

CONSTRUINDO SABERES, FORMANDO PESSOAS E TRANSFORMANDO A PRODUÇÃO ANIMAL

ANALYSIS OF EXPRESSION OF GENES RELATED TO MITOCHONDRIAL FUNCTION ASSOCIATED WITH RESIDUAL FEED INTAKE IN NELLORE CATTLE

Bruna Maria SALATTA*¹, Daniele Fernanda Jovino GIMENEZ¹, Larissa Fernanda Simielli FONSECA¹, Maria Eugênia Zerlotti MERCADANTE^{2,3}, Sarah Figueiredo Martins BONILHA^{2,3}, Gabriela Bonfá FREZARIM¹, Lúcia Galvão de ALBUQUERQUE^{1,2}

*corresponding author: bruna_salatta@hotmail.com

¹São Paulo State University, Faculty of Agricultural and Veterinary Sciences, Jaboticabal São Paulo, Brazil

²National Council for Science and Technological Development (CNPq), Brasília, Brazil

³APTA Center of Beef Cattle, Animal Science Institute, Sertãozinho, SP, Brazil

The Improvement of cattle production efficiency is being targeted through selection for enhanced feed efficiency. Residual feed intake (RFI) in beef cattle is a measure of feed efficiency that is independent of the production level of the animals, such as size and growth rate. Mitochondrial function have pointed to be one of the factors that most influence RFI. Recent studies found a greater loss of electrons in mitochondria of low efficient animals (positive RFI) compared to high efficient animals (negative RFI). Therefore, in this study we aimed to analyze genes related to mitochondrial function in order to understand the transcription mechanisms related to feed efficiency. We analyzed the expression of PPAR α , PPAR γ e NRF1 genes, by quantitative real-time PCR, in liver tissue, of two groups of Nellore cattle, divergently ranked for RFI. A total of 24 non castrated Nellore males (12 positive RFI, 12 negative RFI), belonging to Animal Science Institute, Sertãozinho, SP, were used in this study. The animals were managed in the same contemporary group and were slaughtered in the same day. The NRF1 is an important transcriptional regulator in the regulation and expression of mitochondrial genes, which encodes proteins required for biogenesis and oxidative metabolism. Despite this, expression of the NRF1 gene in this tissue did not differ significantly between animals from positive and negative RFI groups. The expression of the PPAR γ gene was 0.76 times lower in positive RFI animals compared to negative RFI animals, and its expression differs significantly between RFI groups. The genes of the PPAR family act in the regulation of metabolism and play an important role in the use of lipids as energy source. These results suggest that PPAR γ is an important gene related to RFI and could be a potential candidate gene in breeding programs designed to increase the feed efficiency of Nellore cattle.

Keywords: Gene expression, Liver tissue, NRF1, PPAR α , PPAR γ

Acknowledgments: We thank the São Paulo Research Foundation (FAPESP) for providing grant 2009/16118-5.

Promoção e Realização:



Apoio Institucional:



Organização:

