AMSA 2017 - Abstract Submission

Topic: Muscle and Lipid Biology and Biochemistry

AMSA2017-1116

GENE CO-EXPRESSION NETWORK ANALYSIS ASSOCIATED WITH CARCASS TRAITS IN NELLORE STEERS

Bárbara S. Vignato[1], Luiz L. L. Coutinho[2], Aline S. M. Cesar[2], Mirele D. Poleti[2], Luciana C. A. Regitano[3], Júlio Cesar de C. Balieiro[*4]

[1]Animal Science, Universidade de São Paulo, Pirassununga, [2]Animal Science, Universidade de São Paulo, Piracicaba, [3]CPPSE, EMBRAPA, São Carlos, [4]Animal Nutrition and Production, Universidade de São Paulo, Pirassununga, Brazil

Did you submit an intent to participate in the student research poster competition, graduate or undergraduate?: No

Were animal or human subjects used in this research project?: Yes

Do you want your abstract to be considered for the Industry Technical Summary section?** :** No

Objectives: Carcass traits are influenced by a complex network of gene interactions in muscle, so elucidating the relationships between genes and how these genes influence these traits is crucial for understanding the muscle development in animals. This study aimed to identify groups of co-expressed genes in the skeletal muscle of Nellore steers associated with ribeye area (REA) and backfat thickness (BFT), using RNA-Sequencing (RNA-Seq) data.

Materials and Methods: Three hundred and ninety Nellore steers from the Brazilian Agricultural Research Corporation (EMBRAPA/Brazil), were raised in feedlots under identical nutrition and management conditions until slaughter at an average age of 25 months. Samples from *Longissimus dorsi* (LD) muscle located between the 12th and 13th ribs were collected in two time-points: at slaughter for RNA sequencing analysis to guarantee the RNA integrity, and 24 h after slaughtering for REA and BFT evaluations. A total of 43 animals were selected based on their extreme (highest (H) or lowest (L)) GEBVs (Genomic Estimated Breeding Values) for REA and BFT to define groups for differential expression analysis. RNA-Seq data was normalized by the Transcript per million (TPM) procedure. The gene co-expression network analyses was carried out using the "blockwiseModules" function, part of the WGCNA (Weighted Correlation Network Analysis) R package. Modules were merged based on the dissimilarity between their eigengenes, which is the first principal component of each module. For each module, a different color was assigned. Module-trait associations were estimated using the correlation between the eigengene module and the phenotype (REA and BFT). Genes from modules with significant module-trait associations ($P < 0.1$), for at least one trait, were assigned for functional enrichment analysis when their Module Membership (MM) values were greater than 0.7 ($P<0.001$). The functional enrichment analysis was performed by DAVID v6.7 (FDR<0.1).

Results: Thirty-seven modules were identified. Among the modules identified, the Blue (r=0.3), Dark Green (r=0.3) and Salmon (r=0.3) presented significant correlation ($P < 0.10$) with BFT. The Blue module was the largest one, presenting 953 genes (MM>0.7). The functional enrichment analysis of the 953 genes from the Blue module identified 101 Gene Ontology (GO) terms including biological processes, cellular component, and molecular function, and six KEGG pathways. Among the metabolic pathways identified for the Blue module, the Extracellular Matrix - receptor interaction (bta04512) was noteworthy. This pathway was related to GO terms such as proteinaceous extracellular matrix (GO:0005578), extracellular matrix (GO:0031012) and cell-matrix adhesion (GO:0007160). The extracellular matrix (ECM) is a substrate for cell adhesion, growth, and differentiation, which plays an important role in force transmission for muscle contraction, maintenance, and repair, emphasizing its importance for REA. In relation to BFT, ECM plays an important role in adipogenesis.

Conclusion: The approaches used in this study allowed us to identify co-expressed networks correlated with important economic traits, collaborating to better understand the biological processes involved in muscle development and fat deposition in beef cattle.

Keywords: backfat thickness, ribeye area, WGCNA