GENE CO-EXPRESSION NETWORKS OF HEPATIC TISSUE ASSOCIATED WITH RIBEYE AREA IN NELLORE CATTLE

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Abstract:
The ribeye area (REA) shows a positive correlation with carcass weight and animal growth, making it a reliable indicator of muscularity, prime cuts, and the overall edible mass of the carcass. The RNA-seq has opened up opportunities for transcriptional profiling of biological systems. By studying gene expression patterns, RNA-seq provides valuable insights into the interplay between genes and phenotypes, facilitating a deeper understanding of important biological processes. The objective of this study was to construct co-expression networks of genes expressed in the liver of Nellore cattle using Weighted Gene Correlation Network Analysis (WGCNA), and identify hub genes and metabolic pathways regulating REA phenotype. Therefore, in the present study, samples of liver tissue were collected from 90 animals for RNA-seq. The sequencing data was aligned to the reference genome, and the expression data was normalized to log2-CPM. Then, co-expression network analysis was conducted using the WGCNA R package v.1.72-1. The WGCNA applies Pearson correlations to assess the gene expression profiles of all samples, allowing the identification of gene modules based on the dissimilarity of their eigengenes (first principal component within a module). Additionally, a random color is assigned to each module. Then, module-trait associations were found by correlating their eigengenes with REA. As a result, 25 gene modules were identified correlated with REA, highlighting the Grey60 with phenotype correlation=0.2 (p-value=0.07). This module has 103 genes. DAVID (2021) was used to enrichment analysis of those genes. The hub gene in this module is LAMTOR1 also known as p18, enriched for a biological process of cholesterol homeostasis. This gene is a constituent of the ragulator complex (activation of Rag GTPases function), which plays a crucial role in amino acid sensing and activation of mTORC1, a signaling complex that promotes cell growth. Additionally, it is involved in the biogenesis of late endosomes/lysosomes and may regulate receptor recycling through endosomes, as well as, the MAPK signaling pathway by recruiting certain components to late endosomes. Studies suggest that p18 is also implicated in intracellular cholesterol transport from the lysosome to the Endoplasmic Reticulum (ER), where cellular cholesterol levels are sensed. In a particular study, the impact of p18 loss and mTORC1 inhibition on the structure and function of late endosomes/lysosomes was investigated using p18-deficient cells. The findings of the study revealed that knockout (KO) cells exhibited significantly elevated intracellular cholesterol levels. These results are in line with recent observations demonstrating that p18 knockdown leads to the accumulation of intracellular cholesterol. So, the correlation between this gene and REA may be attributed to the fact that its presence is associated with lower intracellular cholesterol levels, which consequently leads to a higher amount of muscle. Furthermore, p18 indirectly influences cellular growth by activating the mTORC1 gene, contributing to its association with the phenotype. These findings help to understand the molecular mechanisms involved in REA regulation in Nellore cattle.
Palavras-chave: Carcass; Correlation; Liver; ;