

*T. Chokan, A. Radko, S. Tarasjuk, A. Szumiec, D. Rubiś. Genetic structure of Ukrainian Mountain Carpathian sheep by use of microsatellite loci*

Significant reduction of sheep population and the lack of clear selection-breeding work in Ukraine, have led to partial and in some cases complete loss of specific gene pools of local breeds. Intensification of the selection process accelerates absorption of uncompetitive breeding material, which primarily is mostly local (native) breeds, reducing their number, in consequence of which is rapidly decreasing natural diversity of animals. Using crossed with imported breeds doesn't solve the general problem of reconstruction and development of the sheep industry, while resulting in the loss of local breeds features, increasing the number of diseases, including genetically caused ones.

The natural basis of Carpathian Mountain sheep is native (local) thick-fiber wool sheep, a typical representative of such sheep breed is Tsakel. Since the middle of last century, by a long reproductive crossbreeding of local thick-fiber wool ewes of Carpathian Mountain sheep with the rams of Tsigay breed, a Ukrainian Carpathian Mountain sheep breed combined with wool-milk-meat-sheep skin direction of productivity was created, and, in 1993, was approved.

To study the polymorphism of microsatellite loci and molecular genetic estimation of Ukrainian Mountain Carpathian sheep we investigated the use of molecular genetic markers – microsatellite DNA sequences recommended by FAO for assessing biodiversity sheep.

Material was taken from both sexes sheep of different age groups in "Bansko" farm, Rakhiv district – mountainous area and "Saldobosh" farm, Khust district, Transcarpathian region – low-lying area in the amount of 49 head.

Genetic analysis of groups of sheep by the use of DNA markers was conducted based on the recommended list of the International Society for Animal Genetics (ISAG), for assessing sheep biodiversity by using different fluorescent coloring for labelling fragments. Given the criteria and recommendations of ISAG, we selected 11 microsatellite loci: Oar304, HSC, Oar129, MAF214, Oar11, INRA063, CSRD247, SPS113, D5S2, MAF65, McM527.

The analysis revealed significant genetic differences in the use of microsatellite markers in sheep of this breed. We found a total of 106 alleles, which number ranges from 6 (D5S2 locus) to 13 (INRA63 locus). The identified alleles were used to determine polymorphism of markers. Based on the calculation of allele frequencies heterozygosity values (H), polymorphic information content (PIC) and inbreeding coefficient ( $F_{IS}$ ) were determined. The results showed that the markers had a high degree of polymorphism.

The polymorphic information content (PIC) averaged 0,740 and ranged from 0,53 (Oar304 locus) to 0,84 (HSC locus). In our studies, the highest polymorphism was typical for INRA 063 locus, which consisted of 13 alleles with polymorphic information content (PIC) – 0,838 and observed heterozygosity ( $H_O$ ) – 0,857. High variability was also detected for loci HSC, Oar11 and SPS113, where it was identified more than 9 alleles, and the value of PIC and  $H_O$  varied from 0,74 and 0,84 (SPS113) to 0,89 and 0,81 (Oar11). The lowest polymorphism was noted for

Oar304 locus where it was found 9 allelic variants, but two of them (164 and 170 bp) had much higher frequency of 0,28 and 0,57. PIC and  $H_O$  values for this locus were 0,53 and 0,47, respectively. The other markers exhibited a similar polymorphism, with the number of alleles in the range of 8-11 and PIC and  $H_O$  values ranging from 0,65 and 0,61 (Oar129) to 0,72 and 0,70 (MAF65).

Thus, information on the genetic structure of Ukrainian Mountain Carpathian sheep breed and its diversity at the genomic level was obtained by use of 11 microsatellite loci. The specific features of the structure of the gene pool were revealed. The analysis showed a significant genetic variability of the studied microsatellite loci. Totally 106 alleles were identified that were used to determine the discussed polymorphism markers. The highest polymorphism was characterized for Oar 11, INRA063 and SPS113 loci which had more than 9 alleles, whereas the index of polymorphism (PIC) and actual heterozygosity ( $H_O$ ) exceeded 0,80. The lowest polymorphism was revealed for Oar304 locus and at the presence of 9 alleles, PIC and  $H_O$  values were 0,53 and 0,47 respectively. Average inbreeding coefficient had low negative value (0,070), indicating almost absent inbreeding within the studied breed.

The obtained information at the appropriate assessment using classical methods of selection and breeding makes it possible to control the genetic structure directly with DNA markers, and the creation of targeted groups of animals through genetic selection based on appropriate economic characteristics.

***Keywords:* genetic structure, sheep, microsatellite loci, polymorphism, genotype, allele**

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