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GENETIC STRUCTURE OF INDIVIDUAL POPULATIONS OF MOUNTAIN CARPATHIAN SHEEPS

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The specific character of genetic structure interbreed Mountain Carpathian groups of sheep with different color of wool under, the molecular-genetic markers, were studied. Revealed the structure of the gene pool, which is characteristic for different groups of sheep breeding. Shows the change in the distribution of allele frequencies depending on the area of breeding and wool color populations studied.

Genetic structure, Mountain Carpathian sheeps, markers, breeding, genotype, phenotype.

Conditioned by a number of factors steady state populations largely depends on the genetic structure. Adapting type occurs at the level of populations that constitute species and their genetic variability determines important properties such as size, performance, longevity, resistance to disease, and others. [1].

Rock formation, the emergence of rock associations, between gene interactions, genetic diversity parameters, conservation of genetic variation in domestic sheep are poorly understood genetics domestication species of animals. For routine maintenance breeding and effective use of genetic resources sheep industry requires constant monitoring of genetic breeding material. Arises the need to use modern methods of investigation of genetic structure of breeds of sheep are kept in farms of different ownership and are used both in production and in breeding work [2].

Keeping sheep in the mountain areas of the Carpathians is specific, which is that in the area there is a possibility of breeding almost exclusively rocks sheep, including Ukrainian Mountain Carpathian (UMC). This breed is well adapted to local conditions, wool, milk and meat production directly sheepskin performance of live weight 30-40 ewes, rams - 50-60 kg [3].

The aim of the research was to study the genetic structure Mountain Carpathian sheep wool of different colors on a color using molecular genetic markers.

Materials and methods research. We investigated the genetic structure Mountain Carpathian sheep with different color wool colors: white, gray and black. Material selected adults of ewes and breeding rams of the lowland breeding areas SFG "Saldobosh" p. Steblivka Hust District (ewes - 115 sheep - 6 goals) and mountainous areas - SFG "Bansko" p. Lug, Rakhiv district, Transcarpathian region (ewes - 115 sheep - 5 goals).

To study the genetic structure of different groups of sheep analyzed genetically determined polymorphism of these genetic and biochemical systems, transport proteins - TF (transferrin), PTF-2 (posttransferyn), HB (hemoglobin), receptor to vitamin D (GC D), intracellular metabolism enzymes - 6 fosfohlyukonatdehidrohenaza 6-PGD (K.F.1.1.1.44.), glucose-6-phosphate dehydrogenase G-6-PD (K.F.1.1.1.49.), metabolic enzymes exogenous substrates - Es plasma esterase: arylesteraza (K.F.3.1.1.2.) adenilkinaza AK (K.F.2.7.4.3.) Creatine CC (K.F.2.7.3.2.), hexokinase Gk (K.F.2.7.1.1.), enzymes Krebs cycle - malate dehydrogenase MDH (K.F.1.1.1.37.), enzymes of glycolysis - fosfohlyukomutaza PGM (K.F.2.7.5.1.), metabolic enzyme purine bases - purynnukleozydfosforylaza PN (K.F.2.4.2.1.).

The study was conducted on erythrocytes and plasma. Blood samples taken from the jugular vein into tubes with heparin, centrifuged (3000 rpm., 15 min.), And then selected the plasma. Red blood cells washed three times with saline. Polymorphism of proteins and enzymes was assessed by electrophoretic separation methods proteins in starch gels (13-14%) in horizontal cells followed by histochemical staining [4, 5]. Allelic variants range transport proteins detected by vertical polyacrylamide gel electrophoresis for Ganne [6]. Mathematical processing (estimates of genetic distances by M. Ney, assessment of genetic equilibrium according to the Hardy-Weinberg law, cluster analysis, genetic distances dendrohrama) was performed using the computer program "BIOSYS-1" [7].

Results. The analysis of thirteen investigated genetic and biochemical systems monomorphic appeared: MDH, PGM, AK, CK, Gk, 6-PGD, G-6-PD.

In the analysis of the genetic structure of the studied groups of sheep found locus-specific structural features of the genetic structure (Table 1).

In the experimental set sheep genetically determined polymorphism for genetic and biochemical following systems: hemoglobin, transferrin, purynnukleozydfosforylazy, arylesterazy receptor and vitamin D.

In the study of locus of hemoglobin (HB) observed two allelic variants, Hb A and Hb B, which differ in electrophoretic mobility in starch gels. No significant intergroup differences in these allelic variants were found, although the highest frequency meetings Hb variant B (0,738) was in animals SFG "Bansko" with black hair. By transferrin locus (TF) found 5 allelic variants: Tf A, Tf B, Tf C, Tf D, Tf E. largest gene frequency at locus C TF was noted in animals SFG "Saldobosh" with white wool - 0.451, while the frequency Tf A was 0,073. For posttransferynu-2 locus revealed two allelic variants - rTf F and Tf S, for which significant intergroup differences were observed. For purynnukleozydfosforylazy locus revealed two allelic variants: with high (H) and low activity (L). The advantage allelic variant purynnukleozydfosforylazy with high activity NP N characteristic of animals SFG "Bansko" with black hair and it will amount to 63%, while the white sheep SFG "Saldobosh" it was 29%.

Table 1. The genetic structure of the studied groups of sheep for polymorphic genetic and biochemical systems

Locus, allele	**Group of animals**					
	SFG "Saldobosh"			**SFG "Bansko"**		
	White wool	Grey wool	Black wool	White wool	Grey wool	Black wool
TF	n - 41	n - 40	n - 40	n - 40	n - 40	n - 40
A	0,073	0,162	0,237	0,200	0,162	0,213
B	0,207	0,162	0,138	0,213	0,200	0,188
C	0,451	0,425	0,450	0,325	0,400	0,338
D	0,268	0,237	0,162	0,262	0,225	0,250
E	0	0,013	0,013	0	0,013	0,013
PTF-2	n - 41	n - 40	n - 40	n - 40	n - 40	n - 40
F	0,707	0,600	0,713	0,662	0,700	0,650
S	0,293	0,400	0,287	0,338	0,300	0,350
HB	n - 41	n - 40	n - 40	n - 40	n - 40	n - 40
A	0,488	0,425	0,400	0,412	0,338	0,262
B	0,512	0,575	0,600	0,587	0,663	0,738

EST	n - 41	n - 40	n - 40	n - 40	n - 40	n - 40
A	0,814	0,800	0,850	0,825	0,800	0,825
B	0,186	0,200	0,150	0,175	0,200	0,175
GC	n - 41	n - 40	n - 40	n - 40	n - 40	n - 40
A	0,415	0,463	0,463	0,412	0,425	0,425
B	0,585	0,538	0,538	0,587	0,575	0,575
PN	phenotype, % n - 41	phenotype, % n - 40	phenotype, % n - 40	phenotype, % n - 40	phenotype, % n - 40	phenotype, % n - 40
H	29	45	40	53	58	63
L	71	55	60	47	42	37

According to the locus of vitamin D receptor identified two allelic variants - GC and GC A B, differing in electrophoretic mobility in polyacrylamide gels, and three genotypes - AA, AB, BB. No significant intergroup differences on the above allelic variants not found.

Using the staining mixture of substrates (alpha and betanaftylatsetatu) in different concentrations, we polymorphism was detected by substrate specificity of plasma esterase - arylesterazy. In forehrami watched two phenotypes that differ in color (red - RR and red and dark brown - RB). Between-group difference of locus by allelic variants arylesterazy unchecked.

While the frequency of allele gene to assess the variability of genetic structure in space and time in a specific area of the genome, the value of heterozygosity characterizes this local population in terms of genetic variability. We have designed and expected heterozygosis available on the locus and average heterozygosis for all loci studied (Table. 2).

Table 2.The average heterozygosis for all loci studied

Groups sheep	H all loci	wool color		
		White wool	Grey wool	Black wool
SFG "Saldobosh"	H actual	0,379±0,084	0,446±0,098	0,388±0,087
	H expected	0,471±0,051	0,505±0,051	0,476±0,059
SFG "Bansko"	H actual	0,425±0,093	0,375±0,081	0,388±0,092
	H expected	0,497±0,060	0,487±0,055	0,478±0,063

Analyzing the data of average heterozygosis at the locus studied groups of animals should be noted that the largest and the smallest value was heterozygous animals with black fur. Thus, the most important locus heterozygosis detected by transferrin in sheep farms "Bansko" (75.3%) and lowest in ewes SFG "Saldobosh" locus for esterase - 25.8%. The average heterozygosis for all loci studied highest (0.446) and the lowest (0.375) was in animals with gray wool.

Based on the index constructed identity dendrohramu to assess the genetic relationship of the studied groups of sheep (Fig. 1).

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.20       .17       .13       .10       .07       .03       .00
+----+----+----+----+----+----+----+----+----+----+----+----+

                                  *************************** "Saldobosh" white wool
                            *******
                            *     *      ******************** "Saldobosh" gray wool
                            *     ********
                            *            ******************** "Saldobosh" black wool
                            *
                            *                **************** "Bansko" white wool
                            *            *****
                            **************   **************** "Bansko" gray wool
                                         *                   "Bansko" black wool
                                         ********************
+----+----+----+----+----+----+----+----+----+----+----+----+
.20       .17       .13       .10       .07       .03       .00
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Figure 1. Dendrohrama genetic interrelations between groups of sheep

Cluster analysis showed that the genetic and biochemical systems of sheep were distributed into two main clusters. Groups of animals are differentiated by ecological and geographical characteristics, that is the main contribution to the formation of the genetic structure of natural selection made factors. Although it should be noted certain characteristics of distribution of genotypes at loci RTF-2 and purynukleotydfosforylazy that certainly made their contribution to the genetic relationships between groups. In dendrohrami group of white sheep SFG "Saldobosh", which have a low incidence purynukleozydfosforylazy with high activity, removed from animals with different color hair and forms a separate cluster.

In conclusion, it should be noted that the systematic breeding work to improve the Ukrainian Mountain Carpathian sheep by using molecular genetic techniques started recently, so research in this area should continue in the expanded animals. In this regard, the development of measures to improve and preserve this breed of sheep is now quite relevant. Using the most common male stud for return crossings, many farms can stabilize their genetic structure, and using molecular genetic markers continue to monitor its dilution or preservation in situ.

Conclusions and prospects for further research. Thus, using molecular genetic markers - genetic and biochemical systems, information on the genetic structure of Ukrainian Mountain Carpathian sheep and its diversity at the genomic level. These results suggest that in its genome gene complexes remained stable despite a rock multistage hybridization, Power and reproductive crossing. Based on molecular genetic analysis identified inside the rock groups that have a significant impact on the selection process within species and populations are found, which survived the most thoroughbred and heterogeneous group of local breeds that are directly associated with the color of wool.

We applied genetic and statistical approaches can be used to monitor the genetic structure of species and groups intrabreed sheep to establish the level of consolidation and phylogenetic relationships between them, with further genetic certification.

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