

GENETIC DIFFERENTIATION DURING BREEDS FORMATION IN CATTLE AND SMALL RUMINANTS IN THE REPUBLIC OF MOLDOVA

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Abstract

The publication presents data on the genetic structure and differentiation of populations in large and small ruminants during breed formation. The objects of the study were aboriginal sheep of the Tsushka breed, the Moldavian type of Karakul sheep, the Moldavian wool-meat-milk type of Tsigai sheep, the local wool-milk type of Tsigai breed, populations of Holstein cows (Dutch breeding origin), and the Moldavian type of Black and White cattle. It was found that the isolating character of differentiation ($D = 0.13; 0.15$) was found in the populations of sheep of the Moldavian type of Karakul and in the indigenous breed of Tsushka, as well as in the local wool-milk type of Tsigai breed and in the Moldavian wool-meat-milk type. The most heterogeneous and remote ($D = 0.24$) were the populations of indigenous sheep of the Tsushka breed and the local wool-milk type of Tsigai breed, as well as the population of the Moldavian type of Black and White cattle ($D = 0.23$) relative to the populations of Holstein cows of the Holland selection.

Keywords: sheep populations, cattle, crossbreeds, genetic distances, identities, divergence

Introduction

The key issue in determining and measuring the differentiation of any populations is the quantitative assessment of the non-random distribution of genetic variability. The studies of divergence of species and genetic differentiation of populations require analysis of heterozygosity and genetic distances, measuring different aspects of variability, which, according to Zinovieva et al. (2016), in the formation of different breeds of sheep at the inter-population level is 8.8 %.

The knowing how genetic variability is distributed among populations has important implications not only for evolutionary biology and ecology, but also for breeding and preserving breeds of productive animals. In domesticated animal species, the natural course of development is disrupted because of different methods of breeding and crossbreeding, both to improve the "old" and to create "new" breeds (Kuznetsov, 2020).

So, for example, Zorina (2018) in her research points to the diversity of selection methods and approaches in creating different types of sheep, and to the peculiarities of natural and climatic breeding conditions, which determine genetic polymorphism to varying degrees, and which can be expressed in differences in the antigenic spectrum of blood. Such an example, according to the author, can be the Trans-Baikal fine-fleeced breed and fine-fleeced sheep breeds of the North Caucasus.

Selecting methods can also set different scenarios for the evolution of populations, directing them towards isolation ($D < 0.1$) or divergence ($D > 0.2$) (Bader, 1998).

Interbreed differentiation also makes it possible to determine the genetic diversity in animal populations. Thus, when studying different breeds of sheep by 12 STR loci bred on the territory of the Republic of Belarus (Cheburanova, 2021), the established genetic distance of 0.0137-0.2130 indicated a possible reduction in the genetic diversity of sheep bred on the territory of this country.

Materials and methods

The study has been carried out in the two projects: 20.80009.5107.12 Strengthening the "food-animal-production" chain through the use of fodder resources new, innovative sanitation methods and schemes, and project 20.80009.5107.20 "Management of the genetic potential and productions of breed animals reproduced and exploited in the pedoclimatic conditions of the Republic of Moldova".

The assessment and features of the genetic structure of sheep populations by blood groups, including 14 antigens, were detected using monospecific serums on native sheep of the Tsushka breed and the bred Moldovan type of Karakul sheep (♀ Tsushka × ♂ Karakul sheep of Uzbek selection), and also on the created Moldovan wool-meat-dairy type of Tsigai sheep (♀ Local × ♂ Priazovsky meat and wool × ♂ Crimean wool and meat) and on the local wool-milk type of Tsigai breed. To establish the degree of differentiation, the local population of the wool-milk type of Tsigai breed and the indigenous breed of sheep Tsushka were compared with each other.

The evaluation of the genetic structure of the population in cows of the Holstein breed (Dutch selection) and the Moldavian type of Black-and-White cattle breed was carried out by the method of lactoprotein electrophoresis according to the Smithies (1955).

The genetic similarity index (I) between two populations using the Nei test (1987) was calculated „ P ”. It was derived using the following formula: $I_k = \sum a_1 \times b_1 / \sqrt{\sum a_1^2 \times \sum b_1^2}$, where, a_1 and b_1 refer to the allele frequencies (Ayala, 1984). The formulation for genetic distance, D , is given by: $D = -\ln I$

Discussion and results

The lactoproteins electrophoresis data obtained allowed us to estimate the proportion of structural genes that are identical in both cattle populations (I) and to estimate the average number of allele substitutions at each locus that occurred during the separate (since 2001) breeding of these breeds (Table 1).

The genetic similarity in our studies between these populations was $I = 0.77$, which, in principle, indicates their commonality in the analyzed lactoproteins, however, a genetic change ($D = 0.23$) is detected between them due to the reproductive isolating mechanism, namely, in breeding of the Black and White breed population "in itself". The Moldavian type of Black and White cattle was created by crossing local cows of Simmental breed (in the northern zone of our republic) and Red Steppe breed (from the southern part of Moldova) with bulls of Holstein and Black and White breeds, respectively (Smirnov E. et al., 2009). In terms of genetic similarity between the created type and the breeds involved in the crossings, the Moldovan type of Black and White cattle was closer ($D = 0.15$ and 0.17) to the parent breed-forming forms of the Simmental and Red Steppe cows (Smirnov et al., 2020). Despite the close relationship of these populations (the common ancestors were Holstein bulls), the value of genetic differentiation indicates that, on average, 23 alleles substitutions have accumulated for every 100 loci.

Table 1. Genetic differentiation between populations of Holstein breed and Moldavian type of Black and White cattle

Systems	Genes	Holstein breed, (n= 180)		Moldavian type of Black and White cattle, (n= 191)		$a_1 \times b_1$	I	D
		a_1	a_1^2	b_1	b_1^2			
AS ₁ -CN	A	0,041	0,0017	0,034	0,0011	0,001394	—	—
	B	0,911	0,8300	0,480	0,2304	0,43728	—	—
	C	0,052	0,0027	0,021	0,0004	0,001092	—	—
	D	—	—	0,462	0,2134	0	—	—
B-CN	A	0,891	0,7938	0,429	0,1840	0,382239	—	—
	B	0,102	0,0104	0,545	0,2970	0,05559	—	—
K-CN	A	0,819	0,6707	0,458	0,2097	0,375102	—	—
	B	0,180	0,0324	0,489	0,2391	0,08802	—	—
BLG	A	0,769	0,5913	0,473	0,2237	0,363737	—	—
	B	0,230	0,0529	0,526	0,2766	0,12098	—	—
Σ	—	—	$\Sigma 2,9859$	—	$\Sigma 1,8754$	$\Sigma 1,825$	—	—
	—	—	—	—	—	—	0,77	0,23

Table 2. Genetic differentiation between populations in sheep of the Moldavian Karakul type and the indigenous Tsushka breed (according to Buzu I, 2012)

Systems	Antigens	Moldavian Karakul type, (n=383)		Indigenous Tsushka breed, black, (n=69)		$a_1 \times b_1$	I	D
		a_1	a_1^2	b_1	b_1^2			
A	Aa	0,58	0,34	0,70	0,49	0,41		
	Ab	0,15	0,02	0,12	0,01	0,02		
B	Bb	0,65	0,42	0,50	0,25	0,32		
	Bd	0,69	0,48	-	-	0,00		
	Bg	0,72	0,52	-	-	0,00		
	Be	0,63	0,40	0,25	0,06	0,16		
	Bi	0,23	0,05	-	-	0,00		
C	Ca	0,91	0,83	0,48	0,23	0,44		
	Cb	0,75	0,56	0,38	0,14	0,28		
D	Da	0,74	0,55	0,56	0,31	0,41		
I	i	0,05	0,00	0,32	0,10	0,02		
	I	0,95	0,90	0,68	0,46	0,65		
M	Ma	0,82	0,67	0,93	0,86	0,76		
R	R	0,35	0,12	0,27	0,07	0,10		
	O	0,60	0,36	0,42	0,18	0,25		
Σ		—	$\Sigma 6,22$	—	$\Sigma 3,16$	$\Sigma 3,82$		
							0,87	0,13

In studies on sheep, the populations turned out to be more similar genetically when creating an intra-breed type of Karakul sheep (Table 2).

As can be seen from the table above, the analyzed populations have retained a lot in common with each other in genetic terms, a slight differentiation of 13% is apparently due to the homogeneity of the ecological and climatic environment during the period of breed formation, which contributed and, apparently, contributes to the greater natural selection of genotypes most adapted to this breeding area. It can be assumed that this happens regardless of the significance of the signs of productivity in animals. Also, the author notes the great genetic remoteness of the Moldovan type of Karakul from the breed-forming paternal form as Karakul of Uzbek selection ($D = 0.2586$).

A high adaptive plasticity and adaptability to environmental conditions was also shown by the bred (created) Moldavian wool-meat-milk type of Tsigai sheep, which turned out to be 85% genetically close to the local population of the wool-milk type of Tsigai breed (Table 3).

Table 3. Genetic differentiation between sheep populations of the local wool-milk type of Tsigai and Moldavian wool-meat-milk type

Systems	Antigens	Moldavian wool-meat-milk type of Tsigai sheep, (n=306)		Local wool-milk type of Tsigai, (n=134)		$a_1 \times b_1$	I	D
		a_1	a_1^2	b_1	b_1^2			
A	Aa	0,64	0,41	0,66	0,44	0,42		
	Ab	0,23	0,05	0,90	0,81	0,21		
B	Bb	0,87	0,76	0,41	0,17	0,36		
	Be	0,29	0,08	0,38	0,14	0,11		
	Bi	-	-	0,53	0,28	0,00		
	Bg	0,33	0,11	0,40	0,16	0,13		
	Bd	-	-	0,72	0,52	0,00		
C	Ca	0,65	0,42	0,41	0,17	0,27		
	Cb	0,95	0,90	0,89	0,79	0,85		
M	Ma	0,62	0,38	0,49	0,24	0,30		
R	R	0,52	0,27	0,70	0,49	0,36		
	O	0,43	0,19	0,28	0,08	0,12		
D	Da	0,55	0,30	0,68	0,46	0,37		
I	i	0,05	0,00	0,01	0,00	0,00		
	I	0,95	0,90	0,99	0,98	0,94		
Σ		–	$\Sigma 4,77$	–	$\Sigma 5,73$	$\Sigma 4,44$		
							0,85	0,15

These data indicate some "interweaving and mixing" of the analyzed populations due to similar selection conditions and the "effect" of the founder which is Tsigai breed.

To establish the genetic distance and to trace the "evolutionary history", local sheep populations were analyzed, table 4.

Genetic differentiation ($D = 0.23$) in the studied populations, in our opinion, is explained by stabilizing selection, the result of which is the geographical separation of the distribution of these sheep. The Tsushka has historically grown in the north part of Moldova, unlike the local wool-milk type of Tsigai, which traditionally, starting from 1769-1791 and after from 1806-1812 (during the period of resettlement of ethnic Bulgarians) was bred in the south of our republic, namely in

the Budjak steppe, where flocks of fat-tailed sheep of Tatars and Nogais used to graze (Lutskanov et al., 2015).

Table 4. Genetic differentiation between local sheep populations

Systems	Antigens	Local wool-milk type of Tsigai breed		Aboriginal breed of Tsushka		$a_1 \times b_1$	I	D
		a_1	a_1^2	b_1	b_1^2			
A	Aa	0,66	0,44	0,70	0,49	0,46		
	Ab	0,90	0,81	0,12	0,01	0,11		
B	Bb	0,41	0,17	0,50	0,25	0,21		
	Be	0,38	0,14	0,25	0,06	0,10		
	Bi	0,53	0,28	-		0,00		
	Bg	0,40	0,16	-		0,00		
	Bd	0,72	0,52	-		0,00		
C	Ca	0,41	0,17	0,48	0,23	0,20		
	Cb	0,89	0,79	0,38	0,14	0,34		
M	Ma	0,49	0,24	0,93	0,86	0,46		
R	R	0,70	0,49	0,27	0,07	0,19		
	O	0,28	0,08	0,42	0,18	0,12		
D	Da	0,68	0,46	0,56	0,31	0,38		
I	i	0,01	0,00	0,32	0,10	0,00		
	I	0,99	0,98	0,68	0,46	0,67		
Σ		—	$\Sigma 5,73$	—	$\Sigma 3,16$	$\Sigma 3,24$		
							0,76	0,24

Natural and ecological conditions, such as the diversity of the feed base, the difference in average daily temperatures (from south to north of Moldova, with 3-4 °C), the greatest amount of precipitation in the north-western part of the country caused phenotypic and genetic differences of local sheep and formed a heterogeneous gene pool of these populations.

Conclusions

The obtained results of genetic studies in local populations of cattle and small ruminants and in more productive breeds and types created with their participation indicate the specific features of the gene pool and the nature of their differentiation.

Thus, the great genetic proximity of the created types of sheep, in comparison with local breeds, can be explained by the fact that they were all bred and further improved in similar natural and climatic conditions of Moldova, while the original maternal basis for them were individuals of the indigenous breed of Tsushka and sheep of the local wool-milk type of Tsigai breed. In addition, in the second half of the 20th century, the main vectors of selection in sheep breeds were an increase in dairy and meat productivity, and the quality of lambskins (curls), while the gene pool of the Karakul breed and Tsigai was intensively used for that, and which together determined the genetic similarity of the studied breeds. Local animal populations (as Moldavian type of Black and White cattle, Tsushka sheep and wool-and-milk type of Tsigai sheep) evolved in the direction of divergence ($D= 0.23; 0.24$) by selecting individuals with high resistance to local climatic conditions and meeting the economic requirements of the time, which finally formed them distinctive gene pool.

The established heterogeneity of populations in sheep of the Tsushka breed and wool-milk type of Tsigai sheep, as well as the Moldovan type of Black and White cattle is a necessary condition for their further preservation, with subsequent selection as maternal bases in various breeding programs and possible inbreeding control.

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