INFLUENCES OF DIETARY ENERGY PLANES ON GROWTH AND HERITABILITY ESTIMATES OF POSTWEANING GROWTH TRAITS IN YOUNG BEEF BULLS

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SUMMARY

The records of 263 young Angus (AN) bulls representing 21 sire families and 270 young Hereford (HE) bulls representing 26 sire families were analyzed to evaluate the influences of dietary energy planes on growth and heritability estimates of postweaning growth traits in young beef bulls. AN bulls were heavier throughout the test period and grew faster in the first 140-d of the test than HE bulls. In the last 28-d period, growth rates in the AN and HE bulls were similar. Although bulls receiving medium-energy diet (MED) were 2.3 kg heavier than those receiving high-energy diet (HED) at the start of the test, the bulls on the HED were 78.7 kg heavier than those on the MED at the end of the test, indicating that the HED resulted in high growth performance of feedlot bulls. Although the estimate of direct heritability (h^2_a) for start of test weight (WT0) was somewhat higher in the HED line (0.19) than in the MED line (0.11), the estimates of h^2_a for end of test weight (WT168), average daily gain on test (ADG0_168) and relative growth rate on test (RGR0_168) were much higher in the MED line than in the HED line. Between the HED and MED lines, maternal heritability estimates (h^2_m) for WT0 and ADG0_168 were similar (0.14 vs. 0.12 and 0.27 vs. 0.24, respectively). The estimate of h^2_m for WT168 was much higher in the HED line (0.28) than in the MED line (0.17). The reverse was true for RGR0_168, with h^2_m being 0.12 in the HED line and 0.33 in the MED line. All direct-maternal genetic correlations (r_{am}) were negative. The estimates of r_{am} for WT0 were high (-0.99) in both the HED and MED lines. Estimates of r_{am} for WT168, ADG0_168 and RGR0_168 were -0.98, -0.62 and -0.86, respectively, in the HED line compared with -0.54, -0.31 and -0.21, respectively, in the MED line, indicating that the antagonism between direct and maternal genetic effects for postweaning growth traits in the MED line was much less than that in the HED line. Total heritability estimates in the MED line (0.25 to 0.41) were substantially larger than those in the HED line (0.09 to 0.14) except for WT0, indicating that after many generations of selection, the MED line retained more genetic variation in postweaning growth traits compared with the HED line. Therefore, selection on individual performance would be more effective in the MED line than in the HED line.

INTRODUCTION

The development of economic traits is dependent on the environment, especially the nutrition plane in which the animals are reared (Hammond, 1947). In other words, the phenotypic expression of a trait is the result of genotype-environment interaction. For effective selection, animals should be raised under conditions in which traits of economic importance are expressed. Under different nutrition planes, the gene complexities affecting a given trait may differ (Falconer, 1981). Therefore, nutrition plane affects growth of animals and the estimation of heritability and consequently affects selection accuracy. Falconer (1960) indicates that, for growth rate, it is better to select on a low plane of nutrition. Dalton (1967), on the other hand, obtained the same results whether he selected animals on a full diet or on one diluted with cellulose. The objective of this study was to investigate the effects of dietary energy planes on growth and estimation of heritabilities of postweaning growth traits in young beef bulls.

MATERIALS AND METHODS

Young Angus (AN) bulls (n = 263) representing 21 sire families and young Hereford (HE) bulls (n = 270) representing 26 sire families, born in the spring of 1984, 1985 and 1986 and fed at the Agriculture and Agri-Food Canada Research Centre, Lethbridge, Alberta, Canada were used for this study. The bulls were progeny from a long term selection project (Bailey et al., 1991). A brief description pertinent to the current study follows. Each breed consisted of two lines. Line 1 calves were fed a high-energy diet (HED) and line 2 calves were fed a medium-energy diet (MED) during a 168-d postweaning gain feedlot test. The HED consisted of 80% concentrate and 20% alfalfa hay cubes. The MED consisted of 100% alfalfa hay cubes. A vitamin-mineral supplement was provided free choice. Immediately after weaning (< 1 wk), bull calves were randomly assigned to individual pens and fed for 168 d. Calves averaged 189 days of age at weaning. Pens were equipped with heated waterers and bulk feeders. Body weights (WT) were obtained every 28 d during the 168-d test (i.e., WT0, WT28, ..., WT168). In addition, average daily gains (ADG) in 28-d intervals (e.g., ADG0_28 = (WT28 - WT0)/28, ADG112_140 = (WT140 - WT112)/28, etc.) and during the entire test period (ADG0_168 = (WT168 - WT0)/168), and relative growth rate (RGR) during the entire test period (RGR0_168 = (lnWT168 - lnWT0)/168) were calculated.

The effects of breed and nutrition plane were analyzed using analysis of variance (SAS, 1988). An individual animal model was used for (co)variance components (Meyer, 1991) within each line as follows:

$$\mathbf{Y} = \mathbf{Xb} + \mathbf{Z_a a} + \mathbf{Z_m m} + \mathbf{e}$$

with $\mathbf{E(Y)} = \mathbf{Xb}$, and

$$\mathbf{Var(Y)} = \mathbf{Z_a A Z^T_a}\sigma^2_a + \mathbf{Z_m A Z^T_m}\sigma^2_m + (\mathbf{Z_a A Z^T_m} + \mathbf{Z_m A Z^T_a})\sigma_{am} + \mathbf{I_n}\sigma^2_e$$

where, **Y** is a n x 1 vector of records; **b** denotes the fixed effects (breed, year, and the covariate weaning weight), and a pooled regression of the traits on weaning weight was assumed; **a** is the vector of direct additive genetic effects with σ^2_a being direct additive genetic variance; **m** is the vector of maternal additive genetic effects with σ^2_m being maternal additive genetic variance; σ_{am} is direct-maternal additive genetic covariance; **e** denotes the vector of residual effects with σ^2_e being residual variance; $\mathbf{X}$, $\mathbf{Z_a}$ and $\mathbf{Z_m}$ are design matrices relating elements of **Y** to the fixed and random effects. With **A** equal to the numerator relationship matrix, the covariance matrix of **a** is given by $\mathbf{A}*\sigma^2_a$ and that of **m** is given by $\mathbf{A}*\sigma^2_m$ for levels of **a** and **m** ordered by animals. The covariance matrix for both **a** and **m** is given by $\mathbf{A}*\sigma_{am}$. The covariance matrix of **e** was assumed to be $\mathbf{I_n}*\sigma^2_e$, $\mathbf{I_n}$ being the identity matrix with the order of the records.

Estimates of direct (h^2_a) and maternal (h^2_m) heritabilities were obtained as ratios of the direct additive (σ^2_a) and maternal additive (σ^2_m) genetic variances to the phenotypic variance (σ^2_p), respectively, and $\sigma^2_p = \sigma^2_a + \sigma^2_m + \sigma_{am} + \sigma^2_e$. Direct-maternal genetic correlation (r_{am}) was estimated as the ratio of σ_{am} to the square root of the product of σ^2_a and σ^2_m. Total heritability h^2_t was estimated according to Dickerson (1947). Sampling variances of h^2_a and h^2_m were obtained from the cubic approximation.

RESULTS AND DISCUSSION

Throughout the feedlot test, AN bulls were heavier than HE bulls ($P < 0.05$, Table 1). At the start of the test, AN bulls were approximately 6 kg heavier than HE bulls. At the end of the test, the difference was approximately 26 kg ($P < 0.05$). In general, during the first 140-d on test, AN bulls grew faster than HE bulls. This may be related to the superior milking ability of their dam. However, in the final 28-d period, growth rates were similar ($P > 0.05$) in the AN and HE bulls. Differential maturing rates perhaps played a role. Gilbert et al. (1993) reported that AN calves had smaller frame scores both at weaning and at the end of the 168-d postweaning gain feedlot test than HE calves.

Bulls on the MED were heavier than those on the HED at the start of the test by 2.3 kg. However, bulls on the HED were heavier and grew faster than those on the MED throughout the test. By the end of the test, bulls on the HED were approximately 78.7 kg (Table 1) heavier than those on the MED. The effects of dietary energy plane on postweaning gain in beef bulls were in agreement with Bailey et al. (1991) and Makarechian et al. (1994).

Table 1. Least squares means ± standard errors of breeds and diets

Trait	Breed		Diet	
	Angus	Hereford	High	Medium
		Weight Measurements		
WT0, kg	197.69±0.68a	191.45±0.71b	193.43±0.58a	195.71±0.58b
WT28, kg	228.28±0.73a	217.08±0.87b	222.78±0.72a	222.58±0.71a
WT56, kg	255.75±0.91a	241.61±1.08b	256.46±0.89a	240.89±0.88b
WT84, kg	289.09±1.11a	270.85±1.31b	296.79±1.09a	263.15±1.07b
WT112, kg	324.69±1.26a	301.36±1.50b	336.56±1.24a	289.49±1.22b
WT140, kg	362.83±1.51a	335.89±1.79b	380.74±1.48a	317.98±1.47b
Wt168, kg	392.93±1.66a	367.25±1.97b	419.45±1.63a	340.73±1.61b
		Average Daily Gains		
ADG0–28, kg/d	1.09±0.03a	0.92±0.03b	1.05±0.03a	0.96±0.03b
ADG28–56, kg/d	0.97±0.02a	0.86±0.03b	1.19±0.02a	0.64±0.02b
ADG56–84, kg/d	1.19±0.02a	1.04±0.03b	1.44±0.02a	0.80±0.02b
ADG84–112, kg/d	1.27±0.02a	1.09±0.03b	1.42±0.02a	0.94±0.02b
ADG112–140, kg/d	1.36±0.03a	1.23±0.03b	1.58±0.03a	1.02±0.03b
ADG140–168, kg/d	1.25±0.04a	1.31±0.05a	1.62±0.04a	0.94±0.04b

WTx is weight taken on the xth day of the test; ADGx_y is average daily gain during the period between the xth and the yth days of the test; RGRx_y is relative growth rate during the period between the xth and the yth days of the test.

a, b Least squares means bearing different letters are significantly different ($P < 0.05$) between breeds or between diets for the same traits.

Although the estimate of direct heritability (h^2_a) for start of test weight (WT0) was somewhat higher in the HED line (0.19) than in the MED line (0.11), the estimates of h^2_a for end of test weight (WT168), average daily gain on test (ADG0_168) and relative growth rate on test (RGR0_168) were much higher in the MED line than in the HED line (Table 2). Maternal heritability estimates (h^2_m) for WT0 and ADG0_168 were similar between the HED line (0.14 and 0.27, respectively) and the MED line (0.12 and 0.24, respectively). The estimate of h^2_m for WT168 was much higher in the HED line (0.28) than that in the MED line (0.17). The reverse was true for RGR0_168, with h^2_m being 0.12 in the HED line and 0.33 in the MED line. All direct-maternal genetic correlations (r_{am}) were negative, ranging from -0.62 to -0.99 in the HED line and from -0.21 to -0.99 in the MED line. The estimates of r_{am} for WT0 were high (-0.99) in both lines. Estimates of r_{am} for WT168, ADG0_168 and RGR0_168 were -0.98, -0.62 and -0.86, respectively, in the HED line compared with -0.54, -0.31 and -0.21, respectively, in the MED line, indicating that the negative direct-maternal genetic correlations for postweaning growth traits in the MED line were much smaller than those in the HED line. Total heritability estimates (h^2_t) in the MED line (0.24 to 0.41) were considerably higher than those in the HED line (0.09 to 0.14) except for WT0 which had low h^2_t in both lines. This indicates that there remained more genetic variation in the MED line than the HED line after many generations of selection.

Table 2. Estimates of heritabilities and direct-maternal genetic correlations

	h^2_a		h^2_m		r_{am}		h^2_t	
Traits	HED	MED	HED	MED	HED	MED	HED	MED
WT0	0.19±0.001	0.11±0.001	0.14±0.001	0.12±0.010	−0.99	−0.99	0.02	0.02
WT168	0.12±0.001	0.37±0.001	0.28±0.001	0.17±0.001	−0.98	−0.54	0.15	0.25
ADG0−168	0.14±0.010	0.41±0.001	0.27±0.001	0.24±0.001	−0.62	−0.31	0.09	0.38
RGR0−168	0.27±0.001	0.35±0.001	0.12±0.001	0.33±0.010	−0.86	−0.21	0.10	0.41

WT0 and WT168 are start and end of test weights, respectively. ADG0_168 and RGR0_168 are average daily gain and relative growth rate on test, respectively.

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