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Estimation of Genetic Parameters and Trends in Pre-Weaning Traits of Beef Lines Subject to Phenotypic Selection

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Abstract : Production records over a twenty-five year period (n=6047) from three synthetic beef lines, Beef Synthetic 1 (BS1), Beef Synthetic 2 (BS2) and Dairy Beef Synthetic (DBS), at the University of Alberta Kinsella Research Station were analyzed to determine genetic parameters and genetic trends for birth weight (BW) and pre-weaning gain to 200-d (WG). The lines were selected for high fertility in females, high pre- and post-weaning gain in males and against high BW in both sexes. The Multiple Traits Derivative Free Restricted Maximum Likelihood (MTDFREML) was used to estimate (co) variance components, direct (h^2_d) and maternal (h^2_m) heritability, direct (r_{gd}) and maternal (r_{gm}) genetic correlations. The h^2_d and h^2_m for BW were 0.45 and 0.10 respectively, and the h^2_d and h^2_m for WG were 0.19 and 0.12 respectively. The r_{gd} and r_{gm} between BW and WG was 0.32 and 0.18 respectively. In BS1, the average direct and maternal breeding value change for BW was 0.08 and 0.00kg yr^{-1} respectively, and for WG was 0.29 and 0.12 kg yr^{-1} respectively. Genetic trends similar to BS1 were observed in the BS2 and DBS lines for BW only. Under commercial situations, by phenotypic selection alone it is possible to improve WG with little or no increase in BW.

Key words : Direct, Maternal, Heritability, Genetic trend, Birth weight, Weaning gain, Synthetic beef cattle

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Introduction

Abbreviations : ALBV, across line breeding value; BS, Beef Synthetic; BW, body weight; D, direct additive genetic; DBS, Dairy Beef Synthetic; EBV, estimated breeding value; M, maternal additive genetic; MTDFREML, multiple traits derivative free restricted maximum likelihood; WG, Weaning gain.

Genetic improvement in beef production traits has been accomplished through selection and crossbreeding. Selection based on expected breeding values (EBV) have been effective in making continuous genetic improvement in production traits (Robinson and Chesnais 1988 and Kennedy *et al.,* 1996), but is primarily used in the beef seed stock industry, although somewhat limited in use under commercial conditions. As such, simple selection criteria based on phenotype, and cross breeding systems that are easy to apply are often used in commercial beef production. Two- and three-breed crossbreeding systems are difficult to sustain especially in small beef operations due to the cost of perpetuating and selecting superior pure breeds for breeding from a sufficiently large genetic base. Hence, synthetic (composite) breeds offer an alternate system that is generally competitive with crossbreeding and easier to manage regardless of herd size (Gregory *et al.,* 1994). However, when the genetic base is small and a few sires are used for breeding, the degree of inbreeding can increase over time, nullifying the advantages of heterosis, especially in traits that are significantly influenced by non-additive genetic effects. The estimation of genetic parameters and genetic trends is essential for developing breeding strategies and the evaluation of such programs. Genetic trend analysis is done to evaluate continuous breeding programs and compare the observed genetic gains with the theoretical expected genetic progress over time. Although many studies assessing genetic parameters (Koots *et al,*. 1994a, 1994b) and genetic trends (Van Vleck, 1996 and Sullivan, 1999) for growth traits in beef cattle can be found in the literature, most studies have focused on non-commercial breeding (seed stock) populations undergoing genetic selection. However, in many non-commercial herds, selection of breeding animals is based solely on phenotype and little information is available in the literature on the analysis of genetic trends in such composite populations. The objectives of this study were to estimate genetic parameters and genetic trends over time in birth weight and weaning gain in three synthetic beef lines, managed as a commercial herd, in which sires were phenotypically selected for high pre-weaning and post-weaning gain, against excessively high birth weights and females selected for high fertility and against calving difficulty.

Materials and Methods

Production records (n=6047), collected from 1962 to 1987, at the Kinsella Beef Research Station of the University of Alberta, were used in this study. The Kinsella ranch was established in 1960 and at that time consisted of foundation breeds of cattle, which were combined to develop one synthetic line, which was later renamed Beef Synthetic 1 (BS1), and a purebred Hereford line. The synthetic line combined Angus for its mothering ability, Galloway for its hardiness and Charolais for muscling and leanness. From 1960-1966, the BS1 and Hereford lines were developed and multiplied and all fertile females retained for breeding. The breed composition of the BS1 line in 1966 was 41.6% Angus, 29.8% Charolais, 26.4% Galloway, 0.6% Brown Swiss and 1.6% comprising of other breeds such as Hereford, Holstein, Brahman and Jersey which were introduced by the foundation breeding animals. In 1970, the composition of BS1 was 37.6% Angus, 35.1% Charolais, 20.3% Galloway, 4.7% Brown Swiss and 2.3% of the other breeds, by 1980, it comprised of about 37% Angus, 34% Charolais, 21% Galloway, 5% Brown Swiss and the remainder comprising other breeds. This breed composition has changed only slightly over the years. The purebred Hereford line was maintained until 1980 and in 1981 the line was crossed with other beef breeds to develop a crossbred line which was later renamed Beef Synthetic 2 (BS2). This line was made up of approximately 60% Hereford and 40% other beef breeds. In 1968, a Dairy Beef Synthetic line (DBS) was developed by crossing the beef lines with large milking breeds such as Holstein and Brown Swiss. In 1975, the Simmental breed was introduced into the DBS line and the approximate composition of this line in 1979 was 28.2% Holstein, 26.2% Brown Swiss, 11.2% Simmental and 34.4% beef breeds. In 1984 this line contained 23% Holstein, 24% Brown Swiss, 12% Simmental and 41% beef breeds that included Angus, Galloway, Hereford, Charolais, and small amounts of Guernsey, Jersey and Brahman. The DBS line was bred to contain approximately 60% dairy and 40% beef breeding. The breed composition of the different lines and management practices were described by Berg (1978), Berg and Makarechian (1980) and Berg *et al.* (1990). Animals at the Kinsella Research Station were cared for in accordance with the Canadian Council of Animal Care (1993) guidelines.

The Kinsella Research Station, located in east central Alberta is managed as a commercial unit. The annual precipitation is approximately 48 cm. Winters in this part of Alberta, Canada persist to the end of March, and April snowstorms often occur. All cattle populations were maintained and managed similarly, and were selected for the same traits. In the early years prior to 1980, selection of breeding sires within each line was based primarily on pre-weaning and post-weaning gain. After 1980, sires with excessively large birth weights were removed from the selection pool. Cows and heifers were bred in single sire breeding groups until 1985, within each breed group on pasture. The breeding period was approximately 60-80 days. Bred females were pregnancy checked four months after exposure to breeding. Females were selected as follows: heifers and cows failing to wean a calf in any year were culled; cows that were given any calving assistance were culled while heifers that needed a hard pull (mechanical device), veterinary assistance or Caesarian section were culled (Berg 1978). Among the culled cows, 51.4% were culled for failure to conceive, 12.1% for calf loss, 10.9% for calving problems, 7.7% for udder defects and 9.2% for other problems (Arthur *et al.,* 1992).

The breeding herds grazed a mixture of native rough fescue and improved pastures year round and were supplemented with an alfalfa-brome hay and green feed (oats) during the winter. Cows were wintered on open range pastures, which were either minimally grazed or not grazed in the previous summer. The pastures contained poplar bluff shelters. Winter supplementation usually began in December and continued through to March. Cows and heifers on the range were given minerals free choice and straw provided for bedding, some of which was eaten. Cows calved in the open range and heifers calved out in a separate pasture, which was easily accessible. At calving, calf birth weight, cow weight and cow body condition score were recorded. Calves were weaned on one day each year usually in September or October. At weaning, the cows weight and body condition score were recorded along with the calf's weaning weight. The weaning weight were adjusted for the age at weaning and pre-weaning gain calculated from birth to weaning.

Statistical Analysis : Two traits, birth weight and pre-weaning gain to 200 days were analyzed. The mult-trait mixed model equation used to obtain estimates of (co) variances and estimated breeding values of each individual animal was:

$$y = x\beta + Z_a d + Z_m m + Z_c c + e$$

where, *y* is a vector of observations; β is a vector of fixed effects (year of birth, combined effects of breed group-sex-age of dam); *d* is a vector of random direct additive genetic effect of the animal; *m* is a vector of random maternal genetic effects; *c* is a vector of random maternal permanent environmental effects, *e* is a vector of random residual effects and X, Z_d, Z_m and Z_c are incidence matrices relating observations to the relevant fixed and random effects respectively. The expectation of the mixed model equation was,

$$E(y) = x\,\beta$$

and the (co) variances structure of the random effects was

$$V\begin{bmatrix} d \\ m \\ c \\ e \end{bmatrix}=\begin{bmatrix} A\sigma_d^2 & A\sigma_{dm} & 0 & 0 \\ A\sigma_{dm} & A\sigma_m^2 & 0 & 0 \\ 0 & 0 & I_c\sigma_c^2 & 0 \\ 0 & 0 & 0 & I_n\sigma_e^2 \end{bmatrix}$$

Where A is the additive genetic relationship matrix, I_c and I_n are identity matrices of order equal to the number of maternal permanent environmental effects and the number of records respectively; , , , and are the additive direct, additive maternal genetic variances, maternal permanent environmental, residual variances and covariance betw- een direct and maternal additive genetic components respectively. The above (co) variance structure of the rando- m effects can be expanded to two traits, as considered in this study and was:

$$V\begin{bmatrix} d_1 \\ m_1 \\ d_2 \\ m_2 \end{bmatrix}=A\otimes\begin{bmatrix} \sigma_{d_1}^2 & \sigma_{d_1m_1} & \sigma_{d_1d_2} & \sigma_{d_1m_2} \\ \sigma_{d_1m_1} & \sigma_{m_1}^2 & \sigma_{d_2m_1} & \sigma_{m_1m_2} \\ \sigma_{d_1d_2} & \sigma_{d_2m_1} & \sigma_{d_2}^2 & \sigma_{d_2m_2} \\ \sigma_{d_1m_2} & \sigma_{m_1m_2} & \sigma_{d_2m_2} & \sigma_{m_2}^2 \end{bmatrix}$$

and

$$V\begin{bmatrix} c_1 \\ c_2 \end{bmatrix}=I_c\otimes\begin{bmatrix} \sigma_{c_1}^2 & \sigma_{c_1c_2} \\ \sigma_{c_1c_2} & \sigma_{c_2}^2 \end{bmatrix}$$

$$V\begin{bmatrix} e_1 \\ e_2 \end{bmatrix}=I_p\otimes\begin{bmatrix} \sigma_{e_1}^2 & \sigma_{e_1e_2} \\ \sigma_{e_1e_2} & \sigma_{e_2}^2 \end{bmatrix}$$

where $\otimes$ is the direct product operator assuming all other co-variances are null. The total additive genetic value a_{ij} animal i of trait j is the summation of direct d_{ij} and maternal m_{ij} additive genetic values of the animal i of traits j ($a_{ij} = d_{ij} + m_{ij}$). Solutions to a_{ij} were across-line estimated breeding values (ALBV) using the procedure described by Sullivan *et al.* (1999). Genetic trends for each synthetic line were determined by regressing ALBV on the year of bi- rth of each line separately. The data from 1966-1987 were used to compute the genetic trends for BS1 and BS2 and the data from 1969-1987 was used to compute the genetic trends for DBS.

The MTDFREML software, (Boldman *et al.,* 1995) which uses a derivative free algorithm (Gracer *et al,.* 1987) was u- sed to obtain the (co) variance log likelihood value and 10^{-8} was used as the convergence criteria. The estimates were obtained for phenotypic variance (σ^2_p), direct heritability ($h^2_d = \sigma^2_d/\sigma^2_p$), maternal heritability ($h^2_m = \sigma^2_m/\sigma^2_p$), ratio of maternal permanent environmental variance to phenotypic variance ($c^2 = \sigma^2_c/\sigma^2_p$) and genetic correlation ($r_{dm} = \sigma_{dm}/\sigma_d\sigma_m$) between direct and maternal genetic effects for the two traits respectively.

Results and Discussion

Means, standard deviations and coefficients of variation overall and by line for BW and WG are shown in Table 1. The values correspond closely with studies that used the same source of data (Pang *et al.,* 1998 and Goonewardene *et al.,* 1999). In general BW of BS1 and BS2 was similar while that of DBS was heavier. The WG of DBS was high- highest followed by BS1 and BS2, which was the lowest.

The inbreeding coefficient for BS1 averaged over the study period was 0.2±0.9% and ranged from 0-3.5%, the ave- average for BS2 was 0.1±0.2% and ranged from 0-0.7% and the average for DBS was 0.6±1.0% and ranged from 0-3.5%.

Genetic Parameter Estimates: Estimates of genetic parameters for BW and WG are shown in Table 2. Phenotypic variances for BW and WG were similar to the values of Tosh *et al.* (1999) and Ferreira *et al.* (1999) respectively. The direct and maternal heritability estimates for BW are similar to Bennett and Gregory (1996) who reported values of 0.47 and 0.08 respectively, Dodenhoff *et al.* (1998) who reported values of 0.45 and 0.10 respe- ctively, and

Tosh *et al.* (1999) who reported values of 0.51 and 0.09 respectively. The heritability of BW in our study is slightly lower than the value of 0.53 (Rodrigeuz-Almeida *et al.,* 1995) and higher than the value of 0.26 (Gregory *et al.,* 1995) reported for beef synthetics in the U.S. Direct and maternal heritability estimates for WG of 0.19 and 0.12 respectively in our study were lower than the values of 0.32 and 0.26 reported by Miller *et al.* (1994). However, our values were within the range in the review by Koots *et al.* (1999 a) and similar to the values of 0.24 and 0.13 averaged across many studies for direct and maternal heritability of WG respectively. In general, lower maternal heritabilities have been reported for beef composites compared to purebreds (Meyer *et al.,* 1993). The direct-maternal correlation for BW of 0.16 was similar to the value of 0.17 (Tosh *et al.,* 1999) and the direct-maternal correlation for WG was negative which is in general similar to the values in the literature for weaning weight and weaning gain (Koots *et al.* 1994a and Tosh *et al.* 1999). The negative correlation between direct and maternal effects for WG may be partly due to genetic antagonism (Tosh *et al.,* 1999) but Meyer (1993) concluded that the mod- erate to strong negative correlations is likely biased. Maternal permanent environmental variance expressed as a proportion of the phenotypic variance was very low for BW similar to the values of Gengler *et al.* (1997) and Tosh *et al.* (1999). The maternal non-genetic estimate for WG (0.15) was higher than the maternal genetic estimate (0.12) and was therefore more important for WG than for BW. These values are in agreement with those of Gengler *et al.* (1997) who found that the maternal permanent environmental estimate was higher than the estimate for maternal heritability of weaning weight in Hereford and Hereford crossbreds. The permanent environment estimates for 100-d weight reported by Bennett and Gregory (1996) in purebreds (0.13) and beef composites (0.11) are also similar to our estimate for WG. The phenotypic correlation between BW and WG was 0.27 and was lower than the phenotypic correlation between BW and weaning weight (Tosh *et al.,* 1999) (0.46) and the other correlations were within the reported range of Koots *et al.* (1994b). The direct and maternal genetic correlations between BW and WG were moderate to low and were lower than the equivalent correlations between BW and weaning weight (Tosh *et al.,* 1999).

Genetic Trends : Direct and maternal contributions to the genetic trends in BW and WG are shown in Table 3. The genetic trend in BW for BS1 and DBS was 90 g yr^{-1}, while the trend for BS2 was negative 40 g yr^{-1}. Maternal genetic trends were either non-existent or very small for BW in all three lines similar to reports of Song and Che snais (1994) and Sullivan *et al.* (1999). Amer *et al.* (1992) reported genetic trends in BW for Hereford, Charolais, Simmental and Limousin of 52, 14, 24 and 14 g yr^{-1}, respectively over 21 year period, while Sullivan *et al.* (1999) reported genetic trends from 1985-1995 in the range of 48 to 226 g yr^{-1} for BW among Limousin, Hereford, Charolais, Simmental and Angus cattle from the Ontario beef genetic evaluation program. Genetic trends for BW in Simmental, Limousin, Charolais, South Devon and Angus from the United Kingdom were reported to be 90, 70, 110, 50 and 117 g yr^{-1} respectively (Crump *et al.,* 1994). In general, genetic trends reflect selection and breeding objectives on each farm and will continue to change over time. In Canadian commercial populations, there is a trend towards lower birth weights in the Simmental, but in Hereford and Charolais cattle BW has increased by 230 and 130 g yr^{-1} respectively from 1990-1995 (Sullivan *et al.,* 1999). However, from 1988-1993, the average changes (not change per year) in BW for Angus, Charolais, Hereford, Limousin and Simmental were 1, -0.2, 2.6, 0.8 and 1.0 kg respectively (Song and Chesnais 1994).

All three commercial synthetic lines showed positive additive genetic trends ($d + m$) for WG with BS1 = 0.41 kg yr^{-1} which was the highest, followed by DBS = 0.28 kg yr^{-1}. The maternal additive genetic contribution in WG was not recognized in BS2 whereas, in BS1 and DBS it was about 29%. The lack of maternal genetic contribution in BS2 robably relates to the breeds used to develop each synthetic line, the genetic variation in WG for each line and lo- wer accuracy of selection (phenotypic selection). In the BS1, the Angus and Galloway were combined with Charolais, whereas in the BDS, dairy breeds such as Simmental, Brown Swiss and Holstein which are milk breeds were combined with beef breeds. However the BS2 is primarily Hereford crossed with other beef breeds and the breed contribution to milk production is less evident in this synthetic (Pang *et al.,* 1998). Sullivan *et al.* (1999) repo- rted genetic trends ($d + m$) in WG to range from 0.45 kg yr^{-1} in the Limousin to 1.95 kg yr^{-1} in the Angus, while the Amer *et al.* (1992) reported lower trends of 0.019 kg yr^{-1} for Charolais, 0.10 kg yr^{-1} for Angus, 0.24 kg yr^{-1} for Simme- ntal and 0.69 kg yr^{-1} for Hereford from 1970-1991. The genetic trend in 100-d weight for Simmental, Limousin, cha- rolais, South Devon and Angus in the U.K. was reported to be 0.84, 0.59, 0.84, 0.57 and 1.33 kg yr^{-1} respectively (Crump *et al.,* 1994). Lower direct genetic trends for weaning weight ranging from –90 to 150 g yr^{-1} were reported for composite beef cattle from two contrasting environments (Tosh and Kemp 2000). The genetic change in WG from 1988-1993 for Angus, Charolais, Hereford, Limousin and Simmental in Canada was estimated at 7.8, 11.0, 13.0, 6.0 and 10.2 kg respectively (Song and Chesnais 1994). These values are not trends per year but averages of totals over six years. These differences in genetic trend in the literature are partially due to differences in breeding programs (selection criteria, selection emphasis, breeding goals) and methods (statistical models) used for genetic evaluation (Khombe and Hays 1994; Crump *et al.,* 1994 and Menissier 1994). Models based on sire components only are known to compute breeding values that indicate less genetic improvement than full animal models (Ferreira *et al.,* 1999). Also, the wide variation in genetic estimates

Table 1: Means, Standard deviations and coefficient of variations for birth weight and weaning gain, overall and by line

Line^z	n	Birth weight (kg)			Weaning gain (kg)		
		Mean	SD	CV%	Mean	SD	CV%
Overall	6047	37.40	5.79	15.49	199.81	32.16	16.09
BS1	2831	36.88	5.62	15.23	199.49	30.55	15.31
BS2	2136	36.83	5.59	15.18	191.95	32.47	16.91
DBS	1080	39.89	5.95	14.92	215.84	29.71	14.76

^{z} BS1-Beef Synthetic 1, BS2-Beef Synthetic 2, DBS-Dairy Beef Synthetic

Table 2: Mean estimates of phenotypic variances (σ_p^2), direct heritability (h_d^2), maternal heritability (h_m^2), maternal permanent variance as a proportion of the phynotypic variance (c^2) for birth weight (BW) and weaning gain (WG), genetic correlation between direct and maternal (r_{dm}) for the same trait, and phenotypic and genetic correlations between traits (BW and WG) of (p_1p_2), (d_1d_2), (m_1m_2), (d_1m_2), (d_2m_1), (c_1c_2) and (e_1e_2)

						Correlations between traits						
Trait^z	σ_p^2	h_d^2	h_m^2	c^2	r_{dm}	p_1p_2	d_1d_2	m_1m_2	d_1m_2	d_2m_1	c_1c_2	e_1e_2
BW	23.71	0.45	0.1	0.01	0.16							
WG	654.2	0.19	0.12	0.15	-0.09							
BW x WG						0.27	0.32	0.18	0.08	0.49	0	0.25

^{z} BW-birth weight, WG-weaning gain

Table 3. Within line genetic trends (kg yr^{-1}) for birth weight (BW) and weaning gain (WG)

	BW		WG	
Line	Direct	Maternal	Direct	Maternal
BS1	0.08±0.01	0.00±0.00	0.29±0.05	0.12±0.06
BS2	-0.04±0.01	0.00±0.01	0.13±0.07	0.00±0.03
DBS	0.06±0.03	0.02±0.01	0.20±0.12	0.08±0.06

^{z} BS1-Beef Synthetic 1, BS2- Beef Synthetic 2, DBS-Dairy Beef Synthetic

Table 4. Mean genetic values and standard deviations for birth weight (BW) and weaning gain (WG) by line

		Line					
		BS1^z		BS2^z		DBS	
^{z}Trait	Effect	Mean	SD	Mean	SD	Mean	SD
	Direct	0.63	2.25	0.05	2.24	0.55	2.43
BW (kg)	Maternal	0.50	0.77	0.14	0.65	0.38	0.73
	Direct + Maternal	1.13	2.61	0.20	2.64	0.93	2.92
	Direct	4.02	6.00	1.04	6.22	2.51	6.71
WG (kg)	Maternal	2.87	4.48	0.65	3.63	3.17	3.28
	Direct + Maternal	6.88	7.73	1.69	8.19	5.68	7.24

^{z} BS1-Beef Synthetic 1, BS2-Beef Synthetic 2, DBS-Dairy Beef Synthetic

in the reviews by Koots *et al*. (1994b) appear to be due to the inadequacy of the statistical models rather than due to real differences in parameter estimates (Tosh *et al.,* 1999).

At Kinsella, high BW bulls were not used for breeding in all three lines and females were selected for fertility and against dystocia (Berg 1978 and Berg 1980). Within each line, breeding bulls were selected on the basis of their pre and post weaning rates of gain. This phenotypic selection for growth rate in bulls combined with the selection against dystocia and selection for high fertility in the females may have resulted in a moderate genetic improvement in WG (0.13- 0.41 kg yr^{-1}) with little increase in BW (-0.04-0.08 kg yr^{-1}). The trend showing little or no increase in BW with moderate increased in WG is beneficial in commercial beef production as high birth weight accounted for about 22% of the dystocia in 2-yr old beef heifers (Naazi *et al.,* 1989). In composite beef cattle, there appears to be sufficient genetic variation in birth weight that is independent of post weaning growth, so that post weaning gains can be increased without obligatory increases in birth weight (Bennett and Gregory, 1996). Based on the heritab- ility estimate for WG (Table 2) and the genetic variation in all three lines (direct genetic variance=122.8, maternal genetic variance=78.8), there appears to be adequate variation in WG to make moderate genetic progress by selecting breeding sires for high pre and post weaning gain. Although the synthetic populations were relatively small, as breeding combinations were planned to avoid the mating of relatives using pedigree information, inbreeding effects are small and not expected to have influenced genetic variances.

Phenotypic selection, results in selection of individuals that show superiority due to different types of gene action expressed in relation to the environment. The types of gene action include additive (direct and maternal), non-additive and genotype x environment interaction effects. However, to a large extent only the additive genetic component in transmitted. In our study, we were able to recognize stronger genetic trends in the BS1 line possibly because its breed structure combining Angus, Charolais and Galloway has remained relatively stable since 1966 (Berg 1980 and Berg *et al.,* 1990), whereas in the BS2 and DBS lines, more breeds have been combined at different stages of their development, resulting in a diversity of genetic combinations over time. For example, in the DBS, the average breed composition in 1984 was 23% Holstein, 24% Brown Swiss, 12% Simmental and 40% beef breeds that included Angus, Galloway, Hereford, Charolais and small amounts of Guernsey, Jersey and Brahman resulting in a mixture of breed combinations. This may have resulted in selection for non-additive effects and heterosis due to specific gene combinations resulting from cross breeding that are not usually transmitted.

Average Breeding Values : Across line estimated mean genetic values for BW and WG are shown in Table 4. Sullivan *et al.* (1999) reported that average ALBV in both BW and WG were associated with large standard deviations. They observed that the variation within breeds is greater than between breeds and that there is now more overlap between breeds. Maternal breeding values expressed as a percentage of the total additive genetic (*d + m*) for WG in BS1 and BS2 were 42 and 39% respectively, whereas, it was 56% for the DBS. In the DBS, more than half the average breeding value for WG was maternally contributed and this is more likely due to the increased milk production, as the DBS line contains 50% dairy genetics introduced by Brown Swiss, Holstein and Simmental. The maternal genetic contribution to weaning traits has been shown to be relative large in some studies in which better milking breeds have been combined with beef breeds (Koch *et al.,* 1995 and Rodriguez-Almeida *et al.,* 1997) and maternal heritability estimates have been reported to be higher in dairy x beef crossbreds (Van Vleck *et al.,* 1996). The maternal contribution of the total genetic responses in WG and weaning weight has been shown to be higher in Angus cross compared to Hereford cross calves that were selected either for high yearling weight or index selected combining yearling weight and muscle score over a 20 year period (Koch *et al.,* 1995). This can be attributed in part to the genes for higher milk production contributed by the Angus compared to the Hereford (Melton *et al.,* 1967).

Conclusions

Genetic parameter estimates and correlations of birth weight and weaning gain compared favorably with values in the literature. The h^2_d and h^2_m for birth weight was 0.45 and 0.10 respectively, and the h^2_d and h^2_m for weaning gain was 0.19 and 0.12 respectively. The r_{gd} and r_{gm} between birth weight and weaning gain was 0.32 and 0.18 respectively. The maternal genetic contribution to weaning gain was higher in the Dairy Beef Synthetic line compared to the two Beef Synthetic lines and the maternal contribution to birth weight was low in all lines. In the Beef Synthetic 1 and Dairy Beef Synthetic, the genetic trend for birth weight was 0.08 kg year^{-1}, and the genetic trend for weaning gain in the Beef Synthetic 2 was -0.04 kg year^{-1}. The genetic trend for weaning gain in the Beef Synthetic 2 was 0.41 kg year^{-1}. Although genetic selection based on expected breeding value is expected to be more effective, under commercial practical conditions by phenotypic selection, it is possible to improve weaning gain with little change in birth weight which is known to be positively associated with calving difficulty.

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