

Assessing Among Flocks Genetic Diversity in Istrian Sheep to Define a Framework for Optimum Contribution Selection

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ABSTRACT: Long-term sustainability of economically important native breeds depends on sufficient genetic diversity necessary to cope with challenges in environment and breeding programs. The objective of this study was to analyse genetic diversity between and within flocks of Istrian sheep to define baseline population structure before implementation of optimum contribution selection. Altogether 719 animals from 12 flocks were genotyped with the Ovine SNP50 BeadChip. After quality control (SNP call rate > 0.9 and individual genotype call rate > 0.9, exclusion of sex-linked SNPs) 47,793 SNPs were used for further analysis. The snpReady package in the R programming environment was used to calculate genomic population parameters. The average population expected heterozygosity (H_E), observed heterozygosity (H_O) and inbreeding coefficient (F) were 0.357, 0.332, and 0.07, respectively. The average pair-wise genetic differentiation between flocks was moderate (0.194) and ranged from 0.016 to 0.413. The first three PC explained 15.8%, 14.9%, and 10.6% of the variation in the population, showing three genetically disconnected clusters. These results indicate that the Istrian sheep has preserved genetic diversity for the implementation of optimum contribution selection.

Keywords: Istrian sheep; genetic diversity; SNPs

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