ZOOTECNIA BRASIL
Centro de Convenções da PUC-GO | Goiânia-GO
27 a 30 de agosto de 2018

55ª REUNIÃO ANUAL DA SOCIEDADE BRASILEIRA DE ZOOTECNIA

ZOO tec
28º CONGRESSO BRASILEIRO DE ZOOTECNIA

CONSTRUINDO SABERES, FORMANDO PESSOAS E TRANSFORMANDO A PRODUÇÃO ANIMAL

GENE CO-EXPRESSION NETWORK ANALYSIS RELATED TO RIBEYE AREA IN NELLORE CATTLE MALES

Danielly Beraldo dos Santos SILVA*[1], Larissa Fernanda Simielli FONSECA[1], Maria Malane Magalhães MUNIZ[1], Ana Fabrícia Braga MAGALHÃES[1], Daniel Guariz PINHEIRO[1], Lucia Galvão de ALBUQUERQUE[1,2]

*corresponding author: daniellyberaldo@gmail.com
[1]São Paulo State University (UNESP), Jaboticabal, São Paulo, Brazil
[2] National Council for Science and Technological Development (CNPq), Brasília, Brazil

RNA-Seq approach was used to identify co-expressed genes in *longissimus thoracis* of uncastrated Nellore males associated with ribeye area (REA). From a total of 80 animals, phenotyped for ribeye area (REA), 15 with the highest REA (HREA) and 15 with the lowest REA (LREA) were analyzed. Transcript correlation networks were generated by Cytoscape (v.3.4) using the Expression Correlation Network application. The similarity matrix was computed using the expression profiles of the differentially expressed genes (289 genes, 183 up-regulated and 106 down-regulated in the HREA group) obtained from Cufflinks2 v.2.1.1 suite of tools. The cuts-off of ≥0.9 and ≤-0.9 were used for Pearson correlation coefficients. The networks metrics (degree distribution, betweenness centrality, network density and clustering coefficient) were determined via NetworkAnalyzer and Cytohubba applications of Cytoscape. The degree of distribution and betweenness centrality were employed as global metrics for identification of the top three hub genes. The co-expression network showed 400 significantly correlated gene pairs (edges), discovered for 150 genes (nodes). The density and the clustering coefficients were 0.036 and 0.327, respectively. When the network distribution degree was investigated, scale-free topology was found ($R2 = 0.708$), indicating the presence of hubs genes: PPP3R1, UBE2G1, and FAM129B. Hub genes are expected to play an important role in biology of the studied organism. Indeed, the hub genes found in this study have been previously described in important pathways that play a role in the animal muscle development and regulation. Functional enrichment analysis showed that PPP3R1 (down-regulated in HREA group) participates in the cGMP-PKG signaling (bta04022), glucagon signaling (bta04922) and oxytocin signaling (bta04921) pathways. These highly correlated genes (PPP3R1, UBE2G1 and FAM129B) are, likely, the main genetic regulators of the remaining differentially expression genes found in this study and may contribute to the development and maintenance of Nellore cattle muscle.

Keywords: Bovine, Expression Correlation, Hub genes, Meat quality, RNA-Seq

Acknowledgments: São Paulo Research Foundation FAPESP (grants #2009/16118-5 and #2015/16850-9).