

Genetic structure analysis of 157 transboundary and local populations of cattle (*Bos taurus*, *Bos indicus* and *Bos grunniens*) based on STR markers

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Motivation and Aim: According to the International Food Organization of the United Nations (FAO), biodiversity conservation is one of the most pressing problems of modern agriculture [1]. To develop breeding programs and programs for the conservation of rare breeds, methods of molecular genetic analysis, including those using STR markers, are widely used. In order to determine the population genetic characteristics, as well as to clarify the phylogenetic relationships of 157 cattle populations from different regions of the world, the analysis of the genetic variability of 12 highly variable microsatellite loci was carried out.

Methods and Algorithms: The study object was the original STR analysis data of 30 cattle populations provided by the laboratory team in the course of previous studies [2], as well as data obtained using microsatellite analysis of 127 populations, from open sources using the Mendeley Data database. Before combining this data into one array the data were reduced to a general form by eliminating nucleotide shifts calculated using heat maps. The genetic distance matrices were calculated using the Hierfstat and PopGenReport packages of the R environment. To reconstruct the phylogenetic tree using the poppr R-package and the Trex-online program the Neighbor-Joining approach was implemented. The visualization of the tree by the type of a circular dendrogram followed by the color identification of clusters was performed using the tools of the ITOL application. Allelic diversity parameters, observed and expected heterozygosity, fixation index, and Hardy-Weinberg equilibrium were calculated using the PopGenReport R-package.

Results: Using STR analysis data, 157 cattle populations from different geoclimatic zones were analyzed in order to study their genetic diversity and phylogenetic relationships. The main attention was paid to the analysis of poorly studied local breeds. Cluster analysis based on genetic distances, as well as plots of data display using principal components analysis, made it possible to distinguish three large groups: 1) yaks (*Bos grunniens*), 2) zebu (*Bos indicus*) and African cattle, and 3) domestic cattle (*Bos taurus*). The greatest phylogenetic distances from a common ancestor were noted for yaks, which correlates with the modern idea of the phylogeny of cattle. The introgression of zebu genes into the gene pool of African cattle has been noted in a number of works [3, 4], which explains their joint clustering. A high level of allelic diversity was identified among cattle breeds from Spain, Italy, Russia, Kyrgyzstan, Brazil, Colombia, Mexico, Mozambique, Egypt, Suriname and Kenya, as well as among Creole cattle. Analyzing the list of private alleles, we noted that all the identified unique allelic variants are

characteristic of local breeds of *Bos taurus* from different countries, populations of domestic Yak and Zebu.

Conclusion: The results obtained during the study can be used to improve the efficiency of breeding and conservation programs of local breeds in different countries.

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References

1. Bélanger J., Pilling D. (Eds.). The State of the World's Biodiversity for Food and Agriculture. FAO Commission on Genetic Resources for Food and Agriculture Assessments. Rome. 2019.
2. Svishcheva G. et al. Microsatellite diversity and phylogenetic relationships among East Eurasian *Bos taurus* breeds with an emphasis on rare and ancient local cattle. *Animals*. 2020;10(9):1493.
3. MacHugh D.E. et al. Microsatellite DNA variation and the evolution, domestication and phylogeography of taurine and zebu cattle (*Bos taurus* and *Bos indicus*). *Genetics*. 1997;146(3):1071-1086.
4. Decker J.E. et al. Worldwide patterns of ancestry, divergence, and admixture in domesticated cattle. *PLoS Genetics*. 2014;10(3):e1004254.