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GENETIC PARAMETERS FOR GROWTH AND CARCASS TRAITS FROM CROSSBREEDING

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Summary

Growth and carcass data from 5 years of a long-term, rotational, crossbreeding project were used to calculate heritabilities and genetic and phenotypic correlations for direct and maternal birth and weaning weight, gain on feed, hot carcass weight, ribeye area, marbling score, and age at slaughter. Angus, Brahman, Hereford, Charolais, Simmental, and Gelbvieh breeds were involved. Heritabilities of traits ranged from low (maternal weaning weight 0.04) to moderate (direct weaning weight 0.41). Direct birth weight, direct weaning weight, gain on feed, and hot carcass weight had moderate to high genetic correlations. Marbling had negative genetic correlations with birth and weaning weight but positive correlations with slaughter age and hot carcass weight.

(Key Words: Breeds, Heritability, Correlations, Carcass Traits, Growth.)

Introduction

With a movement toward more value-based marketing, both growth and carcass traits become more important to producers. Knowledge of the relationships between growth and carcass traits will help producers select cattle that perform in both areas. Our objectives were to determine the heritability of seven growth and carcass traits and to calculate genetic and phenotypic correlations among those traits.

Experimental Procedures

Records from 488 crossbred steer calves were available. Traits of interest were direct and maternal birth and weaning weights, gain on feed, hot carcass weight, ribeye area, marbling score, and age at slaughter. Steers were produced at Louisiana State University (LSU) in the fifth generation of a rotational crossbreeding project carried out in cooperation with KSU. Breeds were Angus, Brahman, Charolais, and Hereford. All F_1 and two-, three-, and four-breed rotational crosses were represented with the restriction that Brahman be included in each cross. Terminal cross sires were mated to F_1 dams and half of each rotational-cross dam group. Gelbvieh was used for the first 3 years and Simmental for the last 2 years as the terminal sire breeds. Angus Hereford F_1 calves also were produced.

Calves were born between mid-January and mid-April. Bull calves were dehorned and castrated in July. Calves were weaned and vaccinated in the first week of September. Approximately 60% of the steers were assigned randomly to a calf management group and shipped to KSU during the first week of October at an average age of 8 months. The remaining 40% made up a yearling management group and were backgrounded on ryegrass pasture at LSU before being shipped to KSU in early May at an average age of 15 months. In 1993, only a calf management group was available, because fewer steers were produced at LSU.

Upon arrival at KSU, steers were weighed, sorted into pens, and placed on feed. The ration consisted of sorghum silage and cracked corn

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plus a soybean meal, urea, and mineral supplement. Silage was reduced from 75 to 15 % of the diet dry matter over a 4-week starting period. Steers were slaughtered at IBP, Inc., Emporia, Kansas, when ultrasound-measured fat thickness was between .3 and .5 inches. Carcass data were collected by members of the KSU faculty. Marbling scores were converted to a numeric value for analysis.

Data were analyzed using a multiple trait DFREML procedure in a full-animal model. The model included pedigree information from all five generations of the project. The model also included fixed effects of year of birth and management group for postweaning traits and year of birth and age of dam for preweaning traits. Heterosis was accounted for by use of regression procedures. Birth date was included as a covariant for birth weight and age at weaning for weaning weight. Gain on feed was adjusted for days on feed by regression procedures. All postweaning traits were adjusted by regression to a common adjusted backfat thickness end point. Two-trait analyses were used to calculate the heritabilities and correlations. Breed differences were accounted for by regression procedures.

Results and Discussion

A total of 488 steers calves was shipped form LSU to KSU; however, because of missing data, only 437 steers were available for analysis of all growth and carcass traits. The steers average 83.2 lb at birth and 521.0 lb at weaning. They had an average hot carcass weight of 718.3 lb, with a 12.9 in^2 ribeye and small^{07} marbling at an average slaughter age of 504 days. Adjusted backfat averaged .42 in., and actual backfat was .37 in.

Heritabilities and genetic and phenotypic correlations for the seven traits are presented in Table 1. Maternal heritabilities were low

in this study. Direct birth and weaning weight had heritabilities (.17 and .41, respectively) lower than most estimates reported earlier for these traits, as did gain on feed and ribeye area. Differences in the model used and the use of a fat-constant end point may have caused these differences. Hot carcass weight and marbling score had moderate heritabilities (.24 and .32, respectively). Days of age at a fat-constant end point had a heritability of .20 in this study.

Maternal birth and weaning weight generally had negative genetic correlations with other traits except ribeye area. No genetic correlations were found between maternal birth weight and gain on feed, hot carcass weight, or days of age. Direct birth weight had little genetic relationship with carcass traits. Direct weaning weight had high positive genetic correlations with gain on feed, hot carcass weight, and ribeye area. Negative correlations were found between direct weaning weight and marbling score and days of age.

Gain on feed had a small negative correlation with hot carcass weight and moderately positive correlations with ribeye area and marbling. The only other negative correlation between postweaning traits was between ribeye area and marbling score (.64).

Days of age had high negative genetic correlations with weaning weight (.56) and gain on feed (1.0) and a moderately negative correlation with ribeye area (.41). The relationship between days of age and hot carcass weight was very low (.07), but marbling score had a moderately positive genetic correlation with days of age (.58).

The results of this study indicate that desirable growth and carcass traits are compatible. Positive correlations between preweaning and postweaning growth indicates that selection for early growth will transfer to faster later growth. Age that an animal reaches an end point of set fat thickness should be reduced by selection for growth rate.

Table 1.   Heritability and Genetic and Phenotypic Correlations [a]

Traits[b]	BWT		WWT		GOF	HCW	REA	MAR	DOA
	D A	M A	D A	M A					
BWT DA	**.17**	-.91	.79	-.0l	.46	.50	0.0	-.07	0.0
BWT MA	NA	**.09**	-.37	-.53	0.0	0.0	.10	-.0l	0.0
WWT DA	.49	NA	**.41**	-.56	.68	1.0	.88	-.20	-.56
WWT MA	NA	NA	NA	**.04**	-.04	-.58	.42	0.0	-.33
GOF	.29	NA	.25	NA	**.17**	-.04	.42	.37	-1.0
HCW	.42	NA	.47	NA	.73	**.24**	.40	.40	.07
REA	.17	NA	.20	NA	.42	.56	**.21**	-.64	-.41
MAR	-.04	NA	-.09	NA	.21	.19	-.01	**.32**	.58
DOA	-.04	NA	0.0	NA	.03	.54	.31	.19	**.20**

[a]Heritabilities are underlined and on the diagonal, genetic correlations are above the diagonal, and phenotypic correlations are below the diagonal.

[b]DA = direct, MA = maternal, BWT = Birth weight, WWT = Weaning weight, GOF = gain on feed, HCW = hot carcass weight, REA = ribeye area, MAR = marbling score, DOA = days of age at slaughter.

NA = not available

Heritabilities and Genetic Correlations

Direct heritabilities estimate the fraction of variation among animals caused by genes received from the parents and range from zero to 1. The dam also provides a maternal environment (uterine environment, milking ability, etc.), which is influenced by the dams own genetics, separate from the genes she passes on to the offspring. The heritability of this maternal environment is referred to a smaternal heritability. Direct heritabilities include a calf s own genetics for growth up to birth, expressed as birth weight heritability, or growth to weaning, expressed as weaning weight heritability, etc.

Correlations indicate the relationship between two traits and can range from -1 to +1. Genetic correlations indicate the relationship between two traits caused by the same genes. For example, some genes that cause rapid growth from birth to weaning also cause rapid growth from weaning to yearling. Some genetic correlations are less obvious. A correlation between maternal weaning weight and direct yearling weight would indicate that some of the genes that influence milk production also influence the individuals s own growth rate . Phenotypic correlations represent relationships between traits, regardless of their cause.