Asian-Australasian Journal of Animal Science (2013)
Volume 26, Issue 1

ABSTRACT

Gene Co-expression Analysis to Characterize Genes Related to Marbling Trait in Hanwoo (Korean) Cattle.

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Marbling (intramuscular fat) is an important trait that affects meat quality and is a casual factor determining the price of beef in the Korean beef market. It is a complex trait and has many biological pathways related to muscle and fat. There is a need to identify functional modules or genes related to marbling traits and investigate their relationships through a weighted gene co-expression network analysis based on the system level. Therefore, we investigated the co-expression relationships of genes related to the 'marbling score' trait and systemically analyzed the network topology in Hanwoo (Korean cattle). As a result, we determined 3 modules (gene groups) that showed statistically significant results for marbling score. In particular, one module (denoted as red) has a statistically significant result for marbling score ($p = 0.008$) and intramuscular fat ($p = 0.02$) and water capacity ($p = 0.006$). From functional enrichment and relationship analysis of the red module, the pathway hub genes (IL6, CHRNE, RB1, INHBA and NPPA) have a direct interaction relationship and share the biological functions related to fat or muscle, such as adipogenesis or muscle growth. This is the first gene network study with m.logissimus in Hanwoo to observe co-expression patterns in divergent marbling phenotypes. It may provide insights into the functional mechanisms of the marbling trait.

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