

Analysis of genetic diversity of indigenous cattle, horse and sheep breeds from the Basque Country.

M. Iriondo, B. Jugo, F. Rendo, A. Solis, L.I. Mazon and A. Estonba*

Department of Animal Biology and Genetics, University of the Basque Country

P.O.B. 644, E-48080 Bilbao, Spain. *e-mail: ggpesrea@lg.eh.es



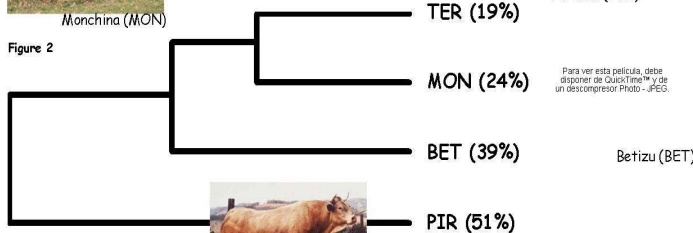
INTRODUCTION

As a consequence of the demand for high-input farming systems, local livestock breeds have become almost totally displaced by commercial breeds during the last decades. The genetic diversity of animals permits farmers to select breeds and develop new breeds in response to environmental changes, the threat of diseases, new findings concerning the nutritional needs of human beings, the evolution of market needs and the needs of society, all of which are immensely difficult to forecast (FAO, 1995). Thus, a strategy is required to maintain the most ample level of genetic variation within the species, a strategy in which the first step is the characterization of the genetic resources available.

The Basque Country comprises an area of geographic transition offering great biological wealth. Its mountainous orography and the conservationist tendencies of local cattle breeders has preserved breeds of diverse species from prehistoric times to the present. Thus, in the Basque Country there exist numerous indigenous breeds. Despite the risk of extinction for some of the breeds, knowledge of the intra and inter-genetic variation of these native breeds is still lacking. The use of genetic markers provides the only tool to assess population genetic structures of most of these native breeds because they lack detailed recorded data concerning history and pedigree.



Figure 2



RESULTS

The variability detected within breeds is slightly higher than those obtained with other European breeds (Arroz *et al.*, 1995; Cañon *et al.*, 2000; Martín-Burniel *et al.*, 1999). The elevated value of H_e in some threatened breeds such as MON and SAS is noteworthy, a characteristic which is worth taking into account whenever undertaking a Selection or Conservation program (table 1). According to the F_{ST} values, the proportion of allelic variation attributed to breed differences in horses would be 16%, a value markedly lower than that obtained in cattle and sheep (4.1% and 3.1% respectively).

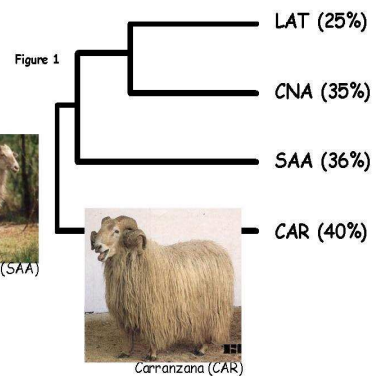
We constructed "diversity trees" with our native breeds with the aim of evaluating the relative contribution of each breed to the global diversity observed and defining objectives of conservation and breeding programs (figures 1, 2 and 3). From these trees it was clear that most of the diversity in cattle lies in the PIR breed (51%), specialized in meat production. Moreover, the semiferal and endangered breed BET also represents a high proportion of diversity (39%). Similarly, in horses, the POT pony, in grave danger of extinction, accumulates the largest part of genetic variability of this species in the Basque Country (59%). Finally, in relation to sheep breeds, the only one in danger of extinction, SAA, contributes 35% of the diversity in this species.

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Table 1. Number of individuals, MNA, H_e , PE, F_{ST} and breed correct allocation values in the 12 breeds. (*) $p < 0.05$ with Bonferroni correction

Species	Breed	n	MNA	H_e	PE	F_{ST}	Breed Assig
CATTLE	PIR	56	6.91±2.63	0.688±0.111	0.9993		93%
	BET	83	7.91±2.51	0.715±0.082	0.9995		87%
	TER	115	8.64±2.54	0.747±0.105	0.9999		83%
	MON	56	7.46±2.51	0.762±0.076	0.9999	0.041±0.005*	92%
HORSE	EHZ	144	7.75±2.45	0.738±0.086	0.9999		71%
	POT	89	8.08±2.54	0.762±0.061	0.9999		80%
	BUR	45	6.25±2.75	0.698±0.132	0.9997		78%
	JNA	62	7.25±2.48	0.744±0.102	0.9999	0.016±0.003*	70%
SHEEP	LAT	264	11.46±3.93	0.765±0.085	0.9999		88%
	CAR	41	8.00±2.10	0.729±0.092	0.9998		98%
	SAA	72	9.46±3.17	0.781±0.087	0.9999		86%
	CNA	60	10.82±2.75	0.790±0.073	0.9999	0.031±0.004*	93%



MATERIALS AND METHODS

MNA, H_e and PE values were calculated using CERVUS software (Marshall *et al.*, 1998). The parameter θ (F_{ST}) according to the formulae of Weir and Cockerham (1984) was calculated using the FSTAT program (Goudet, 1995). The F_{ST} genetic distance (Reynolds *et al.*, 1983; Cavalli-Sforza *et al.*, 1994) was used to measure losses of diversity due to various patterns of breed extinction, as proposed by Weitzman (1993). Employing allelic frequencies and using the maximum likelihood approach, we have estimated the assignment of an individual to a breed using WHICHRUN 4.1 software (Banks and Eicher, 2000).

DISCUSSION

The difference among the F_{ST} values of the species analysed is a result of the combined effects of breed origin, the extent of admixture occurring during breed foundation and development, and random genetic drift. Thus, EHZ and BUR horses originated after genetic contributions from French equine breeds, from two breeds of Basque ponies (POT y JNA, respectively). Besides, the fact that the four horse breeds are semiferal no doubt has influenced in a greater gene flow between these breeds than bovine and ovine breeds. Relatively speaking, the levels of diversity observed among cattle and sheep breeds are higher than those obtained with other breeds of geographical proximity. Thus, the area analyzed in the present work occupies around 15,000 km², the values of F_{ST} for areas like the Iberian Peninsula and France, for example (1,150,000 km²) for bovine breeds is less than double ($F_{ST} = 0.07$; Cañon *et al.*, 2001). This result would indicate the relatively high differentiation between breeds in the Basque Country which can serve as an index of the existent high biodiversity in this small region in Europe.

The extensive capability of DNA markers to distinguish among individuals has been broadly used in parentage testing. The global probability of exclusion (PE) values of 0.999 obtained with 11 microsatellites for each breed make it extremely unlikely that false parentage would not be recognised in the three species. These markers are therefore an effective tool in cattle, horse and sheep parentage verification in these breeds. Furthermore, these results indicate that these DNA markers can be used effectively for issues of traceability of live animals or derived products.

On the other hand, the potential of using individual genotype information to determine the breed membership of a single individual is a topic receiving current interest (Blott *et al.*, 1999; Roques *et al.*, 1999). Potential for discrimination among individuals is essential for effective and accurate management of livestock breeds. Furthermore, a test for breed identity would be valuable for the validation of quality and origin of livestock products. Thus, we obtain correct classification percentages for the individuals in each breed, between 70% and 98%. The largest percentages of correct classification that we obtain are for sheep from the CAR and CNA breeds, along with cows from the PIR and MON breeds. The weaker aggregation observed for the remaining breeds can be explained not only as a function of the number of analysed loci, but also as the genetic differentiation among breeds which influence the breed assignment potential (Bjornstad and Reed, 2001). Even so, and with the aim of reaching values near 99%, we should implement the genetic system used in this study, increasing the number of polymorphic loci analysed in order to apply in an effective manner DNA testing technology for clarifying the population background of individuals with unknown or suspect origin.



Terreña (TER)

Para ver esta película, debe disponer de QuickTime™ y de un decompresor Photo - JPEG.



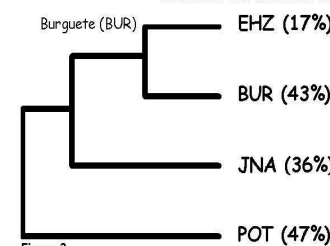
Sasi Ardi (SAA)



Carranzana (CAR)



Euskal Herriko Mendiko Zaldia (EHZ)



Jaca Navarra (JNA)



Pottoka (POT)

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