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

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INTRODUCTION

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.

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.

A research project funded by the Florida Beef Council was designed to 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.

RESULTS

For this project we analyzed data from the Angus-Brahman multibreed herd developed at the University of Florida Beef Research Unit. The herd, initiated in 1989, consists of group of cattle spanning the range from 100% Angus to 100% Brahman. 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
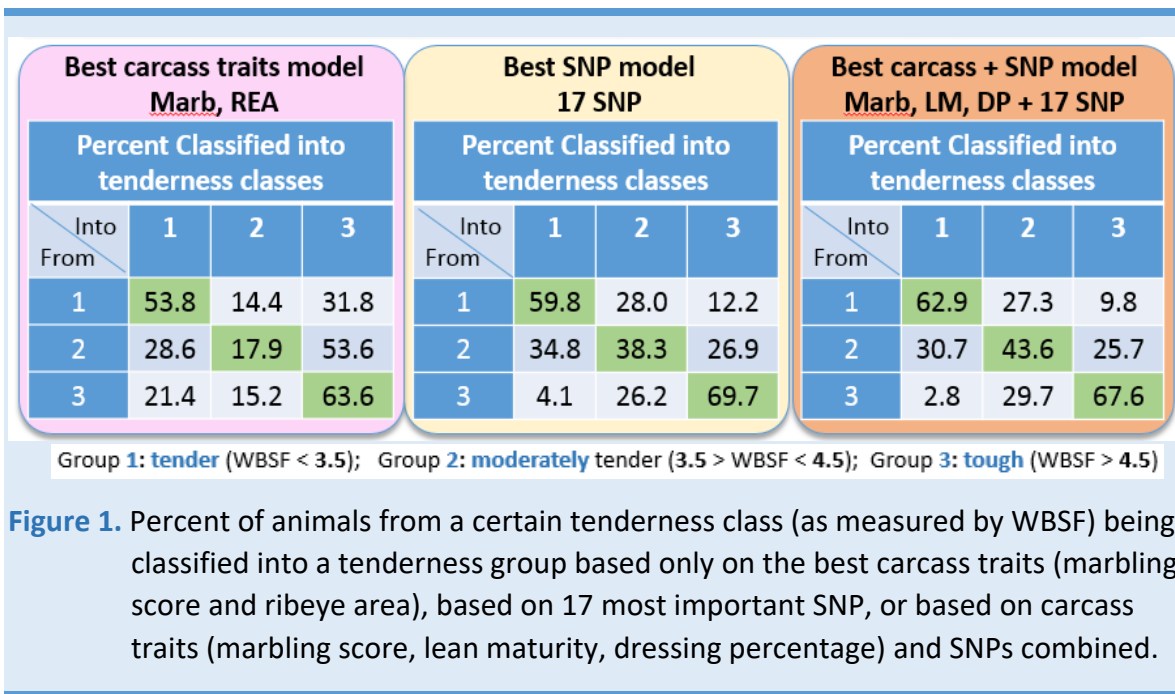
genetic markers that could be used to predict tenderness and assess their feasibility for selection and marketing purposes.

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).

Carcass traits available and the 21 significant SNPs (separate and combined) were used in a discriminant analysis to identify a subset of carcass traits and genetic markers with the highest predictive accuracy across tenderness classes.

Predictive discriminant analyses were performed using best carcass traits predictors alone (marbling score and ribeye area), the best 17 SNP alone (best marker predictors), and best carcass traits and markers combined (marbling score, lean maturity, dressing percentage and 17 SNPs). The results from the predictive discriminant analysis, shown in **Figure 1,** were used to

Best carcass traits model Marb, REA				Best SNP model 17 SNP				Best carcass + SNP model Marb, LM, DP + 17 SNP			
Percent Classified into tenderness classes				**Percent Classified into tenderness classes**				**Percent Classified into tenderness classes**			
Into \ From	**1**	**2**	**3**	Into \ From	**1**	**2**	**3**	Into \ From	**1**	**2**	**3**
1	53.8	14.4	31.8	**1**	59.8	28.0	12.2	**1**	62.9	27.3	9.8
2	28.6	17.9	53.6	**2**	34.8	38.3	26.9	**2**	30.7	43.6	25.7
3	21.4	15.2	63.6	**3**	4.1	26.2	69.7	**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 1. 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.

evaluate the usefulness of carcass traits, DNA markers, or carcass traits and markers combined in predicting tough, moderately tender or tender group membership. 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 2**). 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%.

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

Best carcass traits model Marb, REA				Best SNP model 17 SNP				Best carcass + SNP model Marb, LM, DP + 17 SNP			
Total Error Estimates for tenderness classes				Total Error Estimates for tenderness classes				Total Error Estimates for tenderness classes			
1	2	3	Total	1	2	3	Total	1	2	3	Total
Error Rate 46.2	82.1	36.6	54.9	Error Rate 40.1	61.7	30.3	44.0	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)
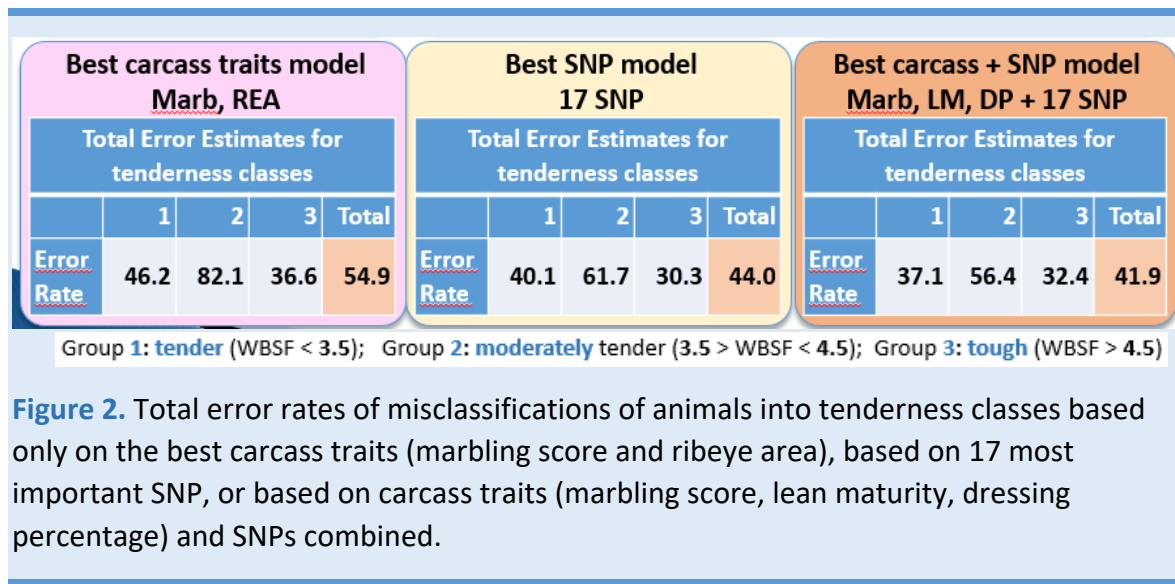
Figure 2. Total error rates of misclassifications of animals into tenderness classes based only on the best carcass traits (marbling score and ribeye area), based on 17 most important SNP, or based on carcass traits (marbling score, lean maturity, dressing percentage) and SNPs combined.

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 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 USDA quality grades. To assess their effectiveness in identifying genetically superior young bulls to be used in a marker assisted selection and management program designed to improve product

quality, these markers will be subsequently validated using a larger dataset supplemented by a genome scan to identify causal mutations. Further investigation of these genomic regions in association with detailed analysis of gene expression and protein activity in this population will allow us to pinpoint and reveal the key players having an impact on beef tenderness.