Genetic structure of Italian Alpine goat populations based on microsatellite markers

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INTRODUCTION

A great variety of local goat populations are present in the Italian Alps. From these populations, some breeds have been recently defined on the basis of their geographical distributions and morphological aspects. The objective of this study was to analyse the genetic structure of seven Italian goat breeds using microsatellite markers to confirm or reconsider their classification into breeds.

MATERIAL AND METHODS

•DATA and MARKERS

A total of 205 animals were sampled from seven goat breeds Roccaverano, Vallesana, Verzaschese, Lariana, Ciavenasca, Trentina and Passiria, farmed on the Italian Alpine ark (Figure 1). DNA was taken from three animals per flock, unrelated for at least two generations. A panel of 26 microsatellites, recommended by FAO and recently used in the EU project Econogene, was analysed on the entire data set.

•GENETIC ANALYSES

Genotypic frequencies at the 26 microsatellite loci were tested for Hardy-Weinberg equilibrium (GenePop software). Within breed diversity parameters, including expected (H*exp*) and observed (H*obs*) heterozygosity and F_{IS} statistics (Weir & Cockerham) were estimated with the Genetix software (Belkhir et al., 2004). The global structure of the population was then analysed by the fixation index F_{ST} (Weir & Cockerham), and a Neighbour-Joining tree was built using the Reynolds genetic distance. Ignoring the breed structure, the Bayesian-based clustering analyses proposed by Pritchard *et al.* (2000) was applied to the entire data set with the aim of delineating clusters of individuals based on their genotypes at multiple loci.

Figure 1: Geographic distribution of the goat breeds Roccaverano (n.1), Vallesana (n.2), Verzaschese (n.3), Lariana (n.4), Ciavenasca (n.5), Trentina (n.6) and Passiria (n.7).

RESULTS

A total of seven microsatellites were in Hardy-Weinberg disequilibrium (P<0.05) and were excluded from the Bayesian-based clustering analysis. Average H*exp* and H*obs* heterozygosities over all loci were respectively 0.68 and 0.62, and the mean F_{IS} was 0.09.

Genetic differentiation was moderate with an overall value $F_{ST} = 0.03$.

The Reynolds genetic distances ranged from a minimum value of 0.011 between Trentina and Passiria breeds, and a maximum value of 0.057 between Vallesana and Verzaschese breeds.

A Neighbour-Joining tree was built, that clustered together breeds following their geographical distribution: Lariana and Ciavenasca, Trentina and Passiria, Verzaschese and Vallesana breeds (Fig. 2).

Ignoring the structure of the metapapulation in breeds, the Bayesian-based clustering analysis correctly assigned to the breed of origin only 63% of individuals. Based on the estimated proportion of membership (Table 1) the seven breeds were reorganized into five different groups (Figure 3).

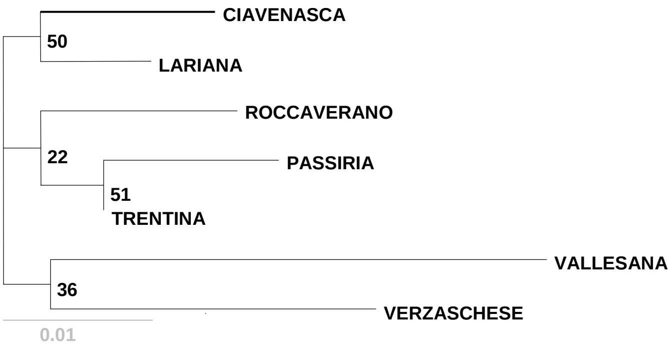

Figure 2: Neighbour-Joining tree based on Reynolds genetic distances among seven goat breeds.

Breed	Inferred Clusters				
	1(red)	2(green)	3(blue)	4(yellow)	5(pink)
Ciavenasca	0.142	0.116	**0.537**	0.061	0.144
Lariana	0.191	0.083	**0.488**	0.099	0.140
Passiria	0.137	0.103	0.111	0.067	**0.582**
Roccaverano	**0.479**	0.121	0.141	0.073	0.186
Trentina	0.200	0.085	0.250	0.128	**0.336**
Vallesana	0.053	**0.771**	0.078	0.041	0.058
Verzaschese	0.067	0.097	0.099	**0.664**	0.074

Table 1: Proportion of membership of the seven analysed breeds in each of the five cluster (colours into parenthesis indicate correspondence to the clusters in Figure 3).

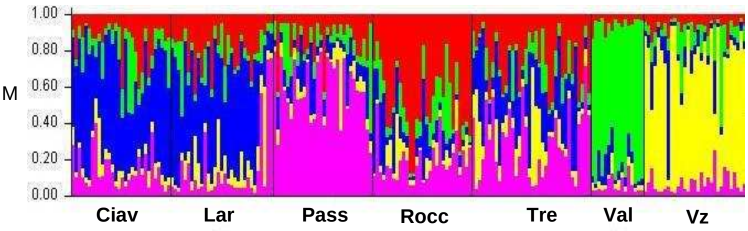

Figure 3: Estimated membership coefficient for each individual in each of the five cluster (represented by five different colours). (Ciav = Ciavenasca, Lar = Lariana, Pass = Passiria, Rocc=Roccaverano, Tre = Trentina, Val = Vallesana, Vz = Verzaschese).

CONCLUSIONS

The genetic analysis of the seven goat breeds from the Italian Alpine ark suggests to reconsider the breed structure defined on the basis of geographical and morphological elements. However, culture differentiation among breeds should be also considered.

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