

## **Project Summary**

### **Genomic Characterization of Feed Efficiency and its Relationship to Carcass Traits**

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# **Genomic Characterization of Feed Efficiency and its Relationship to Carcass Traits: Project Summary**

## **Background**

Economic factors affecting input and feed costs have made feed efficiency an important economically relevant trait to analyze as a component of beef production. Advances in genome technology have aided in the identification of regions of the bovine genome that harbor genes affecting feed efficiency, as well as genes that are important in carcass and meat quality traits. Understanding the interaction between these genes and their expression can be an important area in improving the efficiency of production, as well as the overall beef supply.

This project had two objectives:

1. Identify QTL locations for feed efficiency, carcass and meat traits;
2. Identify candidate genes for feed efficiency based on gene expression data.

## **Methodology**

A group of second generation Nellore-Angus cross calves was used to identify regions of the genome (quantitative trait loci or QTL) that harbor genes affecting feed efficiency, carcass and meat quality traits. The study was conducted on calves born over the course of three years.

The researchers conducted a genome-wide scan using over 7,000 DNA markers and characterized the expression of genes in the liver from animals with extreme phenotypes for feed efficiency.

A Calan gate system was used to evaluate individual feed intake at an average age of 11 to 13 months. Daily feed intake was predicted based on observed weight gain for each animal and standardized input for animal type, age, sex, condition and breed. This model predicted intake was then subtracted from observed intake and the difference defined as model predicted residual consumption (MPRC). Those animals that consumed less than predicted, and thus were more efficient, had negative MPRC. The researchers used this method, instead of traditional residual feed intake, in order to make simultaneous use of data from multiple contemporary groups.

After the finishing period and harvest, carcasses were chilled for 48 hours and trained personnel collected USDA quality and yield grade data including maturity, marbling, fat thickness, adjusted fat thickness, ribeye area, hot carcass weight, as well as kidney, pelvic and heart (KPH) fat. Objective color measurements of the ribeye surface were also collected. One side of each carcass was electrically stimulated

Carcasses were fabricated and the rib section was removed. Rib sections were weighed and separated in the *M. longissimus thoracis*, lean, bone and subcutaneous, intermuscular and channel fat. All components were weighed to ensure a 99 percent recovery of the rib weight. Soft tissue samples were collected for chemical analyses for moisture, fat, protein and ash content.

Steaks were removed from the 12<sup>th</sup>-rib section and were analyzed for chemical fat analysis, sarcomere length and myofibrillar fragmentation index (MFI). The loin was removed from both sides of the carcass and cut into steaks. The most anterior steak from both loins was analyzed for tenderness using Warner Bratzler shear force. The next two steaks were used for subsequent

sensory panel evaluations. Two more steaks from the electrically stimulated side of the carcasses were used for sarcomere length and chemical fat analysis.

Two µg of DNA from 780 animals were genotyped. Liver samples from 28 animals that were categorized by the MPRC calculations as being either extremely efficient or inefficient were collected for DNA analysis. Purified RNA samples from cattle with the most negative MPRC residual values (efficient animals) or the most positive MPRC residual values (inefficient animals) were paired randomly.

## **Findings**

Preliminary, visual appraisal of the microarray scans revealed that there are several genes that were differentially expressed in liver from animals with high and low feed intakes.

Several of the QTL identified in this study have been reported previously. In particular, the marbling QTL on BTA9, and the WBS QTL on BTA 5, 17 and 29 were detected by interval mapping in the Angleton *Bos indicus* x *Bos taurus* cross population and were validated as part of the NCBA Carcass Merit project as CMP QTL9, QTL1, QTL3 and QTL6, respectively. The WBS QTL from the non-electrically stimulated side on BTA29 coincides with CAPN1 that has been commercialized by USDA-ARS.

The hot carcass weight QTL on BTA29 was detected in the Angleton project, while the one on BTA10 was detected in another *Bos indicus* x *Bos taurus* cross population. Marbling QTL on BTA 14, 16, and 17 were also detected in this latter population. The marbling QTL on BTA5 also previously has been described in Japanese black cattle. The yield grade QTL on BTA12 and KPH QTL on BTA17), and the bone percent QTL on BTA5 have also been previously identified.

Many of the QTL identified in this study are novel. In particular, the researchers identified a number of QTL for traits such as WBS from electrically stimulated carcasses that have not previously been described and the researchers felt these warranted further investigation. Initial analysis indicates that genes associated with glucose/insulin metabolism, growth and cellular proliferation, and lipid metabolism are all upregulated in the more efficient animals compared to their less-efficient counterparts. In contrast, genes associated with energy production are upregulated in the inefficient animals. GIMAP4 is an abundant GTPase that is expressed higher in the efficient animals. This group also expressed a greater level of GIMAP6, a related protein of unknown function.

Based on the results, the researchers concluded that the inefficient animals produced and used more energy than the efficient animals, and had less growth and proliferation signaling occurring, at least in the liver. The results help demonstrate how multiple networks of genes can combine to result in vastly different efficiency phenotypes.

## **Implications**

Through this project, the researchers were able to develop a list of quantitative trait loci and candidate genes for feed efficiency. Many of the QTL identified in this study were novel, including several for Warner Bratzler shear force from electrically stimulated carcasses. The determination that genes associated with glucose/insulin metabolism, growth and cellular proliferation and lipid metabolism are upregulated in efficient animals, while genes associated with energy production are

upregulated in inefficient animals, demonstrated that combining QTL mapping with microarray analysis is a very powerful methodology to identify underlying genes affecting traits of interest.

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