Genetic diversity of Albanian sheep breeds as revealed by molecular markers

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Albania is a West Balkan Country with a long tradition in managing livestock. Sheep are an important livestock species in Albania distributed throughout the country, grazing in the natural pasture, with an extensive or semi-extensive management system. Sheep are of great interest, especially for the local community that raise them, as an essential source of milk, meat and wool, mainly for family consumption. Ninety-three animals from three native sheep breeds (Bardhoka, Ruda and Shkodrane) were analyzed for 31 microsatellites, AFLP, 36SNP markers, and mitochondrial DNA. The study was carried out in the frame of the ECONOGENE project. Here we provide the results of genetic structure assessment and genetic variation found within and among breeds. The mean expected heterozygosity and allelic richness over the microsatellite loci and sheep breeds were 0.75 and 8.61, respectively. The individuals were analyzed by three EcoRI/TaqI primer combinations that produced 92 AFLP markers. Nei's G<sub>ST</sub> index was 0.039, indicating a low genetic variation between breeds. Similar results were obtained using SNPs. The mean percentage of individuals correctly assigned estimated by the use of the Bayesian approach was at 45.16%. Mitochondrial DNA analysis revealed a total of 34 haplotypes with a high mean haplotype diversity of 0.968. Phylogenetic analysis showed three lineages A, B and C, where lineages B displayed a star-like phylogeny.

Analysis of molecular variance for each kind of marker revealed that only 4% of the total genetic variation is due to differences between breeds, while differences account for 96% of the diversity among individuals within breeds. Factorial Correspondence Analysis (FCA) and Structure analysis showed a high degree of genetic similarity between individuals, in line with the high level of detected gene flow. Factorial component analysis and model-based clustering did not differentiate sheep breeds. However, they displayed a high level of breed admixture, which is in concordance with the small genetic distance found between breeds.

The results obtained here reflect sheep management in Albania. The breeding programs and herd books have been missing since 1990. The mating is natural, and performance control has not been established. In most cases, there is only one ram per flock that breeds all the ewes, and no controlled mating is applied. The farmer does the selection of the ram without any information or control of their origin, resulting in mating without parentage control. This kind of management probably has facilitated the gene flow and the breed's admixture, resulting in a poor level of genetic differentiation. Responsible Institutions can use these results to design proper breeding programs to conserve the genetic diversity presently existing in Albanian sheep.

Key words: genetic variation, breed admixture, gene flow, genetic distance, genetic differentiation.