Identification of Expression QTLs Targeting Candidate Genes for Residual Feed Intake in Dairy Cattle Using Systems Genomics

Background: Residual feed intake (RFI) is the difference between actual and predicted feed intake and an important factor determining feed efficiency (FE). Recently, 170 candidate genes were associated with RFI, but no expression quantitative trait loci (eQTL) mapping has hitherto been performed on FE related genes in dairy cows. In this study, an integrative systems genetics approach was applied to map eQTLs in Holstein and Jersey cows fed two different diets to improve identification of candidate genes for FE.

Methods: Liver RNA-seq transcriptomics data from nine Holstein and ten Jersey cows that had been fed control (C) or high concentrate (HC) diets were integrated with genomic data (from 777k BovineHD Illumina BeadChip) by using the Matrix eQTL R package. A total of 170 previously identified candidate genes for FE (89 differentially expressed genes (DEGs) between high and low RFI groups and 81 hub genes (HG) in a group of co-expressed genes) were used in the data integration analysis.

Results: From the 241,542 SNPs used in the analysis, we identified 20 significant (FDR < 0.05) local-eQTLs targeting seven candidate genes and 16 significant (FDR < 0.05) local-eQTLs targeting five candidate genes related to RFI for the C and HC diet group analysis, respectively, in a breed-specific way. Conclusions: Interestingly, Holstein and Jersey cows appear to rely on different strategies (lipid and cholesterol metabolism versus immune and inflammatory function) to achieve low RFI. The eQTLs overlapped with QTLs previously associated with FE trait (e.g. dry matter intake, longevity, body weight gain and net merit). The eQTLs and biological pathways identified in this study improve our understanding of the complex biological and genetic mechanisms that determine FE traits in dairy cattle. The identified eQTLs/genetic variants can potentially be used in new genomic selection methods that include biological/functional information on SNPs.

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