

Residual feed intake candidate genes

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Residual feed intake (RFI) is a measure of feed efficiency, an economically important trait in livestock. RFI is affected by many factors including both diet and genetics. RFI of an animal depends on the ability of the animal to consume less feed than expected based on their weight gain and weight maintained during the feed testing period. Recent work has implicated mitochondrial function as being involved in the feed efficiency of livestock and it is well known that genetics and diet have profound influence on mitochondrial function. The objective of this study is to identify genes involved in mitochondrial function that may affect feed efficiency in cattle. Several quantitative trait loci (QTL) affecting feed efficiency were mapped in Jersey x Limousin double backcross progeny from 3 sire families. Based on the QTL mapping results, ten candidate genes related to mitochondrial function were identified. These genes have been sequenced in the 3 sires in order to find DNA variants for association studies. 22 DNA variants were found and among the DNA variants discovered, there are 2 potentially functional single nucleotide polymorphisms (SNPs). DNA variants have been selected for genotyping in the Jersey x Limousin progeny in order to determine if the variants are associated with feed efficiency. One of the DNA variants have shown a significant effect (0.041, $p < 0.05$) with liver percentage which explains the mitochondria activity in liver might have an association with RFI.