Genetic diversity of related sheep breeds Sarda and Pag

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Genetic diversity of sheep is endangered, mostly by the replacement of local breeds with commercial breeds. However, local breeds are adapted to unique environments, rustic, resilient, a reservoir of genetic diversity, and could help with meeting challenges due to climate change and market demand fluctuations. Two examples of local island sheep in the Mediterranean region are the Sardinian White (Sarda) and Pag breeds. Sarda sheep are widely found in Italy, while Pag sheep are a Croatian breed that likely had historical introgression of Sarda. Our aim was to study the genetic structure of these Sarda and Pag breeds to highlight differences and common genomic regions, that might indicate environmental adaptations. Using 50K SNP data from 825 Sarda and 2683 Pag, runs of homozygosity (ROH) were detected using detectRUNS in R, and FST analysis was done using PLINK. Sarda (FROH=0.07±0.04) had more inbreeding than Pag (FROH=0.04±0.05), probably due to lower selection pressure on the latter. A total of five ROH segments were shared between the two breeds. We identified 367 SNPs with a FST > 3 SD from the chromosomic mean or that had a FST in the top 99th percentile. The analysis of genes mapped on shared ROH segments or close to significant SNPs could help understand the history of these two breeds and how past introgression contributed to today's Pag sheep.