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Genome-Wide Association Study of milk production traits in the Russian Black-and-White cattle

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Genome-wide association studies (GWAS) have proven effective for exploring genomic regions associated with quantitative traits in dairy cattle. In this study, we conducted GWAS to seek the candidate genes that are associated with three of the most commonly evaluated milk production traits: daily milk yield (MY), percentage of milk fat (FP) and percentage of milk protein (PP). The dataset included in this study was derived from the national genetic evaluation program in Russia for the Black-and-White dairy cattle. The genotypic data for 644 animals (427 bulls and 217 cows) was used to estimate the effects of 52,445 SNP using weighted single-step GWAS (WssGWAS). SNPs with call rate < 0.90 and those with minor allele frequency < 0.05 were removed from the analysis. The results of the analysis were reported as proportion of the total genetic evaluate genes. The biggest non-overlapping windows were located on chromosomes 7, 8 and 12 for MY, 10, 14, 18, 19 and 20 for FP and 10 for PP. They explained 1.83%, 10.29 % and 0.74% of the total genetic variation for MY, FP and PP, respectively. Different genes were detected within these regions and there are thought to be associated with the studied traits. These genes are involved in various biological processes related to growth, metabolism, control ion fluxes through membranes and hormone secretion.

Biography

Experienced Civil Project Manager with a demonstrated history of working in Roads, Structure, and infrastructure & Electro-Mechanical. Skilled in project management, Schedule & planning, Budgeting and costing, Surveying & QYTs, Invoicing and documents controlling, Precast, AutoCAD, Engineering "Design", materials and store management, and Site, staff, manpower, and equipment management. Strong engineering professional graduated from Mutah University in Jordan.

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