

Population structure and genetic diversity analysis in five rare endangered goat breeds in Austria

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Maintenance of genetic diversity within and between breeds plays an important role for designing sustainable conservation programs. Seven autochthonous goat breeds in the Alpine region were identified by the Austrian national association for gene conservation of farm animals (ÖNGENE) as Austrian endangered goat breeds, which are part of a national conservation program. A set of 47,652 single nucleotide polymorphisms (SNP) for 145 goats from five of these breeds (34 Blobe, 22 Chamois Colored Alpine, 28 Pinzgau, 33 Styrian Pied and 28 Tauern Pied) were used to infer population structure and estimate the genetic diversity, using heterozygosity, average pairwise genetic distance, linkage disequilibrium (LD), effective population size (N_e) and runs of homozygosity (F_{ROH}) in order to evaluate the genetic variability within and between breeds. According to the principal component analysis, a quite clear separation for Tauern Pied and more relation between the other breeds were detected. Six ancestries were identified for these five breeds by ADMIXTURE, where Blobe goats showed two different ancestries in their genetic background. We added the genotype information on 22 Passeier goats from South Tyrol, Italy, whose main habitat along the alpine range is very close to that of the Blobe breed. The Passeier goats showed similar background with some Blobe goats, indicating migration between these two populations. According to the genetic diversity measurements, the highest heterozygosity (0.418) and average pairwise genetic distance (0.320) were observed for Styrian Pied goats and the lowest values were observed for Tauern Pied goats; 0.376 and 0.275. Likewise, highest LD (0.070) with smallest N_e (104) were estimated for Tauern Pied goats. In total, a reasonable amount of genetic diversity and good separation between breeds were observed for the breeds. The low levels of genetic diversity in the Tauern Pied goats were confirmed by the highest levels of genomic inbreeding (0.107 ± 0.033) in this breed, due to a more homogenous founder population compared to the other breeds.