

## MICRORNAS EXPRESSION PROFILE AND FUNCTIONAL ENRICHMENT OF *LONGISSIMUS DORSI* MUSCLE IN NELLORE CATTLE

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MicroRNAs are small regulatory RNAs that play an important role in post-transcriptional gene regulation in many tissues and are associated with numerous biological processes. According to miRBase database (v.21) 793 microRNAs have been identified for cattle, however the majority being identified in *Bos taurus taurus* breeds. This is a small number compared with the 2588 microRNAs deposited for humans. This study aims to characterize the profile of microRNAs expressed in Nellore cattle (*Bos taurus indicus*) muscle, a breed well adapted to the tropical climate and one of the most raised in Brazil. Samples of the *Longissimus dorsi* muscle from 30 animals were obtained and total RNA was extracted by Trizol. MicroRNA libraries were made using TrueSeq Small RNA kit (Illumina), and sequenced on Illumina MiSeq equipment. A total of 32 million reads were generated, which were filtered by quality with FastX software, mapped against the bovine genome UMD3.1 and analyzed by miRDeep2 software. In this study 463 known microRNAs were identified, and the five most representatives were bta-miR-10b, bta-miR-486, bta-miR-133a, bta-miR-26a and bta-miR-143, with an average of reads among samples of: 439,196; 79,588; 50,291; 49,921 and 35,791, respectively. The target genes were identified using the TargetScan database and the probable biological processes in which these genes may be involved were analyzed using Gene Ontology terms by DAVID program tools. Processes related with regulation of transcription factors' activity, protein phosphorylation, cell motility and ATP binding were identified from target genes list according GO terms. Herein, were also identified twenty six potential new microRNAs for cattle. The results provide an overview of the main biological processes that take place in muscle and could be controlled by microRNAs. Furthermore, the newly discovered microRNAs will be deposited in miRBase, which will enable the expansion of the current database for cattle specifically for *Bos indicus* species.

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