

CONSTRUINDO SABERES, FORMANDO PESSOAS E TRANSFORMANDO A PRODUÇÃO ANIMAL

GENES EXPRESSION QUANTIFICATION RELATED TO MITOCHONDRIAL FUNCTION IN NELLORE BULLS DIVERGENTLY CLASSIFIED FOR FEED EFFICIENCY

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Feed represents the most costly factor of the beef cattle production system. In this way, improving feed efficiency traits is critical to increase the system profitability. Currently, residual feed intake (RFI) is one of the main traits used to select feed efficient animals. The RFI is defined as the difference between an animal's actual feed intake and its expected feed intake based on its size and growth, allowing the identification and selection of more efficient animals without selecting for increasing adult weight. However, this technology is very costly and laborious. Recent studies have pointed out mitochondrial function as being a factor of major influence on RFI. Thus, the objective of the present study was to analyze genes involved in mitochondrial function in order to identify molecular markers associated with higher feed efficiency. Peroxisome alpha (PPAR α) and gamma (PPAR γ) proliferation-activated receptors appear to play an important role in regulating the metabolism to use lipids as energy source, providing substrates for mitochondrial oxidation. They are also integrated with other function regulators and mitochondrial biogenesis such as nuclear respiratory factor (NRF1), a transcriptional regulator that plays a key role in the regulation and expression of nuclear and mitochondrial genes. The expressions of the PPAR α , PPAR γ and NRF1 genes were analyzed by quantitative Real Time PCR in muscle tissue (masseter muscle) of two Nellore cattle extremes groups for RFI. Animals were from Animal Science Institute, Sertãozinho, SP, Brazil. A total of 24 non castrated males, belonging to the same contemporary group, evaluated for RFI, were used. There were no significant differences in the relative expressions of the PPAR α , PPAR γ and NRF1 genes between RFI groups. This study did not provide evidence of association between the studied genes and energy efficiency in cattle. Further studies will be necessary to determine potential molecular markers for residual feed intake.

Keywords: Muscle tissue, NRF1, PPAR α , PPAR γ , Real time PCR

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