Thyroglobulin, Calpastatin and Calpain Genetic Markers in Brahman Steers and their Association with Carcass and Tenderness Traits
D. E. Franke and T. D. Bidner, School of Animal Sciences

Findings
- In these Brahman steers, frequencies of favorable thyroglobulin and calpain (CAPN 316 and CAPN 4751) genetic marker alleles were generally lower than found in non-Brahman steers.
- Frequency of the favorable calpastatin genetic marker allele in these Brahman steers was 0.342 and associated with calpastatin enzyme activity and tenderness.
- The difference between favorable and unfavorable homozygous genetic markers CAPN 316 and CAPN 4751 for shear force was about 2.2 lb in aged steaks in these Brahman steers and similar to findings in other breeds.
- Combinations of favorable genetic markers in Brahman steers will predict more tender steaks when aged for 14 days.

Introduction
The Brahman is the primary tropically adapted breed in the Gulf Coast region and contributes to reproductive and maternal advantages of crossbred cows. However, yearling cattle with a high proportion of Brahman inheritance that are fed to U.S. weight and fat thickness endpoints are less tender and have lower carcass quality grades. The American Brahman Breeders Association publishes Brahman sire EPDs for carcass and tenderness traits on a limited number of sires, but the time required to obtain carcass and shear force data for meaningful sire EPDs suggests that other methods for determining genetic merit for carcass and tenderness traits should be identified.

Genetic markers offer an approach to utilize information from major genes that influence traits of consumer importance, particularly when the phenotype is difficult or expensive to measure. A gene at the thyroglobulin locus is associated with deposition of fat thickness and marbling in cattle being fed a high energy diet. Genes at the calpastatin and calpain loci are associated with tenderness in aged steaks of both Brahman and non-Brahman fed cattle.

The objectives of this study were to determine the frequency of favorable genetic markers at the thyroglobulin, calpastatin, and calpain loci in Louisiana born Brahman steers and their association with carcass traits and measures of tenderness in aged steaks.

Materials and Methods
Spring-born purebred paternal half-sib Brahman bull calves (n=467) were purchased at weaning from 17 Brahman producers in Louisiana over a five-year period (1996 to 2000). After purchase, calves were transported to the LSU Agricultural Center Central Station in Baton Rouge where they were castrated, dehorned if necessary, dewormed and vaccinated for appropriate diseases. Calves were back-grounded through autumn each year and placed on ryegrass around the first of December. Calves were grazed for an average of 120 days per year over the five-year period and then shipped to south Texas for feeding. Yearlings were harvested from the feedlot in two or three groups each year as groups reached about 0.4 inch fat thickness and weighed approximately 1150 to 1200 lb. All calves were processed at a major packing plant in Corpus Christi, TX where a Texas A&M Extension Meat Scientist recorded carcass data 24 hours post mortem and supervised the removal of a primal wholesale rib from each steer for
shipment to the LSU Animal Science Department Meats Laboratory. Two, one-inch thick steaks were cut from the large end of each primal rib, trimmed, vacuum-packed and assigned to 7- or 14-day aging.

Each year after steaks from all steers had been aged and frozen, the steaks were thawed and cooked to medium doneness for evaluation. Six half-inch cores were taken from each cooked steak parallel to muscle fibers and the shear force recorded for each core. The average shear force of the six cores taken from each steak became the measure of shear force for tenderness for each steer.

During the grazing period blood samples were taken from each steer. DNA was extracted from the white blood cells and frozen for later assay. When all the steers had been harvested, DNA was shipped to Bovigen LLC (now Pfizer Animal Genetics) in Harahan, LA for determination of thyroglobulin, calpastatin, and calpain genetic marker genotypes in each steer.

Statistical analyses were completed using the Statistical Analysis System (SAS) computer package. Mixed model analysis in SAS was used to determine the association of genetic markers with carcass and tenderness traits.

Results and Discussion

Frequencies for the thyroglobulin, calpastatin, and calpain genetic marker genotypes and alleles are shown in Table 1. Genotypes for the thyroglobulin (TG5) genetic marker are CC, CT, and TT. The favorable allele is T, which is involved with fat deposition in cattle. In these Brahman steers, the frequency of the favorable allele T was 0.004. No favorable TG5 TT genotypes were found in these steers for this genetic marker. The frequency of the favorable TG5 allele T in Bos taurus steers is usually 0.30 or higher suggesting a breed difference.

Genetic marker genotypes for calpain 316 are CC, CG, and GG, and for calpain 4751 are CC, CT, and TT. The C allele in both genetic markers is associated with more tender beef. In this group of Brahman steers, no favorable genotypes for either genetic marker were found. The frequencies for the favorable genetic marker C were 0.031 for calpain 316 and 0.050 for calpain 4751. Generally in new research when the frequency of the minor allele (C in this case) is less than 10%, no further analysis is done because the error of identification is larger than the minor frequency. However, in this case where procedures are well established for assay of calpain genetic markers, further analyses are usually done. Frequencies of the favorable allele for calpain 316 and 4751 in these steers are lower than found in other studies with non-Brahman cattle.

Genotypes for the calpastatin genetic markers in these cattle were CC, CT, and TT. T is the favorable allele for tenderness and had a frequency of 0.658, which is similar to findings in other Brahman steers but lower than found in non-Brahman cattle.

Least squares means for the effects of calpastatin and calpain genetic marker genotypes on calpastatin enzyme activity and shear force are presented in Table 2. Calpastatin genetic markers were associated with calpastatin enzyme measured from a loin muscle sample taken from each steer (P < 0.01). The TT calpastatin genotype had an enzyme level of 4.11 ± 0.07 compared to 4.67 ± 0.16 for genotype CC and 4.51 ± 0.07 for genotype CT. Less calpastatin enzyme ties up less calpain, the enzyme involved in tenderization, and therefore results in more tender meat. The calpastatin genetic markers were also associated with shear force after aging steaks for 14-days, but not for 7-days. It is well known that the longer aging of meat increases tenderization.

Calpain 316 and 4751 genetic markers were generally associated with shear force of steaks aged for 7- and 14-days. Genotypes containing the favorable genetic marker alleles in each genetic marker had lower shear force. No Brahman steers had
the homozygous combination of favorable genetic marker alleles. This result could be expected when the frequency of the favorable genetic marker alleles were as low as shown in Table 1 for calpain 316 and 4751.

Using regression statistical analyses and the effects of favorable and unfavorable genetic marker alleles in the homozygous state, we predicted that Brahman steers with favorable genotype CC for calpain 316 and CC for calpain 4751 would have 2.2 lbs less shear force than Brahman steers with unfavorable genotype GG for calpain 316 and TT for calpain 4751 when their steaks were aged for 14-days. Since the frequencies of the favorable genetic marker alleles were so low for this population, only a very limited number of steers would have the desired homozygous genetic marker genotype.

Increasing the frequency of the favorable genetic marker alleles for shear force should be a primary concern of the Brahman breeder in order to increase tenderness. This applies to the calpastatin and calpain genetic markers studied in this project as well as new genetic markers that are discovered in the future.

### Table 1. Genotypic and allelic frequencies for four genetic markers in the molecular structure of Brahman steers.

<table>
<thead>
<tr>
<th>Genetic marker</th>
<th>Genotype</th>
<th>No</th>
<th>Genotypic frequency</th>
<th>Allele</th>
<th>Allelic frequency</th>
</tr>
</thead>
<tbody>
<tr>
<td>TG5</td>
<td>CC</td>
<td>380</td>
<td>0.9922</td>
<td>C</td>
<td>0.996</td>
</tr>
<tr>
<td></td>
<td>CT</td>
<td>3</td>
<td>0.0078</td>
<td>T</td>
<td>0.004</td>
</tr>
<tr>
<td></td>
<td>TT</td>
<td>0</td>
<td>0.0000</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Calpastatin</td>
<td>CC</td>
<td>41</td>
<td>0.1073</td>
<td>C</td>
<td>0.342</td>
</tr>
<tr>
<td></td>
<td>CT</td>
<td>179</td>
<td>0.4686</td>
<td>T</td>
<td>0.658</td>
</tr>
<tr>
<td></td>
<td>TT</td>
<td>162</td>
<td>0.4241</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Calpain 316</td>
<td>CC</td>
<td>0</td>
<td>0.0000</td>
<td>C</td>
<td>0.031</td>
</tr>
<tr>
<td></td>
<td>CG</td>
<td>24</td>
<td>0.0628</td>
<td>G</td>
<td>0.969</td>
</tr>
<tr>
<td></td>
<td>GG</td>
<td>358</td>
<td>0.9372</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Calpain 4751</td>
<td>CC</td>
<td>0</td>
<td>0.0000</td>
<td>C</td>
<td>0.050</td>
</tr>
<tr>
<td></td>
<td>CT</td>
<td>38</td>
<td>0.0995</td>
<td>T</td>
<td>0.950</td>
</tr>
<tr>
<td></td>
<td>TT</td>
<td>344</td>
<td>0.9005</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Table 2. Level of significance and least squares means (± SE) for the effects of CAST, CAPN 316 and CAPN 4751 genetic marker genotypes on calpastatin and shear force of steaks from Brahman steers.

<table>
<thead>
<tr>
<th>Genetic marker</th>
<th>Calpastatin(^a)</th>
<th>SF7(^a), kg</th>
<th>SF14(^b), kg</th>
</tr>
</thead>
<tbody>
<tr>
<td>CAST</td>
<td>0.0001(^b)</td>
<td>0.7580</td>
<td>0.0192</td>
</tr>
<tr>
<td>CC</td>
<td>4.67 ± 0.16</td>
<td>4.48 ± 0.16</td>
<td>3.80 ± 0.11</td>
</tr>
<tr>
<td>CT</td>
<td>4.51 ± 0.07</td>
<td>4.46 ± 0.09</td>
<td>3.95 ± 0.06</td>
</tr>
<tr>
<td>TT</td>
<td>4.11 ± 0.07</td>
<td>4.39 ± 0.09</td>
<td>3.74 ± 0.06</td>
</tr>
<tr>
<td>CAPN 316</td>
<td>0.8385</td>
<td>0.0616</td>
<td>0.0194</td>
</tr>
<tr>
<td>CC</td>
<td>--</td>
<td>--</td>
<td>--</td>
</tr>
<tr>
<td>CG</td>
<td>4.39 ± 0.19</td>
<td>4.05 ± 0.21</td>
<td>3.50 ± 0.15</td>
</tr>
<tr>
<td>GG</td>
<td>4.35 ± 0.06</td>
<td>4.45 ± 0.07</td>
<td>3.87 ± 0.04</td>
</tr>
<tr>
<td>CAPN 4751</td>
<td>0.7637</td>
<td>0.0575</td>
<td>0.0759</td>
</tr>
<tr>
<td>CC</td>
<td>--</td>
<td>--</td>
<td>--</td>
</tr>
<tr>
<td>CT</td>
<td>4.39 ± 0.14</td>
<td>4.13 ± 0.17</td>
<td>3.64 ± 0.11</td>
</tr>
<tr>
<td>TT</td>
<td>4.35 ± 0.06</td>
<td>4.46 ± 0.07</td>
<td>3.87 ± 0.04</td>
</tr>
</tbody>
</table>

\(^a\)Calpastatin = units of calpastatin activity per gm of muscle sample, SF7 = shear force of steaks aged for 7 days and cooked to medium doneness, and SF14 = shear force of steaks aged for 14 days and cooked to medium doneness.

\(^b\)Significance level
A Comparison of Tropically Adapted F1 Cows for Fertility, Maternal Ability, and Size
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Findings
- Brahman F1 cows had a lower weaning rate as two-year-olds than Beefmaster-, Brangus-, Bonsmara-, or Romosinuano-sired F1 cows, but weaning rates were similar for all tropically adapted cows at 3 years and later ages.
- No differences were found for birth date or birth weight of calves from tropically adapted cows but calves from Brahman F1 cows had greater average daily gain and adjusted 205-day weights than calves from other tropically adapted F1 cows.
- Brahman- and Beefmaster-sired F1 cows were slightly heavier at weaning in October than Bonsmara- and Brangus-sired F1 cows and significantly heavier than Romosinuano-sired F1 cows.
- Brahman- and Bonsmara-sired F1 cows had slightly higher body condition scores at weaning in October than Beefmaster- and Romosinuano-sired F1 cows and significantly higher body condition score than Brangus-sired F1 cows.

Introduction
Output per cow has been greater for Bos indicus x Bos taurus F1 cows than for Bos taurus x Bos taurus F1 cows, especially in subtropical environments. However, in both temperate and subtropical environments, the advantages of Bos indicus x Bos taurus crosses has been tempered by reduced meat tenderness and lower levels of marbling as the proportion of Bos indicus was increased. Concern about these problems has prompted the introduction and evaluation of tropically adapted germplasm into the US. The present experiment was conducted to compare reproductive and maternal performance of F1 females by Beefmaster, Bonsmara, Brangus, and Romosinuano sires in Nebraska and in south Louisiana. First cross cows sired by Brahman bulls served as controls in Louisiana.

Materials and Methods
Semen from 20 Bonsmara, 20 Romosinuano, 22 Beefmaster, and 22 Brangus sires was used to artificially inseminate Angus and composite MARC III (1/4 Angus, 1/4 Hereford, 1/4 Red Poll, and 1/4 Pinzgauer) cows to produce F1 progeny in the spring of 2001 and 2002 at the U.S. Meat Animal Research Center, Clay Center, Nebraska. Bonsmara is a composite breed from South Africa with 5/8 Africaner, 3/16 Hereford, and 3/16 Shorthorn inheritance. Romosinuano was developed in Columbia and introduced into the US from Venezuela. Romosinuano is a Criollo breed which traces back to Bos taurus cattle introduced from Europe 400 to 500 years ago. Beefmaster is an American composite with about 1/2 Brahman, 1/4 Hereford, and 1/4 Shorthorn inheritance. Brangus is also an American composite with about 3/8 Brahman and 5/8 Angus inheritance. When the project started, Brangus and Beefmaster ranked 7th and 8th among beef breeds in registrations, respectively.

In 2001 and 2002, when calves were weaned in October, females sired by the four tropically adapted sire breeds were divided into two groups with about equal numbers per sire breed and sire-dam breed group. One group was transferred to the LSU Agricultural Center and the other group remained at MARC. Management of the F1 females and their progeny was consistent with that generally practiced in commercial
production systems in the respective location. At the Nebraska location, Hereford x Angus F₁ heifers born the same years as the tropically adapted F₁ calves, were introduced and managed as controls to the F₁ heifers. In Louisiana, Brahman x Angus F₁ females born in 2002 were purchased from seven different breeders in Louisiana and introduced as control heifers for the study.

At both locations heifers were exposed as yearlings to MARC III bulls selected for easy calving. Two-year-old and older females were exposed to Charolais bulls selected for easy calving. The breeding season began on April 15 in Louisiana and lasted for 75 days. In Nebraska, the breeding season began on May 1 and lasted for 60 days.

Calves were weaned in mid-September in Louisiana and late October in Nebraska, or when each calf crop averaged about 200 days of age. Calf weight and hip height was recorded at weaning. Cows were palpated at weaning of their calves or about 2 weeks later. Cows were weighed and given a body condition score when palpated.

Preliminary statistical analyses were conducted on the combined data from Nebraska and Louisiana. Of interest were the effects of location, sire breed of cow, location x sire breed of cow, dam breed of cow, cow age, year of record, and sex of calf (when appropriate). Only Beefmaster, Brangus, Bonsmara, and Romosinuano-sired F₁ females were included in the combined analyses. Secondary analyses were conducted for cows located in Louisiana. Brahman F₁ cows were included in these analyses.

Production traits of interest were weaning rate, calf birth date, calf birth weight, calf preweaning average daily gain, calf 205-day weaning weight, calf weaning height, and cow weight and body condition score at weaning.

Results and Discussion

Analysis of the combined data from Nebraska and Louisiana revealed several interesting results. There was no location x cow breed type interaction for any trait. Therefore, the ranking of cow breed types was about the same in each location. However, tropically adapted cow breed types in Nebraska (Beefmaster-, Bonsmara-Brangus- and Romosinuano-sired cows) had a 5% higher weaning rate and nursed calves that gained 0.2 lb/d more during the nursing period than the same tropically adapted cow breed types in Louisiana. These results suggest that, during this period of time, the Nebraska environment was superior for cow-calf production to the environment in Louisiana.

Data collected in Louisiana included information on the control Brahman F₁ cows. Least square means and standard errors for selected traits recorded in Louisiana are given in Table 1. Slightly over 240 cows contributed data in Louisiana and slightly over 1000 calf records were available for study.

A few of the Brahman F₁ heifers purchased in 2003 were born in May and June of 2002. These heifers did not reach puberty early enough to successfully breed during the breeding season resulting in a weaning rate of 33 ± 5% as 2 year olds. Weaning rates of the other breed types of heifers were not different from each other, ranging from 67 ± 5% for Romosinuano-sired F₁ females to 73 ± 4% for Brangus-sired F₁ females. Weaning rates for cows 3 years and older were not different among cow breed types, ranging from 81 ± 4% for Brahman and Brangus-sired F₁ females to 86 ± 3% for Romosinuano-sired F₁ females.

No differences were found among cow breed types for calf birth date or for calf birth weight. The average calving date was the 14th of February. Average birth weight was 81 lbs. Least square means and standard errors for birth weights ranged from 79 ± 1 lb for calves from Brahman F₁.
cows to 83 ± 1 lb for calves from Beefmaster-sired F1 cows.

Calf average daily gain (ADG) was significantly influenced by cow breed types. Calf ADG ranged from 2.3 ± 0.03 lb/d for calves nursing Brahman F1 cows to 1.9 ± 0.02 lb/d for calves nursing Brangus- and Romosinuano-sired F1 cows. Calves nursing Beefmaster- and Bonsmara-sired F1 cows averaged 2.0 ± 0.02 lb/d.

Calf 205-day weaning weight from Brahman F1 cows was greater than from other F1 cows. Heavier weaning weights of calves nursing Brahman F1 cows was most likely due to the superior maternal ability of the Brahman F1 cows as the calves gained at least 0.3 lb/d more than any of the other calves.

Least square means for October cow weights ranged from 1285 ± 11 lb for Brahman F1 cows to 1212 ± 9 lb for Romosinuano F1 females. Brahman- and Bonsmara-sired F1 cows tended to be slightly fatter and Brangus-sired F1 cows tended to be slightly thinner throughout the year than other breed types.

In summary, only small differences existed among these tropically adapted cow breed types for most production traits. However, it is clear that the Brahman F1 cows had greater maternal ability than the other cow breed types resulting in greater calf ADG and adjusted 205-day weaning weight.

Table 1. Least square means and standard errors for cow production traits recorded in Louisiana due to breed type of cow.

<table>
<thead>
<tr>
<th>Breed type of cow</th>
<th>2-yr-old weaning rate, %</th>
<th>3+ yr-old weaning rate, %</th>
<th>Calf average daily gain, lb/d</th>
<th>Calf 205-d wt, lb</th>
<th>Cow October wt, lb</th>
<th>Cow October BCS</th>
</tr>
</thead>
<tbody>
<tr>
<td>Brahman F1</td>
<td>33 ± 5</td>
<td>81 ± 4</td>
<td>2.3 ± 0.03</td>
<td>546 ± 6</td>
<td>1285 ± 11</td>
<td>5.8 ± 0.1</td>
</tr>
<tr>
<td>Beefmaster F1</td>
<td>69 ± 5</td>
<td>84 ± 3</td>
<td>2.0 ± 0.02</td>
<td>495 ± 4</td>
<td>1271 ± 8</td>
<td>5.6 ± 0.1</td>
</tr>
<tr>
<td>Bonsmara F1</td>
<td>71 ± 5</td>
<td>82 ± 3</td>
<td>2.0 ± 0.02</td>
<td>489 ± 4</td>
<td>1250 ± 9</td>
<td>5.8 ± 0.1</td>
</tr>
<tr>
<td>Brangus F1</td>
<td>73 ± 4</td>
<td>81 ± 3</td>
<td>1.9 ± 0.02</td>
<td>474 ± 4</td>
<td>1254 ± 8</td>
<td>5.4 ± 0.1</td>
</tr>
<tr>
<td>Romosinuano F1</td>
<td>67 ± 5</td>
<td>86 ± 3</td>
<td>1.9 ± 0.02</td>
<td>473 ± 4</td>
<td>1212 ± 9</td>
<td>5.6 ± 0.1</td>
</tr>
</tbody>
</table>
Polymorphism in E2FB, UASMS1, UASMS2, A1457G, and C963T Genetic Markers at the Leptin Locus in Brahman Steers and their Association with Carcass Traits

D. E. Franke, T. D. Bidner, M. A. Persica III, School of Animal Sciences and M. C. Canal, Central Research Station

Findings

- In these Brahman steers, the variation among genotypes in all genetic markers was limited and frequencies of favorable alleles were lower than reported in Bos taurus cattle.
- Leptin genetic markers E2FB and C936T were weakly associated with marbling score in these Brahman steers.
- Although several genetic markers appear to be informative in these Brahman cattle, additional data is necessary to confirm frequencies and influences of these genetic markers.

Introduction

Louisiana has approximately 500,000 beef cows managed in some 12,000 operations throughout the state. Most of these operations produce feeder calves that are sold at weaning and a majority of the cows contain some degree of Brahman inheritance. Brahman x Angus and Brahman x Hereford first-cross cows have been recognized for their advantages in fertility and maternal ability. Other Brahman composite commercial cows also may be useful. One concern in crossbreeding systems is that Brahman-sired steers that have been fed in commercial feedlots have been recognized for lower carcass quality and less tender meat when compared to non-Brahman influenced cattle.

One possible solution to earlier identification of steers that will produce acceptable carcasses is to assay for genetic markers for major genes that influence specific traits in the Brahman that increases their acceptability. Genetic markers are sections of DNA that are part of, or closely associated with, specific genes and can be identified by laboratory procedures. Major genes are those that have larger effects on animal performance than minor genes.

Several major genes at a leptin locus have been associated with deposition of fat over the loin and intramuscular fat in growing cattle, in fat deposition of milk and energy balance of dairy cattle, and in postpartum estrus traits in beef and dairy cattle. Therefore, the objective of this study was to investigate the frequency of genetic marker genotypes at the leptin locus in this sample of Brahman steers and their association with several important carcass traits.

Materials and Methods

Spring-born purebred paternal half-sib Brahman bull calves (n=467) were purchased at weaning from 17 Brahman producers in Louisiana over a five-year period (1996 to 2000). After purchase, calves were transported to the LSU AgCenter Central Station in Baton Rouge where they were castrated, dehorned if necessary, dewormed and vaccinated for appropriate diseases. Calves were backgrounded through autumn each year and placed on ryegrass around the first of December. Calves were grazed for an average of 120 days per year over the five-year period and then shipped to south Texas for feeding. Yearlings were harvested from the feedlot in two or three groups each year as groups reached about 0.4 inch fat thickness and weighed approximately 1150 to 1200 lb. All calves were processed at a major packing plant in Corpus Christi, TX where a Texas A&M Extension Meat...
Scientist recorded carcass data 24 hours post mortem and supervised the removal of a primal wholesale rib from each steer for shipment to the LSU Animal Science Department Meats Laboratory. Two, one-inch thick steaks were cut from the large end of each primal rib, trimmed, vacuum-packaged and assigned to 7- or 14-day aging.

Each year after steaks from all steers had been aged and frozen they were thawed and cooked to medium doneness for evaluation. Six half-inch cores were taken from each cooked steak parallel to muscle fibers and the shear force recorded for each core. The average of shear forces from the six cores taken from each steak became the measure of shear force for tenderness for each steer.

Blood samples were taken from each steer during the grazing period. DNA was extracted from the white blood cells and frozen for later assay. When all the steers had been harvested, DNA was shipped to Igenity, a partner with Merial, LLC, for determination of E2FB, UASMS1, UASMS2, A1457G, and C963T genetic marker genotypes at the leptin locus in each steer.

Statistical analyses were completed using the Statistical Analysis System (SAS) computer package. Mixed model analysis in SAS was used to determine the association of genetic markers with carcass and tenderness traits. The statistical model included year-harvest group of steers and E2FB, A1457G, and C963T genetic markers as fixed effects and sire of steer as a random effect.

Results and Discussion

Frequencies of genetic marker genotypes and alleles are given in Table 1. It is clear that even though these Brahman steers came from 17 different herds and 66 different sires, the distribution of genotypes is skewed toward one homozygote or the other. For example, no TT genotype was found for genetic marker UASMS2, resulting in frequencies of 0.991 for allele C and 0.009 for allele T. Generally, when the minor allele frequency is less than 10%, one should not place a lot of emphasis in the statistical results associating genotypes with phenotypes. Genetic markers E2FB and A1457G had minor allele frequencies of 19.5 and 17.3%, respectively, whereas genetic markers UASMS1 and C963T had minor allele frequencies near 10%.

The genetic marker genotypic frequencies found in these Brahman steers are different from those found in Bos taurus steers in the US and Canada where all the leptin marker genotypes appear more balanced. Two of the genetic markers (UASMS1 and C963T) were redundant, meaning that their genotypes across steers were nearly the same. Therefore, the genetic marker UASMS1 was deleted from further analyses. Also, genetic marker UASMS2 was omitted from analyses because adequate variation was not found.

No strong associations were shown between E2FB, A1457G, and C963T genetic marker genotypes and carcass traits in these Brahman steers. Slight associations were shown between marbling score and genotypes of E2FB and C963T genetic markers (P < 0.08). Least squares means for marbling score were 392 ± 4, 400 ± 5, and 362 ± 18 for E2FB genotypes CC, CT, and TT, respectively. Canadian researchers also reported higher marbling scores associated with the E2FB allele C in Bos taurus steers.

For the C963T genetic marker, least squares means for marbling score were 391 ± 3, 409 ± 7, and 375 ± 38 for genotypes CC, CT and TT, respectively. Canadian researchers also reported that allele C was associated with greater marbling score.

Least squares means for calpastatin enzyme level were 4.3 ± 0.06, 4.4 ± 0.08 and 5.2 ± 0.4 for A1457G genetic marker genotypes AA, AG and GG. Higher levels of calpastatin enzyme level are associated with more tender beef. However, no association was shown between A1457G
genotypes and shear force of steaks aged for 7 or 14 days in these steers.

In summary, frequencies of favorable genetic marker alleles in these Brahman steers were lower than found in *Bos taurus* cattle. Because the frequencies of one allele in each genetic marker were low, additional data will be necessary to confirm the use of these genetic markers in Brahman steers.

Table 1. Genotypic and allelic frequencies for genetic markers at a leptin locus in Brahman steers.

<table>
<thead>
<tr>
<th>Genetic Marker</th>
<th>Genotype</th>
<th>No of steers</th>
<th>Genotypic Frequency</th>
<th>Allele</th>
<th>Allelic Frequency</th>
</tr>
</thead>
<tbody>
<tr>
<td>E2FB</td>
<td>CC</td>
<td>245</td>
<td>0.633</td>
<td>C</td>
<td>0.805</td>
</tr>
<tr>
<td></td>
<td>CT</td>
<td>133</td>
<td>0.344</td>
<td>T</td>
<td>0.195</td>
</tr>
<tr>
<td></td>
<td>TT</td>
<td>9</td>
<td>0.023</td>
<td></td>
<td></td>
</tr>
<tr>
<td>UASMS1&lt;sup&gt;a&lt;/sup&gt;</td>
<td>CC</td>
<td>3</td>
<td>0.008</td>
<td>C</td>
<td>0.098</td>
</tr>
<tr>
<td></td>
<td>CT</td>
<td>70</td>
<td>0.180</td>
<td>T</td>
<td>0.902</td>
</tr>
<tr>
<td></td>
<td>TT</td>
<td>316</td>
<td>0.812</td>
<td></td>
<td></td>
</tr>
<tr>
<td>UASMS2&lt;sup&gt;a&lt;/sup&gt;</td>
<td>CC</td>
<td>381</td>
<td>0.982</td>
<td>C</td>
<td>0.991</td>
</tr>
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<td></td>
<td>CT</td>
<td>7</td>
<td>0.018</td>
<td>T</td>
<td>0.009</td>
</tr>
<tr>
<td></td>
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<td>0</td>
<td>0.000</td>
<td></td>
<td></td>
</tr>
<tr>
<td>A1457G</td>
<td>AA</td>
<td>251</td>
<td>0.669</td>
<td>A</td>
<td>0.827</td>
</tr>
<tr>
<td></td>
<td>AG</td>
<td>118</td>
<td>0.315</td>
<td>G</td>
<td>0.173</td>
</tr>
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<td></td>
<td>GG</td>
<td>6</td>
<td>0.016</td>
<td></td>
<td></td>
</tr>
<tr>
<td>C963T</td>
<td>CC</td>
<td>312</td>
<td>0.819</td>
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<td>0.907</td>
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<tr>
<td></td>
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<td>0.176</td>
<td>T</td>
<td>0.093</td>
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<tr>
<td></td>
<td>TT</td>
<td>2</td>
<td>0.005</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<sup>a</sup>Due to a low frequency of one allele and/or a redundancy of genotypes with another marker (i.e. UASMS1 and C963T) there were no further analyses of these genetic markers in association with phenotypic differences in marbling score, Warner-Bratzler shear force values (tenderness), or calpastatin enzyme level.
<table>
<thead>
<tr>
<th>Genetic Marker Genotypes</th>
<th>HCWT(^a), kg</th>
<th>FT, cm</th>
<th>REA, sq cm</th>
<th>MS</th>
<th>SF7, kg</th>
<th>SF14, kg</th>
</tr>
</thead>
<tbody>
<tr>
<td>E2FB</td>
<td>0.636(^b)</td>
<td>0.463</td>
<td>0.362</td>
<td>0.073</td>
<td>0.422</td>
<td>0.680</td>
</tr>
<tr>
<td>CC</td>
<td>338 ± 2</td>
<td>0.89 ± 0.02</td>
<td>86.6 ± 0.5</td>
<td>392 ± 4</td>
<td>4.4 ± 0.06</td>
<td>3.8 ± 0.06</td>
</tr>
<tr>
<td>CT</td>
<td>340 ± 3</td>
<td>0.89 ± 0.03</td>
<td>85.5 ± 0.7</td>
<td>400 ± 5</td>
<td>4.5 ± 0.09</td>
<td>3.9 ± 0.06</td>
</tr>
<tr>
<td>TT</td>
<td>335 ± 10</td>
<td>1.04 ± 0.12</td>
<td>83.9 ± 2.8</td>
<td>362 ± 18</td>
<td>4.3 ± 0.33</td>
<td>3.7 ± 0.24</td>
</tr>
<tr>
<td>A1457G</td>
<td>0.267</td>
<td>0.784</td>
<td>0.671</td>
<td>0.207</td>
<td>0.697</td>
<td>0.114</td>
</tr>
<tr>
<td>AA</td>
<td>339 ± 2</td>
<td>0.89 ± 0.02</td>
<td>86.4 ± 0.5</td>
<td>392 ± 4</td>
<td>4.4 ± 0.06</td>
<td>3.8 ± 0.05</td>
</tr>
<tr>
<td>AG</td>
<td>340 ± 3</td>
<td>0.91 ± 0.04</td>
<td>85.6 ± 0.8</td>
<td>400 ± 5</td>
<td>4.7 ± 0.09</td>
<td>3.9 ± 0.07</td>
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<tr>
<td>GG</td>
<td>320 ± 12</td>
<td>0.85 ± 0.15</td>
<td>85.3 ± 3.5</td>
<td>366 ± 22</td>
<td>4.7 ± 0.41</td>
<td>4.1 ± 0.30</td>
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<tr>
<td>C963T</td>
<td>0.534</td>
<td>0.829</td>
<td>0.862</td>
<td>0.056</td>
<td>0.757</td>
<td>0.994</td>
</tr>
<tr>
<td>CC</td>
<td>338 ± 2</td>
<td>0.88 ± 0.02</td>
<td>86.0 ± 0.5</td>
<td>391 ± 3</td>
<td>4.5 ± 0.06</td>
<td>3.8 ± 0.04</td>
</tr>
<tr>
<td>CT</td>
<td>342 ± 4</td>
<td>0.91 ± 0.04</td>
<td>86.3 ± 1.1</td>
<td>409 ± 7</td>
<td>4.4 ± 0.12</td>
<td>3.8 ± 0.10</td>
</tr>
<tr>
<td>TT</td>
<td>332 ± 21</td>
<td>0.84 ± 0.26</td>
<td>86.1 ± 6.0</td>
<td>375 ± 38</td>
<td>4.4 ± 0.70</td>
<td>3.8 ± 0.50</td>
</tr>
</tbody>
</table>

\(^a\)HCWT = hot carcass weight, FT = fat thickness, REA = ribeye area, MS = marbling score, SF7 = shear force of steaks aged for 7 days, and SF14 = shear force of steaks aged for 14 days.

\(^b\)Significance level
Breed and Genetic Effects on Internal Parasitism, Hair Coat Scores, and Postweaning Liveweight Gains in Angus and Brahman-Influenced Replacement Heifers

W. E. Wyatt, Iberia Research Station, D. E. Franke, School of Animal Sciences, J. E. Miller, Department of Pathobiological Sciences, LSU School of Veterinary Medicine, S. M. DeRouen, Hill Farm Research Station and D. C. Blouin, Department of Experimental Statistics

Findings

• Fecal egg counts (indicator of internal parasitism) were similar between Angus and Brahman-influenced heifers at the Iberia station, but were higher for Brahman-influenced compared to Angus heifers at the Central Research Station.

• Sufficient genetic variation exists for selection for fecal egg count, hair luster and length scores, and postweaning ADG to be effective.

Introduction

Research has shown the positive economic impact that controlling internal parasites has on cow-calf operations. Unfortunately, doing so represents a significant input cost and can cost as much as $10 per cow per year to deworm a cow twice annually (assuming an 1100 lb cow) with an effective anthelmintic product. There is growing concern among the consuming public regarding the use of drugs in meat-producing animals in terms of drug residues. Also, there is some suggestion that continued use of anthelmintic products could lead to the development of a resistant parasite (helminth; i.e., worms) population. All of these factors prompted research scientists in the South and Midwest regions of the United States to collaborate on a regional project (S-1013) entitled “Genetic (Co)Variance of Parasite Resistance, Temperament, and Production Traits of Traditional and Non-Bos Indicus Tropically Adapted Breeds”. The research presented here specifically addresses the objective to “Determine genetic variation in temperament and parasite resistance in beef cattle and their association with economically important traits”. It is important to determine if there is sufficient genetic variation that we might select for resistance to parasitism in beef cattle.

Experimental Approach

Spring-born Angus (131; 17 sires) and Brangus (108; 16 sires) heifers, reared at the Iberia Research Station, were weaned in the fall of their respective birth year (2003-2007; no Brangus heifers were used in 2003) and retained as replacement females (Table 1). Similarly, spring-born Angus (56; 14 sires) and Braford (50; 17 sires) heifers, reared at the Central Research Station, were also weaned in the fall of their respective birth year (2003-2007) and retained as herd replacement females (Table 1). A portion of the Angus heifers at both locations were sired by a common Angus bull (artificial insemination).

At weaning, or within approximately 6 weeks following weaning, heifers were orally administered a fenbendazole drench (10 mg kg⁻¹; Safeguard®). The day heifers were initially dewormed was considered day 0 of the trial for each year. Fecal samples were obtained by rectal palpation on approximate 42-day intervals throughout the postweaning growth period (i.e., 6-8 samplings per heifer). Fecal samples were placed in Styrofoam cups with sealable lids, refrigerated (approximately 39° F),
transported to the Veterinary Science department for analyses (i.e., fecal nematode egg counts and coproculture larvae counts).

Hair luster and length scores were evaluated 4 to 8 times (coincidental with fecal sampling) during the postweaning period.

Within each location, heifers were maintained as one group until on or about April 15 of each year, at which time they were randomly allotted to single sire breeding herds (straightbred matings) for an approximate 80-day breeding season each year (terminating on or about July 5). Annual trials were terminated 1 to 5 weeks following the end of the breeding season. Postweaning gain was calculated based upon first and last weights (260-290 day period).

Fecal egg count data were transformed (EPG; log10 + 1) and day 0 data were deleted. Transformed fecal egg counts and hair scores were pooled (i.e., averaged) within each heifer for purpose of statistical analyses. Postweaning average daily gain (ADG) was calculated for each heifer.

Breed estimates in EPG, hair scores, and postweaning ADG were obtained through the Proc Mixed (REML) procedure within SAS. Year and sire within location by breed were included as random effects. Location, breed, and location x breed were included as fixed effects.

Heritability ($h^2$) and genetic correlation ($r_g$) estimates were obtained using the MTDFREML program. Data were coded for sire, dam, paternal grandsire, paternal granddam, maternal grandsire, and maternal granddam. There were a total of 999 animals with 670 pedigrees used in the analyses. Fixed effects included year, location, and breed type.

Results and Discussion

Fecal egg count (FEC) during the postweaning period was affected ($P < 0.05$) by the location by breed interaction (Table 2). There was no difference between Angus (AN) and Brahman-influenced (BI) heifers at the Iberia station location, but a higher count was observed for BI compared to AN at the Central station location. This was a bit surprising in that previous research, conducted at the Iberia Research Station, had shown that BI cattle had less internal parasitism than British breeds of cattle (Pena, M. T., J E. Miller, W. Wyatt, and M. T. Kearney. 2000. Differences in susceptibility to gastrointestinal nematode infection between Angus and Brangus cattle in south Louisiana. Veterinary Parasitology 89: 51-61).

Hair luster score (5-point score with lower indicating healthier hair coat) was consistently greater ($P < 0.01$) for AN than BI heifers at both locations (Table 2). Hair length score (5-point score with lower indicating shorter hair) was shorter in BI than in AN heifers at both locations, but the breed difference was greater at the Central compared to the Iberia station ($P < 0.01$).

Postweaning ADG was 25% greater ($P < 0.01$) for heifers at the Central compared to the Iberia station (Table 2). Brahman-influenced and AN heifers had similar rates of postweaning gain at the Central station, but BI gained faster than AN heifers during the postweaning period at the Iberia station ($P = 0.11$).

A review of some genetic principles is warranted before proceeding with discussion of Table 3 (information that follows is adapted from the LSU AgCenter’s Master Cattle Producer program and the Beef Improvement Federation’s Guidelines for Uniform Beef Improvement Programs, 8th edition, 2002).

- What can be physically seen or measured can be expressed by the equation:
\( P = G + E; \) where \( P = \text{Phenotype}, \) "what we see"; \( G = \text{Genotype}, \) "true breeding value"; and \( E = \text{Environment}, \) "temporary and permanent environmental effects, e.g., uterine environment, weather, nutrition, forage availability and quality, etc."

- **Breeding value** – The value of an animal as a parent. An individual transmits \( \frac{1}{2} \) of its breeding value to the offspring.

- **Heritability** \((h^2)\) – The proportion of a trait difference among cattle, measured or observed, that is transmitted to the offspring. Heritability varies from zero to one and is expressed as a percent, conventional ranges are as follows: lowly \( h^2 \) = estimates less than 20%, moderately \( h^2 \) = estimates from 20 – 40%, and highly \( h^2 \) = estimates greater than 40%.

- **Selection** – Causing or allowing certain individuals in a population to produce offspring in the next generation. The old concept of “breeding the best to the best” still applies.

- **The higher the heritability** of a trait, the more precisely does the individual performance predict breeding value and the more rapid should be the response due to selection for that trait.

- **Genetic correlations** – Correlations between breeding values for two traits that arise because some of the same genes affect both of them. When two traits (weaning and yearling weight for example) are positively genetically correlated, successful selection for one trait will result in an increase in the other trait as well. When two traits are negatively genetically correlated (birth weight and calving ease, for example), successful selection for one trait will result in a decrease in the other.

Heritability and genetic correlations are presented in Table 3. The reader is cautioned that the number of animals used in this study is not sufficient to obtain highly precise estimates of heritability and genetic correlations. The regional data set, involving other states, will provide more precise estimates. However, heritability estimates for fecal egg count (51%), hair coat luster (80%) and length (80%) scores, and postweaning ADG (36%) were all in the moderate to high range, suggesting that selection for these traits would likely be effective. The genetic correlations among these traits weren’t particularly enlightening (due to lack of precision and perhaps accuracy of the estimates, i.e., high standard errors), but it appears possible (i.e., \( r_g = -0.16 \pm 0.26 \)) that selection for postweaning ADG could result in lower fecal egg counts to some extent.

Table 1. Number of spring-born, fall-weaned heifers by location and year.

<table>
<thead>
<tr>
<th>Birth year</th>
<th>Iberia Research Station</th>
<th>Central Research Station</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Angus</td>
<td>Brangus(^a)</td>
</tr>
<tr>
<td>2003</td>
<td>41</td>
<td>5</td>
</tr>
<tr>
<td>2004</td>
<td>29</td>
<td>31</td>
</tr>
<tr>
<td>2005</td>
<td>41</td>
<td>38</td>
</tr>
<tr>
<td>2006</td>
<td>10</td>
<td>29</td>
</tr>
<tr>
<td>2007</td>
<td>10</td>
<td>10</td>
</tr>
<tr>
<td>Total</td>
<td>131</td>
<td>108</td>
</tr>
</tbody>
</table>

\(^a\)Brangus and Braford heifers were classified as Brahman-influenced for analyses.
Table 2. Location, breed, and location by breed least-squares means for fecal egg count, hair luster and length scores, and postweaning ADG.

<table>
<thead>
<tr>
<th>Effect</th>
<th>FEC (^{adgi})</th>
<th>Hair luster score (^{bf})</th>
<th>Hair length score (^{cdefh})</th>
<th>Postweaning ADG, lb (^{dg})</th>
</tr>
</thead>
<tbody>
<tr>
<td>Location</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Central</td>
<td>31.6</td>
<td>1.8</td>
<td>2.4</td>
<td>1.56</td>
</tr>
<tr>
<td>Iberia</td>
<td>15.8</td>
<td>1.9</td>
<td>2.1</td>
<td>1.24</td>
</tr>
<tr>
<td>Breed</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Angus (AN)</td>
<td>15.8</td>
<td>1.9</td>
<td>2.7</td>
<td>1.37</td>
</tr>
<tr>
<td>Brahman-influenced (BI)</td>
<td>25.1</td>
<td>1.7</td>
<td>1.8</td>
<td>1.43</td>
</tr>
<tr>
<td>Location x breed</td>
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<td></td>
<td></td>
</tr>
<tr>
<td>Central-AN</td>
<td>20.0</td>
<td>2.0</td>
<td>3.1</td>
<td>1.56</td>
</tr>
<tr>
<td>Central-BI</td>
<td>50.1</td>
<td>1.6</td>
<td>1.8</td>
<td>1.57</td>
</tr>
<tr>
<td>Iberia-AN</td>
<td>15.8</td>
<td>1.9</td>
<td>2.3</td>
<td>1.17</td>
</tr>
<tr>
<td>Iberia-BI</td>
<td>15.8</td>
<td>1.8</td>
<td>1.8</td>
<td>1.31</td>
</tr>
<tr>
<td>SE</td>
<td>0.2</td>
<td>0.1</td>
<td>0.2</td>
<td>0.07</td>
</tr>
</tbody>
</table>

\(^{a}\)FEC = fecal egg count (eggs per gram of feces; non-transformed).

\(^{b}\)Five-point subjective hair luster score: 1 = glossy, healthy appearance; 2 = slightly glossy with patches of dull; 3 = intermediate between glossy and dull; 4 = mostly dull, some indication of unthriftiness; and 5 = dull and unthrifty.

\(^{c}\)Five-point subjective hair length score: 1 = short; 2 = shows some winter growth; 3 = intermediate in length; 4 = long in places, but intermediate in others; and 5 = long.

\(^{d}\)Location effect (P < 0.01 and P < 0.05, respectively).

\(^{e}\)Breed effect (P < 0.01 and P < 0.05, respectively).

\(^{h}\)Location x breed effect (P < 0.01 and P < 0.05, respectively).

---

Table 3. Heritability (h\(^2\)) estimates for fecal egg count (FEC), hair luster and length scores, and postweaning ADG and genetic correlations (r\(_{ij}\)) between postweaning ADG and remaining traits.

<table>
<thead>
<tr>
<th>Traits</th>
<th>FEC</th>
<th>Hair luster</th>
<th>Hair length</th>
<th>ADG, lb</th>
</tr>
</thead>
<tbody>
<tr>
<td>FEC</td>
<td>0.51 ± 0.133(^{a})</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Hair luster</td>
<td>0.18 ± 0.192(^{b})</td>
<td>0.80 ± 0.129(^{a})</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Hair length</td>
<td>0.05 ± 0.186(^{b})</td>
<td>0.80 ± 0.136(^{a})</td>
<td></td>
<td></td>
</tr>
<tr>
<td>ADG</td>
<td>-0.16 ± 0.259(^{b})</td>
<td>0.15 ± 0.227(^{b})</td>
<td>0.09 ± 0.248(^{b})</td>
<td>0.36 ± 0.145(^{a})</td>
</tr>
</tbody>
</table>

\(^{a}\)Heritability estimates appear on the diagonal.

\(^{b}\)Genetic correlation estimates are below the diagonal.
Breed and Genetic Effects on Temperament Traits and Postweaning Liveweight Gains in Angus and Brahman-influenced Replacement Heifers

W. E. Wyatt, Iberia Research Station, D. E. Franke, School of Animal Sciences, S. M. DeRouen, Hill Farm Research Station, D. C. Blouin, Department of Experimental Statistics and J. E. Miller, Department of Pathobiological Sciences, LSU School of Veterinary Medicine

Findings

- Measures of heifer temperament (i.e., chute scores and exit velocities) were generally similar between Angus and Brahman-influenced heifers, although the latter scored higher (worse temperament) than Angus heifers at the Central Research Station.

- Temperament in cattle is subject to a level of genetic control (moderate heritability estimates) and therefore selection against ill temperament should be effective in Angus and Brahman-influenced heifers.

- Also, there appears to be a genetic antagonism (negative genetic correlations) between these measures of temperament and heifer postweaning growth, i.e., selection against ill temperament should result in improved postweaning ADG in heifers.

Introduction

Considerable research has shown that carcass and meat quality are affected by temperament. In general terms, the more excitable an animal is, the tougher the meat will be. Also, those animals often may not gain as much weight as calmer animals. Less research has been directed at determining the effect differences in temperament (disposition) may have on heifer productivity. Excitable heifers may not perform as well in terms of reproductive development and performance. It is important to determine the genetic relationship between temperament and growth in developing heifers. Also, does sufficient genetic variation exist that we might effectively select against ill temperament in beef cattle? These concerns prompted research scientists in the South and Midwest regions of the United States to collaborate on a regional project (S-1013) entitled “Genetic (Co)Variance of Parasite Resistance, Temperament, and Production Traits of Traditional and Non-Bos Indicus Tropically Adapted Breeds”. The research presented here specifically addresses the objective to “Determine genetic variation in temperament and parasite resistance in beef cattle and their association with economically important traits”.

Experimental Approach

Spring-born Angus (131; 17 sires) and Brangus (108; 16 sires) heifers, reared at the Iberia Research Station, were weaned in the fall of their respective birth year (2003-2007; no Brangus heifers were used in 2003) and retained as replacement females (Table 1). Similarly, spring-born Angus (56; 14 sires) and Braford (50; 17 sires) heifers, reared at the Central Research Station, were weaned in the fall of their respective birth year (2003-2007) and retained as herd replacement females (Table 1). A portion of the Angus heifers at both locations were sired by a common Angus bull (artificial insemination).
Within 6 weeks following weaning, heifers were weighed (day 0), scored for chute temperament, and time required to traverse 6 feet following exiting of the chute was recorded. Within each location, heifers were maintained as one group until mid-April of each year, at which time they were randomly allotted to single sire breeding herds (straightbred matings) for an approximate 80-day breeding season each year. Annual trials were terminated 1 to 5 weeks following the end of the breeding season, at which time heifers were weighed once again. Postweaning gain was calculated based upon first and last weights (260- to 290-day period) and was expressed as average daily gain (ADG).

Chute temperament score and time required to travel 6 feet were obtained in the following manner. Heifers entered the squeeze chute (quietly and gently handled without use of “hotshot”) and were immediately scored for chute behavior temperament using a 5-point subjective scoring system (i.e., 1 = calm, stands still, no movement; 2 = slightly restless; 3 = restless, shaking chute; 4 = vigorously shaking the chute; and 5 = extremely excited). Heifers diving to the floor of the squeeze chute were automatically given a chute temperament score of 4. Subsequently, squeeze chute side pressure was applied and heifers were weighed. Side pressure was released and the front gate was opened allowing the heifer to exit. Heifers exited straight ahead into a fenced lane, which lead to a loafing pen. A set of electronic timing “eyes” (initiate timing) were placed 6 feet and a second set of “eyes” (terminate timing) were placed 12 feet from the front of the squeeze chute. Velocity (i.e., feet per second) was calculated based upon the elapsed time to traverse the 6 feet between the electronic timing devices. Consequently, heifers exiting the squeeze chute at a faster speed (i.e., greater distance traveled per second) were interpreted as having poorer or worse temperament than heifers exiting at a slower speed (i.e., less distance traveled per second), which were interpreted as being less excitable and having a calmer temperament. Both chute temperament score and exit velocity was obtained 3 to 8 times for each heifer during the postweaning period (heifers were weighed on approximate 45-d intervals during the postweaning period, but chute temperament and exit velocities weren’t assessed or measured each time).

Chute temperament score and exit velocity were pooled (i.e., averaged) within each heifer for purpose of statistical analyses. Postweaning ADG was calculated for each heifer. Brangus, at the Iberia Research Station, and Braford, at the Central Research Station, were recoded as “Brahman-influenced” (% British - % Brahman).

Breed estimates in chute temperament score, chute exit velocity, and postweaning ADG were obtained through the Proc Mixed (REML) procedure within SAS. Year and sire within location by breed were included as random effects. Location, breed, and location x breed were included as fixed effects.

Heritability ($h^2$) and genetic correlations ($r_g$) estimates were obtained using the MTDFREML program. Data were coded for sire, dam, paternal grandsire, paternal granddam, maternal grandsire, and maternal granddam. There were a total of 999 animals with 670 pedigrees used in the analyses. Fixed effects included year, location, and breed type.

**Results and Discussion**

Chute temperament score was affected ($P < 0.05$) by the location by breed type interaction (Table 2). Brahman-influenced heifers at the Central Research Station were more excitable than Angus heifers, but both Brahman-influenced and Angus heifers received similar chute temperament scores at the Iberia Research Station. It is unclear as to why the breed differences varied between the two research stations. However, chute exit velocities were similar
between Angus and Brahman-influenced heifers at both locations (Table 2), although greater ($P < 0.01$) velocities were observed for heifers at the Iberia Research Station compared to the Central Research Station. Postweaning ADG was 25% greater ($P < 0.01$) for heifers at the Central Research Station compared to the Iberia Research Station (Table 2). Brahman-influenced and Angus heifers had similar rates of postweaning gain at the Central station, but Brahman-influenced gained faster than Angus heifers during the postweaning period at the Iberia Research Station ($P = 0.11$).

Heritability and genetic correlations are presented in Table 3. A review of genetic terms is presented in the preceding article (covering internal parasitism resistance and hair coat scores of these same heifers). The reader is cautioned that the number of animals used in this study is not sufficient to obtain highly precise estimates of heritability and genetic correlations. The regional data set, involving other states, will provide more precise estimates.

Heritability estimates for chute temperament score (34%), chute exit velocity (19%), and postweaning ADG (36%) were in the moderate range, suggesting that selection for these traits would likely be effective (Table 3). The heritability estimate for chute temperament score is somewhat higher than estimates reported in Australia (20% on Brahman, Belmont Red, and Santa Gertrudis cattle) and Brazil (20% on Nelore cattle). The heritability estimate for chute exit velocity was very similar to that obtained on tropically adapted British, Sanga-derived, and Zebu cross cattle in Australia. The genetic correlation estimates of temperament traits (chute score and exit velocity) with postweaning ADG were highly negative ($-0.85 \pm 0.260$ and $-0.97 \pm 0.489$, respectively), but were highly variable (i.e., high standard errors; the reader may interpret this to mean that the estimates are not very reliable). These negative correlations would indicate that selection against these traits would potentially result in animals with higher postweaning ADG, which would generally be considered a positive attribute in developing replacement heifers. In summary, these results suggest that bad temperament can effectively be selected against (using some measure of temperament) and would result in positive gain performance during the postweaning period.

<table>
<thead>
<tr>
<th>Birth year</th>
<th>Iberia Research Station</th>
<th>Central Research Station</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Angus</td>
<td>Brangus$^a$</td>
</tr>
<tr>
<td>2003</td>
<td>41</td>
<td>5</td>
</tr>
<tr>
<td>2004</td>
<td>29</td>
<td>31</td>
</tr>
<tr>
<td>2005</td>
<td>41</td>
<td>38</td>
</tr>
<tr>
<td>2006</td>
<td>10</td>
<td>29</td>
</tr>
<tr>
<td>2007</td>
<td>10</td>
<td>10</td>
</tr>
<tr>
<td>Total</td>
<td>131</td>
<td>108</td>
</tr>
</tbody>
</table>

$^a$Brangus and Braford heifers were classified as Brahman-Influenced (BI) for analyses.
Table 2. Location, breed, and location by breed least-squares means for chute temperament score, chute exit velocity, and postweaning ADG.

<table>
<thead>
<tr>
<th>Effect</th>
<th>Chute temperament score</th>
<th>Chute exit velocity, feet/sec</th>
<th>Postweaning ADG, lb</th>
</tr>
</thead>
<tbody>
<tr>
<td>Location</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Central</td>
<td>1.72</td>
<td>8.35</td>
<td>1.56</td>
</tr>
<tr>
<td>Iberia</td>
<td>1.76</td>
<td>9.79</td>
<td>1.24</td>
</tr>
<tr>
<td>Breed</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Angus (AN)</td>
<td>1.65</td>
<td>9.11</td>
<td>1.37</td>
</tr>
<tr>
<td>Brahman-influenced (BI)</td>
<td>1.84</td>
<td>9.03</td>
<td>1.43</td>
</tr>
<tr>
<td>Location x breed</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Central-AN</td>
<td>1.53</td>
<td>8.56</td>
<td>1.56</td>
</tr>
<tr>
<td>Central-BI</td>
<td>1.91</td>
<td>8.13</td>
<td>1.57</td>
</tr>
<tr>
<td>Iberia-AN</td>
<td>1.77</td>
<td>9.65</td>
<td>1.17</td>
</tr>
<tr>
<td>Iberia-BI</td>
<td>1.76</td>
<td>9.94</td>
<td>1.31</td>
</tr>
<tr>
<td>SE</td>
<td>0.10</td>
<td>0.76</td>
<td>0.07</td>
</tr>
</tbody>
</table>

*aChute temperament score is a 5-point subjective score: 1 = calm, stands still, no movement; 2 = slightly restless; 3 = restless, shaking chute; 4 = vigorously shaking the chute; and 5 = extremely excited.

*bChute exit velocity is a measure of the distance traversed (per second) as the heifer exited the squeeze chute.

*cLocation effect (P < 0.01).

*dBreed effect (P < 0.05).

*eLocation x breed effect (P < 0.05).

Table 3. Heritability (h²) and genetic correlations (r_g) estimates for temperament traits and postweaning ADG.

<table>
<thead>
<tr>
<th>Traits</th>
<th>Chute temperament score</th>
<th>Chute exit velocity</th>
<th>Postweaning ADG</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chute temperament score</td>
<td>0.34 ± 0.136a</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Chute exit velocity</td>
<td>0.51 ± 0.308b</td>
<td>0.19 ± 0.141a</td>
<td></td>
</tr>
<tr>
<td>Postweaning ADG</td>
<td>-0.85 ± 0.260b</td>
<td>-0.97 ± 0.489b</td>
<td>0.36 ± 0.145a</td>
</tr>
</tbody>
</table>

*aHeritability estimates appear on the diagonal.

*bGenetic correlation estimates are below the diagonal.