# FORMATION PROCESS STUDY OF ANDALUSIAN BOVINE LOCAL BREEDS IN DANGER OF EXTINCTION

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## ABSTRACT

A paper on breed characterization and genetic relationships among Berrenda en Colorado(BC), Berrenda en Negro (BN), Pajuna (P) and Cardena (C) cattle breeds was presented at a previous EAAP meeting. The present paper involves 168 BN animals (23 farms), 262 BC animals (25 farms), 14 C animals (1 farm) and 51 P animals (3 farms); 32 DNA markers were used for the genetic studies. Gene flow among the four breeds and farms within breeds was estimated: values for among breeds are low, (3,78 and 3,29) among C and Berrenda (BN and BC); little higher among P and Berrenda (BN and BC) (6,71 and 6,89); lower limits were found ( 2,91)among P and Berrenda (BN and BC) and the highest between BN and BC (18,42). The values obtained are not determinants for farms with the breed, especially for Berrenda cattle breeds (BN and BC). The results agree with previous ethnologic studies about common breed origins and mating systems in populations. The divergence times among the populations studied were obtained, resulting 13,22 generations for Berrenda cattle breeds (BN and BC) and 403,75 generations for P and C. These values were obtained without taking into account gene flow among breeds, when previous data show that it is high, at least for Berrenda breeds.

## INTRODUCTION

The four cattle breeds of this paper (Berrenda en Colorado –BC-, Berrenda en Negro –BN-, Pajuna –P- and Cárdena –C-) have the highest level of priority in order to guarantee their conservation (Rodero et al., 1992). A paper on breed characterization and genetic relationships among this four cattle breeds was presented at a previous EAAP meeting (Rodero et al, 2005). In this paper, we are attempting to obtain information about the genetic process for the formation of the four breed studied. (Supported by INIA Project No RZ004-0013)

## MATERIAL AND METHODS

The present paper involves 168 BN animals (23 farms), 262 BC animals (25 farms), 14 C animals (1 farm) and 51 P animals (3 farms); 32 polymorphic loci from the DNA microsatellites were analyzed. These markers were chosen by following the recommendation of FAO (MoDAD), ISAG and those used in the European Project for Biodiversity in Cattle (http://www.ribbsrc.ac.uk)

We are obtained the gene flow (Trexler, 1988) within and between breed, the relation among the excess of heterozygosity and the number of alleles per locus in each breed; and also, the divergence time among breeds. Finally, the different methods (Nei, 1972, Weir and Cockerham. 1984 and Reynols et al, 1983) to determine the genetic distances were compared (Takezaki and Nei, 1996).

## RESULTS AND DISCUSSION

In general, the values obtained for the gene flows among breeds (Table 1) was very variable (p. e. 3,78 and 3,29 among C with BN and BC respectively); little higher among P and both Berrenda breeds (6,71 and 6,89 for BN and BC, respectively); The lower level were found ( 2,91) among P and C and the highest between BN and BC (18,42)). This result agree with previous ethnologic and historic studies about common breeds origins and mating systems in populations (Sanchez Belda, 2003)

In the *Pajuna* breed the gene flows between farms (Table 2) ranged from 8,62 to 10,27; from 1,54 to 10,17 in the *Berrenda en Colorado*, and from 0,88 to 6,33 in the *Berrenda en Negro*. These values are very slight, this cannot be understood as a consequence of the result of crossbreeding of individuals with other from outside farm.

The heterozygosities were high (Table 3), according to the high gene flow among some breeds.

The divergence times among the populations studied (Table 4) resulting 13,22 generations for Berrenda cattle breeds (BN and BC) and 80,75 generations for P and C. These values were obtained without taking into account gene flow among breeds, when previous data show that it is high, at least for Berrenda breeds. Also, these results are according with the historical postulation.

All the parameters of genetic distances (Figure 2) showed the greatest proximity between the two Berrenda breeds and the greatest degree of distance was between the Cárdena and the other breed studied, mainly with the Pajuna.

In the Figure 3 we can see the relation among number of alleles with the excess or deficit of heterozygosities. It should be pointed out more a deficit of heterozygocities than an excess (Cornuet y Luikart, 1996). Only in the Cárdena could have been “bottlenecks”, but not recently

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## TABLES

**Table 1.- Gene flow among four breeds**

| | **BERRENDA EN NEGRO** | **CARDENA** | **PAJUNA** |
|---|---|---|---|
| **BERRENDA COLORADO** | 18,42 | 3,78 | 6,71 |
| **BERRENDA EN NEGRO** | | 3,29 | 6,89 |
| **CARDENA** | | | 2,91 |

**Table 2.- Range of gene flow among flock within breeds**

| | **Minimun** | **Maximun** |
|---|---|---|
| **BERRENDA COLORADO** | 1.54 | 10.17 |
| **BERRENDA EN NEGRO** | 0.88 | 6.33 |
| **PAJUNA** | 8.63 | 10.27 |

**Table 3.- Heterozygosities (standard deviations in parentheses) and number of alleles per locus, averaged over 32 DNA microsatellites.**

| **Breed** | **Mean Heterozygosities** | | | **Mean no. alleles per locus** |
|---|---|---|---|---|
| | **Hexp.** | **H.n.b.** | **Hob** | |
| **BERRENDA COLORADO** | 0.720 (0.132) | 0.722 (0.133) | 0.668 (0.142) | 8.677 |
| **BERRENDA EN NEGRO** | 0.721 (0.109) | 0.723 (0.109) | 0.653 (0.125) | 8.807 |
| **CARDENA** | 0.697 (0.124) | 0.723 (0.129) | 0.678 (0.180) | 5.838 |
| **PAJUNA** | 0.671 (0.152) | 0.681 (0146) | 0.654 (0.167) | 6.613 |

**Table 4.- Divergence times among breeds (t=generation, the time are in years)**

| | **t** | **years** |
|---|---|---|
| **BC - BN** | 13.22 | 165 |
| **BC - C** | 62.72 | 313.62 |
| **BC - P** | 35.88 | 179.39 |
| **BN - C** | 71.86 | 359.28 |
| **BN - P** | 34.90 | 174.7 |
| **P - C** | 80.75 | 403.75 |

**Figure 1- Geographical localization of different breeds**

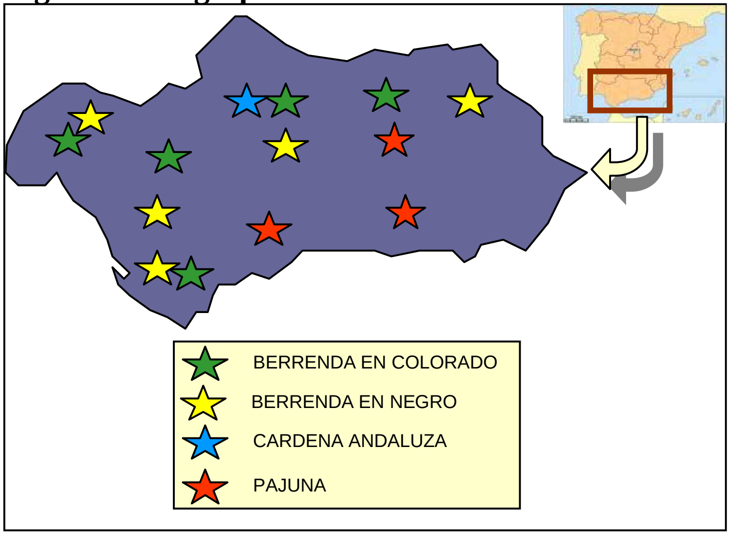

**Figure 2- Genetic distances among breeds**

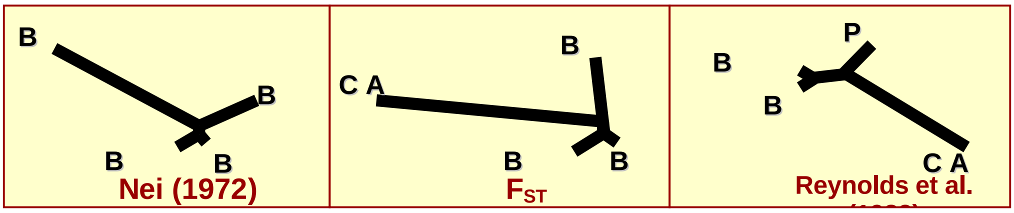

**Figure 3.- Relationship each breed among alleles number and excess of heterozygosity**