

# Genetic Structure of Populations of Kazakh Whiteheaded and Hereford Cattles on the Basis of Microsatellite DNA

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**Abstract:** This work is aimed at determination of genetic dissimilarities between two allied cattle breeds: Kazakh Whiteheaded and Hereford. Hair follicles were analyzed, from which DNA was extracted with subsequent amplification. Identification of amplification products was performed using an ABI Prism 310 genetic analyzer. Allele 147 was detected in Kazakh Whiteheaded cattle in locus BM 2113, there was no such allele in Hereford cattle. Average number of alleles per one locus of Hereford and Kazakh Whiteheaded breeds was 11.82 and 12.27, respectively. Herewith, the number of private alleles in Kazakh Whiteheaded cattle was 10 and in Herefordcattle-11. No confidential difference in average heterozygosity was determined. Analysis of sample allele fund with regard to both considered breeds revealed the characteristics' range for both of them, thus facilitating determination of genetic dissimilarity between the two breeds.

**Keywords:** Kazakh and Hereford Breeds, Allele, Locus, Microsatellites, Heterozygosity

## Introduction

In 1950 in Kazakhstan the first cattle breed was approved: Kazakh Whiteheaded, created on the basis of Kazakh and Kalmyk cattle by cross breeding with servicing bulls of Hereford breed imported from Uruguay and England (Dankvert, 2007; Cherekaev and Cherekaeva, 1973).

In recent decade, aiming at increase in productivity of Kazakh Whiteheaded cattle, Hereford bulls were again used, however, admixture of new blood was applied, that is, with single and double blood admixture.

Therefore, the studies were aimed at determination of genetic properties of Kazakh Whiteheaded and Hereford breeds. Selection of these breeds for studies was based on the fact that Kazakh Whiteheaded breed originated from Hereford cattle; as a consequence, the new breed inherited actually identical color type, conformation and productive properties. Since phenotypic properties of both breeds are the same, it would be interesting to clarify the aspect of genetic similarity of these two breeds.

It is well-known that significant contribution to characteristic of allele variety is made by regional populations, which were formed mainly on the basis

of local cattle with its own unique allele fund and under conditions of relative geographic isolation (Tapio *et al.*, 2010).

Necessity to maintain optimum level of genetic variances and heterozygosity in cattle population is related with the fact that these properties are directly attributed to adaptive abilities of cattle with regard to modified environmental conditions. Without required genetic variety cattle populations lose their evolutionary adaptiveness and become unstable against impacts of pathogenic flora and negative environmental influences (climatic changes, negative impact of hazardous substances (Dubinin and Mashurov, 1986; Stolpovskii, 2010).

Loss of cattle genetic variety leads to significant economic damage.

One of the methods of revealing of genetic dissimilarities between populations, evaluation of population structure is application of anonymous DNA markers-microsatellites. Microsatellites are short (100-200 base pairs) tandem segments of DNA characterized by high extent of polymorphism (Tautz, 1989; De Woody and Avis, 2000).

Numerous data on applied significance of microsatellites are published regarding evaluation of

state and dynamics of allele fund of dairy breed. However, there are few data on genetic variety of beef breed. Herewith, the microsatellite data can be applied both for evaluation of genetic variety in the breeds and between the breeds and genetic mixture of the breeds; average number of alleles (*mna*), observed and expected heterozygosity (*Ho* and *He*) are more widely applied calculated genetic parameters of populations for evaluation of variety in the breed. Average number of alleles per locus, on the one hand, is one of the properties of informative value of analytical system and, on the other hand, serves as a criterion of genetic variety of the studied cattle groups (Gibson *et al.*, 2007; Zinov'eva *et al.*, 2009; Ernst and Zinov'eva, 2008).

Analysis of locus itself as well as revealing of dominating allele variants of this locus is highly important for selection and development of monitoring procedures of genuineness of cattle breeds (Gershenzon, 1974; Sulimova, 2004; Glazko *et al.*, 2013).

## Methods

Hair follicles of 5617 animals of Kazakh Whiteheaded breed, Kazakh population and of 108 animals of Hereford breed imported from abroad were used for analysis. Biological material was sampled in 40 farms situated in various regions of Kazakhstan. Significant difference in amount of samples from the breeds was stipulated by the fact that Hereford breed was supported by at least one hundred years of purely breeding, whereas in Kazakh Whiteheaded breed the fraction of Hereford breed ranges from 50 to 80%, which makes it possible to assume high genetic variety of allele fund of this breed.

DNA was extracted by means of PureLink™ Genomic DNA Kits (Corporate Headquarters: Invitrogen by Life Technologies, USA). Amplification was performed using set of reagents: Stock Marks Bovine Kit (Applied Biosystems, USA) in multi-locus format for 11 loci (Van de Goor *et al.*, 2009). Amplification products were identified using an ABI Prism 310 genetic analyzer (Applied Biosystems, USA) with capillary electrophoresis and laser detection. The obtained graphic results were processed in Gene Mapper 4.0. Polymorphism was characterized by the following properties: Allele frequency and genotype frequency, observed and expected heterozygosity with accounting for the Hardy-Weinberg principle, as well as average heterozygosity in loci, average number of alleles in locus.

Biometric processing of the obtained results was performed according to the existing procedures and equations (Hedrick, 2013; Weir, 1996, Zhivotovskii, 1991; Plokhinskii, 1937; Nurbaev, 2016; Merkur'ev,

1970). Population genetic properties were calculated using statistical package and software written in Fortran Power Station v.1.0.

## Results

Analysis of molecular and genetic peculiarities of the two breeds revealed from 7 to 24 allele variants in loci, herewith, the considered species in each breed had certain range of alleles, their occurrence frequency determined genetic structure of population Table 1.

The lowest number of alleles (7 each) was detected in loci ETH 225 and BM 1824, the highest number of alleles was detected in loci TGLA 122 and TGLA 53, 24 and 19 alleles, respectively. In Hereford breed the average number of alleles per one locus was 11.82; in Kazakh Whiteheaded breed - 12.27.

In Hereford breed the existence of private alleles was detected in four loci and in Kazakh Whiteheaded breed in two loci. Thus, in loci BM 2113 and ETH 3 of Hereford breed there was one private allele in each, in loci TGLA 53 and TGLA 222 and 7, respectively. Private alleles for Kazakh Whiteheaded breed were detected in loci BM 2113 and TGLA 122, their number was 2 and 8, respectively.

Analysis of the obtained data made it possible to determine that the alleles occurred in Hereford breed nearly completely exist in Kazakh Whiteheaded breed. However, in Kazakh Whiteheaded breed allele 147 was detected in locus BM 2113, which was absent in Hereford breed.

In total, in 11 loci of Hereford breed there were 35 alleles with occurrence index above 0.1 and in Kazakh Whiteheaded breed 41, respectively Table 2.

As can be seen, the gene pools of the considered breeds differed not only in spectrum but in allele occurrence frequency. Among the frequently occurred alleles the most spread was allele 103 in locus ETH 3 of both breeds (0.2685 in Hereford and 0.3314 in Kazakh Whiteheaded). It should be mentioned that occurrence frequency of allele 139 in locus BM 2113 was different for the considered breeds (0.1389 in Hereford and 0.208 in Kazakh Whiteheaded) at high confidence according to Student's t-test ( $t = 2.9027$ , d.f. = 1,  $p > 0.05$ ).

Analysis of heterozygosity extent in loci of both breeds made it possible to detect sufficiently high level of this property in all 11 loci. The lowest heterozygosity extent was observed in locus ETH3 of Hereford breed equaling to 0.8357, the highest-in locus TGLA122 of the same breed equaling to 0.9319. In Kazakh Whiteheaded breed the heterozygosity extent in all 11 loci varied from 0.8113 and 0.9211.

**Table 1:** Allele occurrences in 11 loci of Kazakh Whiteheaded and Hereford breeds

Name of loci and alleles											
Allele variants	TGLA 227	BM 2113	TGLA 53	ETH 10	SPS 115	TGLA 126	TGLA 122	INRA 23	ETH 3	ETH 225	BM 1824
1	75	121	154	209	248	109	137	198	103	140	178
2	77	123	156	213	250	111	139	200	109	142	180
3	79	125	158	215	252	113	141	202	115	144	182
4	81	127	160	217	254	115	143	204	117	146	184
5	83	129	162	219	256	117	145	206	119	148	186
6	85	131	164	221	258	119	147	208	121	150	188
7	87	133	166	223	260	121	149	210	123	152	190
8	89	135	168	225	262	123	151	212	125		
9	91	137	170			125	153	214	127		
10	93	139	172				155	216	129		
11	95	141	174				157	218	131		
12	97	143	176				159	220			
13	99	145	178				161	222			
14	101	147*	180				163				
15	103		182				165				
16			184				167				
17			186				169				
18			188				171				
19			190				173				
20							175				
21							177				
22							179				
23							181				
24							183				

Note: \*only in Kazakh Whiteheaded population

**Table 2:** Number of alleles in loci with occurrence frequency above 0.1

Locus	Breed				Locus	Breed			
	Hereford		Kazakh Whiteheaded			Hereford		Kazakh Whiteheaded	
	Allele	Frequency	Allele	Frequency		Allele	frequency	Allele	Frequency
TGLA 227	75	0.1435	75	0.1889	BM				
2113	139	0.1389	139	0.2080					
	81	0.1389	83	0.1344		129	0.1065		
	79	0.1204	-	-	ETH 10	225	0.2593	225	0.2357
TGLA 53	154	0.1898	154	0.2339		213	0.1852	209	0.1575
	156	0.1204	156	0.1409		209	0.1389	213	0.1511
SPS 115	248	0.1898	248	0.2031		-	-	215	0.1256
	250	0.1620	262	0.1544		-	-	219	0.1037
	-	-	252	0.1268	TGLA 126	109	0.1713	109	0.1862
	-	-	250	0.1247		125	0.1574	113	0.1168
	-	-	260	0.1046		119	0.1481	119	0.1155
TGLA 122	143	0.1157	143	0.1244		113	0.1065	125	0.1111
	141	0.1019	141	0.1171		115	0.1065	121	0.1100
			137	0.1072		121	0.1019	-	-
ETH 3	103	0.2685	103	0.3314	INRA 23	198	0.2037	198	0.1949
	109	0.2546	109	0.2269		202	0.1204	200	0.1239
	-	-	115	0.1082		200	0.1157	202	0.1200
ETH 225	148	0.2176	140	0.2158	BM 1824	188	0.2361	188	0.2104
	140	0.2083	148	0.1845		190	0.1852	190	0.1677
	150	0.1713	146	0.1659		178	0.1620	178	0.1553
	146	0.1389	150	0.1565		182	0.1389	180	0.1403
	144	0.1111	144	0.1071		184	0.1343	184	0.1354
						-	-	182	0.1241

## Discussion

The performed molecular and genetic analysis revealed that cattle population of domestic and integrated beef breeds had dissimilarities in genetic parameters. Kazakh Whiteheaded breed has higher genetic variety in terms of allele number in comparison with Hereford breed, which probably can be attributed to gene pool merging of these two breeds of different origin. With regard to locus BM 2113, existence of 14 alleles for Kazakh Whiteheaded breed and 13 alleles for Hereford breed was detected. Hereford breed had no allele148 in locus BM 2113. Hereford breed had private alleles in loci TGLA 122, BM2 113, ETH 3 and TGLA 53; in Kazakh Whiteheaded populations private alleles were detected in loci TGLA 122 and BM 2113, which indicated at unique essence of each breed on the basis of rare alleles of the population.

Average value of heterozygosity of the two breeds demonstrated no confidential difference between the two breeds. For Kazakh Whiteheaded breed this value was 0.8743 and for Hereford breed -0.8808, which indicates at necessity to maintain optimum level of genetic variety and heterozygosity in cattle populations.

## Conclusion

The performed studies demonstrated that the obtained results and analysis of allele variety of the two breed could be applied for development of measures aimed at conservation of unique gene pools, well adopted for local natural and climatic conditions.

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## Author's Contributions

**Adas Tileubekovna Tyngoziyeva:** Participated in all experiments, coordinated the data-analysis and contributed to the writing of the manuscript.

**Talgat Nikolaevich Karymsakov:** Coordinated the mouse work.

**Serik Doldashevich Nurbaev:** Designed the research plan and organized the study.

## Ethics

Authors declared no conflict of interests.

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