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Analysis of *GH1*, *GHR* and *PRL* gene polymorphisms for estimation of the genetic diversity of Buryat and Altai cattle breeds

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Small and unique Buryat and Altai cattle breeds of Turano-Mongolian origin are well adapted to harsh conditions of the continental climate to be their habitat. However, the population-genetic structure of the breeds has been poorly studied. This paper presents the results of analysis of polymorphisms *GH1* (AC_000176.1: BTA 19, exon 5, rs41923484, g.2141C>G, L127V), *GHR* (AC_000177.1: BTA 20, exon 10, rs109300983, g.257A>G, S555G) and *PRL* (AC_000180.1: BTA 23, exon 3, g.35108342A>G) in the samples of Buryat cattle breed of Russia, China and Mongolia, and indigenous Altai cattle breed (Russia) that belong to Turano-Mongolian cattle. The Russian sample of Buryat breed was differentiated from the Mongolian sample based on pairwise *G*-test and F_{ST} values for the *PRL-Rsa*I polymorphism and from the Chinese sample – based on pairwise *G*-test values for the *GH1-Alu*I polymorphism. All the three samples of Buryat breed clearly differed from the sample of Altai breed based on pairwise *G*-test and F_{ST} values for the *GHR-Alu*I polymorphism as well as on the base of F_{ST} values for the joint polymorphism of the three genes. Nei's genetic distances calculated from the three gene polymorphisms also confirmed the difference between the two breeds. The results of AMOVA demonstrated that GHR gene variability (16 %) gave the largest contribution to the differentiation that was confirmed by F_{ST} values (0.12–0.27). The STRUCTURE software enabled us to reveal four clusters, with a specific ratio for each sample, in the Chinese and Mongolian samples of Buryat breed, and in the sample of Altai breed, while the Russian sample of Buryat breed had only three clusters. The differences within the breed level were determined based on the *GH1-Alu*I and *PRL-Rsa*I polymorphisms, while at the inter-breed level – based on the *GHR-Alu*I polymorphism. Linkage disequilibrium analysis demonstrated significant linkage of the following pairs of genes in the Buryat breed: *GH1-GHR*, *GH1-PRL*, *GHR-PRL*.

Key words: *Bos taurus turano-mongolicus*; Buryat cattle; Altai cattle; population genetics; gene polymorphism; *GH1*; *PRL*; *GHR*.

Генетическая изменчивость бурятской и алтайской пород крупного рогатого скота, оцененная на основе анализа полиморфизма генов *GH1*, *GHR* и *PRL*

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Малочисленные уникальные бурятская и алтайская породы крупного рогатого скота турано-монгольского корня хорошо адаптированы к суровым условиям континентального климата региона обитания. Информация о популяционно-генетической структуре этих пород практически отсутствует. В настоящей работе выполнен анализ генетической изменчивости следующих генов-кандидатов: *GH1* (AC_000176.1: хромосома 19, экзон 5, rs41923484, g.2141C>G, L127V), *GHR* (AC_000177.1: хромосома 20, экзон 10, rs109300983, g.257A>G, S555G), *PRL* (AC_000180.1: хромосома 23, экзон 3, g.35108342A>G) в выборках бурятской породы из трех сопредельных государств – России, Китая и Монголии, а также аборигенной алтайской породы (Россия), относящихся в соответствии с происхождением к турано-монгольскому корню. Российская выборка бурятского скота дифференцируется от монгольской выборки этой породы на основе попарных значений *G*-теста и F_{ST} по изменчивости *Rsa*I-локуса гена *PRL* и от китайской выборки – на основе значений *G*-теста для *Alu*I-локуса гена *GH1*. При этом все выборки бурятского скота ведут себя согласованно в отношении алтайской породы, четко отличаясь от нее по данным *G*-теста и F_{ST} для локуса гена *GHR* и по значениям F_{ST} для комплекса локусов генов *PRL*, *GH1* и *GHR*. Генетические расстояния Нея на основе комплекса генов также отделяют бурятскую и алтайскую породу. Наибольший вклад в межпородную дифференциацию двух пород вносит изменчивость гена *GHR*, что зафиксировано в результатах AMOVA (16 %) и F_{ST} (0.12–0.27). Кластерный анализ, выполненный в программе STRUCTURE, выявил четыре кластера в алтайской породе крупного рогатого скота, китайской и монгольской выборках бурятского скота, которые представлены специфично в каждой выборке.

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У российского бурятского скота отсутствует один кластер, его частота в других выборках достигает 15 %. Различия на внутрипородном уровне у бурятской породы определяют локусы генов *PRL* и *GH1*, на межпородном с алтайской породой – исследованный локус гена *GHR*, что отражает неодинаковый вклад разных локусов. Анализ на неравновесие по сцеплению генов доказал достоверное сцепление следующих пар генов у бурятской породы: *GH1-GHR*, *GH1-PRL*, *GHR-PRL*.

Ключевые слова: *Bos taurus turano-mongolicus*; бурятский крупный рогатый скот; алтайский крупный рогатый скот; популяционная генетика; полиморфизм генов; *GH1*; *PRL*; *GHR*.

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As opposed to a majority of European breeds originated from European buffalo *Bos primigenius primigenius* (Hiendleder et al., 2008), Buryat and Altai cattle are of Eastern Asian origin, and based on craniological data and their horn structure, belong to *B. taurus turano-mongolicus* subspecies Kolesnik, 1936, which also includes Kirgiz, Yakutian, Siberian, Soyot, Mongolian, and Manchurian breeds (cited by: Kantanen et al., 2009).

As of today, Kalmykian and Yakutian cattle have been preserved in Russia, along with Buryat and Altai cattle. These breeds are well adapted to harsh conditions of the continental climate and specific habitat features and are characterized with high physical endurance, minimum human involvement in their management, year-round free grazing regime and abilities to maintain viability under low-caloric and deteriorating forage base in certain times of year, digest coarse forage and find it under the snow. These features are facilitated by physiological and morphological adaptations from specific features of digestive system structure and metabolism to developing longer and thicker fur in winter (Lazebnaya et al., 2010).

Lactation yield in Buryat and Altai cattle is not specifically high. According to M.N. Balkov (1962), milk yield in 114 cows in a 305-day lactation period, the number of calvings being four or above, was on average 911 kg with a fat percentage of 4.58. However, the simplicity and low cost of management for these breeds, as well as their high stability against diseases, make it possible to consider them not only unique, but irreplaceable for conventional breeding regions in terms of solving problems of providing environmentally healthy nourishment, preserving historical traditions of the local population, including technologies of making traditional dishes and clothing, and developing agro- and ecotourism. In addition, cattle breeds of such an ancient origin with aforementioned features are rare even on global scale, which makes it possible to consider them an important object for scientific investigation with an opportunity for finding possible uses for their genetic potential in present and future (Dmitriev, Ernest, 1989; Ukhanov et al., 1993; Moiseeva et al., 2006; Mwai et al., 2015; Shabtay, 2015).

Despite the facts above, the genetic features of breeds of Turano-Mongolian origin are rather understudied. Individual candidate genes are investigated in Yakutian and Kalmykian breeds, whose SNPs are associated in cattle with productivity attributes of selection value (Lazebnaya et al., 2010, 2013; Gorlov et al., 2014). Polylocus (ISSR) and monolocus (SSR) DNA markers were used to study a variety of breeds, including Yakutian, Kalmykian, and Mongolian ones (Tapio et al., 2010; Stolpovsky et al., 2011). Whole genome SNP-analysis has been performed recently for a series of Russian breeds, which also included Buryat breed, to investigate their origin, phylogeny, and differentiation (Yurchenko et al., 2017).

Diversity in somatotropic axis genes, which are candidate genes to be associated with milk and meat yield traits, is well researched in individual commercial cattle breeds. Correlation is established between gene polymorphism in growth hormone (*GH1*), its receptor (*GHR*), and prolactin (*PRL*) and growth and development, weight gain rate, meat quality, and protein and fat content in milk (Mitra et al., 1995; Chung et al., 1996; Chrenek et al., 1999; Dybus et al., 2004; Di Stasio et al., 2005). The best-known SNPs for the listed genes are as follows: the ones of *GH1 Alu*I (L127V, exon 5) (Dybus et al., 2004) and *GHR Alu*I genes (AF140284: g.257A > G, exon 10, Ser/Gly) (Di Stasio et al., 2005), and the ones of *PRL Rsa*I gene (A > G, 103 codon, exon 3) (Mitra et al., 1995). Comparative data on the diversity of the listed genes in Buryat and Altai cattle are not available.

The objective of the presented study was to assess the genetic structure in samples from two breeds of Turano-Mongolian origin, specifically Buryat breed from the neighboring territories of China, Mongolia, and Russia to discover diversity patterns within the same breed, and indigenous Russian Altai cattle based on polymorphism analysis for *PRL*, *GH1*, and *GHR* genes.

Materials and methods

Buryat cattle blood samples from three neighboring states, specifically Russia (Ltd. Shuluuta, Buryatia, $n = 51$), Northern Mongolia (Hubsugul aimak, $n = 25$), and China

(Inner Mongolia, $n = 13$), were studied, along with Altai cattle blood from Russia (Yazula rural area, Ulagan district, Altai Republic, $n = 21$).

Polymorphism in *Alu*I of *GH1* (AC_000176.1: chromosome 19, exon 5, rs41923484, g.2141C > G, L127V) (Dybus et al., 2004) and *GHR* genes (AC_000177.1: chromosome 20, exon 10, rs109300983, g.257A > G, S555G) (Di Stasio et al., 2005) and *Rsa*I of *PRL* gene (AC_000180.1: chromosome 23, exon 3, g.35108342 A > G) (Lewin et al., 1992) in cattle was analyzed using PCR RFLP with the following reagent kits: DIAtom™ DNA Prep (IsoGene Lab., Moscow, Russia) for isolating DNA from whole blood, GenPak® PCR Core (IsoGene Lab., Moscow, Russia) for amplification of the analyzed gene segments, restriction endonuclease provided by Thermo Fisher Scientific (USA): *Alu*I for *GH1* and *GHR* genes and *Rsa*I for *PRL* gene (Mitra et al., 1995; Dybus et al., 2004; Di Stasio et al., 2005; Hradecka et al., 2008).

The data were statistically processed using the GenAlEx 6.503 (http://biology-assets.anu.edu.au/GenAlEx/Download_files/GenAlEx %206.503 %20Download.zip), and STRUCTURE 2.3.4. software (https://web.stanford.edu/group/pritchardlab/structure_software/release_versions/v2.3.4/html/structure.html). Benjamini–Hochberg multiple comparison correction was introduced (Benjamini, Hochberg, 1995) to estimate the confidence of $p_{F_{st}}$, $p_{G_{st}}$, and $p_{\chi 2}$ values. Gene linkage was assessed using linkage (D) and correlation (r) coefficients. The confidence of linkage disequilibrium was estimated by the χ^2 test using the Benjamini–Hochberg multiple comparison correction. Cluster analysis of genetic structure based on the complex of studied genes was performed using the STRUCTURE 2.3.4 software. Here, the basic set of models was analyzed with genetic admixture and allele frequency correlation both taken and not taken into account.

Models were analyzed in two modes, i. e. LOCPRIOR and without considering the general matrix division into studied samples. Nine hypotheses on population structure were tested within each model with K varying from 1 to 9. For each K, the simulation was repeated 10 times to collect the required statistical data on likelihood function logarithm values and its average variance. The quantity of possible populations was tested by 1 000 000 burn-in iterations with the first 100 000 iterations being discarded.

Results

Allele frequency distributions for the studied *GH1*, *GHR*, and *PRL* gene loci are presented in Table 1, along with chi-square test results with probability values for each of three candidate genes studied in the cattle samples of Buryat and Altai breeds considered. According to Table 1, allele frequency *L* of *GH1* gene prevails in all samples and varies within the range of 0.654 in Buryat breed from China and up to 0.863 in the Russian sample of the breed. Allele *A* of *PRL* gene is also represented with high frequency in all samples of both breeds, frequency interval is 0.620 for Buryat breed from Mongolia and up to 0.814 in Buryat breed from Russia. Allele frequency distribution for

Table 1. Allele frequencies of *GH1*, *GHR* and *PRL* genes and HWE for Buryat and Altai cattle breeds

Gene	Allele	Altai, $n = 21$	Buryat (China), $n = 13$	Buryat (Mongolia), $n = 25$	Buryat (Russia), $n = 51$
GH1	*L*	0.857	0.654	0.800	0.863
	V	0.143	0.346	0.200	0.137
	χ^2	0.583	0.294	0.000	1.510
	p	0.445	0.588	1.000	0.219
GHR	*A*	0.881	0.577	0.380	0.441
	G	0.119	0.423	0.620	0.559
	χ^2	0.383	0.138	1.868	3.047
	p	0.536	0.710	0.172	0.081
PRL	*A*	0.690	0.731	0.620	0.814
	B	0.310	0.269	0.380	0.186
	χ^2	1.018	0.007	0.110	0.045
	p	0.313	0.935	0.741	0.831

Notes: n – number sampled, χ^2 – chi-square criterion, p – probability.

GHR gene differs from the ones described above for *GH1* and *PRL* genes, i. e. allele frequency *A*, 0.88, prevails in the Altai breed sample and allele frequencies *G*, 0.62 and 0.559, in Buryat breed samples from Mongolia and Russia respectively. It should be noted that the genotype frequency distribution observed showed no deviation from the one expected based on Hardy–Weinberg equilibrium for all *GH1*, *GHR*, and *PRL* gene loci in all samples.

Pairwise *G*-test values for the studied samples with the corresponding probability values are presented in Table 2. According to the Benjamini–Hochberg multiple comparison correction, probability values that fit condition $p < 0.025$ are significant. According to Table 2, differences between the Russian breed sample and Chinese and Mongolian samples were discovered in *Alu*I locus of *GH1* gene and *Rsa*I locus of *PRL* gene, respectively. The difference between the Altai breed and Buryat breed samples was found in *Alu*I locus of *GHR* gene regardless of origin.

Differentiation between the considered Buryat and Altai cattle breed samples was estimated using pairwise values of Wright's fixation index (F_{ST}) for individual genes and their complexes (Table 3). Confident F_{ST} values given the Benjamini–Hochberg multiple comparison correction ($p < 0.025$) were identified by the considered *GHR* gene locus for Altai breed sample paired with Buryat breed samples from China ($F_{ST} = 0.117$), Mongolia ($F_{ST} = 0.269$), and Russia ($F_{ST} = 0.216$). This regularity stands for this parameter in case of gene complexes as well. In addition, Russian Buryat breed sample is differentiated from the Mongolian sample ($F_{ST} = 0.046$) by the studied *PRL* gene locus.

The analysis of Table 3 also shows that significant

Table 2. The pairwise *G*-test and corresponding probability values for each genetic marker

Cattle breed (Region)	Altai (Russia)	Buryat (China)	Buryat (Mongolia)	Buryat (Russia)
			GH1 gene	
Altai (Russia)		0.052	0.469	1.000
Buryat (China)	3.769		0.169	0.020
Buryat (Mongolia)	0.525	1.893		0.326
Buryat (Russia)	0.000	5.424	0.964	
			GHR gene	
Altai (Russia)		0.004	0.000	0.000
Buryat (China)	8.113		0.101	0.216
Buryat (Mongolia)	26.088	2.682		0.472
Buryat (Russia)	26.191	1.533	0.518	
			PRL gene	
Altai (Russia)		0.722	0.479	0.114
Buryat (China)	0.126		0.329	0.360
Buryat (Mongolia)	0.502	0.952		0.011
Buryat (Russia)	2.505	0.836	6.465	

Notes: pairwise *G*-test values for the considered samples are given below the diagonal, the corresponding probability values are above the diagonal.

Table 3. Pairwise genetic differentiation of Buryat and Altai breed samples on the basis of Wright's F-statistics (F_{ST}) and corresponding probability values given separately for the studied loci of *GH1*, *GHR* and *PRL* genes and for a complex of the genes

Cattle breed (Region)	Altai (Russia)	Buryat (China)	Buryat (Mongolia)	Buryat (Russia)
			GH1 gene	
Altai (Russia)		0.085	0.576	1.000
Buryat (China)	0.056		0.292	0.051
Buryat (Mongolia)	0.006	0.027		0.393
Buryat (Russia)	0.000	0.060	0.007	
			GHR gene	
Altai (Russia)		0.011	0.001	0.001
Buryat (China)	0.117		0.123	0.312
Buryat (Mongolia)	0.269	0.039		0.493
Buryat (Russia)	0.216	0.018	0.004	
			PRL gene	
Altai (Russia)		0.790	0.544	0.148
Buryat (China)	0.002		0.449	0.427
Buryat (Mongolia)	0.005	0.014		0.024
Buryat (Russia)	0.020	0.010	0.046	
			GH1, *GHR*, and *PRL* genes	
Altai (Russia)		0.011	0.001	0.001
Buryat (China)	0.058		0.130	0.118
Buryat (Mongolia)	0.108	0.027		0.075
Buryat (Russia)	0.098	0.028	0.019	

Notes: the pairwise values of the F_{ST} coefficient are given below the diagonal, the corresponding probability values are above the diagonal.

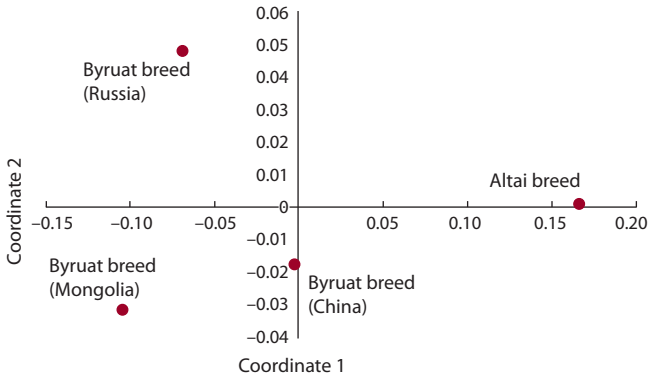

Fig. 1. Principal coordinates analysis (PCoA) of pairwise Nei's genetic distances (Nei, 1978) from the three polymorphisms typed in four samples.

differentiation of Altai breed from Buryat breed samples from various regions is primarily determined by *GHR* gene diversity, which is further confirmed by AMOVA results. Thus, diversity between populations by three genes studied was rather high at 8 %, however for *GHR* gene it was 16 % and for *GH1* and *PRL* genes – 2 %. Ordination of the studied samples in the first two principal coordinates based on pairwise Nei's genetic distance (Nei, 1978) for the gene complex is shown in Fig. 1.

The amount of diversity in the first principal component is 92.33 %, and in the second – 7.67 %. All the studied samples of both breeds are differentiated from each other. The distance from Altai breed to Buryat breeds by samples increases as follows: China, Russia, and Mongolia. Here, the calculations show that average pairwise Nei's genetic distance inside the group formed by Buryat breed samples from various regions (D_{Nei} = 0.071) is over three times as small as average pairwise Nei's genetic distance between Altai breed and each Buryat breed sample from China, Mongolia, and Russia (D_{Nei}= 0.222).

Cluster analysis of genetic structure on the dataset, including the complex genotypes of *GH1*, *GHR*, and *PRL* genes in the Buryat breed samples from three regions, and Altai breed from Russia, was performed using the STRUCTURE software. After various models had been tested taking posterior probability into account, a model with genetic material admixture but with no allele frequency correlation was selected. Based on average likelihood function logarithm values and variances of its estimates obtained in 10 simulation runs with a specified set of respective parameters, the optimum number of clusters (*K*) turned out to be four.

It follows from Fig. 2 and Table 4 that each sample has its own cluster distribution. Most samples show all types of clusters, apart from Buryat breed from Russia, in which one cluster shown in blue in Fig. 2 and present in Table 4 under no. 3 is lacking, whereas its frequency in other samples does not exceed 0.154. In Buryat cattle from China, the presence of cluster 2 shown in green is

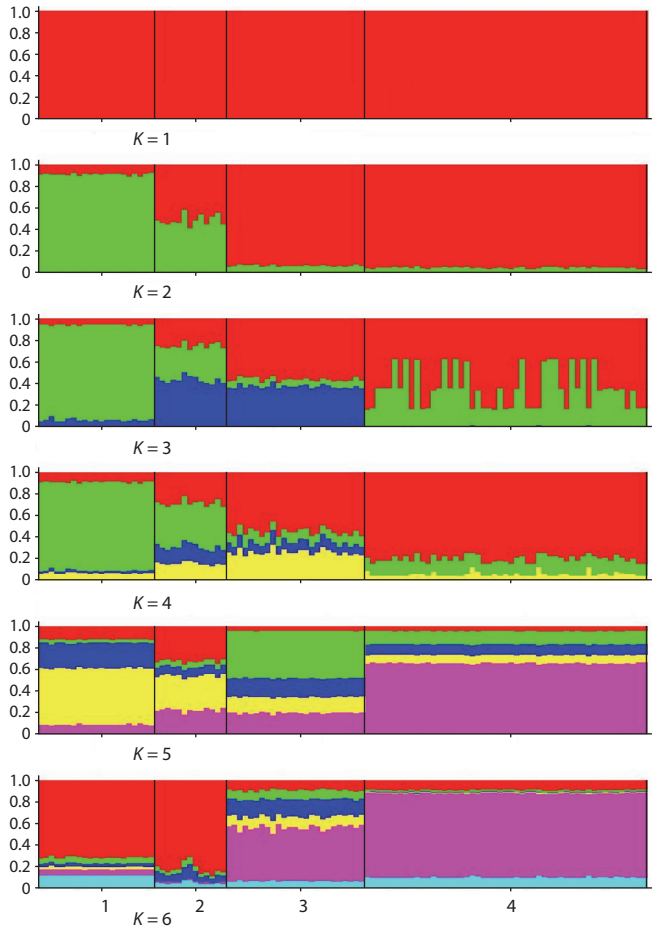

Fig. 2. Bayesian genotypic cluster analysis of the four samples in Buryat and Altai breeds based on the three polymorphisms (*GH1*, *GHR*, and *PRL*) at various values of *K*.

X-axis: 1 – Altai cattle breed, 2 – Buryat cattle breed from China, 3 – Buryat cattle breed from Mongolia, 4 – Buryat cattle breed from Russia; each cluster designated with particular color (description in the text).

high at 0.403, and it is only higher in Altai breed, in which it is vastly prevailing (0.820). Buryat breed sample from China is characterized by the most uniform distribution of various clusters. Buryat and Altai breeds from Russia show the significant prevalence of one cluster, namely clusters 1 and 2 (see Table 4) highlighted in red (0.800) and green respectively.

GH1, GHR, and *PRL* genes in *B. taurus* specimens are localized on different chromosomes, 19, 20, and 23, respectively, however linkages between individual loci remain a possibility. The performed analysis of pairwise linkage in studied loci of three genes in accordance with Benjamini–Hochberg correction showed confident probability values ($p < 0.025$) for loci of the following gene pairs: *GH1-GHR* in Buryat breed from Russia ($D = 0.051$, $r = 0.297$, $p = 0.003$) and Mongolia ($D = 0.076$, $r = 0.391$, $p = 0.006$), *GH1-PRL* genes in all Buryat breed sample pairs ($D = 0.033$–0.099, $r = 0.248$–0.470, $p = 0.012$–0.020), and

Table 4. Percentage of the clusters identified in samples of Altai and Buryat cattle breeds

Cattle breed (Region)	Sample volume	Cluster			
		1	2	3	4
Altai	21	0.088	0.820	0.025	0.067
Buryat (China)	13	0.286	0.403	0.154	0.157
Buryat (Mongolia)	25	0.551	0.093	0.095	0.260
Buryat (Russia)	51	0.800	0.139	0.000	0.061

Table 5. Complex genotypes of *GH1*, *GHR* and *PRL* genes with linkage disequilibrium in Buryat cattle breed

GH1-PRL	*q*	*GH1-GHR*	*q*	*GH1-GHR-PRL*	*q*
China		Mongolia		Russia	
LL-AA	0.308	*LL-AA*	0.080	*LL-AA-AA*	0.196
LL-AB	0.154	*LL-AG*	0.400	*LL-AA-AB*	0.039
LV-AA	0.154	*LL-GG*	0.160	*LL-AG-AA*	0.176
LV-AB	0.231	*LV-AG*	0.200	*LL-AG-AB*	0.039
VV-AA	0.077	*LV-GG*	0.120	*LL-GG-AA*	0.176
VV-BB	0.077	*VV-GG*	0.040	*LL-GG-AB*	0.118
Russia		Russia		*LL-GG-BB*	0.020
LL-AA	0.549	*LL-AA*	0.235	*LV-AA-AA*	0.020
LL-AB	0.196	*LL-AG*	0.216	*LV-AG-AA*	0.098
LL-BB	0.020	*LL-GG*	0.314	*LV-AG-AB*	0.059
LV-AA	0.118	*LV-AA*	0.020	*LV-GG-BB*	0.020
LV-AB	0.059	*LV-AG*	0.157	*VV-GG-AB*	0.039
LV-BB	0.020	*LV-GG*	0.020		
VV-AB	0.039	*VV-GG*	0.039		
Mongolia					
LL-AA	0.280				
LL-AB	0.320				
LL-BB	0.040				
LV-AA	0.120				
LV-AB	0.120				
LV-BB	0.080				
VV-BB	0.040				

Note. *q* is the frequency of the complex genotype.

GHR-PRL genes in Buryat breed from Russia ($D = 0.063$, $r = 0.324$, $p = 0.001$). Complex genotypes based on two and three genes for samples, in which disequilibrium gene linkage is established, are presented in Table 5. According to the provided complex genotype frequencies for *GH1-PRL* genes, the linkage between *L*-allele of *GH1* gene with *A*-allele of *PRL* gene may be assumed in all Buryat breed samples. In addition, according to maximum complex genotype frequencies for *GH1-GHR* genes, *L*-allele of *GH1* gene is also linked to *A*- and *G*-alleles of *GHR* gene in Buryat breeds from Russia and Mongolia. These regularities are also reflected in high complex genotype frequencies for three genes, in which *L*-allele of *GH1* gene, *A*- and *G*-alleles of *GHR* gene, and *A*-allele of *PRL* gene are present in Russian Buryat breed sample.

Discussion

Samples of two breeds of Turano-Mongolian origin, i. e. Buryat breed from China, Mongolia, and Russia and Altai breed from Russia have been compared for the first time in the present paper. In none of these samples the observed genotype frequency distribution deviates from the one expected based on Hardy–Weinberg equilibrium. Russian Buryat breed sample is differentiated from the Mongolian sample of the same breed based on pairwise *G*-test and F_{ST} values regarding diversity in *Rsa*I locus of *PRL* gene and from Chinese sample – based on *G*-test values for *Alu*I locus of *GH1* gene. Here, all Buryat breed samples match in their behavior with respect to Altai breed, i. e. they clearly differ from it based on *G*-test and F_{ST} data for *GHR* gene locus and F_{ST} values for locus complexes of *PRL*, *GH1,* and *GHR* genes. Nei's genetic distances based on gene complexes also isolate the group of Buryat breed samples from Altai breed, which is indicated by the relationship between average pairwise Nei's genetic distance inside the Buryat breed group and average pairwise Nei's genetic distance for Buryat breed samples from China, Mongolia, and Russia and Altai breed. The largest contribution to differentiation between the two breeds is given by *GHR* gene diversity, which is reflected by AMOVA (16 %) and F_{ST} results (0.12–0.27).

Differences in the genetic structure of studied samples were demonstrated by cluster analysis performed using the STRUCTURE software. Four clusters identified in Altai breed, as well as Chinese and Mongolian Buryat breed samples are present in a specific fashion in each sample. However, one cluster with relatively low frequencies in other samples is lacking in Russian Buryat breed. Presence of the same clusters in Buryat and Altai breeds may indicate the unity of origin expressed by belonging to Turano-Mongolian root breed, however their lengthy independent existence affected their genetic structure in the form of prevalence of one of clusters in Altai breed sample. In addition, differentiation within the breed may be observed in Buryat cattle. Note that differences within the breed in Buryat cattle are determined by *PRL* and *GH1* gene loci and differences from Altai breed by the studied *GHR* gene locus, which reflects unequal contributions of various loci to differentiation depending on the level of

comparison. To clarify whether the identified diversity pattern is maintained, when the dataset is expanded, larger-scale research needs to be carried out. However, the results obtained show the necessity of taking diversity in subpopulations into account, while preserving small breeds.

Disequilibrium linkage analysis of the genes considered performed in the paper confidently showed its presence for the following gene pairs in Buryat breed: *GH1-GHR*, *GH1-PRL*, *GHR-PRL*. The use of primarily the same servicing bulls could be considered a possible explanation for the discovered similarity in disequilibrium linkage between alleles of the mentioned genes in all studied cattle samples, however our samples represent independent herds, which makes their mixing impossible. Thus, the discovered similarity in disequilibrium linkage between alleles of the mentioned genes is most likely to result from direct or indirect natural and-or artificial selection. Disequilibrium linkage of *GH1* and *PRL* genes with *GHR* gene does not contradict with the available data on possible competition between prolactin and growth hormone genes for linkage with the latter's receptor (Inoue et al., 2001).

Maintaining genetic diversity and preventing inbreeding are especially important for small indigenous breeds in a critical state. Allele variety of genes subjected to strong selection pressure in commercial breeds may lead to significant allele frequency deviation in one direction or another up to their fixation, which may have a negative effect on their viability under changing climatic and agrobiocenotic conditions. Moreover, genetic potential of indigenous breeds well adapted to harsh ecological and geographical conditions, which also preserve stability against diseases most common for their habitat, may be desired in both conventional livestock breeding and developing new breeds. Given the fact that artificial insemination is rarely practiced in free grazing breeds, it is necessary to develop *in situ* and *ex situ* preservation strategies taking into account DNA marker monitoring. The data obtained are the first population-genetic characteristics of Buryat and Altai breeds based on candidate gene diversity.

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Conflict of interest

The authors declare no conflict of interest.

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