GENETIC AND ENVIRONMENTAL GROWTH TRAIT PARAMETER ESTIMATES FOR BRAHMAN AND BRAHMAN-DERIVATIVE CATTLE\(^1,2\)

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ABSTRACT

Beefmaster, Brahman, Brangus, and Santa Gertrudis field data records were used to determine genetic and environmental parameter estimates using a multiple-trait, pseudo-expectation approach. Adjusted birth weight, 205-d weight, and postweaning gain records were analyzed for each breed. Also, Brangus weaning sheath and navel scores were both analyzed using a single-trait, pseudo-expectation method to determine genetic parameter estimates. Additive birth weight heritability \((h^2_A)\) estimates ranged from .22 to .37 and maternal birth weight heritability \((h^2_M)\) estimates ranged from .12 to .55. Estimates for 205-d weight \(h^2_A\) for the four breeds varied from .21 to .25, and 205-d weight \(h^2_M\) estimates ranged from .15 to .21. Postweaning gain \(h^2_A\) estimates ranged from .16 to .56.

The genetic correlation between direct and maternal portions of birth weight was negative for all breeds. This was also true for the genetic correlation between direct and maternal portions of 205-d weight, except in Brahman cattle, for which it was .15. The genetic correlation between additive portions of birth weight and 205-d weight was large and positive in all breeds. A moderately positive correlation between 205-d weight and postweaning gain was found for all breeds except Santa Gertrudis, whereas the environmental correlation between these two traits was a small to moderately negative estimate in all breeds. Brangus weaning sheath and navel score heritability indicators indicated that genetic change for the size and shape of the sheath and navel area is possible.

Key Words: Growth Traits, Sheath and Navel Score, Brahman Cattle, Heritability, Genetic Effects, Environmental Effects


Introduction

Brahman and Brahman-derivative cattle, such as Brangus, Beefmaster, and Santa Gertrudis, are important beef cattle breeds in the southern and tropical regions of the United States. These cattle are heat- and disease-resistant and have become fixtures in the U.S. beef cattle industry. Genetic and environmental parameter estimates must be obtained for the development of sound breeding programs and National Cattle Evaluation (NCE) programs for these breeds.

Limited information is currently available on genetic and environmental parameter estimates for breeds of Brahman and Brahman-derivative cattle. Aaron et al. (1987) reported heritability and genetic correlation estimates for birth weight and weaning weight using a large herd of Santa Gertrudis cattle and found parameter estimates comparable to those of Bos taurus breeds of cattle. Also, Bertrand and Benyshek (1987) analyzed Brangus birth and weaning weight records and found parameter

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\(^{1}\)A portion of this research was funded by the American Brahman Breeders Association, Houston, TX, the Santa Gertrudis Breeders International, Kingsville, TX, the Beefmaster Breeders Universal, San Antonio, TX, and the International Brangus Breeders Association, San Antonio, TX.

\(^{2}\)This study was partially funded by the Georgia Agric. Exp. Sta. and was part of Hatch Project 873.

\(^{3}\)Anim. and Dairy Sci. Dept.

Received March 2, 1990.

Accepted December 7, 1990.
An important breed characteristic of Brahman and Brahman-derivative cattle is the shape and size of the navel or sheath area. It is undesirable to have too little or too much skin in these areas; excess skin poses possible reproductive and health problems, and insufficient skin represents a lack of breed character. There are few studies in the literature that address this problem or attempt to determine the genetic makeup of these traits.

Therefore, this study was conducted to determine 1) heritability and genetic and environmental correlation estimates for birth weight, weaning weight, and postweaning gain traits for Beefmaster, Brahman, Brangus, and Santa Gertrudis cattle using breed field data information and 2) heritability estimates for Brangus weaning sheath and navel scores.

Materials and Methods

Data Description. All information used in subsequent multiple-trait variance-covariance analyses came from NCE data pools. Breeds analyzed were Beefmaster, Brahman, Brangus, and Santa Gertrudis. Adjusted birth weight (BTHW), 205-d weight (WW), and adjusted 365-d weight (YWT) traits were provided in each data set along with birthdate of the calf, weaning and yearling weight dates, herd, sex, calf management information, and pedigree information. Each breed used Beef Improvement Federation (BIF) Guideline (1986) equations and age of dam correction factors to adjust birth weight and weaning weight records. Yearling weight records were also adjusted using the suggested 365-d weight equation. Adjusted postweaning gain (GAIN) was computed by subtracting WW from YWT. Weaning contemporary groups (WCG) were defined as herd, sex, weaning management code (creep vs no creep), and weaning weight date for each breed. Adjusted postweaning gain contemporary groups were subsets of WCG and also included yearling management code and yearling weight date. These definitions were the same as those used in each breed’s NCE analyses. Birth weight records were assigned to the animals’ WCG definition. This was done to simplify the variance component analyses because it was assumed that both traits analyzed were either defined by the same contemporary group or the second trait was a subset of the first trait. For each breed analyzed in this study, there were many more weaning weight records available for analysis than birth weight records. Thus, by assigning the birth weight record to the WCG definition, all weaning weight records were used in the multiple-trait model variance component procedures.

Subsets of the data were formed consisting of BTHW and WW, BTHW and GAIN, or WW and GAIN information for each breed. These data sets were then used in multiple-trait variance-covariance analyses to estimate variance and covariance parameters for each breed separately.

In addition to the above information, the International Brangus Breeders Association (IBBA) provided weaning sheath and navel scores. Sheath and navel scores were obtained by certified IBBA inspectors at weaning age. These scores ranged from 1 to 5, with a score

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**TABLE 1. SHEATH AND NAVAL SCORE DESCRIPTIONS IN BRANGUS CATTLE**

<table>
<thead>
<tr>
<th>Score</th>
<th>Sheath</th>
<th>Navel</th>
</tr>
</thead>
<tbody>
<tr>
<td>2 Optimum</td>
<td>The sheath is clean and free from excess leather. The prepucial opening is held at a 45° angle to the body wall.</td>
<td>The navel is clean and free from excess leather.</td>
</tr>
<tr>
<td>3 Acceptable</td>
<td>Leather in navel area is slightly in excess of desired amounts. The prepucial opening is at a 90° angle to the body wall.</td>
<td>Leather in the navel is slightly in excess of desired amounts.</td>
</tr>
<tr>
<td>4 Marginal</td>
<td>Excessive loose leather in navel area. Sheath is slightly pendulous. Prepuclal opening is at a 90° angle to the body wall.</td>
<td>Excessive loose leather in navel area.</td>
</tr>
<tr>
<td>5 Unacceptable</td>
<td>Sheath is pendulous. Leather in navel area is greatly in excess of desired amounts. Prepuclal opening may be large.</td>
<td>Leather in navel is greatly in excess of desired amounts.</td>
</tr>
</tbody>
</table>
of 2 being optimum. Table 1 describes the type of sheath or navel that fits each score as defined by the IBBA. Although the scores are considered subjective, they are partially objective because they measure how far the sheath or navel is from the underline of the animal. Bulls and heifers were analyzed separately. Weaning contemporary groups were formed in the manner previously defined. The data sets were analyzed using a single-trait variance-covariance analysis to estimate variance and covariance parameters for each trait.

**Heritabilities and Correlations.** Variance and covariances were estimated using multiple-trait models and equating quadratics

\[
\begin{bmatrix}
  y_1 \\
  y_2
\end{bmatrix}
= \begin{bmatrix}
  X_1 & 0 \\
  0 & X_2
\end{bmatrix}
\begin{bmatrix}
  c_1 \\
  c_2
\end{bmatrix}
+ \begin{bmatrix}
  Z_1 & Z_2 & 0 & 0 \\
  0 & 0 & Z_3 & Z_4
\end{bmatrix}
\begin{bmatrix}
  s_1 \\
  m_1 \\
  s_2 \\
  m_2
\end{bmatrix}
+ \begin{bmatrix}
  e_1 \\
  e_2
\end{bmatrix}
\]

where \( y_1 \) and \( y_2 \) were vectors of progeny records for the first trait and second trait, respectively; \( c_1 \) and \( c_2 \) were fixed contemporary group effects for the two traits; and \( s_1 \) and \( s_2 \), \( m_1 \) and \( m_2 \), and \( e_1 \) and \( e_2 \) were sire, maternal grandsire, and random residual effects, respectively, for the two traits. The \( X \) and \( Z \) matrices were the incidence matrices of 1’s and 0’s relating their specific effect back to the progeny vector. All sires and maternal grandsires were represented in both solution vectors across both traits regardless of whether they had a progeny or grandprogeny for that trait. This method required that the contemporary groups be absorbed into the random effects. In matrix notation, the multiple-trait equations after absorption were as follows:

\[
\begin{bmatrix}
  Z_1' & M_11 & Z_1' & M_12 & Z_2' & M_21 & Z_2' & M_22 \\
  Z_2' & M_21 & Z_2' & M_22 & Z_3' & M_31 & Z_3' & M_32 \\
  Z_3' & M_31 & Z_3' & M_32 & Z_4' & M_41 & Z_4' & M_42
\end{bmatrix}
\begin{bmatrix}
  s_1 \\
  m_1 \\
  s_2 \\
  m_2
\end{bmatrix}
= \begin{bmatrix}
  Y_1 \\
  Y_2
\end{bmatrix}
\]

where

\[
\begin{bmatrix}
  s_1 \\
  m_1 \\
  s_2 \\
  m_2
\end{bmatrix}
= \begin{bmatrix}
  \sigma^2_s & \sigma_{s1m1} & \sigma_{s1s2} & \sigma_{s1m2} \\
  \sigma_{s1m1} & \sigma^2_{m1} & \sigma_{ms1s2} & \sigma_{ms1m2} \\
  \sigma_{s1s2} & \sigma_{ms1s2} & \sigma^2_s & \sigma_{ms2m2} \\
  \sigma_{s1m2} & \sigma_{ms1m2} & \sigma_{ms2m2} & \sigma^2_{m2}
\end{bmatrix}^{-1}
\]

\[
M_{11} = (M_1 - M_2)^{-1} / \sigma^2_e e_1^{-1} + M_2^r r_{11},
M_{12} = M_2^r r_{12},
M_{22} = M_2^r r_{22},
M_1 = J - X_1(X_1'X_1)^{-1}X_1,
M_2 = J - X_2(X_2'X_2)^{-1}X_2,
\]

and

\[
\begin{bmatrix}
  r_{11} \\
  r_{12} \\
  r_{12} \\
  r_{22}
\end{bmatrix}
= \begin{bmatrix}
  \sigma^2_e e_1 & \sigma_{e1e2} \\
  \sigma_{e1e2} & \sigma^2_e e_2
\end{bmatrix}^{-1}
\]
Bertrand and Kriese (1990) described a procedure for absorbing contemporary groups in cases involving two traits, in which there are no missing records for the first trait, there may be missing records for the second trait, and the contemporary groups for the second trait are subsets of the contemporary groups for the first trait. The procedure involves absorbing the contemporary groups separately for each trait, multiplying the absorbed matrices and vectors by the proper values from the inverse residual variance-covariance matrix, and then combining the appropriate matrices and vectors. The hierarchical contemporary group structure between the two traits allows easier absorption of these effects in multiple-trait models in which the residual covariance between the traits is not zero, as was the case in the analyses presented in this study. For the analyses that contained only a sire effect for the second trait, the model was similar except that the maternal grandsire effect was eliminated for the second trait. Pseudo-expectations of quadratic forms and expectations of variances and covariances for each model were described by Kriese et al. (1991). The dataset composed of WW and BTHW progeny records was analyzed using a sire-MGS model for both traits. The two datasets of WW and GAIN and BTHW and GAIN were analyzed using a sire-MGS model for the first trait and a sire model for the second trait. Different models were employed to aid in convergence of variance component solutions. It has been our experience with these multiple-trait models that if a trait is not maternally influenced, it becomes very difficult to estimate the various covariances associated with the model and the solutions will not converge and most probably will diverge.

The expectations for the variance and covariance components using a sire-MGS model for both traits were:

\[
\begin{align*}
E(\sigma^2_{s1}) &= 1/4\sigma^2_A, \\
E(\sigma_{s1s1}) &= 1/8\sigma^2_A + 1/4\sigma_{A1M1}, \\
E(\sigma_{s1s2}) &= 1/4\sigma_{A1A2}, \\
E(\sigma_{s1s2}) &= 1/8\sigma_{A1A2} + 1/4\sigma_{A1M2}, \\
E(\sigma^2_{s1}) &= 1/16\sigma^2_A + 1/4\sigma_{A1M1} + 1/4\sigma_{A2M2}, \\
E(\sigma_{ms1}) &= 1/8\sigma_{A1A2} + 1/4\sigma_{A1M2}, \\
E(\sigma_{ms2}) &= 1/16\sigma^2_A + 1/4\sigma_{A1M1} + 1/4\sigma_{A2M2}.
\end{align*}
\]

For the models that contained only a sire effect for the second trait, the expectations were similar except that terms containing \(ms_2\) and \(M_2\) were eliminated and resulted in the following changes in the residual expectations:

\[
\begin{align*}
E(\sigma_{e1e2}) &= 5/8\sigma_{A1A2} + 3/4\sigma_{M1A2} + \sigma_{e1e2} \\
E(\sigma^2_{e2}) &= 3/4\sigma^2_A + \sigma^2_{e2}.
\end{align*}
\]

Brangus sheath and navel scores were analyzed using a single-trait pseudo-expectation method (Schaeffer, 1986) and a sire-MGS model. The model was as follows:

\[
y = Xc + Z_1s + Z_2ms + e,
\]

where \(y\) was a vector of observed weaning sheath or navel scores and \(c, s, ms, \) and \(e\) were vectors of fixed contemporary group effects and random sire, maternal grandsire, and residual error effects, respectively. \(X, Z_1,\) and \(Z_2\) were incidence matrices of 1's and 0's corresponding to their specific effect.

The expectations for the variance and covariance components under this model were as follows:

\[
\begin{align*}
E(\sigma^2_{s}) &= 1/4\sigma^2_A, \\
E(\sigma_{sms}) &= 1/8\sigma^2_A + 1/4\sigma_{AM}, \\
E(\sigma^2_{ms}) &= 1/16\sigma^2_A + 1/4\sigma_{AM} + 1/4\sigma^2_M, \\
E(\sigma^2_{e}) &= 11/16\sigma^2_A + 3/4\sigma_{AM} + 3/4\sigma^2_M + \sigma^2_e.
\end{align*}
\]

Results and Discussion

Growth Traits. The number of progeny records, contemporary groups, sires, and MGS from each breed's analysis are presented in Table 2. There was a large range of progeny records available for analyses of the different breeds. Tables 3 and 4 contain variance and
covariance components and heritability and genetic correlation estimates for each breed. The variance and covariance components found in these tables were estimated using the outlined expectation equations. For each breed, three two-trait analyses were conducted. There were many more 205-d weight records reported than birth weight or postweaning gain records in each breed. In all four analyses involving birth weight and postweaning gain, there were relatively few postweaning gain records compared with the number of postweaning gain records involved in the analysis with 205-d weight. There was a possibility that the sample of data for the birth weight postweaning gain analyses did not adequately represent the populations. However, except for the Beefmaster BTHW-GAIN dataset, heritabilities from the analyses of BTHW-GAIN, BTHW-WW, and WW-GAIN datasets were within .07 across a trait for each dataset. In most cases, the heritability estimates were within .01. Therefore, except for the Beefmaster BTHW-GAIN analysis, the variance component estimates for BTHW, WW, and GAIN were averaged across the three two-trait analyses for each breed, because the heritabilities were similar across the datasets. In the Beefmaster BTHW-GAIN analysis, there were only 327 GAIN records available for analysis, and the additive gain variance was not taken into consideration when reporting results for this paper. The variance and covariance components are provided for completeness, but the discussion will revolve around the heritability and correlation estimates.

For each breed, heritability estimates were lower than estimates summarized by Woldehawariat et al. (1977) for BTHW, WW, and GAIN. This was not unexpected, because field data estimates are generally lower than heritability estimates from designed studies. Birth weight additive heritability ($h^2_A$) and maternal heritability ($h^2_M$) estimates of .28 and .12 for the Brangus breed were similar to those reported by Bertrand and Benyshek (1987). Additionally, the $h^2_A$ estimate (.34) for Santa Gertrudis BTHW was similar to the heritability reported by Aaron et al. (1987) using King Ranch records. Brahman BTHW estimates of .37 and .18 for $h^2_A$ and $h^2_M$, respectively, were comparable in magnitude to Brangus and Santa Gertrudis estimates. However, the $h^2_A$ estimate (.22) for Beefmaster BTHW was lower in magnitude, and the $h^2_M$ estimate (.55) was much larger in magnitude than those of other Brahman and Brahman-derivative breeds in this study. This could be a function of the relatively small number of Beefmaster BTHW progeny records. All estimates of both additive and maternal heritabilities for BTHW in Brahman and Brahman-derivative cattle suggest that birth weight can be changed by selection in these breeds if desired. The genetic correlation between the additive and maternal portions of BW ($r_{BM}$) was negative in all breeds. The magnitude of $r_{BM}$ was large in all

### TABLE 2. NUMBER OF RECORDS, CONTEMPORARY GROUPS, SIRES, AND MATERNAL GRANDSIRES (MGS) FOR BRAHMAN AND BRAHMAN-DERIVATIVE GROWTH TRAIT ANALYSES

<table>
<thead>
<tr>
<th>Trait^a</th>
<th>Records</th>
<th>Contemporary groups</th>
<th>Sires</th>
<th>MGS</th>
</tr>
</thead>
<tbody>
<tr>
<td>Beefmaster</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>BTHW</td>
<td>2,388</td>
<td>392</td>
<td>361</td>
<td>554</td>
</tr>
<tr>
<td>WW</td>
<td>7,211</td>
<td>1,278</td>
<td>1,040</td>
<td>1,265</td>
</tr>
<tr>
<td>GAIN</td>
<td>1,576</td>
<td>313</td>
<td>364</td>
<td></td>
</tr>
<tr>
<td>Brahman</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>BTHW</td>
<td>5,459</td>
<td>368</td>
<td>363</td>
<td>935</td>
</tr>
<tr>
<td>WW</td>
<td>12,559</td>
<td>950</td>
<td>836</td>
<td>1,513</td>
</tr>
<tr>
<td>GAIN</td>
<td>3,565</td>
<td>376</td>
<td>238</td>
<td></td>
</tr>
<tr>
<td>Brangus</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>BTHW</td>
<td>32,215</td>
<td>3,816</td>
<td>2,141</td>
<td>3,335</td>
</tr>
<tr>
<td>WW</td>
<td>58,932</td>
<td>6,479</td>
<td>3,387</td>
<td>4,424</td>
</tr>
<tr>
<td>GAIN</td>
<td>16,456</td>
<td>1,791</td>
<td>1,029</td>
<td></td>
</tr>
<tr>
<td>Santa Gertrudis</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>BTHW</td>
<td>10,768</td>
<td>948</td>
<td>797</td>
<td>1,749</td>
</tr>
<tr>
<td>WW</td>
<td>23,180</td>
<td>2,649</td>
<td>1,857</td>
<td>3,442</td>
</tr>
<tr>
<td>GAIN</td>
<td>2,868</td>
<td>415</td>
<td>520</td>
<td></td>
</tr>
</tbody>
</table>

^aBTHW = adjusted birth weight; WW = adjusted 205-d weaning weight; GAIN = adjusted postweaning gain.
PARAMETER ESTIMATES FOR ZEBU-DERIVATIVE CATTLE

TABLE 3. GENETIC VARIANCE, COVARIANCE (kg²), HERITABILITY, AND CORRELATION ESTIMATES FOR BEEFMASTER AND SANTA GERTRUDIS CATTLE

<table>
<thead>
<tr>
<th>Trait</th>
<th>Beefmaster</th>
<th>Santa Gertrudis</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>BTHW</td>
<td>WW GAIN</td>
</tr>
<tr>
<td></td>
<td>A</td>
<td>M</td>
</tr>
<tr>
<td>BTHW</td>
<td>A</td>
<td>-3.15</td>
</tr>
<tr>
<td>WW</td>
<td>A</td>
<td>.22</td>
</tr>
<tr>
<td></td>
<td>M</td>
<td>.55</td>
</tr>
<tr>
<td>GAIN</td>
<td>A</td>
<td>131.05</td>
</tr>
<tr>
<td></td>
<td>M</td>
<td>.21</td>
</tr>
</tbody>
</table>

aBTHW = adjusted birth weight; WW = adjusted 205-d weaning weight; GAIN = adjusted postweaning gain.
bCo(variances) are on the first two lines of each trait, heritabilities and correlations are on the next two lines for BTHW and WW. Variances and heritabilities are on the diagonals of each 2 × 2 cell. v = rows of (co)variances h = rows of heritabilities and correlations. GAIN lines contain additive (co)variance, heritability and correlation estimates.
cA = additive; M = maternal.

breeds except Brahman (−.15). Negative rBM estimates were also reported in Brangus cattle (Bertrand and Benyshek, 1987), Simmental cattle (Burford et al., 1981; Garrick et al., 1989), and Hereford cattle (Kriese et al., 1991). In examining WW, h²A (.21) and h²M (.15) estimates in Brangus cattle were very similar to estimates reported by Bertrand and Benyshek (1987). However, the h²A estimate of .25 for Santa Gertrudis WW was lower than that reported by Aaron et al. (1987). Brahman and Beefmaster h²A and h²M estimates were similar in magnitude to Brangus and Santa Gertrudis estimates. These additive and maternal heritabilities suggest that genetic progress can be made for increased weaning weights in Brahman and Brahman-derivative cattle. The genetic correlation between weaning weight direct and weaning weight maternal (rWM) was negative and moderate in magnitude in Brangus and Santa Gertrudis cattle. Moderate, negative rWM correlations were also found in the literature for Brangus and Simmental cattle (Bertrand and Benyshek, 1987; Garrick et al., 1989; Kriese et al., 1991). However, the rWM estimate for Beefmaster cattle was small and negative (−.06), whereas the rWM estimate for Brahman cattle was small and positive (.15). Quass et al. (1985) reported a rWM of −.04 in Simmental cattle. Although the relationship between weaning weight direct and weaning weight maternal is not fully resolved, both weaning weight direct and weaning weight maternal values should be monitored when selecting Brahman and Brahman-derivative cattle to ensure a balance between additive and maternal values. Additionally, the correlation between direct and maternal effects, coupled with moderate heritability estimates, for both BTHW and WW suggests that direct and maternal components are important in Brahman and Brahman-derivative cattle. Additive heritability estimates for GAIN were variable between breeds. Estimates ranged from .15 to .56. However, these estimates are in the range of estimates found in the literature (Woldehawariat et al., 1977; Garrick et al., 1989). All GAIN estimates suggest that cattle can be selected for increased postweaning gains and yearling weights and that genetic progress can be made. A large, positive correlation between direct BTHW and direct WW (rBW) was observable across all breeds. This was in agreement with reported rBW correlation estimates using Hereford and Brangus cattle (Kriese et al., 1991) and Simmental cattle (Garrick et al., 1989) and with other reports (Woldehawariat et al., 1977). However, Quass et al. (1985) and Bourdon and Brinks (1986) found only a small, positive genetic correlation between birth weight and weaning weight in Hereford and Simmental cattle, respectively. Thus, when selecting for increased weaning weights in Brahman and Brahman-derivative cattle, birth weights should be monitored or dystocia problems could arise.
TABLE 4. GENETIC VARIANCE, COVARIANCE (kg²), HERITABILITY, AND CORRELATION ESTIMATES FOR BRAHMAN AND BRANGUS CATTLE

<table>
<thead>
<tr>
<th>Trait</th>
<th>Brahman</th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th>Brangus</th>
<th></th>
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</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>BTHW</td>
<td>WW</td>
<td>GAIN</td>
<td>BTHW</td>
<td>WW</td>
<td>GAIN</td>
<td></td>
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<tr>
<td></td>
<td>A²</td>
<td>M²</td>
<td>A</td>
<td>M</td>
<td>A</td>
<td>M</td>
<td>A</td>
<td>M</td>
<td>A</td>
<td>M</td>
<td>A</td>
</tr>
<tr>
<td>BTHW</td>
<td>-75</td>
<td>18.77 6.25 9.31</td>
<td>5.60 -1.85 12.42 -6.34 2.54</td>
<td></td>
<td></td>
<td></td>
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<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>.37</td>
<td>.35 1.97 12.29</td>
<td>.15 -5.2 9.31 5.60 -1.85 12.42 -6.34 2.54</td>
<td></td>
<td></td>
<td></td>
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<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>WW</td>
<td>109.70 13.75 64.32 121.75 -24.10 28.33</td>
<td></td>
<td></td>
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<td></td>
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<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>.23</td>
<td>.15 1.15</td>
<td>.21 -23 .34</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GAIN</td>
<td>108.04</td>
<td>symmetric</td>
<td>56.65</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

⁴BTHW = adjusted birth weight; WW = adjusted 205-d weaning weight; GAIN = adjusted postweaning gain.
⁵Co(variance) are on the first two lines of each trait, heritabilities and correlations are on the next two lines for BTHW and WW. Variances and heritabilities are on the diagonals of each 2 x 2 cell. v = rows of (co)variances, h = rows of heritabilities and correlations. GAIN lines contain additive (co)variance, heritability and correlation estimates.
⁶A = additive; M = maternal.

Also, large, positive genetic correlations were present between direct WW and direct GAIN (rWG) in the Beefmaster, Brahman, and Brangus populations. This is in agreement with most previous estimates. However, a negative rWG (−.11) was present in the Santa Gertrudis population. This seems contradictory to current theory, which indicates that genes controlling weaning weight growth also affect postweaning growth patterns. Neville et al. (1984a,b) conducted a study that included grade Angus, Polled Hereford, and Santa Gertrudis dams mated to purebred sires of the same breeds. The calves from the grade Santa Gertrudis dams mated to the purebred Santa Gertrudis sires weighed significantly more at birth and weaning and had the highest preweaning ADG in the study. However, this advantage did not carry over to the postweaning phase. Additionally, the Santa Gertrudis data were previously analyzed with 2,090 GAIN records and 15,290 WW records. The previous analysis represented the NCE data bank available at the end of the previous year (1988). As in this current analysis, the rWG was negative but larger in magnitude. With this move toward zero for the Santa Gertrudis rWG, it is probable that the rWG is not negative in the Santa Gertrudis breed. The current negative correlation between weaning weight and gain may be caused by a small sample size, coupled with a possible selection bias in the records that were reported. Often not all animals contained in a weaning contemporary group will have a reported postweaning gain record. This may result in an inaccurate representation of the breed population.

The environmental correlation between WW and GAIN was negative for all breeds (Table 5), which is in agreement with the finding of Garrick et al. (1989). This negative correlation may be due to compensatory gain effects. The environmental correlation between BTHW and GAIN varied greatly between breeds. Estimates ranged from −.06 to .18. Using Hereford and Brangus bull records, moderate, positive correlations have been reported between BTHW and GAIN (Kriese et al., 1991). However, a small, positive correlation between BTHW and GAIN was reported in Simmental cattle (Garrick et al., 1989). Interpretations of these environmental correlations should be made with caution because the method used to estimate environmental correlations is not free of selection bias (Bertrand and Kriese, 1990). However, no environmental correlation was substantially different from literature reports. Thus, Brahman and Brahman-derivative cattle should respond to environmental factors similarly to Bos taurus cattle.

Sheath and Navel Score. Bull and heifer records were analyzed separately because reproduction is intrinsically linked to the sheath, but a relationship between reproduction and navel shape is currently unclear. Also, previous work showed that reranking of sires
PARAMETER ESTIMATES FOR ZEBU-DERIVATIVE CATTLE

TABLE 5. ENVIRONMENTAL VARIANCES, COVARIANCES (kg²), AND CORRELATIONS FOR BRAHMAN AND BRAHMAN-DERIVATIVE CATTLE

<table>
<thead>
<tr>
<th>Trait</th>
<th>Beefmaster</th>
<th>Brahman</th>
<th>Brangus</th>
<th>Santa Gertrudis</th>
</tr>
</thead>
<tbody>
<tr>
<td>BTHW</td>
<td>6.90</td>
<td>11.73</td>
<td>8.1</td>
<td>13.65</td>
</tr>
<tr>
<td>WW</td>
<td>2.3</td>
<td>369.50</td>
<td>-61.11</td>
<td>34</td>
</tr>
<tr>
<td>GAIN</td>
<td>0.02</td>
<td>-25</td>
<td>167.62</td>
<td>19</td>
</tr>
</tbody>
</table>

aVariances are on the diagonal, covariances above the diagonal, and environmental correlations below the diagonal for each breed.

bBTHW = adjusted birth weight; WW = adjusted 205-d weaning weight; GAIN = adjusted postweaning gain.

(Spearman correlation = .52) occurred among sheath and navel score expected progeny differences when sires had both male and female progeny (Kriese et al., 1988). In an additional study, the genetic correlation between weaning sheath and navel score was estimated from bulls having both male and female progeny in the same contemporary group (unpublished data). The genetic correlation was .51, which indicates that many of the same genes control both weaning sheath and navel score but also suggests that weaning sheath and navel scores are not identical traits in males and females.

Table 6 provides the number of weaning sheath and navel observations in each score classification. The data seem to follow a normal distribution. There were a total of 19,820 weaning sheath scores analyzed. These records represented 2,187 WCG, 2,933 MGS, and 2,044 sires. The $h^2_A$ estimate for weaning sheath score was .21; $h^2_M$ was .09. The genetic correlation between the additive and maternal effects was -.39. For the weaning navel score analysis, there were 11,560 records from 1,389 WCG, representing 2,012 MGS and 1,222 sires. The $h^2_A$ and $h^2_M$ estimates for weaning navel score were .21 and .07, respectively. Again, the genetic correlation between additive and maternal effects was large and negative (-.53). Franke and Burns (1985) measured Brahman bull and heifer weaning sheath area and found a heritability estimate of .45. Our study indicates that both weaning sheath and navel score are under a moderate amount of additive genetic control and that improvement can be obtained for the size and shape of the calf's sheath and navel areas during gestation.

Implications

This study was conducted to characterize four breeds of Brahman and Brahman-derivative cattle in terms of genetic and environmental parameters for growth traits. There do not seem to be any genetic parameters contradictory to traditional Bos taurus estimates, although the maternal portion of variation may play a more important role in Brahman and Brahman-derivative cattle. The large, negative genetic correlations for direct growth and maternal portions of variation between and within traits must be considered when selecting within these cattle. Selection for extreme growth or maternal ability could be detrimental for the other trait if it is not monitored because of the antagonistic correlation present between direct and maternal portions of variation. Environmental correlations were of the same direction and magnitude as other reported estimates, indicating that Brahman and Brahman-derivative cattle re-
spond to environmental factors similarly to *Bos taurus* cattle. Also, Brangus sheath and navel scores may be improved through selection.

**Literature Cited**


