Project Summary Product Quality

| | |
|---|---|
| **Project Title:** | Prediction and Assessment of Genomic Breeding Values for Measures of Tenderness and Temperament in *Bos indicus*-*Bos taurus* Crossbreds |
| **Principle Investigator(s):** | D. G. Riley, L. L. Hulsman, R. K. Miller, C. A. Gill, A. D. Herring, J. O. Sanders, & S. O. Peters |
| **Institution(s):** | Texas A&M University & New Mexico State University |
| **Completion Date:** | May 2011 |

## Background

Cattle with some *Bos indicus* background provide advantages to cow-calf producers because of their adaptation to high heat, high humidity, and harsh or poor-quality forages. Consequently, they make up as much as one-third of the U.S. cow herd. The calves from these cows make up a substantial portion of the beef produced annually. Beef from *Bos indicus* cattle has consistently been characterized as tough relative to beef from *Bos taurus* cattle, and as such can negatively influence the eating experience of consumers. This has strong potential to depress demand for beef. *Bos indicus* cattle can also demonstrate poor temperament or disposition and be dangerous to those who work with them. Poor temperament has been genetically associated with increasing toughness of beef. It may be possible to select individuals for improved temperament and indirectly improve the tenderness of beef from cattle. Genomic selection is a term that describes the estimation genotype effects for many DNA markers and adding those to produce a breeding value for each animal.

The objectives of this project were to:
1. Estimate genomic breeding values for all individuals in an F2 mapping population.
2. Compare those with breeding values produced by traditional quantitative methodology.

## Methodology

Cattle for this work were produced as embryos from four Nelore-Angus F1 bulls and 10 Nelore-Angus $F_1$ cows. Additional cattle were half-siblings from the same four bulls and crossbred *Bos indicus-Bos taurus* cows. Females from these crosses, after their first parturition, were mated with $F_2$ bulls and the resulting $F_3$ calves and other crossbred calves from the half-sibling females were first born in 2009.

Temperament of each animal was assessed at weaning (n = 703). Each animal was separated from others in a pen and placed in an alley with four evaluators. Each animal was scored subjectively from 1 to 9 for these characteristics:

- Aggressiveness-the willingness to hit an evaluator
- Flightiness-running or attempting to escape
- Gregariousness-unwillingness to be separated from a group of animals
- Nervousness-examples of distinct (from flightiness) nervous behavior include shaking, urination, etc.
- Overall disposition score-general assessment of temperament; not an average of the other 4 scores.

For each characteristic, high scores represent excesses of these behaviors or poor overall temperament and were undesirable. Low scores indicated calm, non-aggressive animals and good overall temperament. Preliminary analyses indicated that these were strongly correlated and the overall score appeared to be the best representation of an animal's temperament. Warner-Bratzler shear force values were obtained on steaks from steers (n = 312) after conventional feeding, and were obtained for 2010-born steers as validation data with which to compare the predicted values.

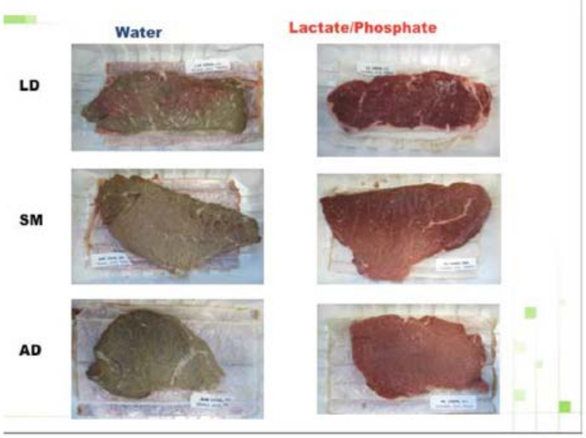
Genotypes from the Bovine 50kSNP chip were used for all F2 heifers and steers (n = 705) and the 2010- born steers. Shear forces and genotypes were obtained for steers from the validation population, and association analyses was completed for Warner-Bratzler shear force. Additionally, genomic correlations between temperament and shear force were considered.

## Findings

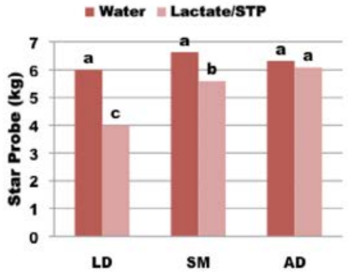
After appropriate quality editing, there were 34,980 SNP marker genotypes that were used in this work. Analyses were completed for temperament score. Several times, researchers separated genotypes and their corresponding records into distinct groups for the two steps of estimating the genetic effects at each marker in one group and then checking those values in the other group. This was done to determine if the best individuals (those with the lowest breeding values for temperament) were consistently identified in these different analyses. This grouping had no effect on the ranking of individuals; the same group of individuals was identified in each set of analyses. Genomic selection procedures did not identify the same individuals as conventional analyses to predict breeding values (those with no marker effects included).

## Implications

These results will serve as foundational investigations for the improvement of beef tenderness in *Bos indicus* steaks, and may result in implementation of a new selective tool utilizing whole genome association and high density marker arrays.



**Lactate/phosphate enhancement improved tenderness values for LD and SM in HIOX-MAP**



$^{abc}$Means having different letters are different ($p < 0.05$).

Funded by
the Beef Checkoff