

Study of Genetic Diversity of Dagestan Mountain Cattle Based on STR-Markers [†]

Valeria Volkova ^{1,*}, Tatiana Deniskova¹, Alexandra Abdelmanova¹, Olga Romanenkova ¹, Abdusalam Khozhokov², Alexander Sermyagin ¹ and Natalia Zinovieva¹

¹ L.K. Ernst Federal Science Center for Animal Husbandry, Dubrovitsy 60, Podolsk Municipal District, 142132 Moscow, Russia; horarka@yandex.ru (T.D.); preevetic@mail.ru (A.A.); y7tteaip@mail.ru (O.R.); alex_sermyagin85@mail.ru (A.S.); n_zinovieva@mail.ru (N.Z.)

² Federal Agricultural Research Center of The Dagestan Republic, Akushinsky Ave., Science Town 30, 367014 Makhachkala, Russia; niva1956@mail.ru

* Correspondence: moonlit_elf@mail.ru

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Abstract: Cheap pasture fodder and a long grazing season are favorable for cattle breeding in the Dagestan Republic of Russia. However, specific natural and geographical conditions including mountain terrain, hypoxia, and high humidity slow down intensification of cattle breeding in this region. Thus, maintenance of genetic diversity of local cattle breeds, which fit well into specific environments, is of special importance for mountain ethnic communities. Dagestan Mountain cattle has valuable biological traits including strong hooves, stamina, and adaptability to extreme mountain conditions. The sample included 32 individuals of Dagestan Mountain cattle collected from private owners in the mountain villages of Dagestan during a scientific expedition. We observed the high level of genetic diversity in Dagestan Mountain cattle as revealed by calculations of the mean number of alleles per locus (6.82 compared to 4.79–5.82 in other breeds) and observed heterozygosity indices ($H_o = 0.73$, that was higher comparing to the other breeds ($H_o = 0.69$) excluding Simmentals and Brown Swiss ($H_o = 0.74$)). Based on STRUCTURE results, the individuals with low level of admixture with other breeds were found within Dagestan Mountain cattle, which can be considered as candidates for using in germ plasm conservation programs.

Keywords: Dagestan Mountain cattle; STR markers; allele frequency

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1. Introduction

Dagestan is a peculiar and interesting region located in the southernmost part of the Russian Federation, on the northeastern slopes of the Greater Caucasus and in the Caspian lowland. Almost half of the territory (48%) is occupied by a mountainous zone. At the same time, large areas of mountain pastures, cheap pasture fodder and a long pasture season favor cattle breeding in the region [1].

In Dagestan, from time immemorial, Great Caucasian and Lesser Caucasian cattle have been bred in the mountains and on the plains. Mountain cattle, which were created by crossing of local cattle with Swiss, Kostroma, and Lebedin breeds, represent a valuable gene pool for obtaining new breeds of cattle. Thus, the Caucasian Brown breed (Dagestan offspring) was resulted from crossbreeding of mountain cattle with Swiss, Brown Carpathian and Lebedin breeds [2].

One of the main reasons for the conservation of gene pool of mountain cattle is predominance and specifics of the mountain terrain, where the intensification of cattle breeding is hampered by natural and geographical conditions. Breeding of highly specialized breeds in the mountain zone is associated with a significant loss of their productivity and premature culling for various reasons [3].

In this regard, the aim of our study is to characterize modern allele pool and to assess genetic diversity of Dagestan Mountain cattle using STR markers.

2. Materials and Methods

For present study, samples of mountain cattle were collected in the Republic of Dagestan within the specially organized scientific expedition in 2019.

Polymorphism of 11 STR loci recommended by ISAG for population genetic studies of cattle was evaluated on a 16-channel capillary genetic analyzer ABI3130xl (Applied Biosystems, USA). Raw allele length data were obtained using the Gene Mapper v.4 software (Applied Biosystems).

To compare genetic diversity levels and to establish genetic links, we used STR profiles of different cattle breeds from the Bioresource collection of the L.K. Ernst Federal Research Center for Animal Husbandry, (Unique Scientific Installation (UNU) "Bank of Genetic Materials of Animals and Birds of the L.K. Ernst Federal Science Center for Animal Husbandry, supported by the Russian Ministry of Science and Higher Education). A total of 132 specimens from 5 cattle breeds was analyzed in our study (Table 1).

Table 1. Sampling information for studied cattle breeds.

Breed	Abbreviation	Sample Number	Breeding Region	Reference
Dagestan mountain	GS	32	The Dagestan Republic	Present study
Brown Swiss, Caucasian branch	BS	13	The Dagestan Republic	Present study
Brown Swiss, Germany	BS_G	27	Germany	Present study
Red Steppe	RS	26	The Dagestan Republic	Present study
Simmental	SIM	32	Oryol region	Present study
Holstein	HOL	34	Holstein Association USA	Holstein Association USA

3. Results

A total of 117 alleles at 11 loci were found in the studied populations. The total number of alleles was 413 and 90 of them was identified in the GS group. We found that there was deficiency of heterozygotes in one locus in the cattle populations bred in the territory of Dagestan (Table 2).

Table 2. Genetic diversity parameters estimated for 11 microsatellite markers by cattle breeds.

Breed		TGLA227	BM2113	TGLA53	ETH10	SPS115	TGLA122	INRA23	TGLA126	BM1818	ETH225	BM1824
GS	Na	11	9	15	5	7	12	7	7	6	7	4
	F	0.069	0.102	0.250	0.123	0.024	-0.080	0.040	-0.154	-0.019	-0.034	0.044
BS	Na	7	6	9	5	4	6	7	4	5	7	4
	F	-0.059	-0.238	0.449	-0.212	-0.083	-0.243	0.096	0.129	0.100	-0.099	-0.022
BS_G	Na	6	7	9	4	5	8	5	3	6	5	4
	F	-0.051	-0.027	-0.101	-0.130	-0.115	-0.004	-0.187	-0.043	0.048	-0.259	0.016
RS	Na	9	6	8	5	6	7	8	4	3	7	4
	F	-0.081	-0.134	0.200	0.065	-0.161	0.050	-0.030	0.439	0.156	-0.099	-0.102
SIM	Na	8	5	11	4	6	8	8	5	4	6	5
	F	-0.204	-0.045	-0.037	-0.303	-0.222	-0.223	0.045	-0.177	-0.001	-0.123	-0.031

HOL	Na	8	5	8	6	4	7	4	5	4	5	4
F	-0.069	0.176	-0.060	0.027	-0.175	0.167	-0.214	0.067	0.047	-0.086	-0.225	

N—No. Alleles; F—fixation index.

Allelic diversity was the highest in the mountain cattle group compared to other studied breeds.

The level of observed heterozygosity was 0.73 in mountain cattle.

Heterozygote deficiency was found in mountain and in the Red Steppe cattle, bred in Dagestan.

We identified a total of 29 private alleles (14 in the GS group) with frequencies varying from 0.016 to 0.148 in the studied populations.

Analysis of the Neighbor Net graph (Figure 1) showed a presence of genetic relationships between the GS, BS, and RS groups as well as provided evidence of a common origin of the BS and BS_G groups. Holsteins and Simmentals formed separate branches.

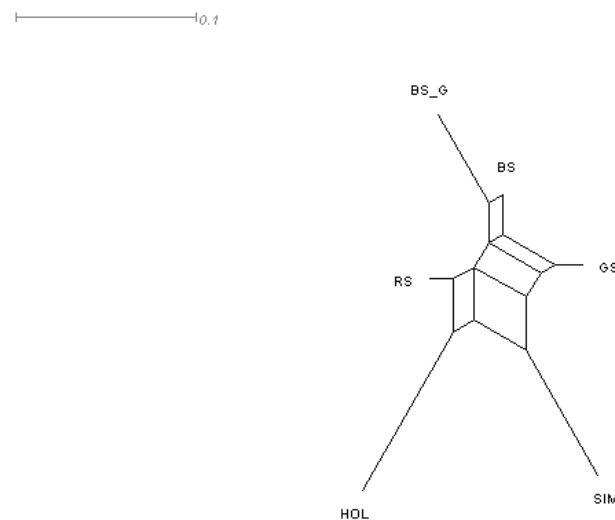


Figure 1. Dendrogram based on pairwise genetic distances (Djost), plotted using the NeighborNet algorithm.

Based on cluster analysis, an endemic population of mountain cattle was identified. Most of the identified endemic animals belonged to the samples from the most remote area, characterized by rocky and rugged terrain. The remaining cattle groups showed a high degree of membership in their own cluster. In addition, we found differences between Brown Swiss from Caucasian branch and those, which were brought from Germany.

Based on different approaches, we found that GS was characterized by high degrees of polymorphism and genetic diversity. This peculiar pattern might correspond to the following factors. The samples of GS were collected from different private owners, which did not provide any information whether their animals were crossed with other breeds or not. Besides the cattle owners in some villages form the united herd, which is moved to the shared pastures and is managed by single herdsman. The united herd includes cattle from different breeds, which probably might be admixed. This agreed with a finding that GS and RS share a part of their genome and that the artificial strain BS is already introgressed by the original genome of the region.

However, the recognition of distinguished group of animals within GS population might indicate on the presence of original endemic GS population in the remote isolated areas of the Dagestan region.

4. Conclusions

Thus, our study provides the most complete data on the state of allelic diversity and genetic differentiation of mountain cattle in the Republic of Dagestan compared to other breeds.

The preservation of the valuable gene pool of mountain cattle is necessary for the further development of animal husbandry in the mountains of Dagestan. Comprehensive conservation programs are required to reduce inbreeding and to increase the effective population size of this local breed cattle.

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