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J Anim Sci 1999. 77:1155-1161.

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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 (Calf_{WG}, Calf_{MY}) and cow (Cow_{WG}, Cow_{MY}) 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 Calf_{WG}, and Tarentaise, Simmental, Gelbvieh, and Maine-Anjou were highest for Cow_{MY}. Heterosis was estimated at 8.00, 2.58, 4.05, and 5.50% of the mean for Calf_{WG}, Cow_{WG}, Calf_{MY}, and Cow_{MY}, respectively. Variance attributable to repeated records on Cow_{MY} represented 9% of phenotypic variance. Heritabilities estimated were .22 and .24 for Calf_{WG} and Cow_{WG} and .04 and .35 for Calf_{MY} and Cow_{MY}. Genetic correlations estimated between Calf_{WG} and Cow_{WG} and between Calf_{MY} and Cow_{MY} were $-.35$ and $-.64$, respectively. A genetic correlation between Cow_{WG} and Cow_{MY} 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

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J. Anim. Sci. 1999. 77:1155–1161

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.

Received March 2, 1998.

Accepted November 2, 1998.

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

Breed group	WG, kg (n = 2,207)			MY, kg (n = 1,826)		
	n ^a	Mean ^b	SD	n	Mean	SD
Angus	811	.258	.179	706	.257	.180
Dairy ^c	462	.084	.086	381	.069	.066
Charolais	1,083	.295	.197	908	.303	.197
Continental ^d	216	.166	.132	132	.120	.126
Gelbvieh	391	.258	.157	352	.252	.152
Hereford ^e	1,308	.374	.379	1,068	.390	.389
Holstein	600	.104	.074	488	.086	.058
Limousin	207	.283	.192	139	.246	.201
Maine-Anjou	850	.300	.178	713	.289	.176
Pinzgauer	351	.284	.162	325	.273	.158
Salers	236	.422	.128	188	.434	.122
Simmental	1,001	.315	.214	904	.310	.212
Shorthorn	700	.081	.117	561	.068	.101
Tarentaise	205	.288	.167	181	.270	.161

^aNumber of animals containing some portion of genes from that breed group.

^bUnits are proportion of purebred.

^cIncluding Jersey, Ayrshire, Brown Swiss, and undescriptive crossbred.

^dIncluding Belgian Blue, Blonde d'Aquitaine, Chianina, Marchigiana, Romagnola, and Parthenais.

^eIncluding polled and horned.

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

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

Breed group	WG, kg (n = 2,207)			MY, kg (n = 1,826)		
	n ^a	Mean ^b	SD	n	Mean	SD
Angus	596	.297	.177	522	.294	.175
Dairy ^c	406	.171	.179	333	.139	.138
Charolais	938	.293	.199	779	.293	.206
Continental ^d	203	.261	.172	128	.156	.079
Gelbvieh	294	.354	.159	274	.358	.156
Hereford ^e	1,226	.434	.408	995	.437	.422
Holstein	641	.197	.150	522	.163	.117
Limousin	128	.275	.160	90	.192	.094
Maine-Anjou	676	.330	.174	585	.326	.173
Pinzgauer	246	.353	.163	237	.359	.161
Salers	63	.444	.112	43	.442	.117
Simmental	855	.433	.281	784	.439	.283
Shorthorn	734	.109	.130	597	.098	.120
Tarentaise	139	.335	.152	134	.338	.152

^aNumber of animals containing some portion of that breed group.

^bUnits are proportion of purebred.

^cIncluding Jersey, Ayrshire, Brown Swiss, and undescriptive crossbred.

^dIncluding Belgian Blue, Blonde d'Aquitaine, Chianina, Marchigiana, Romagnola, and Parthenais.

^eIncluding 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)

Heterozygosity	WG		MY	
	Mean	SD	Mean	SD
Calf	.819	.354	.810	.361
Cow	.743	.419	.728	.427

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:

$$y = YR + PS + T + \mathbf{b}_1\mathbf{X}_1 + \mathbf{b}_2\mathbf{X}_2 + \mathbf{b}_3H_{Calf} + \mathbf{b}_4H_{Cow} + Calf + Cow + PE + e$$

where

- y = observation on WG or MY as described above,
- YR = year of birth of calf associated with observation y , with 14 levels (1980 to 1993) for WG, and 13 levels for MY (1980 to 1992),
- PS = parity of cow \times 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 = calving type with four levels (natural birth or embryo transfer by born as single or twin),
- \mathbf{b}_1 = vector of partial regression coefficients of observation y on proportion of 14 individual breed groups in breed composition of calf associated with observation y ,
- \mathbf{b}_2 = vector of partial regression coefficients of observation y on proportion of 14 individual breed groups in breed composition of cow associated with observation y ,
- \mathbf{X}_1 = vector of proportions of 14 individual breed groups comprising the calf associated with observation y ,
- \mathbf{X}_2 = vector of proportions of 14 individual breed groups comprising the cow associated with observation y ,
- b_3 = partial regression of observation y on level of heterozygosity in the calf,
- b_4 = partial regression of observation y on level of heterozygosity in the cow,

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

Item	Trait	
	WG, kg	MY, kg
No. of animals in analysis	2,926	2,926
No. of records	2,207	1,826
No. of cows with records on progeny	817	693
No. of cows with own records and records on progeny	594	447
No. of missing sires of cows	217	147
No. of sires with records on progeny	261	233
No. of sires of cows	188	170
Mean	210.6	1,623.9
SD	36.0	516.0

- H_{calf} = expected heterozygosity of the calf associated with observation y , based on breed composition of its parents,
 H_{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 .

$$E(y) = YR + PS + T + \mathbf{b}_1\mathbf{X}_1 + \mathbf{b}_2\mathbf{X}_2 + b_3H_{\text{Calf}} + b_4H_{\text{Cow}}$$

$$E \begin{bmatrix} \text{Calf} \\ \text{Cow} \\ \text{PE} \\ e \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}$$

Random effects were distinguished by traits using their respective subscripts,

$$V \begin{bmatrix} \text{Calf}_{\text{WG}} \\ \text{Calf}_{\text{MY}} \\ \text{Cow}_{\text{WG}} \\ \text{Cow}_{\text{MY}} \end{bmatrix} = \begin{bmatrix} \mathbf{Ag}_{11} & \mathbf{Ag}_{12} & \mathbf{Ag}_{13} & \mathbf{Ag}_{14} \\ \mathbf{Ag}_{21} & \mathbf{Ag}_{22} & \mathbf{Ag}_{23} & \mathbf{Ag}_{24} \\ \mathbf{Ag}_{31} & \mathbf{Ag}_{32} & \mathbf{Ag}_{33} & \mathbf{Ag}_{34} \\ \mathbf{Ag}_{41} & \mathbf{Ag}_{42} & \mathbf{Ag}_{43} & \mathbf{Ag}_{44} \end{bmatrix}$$

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

$$V \begin{bmatrix} \text{PE}_{\text{WG}} \\ \text{PE}_{\text{MY}} \end{bmatrix} = \begin{bmatrix} \mathbf{IC}_{11} & \mathbf{IC}_{12} \\ \mathbf{IC}_{21} & \mathbf{IC}_{22} \end{bmatrix}$$

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.

$$V \begin{bmatrix} e_{\text{WG}} \\ e_{\text{MY}} \end{bmatrix} = \begin{bmatrix} \mathbf{Ir}_{11} & \mathbf{Ir}_{12} \\ \mathbf{Ir}_{21} & \mathbf{Ir}_{22} \end{bmatrix}$$

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 Cow_{WG} with PE_{WG} included was close to zero. Without PE_{WG} included, the heritability of Cow_{WG} 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 PE_{WG} for WG.

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

$$SE_{\hat{h}_2} = 4 * \sqrt{\frac{2(1-t)^2[1+(k-1)t]^2}{k(k-1)(s-1)}} \quad [1]$$

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 Cow_{WG} and Cow_{MY} 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):

$$SE_{\hat{r}_g} = \frac{1 - \hat{r}_g^2}{\sqrt{2}} \sqrt{\frac{SE_{\hat{r}_1^2} SE_{\hat{r}_2^2}}{\hat{r}_1^2 \hat{r}_2^2}} \quad [2]$$

where \hat{r}_1^2 and \hat{r}_2^2 are the individual heritability estimates and $SE_{\hat{r}_1^2}$ and $SE_{\hat{r}_2^2}$ 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 Calf_{WG} were similar to those of Núñez-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 Calf_{WG} , whereas this study and that of Núñez-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

Breed	Calf _{WG} ^a		Cow _{WG}		Calf _{MY}		Cow _{MY}	
Angus	-1.70	(6.6) ^b	14.01	(6.3)	-160.29	(92.9)	360.89	(111.3)
Charolais	16.17	(7.4)	14.73	(7.1)	-143.65	(101.8)	346.51	(118.4)
Gelbvieh	1.23	(8.4)	26.08	(7.8)	-148.64	(117.0)	678.31	(135.2)
Maine-Anjou	7.12	(7.5)	24.13	(7.2)	-67.13	(112.6)	619.95	(124.2)
Pinzgauer	-69	(8.0)	16.91	(7.8)	-203.56	(110.5)	467.07	(134.0)
Salers	-3.02	(7.6)	19.09	(11.3)	-254.54	(101.3)	396.11	(199.0)
Simmental	19.99	(7.1)	24.71	(6.2)	-89.97	(104.6)	691.73	(99.6)
Tarentaise	-7.00	(9.5)	22.75	(10.0)	-132.98	(132.0)	792.36	(171.5)

^aCalf_{WG}, Cow_{WG}, Calf_{MY}, and Cow_{MY} are calf and cow contributions to weaning gain (kg) and milk yield (kg), respectively.

^bStandard errors in parentheses.

similarly for cow contribution to weaning gain (Cow_{WG}) in this study and that of Miller et al. (1994) and Núñez-Dominguez et al. (1993). However, the magnitude of breed differences in this study were similar to those found by Núñez-Dominguez et al. (1993), but breed differences for Cow_{WG} were smaller in Miller et al. (1994).

Breed differences for Cow_{MY} generally coincided with breed differences for Cow_{WG}. Breed rankings for milk yield obtained in this study seem consistent with results in the literature. However, some differences among estimates of breed effects for milk yield (Cow_{MY}) existed between studies. This study found Angus and Charolais to be similar for Cow_{MY}, in agreement with Notter et al. (1979). Melton et al. (1967) and Gregory et al. (1992) found Charolais to be greater than Angus. Marshall et al. (1976) found the opposite. Again, breed differences between studies could be due to sampling within a breed. Gregory et al. (1992) found Gelbvieh and Pinzgauer to be similar for milk yield, whereas, in this study, Gelbvieh was superior to Pinzgauer and similar to Simmental. Simmental was high for milk yield in this study and in that of Gregory et al. (1992).

Fiss and Wilton (1992) investigated maternal grand-sire breed of the calf contributions to milk yield within breeding system, using some of the same data as in this study, and found results contradictory to those obtained here. Within LR, Fiss and Wilton (1992) ranked the breeds Charolais, Maine-Anjou, and Simmental in descending order. This was opposite to rankings expected based on breed contributions to

Cow_{WG}, as outlined previously. Within SR, Fiss and Wilton (1992) found Gelbvieh to be higher for Cow_{MY} than Pinzgauer, which was similar to this study. However, Tarentaise was estimated as making the least contribution to milk yield, in contrast to this study, which found Tarentaise to be highest for Cow_{MY} of all breeds. This relatively high value for Cow_{MY} for Tarentaise corresponded to results for Cow_{WG} obtained by Núñez-Dominguez et al. (1993). Kress et al. (1995) also found Tarentaise to be considerably higher in milk yield than Herefords, with a difference of 3.1 kg/d found in later stages of lactation. The four breeds that had high contributions to Cow_{MY} in this study originated as dual-purpose breeds in Europe (Tarentaise, Simmental, Gelbvieh, and Maine-Anjou).

Estimates of heterosis (Table 6) were in general agreement with the literature. Heterosis for Calf_{WG} (8.0%) was higher than reported in the literature; Dillard et al. (1980), Cundiff et al. (1992), Gregory et al. (1992), and Kress et al. (1995) noted estimates ranging from 3 to 5.8%. Heterosis for Cow_{WG}, conversely, was to the low end of the range of 3 to 5.8% reported by Dillard et al. (1980), Cundiff et al. (1992), and Kress et al. (1992).

Similar to findings of Kress et al. (1992), estimated heterosis was higher for Cow_{MY} than that for Cow_{WG}. The estimate of 5.5% observed in this study was within the range of 2.76 to 14.5% reported for beef cattle by Marshall et al. (1976), Gregory et al. (1992), and Kress et al. (1992). Johnston et al. (1995) reported an average 32% heterosis for Cow_{MY}

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

Item	Calf _{WG} ^a		Cow _{WG}		Calf _{MY}		Cow _{MY}	
Heterosis, kg	16.84	(3.4) ^b	5.43	(3.2)	65.69	(53.7)	89.20	(57.3)
Heterosis, % ^c	8.00	(1.6)	2.58	(1.5)	4.05	(3.3)	5.50	(3.5)

^aCalf_{WG}, Cow_{WG}, Calf_{MY}, and Cow_{MY} are calf and cow contributions to weaning gain (kg) and milk yield (kg), respectively.

^bStandard errors in parentheses.

^cExpressed as percentage of the mean.

Table 7. Heritabilities (on diagonal) of and genetic correlations (above diagonal) between calf and cow contributions to 200-d weaning gain and milk yield

	Calf _{WG} ^a		Cow _{WG}		Calf _{MY}		Cow _{MY}	
Calf _{WG}	.22	(.06) ^b	-.35	(.27)	.80	(.15)	-.08	(.26)
Cow _{WG}			.24	(.17)	-.80	(.24)	.76	(.18)
Calf _{MY}					.04	(.05)	-.64	(.34)
Cow _{MY}							.35	(.18)

^aCalf_{WG}, Cow_{WG}, Calf_{MY}, and Cow_{MY} are calf and cow contributions to weaning gain (kg) and milk yield (kg), respectively.

^bStandard errors in parentheses.

in Hereford-Devon crossbred heifers. Estimates of heterosis for Calf_{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 Calf_{MY} would be expected.

The residual correlation between traits was .15. Permanent environment variance for milk yield from repeated records on cows (Cow_{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 (Calf_{WG}) and cow (Cow_{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 (Calf_{MY}) and cow (Cow_{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 Calf_{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 (Calf_{MY}) to be due entirely to calf growth (Calf_{WG}), resulting in Calf_{MY} and Calf_{WG} being identical. Given a heritability for Calf_{WG} of .22, the proportion of the phenotypic variance in MY explained by Calf_{MY} would be .18, a moderate proportion, to result in a heritability for Calf_{MY} of .04.

The genetic correlation between Calf_{WG} and Cow_{WG} (direct and maternal weaning gain) 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 Cow_{WG}, or maternal weaning gain, and Cow_{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.

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