

Genome-wide association study for daily milk yield in Istrian dairy sheep

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The objective of this work was to identify genomic regions associated with daily milk yield in the Croatian native Istrian sheep breed traditionally selected for milk yield. A total of 719 animals (689 ewes and 30 rams) were genotyped using the Illumina OvineSNP50K BeadChip. Genotyped animals and SNPs were included in the analysis after quality control parameters for call rate per animal, call rate per SNP, and MAF set to 0.9, 0.9, and 0.05, respectively. Monomorphic markers and markers with unknown genome position or located on the sex chromosome were also removed. The final number of genotyped animals and markers was 693 and 43,793, respectively. The estimated breeding values obtained by single step genomic BLUP were used as phenotypes to detect significant associations between SNPs and milk yield across the genome. A GWAS analysis was performed with the rrBLUP package in R. Four models were considered: 1) without controlling for population structure (PS) or family relatedness; b) controlling for PS effect; c) controlling for relatedness; and d) controlling for both PS and relatedness. The last one (d) was the most appropriate based on Q-Q plot analysis. After Bonferroni corrections, thresholds were set to $p < 2.47 \times 10^{-6}$ and $p < 4.94 \times 10^{-5}$ (suggestive level), corresponding to $-\log_{10}(p)$ of 5.61 and 4.31, respectively. None of the markers showed significant effect on the former, while five were significant on the latter (suggestive) level (one on chromosomes 5, 6, 13 and two on chromosome 18). Further studies considering a larger sample size will be needed to improve the statistical power of the analysis.