

Glutathione pathway could be associated with meat tenderness in Nellore

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Abstract:

The Nellore cattle breed (*Bos taurus indicus*) is widely used in Brazil due to its robustness and resistance to various parasites and diseases. Among the beef quality parameters, tenderness is a major and preferential characteristics by the consumers. Tenderness is an important economical trait for beef cattle since can increase the value of the beef in the market. However, the metabolic process involved with this trait and the differences between *Bos taurus indicus* and *Bos taurus taurus* breeds are not completely understood. The use of molecular strategies prospecting the pathways involved in these processes may allow the understanding of the meat tenderness. The aim of this study was to identify differentially expressed (DE) genes from two groups of Nellore (high (H) and low (L) EBV for shear force (Kgf), considering H for toughness beef and L for tenderness beef) using RNA-Seq approach. In a previous study, we collected samples of Longissimus dorsi muscle of 310 animals of Nellore cattle. Beefs were evaluated for Warner-Bratzler shear force, after seven and 14 days of maturation. After a BLUP analysis, we selected 17 animals for the L group and 14 animals for the H group. The selected samples were submitted to transcriptome analysis on an Illumina sequencer (Illumina HiScanSQ®). The data were processed using the Tuxedo pipeline. The number of initial reads ranged from 16,228,318 to 51,339,112; while the number of mapped reads ranged, from 9,497,046 to 23,505,716. We identified 16,755 genes and 81 were differentially expressed between H and L groups ($p < 0.1$). Among these, 62 were identified by BioMart-Ensembl. For these genes, metabolic pathways were inferred through the Reactome pathway browser. GATM (L-arginine: glycine amidinotransferase), which had higher expression associated with L is related with amino acids metabolism. BDH1 (D-beta-hydroxybutyrate dehydrogenase), with higher expression associated with H is involved in lipid metabolism. Moreover, enrichment analyses were performed with DAVID tools. The results indicates association of the glutathione transferase activity pathway (with adjusted p -value 1.4×10^{-5} - Benjamini-Hochberg correction) with up-regulated genes in the L group. Glutathione transferases are detoxification enzymes that play a role in the oxidative stress, and could be related with the tenderness process during the conversion of muscle into meat. The analysis showed DE genes between the groups and that the glutathione pathway could be associated with beef tenderness. Finally, the transcriptome analysis allows a better understanding of molecular interactions and mechanisms of genetic regulations that could control meat quality and beef tenderness in Nellore cattle.