

Differentially expressed genes in *Longissimus dorsi* muscle of Nelore steers divergent for average daily gain

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Average daily gain (ADG) is the rate of weight gain per day over a specified period and is an indicator of feed efficiency for beef production. This trait has a positive correlation with dry matter intake and can be adopted by animal breeding programs to improve the profitability of the herd. Recent advances in molecular biology and bioinformatics are being applied to understand the biological processes related to feed efficiency. The aim of this study was to identify differentially expressed genes (DEGs) in *Longissimus dorsi* of Nelore cattle genetically divergent animals for ADG, using RNA sequencing methodology. Also, we aimed to highlight the differences in relation to our previous RNA-Seq study that compared animals with contrasting best linear unbiased prediction (BLUP) values for residual feed intake (RFI) from a smaller population (n=83). Differential gene expression analysis were performed between high and low (n=10) ADG groups chosen from an initial population of 200 Nelore steers based on their BLUP estimates for ADG. The animals chosen as extreme of each phenotype in the two studies were not identical. We found 35 DEGs, being 24 upregulated in high ADG group. The DEGs are involved in metabolism of fatty acids, response to steroid stimulus, fat cell and brown fat cell differentiation, collagen synthesis and homeostatic process. Although the biological processes found in this present study are consistent with our previous findings, we only found an overlap of six DEGs already reported in our previous study. These differences are possibly related to the impact of the initial population used to choose the extreme phenotype animals and to the particularities of each feed efficiency trait. Among the DEGs, we can highlight the fatty acid-binding protein four (*FABP4*) and the Adiponectin, C1Q And Collagen Domain Containing (*ADIPOQ*), upregulated in the high ADG group, related to fatty acid metabolism which were already associated with carcass and meat quality traits in Nelore breed. These preliminary results confirm the literature data enrolling biological functions influencing feed efficiency. More analysis will be necessary to unveil the mechanism of action of these genes in Nelore cattle. We thank FAPESP for funding through the process 2012/23638-8.

Key-Word: RNA-seq, *Bos indicus*, ADG