

## GENETIC CHARACTERISATION OF POPULATIONS OF CATTLE OF HOLSTEIN BREED, CULTIVATED IN THE REPUBLIC OF MOLDOVA

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### Abstract

Are present the results of research and analysis of the antigenic spectrum of blood groups of animals in the Holstein breed SRL 'DOCSANCOM' and STE 'Maximovca'. In both certified herds in EAB locus there is a high frequency of antigen  $G_2$ ,  $O_2$ ,  $Y_2$ ,  $E'_2$ ,  $O'$ ,  $Q'$ ,  $G'$ , which is characteristic for the Holstein breed, many breeds black-and-white root as well as Moldavian type black-and-white cattle. By EAC-locus10 of the studied antigens  $R_1$  antigen is not revealed among animals STE 'Maximovca'. High frequency of antigen  $E$ ,  $R_2$ ,  $W$  and  $X_2$  characterizes the analyzed populations of animals. For single-factor locuses EAJ, EAL, EAM and EAZ observed almost the same concentration of the corresponding antigen in compared animal populations. The average frequency of antigen, or saturation of the studied populations of antigenic factors in the population of animals herd SRL 'DOCSANCOM' is 23.7%, in the animal herds STE 'Maximovca'-24, 5%. The genetic distance between populations of both analyzed populations is of little importance - 0.0687, so they sufficiently close to each other. Concentration of main allele in the herd SRL 'DOCSANKOM' is 0,6213, the herd STE 'Maximovca'-0.6667, of rare 0.2129 and 0.2727 respectively. The degree of homozygosity in the analyzed population is low, at 5.0% (SRL 'DOCSANKOM') and 6.0% (STE 'Maximovca').

**Key words:** Holstein breed, groups of blood, alleles, the index of antigenic similarities.

### INTRODUCTION

The breeding work more goes to the level of genetic analysis of selection processes in cattle breeds. Without knowledge of the genotype of the animal can not fully judge his individuality, heredity and variation, focusing only on the phenotypic traits.

At modern stage of development the selection process in dairy cattle breeding highly relevant is the use of allelic forms of the genes responsible for blood group. Codominant inheritance according to the rules of Mendel allelic genes controlling blood group and their wide variety, to differentiate specific features of the animal directly characterize the genotype (Popov, 1994, 1998). This helps to widen the forms controlling the state specific breeds, types herds from the position of the gene level heredity (Sozinov, 1992; Prokhorenko et al., 1996; Serdyuk et al., 2000).

An essential complement of immunogenetic evaluation of the gene pool of breeds make up

research materials in a separate step, which can be regarded as micropopulation.

Therefore, the aim of our study was to immunogenetic characteristic of a population of Holstein breed herds of Dutch selection, imported to the Republic of Moldova.

### MATERIALS AND METHODS

Material for investigation served the blood sampled from animals of Holstein breed of Dutch breeding herds of cattle SRL 'DOCSANCOM' (n = 202) and STE 'Maximovca' (n = 33).

Blood samples from the animals, the assay of hemolysis of erythrocytes, and the study of blood groups was performed by the standard technique, 1983. Blood group determined hemolytic test using 49 reagents of cattle, unified in international comparative tests, which detect antigens controlled by allelic genes 9 genetic systems. Frequency of antigens and alleles EAB locus (q) determined the standard method.

Immunogenetic indices of similarity (r) and distance (d) between populations were determined by the formula Serebrovsky (1970), the use of genetic similarity (r)-by subtracting d of unity. Identification of alleles EAB locus and subsequent analysis of allele-fund carried out on the following genetic parameters: total number of alleles EAB locus, the total frequency of alleles: basic, rare, the degree of homozygosity (Merkuryeva et al., 1983). The materials obtained were treated on a personal computer.

## RESULTS AND DISCUSSIONS

As a result of research and analysis of the spectrum of blood group antigen of animals Holstein breed found that in SRL 'DOCSANCOM' was found 4 (Q, T<sub>1</sub>, B', U') and STE 'Maximovca'-13 (Z', G<sub>1</sub>, P<sub>1</sub>, P<sub>2</sub>, Q, T<sub>1</sub>, T<sub>2</sub>, P', Y', B'', R<sub>1</sub>, M, U'') antigen of the 49 studied.

By EAA-locus frequency of antigen A<sub>2</sub> was 0,3713 (SRL 'DOCSANCOM') and 0,4848 (STE 'Maximovca').

By EAB-locus of the 25 studied antigens in analyzed herds haven't been identified 3 (Q, T<sub>1</sub>, B') and 9 (G<sub>1</sub>, P<sub>1</sub>, P<sub>2</sub>, Q, T<sub>1</sub>, T<sub>2</sub>, P', Y', B') antigens respectively. Revealed low incidence or absence of antigens I<sub>1</sub>, P<sub>1</sub>, B', K', P', Y'.

It should be noted that in both herds is observed high frequency of antigen G<sub>2</sub>, O<sub>2</sub>, Y<sub>2</sub>, E'<sub>2</sub>, O', Q', G', which is characteristic for the Holstein breed, many breeds black-and-white root and Moldovan type black and white cattle (Focsa et al., 2001), Figure 1. As can be seen, there is almost the same (with minor fluctuations antigen O') the concentration of the above antigens in both animal populations.

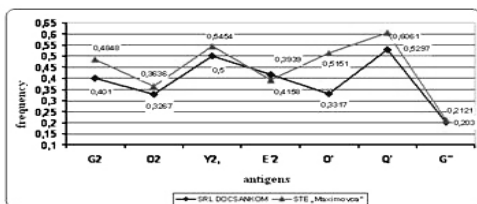


Figure 1. The frequency of some antigens EAB locus

By EAC-10 locus of the studied antigens R<sub>1</sub> antigen was not detected in animals STE

'Maximovca'. High frequency of antigen E, R<sub>2</sub>, W and X<sub>2</sub> characterized a population of animals (Figure 2).

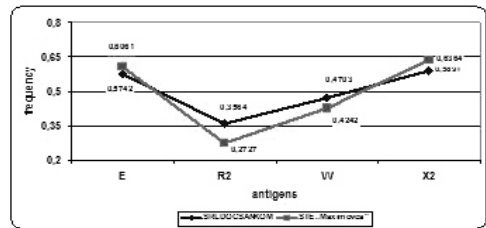


Figure 2. The frequency of some antigens EAC locus

By EAF-locus frequency of F antigen varies from 0,9356 (SRL 'DOCSANCOM') to 1,0 (STE 'Maximovca'). The frequency of V antigen varies from 0,0024 (STE 'Maximovca') to 0,1831 (SRL 'DOCSANCOM').

For single-factor locus EAJ, EAL, EAM and EAZ observed almost the same concentration of the corresponding antigen in the comparable populations of animals (Figure 3).

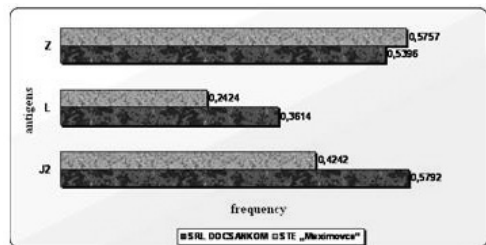


Figure 3. The frequency of antigen J2, L and Z

Antigen M is not detected at animals STE 'Maximovca', but in the herd SRL 'DOCSANCOM' its frequency is 0.0099.

By AES-locus of six studied antigens at the animals of both populations was not detected antigen "U", a significant difference in the frequency of other antigens haven't been identified.

Evaluation saturation of studied population antigenic factors showed (Figure 4) that the animals population of herd SRL "DOCSANCOM" it is 23.7%, at animal herd STE 'Maximovca' a little more – 24.5%.

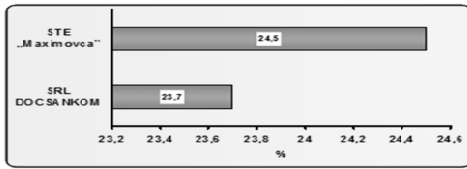


Figure 4. The saturation of cattle populations with antigenic factors

About similarities and some differences between the analyzed populations of animals can be seen Holsteins comparing their genetic structure to EAB-locus alleles.

Genetic structure of the Holstein breed animals studied population presented in Table 1 and Table 2.

Table 1. Genetic structure of the Holstein breed (SRL "DOKSANCOM") respect to alleles EAB locus

No.	allele	n	p	No.	allele	n	p
1.	B <sub>1</sub> P'	1	0.0025	41.	Y <sub>2</sub> B'D'Q'	1	0.0025
2.	B <sub>2</sub> G <sub>1</sub> I <sub>1</sub> P <sub>1</sub>	1	0.0025	42.	Y <sub>2</sub> B'G'	1	0.0025
3.	B <sub>2</sub> G <sub>2</sub>	3	0.0074	43.	Y <sub>2</sub> D'I'Q'	1	0.0025
4.	B <sub>2</sub> G <sub>2</sub> O <sub>2</sub>	1	0.0025	44.	Y <sub>2</sub> D'G'O'	2	0.0050
5.	B <sub>2</sub> G <sub>2</sub> Y <sub>2</sub> I'O'Y'	1	0.0025	45.	Y <sub>2</sub> D'G'O'G?	1	0.0025
6.	B <sub>2</sub> G <sub>2</sub> E' <sub>2</sub> I'J' <sub>2</sub> O'	1	0.0025	46.	Y <sub>2</sub> E' <sub>2</sub>	3	0.0074
7.	B <sub>2</sub> I <sub>1</sub>	1	0.0025	47.	Y <sub>2</sub> E' <sub>2</sub> I'J' <sub>2</sub> O'	1	0.0025
8.	B <sub>2</sub> O <sub>1</sub>	13	0.0322	48.	Y <sub>2</sub> E' <sub>2</sub> J' <sub>2</sub> O'	1	0.0025
9.	B <sub>2</sub> O <sub>1</sub> Y <sub>2</sub> D'	6	0.0148	49.	Y <sub>2</sub> G'	1	0.0025
10.	B <sub>2</sub> O <sub>1</sub> Y <sub>2</sub> E' <sub>3</sub> G'P'Q'G?	2	0.0050	50.	Y <sub>2</sub> G'IP'	1	0.0025
11.	B <sub>2</sub> O <sub>1</sub> Y <sub>2</sub> G'P'Q'G?	1	0.0025	51.	Y <sub>2</sub> G'J' <sub>2</sub> K'O'P'Q'G?	1	0.0025
12.	B <sub>2</sub> O <sub>1</sub> B'	5	0.0124	52.	Y <sub>2</sub> G'O'G?	2	0.0050
13.	B <sub>2</sub> O <sub>2</sub> Y <sub>2</sub>	2	0.0050	53.	Y <sub>2</sub> G'G?	3	0.0074
14.	B <sub>2</sub> Y <sub>2</sub> G'I'OP'Q'G?	1	0.0025	54.	Y <sub>2</sub> I'	1	0.0025
15.	B <sub>2</sub> G'O'Q'	1	0.0025	55.	Y <sub>2</sub> I'O'Y'	1	0.0025
16.	B <sub>2</sub> J' <sub>2</sub> O'	1	0.0025	56.	Y <sub>2</sub> O'	1	0.0025
17.	G <sub>2</sub> O <sub>2</sub>	5	0.0124	57.	B'G'O'	1	0.0025
18.	G <sub>2</sub> O <sub>2</sub> T <sub>2</sub> G'O'	1	0.0025	58.	D'E' <sub>1</sub> G'Q'	1	0.0025
19.	G <sub>2</sub> O <sub>2</sub> Y <sub>2</sub>	1	0.0025	59.	D'G'IT'Q'	1	0.0025
20.	G <sub>2</sub> Y <sub>2</sub> B'I'	1	0.0025	60.	D'G'J' <sub>2</sub> K'O'	2	0.0050
21.	G <sub>2</sub> Y <sub>2</sub> E' <sub>2</sub> Q'	61	0.1510	61.	D'G'O'	23	0.0569
22.	G <sub>2</sub> E' <sub>2</sub>	1	0.0025	62.	E' <sub>2</sub>	4	0.0100
23.	G <sub>2</sub> I'O'G?	1	0.0025	63.	E' <sub>2</sub> G'	1	0.0025
24.	I <sub>1</sub> O <sub>2</sub>	3	0.0074	64.	E' <sub>2</sub> I'	2	0.0050
25.	I <sub>1</sub> B'	2	0.0050	65.	E' <sub>2</sub> J' <sub>2</sub> O'	2	0.0050
26.	I <sub>2</sub>	47	0.1163	66.	E' <sub>2</sub> Q'	2	0.0050
27.	I <sub>2</sub> Q'	1	0.0025	67.	E' <sub>2</sub> G?	1	0.0025
28.	O <sub>2</sub>	16	0.0396	68.	G'J' <sub>2</sub> K'O'G?	1	0.0025
29.	O <sub>2</sub> T <sub>2</sub>	1	0.0025	69.	G'O'Q'	1	0.0025
30.	O <sub>2</sub> Y <sub>2</sub>	1	0.0025	70.	G'O'G?	1	0.0025
31.	O <sub>2</sub> Y <sub>2</sub> D'	1	0.0025	71.	G'G?	1	0.0025
32.	O <sub>2</sub> B'	1	0.0025	72.	I'	5	0.0124
33.	O <sub>2</sub> D'G'Q'	1	0.0025	73.	I'Q'	2	0.0050
34.	O <sub>2</sub> E' <sub>2</sub>	1	0.0025	74.	J' <sub>2</sub> K'O'	8	0.0198
35.	O <sub>2</sub> G'	1	0.0025	75.	J' <sub>2</sub> K'O'Q'	1	0.0025
36.	O <sub>2</sub> I'	3	0.0074	76.	O'	9	0.0223
37.	O <sub>2</sub> J' <sub>2</sub> K'O'	1	0.0025	77.	Q'	22	0.0544
38.	P <sub>1</sub> I'	2	0.0050	78.	G?	17	0.0421
39.	Y <sub>2</sub>	2	0.0050	79.	„b”	14	0.0346
40.	Y <sub>2</sub> B'	1	0.0025				

Table 2. Genetic structure of alleles EAB locus of Holstein cows (STE " Maximovca")

No.	allele	n	p	No.	allele	n	p
1.	B <sub>2</sub> G <sub>2</sub> I <sub>2</sub>	1	0.0151	16.	Y <sub>2</sub> G'O'Q'G'?	1	0.0151
2.	B <sub>2</sub> O <sub>1</sub>	2	0.0303	17.	Y <sub>2</sub> I'O'	1	0.0151
3.	B <sub>2</sub> O <sub>1</sub> Y <sub>2</sub> D'	1	0.0151	18.	Y <sub>2</sub> O'	1	0.0151
4.	B <sub>2</sub> O <sub>1</sub> B'	1	0.0151	19.	B'Q'	1	0.0151
5.	G <sub>2</sub> O <sub>2</sub>	2	0.0303	20.	D'Q'	2	0.0303
6.	G <sub>2</sub> Y <sub>2</sub> E' <sub>2</sub> Q'	13	0.1970	21.	E' <sub>1</sub>	1	0.0151
7.	G <sub>2</sub> D'	1	0.0151	22.	G'O'	1	0.0151
8.	I <sub>2</sub>	7	0.1061	23.	G'O'G'?	1	0.0151
9.	O <sub>1</sub>	1	0.0151	24.	I'	2	0.0303
10.	O <sub>1</sub> D'	1	0.0151	25.	I'Q'	2	0.0303
11.	O <sub>1</sub> D'G'Q'	1	0.0151	26.	O'	1	0.0151
12.	O <sub>1</sub> J' <sub>2</sub> K'O'	4	0.0606	27.	Q'	1	0.0151
13.	O <sub>2</sub> B'	1	0.0151	28.	G'?	4	0.0606
14.	Y <sub>2</sub> D'G'I'O'	1	0.0151	29.	„b”	4	0.0606
15.	Y <sub>2</sub> D'G'O'	2	0.0303				

As can be seen, in the herd SRL 'DOKSANCOM' are revealed 79 alleles, in the herd STE 'Maximovca'-29 alleles.

In both analyzed herds greatest distribution are alleles B<sub>2</sub>O<sub>1</sub>, G<sub>2</sub>Y<sub>2</sub>E'<sub>2</sub>Q', I<sub>2</sub>, I', G'' and the

negative allele „b”. Results of studies found 19 similar alleles in the analyzed populations of animals, Figure 5.

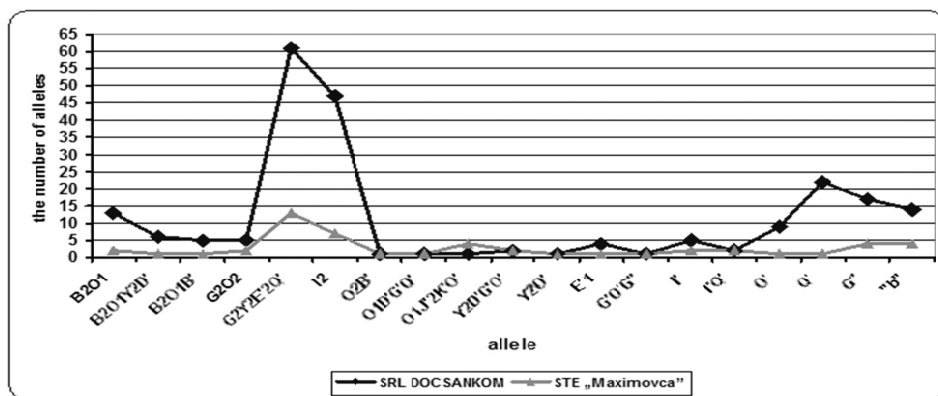


Figure 5. The concentration of the same allele in the analyzed populations of animals of Holstein breed

In the research results (Popov, NA, Eskin, GV, 2000) allelofonde Dutch, Holstein, the German Black and White breed is present most of the alleles detected in the analyzed populations of animals Holsteins.

Intensive use of the gene pool of black-and-White, Dutch and of Holstein breed as improving in many countries of the world leads to a general genetic convergence. In this regard, a high frequency occurs in the case of allele

D'G'O' (0.0569) in the herd SRL 'DOCSANKOM'.

In our earlier study was identified allele D'G'O' 'herds in agricultural firm 'Friendship', STE 'Maximovca' and bull-producing cows of the republic, the incidence of which was 0.0087, 0.0395 and 0.0041, respectively (Smirnov et al., 2007). This allele has been introduced by bull Diamond producer in 1287 of Holstein breed (line Soiling Troyon Rokita 252803).

The genetic distance between populations of both analyzed herds of Holstein cattle has little meaning – 0.0687, so they are close enough to each other-the index of genetic similarity is 0.9313, which indicates that the homogeneity of breed. Similar results were obtained in studies (Svyazhenina, 2012)-the value of genetic similarity indices in Holstein cows of different origin was 0.815 – 0.873, from which comes that in the Tyumen region Highly productive herd of Holstein cattle of breeding, which is almost no different from the representatives of the European selection in genetic plan.

Objectively genetic characteristics of the analyzed populations of animals of Holstein breed reflect such factors as the rate of homozygosity (Ca), the number of effective alleles (Na), the degree of genetic variability (factor V), Table 3.

Table 3. The genetic variability of populations of Holstein breeds cattle

No.	Indices	Name of farms	
		SRL „Docsankom”	STE „Maximovca”
1.	We investigated, goals	202	33
2.	The number of installed alleles:	79	29
	- total	15	11
	- the major	64	18
	- rare		
3.	The total frequency of alleles:	0.6213	0.6667
	- the major	0.2129	0.2727
	- rare		
4.	Coefficient of homozygosity, Ca	0.0501	0.0602
5.	Number of effective alleles, Na	19.9	16.6
6.	The degree of genetic variability, V	95.5	96.9

As can be seen, the concentration of the principal allele in the herd SRL 'DOCSANKOM' was 0.6213, in the herd STE 'Maximovca'-0.6667, 0.2129 and 0.2727 rare respectively. The degree of homozygosity in the analyzed populations is low, at 5.0% (SRL 'DOCSANKOM') and 6.0% (STE 'Maximovca'). A low coefficient of homozygosity (Ca) indicates of significantly higher genetic diversity of studied population of Holsteins breed cattle.

As is known, the state of breed allelofond the level of homozygosity reflects a number of effective alleles. It is found that the animal population of the herd SRL ('DOCSANKOM') was more homozygous, the number of effective alleles equal 19.9.

In general allelofonde of studied herds dominated marker alleles typical Holstein cattle, and revealed differences, their specificity, give the right to assert the valuable in breeding for both populations of cattle.

## CONCLUSIONS

Was established a high frequency of antigen G<sub>2</sub>, O<sub>2</sub>, Y<sub>2</sub>, E'<sub>2</sub>, O', Q', G' in studied populations of SRL 'DOCSANKOM' and STE 'Maximovca' that are characteristic of Holstein breed, breed of Black and White stalk including the Moldavian type of Black and White breed.

Was established 19 alleles identical in both studied populations, the most widespread alleles were B<sub>2</sub>O<sub>1</sub>, G<sub>2</sub>Y<sub>2</sub>E'<sub>2</sub>Q', I<sub>2</sub>, I', G' and recessive allele 'b'.

Level of homozygous in the studied populations was low and amounted to 5.0% (SRL 'DOCSANKOM') and 6.0% (STE 'Maximovca').

It was established that the Holstein breed population of SRL 'DOCSANKOM' is homozygote and the number of effective alleles was 19.9.

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# NUTRITION



