Genomic tools to improve meat quality traits in Angus-Brahman cattle

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PROJECT SUMMARY

This research project had two objectives: (1) develop the genomic tools needed to implement a marker assisted selection program aimed at cumulative and permanent improvement of tenderness in Brahman influenced cattle; (2) explore the feasibility of using genomic markers to supplement carcass traits for a more accurate prediction of tenderness to allow our producers to more effectively respond to consumers' desire for "certified tender" products.

The US Beef Quality audit identified low and inconsistent quality as major impediments to improving domestic demand for beef products. Consumers evaluate the quality of beef at the point of purchase with respect to freshness, marbling, and color, and at the point of consumption where the focus is on quality of eating experience, or palatability described by three sensory traits: tenderness, juiciness and flavor. Ability to deliver a consistently superior quality product is important if beef industry is to maintain and expand its share of the market. These issues are of particular importance for Brahman and Brahman crosses as they are routinely penalized for relatively low marbling score and perceived inferior tenderness. A sustainable strategy to address these issues is via the development of effective selection and management genomic tools. The **goal** of this research was to identify a set of genetic markers strongly associated with the most important beef quality traits in Brahman influenced cattle, particularly tenderness and marbling. These markers will be subsequently validated and their effectiveness in a marker assisted selection and management program designed to improve product quality will be assessed.

Genetic markers are small pieces of DNA, or SNPs, with a known location on a chromosome and associated with a particular gene or trait. Thus, if a set of SNPs that affect carcass quality and palatability traits can be identified, they can be used in selection to identify genetically superior bulls early in life for breeding or can be used to predict palatability for marketing purposes leading to higher and more consistent beef quality product. The expected results are improved demand for US beef, increased profits and more satisfied consumers.
Meat quality and palatability traits, such as marbling, tenderness, juiciness and flavor, are complex traits, controlled by many genes and by the environment. All these traits are measured after the animal is slaughtered, are difficult and costly to measure and have relatively low heritability. Genomic selection provides the best strategy to implement a genetic improvement program for these traits.

For this project, we genotyped critical individuals with a high-density SNP chip which allowed us to impute these genotypes on other individuals. Imputation was used to generate a data set that allowed us to conduct an exploratory study to determine the feasibility of a genomic approach to improve meat quality in Brahman influenced cattle.

RESULTS

For this project we analyzed data from the Angus-Brahman multibreed herd developed at the University of Florida Beef Research Unit (BRU). The herd, initiated in 1989, consists of group of cattle spanning the range from 100% Angus to 100% Brahman. The mating design used to generate the multibreed herd was diallel crosses, where sires from 6 mating groups (Angus, 3/4Angus 1/4Brahman, Brangus, 1/2Angus 1/2Brahman, 1/4Angus 3/4Brahman, and Brahman) were mated across to dams from the same six mating groups. Phenotypic and pedigree records have been collected on these cattle as well as tissue samples for DNA analyses. The phenotype of interest for this project was tenderness assessed by Warner-Bratzler shear force (WBSF).

The project had two steps. First, we performed a genome-wide association study to identify genetic markers that explain variation in tenderness. Second, we identified a subsets of genetic markers that could be used to predict tenderness and assess their feasibility for selection and marketing purposes.

1) <u>Genome-wide association study.</u>

Two hundred key animals from the UF Multibreed herd were genotyped with the GeneSeek Bovine GGP HD150k gene chip (~150,000 genetic markers). Using this genotypic information, we imputed from 3K to 150K on other animals from the Multibreed herd. A genome-wide association study was performed on 418 animals with 150K SNP genotypes and tenderness assessed by WBSF as the focus trait for this study. The genomic heritability for this trait was 0.47. Twelve chromosomes were found to have SNPs with statistically significant association with WBSF, and several more SNPs on other chromosomes were close to reaching significance (**Figure 1**).

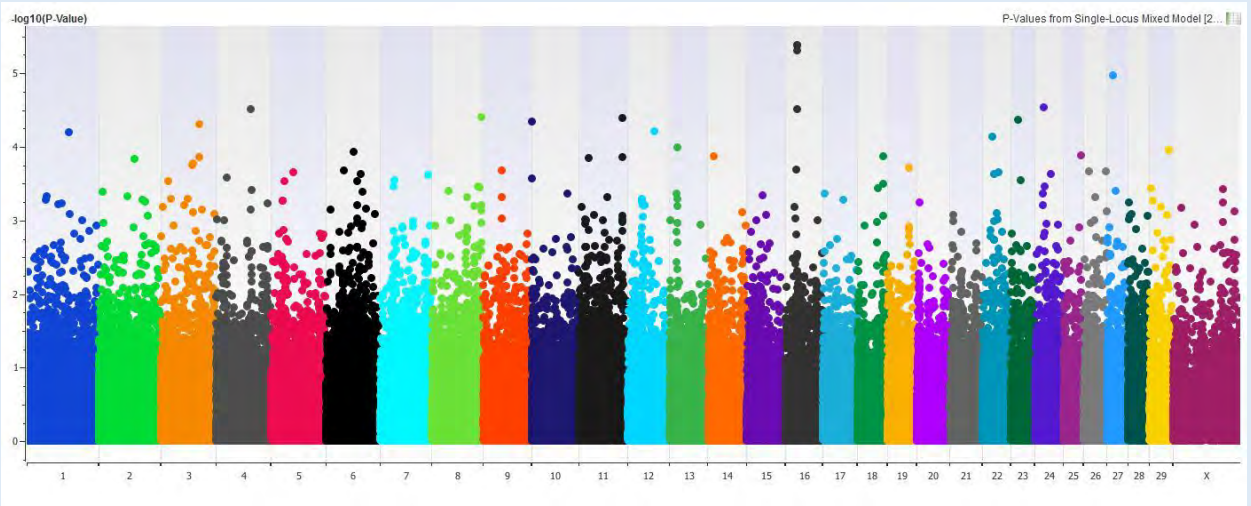

Figure 1. Genome-wide association results for WBSF on 418 multibreed animals with 150K real and imputed genotypes. Genomic location of each SNP across all 29 bovine chromosomes is displayed along the X-axis, with the negative logarithm of the association P-value for each SNP displayed on the Y-axis (each dot represents a SNP). The highest SNPs on each chromosome represent the SNPs stronger associated with WBSF.

An investigation of chromosomal locations with strongest associations with WBSF revealed several genes already established by previous research as being associated and having an impact on beef tenderness: calpain-1 (Chromosome 29) and calpastatin (chromosome 10). Other regions not previously investigated in relation with tenderness proved to contain genes which, based on their biological role, are ideal candidate genes for this study: FHOD3 (formin) which encodes a protein playing a role in actin filament polymerization, ITPR1 gene encodes the inositol 1,4,5-triphosphate (IP3) receptor, an intracellular IP3-gated calcium channel that modulates intracellular calcium signaling and laminin which encodes one of the two B-type lamin proteins and is a component of the nuclear lamina.

2) <u>Strategies to predict eating quality using collected phenotypes enhanced with genomic information.</u> The top 100 SNPs identified from the genome-wide scan were used in a step-wise regression analysis and 21 SNPs were selected as significant for WBSF. Carcass traits available along with the 21 significant SNPs were used in a discriminant analysis to identify a subset of carcass traits and genetic markers with the highest predictive accuracy across tenderness classes. Among all carcass traits, marbling score and ribeye area were identified as significant in predicting tenderness classes.

The dataset was split into 3 tenderness groups based on the WBSF measurement:

- Class 1: **tender** (WBSF < **3.5**, 31.6% of animals)
- Class 2: **moderately** tender (**3.5** > WBSF < **4.5**, 33.6% of animals)
- Class 3: **tough** (WBSF > **4.5**, 34.8% of animals)

Predictive discriminant analyses were performed using marbling score and ribeye area alone (best carcass traits predictors), the best 17 SNP alone (best marker predictors), and best carcass traits and markers combined (marbling score, lean maturity, dressing percentage and 17 SNPs). A linear composite of predictor variables was used to predict group membership. A cross-

Best carcass traits model
Marb, REA

Percent Classified into tenderness classes			
From \ Into	1	2	3
1	53.8	14.4	31.8
2	28.6	17.9	53.6
3	21.4	15.2	63.6

Best SNP model
17 SNP

Percent Classified into tenderness classes			
From \ Into	1	2	3
1	59.8	28.0	12.2
2	34.8	38.3	26.9
3	4.1	26.2	69.7

Best carcass + SNP model
Marb, LM, DP + 17 SNP

Percent Classified into tenderness classes			
From \ Into	1	2	3
1	62.9	27.3	9.8
2	30.7	43.6	25.7
3	2.8	29.7	67.6

Group **1**: **tender** (WBSF < **3.5**); Group **2**: **moderately** tender (**3.5** > WBSF < **4.5**); Group **3**: **tough** (WBSF > **4.5**)

Figure 2. Percent of animals from a certain tenderness class (as measured by WBSF) being classified into a tenderness group based only on the best carcass traits (marbling score and ribeye area), based on 17 most important SNP, or based on carcass traits (marbling score, lean maturity, dressing percentage) and SNPs combined.

validation method was used to estimate error rate when using the discriminant functions to allocate animals to tenderness groups. The results from the predictive discriminant analysis evaluating the usefulness of carcass traits, DNA markers, or carcass traits and markers combined in predicting tough, moderately tender or tender group membership are shown in **Figure 2**. On the diagonal of each table (in green) is the percent of animals correctly classified. It is interesting to note that in all three cases, the moderately tender animals are the most difficult to classify correctly (17.9%, 38.3% and 43.6%, respectively), while the least tender animals had the highest correct classification (63.6%, 69.7% and 67.6%, respectively).

When the prediction of tenderness group membership was based on carcass traits only, the error rate of classification of new observations into tender, moderately tender and tough was 46.2%, 82.1% and 36.6%, respectively (**Figure 3**). The predictive model based on 17 SNP markers alone showed a 20% overall improvement of error rate (from 54.9% to 44%), while the predictive model combining carcass traits and SNP data showed a further improvement to a total error rate of 41.9%. All models performed poorly when classifying observations in moderately tender group, which is expected, given that errors could occur on both directions for this middle group.

Best carcass traits model
Marb, REA

Total Error Estimates for tenderness classes				
	1	2	3	Total
Error Rate	46.2	82.1	36.6	54.9

Best SNP model
17 SNP

Total Error Estimates for tenderness classes				
	1	2	3	Total
Error Rate	40.1	61.7	30.3	44.0

Best carcass + SNP model
Marb, LM, DP + 17 SNP

Total Error Estimates for tenderness classes				
	1	2	3	Total
Error Rate	37.1	56.4	32.4	41.9

Group 1: tender (WBSF < 3.5); Group 2: moderately tender (3.5 > WBSF < 4.5); Group 3: tough (WBSF > 4.5)

Figure 3. Total error rates of misclassifications of animals into tenderness classes based only on the best carcass traits (marbling score and ribeye area), based on 17 most important SNP, or based on carcass traits (marbling score, lean maturity, dressing percentage) and SNPs combined.

Although no errors are desirable, from the consumer and marketing point of view errors may have different consequences. We could speculate that misclassification errors for moderately tender group have relatively small market consequences. If we assume that the price of the product reflects eating quality (as it would with a "certified tender" program), the consumer is paying and expecting average eating quality and this expectation is most likely met. On the other hand, misclassifications of a product with "tough" or "tender" quality may have a greater negative impact on consumers. Again, if we assume the eating quality is positively associated with the price of the product, not meeting quality expectations leads to dissatisfied consumers. This could have important consequences as past experience is a critical factor regarding attitude toward food. A report (SMART, 1994) evaluating the factors contributing to the intent of consumers to repurchase a product concluded that eating quality was the most important factor (65%), followed by price (28%). Unfulfilled eating quality expectations lead to

consumers' dissatisfaction, reduced future beef purchases and lower demand. The negative consequences associated with misclassifications of carcasses with "tender" into "moderately tender" or "tough" groups are of different nature. These errors represent opportunity losses for the industry as the product is undervalued.

IMPLICATIONS. The current exploratory study shows that several genomic regions are associated with tenderness of beef in a multibreed Angus-Brahman population. Investigation of several regions revealed strong candidate genes with possible direct relations to meat tenderization process. A higher-density of SNP markers in a larger population should provide additional evidence and pinpoint to which of these signals are biologically significant.

The predictive analysis reveals that opportunity exists for development and implementation of a system to communicate tenderness attributes to consumers and improve the probability that consumers' eating expectations are met. A predictive model that would assign the product (whole carcasses or components) to appropriate tenderness class based solely on genetic markers, or genetic markers and carcass traits recorded on a routinely basis showed to be significantly better in predicting tenderness relative to current system based on carcass traits alone. A larger dataset and a better set of genetic markers from a high-density genome scan should provide a stronger evidence for the feasibility of this type of prediction.