PRE- AND POSTNATAL DIRECT AND MATERNAL ADDITIVE GENETIC INFLUENCES ON PREWEANING GROWTH TRAITS OF BEEF CALVES

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SUMMARY

In separate analyses, data sets from pedigreed Hereford and Angus herds were used in a sire-dam model and in a sire-maternal grandsire model to obtain variances and covariances of interest for birth weight, gain from birth to weaning and weaning weight (205-d). Estimates of direct additive genetic variance ($\sigma^2_A$), maternal additive genetic variance ($\sigma^2_M$), covariance between direct and maternal additive genetic effects ($\sigma_{AM}$), permanent environmental variance ($\sigma^2_{PE}$) and residual variance ($\sigma^2_e$) were obtained. Estimates of heritability for direct genetic effects ($h^2_A$), maternal genetic effects ($h^2_M$) and the correlation between direct and maternal effects ($r_{AM}$) for birth weight were in Angus .42, .22 and - .12; and in Herefords .58, .22 and -.13, respectively. These values suggest similar prenatal relationships in both herds. For birth to weaning gain, $h^2_A$, $h^2_M$ and $r_{AM}$ were in Angus .57, .15 and -.32; and in Herefords .58, .39 and -.05, respectively. For weaning weight $h^2_A$, $h^2_M$ and $r_{AM}$ were in Angus .63, .16 and -.36; and in Herefords .66, .43 and -.08, respectively. There was relatively greater additive genetic postnatal maternal influence ($h^2_M = .43$ vs .16) among the Herefords than among the Angus. There was a higher correlation ($r_{AM} = -.36$ vs -.08) among Angus for preweaning postnatal growth than among Herefords.

INTRODUCTION

Knowledge of the relative importance of direct and maternal additive genetic effects on growth traits is important to the beef producer when formulating breeding plans. Recent studies have presented procedures for estimating these effects along with certain environmental influences. Most of these studies were with field data and, because of computing constraints, neglected relationships among sires and dams. In the present study, data were available from pedigreed herds of Angus and Hereford cattle under the same management, and computations included the relationship matrix. Of particular interest were comparisons of prenatal growth indicated by birth weight, preweaning postnatal growth indicated by birth to weaning gain and weaning weight, which includes both pre- and postnatal development.

MATERIALS AND METHODS

The data were birth and weaning weight records (adjusted to 205 d) of Angus and Hereford calves reared on the University of Arkansas Experiment Station farm near Fayetteville from 1965 through 1988. Birth and weaning weight records were adjusted for age of dam using additive adjustment factors given by BIF (1986). Birth to weaning average daily gain (ADG) was calculated from these adjusted weights. There were 2,039 birth weight records and 1,835 weaning weight records representing 54 sires and 604 dams in the Hereford data set. In the Angus data set there were 2,514 birth weight records and 2,309 weaning weight records representing 35 sires and 672 dams. There were 48 contemporary groups defined by year and sex of calf (24 years and 2 sexes).

Variances and covariances were estimated using a sire-dam model and a sire-maternal grandsire model as described by Bertrand and Benyshek (1987). The sire-
The dam model was as follows: \( y = Xc + Z_1s + Z_2d + e_1 \), where \( y \) was a vector of progeny records, \( c \) was a vector of fixed contemporary group effects and \( s_1 \), \( d \) and \( e_1 \) were vectors of sire, dam and residual effects, respectively. Mixed model equations were:

\[
\begin{bmatrix}
X'X & X'Z_1 & X'Z_2 \\
Z_1'Z_1 + A^{-1}_s k_1 & Z_1'Z_2 & Z_2'Z_2 + A^{-1}_d k_2
\end{bmatrix}
\begin{bmatrix}
c \\
s \\
d
\end{bmatrix}
=
\begin{bmatrix}
X'y \\
Z_1'y \\
Z_2'y
\end{bmatrix}
\]

where \( A^{-1}_s \) and \( A^{-1}_d \) were the inverses of the matrices of relationships among sires and dams, respectively, and \( k_1 \) and \( k_2 \) were the ratios of error variance to sire and dam variance, respectively. Solutions were obtained by iteration. Convergence for birth weight and 205-day weight variances was assumed when new estimates were within .02 kg of the previous estimates. Convergence for ADG was assumed when new estimates were within .00002 kg of the previous estimates. At each round of iteration, variances were estimated as follows:

\[
\begin{align*}
\sigma^2_{s_1} &= (s'A^{-1}s + trace(A^{-1}C_{11}) \sigma^2_e) / NS \\
\sigma^2_d &= (d'A^{-1}d + trace(A^{-1}C_{11}) \sigma^2_e) / ND \\
\sigma^2_{e_1} &= (y'y - c'X'y - s'Z_1'y - d'Z_2'y) / (N - CG)
\end{align*}
\]

where \( NS \) = number of sires, \( ND \) = number of dams, \( N \) = total number of records, \( CG \) = number of contemporary groups and \( C_{11} \) is the appropriate section of the inverse of the coefficient matrix. Assumed expectations of the variances and covariances were:

\[
\begin{align*}
\sigma^2_{s_1} &= 1/4 \sigma^2_A \\
\sigma^2_d &= 1/4 \sigma^2_A + \sigma^2_M + \sigma^2_H + \sigma^2_{PE} \\
\sigma^2_{e_1} &= 1/2 \sigma^2_A + \sigma^2_M.
\end{align*}
\]

The sire-maternal grandsire model was: \( y = Xc + Z_1s + Z_{mgs} + e_1 \), where \( y \) was a vector of progeny records, \( c \) was a vector of fixed contemporary group effect and \( s_2 \), \( mgs \) and \( e_2 \) were sire, maternal grandsire and residual random effects, respectively. The vectors \( s_2 \) and \( mgs \) included the same animals in the same order. Individuals that were only a sire and not a maternal grandsire had all zeros in the corresponding column in \( Z_2 \). Again an iterative procedure was followed, and convergence was as defined above.

Mixed model equations were as follows:

\[
\begin{bmatrix}
X'X & X'Z_1 & X'Z_2 \\
Z_1'Z_1 + A^{-1}_s \alpha_{11} & Z_1'Z_2 + A^{-1}_s \alpha_{12} & Z_2'Z_2 + A^{-1}_d \alpha_{22}
\end{bmatrix}
\begin{bmatrix}
c \\
s \\
mgs
\end{bmatrix}
=
\begin{bmatrix}
X'y \\
Z_1'y \\
Z_2'y
\end{bmatrix}
\]

where \( A^{-1}_s \) was the same for sires and maternal grandsires. At each round of iteration, variances were estimated as follows:

\[
\begin{align*}
\sigma^2_{s_2} &= (s'A^{-1}s + trace(A^{-1}C_{11}) \sigma^2_e) / NS \\
\sigma^2_{mgs} &= (mgs'A^{-1}mgs + trace(A^{-1}C_{11}) \sigma^2_e) / NS \\
\sigma^2_{e_2} &= (y'y - c'X'y - s'Z_1'y - mgs'Z_2'y) / (N - CG)
\end{align*}
\]

where \( NS \) = number of sires = number of maternal grandsires, \( N \) = total number of records, \( CG \) = number of contemporary groups and \( C_{11} \) is the appropriate section of the inverse of the coefficient matrix. The \( \alpha \)'s were calculated from the following 2 x 2 matrix.

\[
\begin{bmatrix}
\sigma^2_e & \sigma^2_{mgs} \\
\sigma^2_{mgs} & \sigma^2_e
\end{bmatrix}^{-1}
\begin{bmatrix}
\alpha_{11} \\
\alpha_{12}
\end{bmatrix}
\]

Assumed expectations of the variances and covariances were:

\[
\begin{align*}
\sigma^2_{s_2} &= 1/4 \sigma^2_A \\
\sigma^2_{mgs} &= 1/8 \sigma^2_A + 1/4 \sigma_{AM}
\end{align*}
\]
\[
\sigma^2_{\text{MGE}} = 1/16 \sigma^2_A + 1/4 \sigma^2_{AM} + 1/4 \sigma^2_M
\]
\[
\sigma^2_{e_1} = 11/16 \sigma^2_A + 3/4 \sigma^2_{AM} + 3/4 \sigma^2_M + \sigma^2_{PE} + \sigma^2_e.
\]

Therefore, the equations to estimate the genetic variances and covariances associated with direct and maternal genetic predictors in the reduced animal model for a maternally influenced trait were (Bertrand and Benyshek, 1987):

\[
\sigma^2_A = 2 (\sigma^2_{e_1} + \sigma^2_{g_2})
\]
\[
\sigma^2_{AM} = 4 (\sigma^2_{\text{MGE}} - \sigma^2_A/8)
\]
\[
\sigma^2_M = 4 (\sigma^2_{\text{MGE}} - \sigma^2_A/16 - \sigma^2_{AM}/4)
\]
\[
\sigma^2_{PE} = \sigma^2_{e_2} - 3/16 \sigma^2_A - 3/4 \sigma^2_{AM} - 3/4 \sigma^2_M
\]
\[
\sigma^2_e = \sigma^2_{e_1} - \sigma^2_{PE} - 3/4 \sigma^2_M - 3/4 \sigma^2_{AM} - 11/16 \sigma^2_A.
\]

RESULTS

Estimated variances and covariances from the sire-dam model and the sire-maternal grandsire model are presented in Table 1. Direct and maternal genetic estimates generated by equating values in Table 1 to their expected values are presented in Table 2. Values in Table 2 were used to calculate the estimates of genetic parameters presented in Table 3.

DISCUSSION

Values in Table 1 and Table 2 are similar in magnitude to those reported or cited by Wilson et al. (1986), Bertrand and Benyshek (1987) and Trus and Wilton (1988) for birth weight and weaning weight. Angus sire components of variance were consistently smaller than Hereford sire components of variance. Dam components of variance were larger than sire components of variance except for postnatal gain of Angus. Sire components of variance were two to threefold larger than maternal grandsire components of variance.

Estimates of direct additive genetic variance were larger than maternal additive variance in all three traits. Also the covariance between these sources of genetic variation was negative for all three traits. When expressed as heritability (Table 3), values were similar for the breed groups during the prenatal period but differed during the preweaning postnatal growth period. This difference in the breed groups in the direct and maternal genetic relationships for growth is also expressed in weaning weight. Weaning weight maternal effects contain both prenatal and postnatal maternal effects. The variance component associated with permanent environmental effects was negative in all cases except birth weight of Herefords. The extent to which the negative estimates were the result of sampling or the result of some unknown source of bias was not clear. A negative estimate of permanent environmental variance was reported by Bertrand and Benyshek (1987).

Heritability estimates of additive direct, additive maternal and the correlation of direct and maternal additive genetic values are presented in Table 3. Values were similar during the prenatal period for the two breeds but differed during the preweaning postnatal period. There was relatively greater additive genetic postnatal maternal influence (h^2_M = .43 vs .16) among Herefords than among Angus. There was a higher correlation (r_{AM} = -.36 vs -.08) among Angus for preweaning postnatal growth than among Herefords. Knowledge of such diverse genetic relationships should be helpful in formulating selection plans.

REFERENCES

Table 1. Estimates of sire and dam (Co)variances (kg²) from analysis of preweaning growth traits of Hereford and Angus using two models

<table>
<thead>
<tr>
<th>Trait</th>
<th>Breed</th>
<th>Birth Weight</th>
<th>ADG</th>
<th>Weaning Weight</th>
</tr>
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<tr>
<td></td>
<td></td>
<td>A</td>
<td>H</td>
<td>A</td>
</tr>
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<td>Sire-dam model:</td>
<td></td>
<td></td>
<td></td>
<td></td>
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<tr>
<td></td>
<td></td>
<td>1.25</td>
<td>2.73</td>
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<tr>
<td></td>
<td></td>
<td>.91</td>
<td>4.10</td>
<td>.0011</td>
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<td>13.29</td>
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<tr>
<td>Sire-maternal grandsire model:</td>
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<td>2.82</td>
<td>.0013</td>
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<tr>
<td></td>
<td></td>
<td>.96</td>
<td>1.53</td>
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<td>.58</td>
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<tr>
<td></td>
<td></td>
<td>11.11</td>
<td>14.79</td>
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Table 2. Estimates of genetic and environmental variances and covariances of Angus and Hereford preweaning traits

<table>
<thead>
<tr>
<th>Trait</th>
<th>Breed</th>
<th>$\sigma^2_A$</th>
<th>$\sigma_{AM}$</th>
<th>$\sigma^2_M$</th>
<th>$\sigma^2_{PE}$</th>
<th>$\sigma^2_e$</th>
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<tr>
<td>Birth wt</td>
<td>Angus</td>
<td>5.60</td>
<td>-.48</td>
<td>2.92</td>
<td>-5.07</td>
<td>10.49</td>
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<td>Hereford</td>
<td>11.09</td>
<td>-.88</td>
<td>4.25</td>
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<td>Angus</td>
<td>.0054</td>
<td>-.0009</td>
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<td>Hereford</td>
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<td>205-day wt</td>
<td>Angus</td>
<td>282.75</td>
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<td>71.51</td>
<td>-140.66</td>
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<td>400.82</td>
<td>-25.48</td>
<td>258.93</td>
<td>-133.29</td>
<td>107.90</td>
</tr>
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Table 3. Heritability estimates and genetic correlations between direct and maternal effects for preweaning growth traits of Angus and Hereford cattle

<table>
<thead>
<tr>
<th>Trait</th>
<th>Breed</th>
<th>$h^2_A$</th>
<th>$h^2_M$</th>
<th>$r_{AM}$</th>
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<tbody>
<tr>
<td>Birth wt</td>
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<td>.42</td>
<td>.22</td>
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<tr>
<td></td>
<td>Hereford</td>
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<td>.22</td>
<td>-.13</td>
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<tr>
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<td>.57</td>
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<td>-.32</td>
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<tr>
<td></td>
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<td>.58</td>
<td>.39</td>
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<tr>
<td>205-day wt</td>
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<td>-.36</td>
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<tr>
<td></td>
<td>Hereford</td>
<td>.66</td>
<td>.43</td>
<td>-.08</td>
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