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ANALYSIS OF GENETIC STRUCTURE IN UKRAINIAN MOUNTAIN CARPATHIAN SHEEP FROM DIFFERENT BREEDING AREAS BY USE OF DNA MARKERS

T. Chokan[1], PhD, *A. Radko[2]*, Dr. Sc., *S. Tarasjuk[3]*, Dr. Sc., *A. Szumiec[2]*, PhD, *D. Rubis[2]*
tchokan@ukr.net, anna.radko@izoo.krakow.pl, tarasjuk@ukr.net

[1]Institute of Animal Biology of NAAS, Lviv, Ukraine
[2]National Research Institute of Animal Production, Balice near Krakow, Poland
[3]Institute of Fisheries of NAAS, Kyiv, Ukraine

The study and analysis of genetic structure is necessary to monitor changes in the genetic potential and contains information about the processes that occur in populations. The genetic structure of the population is determined mainly by the diversity of the gene pool, which includes both the general properties of species and genetic features that have arisen under adaptation of the population to the specific conditions of its existence. Thus the analysis of the genetic structure of Mountain Carpathian sheep from different breeding areas in the Carpathian region, its monitoring using different types of molecular genetic markers is the issue of vital importance.

Material was taken from sheep of different age groups and both sexes in «Bansko» farm (Rakhiv district) — mountainous area from 25 heads of animals and «Saldobosh» farm (Khust district), Transcarpathian region — low-lying area in the amount of 26 heads.

Genetic analysis of sheep groups, for the use of DNA markers conducted based on the recommended list of the International Society for Animal Genetics (ISAG), for assessing biodiversity sheep by using different fluorescent coloring labeling fragments. In consideration of the criteria and ISAG recommendations, were selected 11 microsatellite loci: Oar304, HSC, Oar129, MAF214, Oar11, INRA063, CSRD247, SPS113, D5S2, MAF65, McM527. Population-genetic processing of results was carried out on the basis of allele frequencies of used markers, using mathematical and statistical programs BIOSYS-1, Cervus 3.0.3, PowerStatsV12 and Excel. The frequency of detected alleles was used to calculate the following parameters: observed heterozygosity — H_O and expected heterozygosity — H_E, inbreeding coefficient — F_{IS}, polymorphic information content — PIC, defined genetic distance and cluster analysis has been conducted.

Microsatellite (STR) in most cases, are characterized by species conservatism, but the analysis revealed a number of markers specific for close groups. These markers are essential in assessing the gene pool of the species. In total 106 alleles detected, the number of which ranges from 4 (locus Oar129) in sheep with low-lying area to 14 (locus INRA63) in animals with mountainous area. Polymorphism Index averaged 0.7420 for animals from mountain areas, which more than 0.0381 of lowland sheep breeding zones. The limits of this indicator were from 0.5334 (locus Oar304) to 0.8472 (locus HSC) in sheep «Bansko» farm and 0.5144 (locus Oar304) to 0.8478 (locus INRA63) in animals «Saldobosh» farm. In our studies, most alleles were detected in the locus of INRA 063 sheep «Bansko» farm at PIC 0.8655 and value of observed heterozygosity — 0.8400. The most specific alleles for flocks of sheep from mountain areas breeding are loci NRA063, and Oar304 for animals of lowlands. Average inbreeding coefficient had a low value in both groups of the (0.0496 and 0.0695 respectively) animals, indicating almost no inbreeding in studied species.

The data indicate significant levels of polymorphism and relatively independent variability of certain types of molecular genetic markers. For the distribution of gene allelic variants and genotypes in studied groups differ from one another, which of course is the result of different factors of natural and artificial selection.