Preliminary analysis of differentially expressed genes involved in meat tenderness in Angus and Nelore beef cattle

Authors: Luís Augusto Eijy Nagai[1,3], Poliana F. Giachetto[1], Fernando F. Cardoso[2], Adhemar Zerlotini[1], Paula R. Kuser-Falcão[1]

Affiliations: [1]Laboratório Multiusuário de Bioinformática, Embrapa Informática Agropecuária, Campinas – SP, Brazil. [2]Embrapa Pecuária Sul, Bagé, RS - Brazil. [3]Univesidade Estadual de Campinas, SP – Brazil.

High-throughput sequencing technologies are responsible for great advances in gene expression research, widening the understanding of the phenotypical characteristics. Over the last years, the data generated through cDNA sequencing (RNA-Seq) have been extensively used. The amount of RNA-Seq data available increased due to improvements in sequencing techniques and low cost, thus becoming an essential tool for transcriptome research. Nevertheless, RNA-Seq experiments must be analyzed with robust, efficient and statistically grounded algorithms. Fortunately, researchers and developers are further advancing such software tools in order to make it possible to focus on data analyze rather than computational tasks such as software installation and file formats.

The *Bos taurus* genome, published and made available in 2009, has enabled studies on traits of interest. Among them, meat tenderness is one of the most important measured attribute. The zebu breeds, mainly Nelore (*Bos indicus*), has wide acceptance in the brazilian market, but has lower productivity and meat quality when compared to taurine breeds, such as Angus (*Bos taurus*). Nowadays, there is a global interest on factors involved with attributes of commercial importance, such as meat tenderness, that justifies the importance of research concerning genetic, molecular and biochemical mechanisms that determine this trait.

In this study, we used the open-source tool EdgeR of the Bioconductor R package to identify differentially expressed genes in a cattle Illumina RNA-seq dataset. We used 150Gb of RNA-Seq data from 18 animals (10 from Angus and 8 from Nelore cattle), and compared the process of align trimmed reads and raw reads against *Bos taurus* Genome using Tophat2. We also performed a functional characterization of such genes in order to identify gene ontology enrichments, which can be related to genetic factors involved in meat tenderness.

Preliminary analysis showed better results from non-trimmed reads alignment. A total of 302 and 449 genes were differentially expressed between tender and tough groups in Angus and Nelore breeds, respectively. From these, we found a significant enrichment in genes related to immune response, skeletal system development, proteolysis, and myoblast cell fate commitment and development. The next step will be to find a relationship between the trait under study and the differentially expressed genes that we found, and validate our results by means of RT-qPCR, using a set of 10 randomly chosen genes.