STUDY OF THE GENETIC VARIABILITY OF THE NEGRA SERRANA GOAT BREED

ESTUDIO DE LA VARIABILIDAD GENÉTICA DE LA RAZA CAPRINA NEGRA SERRANA

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Additional Keywords

Palabras clave adicionales
Raza minoritaria. Polimorfismo bioquímico sanguíneo. Heterocigosidad.

SUMMARY

The Negra Serrana goat breed is considered to be endangered by extinction because of its reduced stocks. In this kind of populations with high risk of reproductive problems due to high consanguinity, it is interesting to know the genetic variability; thus, we used biochemical blood polymorphisms to determine its genetic status and calculate the heterozygosity and inbreeding coefficients both, in the total population as well as in three subpopulations.

We have observed that two of the subpopulations are very similar and show few genetic differences, but they do differ from the third group that shows the greatest heterozygosity and the least inbreeding.

RESUMEN

La población caprina Negra Serrana está considerada como una raza en peligro de extinción, por su reducido número de ejemplares y su reciente reconocimiento oficial. El interés de conocer la variabilidad genética en poblaciones de este tipo, con alto riesgo de problemas reproductivos derivados de una alta consanguinidad, nos indujo a utilizar los polimorfismos bioquímicos sanguíneos para determinar su status genético.

A partir de las frecuencias génicas, se han calculado los coeficientes de heterocigosidad y consanguinidad para el total de la población y cada uno de los tres rebaños que la componen; dos de ellos son similares, el tercero muestra mayor heterocigosidad y menor consanguinidad.

El conjunto poblacional presenta gran déficit de heterocigotos, pero no el tercer rebaño.

INTRODUCTION

The Negra Serrana goat breed recognized by the Junta of Andalucia as an endangered breed, is eminently apt for meat production (Delgado et al., 1992). It survives because of its adaptation to a difficult mountainous

habitat, such as we find in the Jaén region of the Sierra Morena mountains.

Previous knowledge of its zootecni-cal features are complementary and its conservation fits within the necessa-ry pautas according to Primo (1987), Alderson (1985) and Clarke et al. (1989). The study should be intensified because of it deals with a breed threat-ened by extinction on account of its racial indefiniton due to its lack of recognition during so many years.

The Negra Serrana breed, in spite of being pointed out (Cobos, 1950) as a Guadalquivir breed situated in that geographic region, was not included in the official catalogue of Spanish autochthonous breeds until its second edition (Esteban y Tejón, 1986), in which its general traits were described and it was referred to in the popular term of castiza, as it was known by the local people. Afterwards it was studied by Alia (1982) from a produc-tion and morphological point of view. Production studies on the growth of the breed in kids was later broadened by González (1989).

The present work aims to complete the knowlge of this breed from a ba-se of blood polymorphism as well as, evaluating by this method the status of genetic variability in a breed with such a reduced population.

6 polymorphic blood systems were studied:

- In erythrocytes: Haemoglobin (Hb) (Huisman et al., 1958); Catalase (Cat) (Kelly et al., 1971); Protein X (Prot X) (Tucker et al., 1967); Carbonic Anhidrase (CA) (Tucker et al., 1967)
- In plasma: Albumins (Alb) (Rodero et al., 1977); Transferrins (TF) (Efremov and Braend, 1965).

We also measured the level of Na⁺ and K⁺ in erythrocytes, by flame spectrophotometry.

We obtained the genotype and allelic frequencies, both in the total population and separate flocks. We considered the population to be on the Hardy-Weinberg equilibrium.

With the data obtained were able calculate the coefficients of identity among the possible couples within the flock, and from this, estimate the matrix of genetic distances among the populations by which we obtained the philegetic representation of the three populations (flocks).

Using the calculation of heterozy-gousness we got the coefficients of inbreeding (Wright,1965) in each flock (farm) as well as in the overall total of the animals studied.

RESULTS AND DISCUSSION

In figures 1 and 2 we show by striped histograms the level of Na⁺ and K⁺, respectively, for each flock and the overall population. It is no-tiable that the 1st and 3rd flocks, differ greatly in their levels of K⁺ in red cells. Animals with low potassium predominated in the 1st flock, while in the 3rd flock, animals with high

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Figure 1. Levels of Na+ for each flock and the overall population. (Niveles de Na+ eritrocitario en cada rebaño y en la población total).

Figure 2. Levels of K+ for each flock and the overall population. (Niveles de K+ en cada rebaño y en la población total).

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levels of potassium predominated. In flock No. 2 there is a more moderate distribution in the levels.

With respect to the Na⁺ levels, it should be pointed out that the histogram for the 1st flock is that which best fits the representation of the frequencies for the total population.

Table I shows the gene and allele frequencies of each system for each flock and for the total of the animals.

The Hb and Tf systems were monomorphic for the 1st and 2nd populations but not for the 3rd. Furthermore, no polymorphism showed, in any case, the system of Carbonic Anhydrase.

Tables II and III show the matrixes of identity and genetic distances whose results are shown in the dendrogram of figure 3. From all of this, we can appreciate the greatest similarity between the 1st and 2nd flocks, that showed the maximum distance with respect to the 3rd, even though this is closer to the 1st than the 2nd. This last flock (2) had the highest coefficient of inbreeding and the greatest number of heterozygotes, as is observed in the results shown in table IV.

CONCLUSIONS

We have observed in the 3rd group of animals both through visual appreciation of the animals as well as through the analysis of blood polymorphism a great distance with respect to the other flocks, we have inferred

Table I. Allele frequencies of each system for each flock and the total of the animals (N= number of animals). (Frecuencias alélicas en los 3 rebaños y en el total de la población (N= número de animales).

<table>
<thead>
<tr>
<th>Systems</th>
<th>Alleles</th>
<th>Flock1</th>
<th>Flock2</th>
<th>Flock3</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hb</td>
<td>A</td>
<td>1.00</td>
<td>1.00</td>
<td>0.83</td>
<td>0.94</td>
</tr>
<tr>
<td></td>
<td>B</td>
<td>0.00</td>
<td>0.00</td>
<td>0.17</td>
<td>0.06</td>
</tr>
<tr>
<td>(N)</td>
<td></td>
<td>50</td>
<td>38</td>
<td>32</td>
<td>120</td>
</tr>
<tr>
<td>Tf</td>
<td>A</td>
<td>1.00</td>
<td>1.00</td>
<td>0.99</td>
<td>0.99</td>
</tr>
<tr>
<td></td>
<td>B</td>
<td>0.00</td>
<td>0.00</td>
<td>0.01</td>
<td>0.01</td>
</tr>
<tr>
<td></td>
<td>C</td>
<td>0.00</td>
<td>0.00</td>
<td>0.00</td>
<td>0.00</td>
</tr>
<tr>
<td>(N)</td>
<td></td>
<td>50</td>
<td>38</td>
<td>47</td>
<td>135</td>
</tr>
<tr>
<td>Alb</td>
<td>S</td>
<td>0.96</td>
<td>0.885</td>
<td>0.98</td>
<td>0.94</td>
</tr>
<tr>
<td></td>
<td>F</td>
<td>0.04</td>
<td>0.115</td>
<td>0.02</td>
<td>0.06</td>
</tr>
<tr>
<td>(N)</td>
<td></td>
<td>50</td>
<td>38</td>
<td>50</td>
<td>138</td>
</tr>
</tbody>
</table>

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Table III. Matrix of genetic distances between flocks. (Matriz de distancias genéticas entre rebaños).

<table>
<thead>
<tr>
<th></th>
<th>Flock 1</th>
<th>Flock 2</th>
<th>Flock 3</th>
</tr>
</thead>
<tbody>
<tr>
<td>Flock1</td>
<td>0.0000</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Flock2</td>
<td>0.0062</td>
<td>0.0000</td>
<td></td>
</tr>
<tr>
<td>Flock3</td>
<td>0.0074</td>
<td>0.0093</td>
<td>0.0000</td>
</tr>
</tbody>
</table>

that the animals of this group may be the most apt for establishing plans for conservation of this breed, if there exist any problems caused through the high inbreeding and the loss of genes, habitual in reduced flocks. The selection of this group is subject to the condition that the animals fit within the pre-established racial canons, in case that, this difference were not produced by the introduction of rare alleles from other breeds (Clarke et al., 1989).

In the overall animals studied, except for the Hb system, it was noted that the heterocycosity was less that what may be expected in a population on the Hardy-Weinberg equilibrium. The high consanguinity obtained in flocks shows a great deficiency in heterocytotes. For this reason, we suppose that there had been a tendency, direct or indirectly attempted, toward mating endogamically.

Having the best consanguinity in the overall average of the flock, seems to indicate the existence of the "F" value between the certain subpopulations (Jordana et al., 1991). Keeping in mind that this value can be taken as a measure of the genetic distances between them. This may be due to the deviation of the 3rd flock.

Figure 3. Dendrogram showing the genetic affinity of goat populations. (Dendrograma mostrando la afinidad genética de las poblaciones).

Table IV. Coefficients of inbreeding and number of heterozygotes. (Coeficientes de consanguinidad y número de heterozigotos).

<table>
<thead>
<tr>
<th></th>
<th>Flock1</th>
<th>Flock2</th>
<th>Flock3</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hb</td>
<td>0.0000</td>
<td>0.0000</td>
<td>0.0000</td>
<td>0.0000</td>
</tr>
<tr>
<td>Tf</td>
<td>0.0000</td>
<td>0.0000</td>
<td>0.0000</td>
<td>0.0000</td>
</tr>
<tr>
<td>Al</td>
<td>0.0800</td>
<td>0.0768</td>
<td>0.1516</td>
<td>0.2035</td>
</tr>
<tr>
<td>Cat</td>
<td>0.1400</td>
<td>0.1958</td>
<td>0.3422</td>
<td>0.3750</td>
</tr>
<tr>
<td>CA</td>
<td>0.0000</td>
<td>0.0000</td>
<td>0.0000</td>
<td>0.0000</td>
</tr>
<tr>
<td>F</td>
<td>0.1216</td>
<td>0.2197</td>
<td>0.0583</td>
<td>0.2829</td>
</tr>
</tbody>
</table>

REFERENCES


Wright, S. 1965. The interpretation of population structure by F-statistics with special regard to systems of mating. Evolution; 19: 395-420