
Gene expression patterns during intramuscular fat development in cattle

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Abstract :

Deposition of intramuscular fat, or "marbling," in beef cattle contributes significantly to meat quality variables, including juiciness, flavor, and tenderness. The accumulation of intramuscular fat is largely influenced by the genetic background of cattle, as well as their age and nutrition. To identify genes that can be used as early biomarkers for the prediction of marbling capacity, we studied the muscle transcriptome of 2 cattle crossbreeds with contrasting intramuscular fat content. The transcriptomes of marbling LM tissue of heifers from Wagyu x Hereford (WxH; n = 6) and Piedmontese x Hereford (PxH; n = 7) crosses were profiled by using a combination of complementary DNA microarray and quantitative reverse transcription-PCR. Five biopsies of LM were taken from each animal at approximately 3, 7, 12, 20, and 25 mo from birth. Tissue was also collected from the LM of each animal at slaughter (approximately 30 mo). Microarray experiments, conducted on the first 3 biopsies of 2 animals from each crossbreed, identified 97 differentially expressed genes. The gene expression results indicated that the LM transcriptome of animals with high marbling potential (WxH) could be reliably distinguished from less marbled animals (PxH) when the animals were as young as 7 mo of age. At this early age, one cannot reliably determine meaningful differences in intramuscular fat deposition. We observed greater expression of a set of adipogenesis- and lipogenesis-related genes in the LM of young WxH animals compared with their PxH contemporaries. In contrast, genes highly expressed in PxH animals were associated with mitochondrial oxidative activity. Further quantitative reverse transcription-PCR experiments revealed that the messenger RNA of 6 of the lipogenesis-related genes also peaked at the age of 20 to 25 mo in WxH animals. The messenger RNA expression of *ADIPOQ*, *SCD*, and *THRSP* was highly correlated with intramuscular fat content of an individual in WxH animals. Our study provides clear evidence of early molecular changes associated with marbling and also identifies specific time frames when intramuscular fat development in cattle muscle can be detected by using gene expression. This information could be used by animal scientists to design optimal nutrition for high marbling potential. In addition, the genes found to be highly expressed during development of marbling could be used to develop genetic markers or biomarkers to assist with beef production strategies.

Key Word :

cattle, gene expression, intramuscular fat, marbling, microarray, muscle

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