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## GENETIC DIVERSITY OF THE KOSTANAY HORSE BREED USING MICROSATELLITE MARKERS

### ANNOTATION

The article presents the results of the analysis of genetic diversity of the Kostanay breed of 17 loci of DNA microsatellites, including AHT4, AHT5, ASB17, ASB2, ASB23, CA425, HMS1, HMS2, HMS3, HMS6, HMS7, HTG10, HTG4, HTG6, HTG7, LEX3, VHL20. Hair bulbs of 30 heads of horses of Kostanay breed (Kostanay city, Zarechny settlement) were used as biological material for research.

The aim of the work was to characterise the genetic diversity of horses of the Kostanay breed by microsatellite STR-loci.

Genotyping of animals was carried out by PCR, separation and detection of amplification products was carried out by capillary electrophoresis on an 8-capillary 3500 Genetic Analyzer (Applied Biosystems, USA). The results were interpreted in GeneMapper programme, and statistical processing was performed using Microsoft Excel 2010. The following parameters were calculated: allele frequencies, polymorphism level (Ae), degree of observed (Ho) and expected (He) heterozygosity, fixation index (Fis).

As a result of genotyping of the Kostanay breed of horses bred in Zarechny settlement of Kostanay district on the studied microsatellite loci, data characterising the polymorphism of each of the markers were obtained. On 17 microsatellite loci of DNA in horses of Kostanay breed 102 alleles were revealed. The number of alleles per locus varied from 4 to 10. The most informative for the group under study were loci with the highest number of alleles (ASB17, ASB2), the least informative - with the minimum (HMS1, HTG7). The highest observed heterozygosity was at the ASB2 locus (0.900) and the lowest at the HMS2 locus (0.367). The average expected heterozygosity was 0.696, observed heterozygosity was 0.681, and the mean fixation index had a value equal to 0.018.

Thus, characteristic features of polymorphism on all investigated indexes of the studied microsatellite loci of DNA of the Kostanay breed of horses were revealed.

**Key words:** horses, Kostanay breed, microsatellites, locus, DNA.

**Introduction.** In 1887, for the first time 2 state stables were 19haracter – Torgay and Kostanay stables, and 3 years later – Orenburg stables. These stud farms purchased stallions-producers of Kalmyk, Don, purebred riding, Streletskaya breeds. In 1898 a breeding breeding centre was 19haracter, where local Kazakh horses began to breed in purity, selecting the best individuals for further selection work [1].

The best mares were crossed with stallions of Streletskaya and Don breed lines, and their offspring were infused with the blood of thoroughbred riding horses. The mixed breeds obtained in this way met the stated requirements – they had a massive body and strong limbs, and were characterized by productive movements.

In 1920 the breeding ground was transformed into “Kostanay horse breeding farm”, where the breeding work was continued. Kostanay horse breed was registered in 1951 [2]. At present the work on breeding of the Kostanay breed of horses is continued by “Kazak tulpary” LLP, where the work on studying the genetic characteristics of the population and the development of a comprehensive breeding programme continues.

One of the most convenient and widely used markers for DNA-identification in animal genetics are microsatellites. This is a special class of DNA markers, which are DNA fragments with a large number of up to one hundred or more tandemly repeating identical “ motives” [3, 4]. A motif is a short sequence of several (from two to eight) pairs of nucleotides, usually called a “repeat” [5].

Depending on the repeat length, microsatellites are classified into loci with di-, tri-, tetra-, penta-, and hexanucleotide repeats [6]. Thus, a microsatellite, or microsatellite locus (STR locus, Short Tandem Repeats), is a section of DNA located in a particular chromosome and containing short tandem repeats [7, 8].

In horses, the analysed STR loci constitute a standard panel of markers recommended by the International Society of Animal Genetics (ISAG): AHT4, AHT5, ASB17, ASB2, ASB23, CA425, HMS1, HMS2, HMS3, HMS6, HMS7, HTG10, HTG4, HTG6, HTG7, LEX3, VHL20.

In the scientific literature, the first description of microsatellite DNA in horses appeared in the early 1990s [9-13]. To date, more than 24 thousand microsatellite loci have been identified in the horse genome. Many of these loci have dozens of alleles that differ from each other in the number of tandem repeats [14-16].

Knowledge of differences in DNA structure is used in the assessment of intrapopulation diversity and identity of different breeds. A detailed study of the genetic characteristics of the population and the development of a comprehensive breeding programme are necessary for the conservation and further increase of the population [17, 18].

The aim of this study is to characterize the genetic diversity of the Kostanay horse breed by microsatellite STR loci.

**Materials and Methods.** The researches were carried out on the basis of scientific research institute of applied biotechnology NLC “A.Baitursynov Kostanay regional university “. The object of research were horses of Kostanay breed (n=30), bred in “Kazak tulpary” LLP.

For DNA isolation from hair follicles we used a commercial kit “DNA-Extran-2” of “Syntol” company (Moscow). DNA amplification was carried out by PCR in multilocus format using a commercial kit “Cordis Horse” of the company “Gordiz” (Moscow) on the amplifier ProFlex PCR system (Applied Biosystems) according to the manufacturer’s instructions. Amplification products were separated and detected by capillary electrophoresis in automatic mode on a 3500 Genetic Analyzer manufactured by Applied Biosystems. Interpretation of the analysis was performed using GeneMapper software. The final stage of the analysis of amplified fragments is the identification of alleles and establishment of genetic profiles of the studied DNA samples.

The following parameters were calculated during genetic-population analysis: allele frequencies, polymorphism level (Ae), degree of observed (Ho) and degree of observed (He) heterozygosity, fixation index (Fis) [19-21].

**Research Results.** The modern Kostanay horse breed reveals a high level of intra-breed genetic variability. In 17 STR-loci studied by us 102 alleles were identified. The number of alleles in each locus varied from 4 to 10 alleles per locus.

In a study of 30 horses of this breed, the following frequency of allele occurrence was found (Table 1).

Table 1 – Frequency of occurrence of alleles of microsatellite loci in the studied population of horses of Kostanay breed.

Locus	Alleles									
	B	C	D	F	G	L	H	I	J	K
1	2	3	4	5	6	7	8	9	10	11
AHT4							0,167	0,100	0,316	0,017

AHT5									0,200	0,267
ASB17				0,050	0,300		0,050	0,017		0,017
ASB2	0,100									0,183
ASB23						0,283		0,233	0,117	0,100
CA425						0,017		0,133	0,100	
HMS1						0,083		0,083	0,383	
HMS2						0,733	0,033	0,017		0,083
HMS3								0,267		
HMS6									0,033	0,033
HMS7						0,200			0,234	
HTG10						0,017		0,200		0,017
1	2	3	4	5	6	7	8	9	10	11
HTG4						0,017				0,201
HTG6					0,400				0,150	
HTG7										0,267
LEX3				0,067		0,233	0,100			
VHL20						0,033		0,417		
Locus	Alleles									
	M	N	O	P	Q	R	S	T	U	
AHT4			0,350	0,017	0,033					
AHT5	0,217	0,250	0,033		0,033					
ASB17	0,033	0,267	0,133		0,050	0,083				
ASB2	0,033	0,050	0,067	0,167	0,183	0,217				
ASB23							0,217			0,050
CA425	0,200	0,483	0,067							
HMS1	0,451									
HMS2	0,134									
HMS3	0,117	0,033	0,200	0,350		0,033				
HMS6	0,317	0,017	0,033	0,567						
HMS7	0,133	0,333	0,100							
HTG10	0,400		0,232				0,117	0,017		
HTG4	0,750	0,017	0,017							
HTG6	0,067		0,350				0,033			
HTG7	0,117	0,150	0,466							
LEX3	0,083	0,134	0,200	0,183						
VHL20	0,133	0,317		0,100						

As can be seen from Table 1, there are 7 alleles in the locus AHT4. The most widespread was allele J, so, its frequency was 0.316. The lowest frequency was observed for alleles K and P, they occurred with the same frequency of 0.017.

In the locus AHT5 in horses of Kostanay breed 6 alleles were revealed, the highest frequency was observed for allele K (0,267); in the second place - allele N (0,250); the lowest frequency was observed for alleles O and Q (0,033).

The ASB17 locus is the most highly polymorphic in the studied group of horses. Thus, 10 alleles were identified in it. The highest frequency is noted for allele N (0.267); the second place is occupied by allele O (0.133). The lowest frequency is characterized by alleles I (0.017) and K (0.017).

The ASB2 locus contains 8 alleles. The most common allele was the R allele (0.217). Allele M in horses of Kostanay breed was less widespread, as its frequency was 0,033.

In the ASB23 locus, the L allele (0.283) is the most frequent, with the I allele (0.233) in second place. In the studied population of horses of Kostanay breed alleles K (0,100) and U (0,050) are among the rarest.

In locus CA425 in horses of Kostanay breed 6 alleles were revealed, the highest frequency was observed for allele N (0,483); in the second place - allele I (0,133); the lowest frequency was observed for allele L (0,017).

The locus HMS1 is the lowest polymorphic in the studied group of the Kostanay breed of horses. 4 alleles were detected in it. In descending order of frequency there are alleles: M (0,451), J (0,383), L (0,083) and I (0,083).

Five alleles were identified at the HMS2 locus. Thus, in the group of horses of the Kostanay breed, allele L (0.733) was found with the highest frequency, followed by allele M (0.134). Allele I is one of the rarest and its frequency is 0.017.

Six alleles were identified at the HMS3 locus. Allele I has the highest frequency (0.267), while alleles R and N are among the rarest, with a frequency of 0.033.

In the HMS6 locus, the following distribution of alleles is observed. In the studied population of horses of the Kostanay breed, the highest frequency is noted for the allele P (0.567), the lowest - for the allele N (0.017).

In the locus HMS7 in horses of Kostanay breed 5 alleles were revealed. The frequencies of alleles in the group in descending order were: N - 0.333, J - 0.234, L - 0.200, M - 0.133, O - 0.100.

In the studied horse population 7 alleles were detected at the HTG10 locus. The highest frequency was observed for allele M (0.400); the second place was occupied by allele O (0.232); the lowest frequency was observed for alleles L, S and K (0.017).

Five alleles were detected in the HTG4 locus. In the group of horses of Kostanay breed with the highest frequency was allele M (0,750), followed by allele K (0,201). Alleles L, N and O are the least common, their frequency is the same and is 0.017.

In the HTG6 locus the following distribution of alleles is observed. In the group of horses of the Kostanay breed the greatest frequency is noted for alleles G (0,400), and O (0,350). Other alleles have a low frequency (from 0,033 to 0,150).

The HTG7 locus is one of the least polymorphic. Four alleles were identified in it. The O (0.466) and K (0.267) alleles have the highest frequency. The N (0.150) and M (0.117) alleles are the least common.

7 alleles were detected in the LEX3 locus. In horses of the Kostanay breed the most widespread was allele L (0,233). Alleles F (0.067) and M (0.083) were among the less common alleles.

Five alleles were identified at the VHL20 locus. Thus, in the group of Kostanay horses, allele I (0.417) was the most frequent, followed by allele N (0.317). The L allele is one of the rarest, and its frequency is 0.033.

Further we calculated the level of polymorphism, assessed heterozygosity, calculated the values of Wright fixation index (Table 2).

Than the lower the level of polymorphism, the lower the genetic diversity of the population. In our research the level of polymorphism varied from 1.657 in HTG4 locus to 6.250 in ASB2 locus. The average level of polymorphism was 3.758 (Table 2). In the group of Kostanay horses we studied, of the 17 identified STR loci, eight had allele counts greater than the average level of polymorphism and nine had allele counts less than the average level (from 1.657 to 3.719).

Heterozygosity is an important parameter in questions of population genetic dynamics. Heterozygosity serves as a measure of genetic variability of a population and is defined as the average frequency of heterozygous individuals at certain loci. An increase in homozygosity is accompanied by a decrease in genetic and phenotypic diversity and leads to an increase in the homogeneity of populations. In the studied group of the Kostanay breed, the observed and expected heterozygosity for all loci do not differ. The highest level of expected heterozygosity was at the ASB2 locus (0.840), and the lowest at the HTG4 locus (0.397). The average observed heterozygosity was 0.681 and expected heterozygosity was 0.696.

Table 2 – Genetic characterization of polymorphism of Kostanay horses by 17 DNA microsatellites (n=30)

Locus	Number of alleles	Level of polymorphism (AE)	Degree of heterozygosity		Fixation Index (Fis)
			Observed heterozygosity (Ho)	Expected heterozygosity (He)	
1	2	3	4	5	6

AHT4	7	3,814	0,733	0,738	0,007
AHT5	6	4,489	0,867	0,777	-0,116
ASB17	10	5,128	0,800	0,805	0,006
ASB2	8	6,250	0,900	0,840	-0,071
ASB23	6	4,813	0,867	0,792	-0,094
CA425	6	3,267	0,700	0,694	-0,009
1	2	3	4	5	6
HMS1	4	2,752	0,500	0,637	0,215
HMS2	5	1,773	0,367	0,436	0,158
HMS3	6	4,009	0,667	0,751	0,111
HMS6	6	2,353	0,667	0,575	-0,160
HMS7	5	4,286	0,800	0,767	-0,043
HTG10	7	3,719	0,667	0,731	0,088
HTG4	5	1,657	0,500	0,397	-0,261
HTG6	5	3,220	0,667	0,689	0,033
HTG7	4	3,077	0,567	0,675	0,160
LEX3	7	5,980	0,600	0,833	0,280
VHL20	5	3,303	0,700	0,697	-0,004
<b>Average</b>	<b>6</b>	<b>3,758</b>	<b>0,681</b>	<b>0,696</b>	<b>0,018</b>

For each locus, we calculated the values of the Wright fixation index. The Wright fixation index allows us to establish the deviation of heterozygous genotypes from the theoretically expected one. The index value can have both positive and negative values, in the first case it indicates the lack of heterozygotes, in the second case - their excess. For the studied Kostanay breed the shortage of heterozygotes was observed at loci AHT4, ASB17, HMS1, HMS2, HMS3, HTG10, HTG6, HTG7, LEX3; at the same time the index values were insignificant and were in the range from 0.006 to 0.280. An excess of heterozygotes was observed for the remaining loci, where the fixation index ranged from minus 0.004 at the VHL20 locus to minus 0.261 at the HTG4 locus. The mean value of Wright's fixation index showed 0.018.

#### **Conclusion.**

As a result of the study of 30 heads of horses of the Kostanay breed, we investigated and described 17 STR loci, in which 70 alleles were identified: from 4 to 10 alleles per locus. The maximum level of polymorphism was characterised by locus ASB2, and the lowest level - by locus HTG4. The studied group of the Kostanay breed was characterised by a high level of genetic diversity. The average level of observed heterozygosity was 0.681, expected heterozygosity - 0.696. In general, the average index of Fis fixation index (0.018) was determined for the group, which indicates the stability of the genetic structure of this population.

#### **REFERENCES**

- 1 <https://zooclub.ru/loshadi/porody-loshadey/kustanayskaya-loshad.shtml>
- 2 <https://my-horze.ru/kustanayskaya-poroda-loshadey-foto-i-video-harakteristiki-istoriya-mast-eksterer>
- 3 Vieira, M.L. Microsatellite markers: what they mean and why they are so useful [Text] / M.L. Vieira, L. Santini, A.L. Diniz, F. Munhoz Cde // Genet Mol Biol. – 2016. – V. 39(3). – P. 312-328. doi: 10.1590/1678-4685-GMB-2016-0027.
- 4 Tautz, D. Hypervariability of simple sequences as a general source for polymorphic DNA markers [Text] / D. Tautz // Nucleic Acids Research. – 1989. – V. 17. – P. 6463-6471. doi: 10.1093/nar/17.16.6463
- 5 Tautz, D. Notes on the definition and nomenclature of tandemly repetitive DNA sequences [Text] / D. Tautz // DNA Fingerprinting: State of the Science, Basel, Switzerland. - 1993. – V. 67. - P. 21–28. doi: 10.1007/978-3-0348-8583-6\_2.

- 6 Benson, G. Tandem repeats finder: a program to analyze DNA sequences [Text] / G. Benson // *Nucleic Acids Res.* – 1999. – V. 27. – P. 573-580. doi: 10.1093/nar/27.2.573.
- 7 Buschiazzi, E. The rise, fall and renaissance of microsatellites in eukaryotic genomes [Text] / E. Buschiazzi, N.J. Gemell // *Bioessays.* – 2006. – V. 28. – P. 1040-1050. doi: 10.1002/bies.20470.
- 8 Jarne, P. Microsatellites, from molecules to populations and back [Text] / P. Jarne, P.J. Lagoda // *Trends Ecol Evol.* – 1996. – V. 11. – P. 424-429. doi: 10.1016/0169-5347(96)10049-5.
- 9 ZHivotovskij, L.A. Mikrosatellitnaya izmenchivost' v populyacijah cheloveka i metody ee izucheniya [Tekst] / L.A. ZHivotovskij // *Vestnik VOGiS.* – 2006. – № 1. - T. 10. – S. 74–96.
- 10 Ellegren, H. Cloning of highly polymorphic microsatellites in the horse [Text] / H. Ellegren, M. Johansson, K. Sandberg, L. Andersson // *Animal Genetics.* – 1992. - V. 23. – P. 133-142. doi: 10.1111/j.1365-2052.1992.tb00032.x.
- 11 Schlötterer, C. Evolutionary dynamics of microsatellite DNA [Text] / C. Schlötterer // *Chromosoma.* – 2000. – V. 109(6). – P. 365-371. doi: 10.1007/s004120000089.
- 12 Marklund, S. Parentage testing and linkage analysis in the horse using a set of highly polymorphic microsatellites [Text] / S. Marklund, H. Ellegren, S. Eriksson, et al. // *Anim Genet.* – 1994. – V. 25. – P. 19-23. doi: 10.1111/j.1365-2052.1994.tb00050.x.
- 13 Bowling, A.T. Validation of microsatellite markers for routine horse parentage testing [Text] / A.T. Bowling, M.L. Eggleston-Scott, G. Byrns, R.S. Clark, D. Dileanis, E. Wictum // *Anim Genet.* – 1997. – V. 28. – P. 247-252. doi: 10.1111/j.1365-2052.1997.00123.x.
- 14 Chowdhary, B.P. Equine genomics [Text] / B.P. Chowdhary // Wiley-Blackwell. - 2013. - 36 p.
- 15 Bailey, E.F. Horse genetics [Text] / E.F. Bailey, S.A. Bailey // Brooks. CABI. - 2013. - 272 p.
- 16 Kim, S.M. Assessment of genetic diversity using microsatellite markers to compare donkeys (*Equus asinus*) with horses (*Equus caballus*) [Text] / S.M. Kim, S.W. Yun, G.J. Cho // *Anim Biosci.* - 2021. - V. 34(9). – P. 1460-1465. doi: 10.5713/ab.20.0860.
- 17 Bejshova, I.S. Geneticheskoe raznoobrazie aberdin-angusskoj porody s ispol'zovaniem mikrosatellitnyh markerov [Tekst] / I.S. Bejshova, T.V. Ul'yanova, A.ZH. Sidarova // *Fylym zhəne bilim, g.Ural'sk.* – 2020. - № 4-1 (61). – S. 26-31.
- 18 Nei, M. Sampling variances of heterozygosity and genetic distance [Text] / M. Nei, A.K. Roychoudhury // *Genetics.* – 1974. – V. 76. – P. 379-390. doi: 10.1093/genetics/76.2.379.
- 19 Wright, S. Isolation by distance under diverse systems of mating [Text] / S. Wright // *Genetics.* - 1946. - V. 31. - № 1. - P. 39-59. doi: 10.1093/genetics/31.1.39.
- 20 Nei, M. Accuracy of estimated phylogenetic trees from molecular data. II. Gene frequency data [Text] / M. Nei, F. Tajima, Y. Tateno // *Journal of Molecular Evolution.* – 1983. – V. 19. – P. 153–170. doi: 10.1007/BF02300753.
- 21 Merkur'eva, E.K. Geneticheskie osnovy selekcii v skotovodstve [Tekst] / E.K. Merkur'eva // Moskva «Kolos»–1977. – 174 s.

## ТҮЙІН

Мақалада ДНҚ микросателлиттерінің 17 локусы бойынша: АНТ4, АНТ5, АСВ17, АСВ2, АСВ23, СА425, НМС1, НМС2, НМС3, НМС6, НМС7, НТГ10, НТГ4, , НТГ7, ЛЕХ3, VHL20 Қостанай тұқымының генетикалық әртүрлілігін талдау нәтижелері келтірілген. Зерттеу үшін биологиялық материал ретінде Қостанай тұқымының 30 бас жылқысының (Қостанай қ.) шаш талдары пайдаланылды.

Жұмыстың мақсаты микросателлиттік STR-локустар бойынша Қостанай тұқымды жылқылардың генетикалық әртүрлілігін сипаттау болды.

Жануарлардың генотипін анықтау ПЦР әдісімен орындалды, күшейту өнімдерін бөлу және анықтау капиллярлық электрофорез арқылы 8 капиллярлы генетикалық анализатор 3500 Genetic Analyzer (Applied Biosystems, АҚШ) арқылы жүзеге асырылды. Нәтижелер GeneMapper бағдарламасының көмегімен түсіндірілді, статистикалық өңдеу Microsoft Excel 2010 бағдарламасы арқылы орындалды. Келесі параметрлер есептелді: аллель жиіліктері, полиморфизм деңгейі (Ae), байқалу дәрежесі (Ho) және теориялық есептелген (He) гетерозиготалық, фиксация индексі (Fis).

Қостанай облысы Заречное ауылында өсірілетін жылқылардың қостанай тұқымын генотиптеу нәтижесінде зерттелетін микросателлиттік локустар үшін маркерлердің әрқайсысының полиморфизмін сипаттайтын мәліметтер алынды. Қостанай тұқымды жылқылардағы 17 микросателлиттік ДНҚ локустары үшін 102 аллель анықталды. Бір локустағы аллельдердің саны 4-тен 10-ға дейін өзгерді. Зерттеу тобы үшін ең ақпаратты локустар аллельдердің ең көп саны бар локустар (АСВ17, АСВ2), ең аз ақпарат беретін локустар (НМС1, НТГ7). Ең жоғары байқалған

гетерозиготалық ASB2 локусында (0,900), ал ең төменгісі HMS2 локусында (0,367) болды. Күтілетін гетерозиготалықтың орташа деңгейі – 0,696, бақыланатын гетерозиготалық – 0,681, орташа фиксация индексі – 0,018.

Осылайша, Қостанай жылқы тұқымының зерттелетін микросателлиттік ДНК локустарының барлық зерттелген көрсеткіштері бойынша полиморфизмге тән белгілер анықталды.

### РЕЗЮМЕ

В статье представлены результаты анализа генетического разнообразия костанайской породы 17-ти локусам микросателлитов ДНК, включая АНТ4, АНТ5, ASB17, ASB2, ASB23, СА425, HMS1, HMS2, HMS3, HMS6, HMS7, НТГ10, НТГ4, НТГ6, НТГ7, LEX3, VHL20. В качестве биологического материала для исследований использовались волосьяные луковицы 30 голов лошадей костанайской породы (г. Костанай, п. Заречный).

Целью работы было охарактеризовать генетическое разнообразие лошадей костанайской породы по микросателлитным STR-локусам.

Генотипирование животных проводили методом ПЦР, разделение и детекцию продуктов амплификации осуществляли методом капиллярного электрофореза на 8-капиллярном генетическом анализаторе 3500 GeneticAnalyzer (AppliedBiosystems, США). *Интерпретация результатов осуществлялась в программе GeneMapper*, статистическую обработку проводили с использованием программы «Microsoft Excel 2010». Рассчитывали следующие параметры: частоты встречаемости аллелей, уровень полиморфности ( $A_e$ ), степень наблюдаемой ( $H_o$ ) и ожидаемой ( $H_e$ ) гетерозиготности, индекс фиксации ( $Fis$ ).

В результате генотипирования костанайской породы лошадей, разводимых в п. Заречное Костанайского района по изучаемым микросателлитным локусам были получены данные, характеризующие полиморфизм каждого из маркеров. По 17 микросателлитным локусам ДНК у лошадей костанайской породы было выявлено 102 аллеля. Число аллелей на локус варьировало от 4 до 10. Наиболее информативными для исследуемой группы явились локусы с наибольшим числом аллелей (ASB17, ASB2), наименее информативными - с минимальным (HMS1, НТГ7). Наибольшая наблюдаемая гетерозиготность была в локусе ASB2 (0,900), а наименьшая – в локусе HMS2 (0,367). Средний уровень ожидаемой гетерозиготности составлял 0,696, наблюдаемой гетерозиготности – 0,681, средний индекс фиксации имел величину, равную 0,018.

Таким образом, выявлены характерные особенности полиморфизма по всем исследованным показателям изученных микросателлитных локусов ДНК костанайской породы лошадей.