

## NOTA BREVE

# THE GENETIC PROCESS IN THE FORMATION OF THE GRAZALEMA MERINO AND THE LEBRIJA CHURRO SHEEP BREEDS\*

## EL PROCESO GENÉTICO DE FORMACIÓN DEL MERINO DE GRAZALEMA Y DE LA CHURRA LEBRIJANA\*

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### ADDITIONAL KEYWORDS

Genetic erosion. Drift. Sheep. Polymorphisms. External characters.

### PALABRAS CLAVE ADICIONALES

Erosión genética. Deriva. Ovinos. Polimorfismos. Caracteres externos.

### SUMMARY

We study the relationship between the Grazaalema Merino and the Lebrija Churro breeds and the ethnic trunks from which they descend. The drift effect among the various stocks of Grazaalema Merino has also been obtained. Although the total size of the populations investigated does not justify the results obtained for Merinos in terms of erosion coefficients, the effective number and the reproduction schemes are perfectly capable of having produced those. For the Churro types, the differences may be explained by the effect of selection or by the migration of other breeds into the Churro populations, giving rise to the Lebrija Churro through crossbreeding. From the  $f$  values we deduce that even though selection produces the major differences in ethnological traits, the drift is the principal source of differences in blood polymorphisms between pure Merino and the Grazaalema Merino. In the Churro breeds, we must add the effects of selection and geographical situation.

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### RESUMEN

Hemos estudiado las relaciones entre las poblaciones de Merino de Grazaalema y Churro Lebrijano con los troncos étnicos de procedencia. También hemos obtenido el efecto de la deriva entre las distintas ganaderías de Merino de Grazaalema. Si bien el tamaño total de las poblaciones estudiadas no justifica los resultados obtenidos en los Merinos, en lo referente a los coeficientes de erosión, el número efectivo y los planes de reproducción sí pueden haberlos producido. Para los dos tipos de Churras, las diferencias pueden explicarse por efecto de selección o por la entrada en la población Churra Genuina de otras razas lo que formaría la Churra Lebrijana. Al utilizar los valores de  $f$ , deducimos que, si para los caracteres etnológicos la selección produce el principal efecto diferenciador, la deriva genética justifica las diferencias encontradas en las frecuencias alélicas de los polimorfismos sanguíneos entre el Merino puro y el Merino de Grazaalema, mientras que en los Churros se sumaría además la selección y el ambiente geográfico.

In previous research (Rodero *et al.*, 1992) we concluded that the Grazaalema

**Table I.** Allelic frequencies of the stocks and Whalund's variance of the Grazaleta Merino breed. (Frecuencias alélicas en los rebaños de Merino de Grazaleta y su varianza de Whalund's).

Variables	Allele S	Stocks						Whalund's variances	
		Fave n=35	VG n=25	JO n=25	SDM n=30	MBB n=23	EDC n=35	$\bar{\chi}$ Stocks	$\bar{\chi} = 0,029$
Head Profile	Te	0.914	1.000	0.954	0.983	1.000	-	0.870	0,312
	te	0.086	0.000	0.046	0.017	0.000	-	0.130	0,312
Ear orientation	Op	0.557	0.500	0.500	0.500	0.500	0.529	0.569	0,073
	op	0.443	0.500	0.500	0.500	0.500	0.471	0.431	0,073
Ear size	O	0.357	0.000	0.046	0.017	0.000	0.471	0.149	0,290
	o	0.643	1.000	0.954	0.983	1.000	0.529	0.851	0,290
Horns	H <sub>0</sub> <sup>+</sup>	0.239	0.000	0.301	0.258	0.000	0.534	0.222	0,197
	H <sub>0</sub> <sup>P</sup>	0.761	1.000	0.699	0.742	1.000	0.466	0.778	0,197
Pigment pattern	A <sup>wh</sup>	0.635	0.600	0.523	0.598	0.534	0.555	0.574	
	A <sup>b</sup>	0.365	0.200	0.477	0.230	0.258	0.187	0.285	0,065
	a	0.000	0.200	0.000	0.180	0.209	0.258	0.141	
Left super. Nipple	P	0.870	0.566	0.577	0.876	0.626	0.718	0.705	0,079
	p	0.130	0.434	0.423	0.124	0.374	0.282	0.295	0,079
Right super. Nipple	P	0.870	0.490	0.617	0.856	0.72	0.696	0.714	0,085
	p	0.130	0.510	0.383	0.144	0.248	0.304	0.286	0,085
bHb (*)	p <sup>A</sup>	0.132	0.080	0.159	0.200	0.114	0.103	0.131	0,013
	q <sup>B</sup>	0.868	0.920	0.841	0.800	0.886	0.897	0.869	0,013
Tf(*)	p <sup>A</sup>	0.343	0.200	0.318	0.214	0.174	0.235	0.247	0,021
	q <sup>B</sup>	0.271	0.260	0.091	0.482	0.456	0.323	0.314	0,079
	r <sup>C</sup>	0.157	0.220	0.318	0.143	0.193	0.191	0.204	0,020
	s <sup>D</sup>	0.100	0.200	0.182	0.161	0.152	0.132	0.154	0,008
	t <sup>E</sup>	0.129	0.120	0.091	0.000	0.022	0.118	0.080	0,034
Alb(*)	p <sup>S</sup>	1.000	1.000	1.000	1.000	1.000	1.000	1.000	
	q <sup>F</sup>	0.000	0.000	0.000	0.000	0.000	0.000	0.000	
Cat(*)	p <sup>S</sup>	0.514	0.560	0.523	0.550	0.636	0.662	0.574	0,013
	q <sup>F</sup>	0.486	0.440	0.477	0.450	0.364	0.338	0.426	0,013
Prot-X(*)	p	0.044	0.175	0.046	0.087	0.115	0.000	0.078	0,044
	q	0.956	0.825	0.954	0.913	0.885	1.000	0.922	0,044
Ke(*)	p <sup>L</sup>	1.000	1.000	1.000	1.000	1.000	1.000	1.000	
	p <sup>H</sup>	0.000	0.000	0.000	0.000	0.000	0.000	0.000	

$\bar{\chi}$  Stocks = Steady average of frequency of stocks or herds. (\*) = Abbreviation of L-ISAGS.

Merino and the Lebrija Churro breeds were the most endangered sheep among Spanish breeds. The problem is to consider

the Grazaleta Merino and the Lebrija Churro as breeds, or varieties derived from Spanish Merino and from Genuine

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Churro, respectively (Ordás and San Primitivo, 1986). Because of this we assume that the two latter types are original populations from which our Andalusian breeds stem.

The data of biochemical polymorphism systems and external qualitative ethnological variables were obtained from 187 animals from six stocks of Grazalema Merinos, and the animals of Churro Lebrijano breed belong to 2 stocks, one of them (n=185) was used to study blood polymorphisms and the other one (n=72) was used to study external traits.

The genetic determination of the variables employed were made explicit in Rodero *et al.* (1996a). Once calculated the allelic frequencies (Rodero *et al.*, 1996b), the balance situation was checked by an  $\chi^2$  test. Following Jordana *et al.* (1992). The deviation of genetic balance for each polymorphic systems was checked using the *Wright Fixation Index*.

In **table I** are the allelic frequencies obtained for each stock of Grazalema Merino and the Whalund's, variance including ethnological characters. There are few genetically fixed systems and

increased genetic variability due to a weak natural or artificial selection or because of crosses with other breeds.

### ESTIMATE OF THE GENETIC EROSION

The coefficients of genotypic erosion were obtained following Lauvergne *et al.* (1987), by the expression  $e_p = q_e - q_t / 1 - q_t$ , where  $q_e$  is the gene frequencies in the derived population and  $q_t$  is the one in the original population. The erosion coefficient has been obtained only by biochemical polymorphism because of the lack of external attribute data in the original population (**table II**).

If biochemical systems are considered to be selectively neutral, from the  $e_p$  values obtained, positive signs mind that the effect of the breeds must have affected the original ones, while the negative signs only are justified by the drift effect when there are small size populations. Because of the great size of the population, it is necessary to consider other factors.

In Merino populations negative values can not be justified by genetic drift because the size of the populations is large enough to rule out a considerable

**Table II.** The erosion coefficients ( $e_p$ ) and the coefficient of drift change ( $f$ ) obtained by comparison between the purebred Merino and the Grazalema Merino breeds, on the one hand, and the Genuine Churro and the Lebrijana Churro breeds, on the other. (Coeficientes de erosión ( $e_p$ ) y de cambio por deriva ( $f$ ) obtenidos de la comparación entre las razas Merina pura y Merina de Grazalema y entre Churra genuina y Churra Lebrijana).

Systems	Merino breeds		Churro breeds	
	$e_p$ (%)	$f$	$e_p$ (%)	$f$
XProtein	13.60 p.c.	0.4799	-2.90 p.c.	0.0261
Haemoglobin $\beta$	15.44 p.c.	0.2026	3.87 p.c.	0.0306
Transferrin	-3.58 p.c.	0.1389	-5.82 p.c.	0.1043
Albumin	-16.88 p.c.	0.0014	54.30 p.c.	0.4458
$\bar{\chi}$	2.15 p.c.	0.1380	12.36 p.c.	0.1517

influence of other factors. The comparison of the allelic frequencies of purebred Merino and of Grazalema Merino highlights, as does Nguyen *et al.* (1992) in the comparison between purebred and Rambouillet Merino, the loss of certain alleles and almost the fixation of others. The authors account this phenomenon by resorting to the genetic drift effect. We also obtain the drift effect among the various stocks of Grazalema Merino. All the foregoing tends to suggest that, although the total size of the populations does not justify the results obtained for Merinos in erosion coefficients these could have been produced by the effective number and the reproduction schemes.

In the Churro breeds, it can be said that the mean value obtained for  $e_p$  is significative and has a positive sign, which could indicate, that the effect of selection or the influx of animals from populations with different genetic structures, ie. other breeds, which, after crossbreeding with Genuine Churro, must have given rise to Lebrija Churro. Since they are neutral variables we have discarded a possible effect of selection. If  $e_p$  values for each system are observed, the mean obtained is produced basically from the  $e_p$  of the albumin system, which is certainly high. This system is fixed, albeit only in Lebrija Churro population is in a Hardy-Weinberg imbalance. We think, therefore, there must exist some modifying factor of the gene frequencies of the albumin.

#### GENETIC DIFFERENCES BETWEEN ORIGINAL AND DERIVED BREEDS

The analysis in the comparison of original and derived breeds is performed by adopting Lewontin and Krakauer's method (1973), which is based on

obtaining the  $f$  values (drift-induced inbreeding) (**table II**) which examines the temporal changes in the allelic frequencies in small-size populations. The  $f$  corrected by Nguyen *et al.* (1992) are expressed as follows:

$$\hat{f} = \frac{1}{n} \sum \frac{(p_{ix} - p_{iy})^2}{p_{iy}(1 - p_{iy})}$$

where  $n = n^0$ , of alleles in the *locus*,  $p_{ix}$  and  $p_{iy}$  being the frequencies of the allele  $i$  in the derived and in the original populations, respectively. The variation in the gene frequencies among generations or populations is the result of both selection and reproductive structure. If there is a significant heterogeneity among the loci in their coefficient  $f$ , such a heterogeneity can be regarded as evidence that selection has played a part; on the contrary, if all the *loci* are selectively neutral, similar estimates of  $f$  will be produced.

According to Lewontin and Krakauer (1973), the heterogeneity of the various  $\hat{f}$  can be demonstrated starting from the standard error of  $\hat{f}$  by:  $\hat{f} \pm \sqrt{\frac{2}{n-1}}$

when considered as binomial the  $f$  distribution. The heterogeneities of each set of  $f$  values have been tested by dividing the highest value by the lowest one, with 1 and 1 degrees of freedom, and we have obtained  $F = 342.79$ , for Merinos, an extremely significant figure, and  $F = 17.08$  for Churros, which is also significative. In **table II**, it can be noted that, the only system that differs from the others as to  $f$  values is albumin. When the albumin system is eliminated, the significance of these values disappears.

In Merino breeds we have completed the analysis by considering not only the biochemical variables but also the

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external attributes. We have also applied Lewontin and Krakauer's method to the spaciation among the various populations studied of the Grazalema Merino breed. In this breed it was possible to obtain Whalund's variances according to Cavalli-Sforza and Bodmer (1971) as follow:

$$\frac{\sigma^2}{pq}$$

where

$$\sigma_p^2 = \frac{\sum p_i^2}{k} - \bar{p}^2 \quad (\bar{p} = \frac{\sum p_i}{k})$$

$k$  = No. of alleles). From the Whalund's variance in each system we have calculated the mean value  $\bar{f}$  and the obtained variance ( $S_f^2$ ). The expected variance of  $f$  is obtained by

$$\sigma_f^2 = \frac{k\bar{f}^2}{n-1}$$

( $k$  = No. of alleles y  $n$  = No. of populations). The quotient

$$\frac{S_f^2}{\sigma_f^2}$$

is compared to the distribution  $\chi^2$  taking away a degree of freedrom for each *loci*. If the test indicates a difference between  $S_f^2$  and  $\sigma_f^2$ , it is inferred that selection has been operating.

From the calculation of the Whalund variances (**table II**) and from the squared standard errors of the  $F$  coefficients, we have obtained  $S_{obs}^2 = 0.0206$  and  $S_{expected}^2 = 0.00051$  and  $c^2 = 46.27$ , which with 1 and 1 degrees of freedom results in  $p \leq 0.005$ . In other words, because of the

fact that man-selected ethnological characters are included, the spatial heterogeneity of Grazalema Merino is produced by the drift effect and by selection. For this we have researched on various populations of Grazalema Merino and not extrapolating the data from only one lot.

An estimate of the genetic divergence considering all the *loci* was obtained (Nguyen *et al.*, 1992) by means of a weighted mean of all of them:

$$\bar{f} = \frac{\sum [K(n-1)]}{\sum (n-1)}$$

where  $K$  = no. of *loci*. Nguyen *et al.* (1992) compare the mean value of the  $\bar{f}$  coefficients with the mean inbreeding ( $\bar{F}$ ) obtained from genealogies, in order to determine the drift effect or that of selection. We did not have genealogical data available that would make it possible to calculate the  $F$  of each breed, yet, considering the size of the populations and the number of generations that distinguish the members of each breed pair, we have made an approximate estimate of the  $F$  coefficients which yields an approximate result of 0.20 for the Merinos and 0.45 for the Churro breed. These values are higher than the mean of the  $\bar{f}$  of each breed (**table II**), but while in the case of Merinos it stays within the interval of the  $f$  coefficients, there are significant differences with Churros. Due to all this, the genetic drift can be a justification of the differences that were found in the allelic frequencies of the biochemical polymorphism between purebred Merino and Grazalema Merino. Noting that Nguyen *et al.* (1972) find an  $f$  between purebred Merino and Rambouillet Merino of 0.303, while we

obtain  $f=0.138$  between purebred Merino and Grazalema Merino.

Contrarily, in the Churro breeds there is another factor that acts as a distinguisher for the two breeds involved. For Manwel and Baker (1977), the low-frequency electrophoretic variants (think of the Albumin system) can, in many recent cases, represent mutations occurring after the separation of breeds. In our case this factor has little importance. In our study genetic drift is shown to have played an important but not unique part. Besides

this factor one must also reckon with selection and geographical isolation, which must historically have taken part in the development of the Lebrija Churro breed. Teixeira and Altarriba (1992) conclude that the appreciable distance between the Portuguese Churro sheep and the Spanish Churro breed should not be surprising, since these sheep populations were orientated towards different productive purposes such as the ones we have studied, even though they conceal a possible common origin.

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