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### Preliminary analysis on genetic variability and relationships among five native Italian ovine breeds (Appenninica, Garfagnina Bianca, Massese, Pomarancina and Zerasca)

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### Introduction

The intense work of selection of these last years decreased the contribution of locally developed breeds and threatened their existence, but some of them could still play an important role in the animal production systems.

In order to decide what to preserve it is necessary to measure the genetic uniqueness of the breeds.

Aim of this project was to perform a genetic characterization of some Italian endangered sheep breeds. Namely we investigated Pomarancina (PO), Garfagnina bianca (GB) and Zerasca (ZE) breeds; Massese (MS) and Appenninica (AP) were included as reference groups and Pelibuey (PB) breed (Mexico) has been considered as an outgroup.

### Materials and Methods

- Breeds: the number of individuals sampled, of both sexes, was 42 for each breed.

- Molecular analyses: Sheep DNA was prepared from whole blood. The 6 microsatellite loci studied were MCMA8, MCMA11, OARAE119, OARCP49, OARFCB4 and MAF70.

- Data analysis: number of alleles per locus; mean heterozygosity values (observed and expected); gene diversity; coefficient of gene differentiation; phylogenetic trees (NJ method) among populations based on Reynolds genetic distances. The robustness of the dendrogram was evaluated by a bootstrap test with 1000 replicates resampling of loci with replacement.

### Results and discussion

The mean number of alleles per locus ranged from 8.8 (PB) to 12.3 (ZE). Only the out group seems to show a reduced mean number of alleles (Table 1).

The average expected heterozygosities ( $H_S$ ) of the five European breeds lie in a narrow range of 0.80-0.84 (Table 2) indicating that there are no appreciable differences in genetic variability among the breeds.

A large part of the total genetic diversity can be explained by the variation within breeds (91.1%) and to a smaller extent by the variation among breeds ( $G_{ST}=0.089$ ).

*Table 1 – Number of alleles per locus, observed and expected mean heterozygosity values ( $\pm$  standard error).*

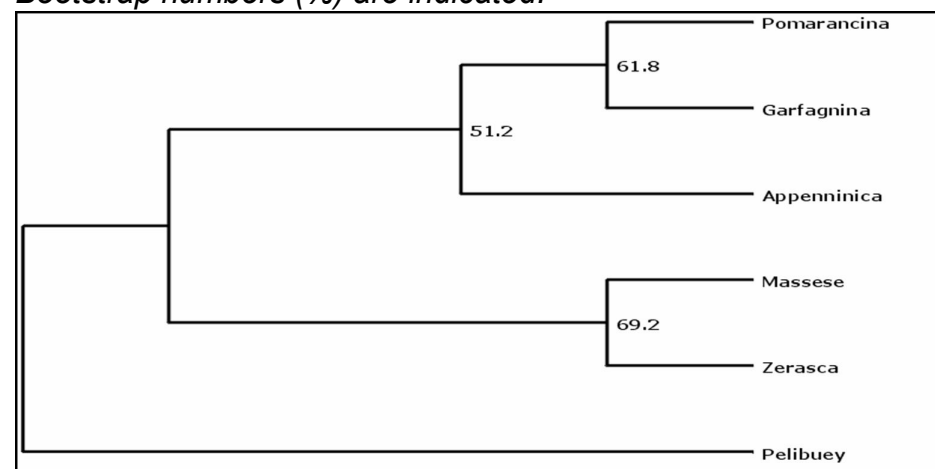
Population	Mean No. of alleles per locus	Mean heterozygosity	
		Observed	Expected
Pomarancina	11.3 $\pm$ 3.4	0.690 $\pm$ 0.161	0.808 $\pm$ 0.027
Garfagnina bianca	10.5 $\pm$ 3.8	0.667 $\pm$ 0.125	0.827 $\pm$ 0.025
Appenninica	10.3 $\pm$ 4.8	0.730 $\pm$ 0.086	0.830 $\pm$ 0.029
Massese	9.3 $\pm$ 2.6	0.591 $\pm$ 0.211	0.818 $\pm$ 0.023
Zerasca	12.3 $\pm$ 2.7	0.635 $\pm$ 0.182	0.836 $\pm$ 0.031
Pelibuey	8.8 $\pm$ 1.7	0.563 $\pm$ 0.151	0.776 $\pm$ 0.035

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Table 2 – Total number and range of observed alleles, average heterozygosity  $H_S$  and  $H_T$  and coefficient of differentiation  $G_{ST}$ .

Locus	Total No. of alleles	Size range in bp.	$H_S$	$H_T$	$G_{ST}$
MCMA8	14	138-172	0.789	0.840	0.062
MCMA11	15	176-222	0.815	0.881	0.075
OARAE119	11	149-185	0.773	0.865	0.106
OARCP49	23	84-138	0.859	0.943	0.089
OARFCB4	15	130-180	0.788	0.895	0.119
MAF70	18	124-162	0.812	0.882	0.080
All loci			0.806	0.885	0.089

Figure 1. NJ tree based on Reynolds' genetic distances. Bootstrap numbers (%) are indicated.



The NJ tree shows (Figure 1):

i) within European breeds clear branching with high reliability (bootstrap value > 80%) was not possible.

ii) both breeds of the miniclust PO and GB are probably influenced by the AP breed forming together a group of Appenninic origin. Although GB breed is considered derived from MS breed it is probable that crosses with AP occurred before the conservation programme started.

iii) the relatedness between the MS and ZE is much closer than among the other breeds and this could be explained with the historical development of this last breed. Both breeds share the same geographical background and recent admixtures with Massese breed cannot be excluded.

Further analyses involving more markers could be carried out to confirm our preliminary results.

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