

ALLELE POOL CHARACTERISTICS OF BASHKIRIA POPULATION OF SIMMENTAL CATTLE USING MICROSATELLITES

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Summary

The allele pool study of Bashkiria population of Simmental cattle using twelve microsatellite loci comparing to pure breed (Novosibirsk, Orel and Austrian) and holsteinized populations was carried out. It was shown that Bashkiria population comparing to other pure breed populations under relative low level of genetic diversity (7.08 ± 0.72 against $7.08-8.83$ alleles per loci) was characterized by the highest number of effective alleles (4.11 ± 0.37 against $3.17-4.00$ alleles per loci). The differences among population (F_{st}) were 3.9 per cent. The highest contribution of Bashkiria population into the total variability of microsatellites was shown. The highest value of similarity coefficient (Q) of individuals of Bashkiria population comparing to other populations was observed: 84.6 ± 2.2 against $36.3-74.9$ per cent. The phylogenetic analysis showed the forming of the separate branch of Bashkiria population on the genealogical tree.

Keywords: microsatellites, Simmental cattle, biodiversity.

Maintenance of genetic diversity in farm animals' breeds is considered as a prerequisite for effective selection and breeding work in both individual herds and breeds (1).

Complete assessment of diversity in animal breeds and creation of their genetic passports requires the study of the greatest possible number of geographically distant populations. A significant contribution into allelic diversity of breeds is provided by regional populations whose allelic pool in most cases was formed in relative geographic isolation on the basis of local cattle carrying own unique alleles (2, 3). Along with it, genetic diversity of local populations is affected by specific regional abiotic factors.

DNA markers are used as a tool in genetic studies of populations and evolutionary issues (1, 4). Microsatellites are the most common type of these markers (3, 5). The applied importance of microsatellites has been confirmed by multiple researches on characterization of new cattle types (6), assessing the state of populations (7), monitoring and management of population structure (8).

Simmental breed is one of the major cattle breeds of a dairy-beef productivity type. According to the World Simmental Fleckvieh Federation (WSFF), there are about 40 million goal. cattle of this breed in the World. In livestock farms of Bashkiria, Simmental is the second largest breed.

The purpose of this work was a comparative study of allelic pool in Bashkir population of Simmental cattle using microsatellites.

Technique. The material for analysis were tissue samples (ear notches) of Simmental cows the Baimak type (Experimental Farm "Baimakskoe", Bashkiria) (SIM_B, $n = 80$). These samples were compared with the biological material derived from different populations of Simmental cows: Siberia (SIM_SIB, $n = 156$), Orel province (SIM_OR, $n = 56$) and Austrian (SIM_A, $n = 89$) purebred populations along with a holsteinized population (SIM_H, $n = 147$) (storage of the Center of Biotechnology and Molecular Diagnostics of the All-Russia Research and Development Institute for Livestock Husbandry (VIZh). DNA extraction and amplification of microsatellites (TGLA126, TGLA122, TGLA227, ILST005, ILST006, ETH185, ETH10, ETH225, BM1818, BM1824, BM2113, SPS115) were performed using the model test system for genetic examination of cattle (LLC "Biostrim", Russia). Detection of results was performed on the genetic analyzer ABI Prism 3130xl ("Applied Biosystems", USA).

Statistical processing of data was conducted according to B. Weir (9), using Microsoft Excel 2007 package with the plugin GenAlEx v. 6.4. The individuals' identity to populations was established using the method of J.K. Pritchard et al. (10) in the software Structure (v. 2.3.1). Calculations were carried out according to the admixture model and correlation model without introducing the prior data about individuals' belonging to a particular population. The analysis was performed considering the most probable number of populations ($k = 5$) and the threshold value of the similarity coefficient (Q) equal to 75% individual genetic identity to own population. Genetic distances were found as described by M. Nei et al. (11).

Results. The analysis of microsatellite allelic profiles revealed the absence of significant differences in diversity between all studied populations of Simmental cattle (Fig. 1).

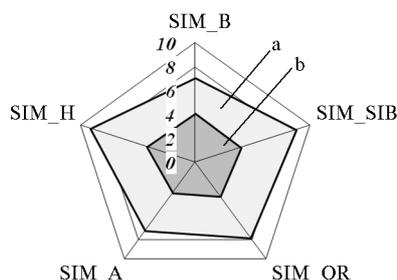


Fig. 1. Characteristics of genetic diversity of microsatellites in studied populations of Simmental cattle: Bashkir (SIM_B), Siberian (SIM_SIB), Orlov (SIM_OR), Austrian (SIM_A) purebred populations and holsteinized (SIM_H) population; a – average number of alleles per locus (N_a), b – number of effective alleles per locus (N_e).

Average number of alleles per locus in various microsatellites ranged from 7.08 ± 0.58 (Austrian population) and 7.08 ± 0.72 (Bashkir population) up to 9.17 ± 1.07 (Holsteinized cattle) while the mean for all populations amounted to 9.00 ± 0.37 . Bashkir

population was characterized by a relatively low genetic diversity and the highest number of effective alleles per locus ($4,11 \pm 0,37$) compared to other purebred populations, in which this index varied from $3,17 \pm 0,24$ to $4,00 \pm 0,47$. Holsteinized population of Simmental cattle showed higher values of the total number of alleles and effective number of alleles per locus, probably owing to the combination of allelic pools of two breeds (Simmental and Holstein Red-Motley).

The analysis of allelic profiles of microsatellite loci revealed their different contributions into inter-population variability (Fig. 2).

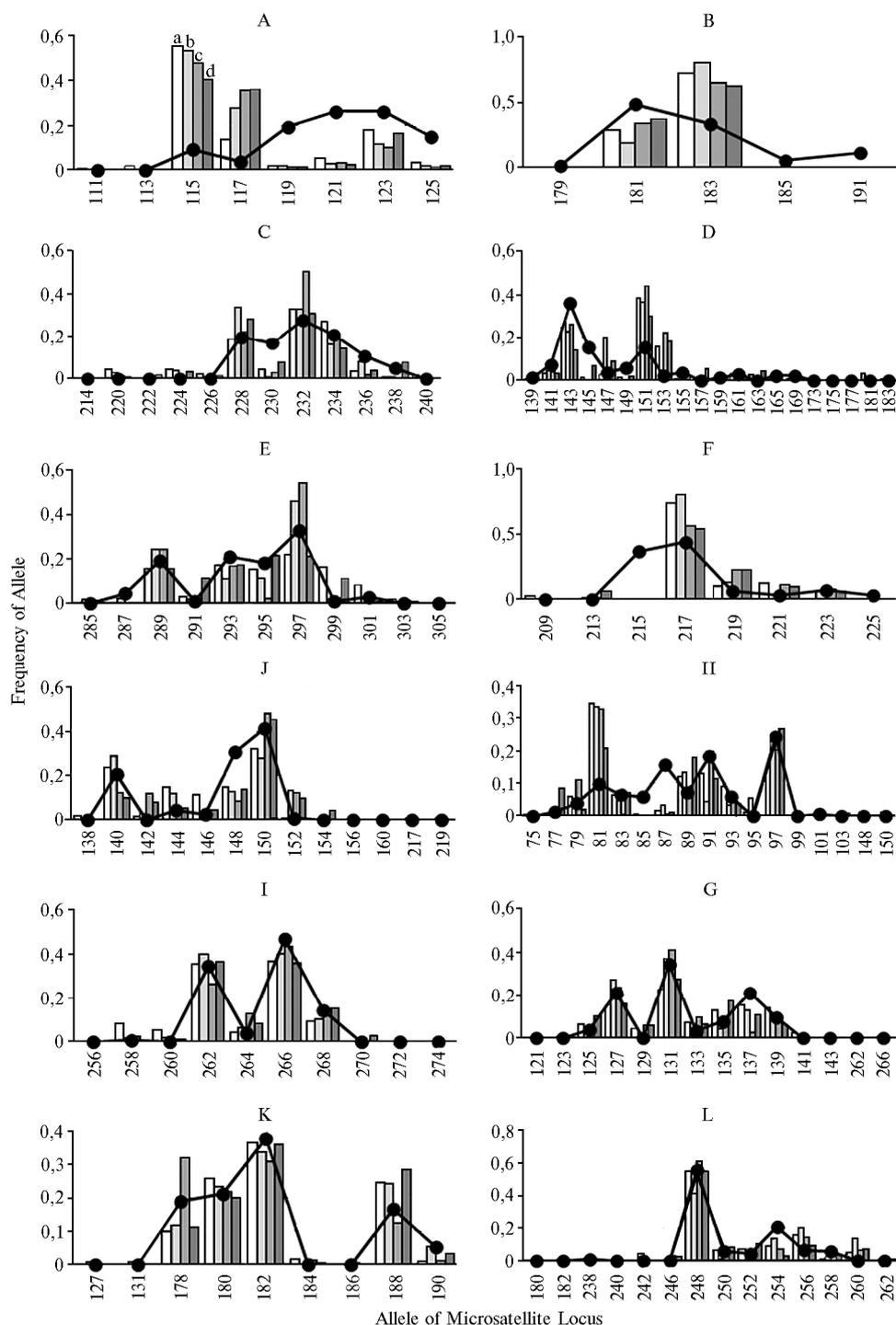


Fig. 2. Comparative characteristics of allelic profiles of Bashkir population of Simmental cattle (diagram) for microsatellite loci: A-L — respectively, TGLA126, ILST005, ETH185, TGLA122, ILST006, ETH10, ETH225, TGLA227, BM1818, BM2113, BM1824, SPS115; a, b, c, d — respectively, Siberian (SIM_SIB), Orlov (SIM_OR), Austrian (SIM_A) purebred populations and holsteinized (SIM_H) population of Simmental cattle.

The lowest value of this characteristic was found in the locus BM1818 (fixation index F_{st} equal to 1,0%), relatively low F_{st} values were established in the loci BM1824, BM2113, SPS115, ETH185 and TGLA227 (respectively, 1,6; 1,9; 2,3; 2,3 and 2,6%). The greatest contribution to inter-population variability was provided by the loci ILST005, ETH10 and TGLA126 (F_{st} values, respectively, 7,5; 8,2 and 8,8%). In total, the differences between populations accounted for 3.9% of the total variability of microsatellites.

The highest contribution into the variability was formed by Bashkir population of Simmental cattle: F_{st} values at paired comparisons with SIM_SIB, SIM_OR, SIM_A and SIM_H populations amounted to, respectively, 3,6; 4,5; 3,8 and 2,9%, whereas in pairs SIM_SIB-SIM_OR, SIM_SIB-SIM_A, SIM_SIB-SIM_H, SIM_OR-SIM_A, SIM_OR-SIM_H and SIM_A-SIM_H values of this index were significantly lower – 1,2; 1,8; 1,2; 1,8; 1,9 and 1,4%.

Results of cluster analysis showed a high degree of genetic consolidation in Bashkir population of Simmental cattle:

similarity factor (Q) averaged $84,6 \pm 2,2\%$, while $86,3\%$ of these animals exhibited the value over 75% (Fig. 3). At the same time, Q values in populations SIM_SIB, SIM_OR, SIM_A and SIM_H amounted to, respectively, $59,1 \pm 2,4$; $45,2 \pm 4,4$; $74,9 \pm 2,2$ and $36,3 \pm 3,2\%$.

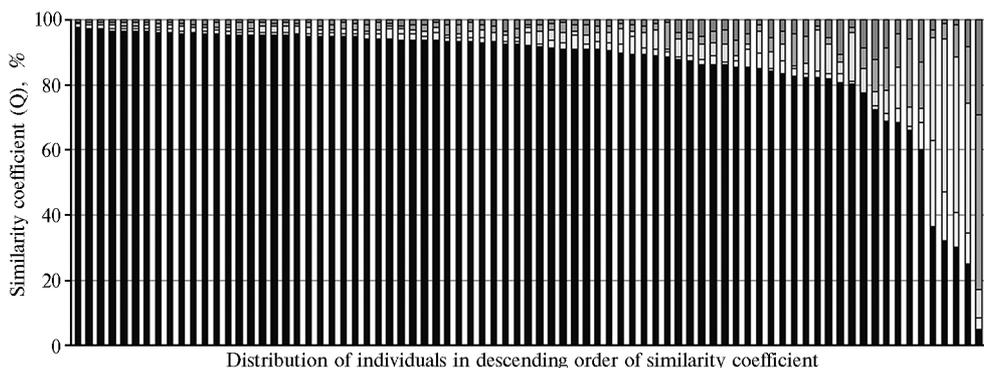


Fig. 3. Clustering of five studied populations of Simmental cattle (Siberian, Orlov, Austrian, Bashkir purebred and holsteinized). Individuals are shown as bars of different color filling ($k = 5$) corresponding to the number of analyzed populations.

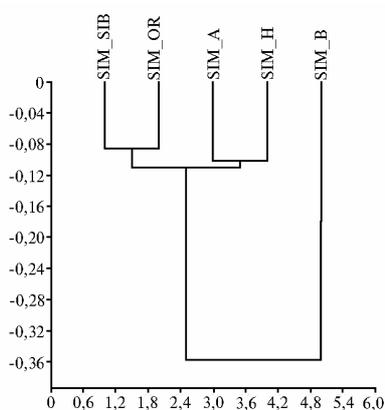


Fig. 4. Dendrogram of phylogenetic relationship of five populations of Simmental cattle designed upon the values of genetic distance according to M. Nei et al. (11) using unweighted pair-group method with arithmetic mean (UMPGA): Siberian (SIM_SIB), Orlov (SIM_OR), Austrian (SIM_A) purebred and holsteinized (SIM_H) populations.

Genealogical tree of the studied populations designed according to M. Nei et al. (11) demonstrated the formation by Bashkir population of a separate branch (Fig. 4) participating the creation of cattle of different origin.

Thus, five populations of Simmental cattle (four thoroughbred and one holsteinized population) were studied and a significant contribution of Bashkir population into the total variability of microsatellite allelic pool of this breed was established. Findings of this research indicate the importance of regional populations for genetic monitoring of cattle breeds.

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