Genomic differentiation between Simmental and Holstein cattle populations from Croatia

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Abstract

The main goal of this study was to identify the most differentiated genome regions (SNPs), those with largest F_{ST} values, between Croatian Simmental and Holstein cattle populations. Our analyses were based on the high-throughput genomic information (Illumina BovineSNP50 BeadChip) obtained from the individuals sampled in Croatian Holstein (72) and Croation Simmental (229) populations. The most differentiated SNPs were identified on the chromosome 2 (ARS-BFGL-NGS-5831), 3 (Hapmap48051-BTA-69046, BTA-67896-nors), 4 (ARS-BFGL-NGS-116590, Hapmap53144-ss46525999, Hapmap51289-BTA-70566), 5 (ARS-BFGL-NGS-39379), 6 (Hapmap60182-rs29025531, Hapmap49292-BTA-75698, ARS-BFGL-NGS-109884), 7 (ARS-BFGL-NGS-11872), 10 (ARS-BFGL-BAC-12251), 11 (ARS-BFGL-NGS-83288, ARS-BFGL-NGS-100141, ARS-BFGL-NGS-89583), 16 (ARS-BFGL-NGS-101656, ARS-BFGL-NGS-106233, BTB-01570194, ARS-BFGL-NGS-22021, ARS-BFGL-NGS-30784, ARS-BFGL-NGS-18487, Hapmap60338-ss46526653, ARS-BFGL-NGS-99802), 20 (Hapmap48214-BTA-121272), 23 (Hapmap54795-rs29014478), 26 (ARS-BFGL-NGS-11271, ARS-BFGL-NGS-101647) and 29 (ARS-BFGL-NGS-115406, Hapmap58266rs29018037, ARS-BFGL-NGS-29788). In addition, we have identified names and functions of those genes that are in the vicinity of the identified SNPs with extreme F_{ST} values. Our analysis will be extended to the population structure analyses with other worldwide Holstein and Simmental populations and the identification of genome regions that are specific for Croatian populations.

Keywords: cattle, genomics, adaptation, selection