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Study of genetic diversity of Dagestan Mountain cattle based on STR-markers

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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.

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.

Valuable biological features:

1. A strong constitution and the presence of strong hooves
2. Survival rate
3. Unpretentiousness
4. Adaptability to extreme mountain conditions

Disadvantages:

1. Low milk productivity
2. Low live weight
3. Weak selection and breeding work

The aim of our study is to characterize modern allele pool and to assess genetic diversity of Dagestan Mountain cattle using STR markers

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

Results

A total of 117 alleles at 11 loci were found in the studied populations. The total num-ber 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.

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 vary-ing from 0.016 to 0.148 in the studied populations.

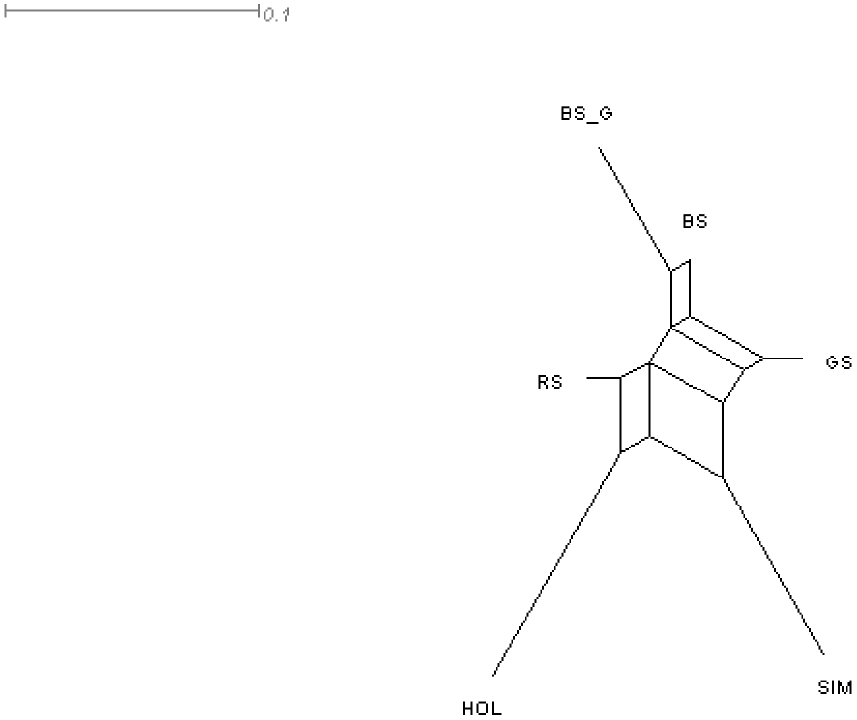
Genetic diversity parameters estimated for 11 microsatellite markers by cattle breeds

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

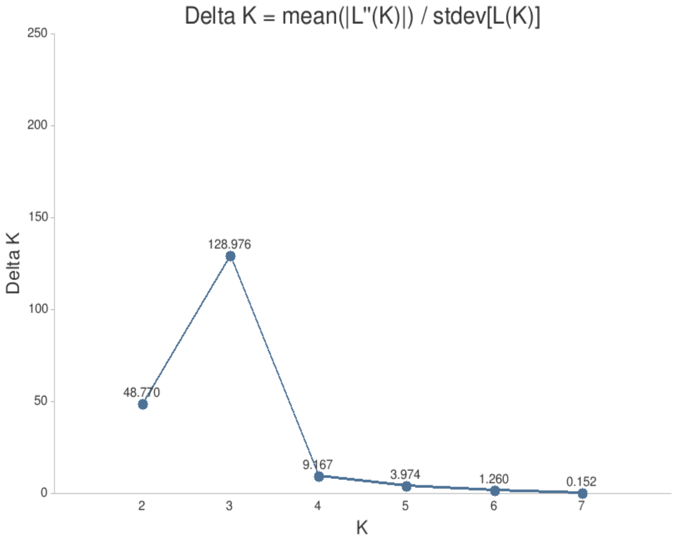
Results

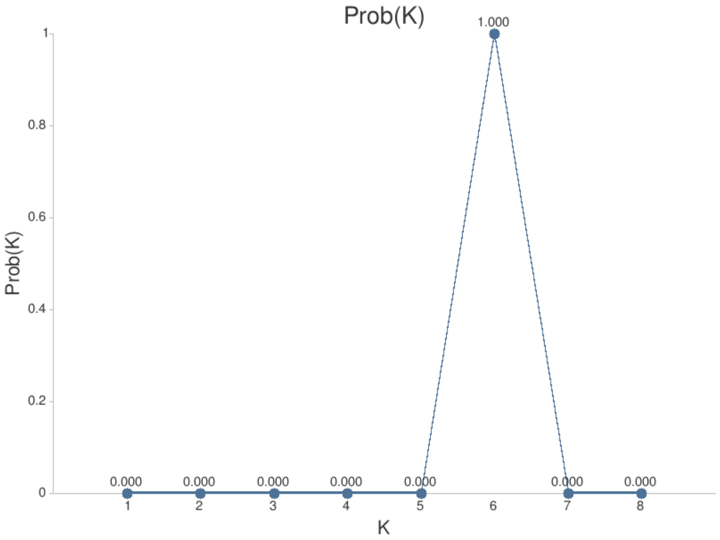
Analysis of the Neighbor Net graph showed a presence of genetic relationships between the GS, BS, and RS groups as well as provided evidence of a common origin of the BS and BS_G groups. Holsteins and Simmentals formed separate branches.

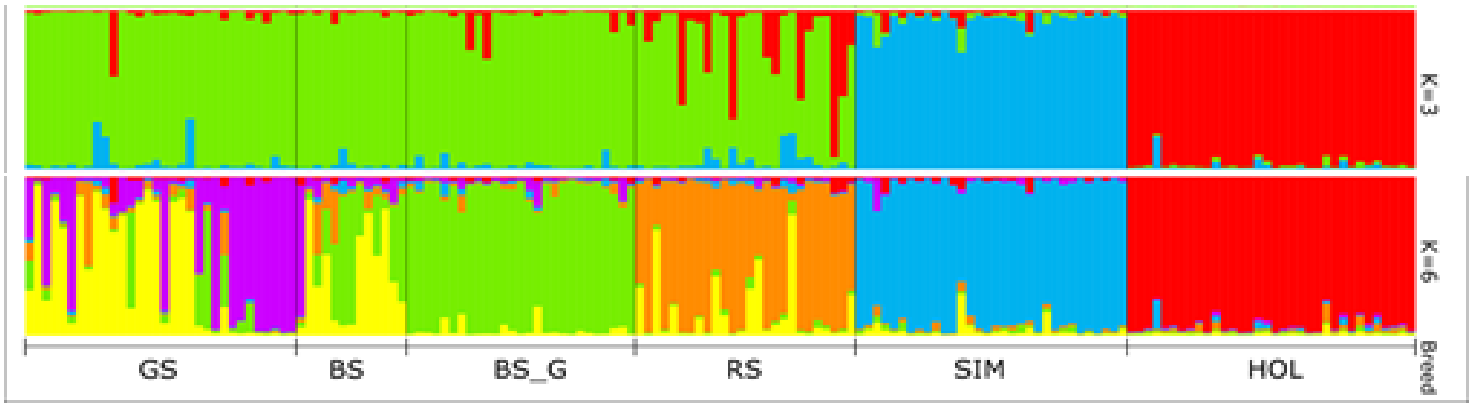


Dendrogram based on pairwise genetic distances (DJost), plotted using the NeighborNet algorithm

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.







Acknowledgments

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Thank you for your attention!

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