Genomic patterns of homozygosity in Istrian sheep

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Summary

The runs of homozygosity (ROH) pattern can provide useful information about the history and genetic structure of livestock populations. The aim of this study was to determine the ROH profile and level of inbreeding in the Istrian sheep using ROH (F_{ROH}) and information on observed and expected homozygosity (F_{HOM}). The subpopulation under study comprised 719 animals genotyped with the OvineSNP50 BeadChip. Analyses were performed using the PLINK toolset (v1.09). After quality control (MAF<0.05; call rate per SNP 0.10 and animal 0.05), 656 animals and 38,351 SNPs were included in the analyses. The minimal number of SNPs in ROH was set to 44, the maximal gap between SNPs was set to 1 Mb, the minimum SNP density was set to 1 SNP every 250 kb, no heterozygotes allowed, no missing SNPs allowed less than 4 Mb, and the minimum length that constituted the ROH was set to 1 Mb. A total of 15,817 autosomal ROHs ranging from 1.9 to 70.1 Mb were detected. On average, there were ~24 ROHs per animal with an average length of ~8.12 Mb. The frequencies of $ROH_{1-4\ Mb}$, $ROH_{4-8\ Mb}$, $ROH_{8-16\ Mb}$, $ROH_{>16\ Mb}$ were 5.6%, 51.4%, 31.4% and 11.6%, respectively. The total length of $ROH_{1-4\ Mb}$, $ROH_{4-8\ Mb}$, $ROH_{8-16\ Mb}$, $ROH_{>16\ Mb}$ in the total length of the genome covered by ROHs was 9.4%, 29.2%, 34.5% and 26.9%, respectively. As suggested for medium-density SNP data, only large ROH segments (>4 Mb) were used to assess inbreeding ($F_{ROH>4Mb}$). The average genomic $F_{ROH>4Mb}$ and F_{HOM} were 0.075 and 0.060, respectively, and the correlation between them was high (r=0.976). The estimated level of genomic inbreeding in this population calls for more attention in planning future matings to decrease inbreeding below the conventionally accepted level (6.25%). The results provide a reliable source of information for developing basic guidelines for implementation of optimum contribution selection.

Keywords: Istrian sheep, runs of homozygosity, genomic inbreeding coefficient