

Conservation genomic analyses of two Croatian autochthonous sheep breeds

M. Spehar¹, M. Ferenčaković², I. Curik², N. Karapandža¹, Z. Barać¹, T. Sinković¹, V. Cubric-Curik²

¹Ministry of Agriculture, Vukovarska 78, 10000 Zagreb, Croatia

²University of Zagreb, Faculty of Agriculture, Svetošimunska cesta 25, 10000 Zagreb, Croatia

Istrian (IS) and Pag (PS) sheep breeds are Croatian autochthonous sheep breeds. We analyzed genotypes of 175 animals (96 IS, and 75 PS) using Illumina OvineSNP50 BeadChip array and estimated genomic inbreeding levels (F_{ROH}) and linkage disequilibrium effective population size (Ne_{LD}). We also defined the genomic position of IS and PS concerning overall 671 animals of 22 Italian, Spanish and some Merino sheep breeds. For this purpose, we used publicly available data from Dryad digital repository. The inbreeding level based on runs of homozygosity (F_{ROH}) was higher in IS compared to PS for $F_{ROH>2Mb}$, 0.08 vs. 0.04, $F_{ROH>8Mb}$, 0.04 vs. 0.03, and $F_{ROH>16Mb}$, 0.02 vs. 0.01 respectively. Software NeEstimator was used to estimate Ne from the parental generation of the sample based on the linkage disequilibrium (LD) method. Estimated Ne_{LD} for IS was 101 (95% CI= 81-130), while higher Ne_{LD} of 222 (95% CI= 161-343) was obtained for PS. Principal Components Analysis of the overall dataset showed separation of both, IS and PS from other breeds. However, PS was placed near to the cluster containing some Italian breeds (Massese, Appenninica, Sardinian White, Comisana, Leccese, and Laticauda) while IS was slightly remote. To our knowledge, this is the first genomic analysis of IS and PS providing valuable insights into their conservation status.