_____ ABSTRACT _____

Identification of microRNA and target gene associated with marbling score in Korean cattle (Hanwoo)

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Marbling is a crucial characteristic in meat quality assessment. In the search for a genetic basis of meat quality, a large number of gene analyses seeking to find loci for a marbling trait have already been reported. However, the influence of microRNA (miRNA) on expression patterns and their ultimate influence on marbling is poorly understood. To better understand post-transcriptional influences on marbling, we applied a microarray analysis to measure the relationship between marbling scores and miRNA and messenger RNA expression in Hanwoo longissimus muscle tissue. Our results build correlations between miRNAs and differentially expressed genes and pathways. Our microarray analysis identified 763 genes and 11 miRNAs that are differentially expressed relative to marbling score. Overall, upregulated miRNAs were associated with downregulated genes. Fifteen genes targeted by miRNAs including insulin-like growth factor 1 (IGF-1) and kruppel-like factor 11 (KLF11), which regulate fatty acid synthase and lipid metabolism. And the expression levels of KLF11 and bta-miR-494 were validated. The results show that downregulated bta-miR-494 was associated with the upregulation of KLF11 gene. Among the differentially expressed genes found to be associated with the marbling score, we identified 15 genes targeted by miRNAs. Furthermore, the expression patterns of the genes KLF11, and bta-miR-494, may influence marbling in Hanwoo.