

THE CHARACTERISTICS OF ALLELE POOL OF YAKUT CATTLE USING MICROSATELLITES

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Summary

The DNA bank of Yakut cattle consisting of 461 samples was created. The study of Yakut cattle population comparing to Holmogor and Mongolia cattle using ten microsatellites was carried out. Essentially lower number of effective alleles per loci (3.46 ± 0.28) in Yakut cattle population was observed that is probably due to limited number of bulls used for breeding. 100 per cent individuals of cattle breeds analyzed were assigned to own populations. The closer relation of Yakut cattle population to Holmogor cattle as to Mongolia cattle was determined.

Keywords: microsatellites, allele pool, polymorphism, cattle, Yakutskaja breed.

Today, biological science pays a lot of attention to characterization of the gene pool of domesticated species and preservation their diversity (1-2). Maintenance of genetic diversity of farm animal species is in focus of the FAO (Food and Agriculture Organization) modern concept on plant genetic resources (3).

Yakut cattle is the unique cattle breed bred in the vast territory of Yakutia (the Republic of Sakha) (4). It is known that cattle inhabited Siberia - from Yakutia to the Pamir, from the Far East to the Urals, in parts of northern India, the Chinese steppes - 2500 years BC (5). This large group of cattle is believed to have a common ancestor *Bos taurus primegenius nomadicus*. According to craniological classification of E.F. Liskun (5), the group of *Bos taurus primegenius* includes aboriginal domestic cattle breeds: Yaroslavl, Kholmogory, Istoben, Tagil, Siberia cattle. Yakut breed is the last representative of native aboriginal cattle of Eastern Asia, related to the Turano-Mongolian root of *Bos taurus* (6). The subspecies *Bos taurus turano-mongolicus* includes Kalmyk, Kyrgyz, Yakut, Siberia, Soyot, Mongolian and Manchurian cattle (7).

Earlier, J. Kantanen et al. has performed a detailed microsatellite analysis of genetic diversity in purebred Yakut cattle and in two hybrid populations of this breed (8); results of these studies have been compared with data on Eurasian cattle breeds bred in the territory of Western Europe and the former Soviet Union (9, 10). This work was continued by the comparative study of mitochondrial DNA, particularly, sequencing the D-loop, and the analysis of Y-chromosomal markers polymorphism in order to determine genetic divergence of *Bos taurus* breeds (11). European cattle breeds diverged 10 000 years ago, after which the modern European and North Asian cattle have been developing as a separate group. Besides, large areas of Eurasian continent and its climatic features have contributed to formation of *Bos taurus turano-mongolicus* cattle type having small craniological differences from *Bos taurus primegenius* (11-12).

Cattle has been bred in Yakutia for thousands years. A local Yakut cattle had been "purebred" until 1929. Later, there was a widespread practice of crossing Yakut cattle with bulls-sires of Kholmogory breed (2), and since 1937 - with Simmental bulls, most of which were the 3rd and 4th generations of descendants from crosses with lines had originated from Switzerland and Germany and brought to Yakutia from the Sychevsky Pedigree Farm (13). Today, there are only 1000-1200 individuals of the "purebred" aboriginal Yakut cattle (2, 14).

The purpose of this research was molecular genetic characterization of allelic pool of Yakut cattle in comparison with Mongolian and Kholmogory cattle breeds.

Technique. The material for analysis were tissue samples (ear notches) of the cattle. The databank of DNA was created using the samples obtained from animals of Yakut breed ($n = 461$) (farms of the State Enterprise "Bytantay", Sakkyryr, Kustur, Taastaakh, Dodor, Kylys and Olom kel', the Republic of Yakutia). Comparative molecular genetic studies were performed upon DNA samples of 23 cows of Yakut breed and two other cattle breeds related to the craniological type *Bos taurus primegenius* including Kholmogory (Pechora type, $n = 39$) and the local Mongolian cattle ($n = 39$).

DNA was isolated using the reagent kit DiatomTM DNA Prep100 ("Laboratory Isogen", Russia). The cattle was genotyped for 10 microsatellite loci (TGLA126, TGLA122, TGLA227, ILST005, ILST006, ETH185, ETH10, ETH225, BM1818 and BM2113) using methodical developments of the Center of Biotechnology and Molecular Diagnosis of the All-Russia Research and Development Institute for Livestock Husbandry (VIZh). DNA analysis and PCR were performed as prescribed (15). Amplification fragments were identified on the genetic analyzer ABI Prism 3130xl ("Applied Biosystems", USA) with capillary electrophoresis and laser detection.

Statistical processing of data was done using GenAEx software (v. 6.4) (16). The identity of cattle to own population was estimated according to D. Paetkau et al. (17). Analysis of results was carried out as described previously (18-24).

Results. Analysis of DNA profiles of the studied breeds showed significantly lower genetic diversity of Yakut cattle (Fig. 1) compared with two other breeds. In Yakut cattle, average number of alleles per locus was $5,60 \pm 0,50$, while in Kholmogory and Mongolian cattle - $7,10 \pm 0,94$ and $8,90 \pm 1,17$, respectively.

A lower genetic diversity of Yakut cattle was reflected by the smaller number of informative and effective alleles - respectively, $3,70 \pm 0,34$ and $3,46 \pm 0,28$ vs $4,60-5,80$ and $4,37 - 4,90$ in Kholmogory and Mongolian breeds.

In Yakut cattle, a reliable deviation from genetic equilibrium was revealed for 3 of 10 microsatellite loci, in Kholmogory breed - for 8 of 10 loci, while in Mongolian cattle, on the contrary, no significant shift from the equilibrium of loci were found. Such

deviation from equilibrium indicates the inbred state of population, which can result from a limited number of producers and a group breeding technology.

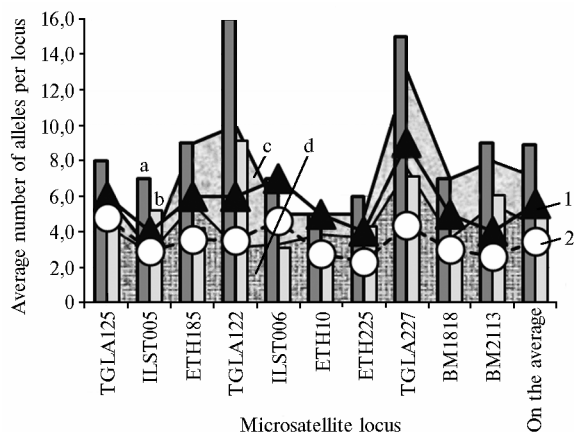


Fig. 1. Allele patterns for 10 microsatellite loci in studied cattle breeds: a, b – respectively, average number of alleles (N_a) and number of effective alleles per locus ($N_e = 4,92 \pm 0,65$) in Mongolian cattle; c, d – the same parameters of Kholmogory breed ($N_e = 4,37 \pm 0,46$); 1 and 2 – the same parameters of Yakut cattle ($N_e = 3,46 \pm 0,28$).

The analysis of calculated levels of observed and expected heterozygosity revealed the deficit of heterozygotes in all studied cattle breeds (Fig. 2).

Minimal deficit of heterozygotes was found in Mongolian cattle (1,0%), a maximal – in Kholmogory (11,9%), while in Yakut breed heterozygote deficit amounted to 8,7%.

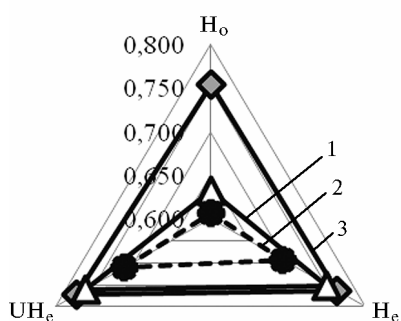


Fig. 2. Observed heterozygosity (H_o), expected heterozygosity (H_e) and unbiased expected heterozygosity (UH_e) degrees in cattle breeds – Kholmogory (1), Yakut (2) and Mongolian (3).

The deficit of heterozygotes was also suggested by positive values of index of fixation F_{is} ranging from 1,4% (population of Mongolian breed) to 16,0% (Kholmogory cattle of Pechora type).

The analysis of genetic consolidation of the animals (17) showed that all individuals of the studied cattle groups were genetically identical to own breeds (Fig. 3).

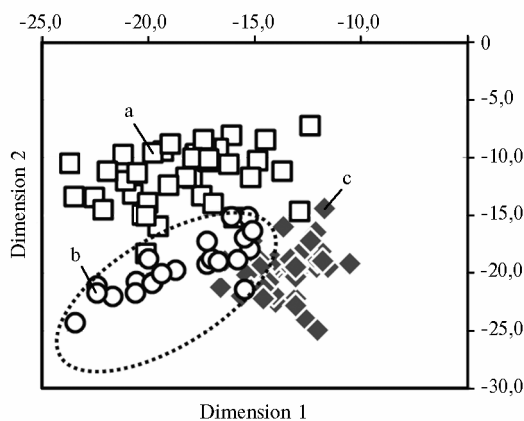


Fig. 3. Population comparison of studied cattle breeds according to D. Paetkau et al. (17): a — Kholmogory breed, b – Yakut cattle, c – Mongolian cattle. Dotted line shows an area occupied by Yakut cattle.

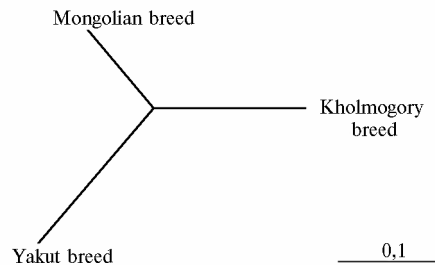


Fig. 4. Genealogical tree of three aboriginal cattle breed designed according to M. Nei et al. (25). Genetic distances between Kholmogory and Yakut breeds 0,378, between Kholmogory and Mongolian breeds — 0,283, between Yakut and Mongolian breeds — 0,360.

The data presented in Figure 3 indicate that Yakut, Mongolian and Kholmogory cattle breeds form distinct clusters including 100% individuals of each studied population. It should be noted that Yakut cattle occupies an intermediate position between Mongolian and Kholmogory breeds.

The analysis of F_{st} values calculated using molecular variance (AMOVA) showed that inter-individual variability amounted to 74%, inter-population and intra-individual - 13%. The comparison of data obtained using R_{st} criterion revealed that total variability was formed by 75% inter-individual variability, 24% inter-population variability and only 1% - intra-individual diversity. The observed differences were reflected by the structure of the genealogical tree (Fig. 4).

According to the analysis of genetic distances (Fig. 4), Yakut breed is genetically somewhat closer to Kholmogory cattle rather than to Mongolian breed, which can be the result of using Kholmogory sires in crosses with Yakut cattle in 1930ies.

Thus, three studied cattle breeds have 100% genetic consolidation. The identified genetic characteristics indicate that aboriginal cattle breeds are the carriers of a unique pool of alleles being the irreplaceable source of valuable genetic resources that must be protected and preserved.

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