

A COMPARATIVE STUDY OF SKELETAL MUSCLE TRANSCRIPTIONAL PROFILES IN TWO CATTLE BREEDS

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It is well-established that different cattle breeds differ in muscle characteristics due to differences in their physiology. Friesian and Chianina are two cattle breeds selected in the past century for milk and meat traits, respectively. This selection may have influenced muscle features and, consequently, muscle quality. Muscle biological traits are controlled by gene expression and gaining insights with respect to differential expression profiles would provide valuable information to better understand the difference in meat quality. To evaluate whether divergent genetic selection was associated with modified patterns of gene expression in longissimus muscle, transcriptional profiles have been analyzed in LD muscle of both breeds using an RNA-seq approach. RNA-seq is a methodology which allows a quantitative measurement of gene expression through massively parallel RNA sequencing. This methodology allows a comprehensive transcriptome analysis, an accurate measure of individual gene expression as well as detection of rare gene transcripts. The comparison of muscle transcriptional profiles revealed significant differences (as estimated by DESeq/edgeR packages) in expression of about 800 genes between the two breeds. Further approaches include resolution of differential expression at transcript isoform level (Cufflinks package). The results reported here will be important to help identify the genes underlying beef quality traits.