

Genomic inbreeding in Istrian sheep – baseline for optimum contribution selection

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The objective of this study was to examine genomic inbreeding based on the runs of homozygosity (ROH) in the population of Istrian sheep, a Croatian dual-purpose breed (milk and meat). The ROH is a kind of “state of the art” methodology in the conservation genetic studies, not only due to effective way to estimate inbreeding, but also due to possibility of distinguishing between distant and recent inbreeding based on the length of the homozygous segments of the genome and their share in the length of the total genome. In addition to estimate overall population genomic inbreeding (F_{ROH}), the aim was also to estimate within flock genomic inbreeding in order to provide baseline for implementation of the optimum contribution selection (OCS) which seeks to provide selection progress with minimal loss of genetic variability. This selection strategy for this native sheep population has been initiated under the project OPTI SHEEP (CSF, IP: 2019-04-3559), and numerous studies are ongoing to set up this selection strategy. This particular study was conducted on 719 genotyped (Ovine 50K SNP BeadChip) sheep from 11 flocks, but after quality control, 656 of them were retained in the inferential statistical analysis. Estimation of ROH segments lengths of different sizes was obtained using the PLINK toolset (v1.09), and post hoc analysis, i.e. estimation of genomic F_{ROH} ($F_{ROH} = \sum_i \text{length}(\text{ROH}_i) / L_{\text{total length of genome covered by SNP}}$) was conducted in R programme. As suggested for medium density SNP data, only large ROH segments (> 4 Mb) were used to estimate F_{ROH} . Individual F_{ROH} ranged from 0.002 to 0.382 with an average of 0.068, and mean flock F_{ROH} ranged from 0.024 to 0.124. Only two flocks had F_{ROH} above 10% ($F_{ROH} = 0.114$ and 0.125). These results represent the first insights into genomic inbreeding at the flock level in this population and they will be used to set up the baseline for the OCS in the very near future. Development of the “pipeline” for including genomic inbreeding in the genetic evaluation system following the OSC principles is also an important practical and applicable contribution of the study.

Key words: Istrian sheep, flocks, inbreeding coefficient, mating scheme