

Genome-wide assesment of inbreeding (F_{ROH}) in Pag sheep

Kasap, A.¹, Špehar, M.², Držaić, V.¹, Mioč, B.¹, Barać, D.², Barać, Z.³, Ramljak, J.¹

¹University of Zagreb Faculty of Agriculture, Svetošimunska 25, Zagreb, Croatia (akasap@agr.hr)

²Croatian Agency for Agriculture and Food, Svetošimunska 25, 10000 Zagreb, Croatia

³Ministry of Agriculture, Ulica grada Vukovara 78, 10000 Zagreb, Croatia

Summary

The study aimed to examine genomic inbreeding with the runs of homozygosity (ROH) methodology in the population of Pag sheep which is a Croatian indigenous dual-purpose breed (milk and meat). This is one of the most recommended methodologies in the recent conservation genetic studies, not only due to ability to estimate genome-wide and chromosome-wide inbreeding, but also due to ability to distinguish recent from ancient inbreeding (based on different lengths of the homozygous segments of the genome). The results of this study have important practical contribution since they provide the baseline for implementation of the optimum contribution selection (OCS), the strategy that seeks to provide selection progress with minimal loss of genetic variability (the strategy initiated in the Pag sheep population by project OPTI SHEEP, CSF, IP: 2019-04-3559). The study was conducted on 749 genotyped (Ovine 50K SNP BeadChip) animals from 10 flocks, but after quality control, 705 of them retained in the final inferential statistical analysis. The detection of ROH segments having different size was obtained using the PLINK toolset (v1.09), while the estimation of genomic F_{ROH} was conducted in R programme ($F_{ROH} = \sum_i \text{length}(\text{ROH}_i)/L_{\text{genome}}$). As suggested for medium density SNP data, only large ROH segments (> 5 Mb) were used to estimate F_{ROH} . Individual $F_{ROH}(>5\text{Mb})$ ranged from 0.002 to 0.363 with an average of 0.026, while mean flock $F_{ROH}(>5\text{Mb})$ ranged from 0.012 to 0.058. In addition to unrevealing the level of genomic inbreeding, another important contribution of the study for conservation of the Pag sheep is development of “pipelines” for calculation and inclusion of F_{ROH} in the routine genetic (genomic) evaluation following the basic principles of OSC.

Key words: Pag sheep, Runs of Homozygosity, Genomic Inbreeding, Optimum Contribution Selection