

ABSTRACT

Transcriptional profiling of skeletal muscle tissue from two breeds of cattle

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We used a 9.6 K cattle muscle/fat cDNA microarray to study gene expression differences between the longuissimus dorsi (LD) muscle of Japanese Black (JB) and Holstein (HOL) cattle. JB cattle exhibit an unusual ability to accumulate intramuscular adipose tissue with fat melting points lower than that in other breeds. The LD biopsies from three JB (Tajima strain) and three HOL animals were used in this breed comparison. Seventeen genes were identified as preferentially expressed in LD samples from JB and seven genes were found to be expressed more highly in HOL. The expression of six selected differentially expressed genes was confirmed by quantitative real-time PCR. The genes more highly expressed in JB are associated with unsaturated fatty acid synthesis, fat deposition, and the thyroid hormone pathway. These results are consistent with the increased amounts and proportions of monounsaturated fatty acids observed in the muscle of JB animals. By discovering as yet uncharacterized genes that are differentially regulated in this comparison, the work may lead us to a better understanding of the regulatory pathways involved in the development of intramuscular adipose tissue.