.120	0.591	0.612	0.652
Nearco	5	13	2.795	0.556	0.635	0.618
Man o'War	5	11	2.705	0.548	0.635	0.559
Mean		13	2.762	0.540	0.628	0.599

Indicators of genetic diversity in Thoroughbred stallions of different lines

Of the 17 markers, the loci HMS 2, ASB 17, LEX 3, HMS 1, and CA425 had a relatively high PIC value (>0.7). This means that individual lines, you need to select those markers that have a higher information content of this line. The PIC value for the lines is in the range from 0.503 to 0.591 (on average-0.540). This means that the studied lines are characterized by an almost equal polymorphism index, which, indirectly, may indicate similar selection approaches when working with these lines.

Discussion. Comparing the results of this study with data from other researchers on Thoroughbred horse breeds showed that our values of genetic diversity indicators are comparable to those obtained Thoroughbred horses from Korea, Bosnia, Italy and Ukraine, with rare exceptions [4-8]. Overall, purebred riding horses have a low level of genetic diversity, with only 86 alleles being classified in our study in 17 small satellite locus.

Conclusions. Analysis of the genetic diversity of representatives of nine lines of Thoroughbred horses showed that the observed differences in indicators, levels of expected and observed heterozygosity, and the polymorphism index arise as a result of not only genotypic differences between the progenitors of the lines, but also differences between the maternal stock in those countries where representatives of the lines were used, against the background of different breeding strategies.

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INFLUENCE OF NODULE BACTERIA ON THE FORMATION OF THE SYMBIOTIC APPARATUS OF ALFALFA

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Abstract: Based on the analysis of the results of previous studies, a review of theoretical and practical data is devoted to the study of salt tolerance and genetic determination of this trait in nodule bacteria Sinorhizobium meliloti - alfalfa symbionts. A collection of natural isolates of the nodule bacterium Sinorhizobium meliloti from nodules of wild species of alfalfa (Medicago polymorpha) and alfalfa plant of the Taisiya varieties were used. The degree of resistance of these strains to salinity and which of them fix nitrogen more efficiently under salinization conditions was discussed, and the effect of different levels of salinity on the growth