

CONSTRUINDO SABERES, FORMANDO PESSOAS E TRANSFORMANDO A PRODUÇÃO ANIMAL

GENE CO-EXPRESSION ANALYSIS IDENTIFIED GENES AND BIOLOGICAL PROCESSES ASSOCIATED WITH CARCASS TRAITS IN NELLORE CATTLE

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Commercial cuts yield is an important trait for beef production, which affects the final value of the products. The ribeye area (REA) and backfat thickness (BFT) are carcass traits used as an indirect measure of meat yield. REA and BFT have strong implication in technological and nutritional characteristics of meat products, muscularity degree and total body fat of beef cattle. In this study, we performed a gene co-expression network analysis to obtain new insights into the gene expression profile of *Longissimus dorsi* (LD) muscle of Nellore steers and associate it with REA and BFT. The co-expression analysis was performed by using the WGCNA (Weighted Correlation Network Analysis) package of R software. Transcript per million (TPM) values from RNA-Sequencing data of 43 animals were used herein. A total of thirty-seven modules were constructed from 14,529 expressed genes in LD muscle according to WGCNA package. Genes of modules with significant module-trait associations (p -value <0.1), for at least one trait, were assigned for functional enrichment analysis when their Module Membership (MM) values were greater than 0.7 (p -value <0.001). The functional enrichment analysis was performed by using BINGO (Biological Networks Gene Ontology) v3.0.3 (FDR <0.05) an app from Cytoscape, and the redundant Gene Ontology (GO) terms were removed using the web server REVIGO (Reduce + Visualize Gene Ontology). From the thirty-seven modules identified, the Blue, Salmon and Dark-green showed a significant correlation (p -value <0.1) with BFT. Among these modules, the Salmon presented sixty-four co-expressed genes (MM >0.7) utilized in the enrichment analysis. The enrichment analysis of this module identified four (FDR <0.05) biological processes (BP): Response to virus (GO:0009615), ISG15-protein conjugation (GO:0032020), Protein catabolic process (GO:0030163) and Proteolysis involved in cellular protein catabolic process (GO:0051603). The *ISG15* gene (Interferon-stimulated gene 15), which codifies an ubiquitin-like protein, appeared in all BP. Previous studies have shown that genes encoding ubiquitin proteins were associated with growth and carcass traits in Nellore cattle. Another interesting gene, annotated in response to virus biological process, was *RSAD2* (radical S-adenosyl methionine domain containing 2). This gene is involved in lipid biosynthesis and, is related to the activation of inflammation

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in obesity states of humans and rodents. In conclusion, this study contributes to the new insights into the genes and biological processes involved in muscle development and fat deposition in beef cattle.

Keywords: backfat thickness, bovine, ribeye area, WGCNA

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