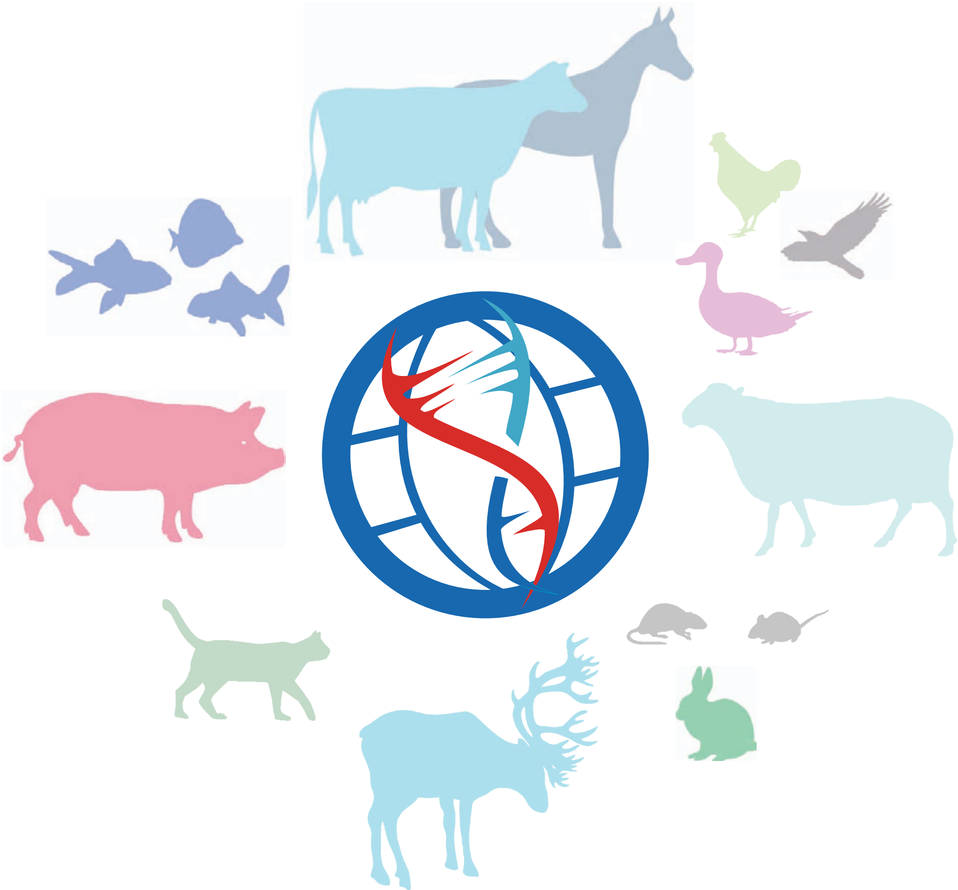
University of Agriculture in Krakow

Faculty of Animal Sciences

International Conference on Biotechnology and Welfare in Animal Science with a session on „7th Poultry Days”



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Intrabreed variability of the Ukrainian Mountain Carpathian sheep genetic structure under using of the different types of molecular genetic markers

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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 with different color wool, its monitoring using different types of molecular genetic markers is the issue of vital importance.

The research of genetic structures using different types of molecular genetic markers (DNA markers – from 11 microsatellite DNA sequences recommended by the FAO for assessing the biodiversity of sheep and genetic and biochemical systems – 13 loci).

Microsatellite (STR) in most cases, are characterized by species conservatism, but the analysis revealed a number of markers specific by close groups. In total 106 alleles were detected, the number of which ranges from 3 (locus MAF65) in sheep with white wool to 12 (locus INRA63) in sheep with gray wool. The high polymorphic information content (PIC) it was averaged 0.740 in groups of sheep with gray wool and ranged from 0.525 (locus Oar304) to 0.851 (locus HSC). In our studies, the highest polymorphism was typical for loci INRA063 in sheep with black wool, which consisted of 13 alleles while the PIC was 0,865 and the observed heterozygosity (HO) – 0.878.

The results of studies on the genetic structure of genetic and biochemical systems indicate the presence of intrabreed genetic differentiation. The data analysis proved that certain genetic and biochemical systems, particularly Tf and PN, can be used as markers for specific characteristics of the genetic structure of the studied groups of animals.

For the distribution of allelic variants of genes and genotypes studied groups differ from one another, which of course is the result of different factors of natural and artificial selection and different approaches in the process of breeding them.