Informational-Statistical Aspects of Genetic Diversity in Tsigai and Tsurcana Ecotypes from Romania

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ABSTRACT

The main objective of this paper is to measure the relationships between the ecotypes belonging to the Tsigai and Tsurcana breeds of Romania and to quantify the genetic diversity within them from the informational statistics point of view, depending on the relief forms of the biotope in which they live, using the genetic variants of some selective genetic markers. The researches were carried out on ecotypes of the most ubiquitous sheep breeds in Romania, Tsigai and Tsurcana whose biotopes are circumscribed by more relief forms: plain, hilly, sub-mountainous and mountainous. The sheep were electrophoretically typified at the determinant loci of haemoglobin and transferrin. Using the allelic frequencies of the haemoglobin and transferrin systems that have been processed by concepts of informational statistics, the differentiation / similarity degree among ecotypes within the two breeds was quantified by the genetic distance (D) and the informational correlation coefficient (R_{xy}), as well as the diversity level (d) of the genetic structures of these ecotypes on the basis of informational energy (e). Also, the heterozygosity degree (Ht) at the Hb and Tf loci was calculated in relation to the genetic diversity level. The paper analyzes the causes of genetic similarities and differentiations among the ecotypes of these two breeds at the level of the two biochemical-genetic loci: allelic distribution of haemoglobin and transferrin, altitude of relief forms, habitat conditions etc. The benefits of such studies are also presented for the improvement, breeding and conservation of the ecotypes of these two sheep breeds from Romania.

Keywords: *ecotype, genetic distance, informational correlation, genetic diversity, sheep.*

INTRODUCTION

The breed as a biological taxonomic entity is specific to the domestic animal breeding domain with an overwhelming contribution of empirical or systematic artificial selection exercised by man to improve the productivity potential of animals. The breed creating is a historical, complex and extremely laborious process, sometimes of very long lasting. Once the breed formed, it is presented as a population or group of populations within a species characterized by common morphological, biochemical, physiological, genetic, productivity and ecological features, all being hereditarily fixed. For this reason, the breed is assimilated to subspecies. Having shaped this profile, a breed

differs from other breeds, precisely through this complex of attributes (Grosu and Drăgănescu, 2003).

The breed created occupies a limited area in which it lives, being adapted to the environmental conditions of the respective biotope. But during its evolution, this area can be expanded or, by migration phenomena in closer or more remote areas, the animals of the same breed adapt to new environmental conditions, conquering areas whose meteorological, geographic and climatic characteristics are different from the original ones in which the breed was created (Scher *et al.*, 2012). Through this process, the ecotypes (biotypes) occur, representing individual groups of the same breed

with their own hereditary properties acquired under the influence of environmental conditions, mostly by natural selection, adapted to the new habitat. The differentiation process of ecotypes can be so emphasized that the reproductive isolation is possible, which creates prerequisites for defining these ecotypes as new breeds (Grosu and Drăgănescu, 2003; Paraschivescu *et al.*, 2009; Gáspárdy, 2011).

The specific features of ecotypes are rather genetic and ecological since the environmental conditions exert selective pressure on the genetic material (Zanoti Casati *et al.*, 1990; Sargent *et al.*, 1999; Gáspárdy, 2011; Ozdemir *et al.*, 2011). Thus, among these subspecific subdivisions, certain biological relationships are established, resulting more or less significant differentiations, leading to an increase in biodiversity within that breed (Paraschivescu *et al.*, 2009).

For this reason, we decided to quantify the relationships among the ecotypes belonging to the Tsigai and Tsurcana breeds of Romania from the informational statistics point of view, depending on the relief forms of the biotope in which they live, using the genetic variants of some selective genetic markers (haemoglobin and transferrin).

MATERIALS AND METHODS

Several ovine populations of the Tsigai and Tsurcana breeds were investigated to reveal some aspects of genetic similarity or diversity among them and within them. The size of these samples was according to the area occupied by each of them (Figs. 1, 2, 7, 8). These populations are in fact the main ecotypes of the two Romanian sheep breeds and were sampled according to the relief forms of their existence areas: plain, hill, sub-mountain and mountain. The altitude as an essential element defining the relief forms is associated with the other environmental conditions in the respective areas: rainfall, luminosity, thermal regime, vegetation for pasture, etc. All these elements outline the complex meteorological, geographic and climatic context in which the ecotypes take their place and influence their productivity standard (to a lesser extent) and their genetic profile (in a wider range).

For the accuracy of the study, we analyzed these two breeds because they are ubiquitous in Romania. Compared to the other two classical Romanian breeds, Palas Merino (spread only in Dobrudja and in the South of our country) and

Botosani Karakul (located in the north-eastern Moldavia), the Tsigai and Tsurcana breeds are spread in several areas of Romania with different weather conditions. In fact, the Palas Merino and Botosani Karakul breeds are not differentiated into ecotypes.

Two biochemical-genetic markers were determined, haemoglobin and transferrin, polymorphic proteins having an essential role in adapting of animal organisms to the environmental conditions and technological factors.

The typifying of individuals at the loci of the two proteins was performed by the horizontal electrophoresis method, having the starch gel as substrate and using the buffer solutions of Tris (hydroxymethyl) aminomethane, EDTA.Na₂, boric acid, citric acid and lithium hydroxide as electrolyte, the recipes for reagents being formulated depending on the protein analyzed. Electrophoresis lasted four hours for haemoglobin and 6-8 hours for transferrin, until the electrophoretic bands migrated to 4 cm, respectively to 11 cm, to the starting line. The power intensity was 40 mA and 50 mA and its voltage was 300 V and 400 V for haemoglobin, respectively for transferrin. The colouring of starch gels was made with an alcoholic-acid solution of 1% amidoschwartz 10B, and their discolouring in a solution of methanol, glacial acetic acid and distilled water (3/1/3). (Hrinca and Vicovan, 2010, 2011).

The degree of genetic differentiation/similarity was calculated in two ways:

- an estimate through the *genetic distance (D)* (according to the Nei method), by the expression:

$$D = -\log_e \frac{J_{x.y}}{(J_x.J_y)^{1/2}} = 2at, \text{ where:}$$

- D = standard genetic distance;
- t = differentiation time;
- a - substitution percentage of genes per locus and per year, whose value is 10⁻⁷.
- J_{xy} = probability of genetic identity between two populations x and y;
- J_x - probability of genetic identity within the population x;
- J_y - probability of genetic identity within the population y;

Fig. 1. Allelic structure at the Hb locus in different Tsigai ecotypes

- a more accurate measurement through the *informational correlation* (C_{xy}) (according to the Onicescu-Ștefănescu method), by the formula (Hrinca, 2015):

$$R_{x,y} = \frac{\sum_{i=1}^n f_x f_y}{\sqrt{(\sum_{i=1}^n f_x^2)(\sum_{i=1}^n f_y^2)}} \text{ where}$$

$R_{x,y}$ – informational coefficient correlation;

f_x and f_y are the frequencies for the population x and y .

The level of *genetic diversity* (d) of these two polymorphic systems was quantified by the *informational energy* (e), according to mathematical monotony:

$d=1-e$, in which

$$e = \frac{(\sum_{i=1}^m p_i^2 - \frac{1}{m})}{(1 - \frac{1}{m})} \text{ where}$$

p = the probability (which ranges from 0 to 1);
 m = number of classes (statuses).

In relation to genetic diversity, the *heterozygosity degree* (Ht) of ecotypes was evaluated by the following expression (Hrinca, 2015):

$$H = \left[\frac{2n}{2n-1} \right] \left[1 - \sum_{i=1}^k x_i^2 \right], \text{ where:}$$

Ht = the heterozygosity of population k ;

n = the number of individuals;

x = the allelic frequency at the locus i .

RESULTS AND DISCUSSIONS

The susceptible number of ecotypes taken in the informational statistics analyzes within each genetic-biochemical system depended on their number typified at the two polymorphic loci.

1. Particularities of biodiversity in the Tsigai ecotypes

The Tsigai ecotypes that have been used to reveal some aspects of biodiversity are defined according to the relief forms in which they carry their existence: plain Tsigai (Rusetu, Buzau County), hill Tsigai (Secuieni, Bacau county), sub mounting Tsigai (Ciuc Depression, Harghita County) and mountain Tsigai (Calimani-Gurghiu Massif, Mures County).

1.1. Allelic structures of biochemical-genetic systems

Allelic structures at the determinant locus of haemoglobin

In the Tsigai breed, the lowest frequency of the Hb^A allele (6.04%) is found in the flocks living on the plain (Rusetu ecotype). Its frequency begins to increase slightly (8.50%) in sheep from hill areas (Secuieni ecotype); in both Tsigai ecotypes the Hb^B allele is very spread (over 90%). On the plateau and in the sub-mountain regions (Ciuc Depression), the Hb^A allele is much more frequent (62.50%)

Fig. 2. Allelic structure at the Tf locus in different Tsigai ecotypes

than the Hb^B allele (37.50%). In the mountain ecotype (Calimani-Gurghiu Massif), the Hb^A allele reaches the highest level of frequency (84.86%), the Hb^B allele having the weakest spread (Fig. 1).

Allelic structures at the determinant locus of transferrin

Three Tsigai ecotypes were typified at the determinant locus of transferrin: the plain ecotype (Rusetu), the hill ecotype (Secuieni) and the mountain ecotype (Moroieni). All nine transferrin alleles are present in the Moroieni Tsigai while in the Secuieni Tsigai there are not the Tf^I and Tf^C alleles. In the Moroieni ecotype, the allele panel is mostly constituted by the Tf^A, Tf^B and Tf^D alleles (each nearly 25%), the other alleles occupying a narrow or sometimes sporadic space such as the Tf^I, Tf^C, Tf^E and Tf^P alleles (less than 1%). In the Secuieni ecotype, almost half of the population individuals possess the Tf^D allele and a quarter of them have the Tf^B allele. Also, the Tf^A allele also records an important frequency (17%). The other four alleles have a very low spread (between 1% and 2.5%). In such a situation it is clear that more transferrin genotypes will be expressed in the Moroieni Tsigai than in the Secuieni Tsigai and the genotypic configurations will be different in the two ecotypes. Although, the plain Tsigai (Rusetu) as nine alleles as the mountain Tsigai, its allelic incidences are relatively similar to those of hill Tsigai; in plain Tsigai the Tf^A and Tf^D alleles are less frequent and the Tf^C and Tf^E alleles are more spread than in hill Tsigai; at the same time, the allele dispersion is more uniform in plain Tsigai,

the ratios among Tf alleles being slightly more balanced than in the hill ecotype (Fig. 2).

1.2. Parameters of informational statistics

Biological relationships

Within the *haemoglobin system*, between the plain and the hill Tsigai, on the one hand, and the sub-mountain and the mountain Tsigai, on the other hand, the genetic distances are very large. The coefficients of informational correlation between the ecotypes from the lowland regions (plain and hill Tsigai) on the one hand are of medium level with sub-mountain Tsigai and have very low values with mountain Tsigai on the other hand. The plain Tsigai is genetically more distant from the sub-mountain Tsigai and especially from the mountain Tsigai compared to the hill Tsigai. There is a very high, almost absolute, genetic similarity between the plain Tsigai and the hill Tsigai, as well as between the pre-mountain Tsigai and the mountain Tsigai, but it is slightly lower than the previous interrelation. The informational-statistical characteristics are concordant with allelic distributions. In the plain and hill ecotypes the Hb^B allele is clearly predominant, while in the sub-mountain ecotypes and especially in the mountain ones the allele Hb^A records high frequencies, but its Hb^B codominant is moderately met in populations, too (Tab. 1, Fig. 3).

Within the *transferrin system*, the informational correlation coefficients achieved at the locus Tf among the three analyzed ecotypes record high values. The closest relationship is established between the plain Tsigai and the hill

Tab. 1. Genetic distances (D) and informational correlation coefficients ($R_{x,y}$) among the Tsigai ecotypes, in terms of structure at the determinant haemoglobin locus

Ecotype	Plain Tsigai	Hill Tsigai	Submountain Tsigai	Mountain Tsigai
Plain Tsigai		0.0004	0.5648	1.4337
Hill Tsigai	0.9996		0.5249	1.3245
Submountain Tsigai	0.5684	0.5916		0.0677
Mountain Tsigai	0.2384	0.2659	0.9345	
$R_{x,y}$

Fig. 3. Informational correlation coefficients ($R_{x,y}$) among the Tsigai ecotypes, in terms of structure at the determinant haemoglobin locus**Tab. 2.** Genetic distances (D) and informational correlation coefficients ($R_{x,y}$) among the Tsigai ecotypes, in terms of structure at the determinant transferrin locus

Ecotype	Plain Tsigai (Rusetu)	Hill Tsigai (Secuieni)	Mountain Tsigai (Moroieni)
Plain Tsigai (Rusetu)		0.0956	0.1203
Hill Tsigai (Secuieni)	0.9088		0.1295
Mountain Tsigai (Moroieni)	0.886	0.8785	
$R_{x,y}$

Fig. 4. Informational correlation coefficients ($R_{x,y}$) among the Tsigai ecotypes, in terms of structure at the determinant transferrin locus

Fig. 5. Coefficients of informational energy (*e*) genetic diversity (*d*) and heterozygosity (*Ht*) at the Hb locus in Tsigai ecotypes from Romania

Fig. 6. Coefficients of informational energy (*e*) genetic diversity (*d*) and heterozygosity (*Ht*) at the Tf locus in Tsigai ecotypes from Romania

Tsigai. The plain Tsigai is slightly more genetically distant than the mountain Tsigai; almost at the same level there is the relationship between the hill Tsigai and the mountain Tsigai (Tab. 2, Fig. 4).

Genetic diversity

The distribution way of alleles within the panels of the genetic-biochemical systems represent the determinant element of the genetic diversity status of the ecotypes. In the *haemoglobin* system, the richest diversity is found in the submountain Tsigai ecotype (Ciuc Depression). This fact happens because the two haemoglobin alleles are spread more evenly than in the other ecotypes. In the ecotypes from low areas, the very high frequency of the Hb^B allele in the detriment of its Hb^A codominant leads to the development of a large informational energy that translates through a moderate genetic diversity. According to the

allelic panel, the haemoglobin diversity of the hill ecotype is higher than of the plain ecotype. In the mountain ecotype, the Hb^A allele dominates the haemoglobin table, but the differences between the frequencies of the two alleles are lower than in the ecotypes from the lower relief areas. In the mountain ecotype, the Hb^A allele dominates the haemoglobin panel, but the differences between the frequencies of the two alleles are lower than in the ecotypes from the lower relief areas. Therefore, although the information energy is relatively large, the genetic diversity reaches a medium level, but it is incomparably lower than that of the submountain ecotype. The submountain Tsigai is the only ecotype in which the informational energy is approximately equal to the genetic diversity at the Hb locus (Fig. 5).

Within the *transferrin* system, in all ecotypes, the genetic diversity is developed due to the emphasized polymorphism at this

Fig. 7. Allelic structure at the Hb locus in different Tsurcana ecotypes

locus materialized by the presence of the nine transferrin alleles (Fig. 6). In the ecotypes from very low regions (plain), as well as in the ones from very high ones (mountain), the genetic diversity achieves very high levels. This situation is explained by the fact that in both ecotypes there is the same number of transferrin alleles (nine) and a better combinatorial capacity of these in transferrin genotypes. Due to the fact that in the plain ecotype the transferrin alleles are more evenly distributed, the genetic diversity is 0.04 more developed than in the mountain ecotype. Compared to these, in the hilly ecotype the transferrin diversity is lower, however achieving an important enough value of the coefficient. One fact that determines this transferrin diversity level of is that there are only seven transferrin alleles in this ecotype, the Tf^F and Tf^G alleles missing from this panel.

From a systemic point of view, the transferrin diversity is much higher than the haemoglobin diversity in most of the Tsigai ecotypes.

2. Particularities of biodiversity in the Tsurcana ecotypes

As with Tsigai, in the Tsurcana too, the biodiversity aspects of its ecotypes were based on the allelic frequencies of the haemoglobin and transferrin systems, depending on the relief forms in which they live: the Tsurcana plain (an isolated nucleus in Dobrudja), the hill Tsurcana (Popăuți), sub-mountain Tsurcana (Caransebeș) and mountain Tsurcana from two massifs: Apuseni

Mountains (West Carpathians) and Meridionali Mountains (South Carpathians).

2.1. Allelic structures of biochemical-genetic systems

Allelic structures at the determinant locus of haemoglobin

The Tsurcana breed from Romania is characterized by large differences concerning the spread of haemoglobin alleles within populations of different areas. In the plain sheep (some isolated populations in Dobrudja left as a result of transhumance) there is almost only the Hb^B allele, the Hb^A allele being only sporadically found. It is a structure similar to that found in Tsurcana of the Hungarian puszta. For Tsurcana from the Meridionali Mountains the preponderance of the Hb^A allele (98%) is specific, while in Tsurcana from the hilly area of Moldavia, the Hb^B allele dominates the haemoglobin pool (79%), and the Hb^A allele has a relatively low spread; moreover, in some populations (in the South Carpathians), the only genotype present is the homozygous one Hb^AHb^A, the Hb^B allele being completely eliminated. As for the hemoglobin table in sub-mountain Tsurcana the configuration of the allelic distributions is more similar to that of the plain and hill ecotypes than to those from mountain areas (Fig.7).

Allelic structures at the determinant locus of transferrin

Of the two Tsurcana ecotypes that were typified at the Tf locus, Caransebes Tsurcana is

Fig. 8. Allelic structure at the Tf locus in different Tsurcana ecotypes

Tab. 3. Genetic distances (D) and informational correlation coefficients ($R_{x,y}$) among the Tsurcana ecotypes, in terms of structure at the determinant haemoglobin locus

Ecotype	Plain Tsurcana (Dobrudja)	Hill Tsurcana (Popauți)	Submountain Tsurcana (Caransebes)	Mountain Tsurcana (Apuseni)	Mountain Tsurcana (Meridionali)
Plain Tsurcana (Dobrudja)		0.0147	0.0264	2.9700	3.4766
Hill Tsurcana (Popauți)	0.9854		0.0017	1.5114	1.6062
Submountain Tsurcana (Caransebes)	0.9739	0.9983		1.2853	1.3591
Mountain Tsurcana (Apuseni)	0.0513	0.2206	0.2766		0.0002
Mountain Tsurcana (Meridionali)	0.0309	0.2006	0.2569	0.9998	
$R_{x,y}$					

more polymorphic than Moldova Tsurcana. In the Caransebes ecotype all nine alleles are found and only seven are present in the Popauti ecotype, lacking the Tf^I and Tf^P marginal alleles. Also, the two ecotypes are also differentiated in terms of allelic distributions. In the Caransebes ecotype, the highest frequency is made by the Tf^D allele (31.4%), followed at a considerable distance by the Tf^A and Tf^B alleles (16% , respectively 18%), while in the ecotype from Moldova the Tf^C allele (34%) is most frequent met and the following alleles, Tf^A and Tf^B (each approximately 22%), have frequencies closer to that of the Tf^C allele. Besides these, only the Tf^C allele (9.6%) in the Caransebes ecotype and the Tf^M allele (11.5%) in

the Moldavian ecotype achieves more substantial frequencies, the other alleles having a very low contribution to the completion of the allelic table in both ecotypes (between 0.5% and 5%) (Fig. 8).

2.2. Parameters of informational statistics

Biological relationships

At the determinant *haemoglobin locus* there is a great genetic similarity among the Tsurcana ecotypes bred in the plain, hill and submountain areas. The similarity is more obvious between the hill and submountain Tsurcana than between these two ecotypes and the plain Tsurcana. All these three ecotypes from regions with lower altitudes differ fundamentally from

Pl.Turc – Plain Tsurcana; Hl.Turc – Hill Tsurcana; Sm.Turc- Submountain Tsurcana; Mt.Turc. - Mountain Tsurcana (Apuseni); MM.Turc - Mountain Tsurcana (Meridionali)

Fig. 9. Informational correlation coefficients ($R_{x,y}$) among the Tsurcana ecotypes, in terms of structure at the determinant haemoglobin locus

Tab. 4. Genetic distances (D) and informational correlation coefficients ($R_{x,y}$) among the Tsurcana ecotypes, in terms of structure at the determinant transferrin locus

Ecotype	Caransebes Tsurcana	Popauti Tsurcana	
Caransebes Tsurcana		0.4281	D
Popauti Tsurcana	0.6517		
$R_{x,y}$

Fig. 10. Informational correlation coefficients ($R_{x,y}$) among the Tsurcana ecotypes, in terms of structure at the determinant transferrin locus

the informational-statistical point of view of the Tsurcana ecotypes from the mountainous regions, the genetic distances between the two of ecotype groups being very large. The Tsurcana ecotypes from plain, hill and sub-mountainous areas are slightly more distant to the mountainous Tsurcana from the Southern Carpathians than to the one from the Apuseni Mountains. Between the two mountain ecotypes, the informational correlation is very strong having an almost absolute value. As with Tsigai, in large part, the informational-statistical characteristics of the Tsurcana ecotypes are concordant with the distributions of the two haemoglobin alleles of each ecotype. In the ecotypes from plain, hilly and sub-mountain areas

the Hb^B allele is clearly predominant, while in the ecotypes from the high mountainous areas only the Hb^A allele is present (in the Meridionali Mountains) or occupies almost all the haemoglobin panel, the Hb^B allele being sporadically spread (in the Apuseni Mountains) (Tab. 3, Fig. 9).

Within the *transferin* system the comparison was made between the Popauti Tsurcana and Caransebes Tsurcana having experimental data only in these two ecotypes. Between these two ecotypes the genetic distance is quite significant and the informational correlation coefficient records a value situated slightly above the medium level (Tab. 4, Fig. 10).

Fig. 11. Coefficients of informational energy (*e*) genetic diversity (*d*) and heterozygosity (*Ht*) at the Hb locus in Tsurcana ecotypes from Romania

Fig. 12. Genetic distances (*D*) and informational correlation coefficients (*R_{xy}*) among the Tsurcana ecotypes, in terms of structure at the determinant transferrin locus

Genetic diversity

The distributional characteristics of the two *haemoglobin alleles* determine the medium or very low levels of genetic diversity at this locus in both ecotypes (Fig. 11). Both in the plain ecotype and in the mountain ecotype from Apuseni the informational energy amount is so great that the haemoglobin diversity is relatively low (in the plain Tsurcana) or extremely low or almost inexistent (in the Tsurcana from West Carpathians); moreover, in the Meridionali ecotype the informational energy is maximal and the genetic diversity is null. In the ecotypes from hilly and sub-mountain areas, due to a more balanced distribution between the two types of alleles, the genetic diversity is developed

having levels above 0.5, especially in sub-mountain Tsurcana. However, in both situations, the informational energy reaches lower values than the genetic diversity coefficients.

Within the *transferrin system*, in both ecotypes analyzed, we find extremely high genetic diversity as a result of the balanced ratios of the transferrin allele frequencies. The distribution uniformity of the transferrin alleles is more pronounced in the Caransebes ecotype than in the Popauti one, fact reflected in the values of their genetic diversity coefficients.

Also, in the Tsurcana ecotypes, the transferrin diversity is more developed than the haemoglobin diversity.

The intensity of biological relationships between ecotypes of the Tsigai and Tsurcana breeds, as well as the characteristics of the genetic diversity within them reflect mainly the particularities of the environmental conditions and, in the alternative, the specificity of the selection criteria and technological factors used for the improvement and breeding process of these breed subdivisions formed according to the relief forms of their habitats. The characteristics of the informational-statistical edifice based on the genetic variants of haemoglobin and transferrin resize the biological relationships among the ecotypes within each breed and quantify with greater accuracy their genetic patrimony at the level of the two polymorphic loci. Compared to the genetic distance, the informational correlation provides more flexibility to the investigational methodology, it is more expressive and has the advantage to benefit of graphic representation.

In general, it comes out a closer relationship among the Tsigai ecotypes than among those of the Tsurcana breed in both biochemical-genetic systems. In the same context, in the ecotypes of both breeds the transferrin diversity achieves higher levels than the haemoglobin diversity. Also, considering the two biochemical-genetic systems, it can be noticed that the Tsigai ecotypes achieve higher levels of genetic diversity than the Tsurcana ecotypes.

The heterozygosity is a first indicator of genetic diversity and an essential factor in increasing this biodiversity. In absolute value, the genetic diversity is higher than the heterozygosity. But there is a direct linearity relation between the genetic diversity level and the heterozygosity degree. The ratio between these two sizes depends on the allele number of polymorphic loci. Thus, in all ecotypes of the Tsigai and Tsurcana breeds the haemoglobin heterozygosity degree differs from the transferrin heterozygosity degree with reference to the genetic diversity levels at these two loci. If the haemoglobin diversity level is twice as high (100%) as haemoglobin heterozygosity degree, the transferrin diversity level is only 12% higher than the haemoglobin heterozygosity degree. And this aspect should be interpreted in the context in which the transferrin diversity is much richer than the haemoglobin diversity (Figs. 5, 6, 11, 12).

These informational statistics analyzes that use genetic markers in the computational algorithm are important tools for evaluating the evolution directions of the Tsigai and Tsurcana ecotypes from Romania and for the substantiation of the preservation and improvement programs for their genetic patrimony.

CONCLUSIONS

The genetic differentiation / similarity degree and the genetic diversity level were quantified in the ecotypes belonging to Tsigai and Tsurcana breeds from Romania by means of informational statistics concepts.

Differences were found among the different ecotypes of the Tsigai and Tsurcana breeds regarding both the biological relationships among them and in terms of genetic diversity, differentiations due to the allele configurations in the haemoglobin and transferrin systems whose fixation is determined by the ecological factors in the existence areas of the ecotypes.

In general, there is a stratification and tiebreaker of the Tsigai and Tsurcana ecotypes from the genetic structure point of view from the Hb and Tf locus level, as well as the values of informational-statistical parameters defining the biodiversity in relation to the relief forms (plain, hill, sub-mountain and mountain) of the areas where the ecotypes live.

From a systemic point of view, the biological relationships are tighter among ecotypes and genetic diversity has higher levels within them in the Tsigai breed compared to the Tsurcana breed.

In the ecotypes of both breeds the transferrin diversity is higher than the haemoglobin diversity, and the difference between the diversity and heterozygosity from the Hb locus is much larger than the difference between the diversity and heterozygosity from the Tf locus.

Determination of informational statistics parameters on genetic basis is useful in the conservation and improvement process of the genetic patrimony of Tsigai and Tsurcana ecotypes.

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