Estimation of Genetic Parameters for Carcass Traits and Their Corresponding Ultrasound Measurements in Crossbred Beef Cattle

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Summary and Implications

Variance parameters including heritabilities, genetic and residual correlations are required for national cattle evaluation. There are huge amounts of data available for estimating such variance parameters for growth traits, but much less data is available for carcass traits. In this study, heritabilities and genetic correlations were estimated using restricted maximum likelihood on carcass weight (CWT), fat thickness (FAT), longissimus muscle area (LMA), marbling score (MRB), birth weight (BW), and ultrasound measurements of fat thickness (UFAT), longissimus muscle area (ULMA) and estimated percentage of intramuscular fat (UIMF) for crossbred cattle with carcass data recorded by the American Simmental Association. A multivariate animal model was fitted using ASREML4 software. The results demonstrate that UIMF measurements provide some useful information for carcass MRB (rg=0.73), but genetic correlations were only moderate between ULMA and LMA (0.56) and were weak between UFAT and FAT (0.38). The implications are that carcass measurements on progeny are the most reliable approach to evaluate carcass traits.

Introduction

American Simmental Association (ASA) like other breed associations has long been using real time ultrasound data in addition to carcass measurements to enhance national cattle evaluations on carcass traits. Studies revealed that evaluations combining ultrasound and carcass data outperform the ones that are based on carcass data alone. To date, most reports of parameters for use in national cattle evaluation were based on bivariate animal model analyses and some have fitted contemporary groups of fixed breed fractions rather than accounting for breed percentages. The objective of this study was to estimate genetic parameters required for evaluating carcass merit in the multi-breed analyses undertaken by International Genetic Solutions, using a single multivariate model fitting major breed percentages as fixed effects.

Materials and Methods

A dataset was constructed using all reliable carcass data from a structured progeny test program, augmented by data from other herds which had ultrasound data on the same sires. Birth weight phenotypic records were available for 72,606 individuals and 9,624 of these had CWT data, while FAT, LMA, and MRB were available for 9,234 individuals. Any ultrasound measures on animals with carcass data was ignored as these animals are not scanned using the same protocols as applied to the seed-stock animals that are routinely scanned but used for breeding and therefore do not typically have carcass data. There were 7,753 ultrasound records for animals without carcass data. Combining carcass data, ultrasound data and birth weight data produced a dataset compromising 16,987 records in analysis. An extended pedigree was used to construct the relationship matrix (n = 165,560).

A single multivariate model including all traits mentioned above could be represented in matrix notation as

$$y = Xb + Zu + e = \begin{bmatrix} y_C \\ y_U \\ y_B \end{bmatrix} = \begin{bmatrix} X_C & 0 & 0 \\ 0 & X_U & 0 \\ 0 & 0 & X_B \end{bmatrix} \begin{bmatrix} b_C \\ b_U \\ b_B \end{bmatrix}$$
$$+ \begin{bmatrix} Z_C & 0 & 0 \\ 0 & Z_U & 0 \\ 0 & 0 & Z_B \end{bmatrix} \begin{bmatrix} u_C \\ u_U \\ u_B \end{bmatrix} + \begin{bmatrix} e_C \\ e_U \\ e_B \end{bmatrix}$$

where X and Z were design matrices relating observations (y) to their respective fixed (b) and random (u) effects, and e was a vector of random residuals. Subscripts denote groups of carcass traits (C: CWT, FAT, LMA, MRB), ultrasound measurements (U: UFAT, ULMA, UIMF), and birth weight (B: BW), respectively for observations and their relative model terms. Random effects were assumed to have null means, and variances Var(u)=$G_0 \otimes A$, Var(e)=$R_0 \otimes I$, where G_0 and R_0 represent the genetic and residual variance/covariance matrices of order 8 being the number of traits being analyzed, while A and I represent the additive relationship matrix and identity matrices of order appropriate to the number of animals in analysis. Because no animal had both carcass and ultrasound data, residual covariances between any carcass and ultrasound traits were not relevant.

Fixed effects for all traits included contemporary groups including sex and the linear regression of five major breed percentages (Angus, Red Angus, Gelbvieh, Simmental and Others). For carcass traits, fixed effects included birth contemporary group and the linear regression of age at harvest in days. Individuals with carcass data were assigned to 889 birth contemporary groups. For ultrasound traits, fixed effects included scan date and the linear regression of age at scanning in days. Animals with ultrasound data were assigned to 328 different scan dates.

For birth weight, fixed effects included birth contemporary group and age of dam (2, 3, 4, 5, 10). Estimates of variance/covariances and associated genetic parameters were obtained by average information REML using ASREML4.

Results and Discussion

Heritability estimates for carcass traits were 0.37, 0.29, 0.33 and 0.43 for carcass weight, fat thickness, longissimus muscle area and marbling score, respectively. Heritability estimates for ultrasound traits were 0.40, 0.44 and 0.44 for fat thickness, longissimus muscle area and intramuscular fat percentage, respectively. Estimated heritability was 0.56 for birth weight. These results indicated that both carcass and ultrasound measurements were moderately heritable. Estimated genetic correlations were 0.46 between carcass weight and birth weight, a low 0.38 between fat thickness and ultrasound fat thickness, a moderate 0.56 between longissimus muscle area and ultrasound longissimus area, and a high 0.73 between marbling score and intramuscular fat percentage, as presented in Table 1. Genetic correlations between carcass traits and their ultrasound indicators varied by trait, indicating that genetic evaluation of some carcass traits like marbling would be enhanced by inclusion of ultrasound data, whereas other traits like fat provide little real information.

Acknowledgments

Table 1. Estimates of heritabilities, genetic and residual correlations between analyzed traits

Trait	CWT	FAT	REA	MRB	FATU	REAU	MRBU	BW
CWT	0.37[a]	0.30[c]	0.37	0.22	N/A[d]	N/A	N/A	0.18
FAT	0.13[b]	0.29	-0.09	0.24	N/A	N/A	N/A	-0.09
REA	0.53	-0.24	0.33	0.04	N/A	N/A	N/A	0.08
MRB	-0.07	0.23	-0.26	0.43	N/A	N/A	N/A	0.00
FATU	-0.02	*0.38[e]*	-0.09	0.16	0.40	0.20	0.17	-0.05
REAU	0.46	0.28	*0.56*	0.01	-0.02	0.44	-0.03	0.10
MRBU	-0.11	0.02	-0.20	*0.73*	0.34	-0.26	0.44	-0.06
BW	0.46	-0.12	0.26	-0.11	-0.14	0.17	-0.17	0.56

a. Heritabilities were presented as diagonal elements
b. Genetic correlations were presented as lower-triangle elements
c. Residual correlations were presented as upper-triangle elements
d. Residual correlations with N/A could not be estimated as no animals had both phenotypes
e. Bold italicized genetic correlations are between the ultrasound measure and its carcass equivalent