

ABSTRACT

Transcriptional profiling of muscle tissue in growing Japanese Black Cattle to identify genes involved with the development of intramuscular fat

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Japanese Black cattle are characterised by a unique ability to deposit intramuscular fat with lower melting temperature. In this study, 3 consecutive biopsies from *Longissimus* muscle tissue were taken and RNA isolated from 3 Japanese Black (Tajima strain) and 3 Holstein animals at age 11–20 months. The gene expression changes in these samples were analysed using a bovine fat/muscle cDNA microarray. A mixed-ANOVA model was fitted to the intensity signals. A total of 335 (4.8%) array elements were identified as differentially expressed genes in this breed × time comparison study. Genes preferentially expressed in Japanese Black are associated with mono-unsaturated fatty acid synthesis, fat deposition, adipogenesis development and muscle regulation, while examples of genes preferentially expressed in Holstein come from functional classes involved in connective tissue and skeletal muscle development. The gene expression differences detected between the *Longissimus* muscle of the 2 breeds give important clues to the molecular basis for the unique features of the Japanese Black breed, such as the onset and rate of adipose tissue development, metabolic differences, and signalling pathways involved in converting carbohydrate to lipid during lipogenesis. These findings will impact on industry management strategies designed to manipulate intramuscular adipose development at different development stages to gain maximum return for beef products.

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