

Observation on Variance and Covariance Estimates for Carcass Traits in Bull and Steer Progeny

A. S. Leaflet R1532

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Summary

Carcass measures from 970 cattle were collected at the Iowa State University Rhodes and McNay research farms over a 6-year period. Data were from bull and steer progeny of composite, Angus, and Simmental sires mated to three composite lines of dams. The objective of this study was to evaluate effects of sex differences on genetic parameter estimates for carcass traits. Estimation of genetic parameters using a three-trait mixed model showed differences between bulls and steers in h^2 and genetic correlations. Heritability for carcass weight, percentage retail product, retail product weight, fat thickness, and longissimus muscle area from bull data were .43, .04, .46, .05, and .21, respectively. The corresponding values for steer data were in order of .32, .24, .40, .42, and .07, respectively. Furthermore, genetic correlations between some of the traits were different both in magnitude and direction when evaluated by sex. The results suggested possible differences in genetic parameter estimates between bulls and steer data. Hence, further study on effects of sex differences on genetic parameter estimation and a designing possible strategy to overcome the problem were emphasized.

Introduction

In a value-based marketing system, the viability of the beef industry will depend on the ability to produce a high-quality, consistent end product. This could be achieved through a clear understanding of lean and fat growth in various sexes and breeds of feedlot cattle. Thus far reports on this topic are limited, not only in number, but also in scope, as they involve single sex evaluations.

To date, sire evaluations for carcass traits have been based solely on steer data. However, the general trend towards use of ultrasound technology is likely to result in a huge amount of information and more rigorous evaluations in the near future. However, some of the most important questions we need to raise today may include, how would genetic parameter estimates behave when estimated from data involving different sexes? and how can we combine carcass

information on an individual and its relatives of varying sexes to have a better animal evaluation?

The objective of this study was to estimate genetic parameters when carcass traits are collected from feedlot cattle of different sexes.

Materials and Methods

Description of Data

Data in this study included carcass information from 970 cattle fed at the Rhodes and McNay research farms of Iowa State University (ISU). These cattle were part of a serial scan and serial slaughter project designed to evaluate sex, age, and frame size differences in carcass composition. Data in 1991 were from progeny of composite sires from the previous ISU beef breeding project. Breed composition of cattle in this project is described by Buttram and Willham (1989) and Northcutt et al. (1991). The remaining data, from 1992 to 1996, came from progeny of purebred Angus and Simmental sires with known expected progeny difference (EPD) and females from the old project. A detailed description of mating plans during the earlier stages of the project is given elsewhere (Hassen and Willham, 1994).

Cattle were assigned to slaughter groups randomly within sire breed, with the first group being slaughtered at an average age of 423 d; subsequent slaughters took place at an average interval of 25 to 30 d. During each slaughter, steers were transported to a commercial packing facility within the next 2 to 3 d after the last scan and slaughtered according to regular plant practices. Carcass traits measured were hot carcass weight (HCW); carcass 12th to 13th rib fat thickness (CFAT); carcass longissimus muscle area (CLMA); percentage kidney, pelvic, and heart fat (KPH); and chemical percentage intramuscular fat (CIMF). Percentage retail product (PRP) and retail product weight (RPW) were computed from the previously listed carcass traits using equations from BIF guidelines (BIF, 1996) and Epley et al. (1970), respectively.

Statistical Analysis

Slaughter traits in this report included HCW, PRP, RPW, CFAT, and CLMA. Effects of sex and breed composition were studied using descriptive statistical tools and analysis of variance techniques (SAS, 1989). Initially, the model included fixed effects of slaughter age (covariate), breed composition (covariate), contemporary group (herd-year-frame size), sex, age of dam, and all possible two- and three-way interactions. None of the interaction effects were significant, and hence, they were dropped from the final model. Age of dam effect was significant ($P < .05$) for HCW, RPW, and CLMA. Information from this analysis

was used to produce the final model for evaluation of genetic parameters.

Genetic parameters were computed using the three-trait mixed model

$$\begin{bmatrix} Y_1 \\ Y_2 \\ Y_3 \end{bmatrix} = \begin{bmatrix} X_1 & 0 & 0 \\ 0 & X_2 & 0 \\ 0 & 0 & X_3 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \\ b_3 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 & 0 \\ 0 & Z_2 & 0 \\ 0 & 0 & Z_3 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \\ a_3 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \\ e_3 \end{bmatrix}$$

where ,

Y_i = vector of observations for the i^{th} trait,

X_i = known incidence matrices relating fixed effects to the vector of observation for the i^{th} trait,

Z_i = known incident matrices relating records for the i^{th} trait to individual animal effects,

b_i = vector of fixed effects corresponding to slaughter age, breed composition, contemporary group, sex, and age of dam,

a_i = vector of direct additive random effects, and

e_i = vector of residual effects.

Fixed effects considered for each of the traits were those that were significant ($P < .05$) in the previous analysis. Means of a_i and e_i are assumed zero, and the following variance-covariance matrix was assumed:

$$\begin{bmatrix} a_1 \\ a_2 \\ a_3 \\ e_1 \\ e_2 \\ e_3 \end{bmatrix} \sim N \left(\begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}, \begin{bmatrix} A\sigma_{a11}^2 & A\sigma_{a12}^2 & A\sigma_{a13}^2 & 0 & 0 & 0 \\ & A\sigma_{a22}^2 & A\sigma_{a23}^2 & 0 & 0 & 0 \\ & & A\sigma_{a33}^2 & 0 & 0 & 0 \\ & & & I\sigma_{e11}^2 & I\sigma_{e12}^2 & I\sigma_{e13}^2 \\ & & & & I\sigma_{e22}^2 & I\sigma_{e23}^2 \\ & & & & & I\sigma_{e33}^2 \end{bmatrix} \right)$$

where,

A = the Wright numerator relationship matrix among all animals including parents without records,

$\sigma_{a_i}^2$ = additive genetic variance for the i^{th} trait, $i = 1, 2, 3$,

$\sigma_{a_{ij}}$ = genetic covariance (additive) between traits i and j ,

$\sigma_{e_i}^2$ = the environmental variance for the i^{th} trait, $i = 1, 2, 3$,

$\sigma_{e_{ij}}$ = the environmental covariance between traits i and

j , and

I = identity matrix.

Genetic parameters were estimated for the overall data, for bulls and steers. A computer package (Boldman et al., 1993) based on Multiple Trait Derivative Free Maximum Likelihood (MTDFREML) algorithm was used to estimate variance components. In order to avoid convergence to a

local maximum, values from several literature sources were also used as starting values. For each of the three-trait combinations, iterations were terminated when the variance among likelihood function values of the simplex function ($-2 \log \Lambda$) was less than 10^{-6} . The output from the initial analysis was used as a prior for the next run. This process was repeated until the change in the value of the convergence criteria and estimates was very small.

Results and Discussion

Differences in breed effect (Simmental minus Angus) from MTDFREML procedures are shown in Table 1. The breed composition of animals was included as a covariate, and therefore solutions in this model represent breed effect for the respective traits. The results indicate the importance of breed direct effect on carcass traits involving Angus and Simmental breeds. The differences suggest that, when expressed as a deviation from Angus solutions, the Simmental breed effect is large ($P < .01$) and positive for HCW, PRP, RPW, and CLMA, and negative for CFAT.

Genetic parameter estimates from a three-trait analysis are depicted in Table 2. An overall h^2 of 0.33 for HCW found in this study is in close agreement with reported estimates by Gregory et al. (1995) for steers in a composite population. However, the same group of authors reported lower estimates of 0.23 and 0.20 for steers of the overall and purebred data, respectively. Error variances were similar across sexes; therefore, the difference between bulls and steers in h^2 for HCW is due to a higher additive genetic variance in bull data (522.6 kg) compared to 322.97 kg for steer data. However, due to a small number of observations per sex, variance components were not subjected to statistical tests of significance.

The h^2 for the overall estimated PRP was extremely low. An error variance value of 5.01 kg for PRP in bulls is closer to the estimate for steers of 4.41 kg. However, the additive genetic variance for estimated PRP of steers was nearly seven times larger (1.40 kg) than that of bulls (.19 kg), leading to a relatively higher h^2 value of 0.24 for steers compared to a h^2 value of .04 for bulls.

The h^2 of estimated RPW for overall data was 0.33; the same as the average of h^2 values reported by Gregory et al. (1995) for composite and purebred steers and is closer to 0.38 for Hereford steer data (Dinkel and Busch, 1973). Benyshek (1981) reported a much larger difference in h^2 estimate for RPW between steers and heifers, but the combined estimate of .45 is much closer to the h^2 estimate of RPW for bulls in this study.

Overall h^2 estimates for CFAT and CLMA were similar. However, there was a clear difference in estimates between bulls and steers. The estimate of h^2 for CLMA in bulls is much closer to the overall estimate in the reports of Gregory et al. (1995) and of Dinkel and Busch (1973) for CLMA adjusted to 272 kg HCW from steer data.

Although the overall genetic correlation between HCW and PRP is closer to zero, the two traits showed a strong association that differed both in magnitude and sign when evaluated by sex. Previous estimates of genetic correlations between these traits for steers were negative but smaller in magnitude. Hence, our results imply that bulls with a good genetic makeup for HCW are likely to have more than average rank in PRP, while the opposite is true for steer progeny. In addition, genetic correlations between PRP and RPW showed a similar magnitude but were opposite in direction when analyzed by sex. Regardless of sex differences, there was a strong positive genetic association between HCW and RPW.

There is a general concern regarding differences in the estimate of genetic parameter by sex. Several previous reports also have shown these differences for carcass and production traits. In agreement with our results, some reports not only underscore differences in magnitude of estimates by sex, but also in their direction (Mohiuddin, 1993; Koots et al., 1994). However, to date, no conclusive recommendation exists regarding how to make best use of information when data are generated from bulls, steers and heifer, progeny.

Results of this study suggest that selection for HCW, using data from steer progeny, would increase CLMA, CFAT, and RPW, but would reduce PRP. The large and negative correlation between CFAT and PRP for steers confirms the strong pleiotropic action among genes influencing these traits, signifying that selection against CFAT would be most efficient to increasing PRP.

On the other hand, if data from bull progeny are considered, the same breeding objective as the above would increase CLMA and RPW. However, it also would result in an increase in PRP and a decrease in CFAT. That is, the same breeding objective is likely not only to result in a different rate of direct and correlated genetic change, but may also result in an opposite directional change in correlated response depending on the sex of progeny used as a source of information. Furthermore, the strong and positive genetic correlation between CLMA and PRP in bulls makes selection for CLMA a better alternative to selecting against CFAT to bring about a positive change in PRP.

Data used in this study are quite small to provide strong recommendations. However, these results and reports from previous work suggest possible differences in genetic parameter estimates between bulls and steer data. Therefore, further attempts should be made to make a more rigorous study of sex effects on genetic parameter estimation and to design a possible strategy to overcome the problem.

Implications

There exists a difference in breed direct effect large enough to make a choice between breeds for a specific breeding objective. The large genetic

variation between individuals within a breed can be used to measure carcass traits and to make genetic improvement through selection. However, if data from individuals of different sexes are to be used for genetic evaluation, possible differences in variance components need to be considered.

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Table 1. Least squares means of carcass traits and differences in breed effect.

Trait ^a	Breed effect (Simmental minus Angus)		
	Overall	Bull	Steer
HCW, kg	36.51 ± 8.24**	41.98 ± 11.24**	24.06 ± 12.40**
PRP	4.32 ± .48**	3.94 ± .60**	5.66 ± .99**
RPW, kg	28.20 ± 4.52**	30.83 ± 6.24**	22.75 ± 6.45**
CLMA, cm ²	13.42 ± 1.75**	13.90 ± 2.50**	13.52 ± 2.35**
CFAT, cm	-.79 ± .008**	-.769 ± .009**	-.915 ± .157**

^aHCW = Hot carcass weight; PRP = Percentage retail product; RPW = Retail product weight;

CLMA = carcass longissimus muscle area; CFAT = Carcass fat thickness.

** P < .01.

Table 2. Heritability, genetic, and phenotypic correlation between carcass traits^a.

Traits	h ^{2c}	Traits ^b				
		HCW	PRP	RPW	CFAT	CLMA
-----Overall-----						
HCW	.33		.24	.99	.25	.76
PRP	.07	-.18		.21	-.74	.57
RPW	.33	.98	.04		-.36	.82
CFAT	.14	.17	-.82	-.01		-.30
CLMA	.15	.53	.52	.66	-.15	
-----Bulls-----						
HCW	.43		.64	.99	-.94	.67
PRP	.04	.12		.69	-.31	.93
RPW	.46	.98	.07		-.88	.82
CFAT	.05	.11	-.78	-.04		-.99
CLMA	.21	.55	.53	.68	-.13	
-----Steers-----						
HCW	.32		-.45	.99	.25	.88
PRP	.24	.24		-.65	-.90	-.18
RPW	.40	.98	-.03		-.09	-.36
CFAT	.42	.24	-.86	.02		
CLMA	.07	.51	.51	.64	-.21	

^aValues above diagonal are genetic correlation, and those below diagonal are phenotypic correlation.

^bHCW = Hot carcass weight; PRP = Percentage retail product; RPW = Retail product weight;

CLMA = Carcass longissimus muscle area; CFAT = Carcass fat thickness.

^cSE of h² for the overall data were .11 (HCW), .09 (PRP), .11(RPW), .09 (CFAT), and .09 (CLMA).