Genetic Relationships Among Direct and Maternal Components of Milk Yield and Maternal Weaning Gain in a Multibreed Beef Herd

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ABSTRACT: Data spanning 1980 to 1993 from a multibreed beef herd including primarily eight breeds (Angus, Charolais, Gelbvieh, Hereford, Maine-Anjou, Pinzgauer, Simmental, and Tarentaise) were used to obtain 2,207 records on 200-d weaning gain (WG) and 1,826 records on 200-d milk yield (MY), obtained by machine milking after oxytocin injection. Estimates of (co)variances for the two traits (WG and MY) were obtained with REML with breed of calf, breed of cow, and heterotic effects modeled for the two traits. Animal effects of calf (CalfWG, CalfMY) and cow (CowWG, CowMY) contributions to each trait were modeled including 2,926 animals. The permanent environmental effect of the cow was modeled for MY, with 693 levels. Estimates of breed differences were generally similar to literature estimates. Simmental, Charolais, and Maine-Anjou were highest for CalfWG, and Tarentaise, Simmental, Gelbvieh, and Maine-Anjou were highest for CowMY. Heterosis was estimated at 8.00, 2.58, 4.05, and 5.50% of the mean for CalfWG, CowWG, CalfMY, and CowMY, respectively. Variance attributable to repeated records on CowMY represented 9% of phenotypic variance. Heritabilities estimated were .22 and .24 for CalfWG and CowWG and .04 and .35 for CalfMY and CowMY. Genetic correlations estimated between CalfWG and CowWG and between CalfMY and CowMY were −.35 and −.64, respectively. A genetic correlation between CowWG and CowMY of .76 indicates that maternal weaning gain evaluations are a good predictor of a cow’s potential for milk yield.

Key Words: Beef Cattle, Milk Yield, Maternal Effects, Genetic Parameters, Breed Differences

Introduction

Milk yield of beef cows is positively related to efficiency of beef production from birth to weaning (Kress et al., 1969; Marshall et al., 1976; Freking and Marshall, 1992) and from birth to slaughter (Brown and Dinkel, 1982; Miller et al., 1999). Evaluating animals for milk yield when selecting in commercial situations is accomplished through genetic evaluations for maternal weaning gain, often referred to inappropriately as milk, because milk yield is not measured directly.

Maternal weaning gain evaluations split weaning gain of the calf into a contribution from calf growth (direct weaning gain) and from maternal environment of the cow (maternal weaning gain). Similarly, milk yield of the cow can be considered as a trait influenced by the calf and the cow. The calf can influence milk yield of the cow through demand for milk and nursing frequency (Drewry et al., 1959; Mezzadra et al., 1989).

The value of maternal weaning gain as an indicator of milk yield is often questioned. A correlation of .8 and heritabilities of .12 and .17 for direct milk yield and maternal weaning gain, respectively, have been reported (Meyer et al., 1994). More estimates of the genetic correlation between maternal weaning gain and milk yield are required. This genetic correlation is important because it determines how effective selection for the indicator trait, maternal weaning gain, can be at changing the economically important trait, milk yield.

The objective of this study was to estimate (co)variance components for cow and calf contributions to weaning gain and milk yield. (Co)variance estimates provide an estimate of the genetic correlation between maternal (cow contribution) weaning gain and direct (cow contribution) milk yield. A secondary objective was to obtain breed differences and heterosis estimates for direct and maternal weaning gain and milk yield.
Materials and Methods

Data

Data were collected at the Elora Beef Research Centre from 1980 to 1993. Breed composition of the animals generally was the result of three breeding systems, Herefords (HE; purebred Herefords), large rotational (LR; rotational cross of Charolais, Simmental, and Maine-Anjou), and small rotational (SR; rotational cross of Angus, Gelbvieh, Pinzgauer, and Tarentaise that evolved into a rotational cross of Angus, Hereford, and Salers). Formation of these breeding systems and variation from the prescribed rotational crosses led to variation and overlap in breed composition within and between breeding systems. Breed composition of calves and cows is described in Tables 1 and 2. Breed composition heterozygosity of calves and cows is presented in Table 3. A more complete description of the cattle and their management is provided in McMorris and Wilton (1986).

Weaning gain (WG) adjusted to 200 d was calculated as the difference in weight between birth

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**Table 1. Breed constitution of calves contributing to records on 200-d weaning gain (WG) or milk yield (MY)**

<table>
<thead>
<tr>
<th>Breed group</th>
<th>n&lt;sup&gt;a&lt;/sup&gt;</th>
<th>Mean&lt;sup&gt;b&lt;/sup&gt;</th>
<th>SD</th>
<th>n</th>
<th>Mean</th>
<th>SD</th>
</tr>
</thead>
<tbody>
<tr>
<td>Angus</td>
<td>811</td>
<td>.258</td>
<td>.179</td>
<td>706</td>
<td>.257</td>
<td>.180</td>
</tr>
<tr>
<td>Dairy&lt;sup&gt;c&lt;/sup&gt;</td>
<td>462</td>
<td>.084</td>
<td>.086</td>
<td>381</td>
<td>.069</td>
<td>.066</td>
</tr>
<tr>
<td>Charolais</td>
<td>1,083</td>
<td>.295</td>
<td>.197</td>
<td>908</td>
<td>.303</td>
<td>.197</td>
</tr>
<tr>
<td>Continental&lt;sup&gt;d&lt;/sup&gt;</td>
<td>216</td>
<td>.166</td>
<td>.132</td>
<td>132</td>
<td>.120</td>
<td>.126</td>
</tr>
<tr>
<td>Gelbvieh</td>
<td>391</td>
<td>.258</td>
<td>.157</td>
<td>352</td>
<td>.252</td>
<td>.152</td>
</tr>
<tr>
<td>Hereford&lt;sup&gt;e&lt;/sup&gt;</td>
<td>1,308</td>
<td>.374</td>
<td>.379</td>
<td>1,068</td>
<td>.390</td>
<td>.389</td>
</tr>
<tr>
<td>Holstein</td>
<td>600</td>
<td>.104</td>
<td>.074</td>
<td>488</td>
<td>.086</td>
<td>.058</td>
</tr>
<tr>
<td>Limousin</td>
<td>207</td>
<td>.283</td>
<td>.192</td>
<td>139</td>
<td>.246</td>
<td>.135</td>
</tr>
<tr>
<td>Maine-Anjou</td>
<td>850</td>
<td>.300</td>
<td>.178</td>
<td>713</td>
<td>.289</td>
<td>.176</td>
</tr>
<tr>
<td>Pinzgauer</td>
<td>351</td>
<td>.284</td>
<td>.162</td>
<td>325</td>
<td>.273</td>
<td>.158</td>
</tr>
<tr>
<td>Salers</td>
<td>236</td>
<td>.422</td>
<td>.128</td>
<td>188</td>
<td>.434</td>
<td>.122</td>
</tr>
<tr>
<td>Simmental</td>
<td>1,001</td>
<td>.315</td>
<td>.214</td>
<td>904</td>
<td>.310</td>
<td>.212</td>
</tr>
<tr>
<td>Shorthorn</td>
<td>700</td>
<td>.081</td>
<td>.117</td>
<td>561</td>
<td>.068</td>
<td>.101</td>
</tr>
<tr>
<td>Tarentaise</td>
<td>205</td>
<td>.288</td>
<td>.167</td>
<td>181</td>
<td>.270</td>
<td>.161</td>
</tr>
</tbody>
</table>

<sup>a</sup>Number of animals containing some portion of genes from that breed group.
<sup>b</sup>Units are proportion of purebred.
<sup>c</sup>Including Jersey, Ayrshire, Brown Swiss, and undescriptive crossbred.
<sup>d</sup>Including Belgian Blue, Blonde d’Aquitaine, Chianina, Marchigiana, Romagnola, and Parthenais.
<sup>e</sup>Including polled and horned.

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**Table 2. Breed constitution of cows contributing to records on 200-d weaning gain (WG) or milk yield (MY)**

<table>
<thead>
<tr>
<th>Breed group</th>
<th>n&lt;sup&gt;a&lt;/sup&gt;</th>
<th>Mean&lt;sup&gt;b&lt;/sup&gt;</th>
<th>SD</th>
<th>n</th>
<th>Mean</th>
<th>SD</th>
</tr>
</thead>
<tbody>
<tr>
<td>Angus</td>
<td>596</td>
<td>.297</td>
<td>.177</td>
<td>522</td>
<td>.294</td>
<td>.175</td>
</tr>
<tr>
<td>Dairy&lt;sup&gt;c&lt;/sup&gt;</td>
<td>406</td>
<td>.171</td>
<td>.179</td>
<td>333</td>
<td>.139</td>
<td>.138</td>
</tr>
<tr>
<td>Charolais</td>
<td>938</td>
<td>.293</td>
<td>.199</td>
<td>779</td>
<td>.293</td>
<td>.206</td>
</tr>
<tr>
<td>Continental&lt;sup&gt;d&lt;/sup&gt;</td>
<td>203</td>
<td>.261</td>
<td>.172</td>
<td>128</td>
<td>.156</td>
<td>.079</td>
</tr>
<tr>
<td>Gelbvieh</td>
<td>294</td>
<td>.354</td>
<td>.159</td>
<td>274</td>
<td>.358</td>
<td>.156</td>
</tr>
<tr>
<td>Hereford&lt;sup&gt;e&lt;/sup&gt;</td>
<td>1,226</td>
<td>.434</td>
<td>.408</td>
<td>975</td>
<td>.437</td>
<td>.422</td>
</tr>
<tr>
<td>Holstein</td>
<td>641</td>
<td>.197</td>
<td>.150</td>
<td>522</td>
<td>.163</td>
<td>.117</td>
</tr>
<tr>
<td>Limousin</td>
<td>128</td>
<td>.275</td>
<td>.160</td>
<td>90</td>
<td>.192</td>
<td>.094</td>
</tr>
<tr>
<td>Maine-Anjou</td>
<td>676</td>
<td>.330</td>
<td>.174</td>
<td>585</td>
<td>.326</td>
<td>.173</td>
</tr>
<tr>
<td>Pinzgauer</td>
<td>246</td>
<td>.353</td>
<td>.163</td>
<td>237</td>
<td>.359</td>
<td>.161</td>
</tr>
<tr>
<td>Salers</td>
<td>63</td>
<td>.444</td>
<td>.112</td>
<td>43</td>
<td>.442</td>
<td>.117</td>
</tr>
<tr>
<td>Simmental</td>
<td>855</td>
<td>.433</td>
<td>.281</td>
<td>784</td>
<td>.439</td>
<td>.283</td>
</tr>
<tr>
<td>Shorthorn</td>
<td>734</td>
<td>.109</td>
<td>.130</td>
<td>597</td>
<td>.098</td>
<td>.120</td>
</tr>
<tr>
<td>Tarentaise</td>
<td>139</td>
<td>.335</td>
<td>.152</td>
<td>134</td>
<td>.338</td>
<td>.152</td>
</tr>
</tbody>
</table>

<sup>a</sup>Number of animals containing some portion of that breed group.
<sup>b</sup>Units are proportion of purebred.
<sup>c</sup>Including Jersey, Ayrshire, Brown Swiss, and undescriptive crossbred.
<sup>d</sup>Including Belgian Blue, Blonde d’Aquitaine, Chianina, Marchigiana, Romagnola, and Parthenais.
<sup>e</sup>Including polled and horned.
Table 3. Mean and standard deviation of heterozygosity of breed composition of animals contributing to records on weaning gain (WG) and milk yield (MY)

<table>
<thead>
<tr>
<th>Heterozygosity</th>
<th>WG</th>
<th>MY</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Mean</td>
<td>SD</td>
</tr>
<tr>
<td>Calf</td>
<td>.819</td>
<td>.354</td>
</tr>
<tr>
<td>Cow</td>
<td>.743</td>
<td>.419</td>
</tr>
</tbody>
</table>

and weaning divided by weaning age and multiplied by 200 d. Milk yield records for cows were determined using machine milking following oxytocin injection after a 6-h calf removal. Two to four milk yield records per lactation were used to estimate 200-d milk yield (MY) using the methods described in Miller et al. (1999), who based their methods on those of Clutter and Nielsen (1987). Briefly, to estimate 200-d MY, cows were assigned to one of the three breeding systems based on a cow's sire breed belonging to either LR or SR, with all purebred Hereford cows belonging to HE and all other Hereford-sired cows belonging to SR. Each of these three breeding systems was split into two groups based on parity of cow being ≤2 or >2. Linear regressions of 24-h milk yield on day of lactation within cow-calf pair were pooled to yield a representative trend within each of the six groups. Average deviation of the individual milk yield measurements for any one cow during a lactation from that predicted based on the group trend and day of lactation were used to shift the group trend, and milk yield of the cow (200-d, kg) was then the area under this deviated trend.

Data used for analysis are described in Table 4. There were 2,207 WG records for 817 cows and 1,826 MY records for 693 cows.

Analysis

Estimates of (co)variance components were obtained using the software MTDFREML (Boldman et al., 1993), which uses restricted maximum likelihood (REML) implementing a derivative-free algorithm. A minimum of two cold restarts were performed to check for global maxima. A variance of 10^{-8} of simplex function values was chosen as the convergence criterion.

Random animal effects in the model were Calf[WG], Cow[WG], Calf[MY], and Cow[MY], where Calf[WG] is the calf's contribution to growth through its genetic potential for growth inherited from the sire and dam, often referred to as direct weaning gain; Cow[WG] is the genetic component of the environment that the cow provides for calf growth, including nutrition (milk), often referred to as maternal weaning gain; Calf[MY] is the calf's genetic contribution to milk yield of the cow that is raising it through the calf's genetic component of nursing stimulus; and Cow[MY] is the cow's genetic potential for milk yield. Dam was distinct from the cow raising the calf because these data include embryo transfers.

The following full model was assumed for each of the traits:

\[
y = YR + PS + T + b_1X_1 + b_2X_2 + b_3H_{Calf} + b_4H_{Cow} + Calf + Cow + PE + e
\]

where

\[
y = \text{observation on WG or MY as described above},
\]

\[
YR = \text{year of birth of calf associated with observation } y, \text{ with 14 levels (1980 to 1993) for WG, and 13 levels for MY (1980 to 1992)},
\]

\[
PS = \text{parity of cow } \times \text{ sex of calf interaction with five levels for parity (parities 1, 2, 3, 4, and 5 or greater) and two sexes (heifer and bull)},
\]

\[
T = \text{calving type with four levels (natural birth or embryo transfer by born as single or twin)},
\]

\[
b_1 = \text{vector of partial regression coefficients of observation } y \text{ on proportion of 14 individual breed groups in breed composition of calf associated with observation } y,
\]

\[
b_2 = \text{vector of partial regression coefficients of observation } y \text{ on proportion of 14 individual breed groups in breed composition of cow associated with observation } y,
\]

\[
X_1 = \text{vector of proportions of 14 individual breed groups comprising the calf associated with observation } y,
\]

\[
X_2 = \text{vector of proportions of 14 individual breed groups comprising the cow associated with observation } y,
\]

\[
b_3 = \text{partial regression of observation } y \text{ on level of heterozygosity in the calf},
\]

\[
b_4 = \text{partial regression of observation } y \text{ on level of heterozygosity in the cow},
\]

Table 4. Characteristics of data on 200-d weaning gain (WG) and milk yield (MY)

<table>
<thead>
<tr>
<th>Item</th>
<th>Trait</th>
<th>WG, kg</th>
<th>MY, kg</th>
</tr>
</thead>
<tbody>
<tr>
<td>No. of animals in analysis</td>
<td></td>
<td>2,926</td>
<td>2,926</td>
</tr>
<tr>
<td>No. of records</td>
<td></td>
<td>2,207</td>
<td>1,826</td>
</tr>
<tr>
<td>No. of cows with records on progeny</td>
<td></td>
<td>817</td>
<td>693</td>
</tr>
<tr>
<td>No. of cows with own records and records on progeny</td>
<td></td>
<td>594</td>
<td>447</td>
</tr>
<tr>
<td>No. of missing sires of cows</td>
<td></td>
<td>217</td>
<td>147</td>
</tr>
<tr>
<td>No. of sires with records on progeny</td>
<td></td>
<td>261</td>
<td>239</td>
</tr>
<tr>
<td>No. of sires of cows</td>
<td></td>
<td>188</td>
<td>170</td>
</tr>
<tr>
<td>Mean</td>
<td></td>
<td>210.6</td>
<td>1,623.9</td>
</tr>
<tr>
<td>SD</td>
<td></td>
<td>36.0</td>
<td>516.0</td>
</tr>
</tbody>
</table>
\(H_{\text{Calf}}\) = expected heterozygosity of the calf associated with observation \(y\), based on breed composition of its parents,
\(H_{\text{Cow}}\) = expected heterozygosity of the cow associated with observation \(y\), based on breed composition of its parents,
Calf = additive genetic effect of the calf associated with observation \(y\),
Cow = additive genetic effect of the cow associated with observation \(y\),
PE = permanent environment effect of the cow associated with observation \(y\), and
e = residual associated with observation \(y\).

\[
E(y) = YR + PS + T + b_1X_1 + b_2X_2 + b_3H_{\text{Calf}} + b_4H_{\text{Cow}}
\]

Random effects were distinguished by traits using their respective subscripts,
\[
V = \begin{bmatrix}
\mathbf{A}_{\text{Calf}} & \mathbf{A}_{\text{MY}} & \mathbf{A}_{\text{Cow}} & \mathbf{A}_{\text{MY}} \\
\mathbf{A}_{\text{Calf}} & \mathbf{A}_{\text{MY}} & \mathbf{A}_{\text{Cow}} & \mathbf{A}_{\text{MY}} \\
\mathbf{A}_{\text{Cow}} & \mathbf{A}_{\text{MY}} & \mathbf{A}_{\text{Cow}} & \mathbf{A}_{\text{MY}} \\
\mathbf{A}_{\text{Cow}} & \mathbf{A}_{\text{MY}} & \mathbf{A}_{\text{Cow}} & \mathbf{A}_{\text{MY}} \\
\end{bmatrix}
\]

where \(\mathbf{A}\) is the numerator relationship matrix and \(g_{ij}\) represents the genetic (co)variance between genetic traits \(i\) and \(j\). Genetic traits \(\text{Calf}_{\text{WG}}, \text{Calf}_{\text{MY}}, \text{Cow}_{\text{WG}}\), and \(\text{Cow}_{\text{MY}}\) were represented as 1 to 4, respectively.

\[
V = \begin{bmatrix}
\mathbf{C}_1 & \mathbf{C}_2 \\
\mathbf{C}_1 & \mathbf{C}_2 \\
\end{bmatrix}
\]

where \(\mathbf{I}\) is an identity matrix and \(C_{ij}\) is the (co)variance between permanent environment effects of the dam associated with traits \(i\) and \(j\). Traits WG and MY were represented as traits 1 and 2, respectively.

\[
V = \begin{bmatrix}
\mathbf{r}_{11} & \mathbf{r}_{12} \\
\mathbf{r}_{11} & \mathbf{r}_{12} \\
\end{bmatrix}
\]

where \(\mathbf{I}\) is an identity matrix and \(r_{ij}\) is the (co)variance between residuals associated with traits \(i\) and \(j\). Traits WG and MY were represented as traits 1 and 2, respectively.

The model assumes the same genetic, permanent environment, and residual (co)variance matrices for the 14 breed groups. All unknown parents were assumed to come from the same unrelated, non-inbred base population regardless of breed. The 14 breed groups are defined in Table 1.

To remove dependencies among breed group effects, Hereford breed group solutions were constrained to zero. The MY and WG were first analyzed separately to determine random effects to include in the model. Removal of any (co)variance components resulted in a significant \((P < .05)\) reduction in the log likelihood. However, the heritability estimate of CowWG with PEWG included was close to zero. Without PEWG included, the heritability of CowWG was as expected based on literature estimates (Koots et al., 1994a). The resulting model for analysis included the full model for MY and the full model excluding PEWG for WG.

Standard errors for heritability estimates were approximated using the following formula provided in Koots (1994):

\[
\text{SE}_{\hat{h}_2} = 4 \sqrt{\frac{2(1 - t)(1 + (k - 1)t)^2}{k(k - 1)(s - 1)}}
\]

where \(t\) = the intraclass correlation, approximated by \(h^2/4\) for paternal half-sib estimates, \(k\) = average number of offspring per sire, and \(s\) = number of sires.

Standard errors of heritability for CowWG and CowMY were obtained substituting \(s\) with the number of sires of cows with records on progeny and \(k\) with the average number of cow progeny per sire in \(s\) (Table 4).

Standard errors of genetic correlation estimates were obtained using the following formula in Koots (1994):

\[
\text{SE}_{\hat{r}_{ij}} = \frac{1 - \hat{r}_{ij}^2}{\sqrt{2} \sqrt{\text{SE}_{\hat{h}_1} \text{SE}_{\hat{h}_2}}}
\]

where \(\hat{h}_1^2\) and \(\hat{h}_2^2\) are the individual heritability estimates and \(\text{SE}_{\hat{h}_1}\) and \(\text{SE}_{\hat{h}_2}\) are the standard errors of the heritability estimates calculated in [1].

**Results and Discussion**

Estimates of average breed effects of calf and cow contributions to weaning gain and milk yield are presented in Table 5. Generally, breed differences were estimated with low precision. Breed differences for CalfWG were similar to those of Nuñez-Dominguez et al. (1993) and Miller et al. (1994). Comparisons of breed differences across studies are difficult considering the possible variance in sampling of animals within a breed. For example, Miller et al. (1994) found Angus to be greater than Hereford for CalfWG, whereas this study and that of Nuñez-Dominguez et al. (1993) found the opposite. Sampling of animals within Hereford and Angus breeds could likely account for the differences between studies. Breeds ranked
Table 5. Breed differences relative to Hereford for calf and cow contributions to 200-d weaning gain and milk yield

<table>
<thead>
<tr>
<th>Breed</th>
<th>CalfWG</th>
<th>CowWG</th>
<th>CalfMY</th>
<th>CowMY</th>
</tr>
</thead>
<tbody>
<tr>
<td>Angus</td>
<td>−1.70</td>
<td>(6.6)</td>
<td>−160.29</td>
<td>(92.9)</td>
</tr>
<tr>
<td>Charolais</td>
<td>16.17</td>
<td>(7.4)</td>
<td>−143.65</td>
<td>(101.8)</td>
</tr>
<tr>
<td>Gelbvieh</td>
<td>1.23</td>
<td>(8.4)</td>
<td>−148.64</td>
<td>(117.0)</td>
</tr>
<tr>
<td>Maine-Anjou</td>
<td>7.12</td>
<td>(7.5)</td>
<td>−67.13</td>
<td>(112.6)</td>
</tr>
<tr>
<td>Pinzgauer</td>
<td>−1.69</td>
<td>(8.0)</td>
<td>−203.56</td>
<td>(110.5)</td>
</tr>
<tr>
<td>Salers</td>
<td>−3.02</td>
<td>(7.6)</td>
<td>−254.54</td>
<td>(101.3)</td>
</tr>
<tr>
<td>Simmental</td>
<td>19.99</td>
<td>(7.1)</td>
<td>−89.97</td>
<td>(104.6)</td>
</tr>
<tr>
<td>Tarentaise</td>
<td>−7.00</td>
<td>(9.5)</td>
<td>−132.98</td>
<td>(132.0)</td>
</tr>
</tbody>
</table>

*CalfWG, CowWG, CalfMY, and CowMY are calf and cow contributions to weaning gain (kg) and milk yield (kg), respectively.*

Table 6. Estimates of heterosis for cow and calf contribution to 200-d weaning gain and milk yield

<table>
<thead>
<tr>
<th>Item</th>
<th>CalfWG</th>
<th>CowWG</th>
<th>CalfMY</th>
<th>CowMY</th>
</tr>
</thead>
<tbody>
<tr>
<td>Heterosis, kg</td>
<td>16.84</td>
<td>(3.4)</td>
<td>5.43</td>
<td>(3.2)</td>
</tr>
<tr>
<td>Heterosis, %</td>
<td>8.00</td>
<td>(1.6)</td>
<td>2.58</td>
<td>(1.5)</td>
</tr>
</tbody>
</table>

*CalfWG, CowWG, CalfMY, and CowMY are calf and cow contributions to weaning gain (kg) and milk yield (kg), respectively.*

*Standard errors in parentheses.*

*Expressed as percentage of the mean.*
in Hereford-Devon crossbred heifers. Estimates of heterosis for $C_{\text{MY}}$ were not found. However, the literature indicates that milk yield of the dam was affected by growth of the calf; faster-growing calves stimulate more milk (Butson and Berg, 1984; Mezzadra et al., 1989; McCarter et al., 1991). With heterozygosity of the calf affecting calf growth, an effect of heterosis of the calf on $C_{\text{MY}}$ would be expected.

The residual correlation between traits was .15. Permanent environment variance for milk yield from repeated records on cows ($C_{\text{PE}}$) represented 9% of phenotypic variance. This estimate of permanent environment variance as a proportion of phenotypic is similar to the .11 obtained by Meyer et al. (1994) in Herefords and lower than the .17 obtained by Fan et al. (1996) analyzing a subset of these data without fitting the additive genetic effect of the calf.

Heritabilities and genetic correlations are presented in Table 7. Heritabilities of the calf ($C_{\text{WG}}$) and cow ($C_{\text{WG}}$) contribution to weaning gain of .22 and .24, respectively, were similar to those found in the literature. Koots et al. (1994a,b) provided a review of genetic parameters and reported that direct and maternal weaning gain had pooled estimates of heritability of .27 and .23, respectively. Heritability of calf ($C_{\text{MY}}$) and cow ($C_{\text{MY}}$) contribution to MY were .04 and .35, respectively. Meyer (1994) estimated the heritability of MY in Herefords to be .12. The estimate of .35 obtained in this study was comparable to the .44, .28, and .26 found in studies by Dillard et al. (1978), Diaz et al. (1992), and Fan et al. (1996), respectively. Heritability for milk yield was also in agreement with that observed in dairy cattle, for which estimates of .44 have recently been reported (Boettcher and Gibson, 1997) and a value of .33 is used for genetic evaluations in Canada as cited by Boettcher and Gibson (1997). The low (.04) estimate of heritability for $C_{\text{MY}}$ could be expected given that only a portion of the variance in MY would be due to nursing stimulus. For example, consider the calf’s influence on milk yield ($C_{\text{MY}}$) to be due entirely to calf growth ($C_{\text{WG}}$), resulting in $C_{\text{MY}}$ and $C_{\text{WG}}$ being identical. Given a heritability for $C_{\text{WG}}$ of .22, the proportion of the phenotypic variance in MY explained by $C_{\text{MY}}$ would be .18, a moderate proportion, to result in a heritability for $C_{\text{MY}}$ of .04.

The genetic correlation between $C_{\text{WG}}$ and $C_{\text{MY}}$ of .04 is of great concern in the industry. Previous studies have indicated a negative relationship. Koots et al. (1994b) reported an average genetic correlation of −.25, based on nine studies, which was of less magnitude than the estimate obtained here (−.35). Although the literature indicates a negative relationship, genetic evaluation systems often use a zero covariance in response to breeder concerns that maternal weaning gain evaluations of high-growth nonparent bulls are suppressed by a negative covariance.

Robinson (1996a,b) proposed that the real genetic correlation between direct and maternal weaning gain is not negative. When estimating genetic covariance between cow and calf contributions to weaning gain, a major source of information is cows that have their own weaning gain record as a calf and then become cows. Such animals express both their potential for calf and cow contribution for weaning gain. This was pointed out by K. Meyer (personal communication). The proportion of cows that have a record in the data as a calf was high, at 73 and 65% for WG and MY, respectively (Table 4). Further research into the relationship between data structure and the genetic covariance between direct and maternal weaning gain is warranted.

The genetic correlation estimated between $C_{\text{WG}}$, or maternal weaning gain, and $C_{\text{MY}}$, or milk yield, was high (.76) and in agreement with that of Meyer et al. (1994) (.80). This high genetic correlation indicates that maternal weaning gain evaluations are good indicators of cow milk yield. This is in agreement with studies of the relationships between cow contributions to weaning gain EPD and actual milk yield (Diaz et al., 1992; Marston et al., 1992; Mallinckrodt et al., 1993). Considering the benefits of increased milk yield (Miller et al., 1999), producers could use maternal weaning gain evaluations to improve the profit of beef production from birth to slaughter when management is sufficient to maintain reproduction with increasing milk yield.

### Implications

The genetic correlation between milk yield and maternal weaning gain was estimated to be high. This
high correlation indicates that maternal weaning gain evaluations are a good indicator of milk yield. Milk yield is a trait of economic importance in beef production and can effectively be selected for in a breeding program, indirectly through maternal weaning gain evaluations.

Literature Cited


