

Changes muscle gene expression profile in *Bos indicus* cows submitted to medium and high gain rates during recovery from undernutrition

Daiane A. Fausto*¹; André L. J. Ferraz²; Eduardo F. Delgado¹; Sônia C. S. Andrade¹; Luis L. Coutinho¹; Gelson L. D. Feijó³

*Doctoral Student, "Luiz de Queiroz" College of Agricultural / University of Sao Paulo; Av. Padua Dias 11; Piracicaba, Sao Paulo 13418 900 Brazil;

¹"Luiz de Queiroz" College of Agricultural / University of Sao Paulo, Piracicaba, SP, Brazil;

²Mato Grosso do Sul State University, Aquidauana, MS, Brazil; ³Beef Cattle Research Center / Embrapa, Campo Grande, MS, Brazil.

*daianefausto@usp.br

The differential growth rate during recovery from undernutrition in mature animals may change the remodeling process in the stromal and myofibrillar proteins as well as in the proteolytic system. The gene expression profile screening based on number of readings obtained from the cDNA libraries may give important information regarding tissues changes during weight recovery. The objective of this study was to assess changes muscle gene expression profile in *Bos indicus* cull cows submitted to medium and high gain rates during recovery from undernutrition. The experiment was held at the Brazilian National Beef Cattle Research Center / Embrapa with Nellore females between five and sixteen years old. Thirty one cows with low body condition score were randomly assigned to control - CON (n = 4), high recovery gain - HG (n = 11; 1.2 kg of live weight gain) and medium recovery gain - MG (n = 16; 0.6 kg of live weight gain) during the dry season. The diet was formulated based on ingredients nutritional values from National Research Council. The animals were slaughtered serially at 0 (CON), 51, 74 and 104 days of feedlot. The comparison was made between the cows in CON with each recovery gain treatment. The analysis was performed with *Longissimus dorsi* samples collected immediately after slaughter and frozen in liquid nitrogen. After extraction of total RNA, analysis of RNA integrity number, separation of mRNA from the total RNA and clusterization the samples were loaded to the sequencer (HiScanSQ, Illumina). Data normalization and analysis of differential expression were done by the DESeq procedure of the R program, followed by the correction by Benjamini - Hochberg multiple tests for the p values obtained. There were about 13,000 genes that have their expression quantitatively measured. Differences in the expression level of 463 and 56 genes were observed for CON versus HG and CON versus MG comparisons, respectively. Those genes may be grouped by the biological function in to protein turnover, extracellular matrix and tissue remodeling. The Cathepsin precursor, E3 Ubiquitin protein ligase, Proteasome subunit alpha type 7 and Ubiquitin hydrolase were up-regulated in CON. Those genes are involved in higher muscle protein degradation (catabolism) which is related to muscle mass waste. There was regulation of genes involved in connective tissue remodeling for either recovery gain treatments, such as: Collagen type IV subunits 1 and 2, Exostosin - like 1, Mitogen activated protein kinase, Serpin, Sparc and Syndecan - 3. There was differential expression in HG of the genes Collagen type 1 alpha 2, Collagen type 3 alpha 1, Collagen type 5 alpha 3, Extracellular Matrix protein, Fibronectin, Heparan sulfate and Procollagen C - endopeptidase enhancer suggesting a more pronounced extracellular matrix renewal. Genes like elongation of long chain fatty acids, diacylglycerol lipase and leptin related to adipose tissue were also difference expressed in HG. The intramuscular connective tissues as well as the muscle tissue have their gene expression changed during recovery from undernutrition in a way that is consistent with the remodeling of the stromal proteins at the extracellular matrix.

Keywords: collagen, connective tissue, extracellular matrix, growth, proteoglycan, renewal

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