Genomic and transcriptomic profiling reveals candidate genes and biomarkers to improve feed efficiency in Danish dairy cattle

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High feed cost and carbon footprint from dairy cattle production require an improvement of feed efficiency (FE) in dairy cows. Particularly, it would be ideal to select and breed cows that have a low feed intake but sustain a high milk production. To identify and select animals with high FE, it might be helpful to understand the biological mechanisms and the role of gene expression patterns across the whole genome (transcriptomics).

In the present study, the high throughput of RNA sequencing was used to detect genes that are differentially expressed (DE) between Danish Holstein and Jersey dairy cows having either a high or low FE and to identify molecular pathways involved.

Ten Jersey and nine Holstein cows were used in the experiment and divided into two FE groups depending on their FE status. The two FE groups received a Control (C) and High Concentrate (HC) diet containing 70:30 and 40:60 ratio of forage:concentrate, respectively. This enabled us to compare the interaction between FE status and diet.

Liver biopsies were obtained and the extracted mRNA was analyzed by paired end RNA sequencing. This resulted in an average of 57 million reads per sample. The RNAseq gene expression data were then analyzed using statistical-bioinformatics pipelines to identify DE genes and subsequently the functional enrichment. We compared gene expressions of the FE groups, and identified 70 and 19 DE genes in Holstein and Jersey, respectively. An interaction term (FE x diet) detected two significantly DE genes in Jersey cows. The functional enrichment analysis of the DE genes showed involvement in pathways that regulate FE, such as primary immunodeficiency, retinol metabolism, starch and sucrose metabolism, arachidonic acid metabolism and drug metabolism cytochrome P450.

In conclusion, the transcriptomics approach was effective in identifying DE genes and understanding their biological function. These findings could contribute to the development of biomarkers for FE and to improving augmented genomic selection procedures that makes use of functional information.

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