Сәкен Сейфуллин атындағы Қазақ агротехникалық зерттеу университетінің Ғылым жаршысы (пәнаралық) =Вестник науки Казахского агротехнического исследовательского университета имени Сакена Сейфуллина (междисциплинарный). — Астана: С. Сейфуллин атындағы Қазақ агротехникалық зерттеу университеті, 2024. -№ 3 (122). - Р. 84-93.- ISSN 2710-3757, ISSN 2079-939X

doi.org/ 10.51452/kazatu.2024.3(122).1756 UDC 636.1.082

Breeding work with kazakh horses Zhabe type

Kairat Zh. Iskhan¹ , Abzal K. Makhmutov² , Vitaly M. Strochkov³ , Dinara I. Kabylbekova² , Shinara N. Kassymbekova² , Zhanat Zh. Bimenova¹

¹N.O. Bazanova Department of Physiology, Morphology and Biochemistry, Faculty of Veterinary Kazakh National Agrarian Research University, Almaty, Kazakhstan

²Department of obstetrics, surgery and reproductive biotechnology, Faculty of Veterinary Kazakh National Agrarian Research University, Almaty, Kazakhstan

³Senior Researcher of the laboratory "Green Biotechnology and Cellular Engineering Kazakh National Agrarian Research University, Almaty, Kazakhstan

Corresponding author: Kairat Zh. Iskhan: Kayrat_ishan@mail.ru
Co-authors: (1: AK) Makhmutov: abazik-83@mail.ru; (2: VS) vstrochkov@gmail.com
(3: DK) dna_03@bk.ru; (4: KN) kasymbekova-s@mail.ru; (6: ZhB) zhan_225@mail.ru
Received: 14-08-2024 Accepted: 18-09-2024 Published online: 30-09-2024

Abstract

Background and Aim. Kazakh horses of Zhabe type differ from local horses in their higher live weight and larger body measurements. Breeding work with Kazakh horses of the Zhabe type is carried out at Tailak farm in Zharminsky district of East Kazakhstan through targeted reproduction, cultivation, and widespread use of the best individuals based on their origin, exterior, productivity, adaptation to year-round grazing, and quality of offspring from stallions and mares. Individuals that are not up to these standards are strictly culled. The aim of the research is to determine meat productivity and study genetic characteristics of a sample of modern population of Kazakh horses of Zhabe type using DNA markers.

Materials and Methods. The material for the study was DNA genotyping data from 20 horses of the Kazakh breed type Zhabe. The horses were genotyped according to 17 STR loci recommended by the International Society for Animal Genetics (ISAG). The international alphabetical code was used to identify alleles. Genetic and population analyses were performed using the GenAIEx software 6.5. The following indicators were calculated: the average number of alleles per locus (Na), the effective number of alleles (Ne), levels of expected (He) and observed heterozygosity (Ho), and inbreeding coefficient (FIS).

Results. A study on 17 STR loci of DNA in Kazakh horses Zhabe type has shown that they have a unique allele pool with a significant number of identified alleles and high genetic variability. The average inbreeding coefficient (FIS) is negative (-0.059), indicating that the genetic diversity of this breed is preserved within this group.

Conclusion. The improvement of these horses is achieved through breeding and cultivation of animals with high genetic potential for productivity, which is passed down through generations of descendants. This is done by carefully selecting horses with desirable traits for breeding.

Key words: exterior; live weight; measurements; STR markers; selection.

Introduction

In the context of the qualitative transformation of horse breeding in Kazakhstan, the role of Kazakh horses Zhabe type as meat and dairy animals is exceptional. They occupy the largest proportion of the breeds used in production, accounting for 34.5% of all horses in the country. These animals are highly valued for their ability to adapt to various living conditions, their endurance, and their meat and dairy qualities.

At the age of two and a half years, Zhabe horses can reach a live weight of 350-370 kilograms on a single feed, making them highly profitable for meat production [1].

Rzabaev et al. [2] noted that breeding work with Zhabe horses began in the Emba stud farm in the Aktobe region in the 1930s, and many generations of breeders have worked to create the modern Zhabe horse. The basis for the modern population of Zhabe type horses was formed by four genealogical lines of stud stallions from the Emben stud farm - Zamok, born in 1927; Berkut, born in 1929; Zaur, born in 1929, and Pisatel, born in 1928. These lines produced the most numerous and high-quality offspring, which played a major role in creating the factory lines Zubr 46-59 and Barhat 15-57 in 1982, followed by the creation and testing of the lines Bracelet 13-74, Zadornyy 51-76 and Pamir 127-78 at the Altai Karpyk Saydaly Sary Tok stud farm in the Pavlodar region in 2010 [3, 4].

In addition to purebred breeding, Kazakh Zhabe horse type were used in crossbreeding with the Bashkir breed to improve meat and adaptability to year-round grazing conditions. Positive results were also obtained from crossing Yakut mares with Zhabe stallions. With the purebred breeding of Kazakh horses of the Zhabe type, based on their genetic characteristics, it is possible to not only obtain individual outstanding animals, but also create genotypes that have great breeding value.

With the development of molecular genetic methods and DNA technology, it became possible to evaluate differences in phenotype between breeds and their structural elements. This is important for effective planning of animal breeding, as well as for conservation of endangered breeds. Microsatellite polymorphism, also known as short tandem repeats (STRs), was first described in horses by Ellegren et al. [5, 6] and Marklund et al. [7]. Microsatellites are used to assess genetic diversity and build genetic maps. They have also been used to map quantitative trait loci and test pedigrees [8, 9]. STRs have become a valuable tool for verifying pedigrees and registering horses [10, 11].

In 1998, an international group of researchers organized a seminar on equine genetics at the International Society for Animal Genetics (ISAG). This group created a panel of nine STRs for typing horse DNA. In 2011, three more STR loci were added (ASB17, ASB23, and HMS2) [12].

Studying microsatellite loci can help us solve several problems. It can determine whether there is a population structure within a species (in space, time, or other aspects). It can also assess the connectivity between populations through gene flow. Finally, it can evaluate the effective population size and genetic diversity within a given population [13].

The purpose of this research is to investigate the meat productivity and genetic structure of the Zhabe type of the Kazakh horse using microsatellite DNA markers.

Materials and Methods

To study the meat quality of Kazakh horses of the Zhabe type, a control slaughter was conducted after the autumn feeding at the slaughterhouse of the Tailak farm in the East Kazakhstan region. The study used the method of determining the meat productivity of horses [14] and in accordance with STRK 1303-2004 [15], which are adopted in the technical specifications of the meat industry. The material for the study was DNA genotyping data from 20 horses of the Kazakh breed type Zhabe. The sample consisted of 10 adult mares and 10 outstanding sire stallions, with measurements typical of Kazakh horses of the Zhaba type, to identify unrelated individuals, which will then be sent for whole genome sequencing. STR-genotyping was conducted in the laboratory of genetics Institute of Applied Biotechnology at the Kostanay Regional University named after Akhmet Baitursynov, using the ABI 3100 Applied Biosystems genetic analyzer. The horses were genotyped according to 17 STR loci recommended by the International Society for Animal Genetics (ISAG): AHT4, AHT5, ASB2, ASB17, ASB23, CA425, HMS1, HMS2, HMS3, HMS6, HMS7, HTG4, HTG6, HTG7, HTG10, LEX3, VHL20. The international alphabetical code was used to identify alleles. Genetic and population analyses were performed using the GenAIEx software 6.5. The following indicators were calculated: the average

number of alleles per locus (Na), the effective number of alleles (Ne), levels of expected (He) and observed heterozygosity (Ho), and inbreeding coefficient (FIS).

Results

At the Tailak farm, located in the East Kazakhstan region, Kazakh horses Zhabe type are bred using pure breeding methods. The goal of this method is to preserve and improve the pedigree qualities of these horses.

The biological features of pure breeding are aimed at preserving and enhancing the productivity and hereditary characteristics of horses of the desired type. The table below shows the class composition of the farm Tailak horse population by gender and age group for the year 2023.

Tuble 1 Class composition of Tunak latin horses by gender and age groups							
Gender and age	Total	Including					
group	heads	elite		I class		II class	
		n	%	n	%	n	% Breeding
Stallions	26	26	100	-	-	-	-
Mares	449	171	38.1	180	40.1	98	21.8
Stallions 2.5 years	old 139	54	38.8	60	43.2	25	18.8
Stallions 1.5 years	old 121	39	32.23	47	38.84	35	28.93
Maresки 2.5years	old 137	49	35.8	56	40.9	32	23.3
Mares 1.5 years	old 150	47	31.3	58	38.7	45	30.0

Table 1 – Class composition of Tailak farm horses by gender and age groups

As can be seen from the data presented in Table 1, all of the breeding stallions (n=26) were rated only as elite. Of the 499 mares on the farm, 38.1% were elite, 40.1% first class, and 21.8% second class. 2.5-year-old stallions, in the number of 139 heads, had 54 elite heads (38.8%), 60 heads class I (43.2%), and 25 heads class II (18%). Stallions 1.5 years old, in the number of 121 heads, were classified as: elite - 32%, class I - 39%, and class II - 29%. Mares 2.5 and 1.5 years old had an elite percentage ranging from 36% to 32% for class I and 24% to 27% for class II.

The average measurements and live weights of adult horses are compared to the data from the guidelines for the evaluation of productive horses in Table 2.

Indicators		Stallions		Mares		
	according to the instructions	farm Tailak n=26	result	according to the instructions	farm Tailak n=449	result
Height at the withers, cm	143	145.7±0.57	±2.7	140	142.8±0.52	±2.8
Oblique body length, cm	148	152.3±0.61	±4.3	145	147.6±0.59	±2.6
Chest circumference, cm	177	183.5±0.73	±6.5	175	179.7±0.68	±4.7
Metacarpal circumference, cm	19.0	19.5±0.19	±0.5	18.5	19.0±0.12	±0.5
Live weight, kg	430	491.4±3.78	±61.4	410	445.2±.,12	±35.2

Table 2 – Measurements and live weight of adult Kazakh horses of Zhabe type

From the data in Table 2, it can be seen that the average body measurements and live weight of breeding stallions are above the standard for class I horses. Specifically, they are 2.7 centimeters taller at the withers, 4.3 centimeters longer in oblique body length, 6.5 centimeters broader in chest circumference, 0.5 cm larger in metacarpal circumference, and 61.4 kg heavier in live weight, which is a 14.3% increase. For mares, the corresponding averages are 2.8 cm taller, 2.6 cm longer, 0.5 cm wider, and 35.2 kg heavier, representing an 8.6% increase in live weight compared to the standard.

Table 3 shows the body measurements and live weight for 1.5- and 2.5-year-old Kazakh horse Zhabe type.

Table 3 – Measurements and	l live	weight	of horses
----------------------------	--------	--------	-----------

			Live				
Age, years	n	Height at the withers	Oblique body length	Chest circumference	Metacarpal circumference	weight, kg	
	stallions						
1.5	121	132.6±0.57	131.4±0.62	156.3±0.72	16.1±0.13	286.5±3.9	
2.5	193	138.3±0.69	139.5±0.73	165.6±0.79	17.2±0.11	365.7±4.6	
	mares						
1.5	137	131.2±0.61	130.4±0.68	154.8±0.68	16.0±0.12	270.3±4.1	
2.5	150	136.5±0.72	136.8±0.75	161.2±0.74	16.5±0.10	334.6±3.8	

Based on the data from Table 3, we can observe that 1.5-year-old male horses have the following body measurements in centimeters: height at the withers is 132.6 cm, oblique body length is 131.4 cm, chest circumference is 156.3 cm, metacarpal circumference is 16.1 cm, and live weight is 286.5 kg. For 1.5-year-old mares, the corresponding measurements are as follows: height at the withers is 131.2 cm, oblique trunk length is 130.4 cm, chest circumference is 154.8 cm, metacarpal circumference is 16 cm, and live weight is 270.3 kg.

Stallions that are two and a half years old have good body measurements. Their height at the withers is 138.3 centimeters, their oblique body length is 139.5 centimeters, chest circumference is 165.6 centimeters, metacarpal circumference is 17.2 centimeters and their live weight is 365.7 kilograms. Mares have a slightly smaller height at the withers - 136.5 centimeters - and a slightly shorter oblique body length - 136.8 centimeters. However, they still have a large chest circumference - 161.2 centimeters - and metacarpal circumference - 16.5 centimeters. The average values of these measurements and live weight meet the requirements for elite and I-class horses. This indicates good growth and development from an early age, achieved under conditions of year-round grazing and breeding.

In autumn, after the rains, the secondary vegetation of the pasture begins to grow. This increases the nutritional value of the grass, the air temperature decreases and blood-sucking insects disappear. These factors all contribute to lengthening the grazing time for horses and increasing their live weight during this period.

Table 4 shows the changes in stallion live weight during the autumn feeding period.

Table 4 – Live weight and average daily gains of stallions during the autumn feeding period (n=10 heads)

Groups	Unit		Weigh-in date (2023)					
		5.10	15.10	25.10	4.11	14.11	24.11	
Stallions 1.5	kg	278.7	281.8	283.8	284.8	285.3	285.7	
years old	g	-	310	200	100	50	40	
Stallions 2.5	kg	353.8	357.2	359.5	360.6	361.4	361.8	
years old	g	-	340	230	40	80	40	

The most intense feeding period occurred between October 5 and 25, during which time the horses gained between 255 and 285 grams per day. After this period, the gains began to decrease as the horses reached their peak level of fatness.

According to the data in Table 4, the stallions that survived the summer heat had a lower average body fat content than usual. After the 20th day of feeding, their daily weight gain decreased gradually, reaching only 40 grams in the last 11 days.

To assess the meat productivity of Kazakh horses Zhabe type, a slaughter of 2.5-year-old stallions was performed on November 24, 2023 at the Tailak slaughterhouse after the autumn feeding. The results showed that the carcass weight of the stallions after feeding was quite high, reaching 194 kg.

The slaughter yield was 53.9% and the pre-slaughter live weight was 360 kg. When analyzing the morphological composition of each cut and the entire carcass, we determined the proportion of boneless meat and bone (Table 5).

TC 1 1 C N C 1 1 1 1 1	•,•	C1	1 1
Table 5 – Morphological	composition	ot horse card	easses hy orade
radic 5 Widipilological	composition	or morse care	asses by grade

	Tissue						
Carcass cuts	Pu	ılp	Bone				
	kg	%	Kg	%			
Zhaya	1.8	1.1		-			
Kazy	20.0	12.3	1.4	4.5			
I Grade	77.3	47.5	11.4	36.4			
II Grade	59.8	36.8	14.0	44.7			
III Grade	3.8	2.3	4.5	14.4			
Total in carcass	162.7	100	31.3	100			

From the above data, we can see that the highest pulp yield in the carcasses of stallions was observed in Grade I at 47.5%, followed by Grade II at 36.8% and kazy at 12.3%. The lowest amount of pulp was found in Grade III at 2.3%. The largest number of bones in the carcass was found in Grade II at 44.7%, followed by Grade I at 36.4% and Grade III with 14.4% bones. The smallest number of bones was found in kazy at 4.5%. Overall, there was 5.2 kg of meat per 1 kg of bone.

Based on our analysis of the morphological composition of stallion carcasses, we can conclude that the pulp yield increased in younger animals after autumn feeding.

The modern Kazakh horse breed of the Zhabe type shows a high level of intra-breed genetic variability within the sample of studied horses (Fig. 1)

111 different alleles were found in the 17 short tandem repeat (STR) loci that were studied. The number of alleles in 20 horses tested per locus ranged from 4 to 9, with an average of 6.529 alleles for each locus. The highest number of alleles was found in the autosomal loci ASB17 (9 alleles), AB2 (8 alleles), CA425 (8 alleles). HTG10 and VHL20 (8 loci each) Table 6.

Table 6 – Alleles identified in the experimental sample of the Kazakh horse breed Zhabe type (n=20)

No॒	Locus	Localization (chromosome)	Number of alleles per locus (Na)	Alleles
1	AHT4	24	7	H**, O**, N, K*, L*, J*, I*
2	AHT5	8	6	K**, M*, J**, O**, N, I*
3	ASB2	15	8	K, O*, Q, B, N, M*, P*, I*
4	ASB17	2	9	H*, R**, N, M, L*, G*, Q*, F*, K*
5	ASB23	3	7	K**, U, J*, S**, I, H*, L*
6	CA425	28	8	G, O*, L*, N**, F*, M**, I*, J*
7	HMS1	15	5	J**, M**, K*, N*, I*
8	HMS2	10	6	J, K, H, I**, M*, L
9	HMS3	9	6	P**, Q*, O, M**, R*, N*
10	HMS6	4	6	O**, Q*, L, P, M, K
11	HMS7	1	6	J*, L**, M*, K*, N**, O*
12	HTG4	9	5	M**, P*, L, K, O*
13	HTG6	15	5	J, O**, I, M*, G
14	HTG7	4	4	K**, O**, M**, N
15	HTG10	21	8	M, Q*, R, O**, P*, N*, S*, L*
16	LEX3	X	7	L**, N, M*, F*, K*, P*, H*
17	VHL20	30	8	M, Q, I, N, R, O, P, J

Notes: * alleles that are rare for the population with an occurrence frequency of <5.0%

^{**} alleles with a frequency of occurrence ≥50.0%

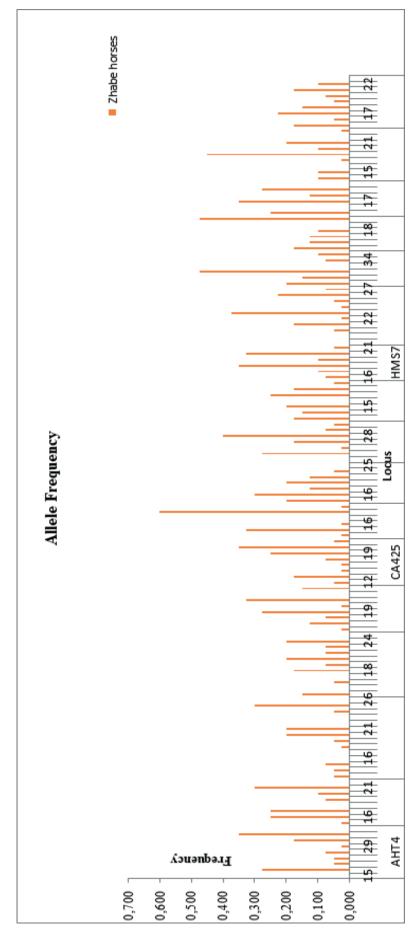


Figure 1 – Allele frequencies for the population of Kazakh horses breed type Zhabe (n=20) with a graph showing the distribution of loci for codominant data

The number of effective alleles at each locus varied significantly, ranging from 2,139 (HMS1) to 6,557 (ASB2), with an average of 4,340 alleles per locus. The observed heterozygosity also varied significantly, from 0.400 (LEX3) to 1,000 (AHT5), with an average of 0.794. (Table 7).

Table 7 – Genetic characteristics of the Kazakh horse breed type Zhabe according to 17 STR DNA loci (n=20)

Locus	Na	Ne	Но	Не	FIS
AHT4	7	4.167	0.900	0.760	-0.184
AHT5	6	4.324	1.000	0.769	-0.301
ASB2	8	6.557	0.850	0.848	-0.003
ASB17	9	5.369	0.850	0.814	-0.045
ASB23	7	4.420	0.850	0.774	-0.099
CA425	8	4.396	0.700	0.773	0.094
HMS1	5	2.139	0.700	0.533	-0.315
HMS2	6	4.908	0.850	0.796	-0.068
HMS3	6	3.636	0.850	0.725	-0.172
HMS6	6	5.298	0.850	0.811	-0.048
HMS7	6	3.902	0.800	0.744	-0.076
HTG4	5	3.292	0.900	0.696	-0.293
HTG6	5	3.361	0.800	0.703	-0.139
HTG7	4	3.620	0.600	0.724	0.171
HTG10	8	4.278	0.700	0.766	0.086
LEX3	7	3.653	0.400	0.726	0.449
VHL20	8	6.452	0.900	0.845	-0.065
Average	e value*	4.340	0.794	0.753	-0.059

Na – number of detected alleles; Ne – number of effective alleles; Ho – observed heterozygosity He – expected heterozygosity; FIS – individual fixation index

Discussion and Conclusion

Based on the results of the study, the average number of alleles per locus (Na), the effective number of alleles (Ne), and the expected (He) and observed (Ho) levels of heterozygosity indicate that the intrapopulation genetic diversity of the Kazakh horses Zhabe type is high. This suggests that this breed has significant genetic potential. FIS is an individual fixation index, which indicates a decrease in heterozygosity due to non-random mating and is a measure of the difference in genotypic frequencies from those expected in Hardy-Weinberg equilibrium within subpopulations, in terms of either a lack or an excess of heterozygotes.

At FIS >0, there is a deficit of heterozygous individuals (related mating), while at FIS <0, there is an excess of heterozygotes (unrelated mating). At FIS=0, mating is random. The highest calculated values of FIS were observed for the loci HTG7 and LEX3, with averages of 0.171 and 0.449, respectively. The average FIS value was -0.059, indicating that the inbreeding coefficient is negative, suggesting that the genetic diversity within the Kazakh horses Zhabe type is maintained within the analyzed population.

Breeding work with Kazakh horses Zhabe type is carried out at the Tailak farm in the Zharminsky district of East Kazakhstan region. This involves the purposeful reproduction, cultivation, and widespread use of horses with the best origin, exterior, productivity, and adaptability to year-round grazing. Strict culling is also used to remove the worst individuals based on these characteristics.

Kazakh horses Zhabe type differ from other local horses by their higher live weight and larger body measurements. The results of a study on 17 short tandem repeat (STR) loci in the DNA of Kazakh Zhabe horses indicate that they have a allele pool with a significant number of identified alleles and high genetic diversity. These findings will be used to compare the allele pools of other local breeds with similar productive characteristics and to update the genetic database.

Authors' Contributions

KI, AM and VS: Conceptualized and designed the study, conducted a comprehensive literature search, analyzed the gathered data and drafted the manuscript. DK, ShK and ST: Conducted the final revision and proofreading of the manuscript. All authors have read, reviewed, and approved the final manuscrip.

Information on funding

This work was carried out within the framework of grant funding for scientific and (or) and technical projects for 2022–2024 of the Ministry Education and Science of the Republic of Kazakhstan AP19677892 "Preservation and assessment of the genetic diversity of horses of the Kazakh breed using whole genome sequencing".

References

- 1 Акимбеков, АР., Юлдашбаев, ЮА. (2017). Продуктивность казахских лошадей типа жабе при разведении по линиям. Зоотехния, 5, 13.
- 2 Рзабаев, С., Рзабаев, ТС, Рзабаев, КС. (2021). Высокопродуктивный генофонд местных пород лошадей табунного содержания республики Казахстан. Актобе: 83.
- 3 Рзабаев, С., Рзабаев, ТС, Рзабаев, КС. (2022). Селекционные достижения по продуктивному коневодству Актюбинской популяции за годы независимости Казахстана Актобе: 84.
- 4 Кузнецов, ВМ. (2021). Оценка генетической дифференциации популяций молекулярным дисперсионным анализом (аналитический обзор). *Аграрная наука Евро-Северо-Востока*, 22(2), 167-187.
- 5 Ellegren, H., Jihansson, M., Sandberg, K., Andersson, L. (1992). Cloning of highly polymorphic microsatellites in the horse. Animal Genetics, 23, 133-42. DOI: 10.1111/j.1365-2052. 1992.tb00032.x.
- 6 Marklund, S., Ellegren, H., Eriksson, S., Sandberg, K., Andersson, L. (1994). Parentage testing and linkage analysis in the horse using a set of highly polymorphic horse microsatellites. *Animal Genetics*, 5, 19-23.
- 7 Li, C., Wang, Z., Liu, B. Yang, Sh., Zhu, Zh., Fan, B., Shuhong Zhao, M.Y., Li, K. (2004). Evaluation of the genetic relationship among ten Chinese indigenous pig breeds with twenty-six microsatellite markers. *Asian-Australas Journal of Animal Scienes*, 17, 441-444. DOI:10.5713/ajas.2004.441.
- 8 Zhang, JH, Xiong, YZ, Deng, CY. (2005). Correlations of genic heterozygosity and variances with heterosis in a pig population revealed by microsatellite DNA marker. *Asian-Australas Journal of Animal Scienes*, 18, 5: 620-625.
- 9 Bowling, AT, Eggleston-Stott, ML, Byrns, G., Clark, RS, Dileanis, S., Wictum, E. (1997). Validation of microsatellite markers for routine horse parentage testing. *Animal Genetics*, 28, 247-52.
- 10 Van de Goor, LH, van Haeringen, WA, Lenstra, JA. (2011). Population studies of 17 equine STR for forensic and phylogenetic analysis. *Animal Genetics*, 42(6), 627-633.
- 11 Галинская, Т., Щепетов, Д., Лысенков, С., (2019). Предубеждения о микросателлитных исследованиях и как им противостоять. *Генетика*, 55, 617-632.
 - 12 Методика определения мясной продуктивности лошадей. (1974). ВНИИК, Москва: 5-22.
- 13 Стандарт Республики Казахстан. СТ РК 1303-2015 Мясо и мясные продукты. Изделия национальные конские. (2015). Технические условия. 34.
- 14 Van De Goor, LHP, Panneman, H., Van Haeringen, WA. (2010). A proposal for standardization in forensic equine DNA typing: allele nomenclature for 17 equine-specific STR loci. *Animal Genetics*, 41(2), 122-127.
- 15 Peakall, R., Smouse, PE. (2012). GenAlEx 6.5: genetic analysis in Excel. Population genetic software for teaching and research an update. *Bioinformatics*, 28, 2537-2539.

References

1 Akimbekov, AR, Yuldashbaev, YuA. (2017). Produktivnost' kazahskih loshadej tipa zhabe pri razvedenii po linijam. *Zootehniya*, 5, 13. [In Russ].

- 2 Rzabaev, S., Rzabaev, TS, Rzabaev, KS. (2021). Vysokoproduktivnyi genofond mestnyh porod loshadej tabunnogo soderzhaniya respubliki Kazahstan. Aktobe: 83. [In Russ].
- 3 Rzabaev, S., Rzabaev, TS, Rzabaev, KS. (2022). Selekcionnye dostizhenija po produktivnomu konevodstvu Aktyubinskoi populyacii za gody nezavisimosti Kazahstana. Aktobe: 84. [In Russ].
- 4 Kuznecov, VM. (2021). Ocenka geneticheskoi differenciacii populyacii molekulyarnym dispersionnym analizom (analiticheskii obzor). *Agrarnaya nauka Evro-Severo-Vostoka*, 22(2), 167-187. [In Russ].
- 5 Ellegren, H., Jihansson, M., Sandberg, K., Andersson, L. (1992). Cloning of highly polymorphic microsatellites in the horse. Animal Genetics, 23, 133-42. DOI: 10.1111/j.1365-2052. 1992.tb00032.x.
- 6 Marklund, S., Ellegren, H., Eriksson, S., Sandberg, K., Andersson, L. (1994). Parentage testing and linkage analysis in the horse using a set of highly polymorphic horse microsatellites. *Animal Genetics*, 5, 19-23.
- 7 Li, C., Wang, Z., Liu, B. Yang, Sh., Zhu, Zh., Fan, B., Shuhong Zhao, MY, Li, K. (2004). Evaluation of the genetic relationship among ten Chinese indigenous pig breeds with twenty-six microsatellite markers. *Asian-Australas Journal of Animal Scienes*, 17, 441-444. DOI:10.5713/ajas.2004.44110.
- 8 Zhang, JH, Xiong, YZ, Deng, CY. (2005). Correlations of genic heterozygosity and variances with heterosis in a pig population revealed by microsatellite DNA marker. *Asian-Australas Journal of Animal Scienes*, 18, 5: 620-625.
- 9 Bowling, AT, Eggleston-Stott, ML, Byrns, G., Clark, RS, Dileanis, S., Wictum, E. (1997). Validation of microsatellite markers for routine horse parentage testing. *Animal Genetics*, 28, 247-52.
- 10 Van de Goor, LH, van Haeringen, WA, Lenstra, JA. (2011). Population studies of 17 equine STR for forensic and phylogenetic analysis. *Animal Genetics*, 42(6), 627-633.
- 11 Galinskaja, T., Shhepetov, D., Lysenkov, S., (2019). Predubezhdenija o mikrosatellitnyh issledovanijah i kak im protivostojat'. Genetika, 55, 617-632. [In Russ].
 - 12 Metodika opredelenija mjasnoj produktivnosti loshadei. (1974). VNIIK, Moskva: 5-22. [In Russ].
- 13 Standart Respubliki Kazahstan. ST RK 1303-2015 Myaso i myasnye produkty. Izdeliya nacional'nye konskie. (2015). Tehnicheskie usloviya, 34. [In Russ].
- 14 Van De Goor, LHP, Panneman, H., Van Haeringen, WA. (2010). A proposal for standardization in forensic equine DNA typing: allele nomenclature for 17 equine-specific STR loci. *Animal Genetics*, 41(2), 122-127.
- 15 Peakall, R., Smouse, PE. (2012). GenAlEx 6.5: genetic analysis in Excel. Population genetic software for teaching and research an update. *Bioinformatics*, 28, 2537-2539.

Қазақ жабе типіндегі жылқыны асылдандыру жұмыстары

Исхан Қ.Ж., Махмутов А.Х., Строчков В.М., Кабылбекова Д.И., Касымбекова Ш.Н., Бименова Ж.Ж.

Түйін

Негізі және мақсаты. Жабе типті қазақ жылқылары жергілікті жылқылардан тірі салмағының жоғарылығымен және денесінің үлкендігімен ерекшеленеді. Шығыс Қазақстан облысы, Жарма ауданындағы «Тайлақ» шаруа қожалығында «Жабе» типті қазақ жылқыларымен асыл тұқымды мал тұқымын асылдандыру жұмысы, олардың шығу тегін, сыртқы түрін, өнімділігін, жыл бойы жайылымға жарамдылығын және айғырлар мен биелердің ұрпақтарының сапасын ескере отырып, үздік дараларды мақсатты түрде көбейту, өсіру және кеңінен пайдалану жолымен жүргізілді. Осы сипаттарға сәйкес келмейтіндерінен қатаң түрде бас тартылады. Зерттеудің мақсаты ет өнімділігін анықтау және ДНҚ маркерлерінің көмегімен жабе типті қазақ жылқыларының қазіргі популяциясының үлгісінің генетикалық сипаттамаларын зерттеу болып табылады.

Материалдар мен әдістер. Зерттеуге материал ретінде Жабе типті қазақ тұқымды 20 жылқының ДНҚ генотиптік деректері алынды. Жылқылар Халықаралық жануарлар генетикасы қоғамы (ISAG) ұсынған 17 STR loci бойынша генотиптелді. Аллельдерді анықтау үшін халықаралық алфавиттік код қолданылды. Генетикалық және популяциялық талдаулар GenAIEx

бағдарламалық құралының 6.5 көмегімен орындалды. Төмендегі көрсеткіштер есептелді: бір локусқа келетін аллельдердің орташа саны (Na), аллелдердің тиімді саны (Ne), күтілетін (He) және байқалған гетерозиготалық (Ho) деңгейлері және инбрединг коэффициенті (FIS).

Нәтижелер. Жабе типті қазақ жылқыларының ДНҚ-ның 17 STR локусын зерттеу олардың анықталған аллельдердің айтарлықтай саны мен жоғары генетикалық өзгергіштігі бар бірегей аллельдік қоры бар екенін көрсетті. Орташа инбридинг коэффициенті (FIS) теріс (-0,059), бұл тұқымның генетикалық әртүрлілігі осы топ ішінде сақталғанын көрсетеді.

Қорытынды. Бұл жылқылардың жетілдірілуі ұрпақтан-ұрпаққа берілетін өнімділік үшін генетикалық потенциалы жоғары жануарларды өсіру және өсіру арқылы жүзеге асырылады. Бұл өсіруге қажетті қасиеттері бар жылқыларды мұқият таңдау арқылы жасалады.

Кілт сөздер: тірі салмақ; экстерьер; селекция; STR маркерлер; өлшемдер; таңдау.

Племенная работа с казахскими лошадьми типа Жабе

Исхан К.Ж., Махмутов А.Х., Строчков В.М., Кабылбекова Д.И., Касымбекова Ш.Н., Бименова Ж.Ж.

Аннотация

Предпосылка и цель. Казахские лошади типа Жабе отличаются от местных лошадей более высокой живой массой и крупными размерами тела. Племенная работа с казахскими лошадьми типа Жабе ведется в хозяйстве «Тайлак» Жарминского района Восточно-Казахстанской области путем целенаправленного воспроизводства, выращивания и широкого использования лучших особей по происхождению, экстерьеру, продуктивности, приспособленности к круглогодовому выпасу и качеству потомства от жеребцов и кобыл. Особи, не соответствующие этим стандартам, строго выбраковываются. Целью исследований является определение мясной продуктивности и изучение генетических особенностей выборки современной популяции казахских лошадей типа Жабе с использованием ДНК-маркеров.

Материалы и методы. Материалом для исследования послужили данные генотипирования ДНК 20 лошадей казахской породы типа Жабе. Генотипирование лошадей проводили по 17 STR-локусам, рекомендованным Международным обществом генетики животных (ISAG). Для идентификации аллелей использовали международный алфавитный код. Генетический и популяционный анализы проводили с использованием программного обеспечения GenAIEx 6.5. Рассчитывали следующие показатели: среднее число аллелей на локус (Na), эффективное число аллелей (Ne), уровни ожидаемой (He) и наблюдаемой гетерозиготности (Ho), коэффициент инбридинга (FIS).

Результаты. Исследование 17 STR-локусов ДНК казахских лошадей типа Жабе показало, что они имеют аллелофонд со значительным числом идентифицированных аллелей и высокой генетической изменчивостью. Средний коэффициент инбридинга (FIS) отрицательный (-0,059), что свидетельствует о сохранении генетического разнообразия данной породы в пределах данной группы.

Заключение. Улучшение этих лошадей достигается путем разведения и выращивания животных с высоким генетическим потенциалом продуктивности, который передается из поколения в поколение. Это осуществляется путем тщательного отбора лошадей с желаемыми признаками для разведения.

Ключевые слова: живая масса; экстерьер; отбор; STR маркеры; промеры; селекция.