00-15 *LDHB* gene has allele-specific expression in liver of Nelore cattle extremes for feed efficiency

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Feed efficiency is a multi-factorial trait of a large economic importance for cattle. Although previous studies reported gene expression differences associated with this trait the contribution of allele-specific expression (ASE) remains largely unknown. In this study, we analyzed ASE in liver samples of 30 Nelore cattle steers in two genetically divergent groups for residual feed intake (RFI) searching for genes with ASE linked to feed efficiency. Based on genotype data obtained using the Illumina BovineHD BeadChip, we computed the frequency of reads from RNA-seq data mapped to each allele of heterozygous individuals and applied a binomial test to identify loci of ASE. We detected significant differences in expression among alleles for seven SNPs (single nucleotide polymorphisms) that were tested significantly in >90% of the samples. Amid them, we selected the *LDHB* gene that has been previously associated with feed efficiency in chickens. The *LDHB* gene carries out functions in carbohydrate, carboxylic acid and oxidation-reduction metabolic processes important for glycolysis. These biological processes were associated with feed efficiency and cell energy balance in previous studies. Since the SNP found on *LDHB* is located at 3'UTR, we studied whether a putative microRNA binding site near or at the SNP site could exist and account for the regulation of gene expression. We found that the Bta-miR-139 binds at the SNP site of *LDHB*. This miRNA was also identified by the group in a previous study with expressed microRNA in the liver. Thus, we theorized that the Bta-miR-139 miRNA affects the expression of the *LDHB* gene and may contribute to ASE. Therefore, these results complement our understanding of the ASE profile of the *LDHB* gene and contribute to explain more accurately the differences in gene expression identified in Nelore steers genetically divergent for RFI.

Keywords: Cattle, residual feed intake, differential expression, microRNA.

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