# Estimation of genetic and phenotypic parameters for ultrasound and carcass merit traits in crossbred beef cattle

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Miar, Y., Plastow, G. S., Bruce, H. L., Moore, S. S., Durunna, O. N., Nkrumah, J. D. and Wang, Z. 2014. **Estimation of genetic and phenotypic parameters for ultrasound and carcass merit traits in crossbred beef cattle**. Can. J. Anim. Sci. **94**: 273–280. Ultrasound measurements of 852 crossbred steers along with carcass merit measurements on 756 of them were used to examine their genetic and phenotypic parameters. Traits including ultrasound backfat thickness (UBF), ultrasound ribeye area (UREA), ultrasound marbling (UMAR), carcass weight (CWT), carcass grade fat (CGF), carcass average backfat thickness (CABF), carcass ribeye area (CREA), carcass marbling score (CMAR), and carcass lean meat yield (CLMY) were measured on 6 yr of residual feed intake trials from 2003 to 2008. Pairwise bivariate animal models were performed for each combination of traits using ASReml software to estimate heritability, phenotypic and genetic correlations among the traits. Significant fixed effects (contemporary group, and sire breed), covariates (age of dam, slaughter weight, and start test age of animal), and random additive effect were fitted in the models. The heritability estimates for UBF, UREA, UMAR, CWT, CGF, CABF, CREA, CMAR, and CLMY were 0.31, 0.17, 0.37, 0.40, 0.22, 0.25, 0.24, 0.38, and 0.28, respectively. Most of the phenotypic correlations were significant ($P < 0.05$). CWT had low to moderate phenotypic correlations with most of the traits. Results show that heavier CWT tends to have more UREA, CGF, CABF, and CREA. Genetic correlations among these traits varied from weak to strong, but most of them were not significantly different from zero. Greater CREA may lead to decreased UMAR, and UBF due to negative genetic correlations ($-0.56 \pm 0.32$, and $-0.45 \pm 0.23$, respectively). The results support the potential value of ultrasound technology in crossbreed beef cattle breeding programs to generate indicator traits for carcass quality. In addition, carcass lean meat yield correlated favourably with backfat thickness and rib eye area but correlated unfavourably with UMAR. The estimated genetic parameters for ultrasound and carcass merit traits can be incorporated into breeding programs that emphasize carcass quality in Canadian crossbred beef cattle populations.

**Key words:** Beef cattle, carcass merit, genetic parameters, heritability, ultrasound

Miar, Y., Plastow, G. S., Bruce, H. L., Moore, S. S., Durunna, O. N., Nkrumah, J. D. et Wang, Z. 2014. **Évaluation de paramètres génétiques et phénotypiques par échographie et caractéristiques de qualité des carcasses chez les bovins de boucherie croisés**. Can. J. Anim. Sci. **94**: 273–280. Les mesures par échographie de 852 bouvillons croisés ainsi que les mesures de qualité de la carcasse de 756 d'entre eux ont été utilisées pour examiner leurs paramètres génétiques et phénotypiques. Les caractéristiques, qui comprennent l'épaisseur du gras dorsal déterminé par échographie (UBF - « ultrasound backfat thickness »), l'aire du faux-filet déterminée par échographie (UREA - « ultrasound ribeye area »), le persillage déterminé par échographie (UMAR - « ultrasound marbling »), le poids de carcasse (CWT - « carcass weight »), l'indice de gras de couverture de la carcasse (CGF - « carcass grade fat »), l'épaisseur moyenne du gras dorsal (CABF - « carcass average backfat thickness »), l'aire du faux-filet de la carcasse (CREA - « carcass ribeye area »), la cote de persillage de la carcasse (CMAR - « carcass marbling score »), et le rendement en viande maigre de la carcasse (CLMY - « carcass lean meat yield »), ont été mesurées lors d'études sur la prise alimentaire résiduelle pendant 6 ans, entre 2003 et 2008. Des analyses en modèles bivariés par paires d'animaux ont été effectuées pour chaque combinaison de caractéristiques au moyen du logiciel ASReml pour évaluer l'héritabilité et les corrélations phénotypiques et génétiques entre les caractéristiques. Les effets fixes significatifs (groupe de contemporains et race du géniteur), les covariables (âge de la mère, poids à l'abattage et âge de l'animal au début des analyses) et les effets aléatoires additifs ont été inclus dans les modèles. Les évaluations d'héritabilité pour UBF, UREA, UMAR, CWT, CGF, CABF, CREA, CMAR, et CLMY étaient de 0,31; 0,17; 0,37; 0,40; 0,22; 0,25; 0,24; 0,38 et 0,28 respectivement. La plupart des corrélations phénotypiques étaient significatives ($P < 0,05$). Le CWT avait une corrélation phénotypique de faible à modérée avec la plupart des caractéristiques. Les résultats démontrent que des CWT plus élevés tendent vers des niveaux plus élevés de UREA, CGF, CABF et CREA. Les corrélations génétiques parmi ces caractéristiques variaient de faible à forte, mais la plupart n'étaient pas significativement différentes de zéro. Une plus grande CREA peut occasionner des niveaux réduits de UMAR et de UBF imputables aux corrélations génétiques négatives ($-0,56 \pm 0,32$ et $-0,45 \pm 0,23$; respectivement). Les résultats

**Abbreviations:** **CABF**, carcass average backfat thickness; **CGF**, carcass grade fat; **CLMY**, carcass lean meat yield; **CMAR**, carcass marbling score; **CREA**, carcass ribeye area; **CWT**, carcass weight; **UBF**, ultrasound backfat thickness; **UMAR**, ultrasound marbling; **UREA**, ultrasound ribeye area

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soutiennent la valeur potentielle de l'utilisation de la technologie d'échographie dans les programmes d'élevage des bovins de boucherie pour obtenir des caractéristiques indicatrices de qualité de carcasse. De plus, il y avait une corrélation favorable entre le rendement en viande maigre de la carcasse et l'épaisseur du gras dorsal et l'aire du faux-filet, mais une corrélation négative avec le UMAR. Les paramètres génétiques évalués par échographie pour les caractéristiques de qualité des carcasses peuvent être incorporés dans les programmes d'élevage qui font valoir la qualité de carcasse des populations canadiennes de bovins de boucherie croisés.

**Mots clés:** Bovins de boucherie, qualité de la carcasse, paramètres génétiques, héritabilité, échographie

The major focus of traditional beef breeding programs is on production efficiency in traits of interest such as reproductive, growth and feed efficiency performance. More recently, many beef producers have paid more attention to lean meat content as well as marbling and quality grade to better meet consumer demands. Miller et al. (2001) revealed that consumers would pay more for tender beef. In fact, approximately 80% of consumers would buy steaks form the retailer if they were consistently tender (Pratt et al. 2013). This led to the development of breeding objectives that include beef carcass merit traits. Increasing muscle tissue and decreasing fat are two major objectives of beef genetic improvement programs that are consistent with consumer demands and preferences. Development of ultrasound technology has made it feasible to collect carcass composition traits on live animals as indicator traits for carcass merit. Thus, ultrasound traits have become important to beef cattle producers. The traits, such as amount of backfat, are also important factors in determining cutability, and the amount of intramuscular fat influences meat quality (Wheeler et al. 1994). Selection for lean meat might decrease fat content that is related to both carcass quality and yield (Wheeler et al. 1994). Utrera and Van Vleck (2004), in a review of 72 papers, and Koots et al. (1994a) reported that the heritability of different carcass traits is moderate to high. Genetic improvement of lean meat yield and carcass quality in beef breeding program requires estimating the genetic and phenotypic parameters of these carcass traits. In addition, genetic correlations between ultrasound measurements and corresponding carcass quality traits need to be confirmed before being implemented in breeding schemes to select carcass merits using ultrasound measurements. The genetic and phenotypic parameters for these traits have not previously been examined for the Kinsella crossbred beef population despite its importance. The objective of this study was to estimate the phenotypic and genetic parameters for different ultrasound and carcass merit traits in this crossbred beef cattle population.

## MATERIALS AND METHODS

The steers used in this study were cared for according to Canadian Council on Animal Care (1993) guidelines.

### Animals and Management

Crossbred steers ($n = 852$) were used in 6 yr of feeding trials conducted at the University of Alberta's Kinsella research station in Alberta, Canada, from 2003 to 2008. The steers were born in the spring of each year from 116 crossbred sires mated to 621 crossbred dams on pasture. The composition of this population has been previously described by Nkrumah et al. (2007) and Durunna et al. (2011). Briefly, the crossbred dams were crosses between Angus or Charolais bulls and composite dams generated from three composite cattle lines, namely Beef Synthetic 1, Beef Synthetic 2, and Dairy × Beef Synthetic. The beef synthetic 1 was made up of 33% Angus, 33% Charolais, about 20% Galloway, and some other beef breeds. The beef synthetic 2 was composed of about 60% Hereford and 40% other beef breeds. Dairy × Beef Synthetic was made up of about 60% dairy breeds (Holstein, Brown Swiss, or Simmental) and 40% beef breeds (such as Angus and Charolais) (Goonewardene et al. 2003). The crossbred sires were bulls selected from crosses between crossbred, Angus, or Charolais bulls and the crossbred dams.

The Growsafe automated feeding system (Growsafe® Systems Ltd., Airdrie, AB) was used for feeding animals at the Kinsella Research Station. Feed and clean drinking water were offered ad libitum throughout the test periods. Approximately 90 animals were included per test with two tests conducted each year. The animals were 224 (SD = 42) d of age at the beginning of testing and they were in the feeding test for a total of 84 d. In year 1, the steers received a ration that consisted of 80.0% dry-rolled corn, 13.5% alfalfa hay pellet, 5% feedlot supplement (32% crude protein beef supplement), and 1.5% canola oil. This ration had a metabolizable energy content of approximately 2.90 Mcal $kg^{-1}$ and 12.5% crude protein (as-fed basis). In years 2 and 3, the ration was composed of 64.5% barley grain, 20% oat grain, 9.0% alfalfa hay pellet, 5.0% beef feedlot supplement, and 1.5% canola oil. This ration had a metabolizable energy content of approximately 2.91 Mcal $kg^{-1}$ and 14% crude protein (as-fed basis). In years 4, 5, and 6, the steers received a diet composed of about 57% barley, 28% oats, 10% alfalfa pellets, and 5% feedlot supplement, supplying approximately 2.9 Mcal $kg^{-1}$ of metabolizable energy (as-fed basis). The diet in year 1 was corn instead of barley and oats because of a feed barley shortage in 2003. Steers were produced from a multiple-sire breeding program on pasture and the sire of each calf was later determined using a panel of microsatellite markers before 2006 (Nkrumah et al. 2007) but rest of them were verified using single nucleotide polymorphisms.

## Traits Studied and Data Collection

Carcass and ultrasound measurements have been described previously by Nkrumah et al. (2004). Briefly, ultrasound measurements of 12th/13th rib fat depth (backfat thickness) (UBF), longissimus muscle (LM) area (UREA), and marbling score (UMAR) were taken at the end of the test (Durunna et al. 2011) with an Aloka 500V realtime ultrasound with a 17-cm, 3.5-MHz linear array transducer (Overseas Monitor Corporation Ltd., Richmond, BC). After ultrasound measurements at the end of each test, steers were shipped to a commercial packing plant where they were slaughtered the following day and standard carcass data were collected after a 24-h chill at $-4°C$ (Nkrumah et al. 2004).

Carcass merit traits were evaluated according to the Canadian beef carcass grading system (Agriculture Canada 1992). The carcass weight (CWT) of each animal was determined as the sum of the weights of the left and right halves of the carcass after 24-h chill at $-4°C$. Carcass grade fat (CGF) was measured at the 12th/13th rib of each carcass. Carcass average backfat thickness (CABF) was measured over the ribeye muscle area at the 12th rib. Carcass ribeye area (CREA) was taken on the cross section of the ribeye muscle area between the 12th and 13th ribs. Carcass marbling score (CMAR) is a measure of intramuscular fat and can be classified as 1 to $<2$ units = trace marbling of 100 to 199 (Canada A quality grade); 2 to $<3$ units = slight marbling of 200 to 299 (Canada AA quality grade); 3 to $<4$ units = small to moderate marbling of 300 to 399 (Canada AAA quality grade); and $\geq 4$ units = slightly abundant or more marbling of 400 to 499 (Canada Prime). Carcass lean meat yield (CLMY) is an estimate of saleable meat and was estimated according to the equations: lean meat yield (%) = 57.96 + [0.202 × (longissimus thoracis area (cm$^2$)] – [0.027 × warm carcass weight (kg)] – [0.703 × average backfat thickness (mm)] as described by Basarab et al. (2003).

## Statistical and Genetic Analyses

There were 852 steers with ultrasound and 766 steers with carcass merit records (Table 1). Genetic and phenotypic (co)variances were estimated for the crossbred beef cattle population using pairwise bivariate animal models with the statistical software ASReml 3.0 (Gilmour et al. 2009) since the multivariate model could not reach to its convergence. Relevant fixed and random effects for ultrasound and carcass traits are presented in Table 2. The animal model included random additive polygenic effects in the final model for all traits. Age of dam, slaughter weight, and start age of animal on test were included in the model as linear covariates. Contemporary group (combination of test groups and years), and breed of the sire were included in the model as fixed effects. The model is given by:

$$\begin{bmatrix} Y_1 \\ Y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix},$$

where $y_1$ and $y_2$ are the vectors of phenotypic measurements for traits 1 and 2, respectively; $x_1$ and $x_1$ are incidence matrices relating the fixed effects to vectors $y_1$ and $y_1$, respectively; $b_I$ and $b_1$ are the vectors of fixed effects (contemporary group, sire-breed, dam age, slaughter weight and start age) for traits 1 and 2, respectively; $Z_1$ and $Z_2$ incidence matrices relating the phenotypic observations to the vector of polygenic (a) effects for traits 1 and 2, respectively; and $e_1$ and $e_1$ are the vectors of random residuals for the traits 1 and 2, respectively.

The expectations and variances were

$$E\begin{bmatrix} Y_1 \\ Y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix},$$

and

$$V\begin{bmatrix} a_1 \\ a_2 \\ e_1 \\ e_2 \end{bmatrix} = \begin{bmatrix} A\sigma^2_{a1} & A\sigma_{a12} & 0 & 0 \\ A\sigma_{a21} & A\sigma^2_{a2} & 0 & 0 \\ 0 & 0 & I\sigma^2_{e1} & I\sigma_{e12} \\ 0 & 0 & I\sigma_{e21} & I\sigma^2_{e2} \end{bmatrix}$$

where $a$ and $e$ were assumed to be normally distributed with mean of zero and (co)variances $A\sigma^2_a$ and $I\sigma^2_e$ for $a$ and $e$, respectively. The $A$ is the additive relationship

**Table 1. Descriptive statistics of the ultrasound and carcass merit traits**

| Traits | Steers ($n$) | Mean | SD | Range | Coefficient of variation |
|---|---|---|---|---|---|
| Ultrasound backfat thickness (mm) | 852 | 8.80 | 2.98 | 1.89–26.81 | 33.83 |
| Ultrasound ribeye area (cm$^2$) | 852 | 79.07 | 10.02 | 52.94–119.82 | 12.68 |
| Ultrasound marbling score | 852 | 5.14 | 0.73 | 3.20–8.65 | 14.14 |
| Carcass weight (kg) | 765 | 316.17 | 29.38 | 207.20–401.25 | 9.29 |
| Carcass grade fat (mm) | 766 | 11.04 | 3.96 | 2.00–26.00 | 35.87 |
| Carcass average backfat thickness (mm) | 766 | 12.42 | 3.96 | 2.67–26.67 | 31.90 |
| Carcass ribeye area (cm$^2$) | 766 | 82.88 | 8.47 | 53.00–113.00 | 10.21 |
| Carcass marbling score | 766 | 2.19 | 0.53 | 1.00–3.00 | 24.41 |
| Carcass lean meat yield (%) | 766 | 57.43 | 3.67 | 44.67–66.18 | 6.38 |

**Table 2. Significance of fixed effects and the random effect included in the models for the analysis of ultrasound and carcass merit traits**

| | Fixed effects | | | | | Random effect |
|---|---|---|---|---|---|---|
| Traits$^z$ | Sire breed | Contemporary group | Dam age | Slaughter weight | Start age | Animal |
| UBF | ** | ** | | ** | | ✓ |
| UREA | ** | ** | | ** | | ✓ |
| UMAR | ** | ** | * | | | ✓ |
| CWT | * | ** | | | ** | ✓ |
| CGF | ** | ** | | ** | | ✓ |
| CABF | ** | ** | | ** | | ✓ |
| CREA | ** | ** | * | ** | | ✓ |
| CMAR | ** | ** | ** | * | | ✓ |
| CLMY | ** | ** | ** | ** | | ✓ |

$^z$UBF, ultrasound backfat thickness (mm); UREA, ultrasound ribeye area (cm$^2$); UMAR, ultrasound marbling score; CWT, carcass weight (kg); CGF, carcass grade fat (mm); CABF, carcass average backfat thickness (mm); CREA, carcass ribeye area (cm$^2$); CMAR, carcass marbling score; CLMY, carcass lean meat yield (%).
*, ** indicate $P < 0.10$ and $P < 0.05$, respectively.

matrix, $\sigma_a^2$ is the additive genetic variance of random polygenic effect, and $I$ is an identity matrix with order equal to the number of animals. Heritability was estimated using variance components obtained from the bivariate analyses:

$$h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_e^2}$$

A preliminary univariate animal model for each trait was carried out to obtain initial values of (co)variance parameters that were then used in subsequent bivariate analyses. Pairwise bivariate analyses were performed for each combination of traits. The two-trait individual animal model used to estimate (co)variance components was used to calculate the phenotypic and genetic correlations as well as the heritability as implemented in ASReml 3.0 (Gilmour et al. 2009). The phenotypic, genetic correlation coefficients, the heritability and their standard errors are reported in Table 3. Heritabilities were the average estimates of corresponding pairwise bivariate analyses.

## RESULTS AND DISCUSSION

### Heritability

The heritability estimates of the traits are presented in Table 3 (diagonal elements). Estimates of heritability were from moderate to high except for UREA, which was estimated to have low heritability. Ultrasound and carcass traits generally have been reported as moderate to high heritable traits in previous studies. Several factors influence the heritability estimates, which may include the end-point adjustment, such as age or weight adjustment, sampling, population size (Benyshek 1981; Koots et al. 1994a), complete pedigree and effect of heterosis in crossbred populations. Results from this study suggest that there is good opportunity for genetic improvement of carcass merit traits in this population since the heritability estimates for these traits range from moderate to high.

For UBF, the estimate in this study (0.31 ± 0.11) was very comparable with the moderate estimate of 0.30 reported by Robinson et al. (1993) in Angus and Hereford cattle. Although it was higher than the 0.11 reported by Moser et al. (1998) and 0.14 reported by Johnson et al. (1993). The low estimate of heritability in Johnson et al. (1993), and Moser et al. (1998) may be due to lower average of UBF at the 12th rib of Brangus calves compared with the measurements in two ribs, 12th and 13th, in our study (4.4 and 4.7 vs. 8.8 mm, respectively) and also their age-constant UBF compared with weight-constant UBF in our study. Kemp et al. (2002) reported age-adjusted heritability of 0.39 for UBF in Angus steers. The differences between the heritability reported here and Kemp et al. (2002) may be due to differences in breeds (Crossbred vs. Angus), smaller sample size in our study compared with their

**Table 3. Estimates of genetic (below diagonal) and phenotypic (above diagonal) correlations, heritabilities (diagonal) and their standard error of estimates among ultrasound and carcass merit traits**

| Traits$^z$ | UBF | UREA | UMAR | CWT | CGF | CABF | CREA | CMAR | CLMY |
|---|---|---|---|---|---|---|---|---|---|
| UBF | **0.31 ± 0.11*** | −0.03 ± 0.04 | 0.34 ± 0.03* | −0.05 ± 0.05 | 0.68 ± 0.02* | 0.68 ± 0.02* | −0.31 ± 0.04* | 0.26 ± 0.04* | −0.65 ± 0.02* |
| UREA | −0.17 ± 0.30 | **0.17 ± 0.09** | −0.03 ± 0.04 | 0.30 ± 0.04* | −0.01 ± 0.04 | 0.00 ± 0.04 | 0.40 ± 0.03* | −0.08 ± 0.04* | 0.15 ± 0.04* |
| UMAR | 0.60 ± 0.18* | −0.42 ± 0.32 | **0.37 ± 0.11*** | 0.13 ± 0.04* | 0.30 ± 0.04* | 0.31 ± 0.04* | −0.22 ± 0.04* | 0.39 ± 0.03* | −0.33 ± 0.04* |
| CWT | −0.34 ± 0.23 | −0.16 ± 0.40 | 0.33 ± 0.22 | **0.40 ± 0.12*** | 0.20 ± 0.04* | 0.21 ± 0.04* | 0.39 ± 0.04* | 0.15 ± 0.05* | −0.16 ± 0.05* |
| CGF | 0.90 ± 0.13* | −0.44 ± 0.34 | 0.43 ± 0.24 | 0.08 ± 0.28 | **0.22 ± 0.10*** | 0.96 ± 0.00* | −0.33 ± 0.03* | 0.30 ± 0.04* | −0.89 ± 0.01* |
| CABF | 0.90 ± 0.15* | −0.46 ± 0.33 | 0.35 ± 0.25 | 0.18 ± 0.27 | 0.97 ± 0.02* | **0.27 ± 0.12*** | −0.33 ± 0.03* | 0.32 ± 0.04* | −0.92 ± 0.01* |
| CREA | −0.45 ± 0.23* | 0.53 ± 0.26* | −0.56 ± 0.23* | 0.07 ± 0.29 | −0.40 ± 0.29 | −0.24 ± 0.30 | **0.24 ± 0.10*** | −0.17 ± 0.04* | 0.66 ± 0.02* |
| CMAR | 0.33 ± 0.23 | −0.36 ± 0.32 | 0.61 ± 0.17* | 0.06 ± 0.25 | 0.19 ± 0.27 | 0.14 ± 0.26 | −0.35 ± 0.25 | **0.38 ± 0.12*** | −0.33 ± 0.04* |
| CLMY | −0.82 ± 0.12* | 0.51 ± 0.30 | −0.62 ± 0.20* | −0.27 ± 0.25 | −0.91 ± 0.06* | −0.91 ± 0.05* | 0.62 ± 0.19* | −0.34 ± 0.24 | **0.28 ± 0.11*** |

$^z$UBF, ultrasound backfat thickness (mm); UREA, ultrasound ribeye area (cm$^2$); UMAR, ultrasound marbling score; CWT, carcass weight (kg); CGF, carcass grade fat (mm); CABF, carcass average backfat thickness (mm); CREA, carcass ribeye area (cm$^2$); CMAR, carcass marbling score; CLMY, carcass lean meat yield (%).
*$P < 0.05$.

study (852 vs. 10 569), and their age-constant estimates in contrast to the present study on weight.

For UREA, our low heritability estimate (0.17 ± 0.09) indicates the presence of small additive genetic effect on UREA. This low heritability estimate for UREA was in agreement with Mao et al. (2013) who reported heritability of 0.11 for this trait on Angus cattle steers. Arnold et al. (1991) reported heritabilities for UREA to be 0.25 for weight-constant, and 0.28 for age-constant estimates in Hereford cattle. Other studies have shown moderate-to-high heritabilities for UREA ranging from 0.21 to 0.68 (Robinson et al. 1993; Johnson et al. 1993; Reverter et al. 2000). The differences with those previous studies may be due to using more homogeneous genetic backgrounds and populations for this trait. In addition to differences in population, sample size, and statistical models used for (co)variance estimation were different from previous studies. For example, Arnold et al. (1991) used the Hereford breed in comparison with the crossbred beef cattle used in our study. Also, Reverter et al. (2000) used a much larger sample size than our study (3989 for Angus and 1637 for Hereford vs. 852).

Marbling is one the most important quality traits as per consumer's demands. The amount of marbling depends on the implementation of different beef breeding and management techniques, which may be one of the reasons for the variation, observed in the estimation of UMAR. The heritability of UMAR was moderate in the present study (0.37 ± 0.11). UMAR has been reported to be a moderately heritable trait. Koots et al. (1994a) reported the moderate heritability of 0.38 as the average heritability of many previous studies, which is in good agreement with our estimate. However, Devitt and Wilton (2001) and Reverter et al. (2000) reported heritability of 0.24 and 0.47 for UMAR, respectively. Several factors may contribute to these differences. First, bulls and heifers from Hereford and Angus were used in the Reverter et al. (2000) study compared to crossbred steers in this study. Second, the prediction of intramuscular fat from ultrasound images may be more accurate in their study because they analyzed at least three images from which to predict an average UMAR.

For CWT, the estimate in this study (0.40 ± 0.12) was in agreement with the average of all studies reviewed by Utrera and Van Vleck (2004) (0.40), Marshal (1994) (0.42), the experimental studies by Newman et al. (2002) (0.40), and Koch et al. (1982) (0.43). Although our estimate was lower than those reported by Devitt and Wilton (2001) for steers (0.47), Crews et al. (2003) for Simmental steers (0.48), Reverter et al. (2000) for Hereford (0.54), and Moser et al. (1998) for Brangus steers and heifers (0.59), the similarities in the estimates of our study with these previous studies may be due to a similar (age-constant) statistical model in the estimations compared with that used weight-constant adjustment. Besides the model, the present study was more similar to the estimates reported by previous studies using steers rather than bulls. The estimated heritability of CGF in this study (0.22 ± 0.10) was in good agreement with the heritability estimate of 0.23 by Bergen et al. (2006) for grade fat in the body cavity of finished feedlot steers. However, limited studies on heritability estimation of CGF make it difficult to compare our estimation with literature reviews.

Heritability estimates for basic carcass yield component traits were 0.27 ± 0.12, 0.24 ± 0.10, and 0.38 ± 0.12 for CABF, CREA, and CMAR, respectively. Utrera and Van Vleck (2004) summarized heritability estimates published up to 2004, and the averages across end points heritability in that summary for CABF, CREA, and CMAR were 0.36, 0.40, and 0.37, respectively. For CABF, the estimate in this study (0.27 ± 0.12) was similar to those estimates cited in the literature. For example, it was similar to those of Reverter et al. (2000) for Angus and Hereford, Newman et al. (2002) for backfat thickness over the rump, and the average heritability estimates adjusted by backfat thickness in the summary by Utrera and Van Vleck (2004) (0.27–0.28, 0.28, and 0.29, respectively). For CREA, Utrera and Van Vleck (2004) reported a large range from 0.01 to 0.97. The heritability estimate for CREA in this study (0.24 ± 0.10) was more similar to those of Gregory et al. (1995), Hoque et al. (2002) but lower than the mean estimate reported in Utrera and Van Vleck (2004) (0.22, 0.18, and 0.40, respectively). The similarities between our estimate of CREA and those of previous studies may be due to the adjustment for backfat thickness in the model, and a similar population but differences may be due to the model for variance estimation. Marbling is an estimate of intramuscular fat that is associated with backfat thickness. For this reason, backfat adjustment of marbling may reduce the additive genetic variance that is not removed by slaughter weight adjustment. However, the moderate heritability of CMAR in this study suggests that genetic improvement of marbling may be possible independently from improvement of leanness. It appears that the estimate of CMAR is in the range of previous studies. Most of studies estimated a moderate range of heritability for CMAR from 0.30 to 0.57 that is in agreement with our results. Estimated heritability (0.38 ± 0.12) in this study was in good agreement with the average heritability (0.37) in the review by Utrera and Van Vleck (2004), and was close to that of Devitt and Wilton (2001) (0.43), and Benyshek (1981) for Hereford (0.47).

The estimated heritability of CLMY in this study was 0.28 ± 0.11, which was similar (0.26) to reports by the American Simmental Association (1993) for Simmental, and close to the average heritability for CLMY reported by Utrera and Van Vleck (2004) (0.36), and Marshall (1994) (0.36). Although there have been limited studies on parameter estimation of ultrasound and carcass traits in beef cattle, most of our heritability estimates were within the ranges published.

## Phenotypic Correlations

Table 3 lists the phenotypic correlations among ultrasound and carcass merit traits in this population (above diagonal elements). Several phenotypic correlations were lower than the corresponding genetic correlations. This is expected, in part, because the heritability estimates in our study indicated the importance of non-additive genetic and environmental contributions to the phenotypic variation. This does not indicate that a negative environmental correlation exists. A negative environmental correlation exists only when the ratio of phenotypic correlation to the genetic correlation is less than geometric mean of heritabilities for two traits (Searle 1961). None of our estimations had negative environmental correlations. Most of the phenotypic correlations were significant ($P < 0.05$). The phenotypic correlation between UREA and UBF ($-0.03 \pm 0.04$), UMAR ($-0.03 \pm 0.04$), CGF ($-0.01 \pm 0.04$), and CABF ($-0.00 \pm 0.04$) were not significantly different from zero ($P < 0.05$). In addition, the phenotypic correlation of UBF and CWT was not significantly different from zero ($-0.05 \pm 0.05$) ($P < 0.05$).

Genetic improvement of multiple-traits can be difficult because of the antagonistic genetic relationships between some traits. Selection for these traits can be achieved through genomic approaches such as marker-assisted selection. Our study showed that almost all estimates of phenotypic correlations were close to the literature reviews by Marshall (1994), Koots et al. (1994b), and Pariacote et al. (1998). The North American beef industry uses marbling as one of the primary factors affecting carcass quality of cattle. The phenotypic correlation between CMAR and CABF ($0.32 \pm 0.04$) was moderate. This result is in the range of estimates (0.12–0.38) reviewed by Marshall (1994). However, this result is a little larger than the literature review by Koots et al. (1994b), who reported an unweighted average of 0.22. Pariacote et al. (1998) also reported a low phenotypic correlation estimate for Shorthorn beef cattle (0.20).

There were low-to-moderate correlations for CWT with most of the traits of this study. Results show that animals with heavier CWT tend to have more UREA, CGF, CABF, and CREA and less CLMY than animals with lighter carcasses, which is in agreement with other publications (Marshall 1994; Pariacote et al. 1998). In the present study, heavier carcass was correlated with a small increase in marbling (both ultrasound and carcass) that is favourable.

## Genetic Correlations

Table 3 presents the genetic correlations among ultrasound and carcass merit traits in this population (below diagonal elements). Genetic correlations varied from weak to strong among the different ultrasound and carcass merit traits within the study. Most genetic correlations were not significantly different from zero ($P > 0.05$), which might be due to a shallow pedigree, since only one paternal generation was available in this study, relatively small sample size, and the possibility of heterosis in the crossbred population. All genetic correlations between CWT and other traits were not significant (minimum $0.06 \pm 0.25$; maximum $-0.34 \pm 0.23$). The CGF was strongly correlated with CABF ($0.97 \pm 0.02$), UBF ($0.90 \pm 0.13$), and CLMY ($-0.91 \pm 0.06$) which seems to be overestimated due to the relatively small sample size in the current study and shallow pedigree as discussed. CABF was also negatively correlated with CLMY ($-0.91 \pm 0.05$). CABF was also strongly correlated with UBF ($0.90 \pm 0.15$). Devitt and Wilton (2001) showed that ultrasound backfat depth has strong positive genetic correlation with carcass average backfat thickness (0.88), which is in agreement with our results.

The genetic correlations between CMAR and other traits were not significant except for correlation with UMAR, with a magnitude of $0.61 \pm 0.17$. The genetic correlations between CREA and UBF ($-0.45 \pm 0.23$), UREA ($0.53 \pm 0.26$), and UMAR ($-0.56 \pm 0.23$) were significantly different from zero ($P < 0.05$). CLMY was also positively correlated with CREA ($0.62 \pm 0.19$) but negatively correlated with UBF ($-0.82 \pm 0.12$), CABF ($-0.91 \pm 0.05$), UMAR ($-0.62 \pm 0.20$), and CGF ($-0.91 \pm 0.06$). The genetic correlations between UBF and other traits were from moderate to very strong (minimum $0.33 \pm 0.23$; maximum $0.90 \pm 0.13$) except with the UREA ($-0.17 \pm 0.30$).

The genetic correlations between UMAR and other traits were between moderate and strong (minimum $0.33 \pm 0.22$; maximum $-0.62 \pm 0.20$). It seems that selection for UMAR may increase UBF and CMAR in this population because they have strong positive genetic correlation ($0.60 \pm 0.18$, and $0.61 \pm 0.17$, respectively). Kemp et al. (2002) reported very strong genetic correlation (0.90) between carcass and ultrasound marbling in Angus steers, which is in agreement with our results.

It was expected that the UREA would have positive genetic correlations with CREA, which was confirmed by our estimate ($0.53 \pm 0.26$). This result is comparable with Kemp et al. (2002), who reported a genetic correlation between carcass and ultrasound longissimus area of 0.58. Moser et al. (1998), and Devitt and Wilton (2001) reported similar results to ours (0.66). Although Crews et al. (2003) reported a much larger genetic correlation between UREA and CREA (0.80), most researchers reported moderate to strong genetic correlation between ultrasound and carcass ribeye area. The weakest genetic correlation between ultrasound measures and their corresponding carcass measurements in the present study was between UREA and CREA. This may be due to the difficulty of measuring UREA in comparison to others. Genetic correlations between ultrasound and corresponding carcass traits have also been investigated by other researchers (Reverter et al. 2000; Kemp et al. 2002). The results of this study show that selection based on CREA will lead to increased CLMY ($0.62 \pm 0.19$), and decreased UBF ($-0.45 \pm 0.23$). Many studies have suggested that there is a negative correlation between longissimus muscle area and backfat thickness but it depends on the population studied and the model of its estimation. However, we used different statistical models and initial values for (co)variance estimates for all bivariate analyses, but some standard errors are still large, which might be due to the relatively small sample size and population structure of crossbred beef cattle used in the present study.

In conclusion, characterization of carcass merit and ultrasound traits and their relationships in crossbred beef cattle will provide not only insight into the biological basis of carcass quality but also a valuable reference to develop effective genetic improvement programs for carcass traits in the studied population. The results indicate that ultrasound measurements of backfat thickness, marbling score, and ribeye area have strong genetic correlations with the corresponding measurements of carcass merit. This provides evidence of potential value of ultrasound technology in crossbred beef cattle genetic improvement programs to use ultrasound measurements as indicators for carcass merit traits. The findings of this study also suggest that genetic selection for increased lean meat yield will lead to decreased fat content. We concluded that the positive genetic correlations between carcass yield and quality traits would imply that beef carcass quality traits may be improved without any adverse genetic effect among these traits. In addition, moderate to high estimates of heritability of the ultrasound and carcass merit traits would indicate a good opportunity for improving carcass merit traits in crossbred beef cattle.

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