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Transcriptome profile in Longissimus dorsi muscle from Nellore steers with extreme GEBV for intramuscular fat percentage

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Abstract:

Introduction: Next generation sequencing (NGS) technology provides a platform via which to thoroughly characterize the transcriptome. It has been shown to have a greater accuracy in the determination of gene expression levels and the identification of differentialy expressed genes or transcripts as compared to other techniques. The deposition of intramuscular fat (IMF) is controlled by several genes, which participate directly, or indirectly in adipogenesis and fat metabolism. Intramuscular fat quantity is an important economic phenotype, which influences the sensorial and nutritional value of beef. Previous research has documented that muscle and fat tissues from Bos indicus cattle develop in a different manner than Bos taurus breeds. Objectives: The goal of this study was to identify differentially expressed (DE) genes in the Longissimus dorsi (LD) muscle in steers of the Nellore breed that exhibit extreme genomic estimated breeding value (GEBV) for (IMF). This should lead to the identification of pathways that control IMF. Methods: Genomic Best Linear Unbiased Prediction (GBLUP) was used to rank 310 animals based on genomic estimated breeding values (GEBVs) for IMF, using ASREML software (Gilmour et al., 2006). Seven animals with high (H) and seven with low (L) GEBV were used for RNA sequencing. The DESeq software (Anders and Huber, 2010) was used to identify DE genes. Read count data was filtered as follows: i) genes with zero count were removed (unexpressed); ii) genes with less than 1 read per sample on average were removed (very lowly expressed); iii) genes that were not present in at least three samples were removed (rarely expressed). After filtering, a total of 16,102 genes were analyzed for differential expression using the "nbinomTest" function of DESeq to fit a negative binomial distribution of the expression level. The Benjamini-Hochberg procedure was used to control false discovery rate (FDR) at 10%. The Database for Annotation, Visualization and Integrated Discovery (DAVID) v6.7 to ol (Huang et al., 2009) was used to detect pathway level changes in gene expression. While pathway enrichment analysis was performed using Pathway Studio (Ariande Genomics, MD)(Nikitin et al., 2003), which is based on literature databases. Results: A total of 77 DE genes were identified between H and L groups. Pathway analysis from Pathway Studio software revealed four major gene networks related to lipid metabolism: oxidized low density lipoprotein (LDL), retinoic acid, reactive oxygen species (ROS) and non-oxidative (NO) pathways. Conclusions: The RNA-Seq data obtained in this study allowed the identification of genes differentially expressed between animals with high and low GEBV for intramuscular fat deposition. In addition, based on this data important pathways involved with lipid metabolism were built and revealed.