Leccese sheep breed from Apulia: evidence of genetic sub-structuring from STR loci

Francesca Cecchi[1], Elena Ciani[2], Elisabetta Castellana[2], Elisa Mazzanti[1], Roberta Ciampolini[1]

[1]Dipartimento di Produzioni Animali, Università di Pisa, Italy

[2]Dipartimento di Fisiologia Generale ed Ambientale, Università di Bari, Italy

Corresponding author: Elena Ciani. Dipartimento di Fisiologia Generale ed Ambientale, Università di Bari. Via Amendola 165/a, 70126 Bari, Italy - Tel. +39 080 5442413 - Fax: **+39 080 5443388** - Email: **elenaciani@** biologia.uniba.it

ABSTRACT

Leccese is an originally triple-purpose sheep breed from Southern Italy. Due to major changes in rural society and livestock production, the breed has experienced in the last decades a drastic population size reduction. Nowadays roughly one thousand animals are reared in about ten farms located in Apulia. In order to evaluate the genetic variability within the Leccese breed, a total of 97 animals, sampled from five different farms in the provinces of Bari, Taranto, Brindisi, and Lecce were genotyped at 19 microsatellite loci belonging to the ISAG-FAO panel for Domestic Animal Diversity. Samples were chosen according to genealogical records in order to minimize relatedness among animals. Although being a local bottlenecked breed, the Leccese sample displayed a valuable number of alleles (187 over 19 loci, with a minimum of 4 in BM1824 and OarFCB193 and a maximum of 16 in MAF70 and MCM140). A high proportion of private alleles was observed for each farm (7.7 alleles on average). In addition, a high level of linkage disequilibrium was observed in the total sample, also among non syntenic locus pairs, suggesting the presence of population sub-structuring. To test the hypothesis of a genetic partitioning at the farm hierarchical level we first calculated the pair-wise FST between the different farms, which highlighted significant (P<0.001) though moderate values (0.055 to 0.065). Then, we performed both a likelihood-based and a Bayesian population assignment test, respectively implemented in the Arlequin and Structure software packages, in order to verify the degree of differentiation between the five farms. A correct allocation was obtained for 96.9% of animals by using the Arlequin software and 92.8% when using Structure, thus highlighting a clear genetic differentiation at the farm level, counterbalanced by a marked within-herd genetic similarity. These results suggest that reproductive isolation and/or different selection strategies across farms contributed to the observed pattern of genetic sub-structuring; this should be seriously taken into consideration, due to the critical implications for the breed conservation.