

CONSTRUINDO SABERES, FORMANDO PESSOAS E TRANSFORMANDO A PRODUÇÃO ANIMAL

## EXPLORATION OF ALTERNATIVE SPLICING EVENTS IN MUSCLE TISSUE OF THE NELLORE CATTLE DIVERGENT FOR RIBEYE AREA

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Studying gene expression using RNASeq approach, especially for examining the existence of alternative splicing (AS) events aiming to understand individual differences in carcass traits in bovine, is a challenging task. For this purpose, transcriptome RNA-Seq data was used to identify differentially alternative splicing (DAS) events, and their associated genes in uncastrated Nellore male, phenotypically divergent for ribeye area (REA). A total of 30 animals were selected based on their divergent REA phenotype, 15 with high REA (HREA) and 15 with low REA (LREA). The JuncBASE package (exon-centric approach) was used to identify AS events (cassette exon, mutually exclusive exon, coordinate cassette exon, alternative 5' and 3' splice sites, intron retention, alternative first and last exon). A total of 166 transcript isoforms were DAS ( $p \leq 0.05$ ) between the groups. Cassette exon (N=49), alternative 3' splice (N=46) and alternative 5' splice (N=42) sites were the most frequent events, whereas the least frequent were: coordinate cassette exon (N=10), alternative first exon (N=8), alternative last exon (N=6) and retained intron (N=5). Mutually exclusion exon was not found. Of the DAS events (N=166), 54 were known and 112 novel events. The DAS events were transcribed from 125 genes with roles in the immune system, muscle development and regulation. Our results revealed that, REA phenotype in Nellore cattle is controlled by various genes with DAS events. From these predicted events, LRRFIP1, RCAN1, and RHOBTB1 were identified as hub genes. These genes play roles in muscle cell development, proliferation and regulation in animals. Therefore, it provides an attractive model for the study of molecular mechanisms of REA trait of Nellore. The multiple DAS events and their large numbers of associated genes, reveals the complexity of the muscle development transcriptome in Nellore cattle.

**Keywords:** Bovine, Carcass trait, Hub genes, Splice event, Transcriptomic

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