LACK OF SIRE BY DIET INTERACTIONS IN HEREFORD AND ANGUS CALVES FED ONE OF TWO DIETS

D. R. C. Bailey, R. P. Gilbert and J. E. Lawson
Agriculture Canada Research Station, Lethbridge, Alberta T1J 4B1

SUMMARY

Prior to the initiation of a selection project, foundation herds of Hereford and Angus cattle were created and their progeny evaluated during a 4-yr period (1964 to 1967) for 168-d postweaning gain on either a high- or medium-energy diet. Hereford and Angus calves receiving the high energy diet gained more (P < .01) than their contemporaries fed the medium energy diet. Sire differences were only significant in the Angus. Sire x diet interactions were not significant in either breed. When gain by progeny of each sire on each diet was considered as two distinct traits, the genetic correlation between gain on the two diets was not different from 1.0 for the Angus. The genetic correlation for gain in the Herefords could not be estimated because of a negative sire variance component estimate. These results indicate that sires rank the same based on progeny performance on either diet.

INTRODUCTION

Falconer (1952) suggested that the environment in which selection is practiced can be either a) the conditions in which the breed will be expected to live, or b) conditions more favorable for expression of the desired character. Existence of a genotype by environment interaction would reduce the effectiveness of selection, i.e., when the superior genotype in one environment is not superior in another environment (Eisen and Saxton, 1983). However, if the genotype by environment interaction is not important, response would be greatest when selection is practiced in the environment where the highest heritability is expressed (Falconer, 1952).

Absence of Sire by Diet (nutritional environment) interactions would indicate that ranking of sires based on progeny performance would be unaffected by differences in diets, i.e., the correlation between their breeding values (genetic correlation) in the different environments should be 1.0. The practical importance of an absence of Sire by Diet interactions is that selection programs are less sensitive to feedstuff availability and(or) economic fluctuations. The objectives of this study were to determine the importance of sire by diet interactions for 168-d postweaning gain.

MATERIALS AND METHODS

This research was conducted at the Agriculture Canada Onefour Substation located in the short grass prairie region of southeastern Alberta, near Manyberries. The Angus and Hereford cattle in this study were unselected progeny from foundation animals accumulated for a long-term selection experiment. Management of the cattle is described in Bailey et al (1988). Both herds were maintained as one group except during the breeding season and when the calves were fed one of two diets during the 168-d postweaning gain test. Herd Management. In June, 1963, each herd was subdivided into two lines (108 cows per line). Cows were stratified by age group (1 through 6 yr), herd of origin, and where applicable, sire of cow within herd of origin, and assigned at random to their respective line. Within each breed, cows were assigned randomly to one of

307
twelve 18-cow breeding groups. Each breeding group contained cows from both lines and all six age categories. One half of the 12 bulls in each breed used in 1963 (to produce the 1964 calves) were mated to the same cows (i.e., breeding group) in 1964. Each of the remaining bulls was assigned randomly to, and mated with, one of the remaining breeding groups. In subsequent years, a random half of the sires was mated to the same cows (breeding group) in two consecutive years; the other sires were randomly allotted to the remaining groups as described above.

Immediately after weaning, all calves were assigned to one of eight pens by breed (Angus, Hereford), sex (bull, heifer), and diet (a high energy diet, HED: 80% grain-20% alfalfa hay; or a medium energy diet, MED: 100% alfalfa hay) for a 168-d postweaning gain test.

Statistical Analyses. The data were analyzed separately for each breed by least squares procedures for unbalanced data (the GLM procedure; SAS, 1985). The mating structure used in the foundation herds required dams to be nested within selection line and sires to be cross-classified with line. Diet was equivalent to line (within breed). Therefore, the linear model was

\[ y_{ijklm} = \mu + s_i + d_j + s_d_{ij} + c_{ijk} + y_{mr} + s_x_{jn} + d_y_{rjm} + d_x_{jn} + e_{ijklmnp} \]  

where

- \( y_{ijklm} \) = observed values for postweaning gain,
- \( \mu \) = the overall mean when equal subclass numbers exist,
- \( s_i \) = the random effect of the ith sire, \( s \sim N(0, \sigma_s^2) \),
- \( d_j \) = the fixed effect of the jth diet,
- \( s_d_{ij} \) = the random effect of the interaction between the ith sire and the jth diet, \( s_d \sim N(0, \sigma_{sd}^2) \),
- \( c_{ijk} \) = the random effect of the kth dam within the ijth subclass, \( d \sim N(0, \sigma_d^2) \),
- \( y_{mr} \) = the fixed effect of the mth year,
- \( s_x_{jn} \) = the fixed effect of the nth sex, and
- \( d_y_{rjm} \) = the interaction of diet and year,
- \( d_x_{jn} \) = the interaction of diet and sex, and
- \( e_{ijklmnop} \) = the random error associated with each observed value, \( e \sim N(0, \sigma_e^2) \).

Genetic Correlations. Variance and covariance components were calculated by equating mean squares and cross products from the ANOVA to their expectations. Genetic correlations may be calculated from two approaches: from the variance components of a two-way ANOVA (Dickerson, 1962; Yamada, 1962), or from a one-way ANOVA by assuming that a trait measured in two environments represents two different traits (Falconer, 1952; Yamada 1962).

In the two-way ANOVA approach the Sire by Diet interaction variance component can be partitioned into a portion associated with the genetic correlation and a portion associated with the heterogeneity of genetic variances measured in each environment (Robertson, 1959; Dickerson, 1962, Yamada, 1962; Eisen and Saxton, 1983). The genetic correlation (r_g) was estimated using the variance components from model [1] above in the equation for a mixed model from Yamada (1962):

\[ r_g = \frac{\hat{\sigma}_5^2 - .5\hat{\sigma}_{sd}^2}{\hat{\sigma}_5^2 + .5\hat{\sigma}_{sd}^2 - .5(\hat{\sigma}_1 - \hat{\sigma}_2)^2} \]  

where \( \hat{\sigma}_5^2 \) and \( \hat{\sigma}_{sd}^2 \) are the sire and sire by diet variance components described above; \( \hat{\sigma}_1 \) and \( \hat{\sigma}_2 \) are the square roots of the estimated sire variances in the HED
and MED environments; and 

\[0.5(\hat{\sigma}_1^2 - \hat{\sigma}_2^2)\] is the adjustment for heterogeneity of genetic variances between environments (i.e., diets).

The within-diet (environment) variance components for each breed used in [3] were estimated from

\[\text{GAIN} = \mu + s_i + d_{ik} + y_{rm} + s_{xn} + e_{ikmnp}\] [3]

where the elements of the linear model are the same as described for [1] above except the data were analyzed within breed and diet.

The genetic correlation was also estimated by considering GAIN on each diet as a separate trait. The data for each diet were averaged by sire, year, and sex and analyzed using multivariate analysis of variance (MANOVA statement in SAS/GLM; SAS, 1985) of

\[\text{GAINH} = \mu + s_i + y_{rm} + s_{xn} + e_{imnp}\] [4]

where GAINH and GAINM are the respective GAIN means for HED and MED; the rest of the model is as described in [1] above. The equation used to estimate the genetic correlation was

\[\hat{r}_g = \frac{\hat{\text{COV}}_{HM}}{\hat{\sigma}_s^H \cdot \hat{\sigma}_s^M}\] [5]

where \(\hat{\text{COV}}_{HM}\) is the mean cross product for sire from the multivariate analysis of [4], and \(\hat{\sigma}_s^H\) and \(\hat{\sigma}_s^M\) are the respective square roots of the sire variance estimates from the GAINH and GAINM ANOVA (model [4]). Approximate standard errors for the genetic correlation coefficients were calculated using the equations developed by Tallis (1959).

RESULTS AND DISCUSSION

Variance Components. Variance components estimated from models [1], [3], and [4] are shown in Tables 1, 2, and 3, respectively. The values of the variance component estimates are consistent with the results of the ANOVA. Where negative or extremely small positive variances existed, corresponding hypothesis tests indicated that the variance was zero, e.g., the Sire by Line interactions for the Angus in Table 4 and the corresponding negative variance component estimates in Table 6. Searle (1971, pp. 407) suggests that a zero variance component may indicate 1) an incorrect linear model, or 2) an unbiased estimate of a variance that actually is zero. One procedure he recommends (his method ii) is to accept the negative estimate as evidence that the true value is zero and use zero in place of the negative estimate. He (Searle, 1971) cautions that such estimates are no longer unbiased.

Genetic Correlations. The negative (or zero) estimate of the sire variance for GAIN on the HED (Table 2) and a negative sire by diet interaction for GAIN in the Angus (Table 1) prevented estimation of the genetic correlation for GAIN using equation [2]. Similarly, the negative sire variance estimate for GAINH in the Herefords precluded estimation of the genetic correlation for GAIN using equation [5]. The genetic correlation in the Angus when GAIN on each diet was considered to be different traits (equation [5]) was not different from 1.0 (Table 3). The lack of Sire by Diet interactions for GAIN in both breeds and the genetic correlation for gain on the two diets for the Angus cattle indicate that sire ranking based on progeny performance is unaffected by the level of dietary energy.
REFERENCES


TABLE 1. ESTIMATED VARIANCE COMPONENTS FROM WITHIN BREED ANALYSES\(^a\)

<table>
<thead>
<tr>
<th>Variance component</th>
<th>Hereford</th>
<th>Angus</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sire</td>
<td>1.24</td>
<td>19.42</td>
</tr>
<tr>
<td>Sire x Diet</td>
<td>1.38</td>
<td>-3.52</td>
</tr>
<tr>
<td>Cow (Sire x Diet)</td>
<td>80.76</td>
<td>113.52</td>
</tr>
<tr>
<td>Residual</td>
<td>207.14</td>
<td>202.96</td>
</tr>
</tbody>
</table>

\(^a\)See model [1] description in text.

TABLE 2. ESTIMATED VARIANCE COMPONENTS AND HERITABILITIES FROM WITHIN BREED AND DIET ANALYSIS OF GAIN\(^a\)

<table>
<thead>
<tr>
<th>Variance component</th>
<th>HED</th>
<th>MED</th>
<th>HED</th>
<th>MED</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sire</td>
<td>-9.17</td>
<td>16.73</td>
<td>22.65</td>
<td>9.46</td>
</tr>
<tr>
<td>Cow (Sire)</td>
<td>127.71</td>
<td>32.32</td>
<td>173.30</td>
<td>53.09</td>
</tr>
<tr>
<td>Residual</td>
<td>253.98</td>
<td>147.58</td>
<td>239.51</td>
<td>172.26</td>
</tr>
</tbody>
</table>

\(^a\)See model [3] description in text.

TABLE 3. ESTIMATED VARIANCE COMPONENTS AND HERITABILITIES FROM WITHIN BREED ANALYSES OF GAIN AS TWO DISTINCT TRAITS (GAINH AND GAINM)\(^a\)

<table>
<thead>
<tr>
<th>Variance component</th>
<th>GAINH</th>
<th>GAINM</th>
<th>GAINH</th>
<th>GAINM</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sire</td>
<td>-8.57</td>
<td>12.08</td>
<td>26.08</td>
<td>9.16</td>
</tr>
<tr>
<td>Residual</td>
<td>133.76</td>
<td>68.31</td>
<td>148.37</td>
<td>62.63</td>
</tr>
<tr>
<td>(r_g)</td>
<td>1.42</td>
<td>.55</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

\(^a\)GAINH, GAINM = postweaning gain on high- or medium-energy diet, respectively. See description of model [4] in text.

\(^b\)Genetic correlation.