

GENETIC CHARACTERIZATION OF THE "CRIOULA LANADA" SHEEP FROM SOUTHERN BRAZIL

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ABSTRACT

The genetic variability of six protein systems was investigated in a rare woolled sheep (Crioula Lanada) from Brazil. Genetic distance analysis between this flock and various Spanish sheep breeds shows great similarity between the Crioula and Lacha breeds, which does not agree with the former's presumed origin. Comparison with Romney Marsh and Corriedale breeds from the same region of Brazil shows great mutual similarity, suggesting gene exchange among these animals.

INTRODUCTION

There is nowadays an increasing interest in rare or indigenous breeds of sheep, especially those that are in danger of extinction. Blood genetic polymorphisms provide convenient means to characterize them, verify their relationships with other breeds, and also to investigate the presence of linkage groups which might be employed in production. Such studies have already been carried out on rare Dutch, British, Italian and African sheep breeds (Buis and Tucker, 1983; Clarke *et al.*, 1989a, 1989b; Zanotti Casati *et al.*, 1990).

In Brazil, the Brazilian Agricultural Research Corporation (EMBRAPA) has been developing a program for preservation and evaluation of a rare-wooled sheep, named Crioula Lanada. According to Mariante and Trovo (1989), there are a small number of flocks in Southern Latin America. This breed probably originated from the

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Spanish sheep "Churra" brought to South America during the colonization period. In comparison with breeds specialized for wool production, Crioula sheep produce a very coarse black, white and agouti wool, not suitable for industrialization. However, the breed presents evidence of high precocity and fertility (Mariante and Trovo, 1989).

We describe some genetic markers of Crioula sheep found in Southern Brazil and make some inferences about their origin.

MATERIAL AND METHODS

Blood samples of 91 animals were obtained from the jugular vein. These samples were placed in tubes with ACD, refrigerated shortly after collection, and carried to the laboratory as soon as possible. Red cells were separated, washed in saline solution and glycerolized according to Weimer *et al.* (1981). Plasma and red cells were stored at -20°C until the tests, that were mainly performed by horizontal starch gel electrophoresis. Plasma was used for typing albumin (Tucker, 1968), transferrin and slow alpha-2 macroglobulin (Ferguson and Wallace, 1961, modified by Valenta *et al.*, 1976) and ceruloplasmin (Imlah, 1964), while red cell lysates were employed for testing hemoglobin (Huehns, 1968) and catalase (Harris and Hopkinson, 1976), the last with the samples diluted 30 to 50 times, as suggested by Baker and Manwell (1977). Arylesterase was typed in plasma, using the quick tube test according to Tucker *et al.* (1967). The albumin and transferin phenotypes were compared with international standards kindly provided by Dr. E.M. Tucker. Gene frequencies were calculated by the gene counting method for the codominant alleles or by assuming Hardy-Weinberg equilibrium for arylesterase. Genetic distances were estimated according to Rogers (1972) and Nei (1978), using the Biosys program of Swofford and Selander (1981).

RESULTS AND DISCUSSION

Genetic variability

The number of animals tested varied in different systems due to various technical reasons, such as denaturation of some proteins and hemolysis.

Two plasma proteins, slow alpha-2 macroglobulin (AP) and ceruloplasmin (CP), were monomorphic. Studies involving these two proteins have also failed to find variation in Merino and Poll Dorset sheep (Manwell and Baker, 1977). For the five other systems, the gene frequencies can be found in Table I. For hemoglobin two alleles were found, the rarer of them, *HB A*, having a frequency of 0.33. This value is very similar to those found for Spanish Merino sheep (Rodero *et al.*, 1982; Morera *et al.*, 1983), and for Romney Marsh sheep from Rio Grande do Sul, Brazil (Weimer *et al.*, 1984).

Table I - Phenotype distribution and gene frequencies of four protein systems in Crioula sheep.

Loci	Phenotypes			Gene frequency	
		No.	Frequency		
HB	HB A	11	0.13	<i>HB A</i>	0.33
	HB AB	36	0.41	<i>HB B</i>	0.67
	HB B	40	0.45		
	Total	87			
ALB	ALB S	90	0.99	<i>ALB S</i>	0.994
	ALB ST	1	0.01	<i>ALB T</i>	0.006
	Total	91			
TF	TF A	2	0.03	<i>TF A</i>	0.16
	TF AB	16	0.20	<i>TF B</i>	0.35
	TF AC	2	0.03	<i>TF C</i>	0.35
	TF AD	1	0.01	<i>TF D</i>	0.11
	TF AE	2	0.03	<i>TF E</i>	0.03
	TF B	7	0.09		
	TF BC	18	0.23		
	TF BD	7	0.09		
	TF C	13	0.17		
	TF CD	8	0.10		
	TF CE	1	0.01		
	TF DE	1	0.01		
	Total	78			
CAT	CAT F	18	0.28	<i>CAT F</i>	0.41
	CAT FS	17	0.27	<i>CAT S</i>	0.59
	CAT S	17	0.45		
	Total	52			
ESA	ESA +	5	0.07	<i>ESA +</i>	0.04
	ESA -	66	0.93	<i>ESA -</i>	0.96
	Total	71			

For transferrin, five alleles were found, whose frequencies were quite different from those for Spanish sheep, mainly due to a high value for *TF C* and low frequency of *TF D* (Rodero *et al.*, 1982).

For albumin the only variation found was a single heterozygote for *ALB S* and an allele slower than *ALB W*. Only one variant slower than *ALB W* has been described till now: *ALB T* found in an Indian sheep population (Krishnamurthy *et al.*, 1974). The variant found here seems to have the same electrophoretic pattern as *ALB T*, but only a side by side comparison in a single electrophoresis gel could confirm this result.

Two alleles were found for the catalase locus, with frequencies around 0.5. This result is very similar to those found for Australian Merino sheep (Manwell and Baker, 1977).

Regarding esterase, we found a gene frequency for *ESA-* of 0.96. There is great variation in the frequency of this allele in different breeds, with values ranging from 0.51 in a rare Dutch breed (Buis and Tucker, 1983) to 1.0 in Merino from the United States of America (Tucker *et al.*, 1967). However, in most breeds *ESA-* has a value above 0.9.

Genetic distance

Genetic distance analysis was made between the Crioula sheep and 11 Spanish breeds. Two other sheep breeds (Romney Marsh and Corriedale) from the same region of Brazil were also included in the analysis in order to verify environmental effects on the genetic background of this breed. Since we did not encounter gene frequency data for four systems in Spanish breeds, this analysis was made considering only HB, TF and ALB loci. The gene frequencies were compiled from Vallejo *et al.* (1975), Rodero *et al.* (1982) and Weimer *et al.* (1984). For the Brazilian breeds we do not have data for ALB; therefore this frequency was estimated by the arithmetic average of the other breeds. Since this is a conservative estimate, it was not expected to provoke a great deviation in the relationships.

Table II gives the genetic distances matrix and Figure 1 shows the phenogram, both obtained using Rogers distance. Similar results were found with Nei distance, but the cophenetic correlation was lower than that obtained with Rogers estimate. Excluding Romney Marsh and Corriedale from the calculation, no difference in relationships was verified. However, these results must be interpreted carefully because the analysis was made involving only three loci. As pointed out by Nei (1975), if one is interested in the relative values of genetic relationships among several taxa, the distances based on few polymorphic loci are useful. As can be seen, Crioula cluster first with Lacha and then with Romney Marsh and Corriedale. The Churra breed, which was believed to be the main breed for the origin of Crioula sheep, is at a great distance from it. These results can explain the great morphological difference between these breeds, and the close similarity between Lacha and Crioula phenotypes, as described by Muñoz and Tejon (1980). However, we can not exclude the possibility that Churra was one of the breeds involved in the ancestry of Crioula sheep. The great similarity of this flock with Romney

Table II - Genetic distances matrix among fourteen sheep breeds.

Population	1	2	3	4	5	6	7	8	9	10	11	12	13
01. Crioula													
02. Rasa	.131												
03. Manchega	.135	.047											
04. Castellana Blanca	.082	.125	.148										
05. Castellana Negra	.140	.044	.051	.123									
06. Lacha	.053	.091	.089	.088	.102								
07. Lacha II	.053	.094	.087	.091	.105	.003							
08. Talavcrana	.182	.168	.206	.132	.170	.167	.170						
09. Segurcña	.171	.074	.067	.182	.085	.128	.131	.213					
10. Churra Tensina	.162	.060	.063	.152	.060	.130	.128	.173	.048				
11. Churra Ordeño	.193	.169	.150	.191	.128	.180	.183	.260	.145	.142			
12. Spanish Merino	.121	.084	.125	.088	.103	.099	.101	.115	.139	.111	.227		
13. Corriedale	.104	.138	.138	.097	.149	.081	.084	.113	.187	.188	.242	.117	
14. Romney Marsh	.083	.100	.106	.107	.121	.064	.067	.169	.154	.157	.223	.090	.071

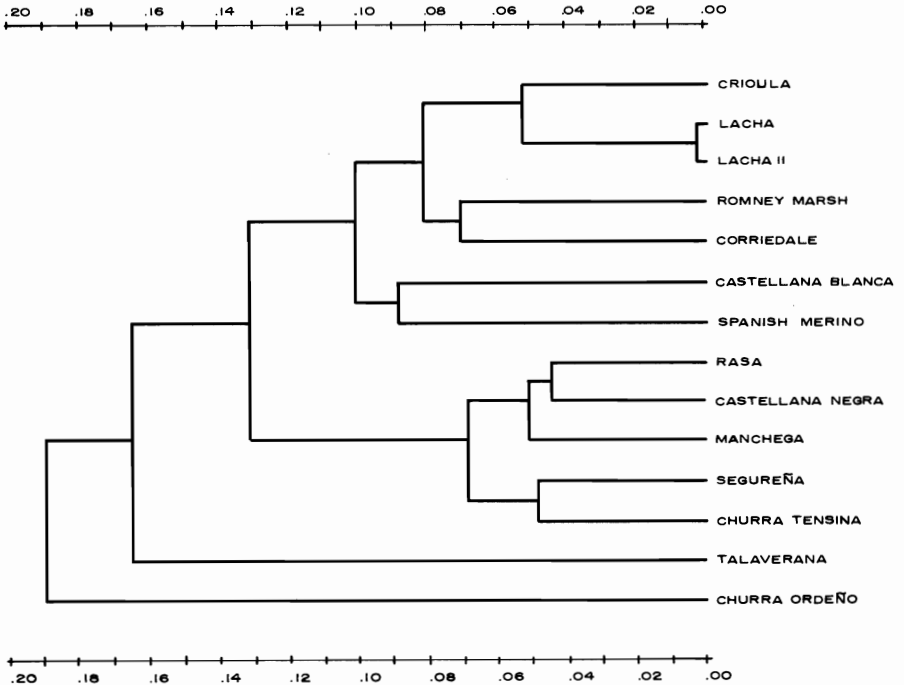


Figure 1 - Dendrogram showing the genetic relationships among 14 sheep breeds based on Rogers distances.

Marsh and Corriedale raised in Southern Brazil suggests gene exchange among these breeds after their introduction into this region or, less probably, that some of their genetic traits can be related to the common environment in which these animals live. These results highlight the need for thorough studies in such "local breeds" of sheep before their inclusion in preservation programmes.

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RESUMO

Um rebanho ovino Crioulo Lanado do Brasil, foi investigado quanto à variabilidade genética em seis sistemas proteicos. Análises de distância genética com diferentes raças espanholas mostraram uma maior similaridade deste rebanho com as ovelhas Lacha o que não concorda com a origem histórica proposta. Verificou-se grande semelhança entre estes animais e os ovinos Corriedale e Romney Marsh, criados na mesma região do Brasil, o que sugere a ocorrência de fluxo gênico entre eles.

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