

GENETIC DISTANCES BETWEEN SPANISH SHEEP BREEDS. (1).

(DISTANCIAS GENÉTICAS ENTRE RAZAS OVINAS ESPAÑOLAS).

por

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Summary

We have estimated the genetic distances and have constructed genealogical trees of the Spanish sheep breeds, taking into account the polymorphisms of hemoglobin, albumin, transferrin, arylesterases, and of potasium levels.

The results obtained indicate the phylogenetic relationship of the breeds studies; they are similar to the ones presented by ethnologists.

The genetic distances of the sub-breeds and varieties of the Rasa Aragonesa breed are also included, arriving at the conclusion that one of them (Ansotana) must be classified as a group with different characteristics.

Resumen

Se han estudiado las distancias genéticas y construido el árbol genealógico de las razas ovinas españolas considerando los polimorfismos de la hemoglobina, albúmina, transferrinas, arilesterasas y niveles de potasio.

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Los resultados obtenidos indican la relación filogenética de las razas estudiadas, similar a las presentadas por los etnólogos.

Las distancias genéticas de las subrazas y variedades de la raza aragonesa se incluyen también, llegándose a la conclusión de que una de ellas, la Ansotana, puede ser clasificada como un grupo con características diferentes.

As indicated by Kidd (1974) and other authorities, knowledge of the genetic relations in breed as a valuable aid, not only for knowledge as to how they are formed, but also that of the formation of the breeding plans of the offspring. Kidd also points out that the variations in the gene frequencies of the polymorphisms give quantitative genetic data for the measuring of evolutive differences among populations.

The knowledge of the genetic distances may help us in the prediction of the heterosis of the crosses that can be made.

In consideration of these points, we have initiated a study of genetic distances among the different Spanish sheep breeds, of which this is the initial work.

The Spanish sheep population is constituted by relatively large number of breeds which can still be considered as for the greater part being in a pure state. They therefore represent a source of specific germ plasma, and very appropriate material for this kind of analysis.

Materials and methods

The number of samples studied were 2146. These samples were distributed among the different breeds as follows: Churra 342, Lancha 186, Manchega 160, Black Castillian 145, White Castillian 149, Segureña 117, Talaverana 149, Rasa 98, and Spanish Merino 800.

The polymorphic systems used were: hemoglobins, albumins, transferrins, arylesterases and potassium levels. The genetic distances were computed according to the method used by Kidd and Pirchner (13), for di as well as for multiallelic loci.

Elaboration of the genealogical tree has been made by analysis of the group according to Edwards and Cavalli-Sforza (4).

The breeds studied were: Rasa, Manchega, Black Castillian, White

Castillian, Lacha, Talaverana, Segureña, Churra and Spanish Merino.

For the electrophoretic study the following methods were used:

- Hemoglobins : Huisman, T.H.J. (7).
Albumins: Efremov, G. and M. Braend (5)
Transferrins: Kristjansson, F.K. (15)
Arylesterases: Gahne, B. and M. Goransson (6)
Potasium: Spectrophotometric. The potasium's genotypes have been determined by the data of two generations.

These methods have been adapted to the conditions of our laboratory.

Results

In Table nº 1 the gene frequencies of the different groups studied are given, and in nº 2, the genetic distances initially obtained.

Chart of genetic distances of the sub-breeds and varieties of the Rasa Aragonesa breed was made, which is shown in Table nº 3. The average distance in this table is equal to 0.1236. When we eliminate the Ansotana variety this average decreases to 0.0702.

All the possible combinations of the tree were reduced to 78. The tree represented in Fig. 1 is the best. Those combinations in each breed which were the nearest and the farthest were taken into account.

Beginning with the genealogical tree and taking into account the historical data, we have constructed Map number 1.

Discussion

The Churra and Lacha are considered (Aparicio (1)) from an ethnological point of view, as being of an orthoid descendance, having come from the European mouflon, a legacy from the forms denominated by Duerst Ovis aries Studerys and diverse groups of this type. This grouping is distributed throughout the Spanish littoral with the exception of the East.

Two groups are studied in the Churra breed: the Churra Tensina and the milk Churra, fairly differentiated, with the latter having been selected for milk production.

The celoid breeds are represented in Spain by the Merino breed, which have influenced the other Spanish breeds by their extension over the country since the Middle Ages. It most probably proceeds from Ovis aries Vigney.

The cyrtoid groups are comprised of the breeds which we can estimate as proceeding from the trunk Sanson denominated Ovis aries Ligenien, and which, after penetrating into Spain from the Catalonian Pyrenses invaded Aragon and Castille forming the Aragonese, Manchega, Castillian and possibly Segureña breeds.

In the determination of the gene frequencies, various subraces of the Rasa breed were included, such as the Monegrina, the Ansotan, the Roya, the Soriana Ojalada and Genuina. In the studies of the distances only the Genuina group was taken into account.

We include the Talaveran breed which was possibly formed by cross-breeding between the Manchega and Merino breeds.

From the genealogical trees presented in graph number 1 we can make different conclusions. The Churra Tensina and the Churra de Ordeño are clearly differentiated through a distinct selective process, either because of different selection objectives or through the action of another breed which was used to improve the breed to obtain the specialization in production that was pursued.

The Lacha breed does appear next to the Churra de Ordeño, in agreement with the data of the classic ethnology, which puts them in the same trunk.

The Merina breed appears to be influential mainly in the following breeds: Rasa Aragonesa, Churra Tensina and Talaverana. The Talaverana breed appears to originate from both the Rasa and Merino animals and not directly from the latter ones across the Talaverana.

The animals in the Black Castillian and White Castillian groups, even though close, do not seem so alike, if you consider the variables of a same breed. The Black Castillian seems to be closely attached to the Manchega, which coincides in its cyrtoid characteristics and in the area of distribution. It also agrees with the more primitive origin of the Black Castillian and its possible influence on the Manchega. The Whi-

te Castillian is from more recent selection.

The Segureña breed is nearer the group of Manchega and Castillian breeds.

In general, the results obtained are in agreement with the notions previously expounded by ethnologic, and with the distribution of the breeds.

From Table 3. giving distances of the populations of the Rasa Aragonesa breed, it must be inferred that the inclusion of the Ansotana population modifies substantially the value of the average distance. Therefore it must be considered as a different group, at least inferred from the polymorphism studied.

A first study was made before having the data corresponding to the arylesterases and the results obtained did not differ significantly from those that are produced in this project, and which are shown in table 2 and figure 1.

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Table I. Gene frequencies of Spanish sheep breeds polymorphisms.

Breeds	HbA	HbB	AlS	AlF	AlV	TfA	TfB	TfC	TfD	TfE	TfS	K _L	K _H	Es ^a	Es ^b	Es ^c
Rasa	0.199	0.801	0.990	0.010	-	0.213	0.159	0.206	0.368	0.054	-	0.940	0.060	0.189	0.597	0.214
Manchega	0.159	0.841	1	0.0	-	0.242	0.138	0.216	0.262	0.107	0.035	1	-	0.113	0.775	0.112
Castellana negra	0.173	0.827	0.970	0.030	-	0.181	0.233	0.144	0.331	0.111	-	1	-	0.124	0.741	0.135
Castellana blanca	0.381	0.619	0.990	0.010	-	0.133	0.398	0.162	0.281	0.026	-	1	-	0.242	0.611	0.147
Lacha	0.306	0.694	0.990	0.010	-	0.204	0.225	0.288	0.169	0.114	-	1	-	0.124	0.656	0.220
Talavera-na	0.515	0.485	0.900	0.100	-	0.097	0.211	0.203	0.416	0.073	-	0.860	0.140	0.289	0.487	0.224
Segureña	0.097	0.903	0.990	0.010	-	0.127	0.083	0.297	0.352	0.141	-	1	-	0.128	0.692	0.180
Churra tensina	0.120	0.880	1	-	-	0.101	0.188	0.210	0.407	0.094	-	0.890	0.110	0.290	0.529	0.183
Churra ordeño	0.061	0.939	0.930	0.070	-	0.115	0.440	0.088	0.126	0.231	-	1	-	0.330	0.381	0.289
Merino español	0.348	0.652	0.983	0.013	0.004	0.168	0.150	0.131	0.467	0.075	0.003	0.906	0.094	0.320	0.500	0.180

Table II. Genetic distances between Spanish sheep breed by the Kidd and Pirchner method(13) (Lower part gives squared distance).

Breeds	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)
(1) Churra tensina	-	0.4139	0.3519	0.3416	0.3103	0.3552	0.3165	0.3559	0.1685	0.2398
(2) Churra ordeño	0.1713	-	0.3877	0.4532	0.3458	0.4093	0.3390	0.5207	0.4176	0.4845
(3) Lacha	0.1238	0.1503	-	0.2419	0.1997	0.2335	0.2472	0.4677	0.2516	0.3537
(4) Manchega	0.1167	0.2054	0.0585	-	0.2042	0.3434	0.1852	0.5027	0.2753	0.3813
(5) Castellana negra	0.0963	0.1196	0.0399	0.0417	-	0.2648	0.1819	0.4087	0.2218	0.3280
(6) Castellana blanca	0.1262	0.1675	0.0545	0.1179	0.0701	-	0.2827	0.3460	0.2711	0.3111
(7) Segureña	0.1002	0.1149	0.0612	0.0343	0.0331	0.0799	-	0.4703	0.2596	0.3617
(8) Talavera	0.1267	0.2711	0.2187	0.2527	0.1670	0.1197	0.2212	-	0.2997	0.2390
(9) Rasa	0.0284	0.1744	0.0633	0.0758	0.0492	0.0735	0.0674	0.0898	-	0.1962
(10) Merina	0.0576	0.2347	0.1251	0.1454	0.1076	0.0968	0.1308	0.0571	0.0385	-

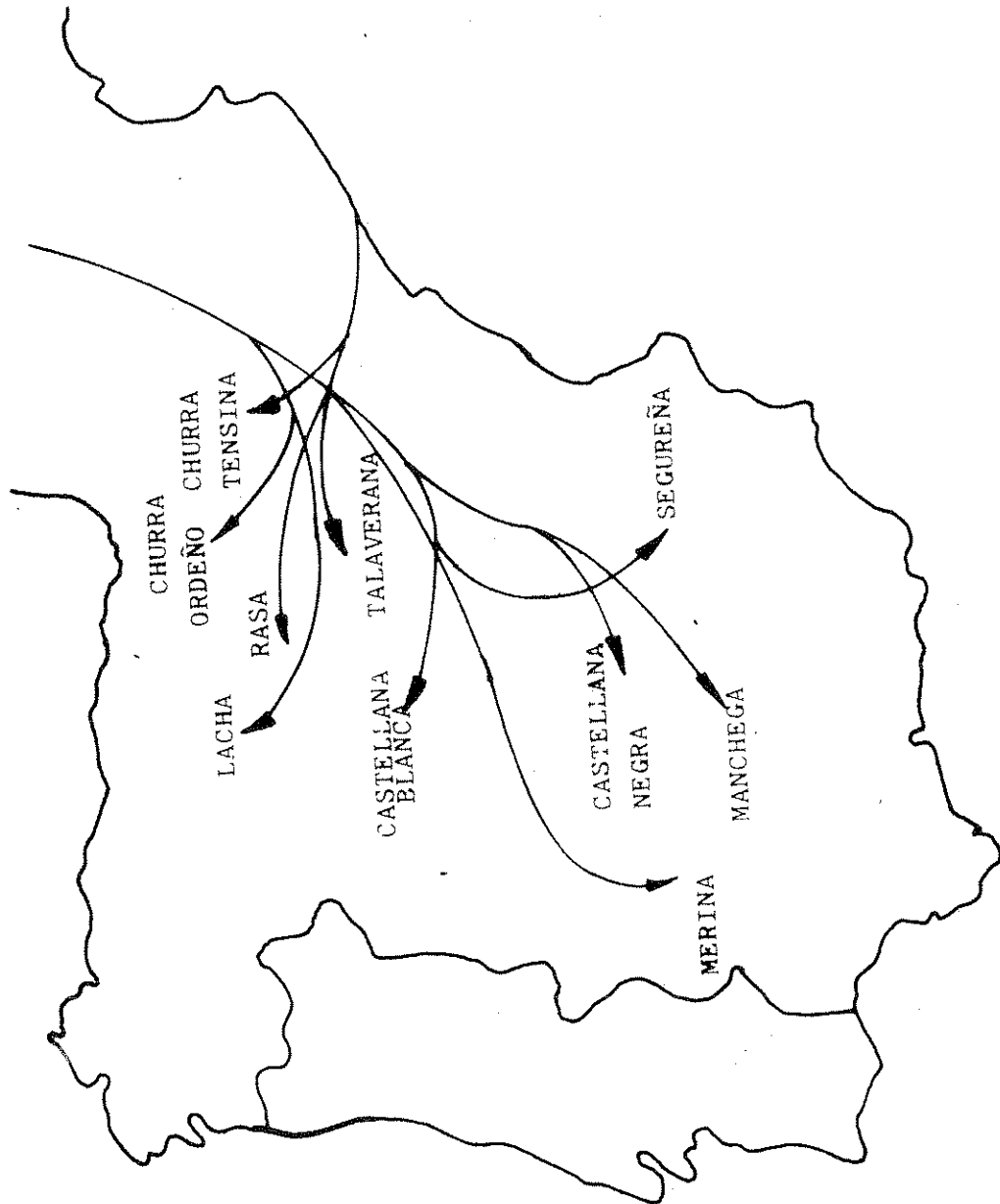
Table III. Genetic distances between Rasa breed populations.

	Genuino	Monegrino	Ansotano	Roya	Ojalado
Genuino					
Monegrino	0.0727				
Ansotano	0.1957	0.1533			
Roya	0.0705	0.0805	0.2338		
Ojalado	0.0714	0.0781	0.2314	0.0482	

Average distance= 0.1236

Average distance excluding Ansotana population= 0.0702

Figura 1. A phylogenetic tree of breeds studied projected on a Spanish map to show correspondence with possible routes of migration.



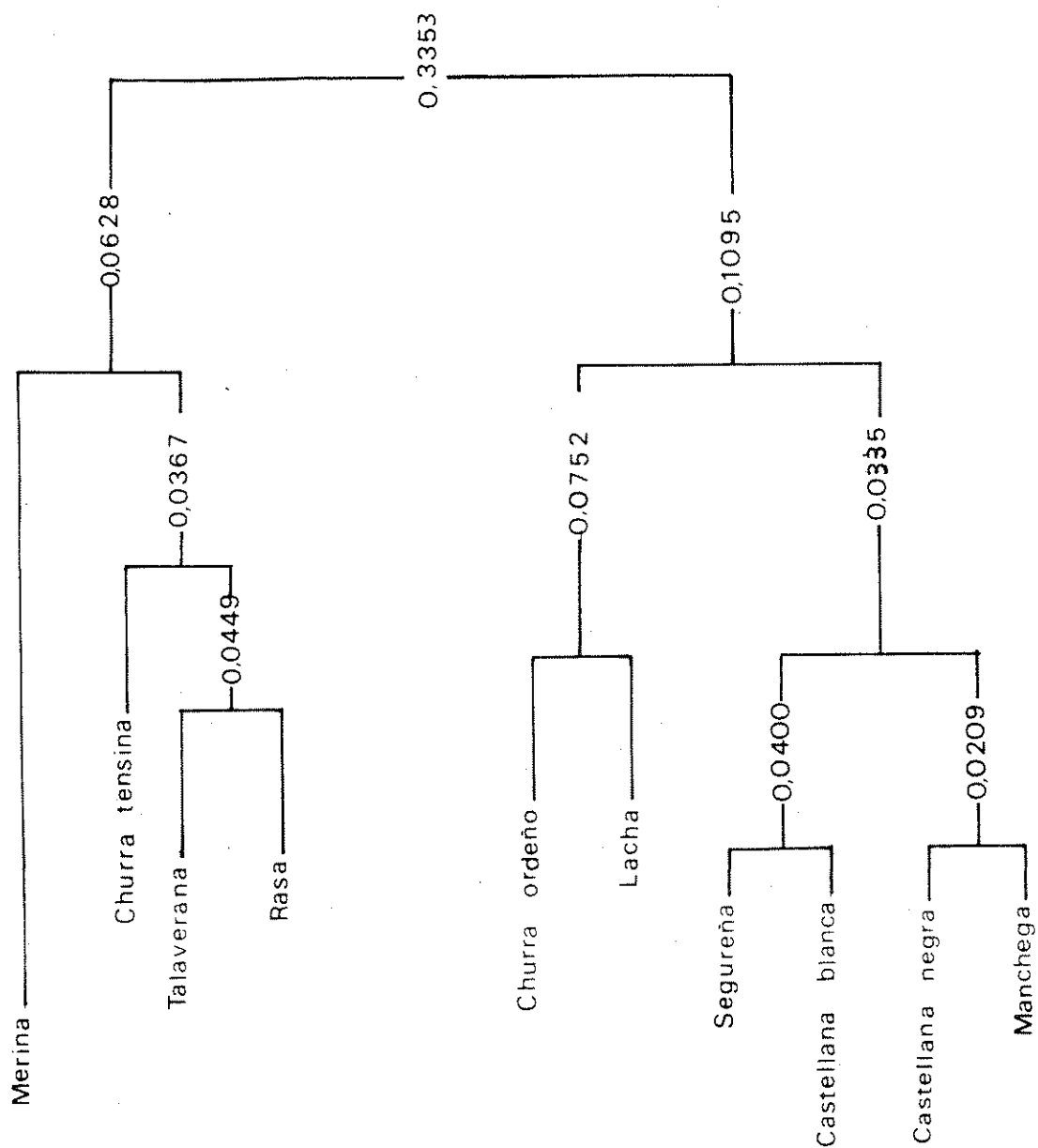


Figura 2. Phylogenetic tree of principal Spanish breeds computed from analysis of groups methods with indication of genetics distances between groups.

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