

Genomic inbreeding of Nicastrese: conservation of an autochthonous Italian goat breed

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Nicastrese is a goat population from Southern Italy. In 2019 there were 6254 individuals from 105 herds. Recently, within the national project *Conservation, Health and Efficiency Empowerment of Small Ruminant* (CHEESR), coordinated by the National Breeders Association, a sample of Nicastrese individuals were genotyped. The objective of this work was to analyse breed structure (BS) and calculate inbreeding in Nicastrese goat using Runs of Homozygosity (ROH) estimated from genomic information. Data came from 100 individuals split in 2 subsets. The first one included 30 unrelated animals sampled from 10 farms. The second subset included 23 and 47 goats sampled from two different and large herds, namely A (n=223) and B (n=220). The official lab of Italian Animal Breeders Association performed DNA extraction and genotyping with a medium density (50k) Goat SNP chip. ROH were estimated as follows: a ROH length of ≥ 1 Mb, a sliding window of 20 SNP with no heterozygous tolerated. ROH inbreeding coefficients (F_{ROH}) were calculated as the proportion of the autosomal genome covered by ROH. ROH analysis allowed us to evaluate both the level of inbreeding in the population and the differences among farms. Herd B showed a very high level of outbreeding across all classes of ROH length (1-2, 2-4, 4-8, 8-16, >16 Mb). Herd A had a F_{ROH} similar to the one found in BS. In all the subsets, we observed a high ROH number on chromosomes (CHI) 6 and 12. The large number of ROH identified on CHI 6 are consistent with the dairy purpose of this breed and may indicate an artificial selection or a natural selection directed at offspring preservation. CHI 12 contains a syntenic region, both in cattle and sheep, where selection signals were already identified by other studies. The investigation of ROH in different farms can give useful indications for the management of the breed's biodiversity and originality.