Genetic relationships between seven Spanish native breeds of cattle

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Summary. Ten genetic markers were studied in seven Spanish native cattle breeds, using a total of 725 animals. Of the ten, two were found to be monomorphic in all seven breeds. The genetic relationships of the seven breeds are estimated by three different genetic-statistical methods (genetic distances, main coordinate analysis and cluster analysis), which indicate three clearly distinct groups of populations: one where the Cárdena Andaluza and Alistana Sanabresa are very closely related, one comprising Sayaguesa, Morucha, Asturiana de los Valles and Asturiana de la Montaña cattle, and a third, genetically distant from the other two, comprising only Blanca Cacereña. The dendrogram drawn from the genetic distances matrix would seem to imply that the seven breeds are descended from different ancestors.

Keywords: Spanish cattle breeds, biochemical polymorphisms, genetic relationships

Introduction

The quantification of kinship between breeds of any species of animal has always been a problem for those researching into evolutionary processes. In cattle especially a great many authors have used the differences observed in genic frequencies of the variants of blood groups and biochemical polymorphisms to compare populations and breeds. However, the most widely used method of establishing possible relationships between different populations has been the calculation of genetic distances (Kidd 1969, 1974; Kidd & Sgaramella-Zonta 1972; Abe *et al.* 1975, 1977; Vallejo 1978; Kidd *et al.* 1980; Astolfi *et al.* 1983; Gonzalez-Sevilla & Vallejo 1983; Vallejo 1983).

Genetic distance can be measured in many different ways. According to Cedric & Smith (1977), generally speaking, each measurement of genetic distance has its own features, and the 'best distance' will depend on the purpose to which it is to be applied. To obtain a descriptive measurement of the degree of difference between populations, any method is valid. On the other hand, different methods of measuring genetic distance gave similar results to Chakraborty & Tateno (1976) and Aupetit (1985).

The purpose of this paper is to study the genetic relationships of seven native Spanish breeds of cattle from gene frequencies of ten genetic blood systems using three genetic-statistical methods: genetic distances, main coordinate analysis and cluster analysis.

Materials and methods

We used a total of 725 blood samples distributed thus among the seven Spanish cattle breeds: Sayaguesa (147), Morucha (101), Alistana Sanabresa (157), Blanca Cacereña (62), Cárdena Andaluza (25), Asturiana de los Valles (127) and Asturiana de la Montaña (106). The sampling of each breed was carried out at random.

The description of the breeds is derived from Sanchez (1981).

Sayaguesa. This is a medium-sized animal with concave profile and hook-shaped horns. The coat colour is black. It is concentrated in the Zamora region. There are about 4000 cows.

Morucha. This is a medium-sized animal with straight profile and hook-shaped horns. It is black or livid. It is concentrated in the Salamanca region, being the third most important Spanish breed numerically (about 147000 head).

Alistana Sanabresa. This is a medium-sized animal with concave profile and hook- or lyre-shaped horns. The coat colour is brown. It is concentrated in the Zamora region. There are about 14000 head.

Blanca Cacereña. This is a medium-sized animal with straight profile and hook-shaped horns. It is white. There are about 400 head concentrated in the Extremadura region.

Cárdena Andaluza. This is a medium- or small-sized animal with straight profile and hook-shaped horns. It is livid. The number of animals is small, there are only about 200 head concentrated in the Andalucia region.

Asturiana de los Valles. This is a medium-sized animal with a straight or slightly convex profile and variable horns. It is dark chestnut. There are about 40000 cows concentrated in the Asturias region.

Asturiana de la Montaña. This is a medium-sized animal with subconvex profile and variable horns. The coat colour is brown. There are about 2000 cows concentrated in the Asturias region.

All breeds described are meat producers.

Ten genetic systems were analysed, comprising six red-cell ones: haemoglobin (Hb), diaphorase (Dia), catalase (Cat), carbonic anhydrase (CA), purine nucleoside phosphorylase (NP) and red-cell potassium (Ke); and four plasmatic ones: amilase (AmI), ceruloplasmin (Cp), albumin (Al) and transferrin (Tf). Erythrocyte potassium was analysed by flame photometry using K^+ concentrations in blood and plasma with correction of the haematocrit value according to the method described by King & Wootton (1956). The other markers were identified by horizontal electrophoresis on starch gel and using the specific technique for each: haemoglobin (Braend 1963), diaphorase and catalase (Valenta *et al.* 1967), purine nucleoside phosphorylase and carbonic anhydrase (Tucker *et al.* 1967), amylase (Trowbridge &

Hines 1979), ceruloplasmin and albumin (Kristjansson 1963) and transferrin (Poulik 1957).

Genetic distances were estimated according to Nei's method (1972).

Main coordinate analysis was performed using methodology described by Mallo (1985).

The dendrogram was drawn from the genetic distances matrix according to the method proposed by Sneath & Sokal (1973).

Results

Table 1 shows the gene frequencies obtained for each locus and breed. It is to be noticed that the diaphorase and catalase systems were monomorphic in all the breeds studied and that the Hb^A, CA^S, NP^L, K^L and Al^F alleles were the most frequent in all breeds. With regard to the AmI system, both alleles show high frequencies though,

Table 1. Gene frequencies in seven native Spanish cattle breeds for ten genetic systems

Loci	Alleles	Sayaguesa (147)	Morucha (101)	Alistana Sanabresa (157)	Blanca Cacereña (62)	Cárdena Andaluza (25)	Asturiana de los Valles (127)	Asturiana de la Montaña (106)
Hb	Hb^A	0·83	0·84	0·99	0·71	0·96	0·91	0·79
	Hb^B	0·17	0·16	0·01	0·29	0·04	0·09	0·21
Dia	Dia^F	0·00	0·00	0·00	0·00	0·00	0·00	0·00
	Dia^S	1·00	1·00	1·00	1·00	1·00	1·00	1·00
Cat	Cat^F	0·00	0·00	0·00	0·00	0·00	0·00	0·00
	Cat^S	1·00	1·00	1·00	1·00	1·00	1·00	1·00
CA	CA^F	0·28	0·28	0·08	0·33	0·00	0·13	0·23
	CA^S	0·72	0·72	0·92	0·67	1·00	0·87	0·77
NP	NP^H	0·14	0·20	0·01	0·48	0·04	0·28	0·26
	NP^L	0·86	0·80	0·99	0·52	0·96	0·72	0·74
Ke	K^L	0·68	0·83	0·78	1·00	0·80	0·78	0·81
	K^h	0·32	0·17	0·22	0·00	0·20	0·22	0·19
AmI	AmI^B	0·59	0·58	0·47	0·77	0·32	0·58	0·64
	AmI^C	0·41	0·42	0·53	0·23	0·68	0·42	0·36
Cp	Cp^A	0·72	0·82	0·79	0·09	0·56	0·79	0·69
	Cp^B	0·11	0·03	0·01	0·00	0·02	0·03	0·14
	Cp^C	0·17	0·15	0·20	0·91	0·42	0·18	0·17
Al	Al^F	0·96	0·89	0·90	0·56	1·00	0·99	0·99
	Al^S	0·04	0·11	0·10	0·44	0·00	0·01	0·01
Tf	Tf^A	0·54	0·41	0·54	0·92	0·68	0·46	0·27
	Tf^D	0·44	0·51	0·45	0·08	0·32	0·51	0·72
	Tf^E	0·02	0·08	0·01	0·00	0·00	0·03	0·01

Number of animals is given in parenthesis

while in Alistana Sanabresa and Cárdena Andaluza AmI^C is the more frequent allele, in the remaining breeds studied it is AmI^B. As for the Cp system, Cp^B allele was not detected in Blanca Cacereña, while in the other races it has low frequencies, ranging from 0·01 in Alistana Sanabresa to 0·14 in Asturiana de la Montaña. There is a remarkably low frequency of Cp^a (0·09) in Blanca Cacereña, which is not only the lowest frequency among the breeds studied, but according to the bibliography consulted, the lowest for any breed in the world. Blanca Cacereña also has a very high frequency of Tf^A (0·92).

Table 2 shows Nei's genetic distance (D) matrix for the seven breeds. The values range from 0·007 (Morucha-Sayaguesa and Morucha-Asturiana de los Valles) to 0·180 (Blanca Cacereña-Alistana Sanabresa). Blanca Cacereña is very distant from the others, with D values ranging from 0·149 (Blanca Cacereña-Cárdena Andaluza) to 0·180 (Blanca Cacereña-Alistana Sanabresa), which, according to Nei (1976), are of the order of the distances between subspecies (0·02–0·2), although Nei himself does point out that it is not easy to distinguish between local breeds and subspecies. It may also be seen from Table 2 that the distances between Cárdena Andaluza and the rest of the breeds are relatively great (0·031–0·149), except the one separating it from Alistana Sanabresa (0·014).

To show the genetic relationships between the seven breeds studied we used the main coordinate analysis method, which, being based on Nei's similarity matrix, gives a matrix of Euclidean distances after transformation, to obtain a synthetic and easily followed representation of the relationships between populations in a limited space, in such a way that the distances within this subspace reflect as efficiently as possible the distances or similarities between the original data.

Table 3 shows the variance (V) for each main coordinate together with the explained variance (EV) and the accumulated explained variance (AEV) for the seven main coordinates.

The first two main coordinates are seen to give 91·6% of the total dispersal, a sufficiently high percentage for a Euclidean representation of the distances under consideration. Therefore in a plane, the seven breeds of cattle may be shown, with a loss of only 8·4% of the information supplied by the genetic distances.

In Fig. 1 we can see that Blanca Cacereña (4) is very distant from the other breeds, which in turn form two groups shown in two quadrants: one containing Alistana Sanabresa (3) and Cárdena Andaluza (5), and the other comprising Sayaguesa (1), Asturiana de los Valles (6), Morucha (2) and Asturiana de la Montaña (7).

Using cluster analysis we draw the dendrogram (Fig. 2), based on the matrix of genetic distances (Table 2). It shows a first differentiation of two groups of populations: (1) Blanca Cacereña and (2) the remaining breeds, which are divided into: (a) Morucha, Asturiana de los Valles, Sayaguesa and Asturiana de la Montaña; (b) Cárdena Andaluza and Alistana Sanabresa.

Discussion

The three methods used in the present study of the genetic relationships of seven breeds show that there is a high genetic affinity between, on the one hand, the

Table 2. Genetic distances between seven cattle breeds (estimated from gene frequencies of 10 loci)

	Sayaguesa	Morucha	Alistana Sanabresa	Blanca Cacereña	Cárdena Andaluza	Asturiana de los Valles	Asturiana de la Montaña
Sayaguesa	—						
Morucha	0·007						
Alistana Sanabresa	0·013	0·017					
Blanca Cacereña	0·153	0·155	0·180				
Cárdena Andaluza	0·032	0·042	0·014	0·149			
Asturiana de los Valles	0·009	0·007	0·014	0·157	0·031		
Asturiana de la Montaña	0·016	0·010	0·032	0·174	0·057	0·011	—

Table 3. Explained variance

MC	1	2	3	4	5	6	7
V	0·244	0·070	0·013	0·007	0·005	0·003	0·000
EV	71·17	20·44	3·86	2·13	1·49	0·92	0·01
AEV	71·17	91·60	95·46	97·59	99·08	99·99	100·00

MC : main coordinates
V   : variance
EV : explained variance (in percentage)
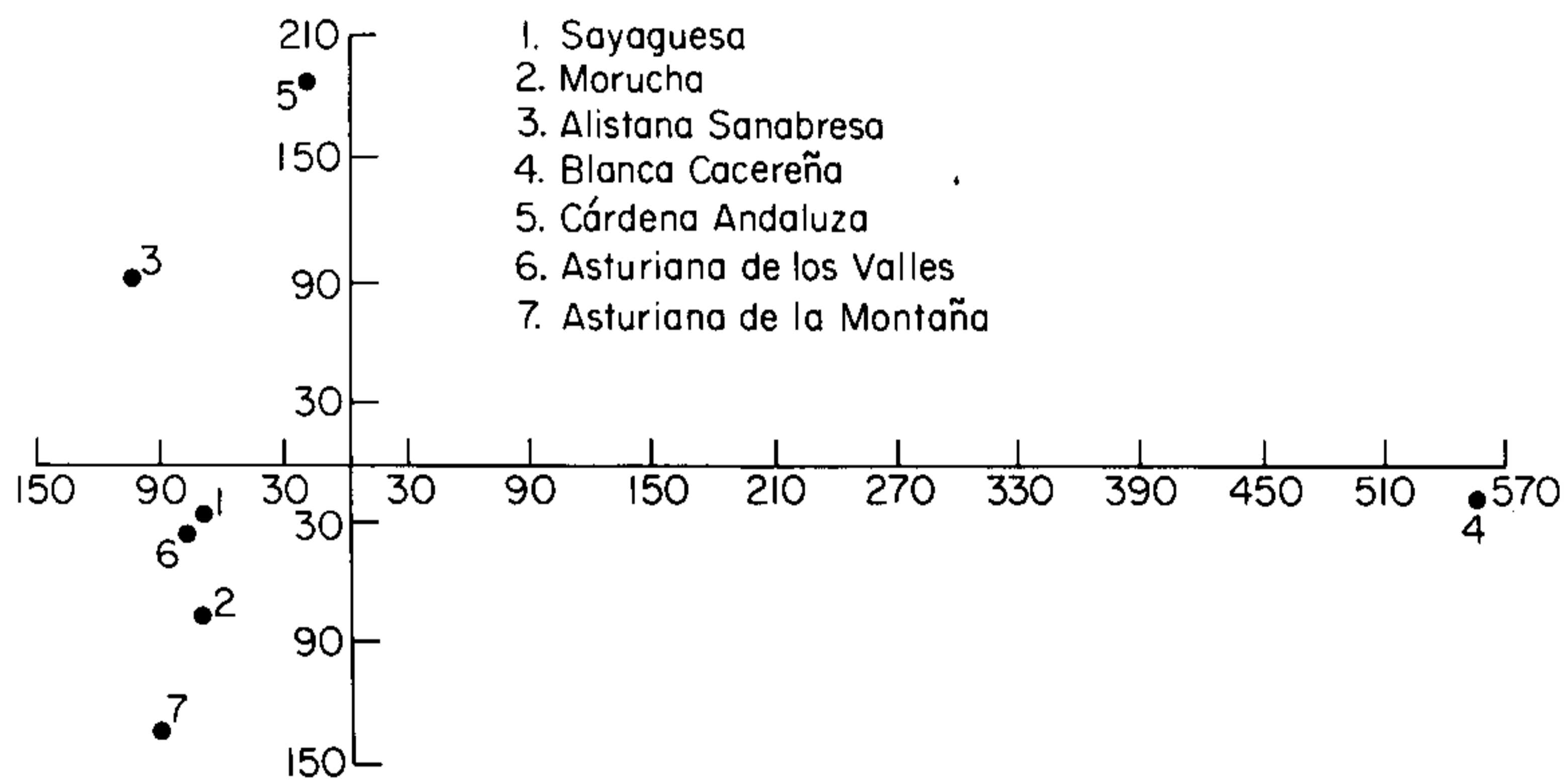AEV : accumulated explained variance (in percentage)

Figure 1. Representation of seven cattle breeds by main coordinate analysis.
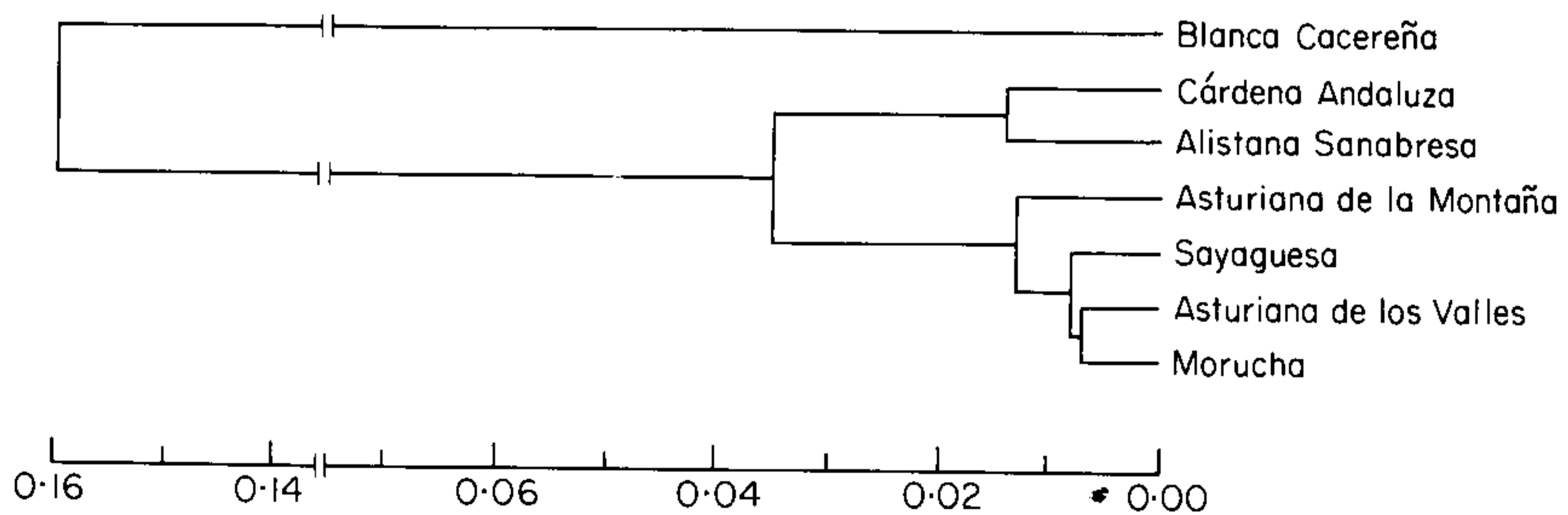

Figure 2. Dendrogram showing the genetic relationships between seven Spanish cattle breeds.

Morucha, Asturiana de los Valles, Sayaguesa and Asturiana de la Montaña and, on the other, the Cárdena Andaluza and the Alistana Sanabresa, all these breeds being very distant genetically from Blanca Cacereña.

The phylogenetic tree, or dendrogram, is the first step towards attempting to study or establish the evolutionary processes of species. The origins of domestic cattle, and therefore those of our native cattle, are by no means clear. From the dendrogram in Fig. 2, we would infer that the native Spanish breeds studied come from two branches: one which gave rise to Blanca Cacereña and one which produced the other six breeds studied here, which bears out the diphyletic theory of two primitive forms: *Bos primigenius* and *Bos brachycerus*, from which all modern cattle are descended.

Our results are in agreement with those of several authors (Kidd & Sgaramella-Zonta 1972; Abe *et al*. 1977; Vallejo 1978; Astolfi *et al*. 1983), who have also pointed out two differentiated branches for various breeds of cattle. We should like to point out, however, that this does not always happen, as may be seen from the work of Abe *et al*. (1975) and Kidd *et al*. (1980).

We should like to emphasize the fact that while the dendrogram shows the genetic relationships between breeds, it cannot show the actual evolutionary history of populations if they are not completely isolated (Nei 1975). The present study therefore questions again some traditional ethnological concepts, although it does not establish any definite theses, as these would require a much more in-depth study, involving a greater number of loci and also other types of data, such as morphometric, which would afford complementary information to clear up the genetic relationships and the evolutionary history of our native breeds.

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