GENETIC PARAMETERS AND BREED DIFFERENCES FOR FEED EFFICIENCY, GROWTH AND CARCASS TRAITS OF BEEF BULLS

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Summary

Genetic relationships between feed efficiency, growth, and live ultrasound measurements of carcass traits from centrally tested beef bulls were studied. Feed traits included average daily dry matter intake (FI), feed conversion ratio and residual feed intake (intake adjusted for either production (RFIp) or production and composition (RFIc)). Growth traits were average daily gain (ADG), mid-test metabolic body weight (body weight$^{0.75}$), and hip height. Carcass traits included backfat, rib eye area, and intramuscular fat (IFAT). Scrotal circumference was also analyzed. Data included purebred bulls from six breeds tested from 1991 to 2000 in Ontario. Bulls were measured every 28 days for individual feed intake and weight, and at the end of test for carcass traits. The number of records per trait ranged from 2,284 (FI) to 13,319 (ADG). Effects of test group, breed, age at end of test, herd of origin, and animal were modeled. Except for IFAT (0.14), heritability estimates were moderate to high for all traits (0.30 to 0.55). RFIp and RFIc were highly genetically correlated (0.99) across breeds, but corresponding breed differences changed. Genetic correlations of RFIc with ADG and backfat were essentially zero, which indicate that selection on residual feed intake could be implemented to reduce feed intake and improve feed conversion without compromising growth and leanness.

Introduction

Bull testing and evaluation have a long history and are the cornerstones of beef cattle genetic improvement programs in Ontario. To evaluate performance, bulls are housed together in central evaluation stations. The main aim of a central performance test is to fairly compare beef bulls under uniform management and environmental conditions. Accurate genetic evaluations for traits affecting profit are critical to the long-term competitiveness of Ontario beef producers. These genetic evaluations require estimates of genetic parameters, which are used in the calculation of Expected Progeny Differences (EPD's) and Across Breed Comparisons (ABC's), as estimates of an animal's additive genetic merit both within and across breeds, respectively. Updated and new estimates of genetic parameters and breed differences will improve genetic evaluations and allow the evaluation of new traits. The objectives of this research were to estimate genetic parameters for growth, carcass, and feed efficiency traits for bulls tested in central evaluation stations in Ontario, as well as, to estimate corresponding breed differences.

Material and Methods

Data. Bull test data used in this study were a subset of data collected through the Bull Evaluation Program in Ontario from purebred bulls that were evaluated from 1991 to 2000. Bulls entered the evaluation centers at a minimum weight of 399 lb and a maximum age of 290 days. Age ranges within evaluation centers did not exceed 90 days. After a 28-day adjustment period to minimize pretest effects, bulls began an official evaluation period. Individual body weight was measured every 28 days and dry matter consumption every 7 days during the test period. The official evaluation length was 140 days up to 1995 (inclusive). From 1996 forward, the official evaluation length was 112 days. At the end of the evaluation period ultrasound measurements of rib eye area (REA), backfat thickness (BF), and percentage of intramuscular fat (IFAT) were obtained by an Animal Ultrasound Practitioner- certified technician. Measurements of REA and BF were calculated from an image of the longissimus (rib eye) muscle between the 12th and 13th ribs, whereas IFAT measurements were calculated from four images of longissimus muscle across the 11th and 13th ribs. Average daily weight gain (ADG) and daily dry matter intake (FI) were calculated as the linear regression coefficient of weight or total feed consumed on the actual day of measurement (every 28 days). Feed conversion ratio (FCR) was defined as FI/ADG and residual feed intake was calculated as the actual FI minus the expected FI. At the end of the evaluation period, measurements of scrotal circumference (SC) and hip height (HH) were made. A total of 2,284 records were available on FI, FCR, and residual feed intake, 3,685 records on IFAT, 5,364 records on REA, and more than 13,100 records on ADG, BF, SC, and HH. Test groups were defined as bulls fed at the same evaluation center with the same starting test date. Bulls from the following breeds were present in the edited data set used for analyses: Charolais, Limousin, Simmental, Hereford, Angus (Red and Black), and Blonde d'Aquitaine.

Residual feed intake. Feed intake adjusted for production (residual feed intake, RFIp) was calculated as the difference between actual FI and the expected feed requirements for maintenance of body weight (through mid-test metabolic body weight (body weight$^{0.75}$)) and growth (through ADG). Feed intake adjusted for production and composition of gain (RFIc) was calculated as the difference between actual FI and the expected feed requirements for maintenance of body weight and growth, and composition of growth (through BF). An example is given in Table 1 for bulls within and across breeds with similar size and growth but different feed intake. These bulls have different RFI. Unlike FCR, where faster growing bulls have better FCR, residual feed intake is independent of production. The attraction of residual feed intake is that it could be more related to some underlying mechanism controlling efficiency of feed utilization, which may translate more directly to efficiency in mature cows for maintenance, a trait of great economic significance and on which has been hard to select for. However, more research is needed to understand the relationship of residual feed intake and maintenance efficiency in cows.

Analyses. Effects of test group, breed, age at end of test (linear effect within breed) and herd of origin were accounted for in the analyses of animal genetic effects. The adjustment for age of bull at end of test converted the records of all bulls to the same age of 380 days at the end of test (overall mean value). The average ages at end of test were similar among all breeds, ranging from 376.7 to 383.1 days.

Breed differences. Breed differences were expressed as differences relative to Charolais.

Results and Discussion

Genetic and environmental parameters. The results in Table 2 indicate that the traits measured in the bull evaluation program are moderate to highly heritable (0.30 to 0.55) with the exception of IFAT (0.14). This indicates that genetic change can be made by selection for these traits. RFIp and RFIc had similar heritabilities, which were higher than heritabilities for ADG. Genetic correlations (Table 3) indicated that RFIp and RFIc were highly correlated with each other (0.99) and highly correlated with FCR ($\bar{r} = 0.68$). RFIp was not genetically associated with ADG and tended to be lowly correlated with BF (0.16) and MW (-0.17), while RFIc was not associated with both ADG and BF and tended to be lowly correlated with MW (-0.18). RFIp and RFIc were more correlated with FI than was FCR ($\bar{r} = 0.80$ vs. 0.39). FCR was not correlated with BF, but was correlated with ADG (-0.52) and REA (-0.28). RFIp and RFIc tended to be correlated with REA (-0.17 and -0.19) and were not associated with IFAT and HH.

Although bulls go through a 28-day adjustment period to remove different management factors that might carry over from the herd of origin, this effect can be quantified. Determined here was the proportion of the total variation (phenotypic) explained by the herd of origin, which would be independent of genetic differences between herds. Other studies showed that herd of origin effects of around 8% were important and should be accounted for in genetic evaluation of weight gain on station test. Contribution of herd of origin to phenotypic variance ranged from 2 to 20% (Table 2). Traits related to body size, such as MW, HH and REA, were the most affected (20, 15, and 9%, respectively). Contrary to weight, ADG was much less influenced (5%). The least affected trait by herd of origin effect was FI (2%). FCR was more affected by herd of origin effect than both RFIp and RFIc (0.07 vs. an average of 0.04 for RFI traits).

Breed differences. Table 4 presents the breed difference estimates. Breed differences for growth rate (ADG), size (MW, HH), fatness (BF, IFAT), and scrotal circumference were similar to those previously published from the bull evaluation program. Evaluating feed intake and related feed efficiency traits (Table 4) on the other hand have brought new insights into differences among breeds for these important traits. Generally, because FCR is influenced by growth, we might expect breeds to rank similarly for growth and FCR. Blonde d'Aquitaine and Limousin are examples of two breeds that are slower growing, but have superior FCR (lower FCR is better).

Residual feed intake is a trait that should be independent of production and an indicator of efficiency of feed utilization. For this trait, the leaner breeds, Blonde and Limousin, were superior (RFIp). Because it takes less feed to put on a pound of lean compared to fat, it could be argued that this is not surprising. To further remove this influencing factor of composition of gain, RFIc was derived, which adjusts for composition through an adjustment for backfat. Adjustment to a common backfat thickness could be justified given that the commercial endpoint in steers is generally backfat or finish constant. Noticeably, the fattest breeds (highest BF and IFAT), Hereford and Angus, improve considerably through the adjustment for fatness, with Hereford changing rank significantly. Feed intake of Hereford, adjusted to a common level of production and composition (RFIc) approximated that of Limousin (Table 4). However the adjustment for fat did not completely remove the relationship between fatness and residual feed intake across breeds. The two leanest breeds, Blonde d'Aquitaine and Limousin remained the most efficient based on residual feed intake with or without adjusting for fat. Likewise, Angus remained the least efficient with or without adjusting for fat.

Conclusions

This study has shown that in young growing beef bulls from six different breeds there exists genetic variation in feed intake that is largely independent of size, growth rate and growth composition (fat vs. lean). Genetic parameter estimates indicate that selection based on residual feed intake could be implemented to reduce feed intake and improve feed conversion without compromising growth and leanness. A possible correlated response on size should, however, be monitored. Breed differences for residual feed intake change for breeds with more fat deposition when feed intake is adjusted for composition of the gain in addition to adjustments for metabolic body weight (body weight$^{0.75}$) and weight gain.

Significance to Industry

Given the wide range of traits, which may be considered in beef production, effective selection for increased profitability relies upon genetic evaluation for those traits that affect profit. Genetic parameters and breed differences have been estimated for a number of traits related to profit in beef production allowing more accurate EPD's and resulting selection decisions.

Acknowledgments

The authors thank Beef Improvement Ontario (BIO) for providing data; BIO and Natural Sciences and Engineering Research Council for financial support; and the Canadian Foundation for Innovation, Ontario Innovation Trust, and Compaq for support of required computing infrastructure.

Table 1. Example of differences in feed efficiency within (bull 1 vs. 2) and across (bull 3 vs. 4) breeds

Bull - Breed	ADG[a] (lb/d)	FI (lb/d)	RFIc (lb/d)	FCR (lb/lb)	BF (mm)	HH (in)	REA (in^2)	MW ($lb^{0.75}$)	TG	SA (d)
1 Simmental	4.57	22.74	-1.62	4.98	5.0	52.0	12.7	184.5	199821	246
2 Simmental	4.56	26.37	2.17	5.78	5.0	52.0	13.1	182.7	199821	254
3 Limousin	4.16	19.29	-3.58	4.64	3.0	53.5	12.6	175.5	200012	252
4 Charolais	4.17	23.63	0.48	5.67	3.0	53.0	12.2	179.1	200012	246

[a] ADG= average daily gain; FI= daily dry matter intake; RFIc= residual feed intake with extra adjustment for BF; FCR= feed conversion ratio; BF= backfat thickness; HH= hip height; REA= rib eye area; MW= mid-test metabolic weight; TG= test group; SA= starting age.

Table 2. Phenotypic mean (Mean) and average[a] estimated phenotypic variances ($\hat{\sigma}_p^2$), heritabilities (h^2), and herd of origin by phenotypic variance ratios (c^2) for station-tested bull traits

	Bull traits[b]										
	RFIp (lb/d)	RFIc (lb/d)	FCR (lb/lb)	FI (lb/d)	ADG (lb/d)	BF (mm)	REA (in^2)	IFAT (%)_	MW ($lb^{0.75}$)	HH (in)	SC (cm)
Mean	0.00	0.04	5.53	21.25	3.83	4.30	12.89	3.44	173.67	52.87	33.50
$\hat{\sigma}_p^2$	3.79	3.64	0.42	5.05	0.19	1.96	1.56	0.76	149.17	2.55	6.21
h^2	0.38	0.39	0.37	0.44	0.35	0.36	0.30	0.14	0.35	0.55	0.48
(SE[c])	(0.07)	(0.07)	(0.06)	(0.06)	(0.03)	(0.03)	(0.04)	(0.05)	(0.02)	(0.03)	(0.03)
c^2	0.04	0.03	0.07	0.02	0.05	0.05	0.09	0.04	0.20	0.15	0.04
(SE)	(0.02)	(0.02)	(0.02)	(0.01)	(0.01)	(0.01)	(0.02)	(0.02)	(0.01)	(0.01)	(0.01)

[a] Average estimates from ten pairwise two-trait analyses for each trait.
[b] RFIp= residual feed intake; RFIc= residual feed intake with extra adjustment for BF; FCR= feed conversion ratio; FI= daily dry matter intake; ADG= average daily gain; BF= backfat thickness; REA= rib eye area; IFAT= intramuscular fat; MW= mid-test metabolic weight; HH= hip height; SC= scrotal circumference.
[c] SE= average standard error of the estimates from ten pairwise two-trait analyses.

Table 3. Genetic (above diagonal) and phenotypic (below diagonal) correlations between station-tested bull traits

	Bull traits[a]										
	RFIp	RFIc	FCR	FI	ADG	BF	REA	IFAT	MW	HH	SC
RFIp		0.99*	0.69*	0.81*	0.01	0.16	-0.17	-0.02	-0.17	-0.05	0.15
RFIc	0.98*		0.68*	0.78*	-0.02	-0.01	-0.19	-0.06	-0.18	-0.02	0.12
FCR	0.76*	0.74*		0.39*	-0.52*	0.03	-0.28*	0.13	-0.13	-0.14	0.06
FI	0.81*	0.78*	0.47*		0.50*	0.24*	0.11	-0.11	0.36*	0.26*	0.33*
ADG	-0.06	-0.08	-0.58*	0.44*		0.14*	0.42*	-0.35*	0.56*	0.37*	0.24*
BF	0.17*	-0.01	0.14*	0.28*	0.13*		-0.10	0.24	0.15*	-0.17*	0.19*
REA	-0.10	-0.10	-0.07*	0.12*	0.22*	0.12*		-0.69*	0.46*	0.01	0.05
IFAT	0.05	0.04	0.07	0.05	-0.02	0.15*	-0.10*		-0.05	0.00	-0.12
MW	-0.11	-0.13	0.05	0.40*	0.36*	0.27*	0.47*	0.02		0.55*	0.31*
HH	-0.09	-0.08	-0.03	0.24*	0.30*	0.04	0.19*	0.03	0.63*		0.16*
SC	0.02	0.01	0.03	0.21*	0.21*	0.14*	0.18*	0.02	0.41*	0.29*	

[a] RFIp= residual feed intake; RFIc= residual feed intake with extra adjustment for BF; FCR= feed conversion ratio; FI= daily dry matter intake; ADG= average daily gain; BF= backfat thickness; REA= rib eye area; IFAT= intramuscular fat; MW= mid-test metabolic weight; HH= hip height; SC= scrotal circumference**.**

* Significant at $P < 0.05$ by t-test.

Table 4. Breed difference estimates for traits related to feed efficiency, growth and body composition of station-tested beef bulls

Breed[a]	RFIp[b] (lb/d)	RFIc (lb/d)	FCR (lb/lb)	FI (lb/d)	ADG (lb/d)	BF (mm)	IFAT (%)	REA (in^2)	MW ($lb^{0.75}$)	HH (in)	SC (cm)
CH	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
LM	-0.71	-0.73	-0.04	-2.49	-0.44	-0.20	-0.32	0.44	-12.21	-0.46	-2.97
AA	1.10	0.42	0.38	0.11	-0.22	2.64	1.10	-1.67	-6.84	-0.87	0.89
SM	0.33	0.33	0.15	0.42	-0.04	0.28	-0.05	-0.02	5.34	0.22	2.44
HE	0.13	-0.64	0.15	-1.39	-0.37	2.93	0.15	-2.06	-10.98	-0.89	-0.92
BD	-1.06	-0.84	-0.13	-2.14	-0.31	-1.22	-0.53	1.20	-8.12	-0.32	-2.75

[a] Charolais, Limousin, Angus, Simmental, Hereford and Blonde d'Aquitaine, respectively.

[b] RFIp= residual feed intake; RFIc= residual feed intake with extra adjustment for BF; FCR= feed conversion ratio; FI= daily dry matter intake; ADG= average daily gain; BF= backfat thickness; IFAT= intramuscular fat; REA= rib eye area; MW= mid-test metabolic weight; HH= hip height; SC= scrotal circumference.