Session 70 Poster 23

SNP-based genetic diversity in Pag sheep - preliminary results

J. Ramljak¹, M. Špehar², A. Kasap¹, B. Mioč¹, I. Širić¹, A. Ivanković¹, D. Barać², Z. Barać³ and V. Držaić¹

¹University of Zagreb Faculty of Agriculture, Department of Animal Science and Technology, Svetošimunska 25, 10000

Zagreb, Croatia, ²Croatian Agency for Agriculture and Food, Svetošimunska 25, 10000 Zagreb, Croatia, ³Ministry of Agriculture, Ulica grada Vukovara 78, 10000 Zagreb, Croatia; jramljak@agr.hr

Sheep breeding has been present in Croatia for centuries, especially in coastal and island areas, where the harsh and unfavourable climate has affected the adaptability and survival of populations. Pag sheep is a local breed, bred exclusively in the restricted area, the Pag island. The economic importance for the inhabitants lies in the production of the well-known hard cheese and, to a lesser extent, lamb meat. In general, intensive production, limitation of the breeding area and control of gene flow lead to erosion of genetic variability and inbreeding. The aim of this research was to obtain preliminary results on the genetic structure of Pag sheep using SNP markers. A total of 100 randomly sampled animals from 10 flocks were genotyped using the Ovine SNP50 BeadChip. After quality control for call rates per SNP and animal and minor allele frequency, 45,224 autosomal SNPs and 100 individuals were available for analysis. Principal component analysis (PCA) was performed based on multidimensional scaling (MDS) to analyse population structure. Two clusters were separated by PCA (PC1, 3.79% and PC2, 3.73%) while the majority of individuals occupied an intermediate position. The population parameters determined in the studied sample were: observed heterozygosity (0.410), expected heterozygosity and Nei's genetic diversity (both 0.420) and inbreeding coefficient (-0.01), respectively. According to the results, the Pag sheep has preserved considerable genetic diversity with a low level of inbreeding. However, further studies with a larger data set and additional breeds are needed to confirm the results of this preliminary study.