

# Genetic correlations between live yearling bull and steer carcass traits adjusted to different slaughter end points. 1. Carcass lean percentage<sup>1,2</sup>

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**ABSTRACT:** We studied genetic relationships between age-constant live yearling beef bull growth and ultrasound traits and steer carcass traits with dissected steer carcass lean percentage adjusted to slaughter age-, HCW-, fat depth-, and marbling score-constant end points. Three measures of steer carcass lean percentage were used. Blue Tag lean percentage (BTLean) was predicted from HCW, fat depth, and LM area measurements. Ruler lean percentage (RulerLean) was predicted from carcass fat depth and LM depth and width measurements. Dissected lean percentage (DissLean) was based on dissection of the 10–11–12th rib section. Both BTLean ( $h^2 = 0.30$  to  $0.44$ ) and DissLean ( $h^2 = 0.34$  to  $0.39$ ) were more heritable than RulerLean ( $h^2 = 0.05$  to  $0.14$ ) at all end points. Genetic correlations among DissLean and RulerLean ( $r_g = 0.61$  to  $0.70$ ), DissLean and BTLean ( $r_g = 0.56$  to  $0.72$ ), and BTLean and RulerLean ( $r_g = 0.59$  to  $0.90$ ) indicated that these traits were not genetically identical. Adjusting DissLean to different end points changed the magnitude, but generally not the direction, of genetic correlations with indicator traits. Ultrasound scan-age-constant live yearling bull lean percentage estimates were heritable ( $h^2 = 0.26$  to  $0.42$ ) and genetically correlated with each

other ( $r_g = 0.68$  to  $0.99$ ) but had greater correlations with DissLean at slaughter age ( $r_g = 0.24$  to  $0.48$ ) and HCW ( $r_g = 0.16$  to  $0.40$ ) end points than at fat depth ( $r_g = -0.08$  to  $0.13$ ) and marbling score ( $r_g = 0.02$  to  $0.11$ ) end points. Scan-age-constant yearling bull ultrasound fat depth also had stronger correlations with DissLean at slaughter age ( $r_g = -0.34$ ) and HCW ( $r_g = -0.25$ ) than at fat depth ( $r_g = -0.02$ ) and marbling score ( $r_g = -0.03$ ) end points. Yearling bull scan-age-constant ultrasound LM area was positively correlated with DissLean at all endpoints ( $r_g = 0.11$  to  $0.23$ ). Genetic correlations between yearling bull LM method 1 width ( $r_g = 0.38$  to  $0.56$ ) and method 2 depth ( $r_g = -0.17$  to  $-0.38$ ) measurements with DissLean suggested that LM shape may be a valuable addition to genetic improvement programs for carcass lean percentage at slaughter age, HCW, and fat depth constant end points. At all end points, steer carcass fat depth ( $r_g = -0.60$  to  $-0.64$ ) and LM area ( $r_g = 0.48$  to  $0.59$ ) had stronger associations with DissLean than did corresponding live yearling bull measurements. Improved methods that combine live ultrasound and carcass traits would be beneficial for evaluating carcass lean percentage at fat depth or marbling score end points.

**Key words:** cattle, end point, genetic parameter, selection, ultrasound

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## INTRODUCTION

Yearling bull ultrasound measurements are heritable and genetically correlated with corresponding

slaughter age-constant steer carcass traits (Devitt and Wilton, 2001; Crews et al., 2003; Bergen et al., 2005b). Because specific price premiums or discounts are generally not applied to carcass fat depth or LM size, a genetic

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evaluation for carcass lean percentage may be preferable to separate genetic evaluations for indicator traits. However, information regarding genetic relationships between yearling bull ultrasound measurements with dissected steer carcass lean percentage is limited to one study in Australia (Reverter et al., 2000) and one in North America (Crews and Kemp, 2001).

Alternative slaughter end points have also received considerable attention recently. North American genetic evaluations adjust both yearling seedstock ultrasound and steer carcass data to age-constant end points (BIF, 2002). Adjusting seedstock data to an age-constant basis is reasonable because postweaning growth tests generally conclude near 365 d of age (Schenkel et al., 2004). In contrast, commercial cattle are marketed based on price premiums or discounts for HCW, yield or quality grade, seasonal price considerations, and production costs. Sire rankings change considerably when progeny carcass data are adjusted to different slaughter end points. Shanks et al. (2001) found that slaughter age-constant EPD for percent retail yield (estimated from HCW, KPH fat, subcutaneous fat depth, and LM area measurements) were highly correlated with percent retail yield EPD evaluated at a constant HCW ( $r = 0.966$ ) but less strongly correlated at marbling score ( $r = 0.881$ ) and fat depth constant end points ( $r = 0.156$ ). This study evaluated genetic relationships between age-constant live yearling beef bull growth and ultrasound traits and steer carcass traits with dissected steer carcass lean percentage adjusted to slaughter age-, HCW-, fat depth-, and marbling score-constant end points.

## MATERIALS AND METHODS

### *Animals and Data*

Growth and ultrasound data from yearling beef bulls and carcass data from finished crossbred feedlot steers were used in this study. Young beef bulls ( $n = 2,172$ ) were born between 1993 and 2002 in private seedstock herds and evaluated in centralized postweaning growth test and feed efficiency stations operated by Beef Improvement Ontario's Bull Evaluation Program. There were 615 preweaning contemporary groups (herd of origin  $\times$  year) containing up to 25 bulls; 26% of observations were from preweaning contemporary groups containing at least 10 bulls. Because of these small groups, preweaning herd of origin effects would not be well estimated as a fixed effect. Consequently, preweaning herd of origin was fitted as a random effect in the genetic models for bull traits described later. Treating small contemporary groups as a random effect increases the effective number of progeny through the use of interclass information from relatives in other contemporary groups (Van Vleck, 1987). Studies using simulation models with random contemporary groups produced EBV with greater accuracy, lower bias, and lower mean squared error than models with fixed contemporary

groups, except when the best sires were represented in the worst contemporary groups (Visscher and Goddard, 1993) or when unrealistically extreme preferential treatment was applied to progeny of superior sires (Oikawa and Sato, 1997). Treating preweaning herd of origin as a random effect also allowed us to determine the effect of preweaning herd of origin on the phenotypic variance of yearling bull traits, which can be substantial for growth traits and LM area (Schenkel et al., 2004).

There were 35 postweaning contemporary groups (test station  $\times$  year  $\times$  start of test date), all of which contained at least 15 bulls. Postweaning contemporary group was treated as a fixed effect in the genetic models described below. Schenkel et al. (2004) described eligibility requirements, nutritional management, and data collection protocols at the test stations. Bulls had to be  $>181$  kg and  $<291$  d of age to enter a test station. Age range within a test group was restricted to 90 d. Following a 28 d adjustment period, bulls were fed a diet containing (DM basis) 15.0 to 15.8% crude protein, 64.1 to 66.8% TDN, and 9.7 to 10.1 MJ kg<sup>-1</sup> ME for 140 (until 1995) or 112 d (after 1995). End of test weight, total postweaning gain (end to start weight), hip height, and ultrasound measurements were collected near 365 d of age.

Ultrasonic 12–13th rib fat depth, LM area, and method 1 and 2 LM depth and width were measured from ultrasound images archived by Beef Improvement Ontario. Method 1 measured maximum LM depth and width through the center of the LM. Method 2 LM depth was measured from the lateral edge of the acorn fat to the point of maximum depth, and width was measured from the lateral edge of the acorn fat and extended to the extreme edge of the LM, distal to the spine. These measurements are illustrated in Bergen et al. (2003). In some cases, archived images could not be located or recovered, resulting in 1,488 ultrasound fat depth and LM size records. Ultrasound intramuscular fat estimates (Beef Quality Objective Measurement software; Critical Visions Incorporated, Atlanta, GA) were available for 1,308 bulls tested from 1996 onwards. Live estimates of lean percentage were calculated for all bulls using equations shown in Table 1. These equations have been developed and verified in previous studies (Dikeman et al., 1998; Tait et al., 2002; Bergen et al., 2003; Greiner et al. 2003).

Sire and dam breed compositions were used to calculate the breed composition and expected heterozygosity of each bull. Approximately 77% of bulls were fullblood (100% of breed composition contributed by a single breed), 16% were purebred (87.5 to 100% of breed composition contributed by a single breed), and 7% were crossbred ( $<87.5\%$  of breed composition contributed by a single breed). The main breeds represented in the current study were Angus, Charolais, Hereford, Simmental, Limousin, Blonde d'Aquitaine, and Gelbvieh; no other breed accounted for more than 12.5% of the total breed composition of any bull.

**Table 1.** Previously published equations predicting carcass lean meat yield percentage based on live preslaughter measurements

Equation	Intercept	Regression coefficient		Weight, kg
		12–13th rib fat depth, mm	12–13th rib LM size, cm <sup>2</sup>	
Equations incorporating live yearling bull weight and ultrasound measurements				
C-5U <sup>1</sup>	63.11	-0.391	0.19	-0.03
PRPRD1 <sup>2</sup>	69.32	-0.85	0.14	-0.01
USLean <sup>3</sup>	60.69	-1.00	0.12	
Eq. 4 <sup>3</sup>	60.82	-1.01	0.10	
Eq. 5 <sup>3</sup>	60.07	-1.05	0.12	
Eq. 6 <sup>3</sup>	56.09	-1.13	1.09 <sup>4</sup>	
			1.04 <sup>5</sup>	
Equation utilizing steer carcass measurements				
BTLean <sup>6</sup>	57.96	-0.70	0.20	-0.003

<sup>1</sup>Equation developed by Dikeman et al. (1998) and Tait et al. (2002) using ultrasound fat depth, LM area (cm<sup>2</sup>), and predicted HCW (kg) = -19.11 + (0.55\*yearling weight) + (0.29\*ultrasound LM area, cm<sup>2</sup>) + (17.16\*yearling weight, kg per day of age).

<sup>2</sup>Equation reported by Greiner et al. (2003) using ultrasound fat depth, traced LM area (cm<sup>2</sup>), and live weight.

<sup>3</sup>Equations reported by Bergen et al. (2003) using ultrasound fat depth and either traced LM area (cm<sup>2</sup>; USLEAN), method 1 LM depth × width (cm<sup>2</sup>; Eq. 4), method 2 LM depth × width (cm<sup>2</sup>; Eq. 5), or method 1 and 2 LM depths (cm; Eq. 6).

<sup>4</sup>Method 1 LM depth (cm).

<sup>5</sup>Method 2 LM depth (cm).

<sup>6</sup>Equation developed by Agriculture and Agri-Food Canada to predict whole-side lean meat yield based on HCW, fat depth and LM area (Bergen et al., 1996). BTLean = Blue Tag lean percentage.

Animal management protocols were approved by the University of Guelph Animal Care committee following Canadian Council on Animal Care (1993) guidelines or followed standard commercial bull test station management procedures established and supervised by Beef Improvement Ontario. Summary statistics for live yearling bull lean meat yield traits are shown in Table 2. Summary statistics for individual bull traits have been presented in an earlier report (Bergen et al., 2005b).

Steers (n = 1,031) were born between 1996 and 2002 as part of a long-term breeding project conducted by the University of Guelph at the Elora Beef Research Center, New Liskeard Agricultural Research Station and Agriculture and Agri-Food Canada's Kapuskasing Research Station. There were 39 preweaning contemporary groups (farm of birth × year of birth × season of birth) ranging in size from 7 to 53 steers. Over 96% of observations were from preweaning contemporary groups containing at least 10 steers, allowing steer pre-

**Table 2.** Summary statistics for yearling bull ultrasound and finished feedlot steer carcass lean meat yield traits

Trait	No. records	Mean	SD	Minimum	Maximum
Live ultrasound lean meat yield percentage estimates in yearling bulls <sup>1</sup>					
C-5U	1,480	69.06	2.35	61.70	76.50
PRPRD1	1,480	71.72	2.87	59.06	78.61
USLean	1,488	67.00	3.01	53.61	73.36
Eq. 4	1,488	67.27	3.00	52.98	74.32
Eq. 5	1,488	66.82	3.16	52.32	73.99
Eq. 6	1,488	66.90	3.23	51.58	74.15
Carcass lean meat yield percentage estimates in finished feedlot steers					
BTLean <sup>1,2</sup>	1,027	59.92	2.51	49.35	70.21
RulerLean <sup>3</sup>	1,019	59.77	1.83	52.00	65.00
DissLean <sup>4</sup>	1,025	56.06	3.82	32.69	66.22

<sup>1</sup>Equations described in Table 1.

<sup>2</sup>Carcass lean meat yield percentage predicted from HCW, fat depth, and LM area. BTLean = Blue Tag lean percentage.

<sup>3</sup>Carcass lean meat yield percentage predicted from carcass fat depth and LM depth and width using the Canadian beef grading ruler. RulerLean = ruler lean percentage.

<sup>4</sup>Carcass lean meat yield percentage based on dissection of the 10–11–12th rib section. DissLean = dissected lean percentage.

weaning contemporary group to be fit as a fixed effect in subsequent genetic models.

All steers were fed from weaning to slaughter at the University of Guelph's Elora Beef Research Center. Steers were grouped into 62 postweaning contemporary groups (experimental treatment  $\times$  year of slaughter  $\times$  season of slaughter) containing 5 to 58 animals; 89% of observations were from postweaning contemporary groups containing at least 10 steers. Postweaning steer contemporary group was treated as a fixed effect in genetic models described below. Many of the experimental treatments were comparisons of corn varieties or dietary energy levels. Consequently, steers were also classified into 2 feedlot regime groups according to whether they were fed a high grain diet from weaning to slaughter ( $n = 499$ ) or were backgrounded on forage or limit fed grain diets before high grain finishing ( $n = 532$ ).

Steers were slaughtered at a federally inspected abattoir operated by the University of Guelph. Hot carcass weight, grade fat depth, traced LM area, and visual carcass marbling score were recorded for all steers. Three estimates of carcass lean percentage (based on complete separation of fat, lean, and bone) were used. Blue Tag lean percentage (**BTLean**) was predicted from HCW, fat depth, and LM area measurements using an equation developed at Agriculture and Agri-Food Canada's Lacombe Research Center (Bergen et al., 1996). This estimate (described in Table 1) is not routinely collected but can be obtained from Canadian packing plants on a fee-for-service basis. Ruler lean percentage (**RulerLean**) was predicted from carcass fat depth and LM area measurements obtained using the Canadian yield grade ruler (Canadian Beef Grading Agency, 2005). Routine Canadian carcass yield grades are based on this estimate. In this procedure, minimum subcutaneous carcass fat depth is measured over the fourth quarter of the LM, distal to the spine. Fat depth is categorized by 2 mm increments into fat classes 1 ( $\geq 2$  mm but  $< 4$  mm) to 9 ( $\geq 18$  mm but  $< 20$  mm). Maximum LM depth and width are measured perpendicular to each other through the center of the LM. Muscle depth is categorized into class 1 ( $< 63$  mm), 2 (63 to 70 mm), or 3 ( $> 70$  mm). Muscle width is categorized into class 1 ( $< 140$  mm), 2 (140 to 150 mm), or 3 ( $> 150$  mm). Muscle depth and width are then combined into muscle score 1 (depth class 1 and width class 1, depth class 1 and width class 2, or depth class 2 and width class 1), 2 (depth class 1 and width class 3, depth class 2 and width class 2, or depth class 3 and width class 1), 3 (depth class 2 and width class 3 or depth class 3 and width class 2), or 4 (depth class 3 and width class 3). Finally, RulerLean is estimated by combining fat class and muscle score. The RulerLean estimates range from 49% (fat class 10 and muscle score 1) to 65% (fat class 1 and muscle score 4). Dissected lean percentage (**DissLean**) was estimated based on complete separation of a 21 cm rib section (corresponding approximately to the 10–11–12th ribs) into lean, bone, subcutaneous, inter-

muscular, and body cavity fat following procedures originally developed by Hankins and Howe (1946).

All steers were crossbred, with predominantly Angus, Simmental and Charolais breeding. Sire and dam breed compositions were used to calculate the breed composition and expected heterozygosity of each steer. Experimental procedures were approved by the University of Guelph's Animal Care Committee and followed guidelines established by the Canadian Council on Animal Care (1993). Summary statistics for individual steer carcass traits have been presented in an earlier report (Bergen et al., 2005b). Summary statistics for carcass lean percentage estimates and covariate traits are shown in Tables 2 and 3, respectively.

## Analyses

The pedigree file contained 10,068 animals, and animals with records had an average of 4.1 ancestors. The degree of genetic connectedness was estimated by calculating the total number of direct genetic links (due to common sires and dams) between bull and steer postweaning groups (Roso et al., 2004). Subsequent genetic analyses were conducted in ASREML (Gilmour et al., 2000).

Pairwise analyses were performed to estimate (co-)variance components and effects of covariates, contemporary group, feedlot regimen, breed, and expected heterozygosity using the following models:

pairwise analyses between live estimates of yearling bull lean percentage:

$$\begin{bmatrix} y_{\text{Bull}_1} \\ y_{\text{Bull}_2} \end{bmatrix} = \begin{bmatrix} X_{\text{Bull}_1} & 0 \\ 0 & X_{\text{Bull}_2} \end{bmatrix} \begin{bmatrix} b_{\text{Bull}_1} \\ b_{\text{Bull}_2} \end{bmatrix} + \begin{bmatrix} Z_{\text{Bull}_1} & 0 \\ 0 & Z_{\text{Bull}_2} \end{bmatrix} \begin{bmatrix} a_{\text{Bull}_1} \\ a_{\text{Bull}_2} \end{bmatrix} \\ + \begin{bmatrix} W_{\text{Bull}_1} & 0 \\ 0 & W_{\text{Bull}_2} \end{bmatrix} \begin{bmatrix} h_{\text{Bull}_1} \\ h_{\text{Bull}_2} \end{bmatrix} + \begin{bmatrix} e_{\text{Bull}_1} \\ e_{\text{Bull}_2} \end{bmatrix};$$

pairwise analyses between steer carcass traits:

$$\begin{bmatrix} y_{\text{Steer}_1} \\ y_{\text{Steer}_2} \end{bmatrix} = \begin{bmatrix} X_{\text{Steer}_1} & 0 \\ 0 & X_{\text{Steer}_2} \end{bmatrix} \begin{bmatrix} b_{\text{Steer}_1} \\ b_{\text{Steer}_2} \end{bmatrix} \\ + \begin{bmatrix} Z_{\text{Steer}_2} & 0 \\ 0 & Z_{\text{Steer}_2} \end{bmatrix} \begin{bmatrix} a_{\text{Steer}_1} \\ a_{\text{Steer}_2} \end{bmatrix} + \begin{bmatrix} e_{\text{Steer}_1} \\ e_{\text{Steer}_2} \end{bmatrix};$$

pairwise analyses between live bull traits with steer carcass traits:

$$\begin{bmatrix} y_{\text{Bull}} \\ y_{\text{Steer}} \end{bmatrix} = \begin{bmatrix} X_{\text{Bull}} & 0 \\ 0 & X_{\text{Steer}} \end{bmatrix} \begin{bmatrix} b_{\text{Bull}} \\ b_{\text{Steer}} \end{bmatrix} \\ + \begin{bmatrix} Z_{\text{Bull}} & 0 \\ 0 & Z_{\text{Steer}} \end{bmatrix} \begin{bmatrix} a_{\text{Bull}} \\ a_{\text{Steer}} \end{bmatrix} + \begin{bmatrix} W_{\text{Bull}} & 0 \\ 0 & 0 \end{bmatrix} \begin{bmatrix} h_{\text{Bull}} \\ 0 \end{bmatrix} + \begin{bmatrix} e_{\text{Bull}} \\ e_{\text{Steer}} \end{bmatrix};$$

in which  $y_{\text{Bull}}$  and  $y_{\text{Steer}}$  are vectors of measurements for bull and steer traits, respectively,

**Table 3.** Summary statistics for finished feedlot steer slaughter end point covariate traits

Slaughter end point covariates for steer carcass traits	Feedlot regimen			
	High grain finishing from weaning to slaughter		Backgrounded before high grain finishing	
	Mean	SD	Mean	SD
Slaughter age, d	426	62	478	76
HCW, kg	337.0	51.5	361.3	62.2
12–13th rib subcutaneous grade fat depth, mm	8.8	2.1	8.8	2.2
12–13th rib visual marbling score <sup>1</sup>	5.0	0.7	5.1	0.7

<sup>1</sup>≤3.0 = devoid; 3.1 to 4.0 = traces; 4.1 to 5.9 = slight; 6.0 to 7.0 = small to moderate; and ≥7.0 = slightly abundant to abundant.

$X_{\text{Bull}}$  and  $X_{\text{Steer}}$  are known incidence matrices of fixed classification and covariate effects influencing bull and steer traits, respectively;  $b_{\text{Bull}}$  and  $b_{\text{Steer}}$  are vectors of fixed classification and covariate effects influencing bull (postweaning contemporary group and regressions on breed, expected breed heterozygosity, and scan age) and steer (pre- and postweaning contemporary group and feedlot regimen effects, and regressions on breed, expected breed heterozygosity, and the appropriate slaughter end point covariate within feedlot regimen) traits, respectively.  $Z_{\text{Bull}}$  and  $Z_{\text{Steer}}$  are known incidence matrices of animals with observations for bull and steer traits, respectively;  $a_{\text{Bull}}$  and  $a_{\text{Steer}}$  are random vectors of unknown animal additive genetic effects for bull and steer traits, respectively.  $W_{\text{Bull}}$  is a known incidence matrix of preweaning contemporary group effects for bull traits;  $h_{\text{Bull}}$  is a random vector of unknown preweaning contemporary group effects for bull traits; and  $e_{\text{Bull}}$  and  $e_{\text{Steer}}$  are random vectors of unknown residual effects affecting bull and steer traits, respectively.

The expected mean of random effects was assumed to be zero, with (co)variance matrices

$$\text{Var} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} = \begin{bmatrix} A\sigma_{a_1}^2 & A\sigma_{a_{12}} \\ A\sigma_{a_{12}} & A\sigma_{a_2}^2 \end{bmatrix},$$

in which  $A$  is the numerator relationship matrix,  $\sigma_{a_1}^2$  is the additive genetic variance of trait 1,  $\sigma_{a_2}^2$  is the additive genetic variance of trait 2, and  $\sigma_{a_{12}}$  is the additive genetic (co)variance between traits 1 and 2;

$$\text{Var} \begin{bmatrix} h_1 \\ h_2 \end{bmatrix} = \begin{bmatrix} I\sigma_{h_1}^2 & I\sigma_{h_{12}} \\ I\sigma_{h_{12}} & I\sigma_{h_2}^2 \end{bmatrix},$$

in which  $I$  is an identity matrix of order equal to the number of preweaning herd of origin bull contemporary groups,  $\sigma_{h_1}^2$  is the variance attributable to herd of origin for bull trait 1,  $\sigma_{h_2}^2$  is the variance attributable to herd

of origin for bull trait 2, and  $\sigma_{h_{12}}$  is the herd of origin (co)variance between bull traits 1 and 2; and

$$\text{Var} (e) = \begin{bmatrix} I\sigma_{e_1}^2 & I\sigma_{e_{12}} \\ I\sigma_{e_{12}} & I\sigma_{e_2}^2 \end{bmatrix},$$

in which  $I$  is an identity matrix of order equal to the number of observations,  $\sigma_{e_1}^2$  is the residual variance of trait 1,  $\sigma_{e_2}^2$  is the residual variance of trait 2, and  $\sigma_{e_{12}}$  is the residual (co)variance between traits 1 and 2 measured in the same gender of animal. Because live bull and steer carcass data were not available for the same animal, bivariate models involving both bull and steer traits assumed

$$\text{Var} (e) = \begin{bmatrix} I\sigma_{e_1}^2 & 0 \\ 0 & I\sigma_{e_2}^2 \end{bmatrix}.$$

After accounting for the fixed breed effect in the animal model, homogeneous genetic, herd of origin, and residual (co)variance were assumed across all breeds, and all unknown sires and dams were assumed to originate from the same noninbred base population regardless of breed. For summary purposes, heterosis and breed effects as well as phenotypic, additive genetic, and preweaning bull contemporary group variances were calculated as the average solution from the pairwise analyses performed for each trait. Breed effects were expressed relative to the Charolais breed, which was constrained to zero.

Scan age was used as a covariate for yearling bull traits in all animal models. Since Beef Improvement Ontario's Bull Evaluation Program controls both minimum start of test age as well as the allowable age range in a given test group, scan age was regressed across postweaning bull contemporary groups. However, since nutritional management (feedlot regimen) affects slaughter age through its influence on rates of weight, fat, and muscle deposition (Vaage et al., 1998; Block et

**Table 4.** End point covariate, heterosis, and breed solutions for yearling bull ultrasound lean meat yield traits

Trait	Covariate	Covariate solution	Heterosis ±SE, %	Breed <sup>1</sup>					
				Angus	Hereford	Simmental	Limousin	Blonde d' Aquitaine	Gelbvieh
C-5U, <sup>2</sup> %	Scan age, d	-0.008 ± 0.002	-0.2 ± 0.4	-3.12	-3.72	0.33	1.63	2.40	0.18
PRPRD1, <sup>2</sup> %	Scan age, d	-0.012 ± 0.002	-0.2 ± 0.4	-6.20	-6.72	-0.27	1.16	2.63	0.16
USLean, <sup>2</sup> %	Scan age, d	-0.003 ± 0.002	0.0 ± 0.5	-6.77	-5.36	-0.22	0.62	2.23	-0.12
Eq. 4, <sup>2</sup> %	Scan age, d	-0.002 ± 0.002	0.1 ± 0.5	-6.73	-5.36	-0.27	0.55	2.09	-0.13
Eq. 5, <sup>2</sup> %	Scan age, d	-0.005 ± 0.003	-0.2 ± 0.5	-6.86	-5.64	-0.37	0.65	2.13	-0.16
Eq. 6, <sup>2</sup> %	Scan age, d	-0.004 ± 0.003	-0.3 ± 0.5	-6.67	-5.44	-0.32	0.52	2.02	-0.16

<sup>1</sup>SE for breed effects were similar among traits and ranged from 0.18 to 0.36%.

<sup>2</sup>Equations described in Table 1.

al., 2001), adjusting all steers to a common end point across feedlot regimes may be inappropriate. Consequently, steer carcass traits were adjusted to slaughter age, HCW, carcass fat depth, or carcass marbling score constant end points by regressing the appropriate slaughter end point covariate within feedlot regimen (i.e., high grain from weaning to slaughter vs. backgrounding before high grain finishing). Breed effects were estimated by regressing the dependent variable on the percentage of total breed composition contributed by each breed.

## RESULTS AND DISCUSSION

### Genetic Connectedness

Direct genetic ties (i.e., through common sires or dams) connected all bull and steer postweaning contemporary groups; no postweaning contemporary group was genetically isolated. Each bull postweaning contemporary group had an average of 356 (ranging from 44 to 888) direct genetic ties to bulls or steers in other contemporary groups. Each steer postweaning contemporary group had more than 300 direct genetic ties to bulls or steers in other contemporary groups. The steers were the progeny of 76 sires, 47 of which had their own ultrasound records or at least 3 intact male progeny with ultrasound records.

### Summary Statistics

The C-5U and PRPRD1 equations predict carcass lean percentage with lean trim mathematically adjusted to contain 20% fat (Dikeman et al., 1998; Greiner et al., 2003), but this adjustment was not used for the other equations (Bergen et al., 2003). Consequently, means for live animal lean percentage equations C-5U and PRPRD1 were numerically greater than for equations USLean, Eq. 4, Eq. 5, and Eq. 6 (Table 2).

Feedlot regimen influenced steer carcass characteristics (Table 3). Steers fed a high grain finishing diet from weaning to slaughter were 52 d younger and 24 kg lighter than steers backgrounded before finishing. Levels of backfat and marbling were similar between the 2 feedlot regimes. Although attempts were made to

slaughter cattle at a backfat constant end point, CV were no lower for carcass fat depth (23.86% and 25.00% for high grain and backgrounded steers, respectively) than for slaughter age (14.55% and 15.90%, respectively), HCW (15.28 and 17.22%, respectively), or marbling score (14.00 and 13.72%, respectively). This suggests that all traits varied sufficiently to justify the end point adjustments.

### Covariate Solutions, Heterosis and Breed Solutions for Lean Meat Yield: Bull Traits

As mentioned previously, all yearling bull traits were adjusted to an ultrasound scan-age-constant end point. Scan age covariate solutions were negative for all live lean percentage estimates, indicating that lean percentage of the carcass declines with increasing age (Table 4). Heterosis estimates (expressed as a percent of the phenotypic mean) for live yearling bull lean percentage estimates were low (Table 4). Heterosis estimates for individual scan-age-constant yearling bull growth and ultrasound traits exhibited a wider range in an earlier study (0.19 to 5.62%) but only approached significance ( $P < 0.10$ ) for yearling weight and postweaning gain (Bergen et al., 2005b). Breed solutions for live yearling bull ultrasound lean percentage estimates showed expected patterns. Limousin and Blonde d' Aquitaine had the highest live ultrasound lean percentage; Simmental, Gelbvieh, and Charolais were intermediate; and Angus and Hereford had the lowest live ultrasound lean percentages (Table 4).

### Covariate Solutions, Heterosis and Breed Solutions for Lean Meat Yield Adjusted to Alternative End Points: Steer Traits

In contrast to yearling bull traits, steer carcass traits were adjusted to slaughter age, HCW, fat depth, and marbling score constant end points within feedlot regimen. Differences between feedlot regimes were observed for steer carcass traits (Table 5). For every kilogram increase in HCW, steers fed a high grain diet from weaning to slaughter deposited subcutaneous fat and marbling more rapidly ( $P < 0.10$ ) as steers backgrounded before high grain finishing. Carcass lean per-

Table 5. End point covariate, heterosis, and breed solutions for finished feedlot steer carcass traits

Trait	Covariate	Covariate solution within feedlot regimen <sup>2</sup>			Heterosis $\pm$ SE, %	Breed <sup>1</sup>					
		HG	BG			Angus	Hereford	Simmental	Limousin	Aquitaine	Blonde d'
HCW, kg	Slaughter age, d	0.69 $\pm$ 0.05 <sup>y</sup>	0.79 $\pm$ 0.04 <sup>z</sup>	4.6 $\pm$ 2.1 <sup>†</sup>	-57.74	-73.6	-35.94	-28.04	-6.87	-62.20	
	Carcass fat depth, mm	5.04 $\pm$ 0.87	5.88 $\pm$ 0.84	2.0 $\pm$ 2.4	-102.83	-117.33	-54.28	-46.30	-2.52	-95.53	
	Marbling score, units <sup>3</sup>	9.61 $\pm$ 2.30	10.47 $\pm$ 2.66	0.7 $\pm$ 2.5	-109.31	-111.80	-57.77	-45.08	-8.44	-98.98	
12 to 13th rib grade fat depth, mm	Slaughter age, d	0.012 $\pm$ 0.003	0.017 $\pm$ 0.003	-0.9 $\pm$ 4.9	1.21	1.68	0.11	0.66	-0.21	0.27	
	HCW, kg	0.017 $\pm$ 0.002 <sup>z</sup>	0.013 $\pm$ 0.002 <sup>y</sup>	-4.1 $\pm$ 4.8	1.86	2.48	0.59	0.94	-0.09	0.84	
	Marbling score, units	0.100 $\pm$ 0.119 <sup>y</sup>	0.656 $\pm$ 0.139 <sup>z</sup>	4.2 $\pm$ 4.9	0.16	1.00	-0.34	0.33	-0.35	-0.65	
12 to 13th rib LM area, cm <sup>2</sup>	Slaughter age, d	0.10 $\pm$ 0.01	0.12 $\pm$ 0.01	4.4 $\pm$ 2.4	-13.54	-20.17	-4.46	8.06	10.48	-7.32	
	HCW, kg	0.15 $\pm$ 0.01	0.16 $\pm$ 0.01	1.1 $\pm$ 2.1	-3.98	-8.91	1.76	12.77	10.67	2.79	
	Carcass fat depth, mm	0.11 $\pm$ 0.24	0.25 $\pm$ 0.23	2.5 $\pm$ 2.6	-19.95	-26.30	-7.15	5.40	10.86	-12.87	
12 to 13th rib marbling score <sup>3</sup>	Marbling score, units	1.40 $\pm$ 0.61	1.08 $\pm$ 0.71	1.9 $\pm$ 2.6	-21.11	-26.25	-7.61	5.33	10.19	-12.91	
	Slaughter age, d	0.0061 $\pm$ 0.0009	0.0039 $\pm$ 0.0008	4.0 $\pm$ 2.7	0.66	-0.09	0.12	-0.15	0.22	-0.09	
	HCW, kg	0.0005 $\pm$ 0.0001 <sup>z</sup>	0.0002 $\pm$ 0.0001 <sup>y</sup>	2.8 $\pm$ 2.7	0.74	0.05	0.20	-0.12	0.33	0.01	
BTLean, <sup>4</sup> %	Carcass fat depth, mm	0.0054 $\pm$ 0.0015	0.0059 $\pm$ 0.0014	3.1 $\pm$ 2.7	0.36	-0.40	0.01	-0.27	0.24	-0.32	
	Slaughter age, d	-0.007 $\pm$ 0.003	-0.009 $\pm$ 0.003	0.5 $\pm$ 0.9	-2.11	-3.52	-0.05	1.87	2.21	-0.07	
	HCW, kg	-0.008 $\pm$ 0.003	-0.004 $\pm$ 0.002	0.7 $\pm$ 0.9	-2.19	-3.69	-0.12	1.89	2.07	-0.13	
RulerLean, <sup>5</sup> %	Carcass fat depth, mm	-0.816 $\pm$ 0.038	-0.810 $\pm$ 0.037	0.4 $\pm$ 0.6	-1.24	-2.19	0.05	2.36	2.22	-0.02	
	Marbling score, units	-0.062 $\pm$ 0.137 <sup>z</sup>	-0.510 $\pm$ 0.160 <sup>y</sup>	0.8 $\pm$ 0.9	-1.47	-3.14	0.22	2.04	2.35	0.44	
	Slaughter age, d	0.000 $\pm$ 0.003 <sup>z</sup>	-0.005 $\pm$ 0.003 <sup>y</sup>	0.3 $\pm$ 0.6	-1.98	-2.69	-0.90	-0.29	0.14	-1.61	
DissLean, <sup>6</sup> %	HCW, kg	0.001 $\pm$ 0.002	0.001 $\pm$ 0.002	0.4 $\pm$ 0.6	-1.82	-2.60	-0.80	-0.17	0.13	-1.46	
	Carcass fat depth, mm	-0.705 $\pm$ 0.029	-0.675 $\pm$ 0.027	-0.1 $\pm$ 0.0	-1.55	-1.97	-0.95	0.12	0.16	-1.85	
	Marbling score, units	-0.109 $\pm$ 0.136 <sup>z</sup>	-0.303 $\pm$ 0.126 <sup>y</sup>	0.5 $\pm$ 0.6	-1.83	-2.80	-0.85	-0.26	0.22	-1.52	
	Slaughter age, d	-0.015 $\pm$ 0.005	-0.020 $\pm$ 0.005	-0.7 $\pm$ 1.4	-4.61	-8.04	-1.02	1.94	1.98	-1.07	
	HCW, kg	-0.012 $\pm$ 0.004	-0.004 $\pm$ 0.004	-0.1 $\pm$ 1.4	-4.40	-7.99	-1.00	2.12	1.65	-0.92	
	Carcass fat depth, mm	-0.68 $\pm$ 0.08	-0.52 $\pm$ 0.07	-0.5 $\pm$ 1.3	-3.41	-6.57	-0.63	2.63	1.74	-0.41	
	Marbling score, units	-0.89 $\pm$ 0.23	-1.24 $\pm$ 0.24	0.5 $\pm$ 1.4	-2.63	-7.17	-0.15	2.40	2.49	-0.10	

<sup>z,y</sup>Values in the same row with different superscripts differ,  $P \leq 0.10$ .

<sup>1</sup>SE values for breed effects were similar across end points, and ranged from 11.10 to 29.21 kg (HCW), 0.59 to 1.32 mm (grade fat depth), 2.69 to 7.24 cm<sup>2</sup> (LM area), 0.20 to 0.45 units (marbling score), 0.52 to 1.72% (BTLean), 0.32 to 1.17% (RulerLean), and 1.02 to 2.50% (DissLean).

<sup>2</sup>HG: steers fed a high grain diet from weaning to slaughter; BG: steers backgrounded before high grain finishing.

<sup>3</sup> $\leq 3.0$  = devoid; 3.1 to 4.0 = slight; 4.1 to 5.9 = moderate; and  $\geq 7.0$  = slightly abundant to abundant.

<sup>4</sup>Carcass lean meat yield percentage predicted from HCW, fat depth, and LM area. Equation described in Table 1. BTLean = Blue Tag lean percentage.

<sup>5</sup>Carcass lean meat yield percentage predicted from carcass fat depth and width using the Canadian beef grading ruler. Equation described in text. RulerLean = ruler lean percentage.

<sup>6</sup>Carcass lean meat yield percentage based on dissection of the 10–11–12th rib section. DissLean = dissected lean percentage.

<sup>†</sup>Heterosis value differed from zero,  $P \leq 0.10$ .

centage traits showed the opposite trend (Table 5). For every unit increase in marbling score, high grain steers deposited less ( $P < 0.10$ ) subcutaneous fat than backgrounded steers (Table 5); both BTLean and RulerLean declined more slowly ( $P < 0.10$ ) in high grain steers than in backgrounded steers (Table 5). Although backgrounding appeared to delay the onset of fattening, increase HCW, and increase lean percentage, it did not improve marbling score. Other researchers have shown similar results (Vaage et al., 1998; Block et al., 2001). With the exception of the fat constant end point, differences between feedlot regimes ( $P < 0.10$ ) were observed for at least one trait in the current study. Feedlot regimes should be considered when adjusting carcass traits to a common slaughter end point in genetic evaluations when data from backgrounded and nonbackgrounded cattle are being used.

Heterosis estimates only approached significance ( $P < 0.10$ ) for slaughter age-constant steer HCW (Table 5). Marshall (1994) reported a similar range of heterosis estimates for age-constant carcass traits. Johnston et al. (1992) reported weight constant heterosis estimates of 7.4% and -0.7% for HCW and LM area, respectively. As expected, British (Angus and Hereford) steers had lighter, fatter carcasses with smaller LM area than Continental (Charolais, Simmental, Gelbvieh, Limousin, and Blonde d'Aquitaine) steers (Table 5). Marbling levels were highest for Angus, with similar levels among the remaining breeds (Table 5); similar results have been observed elsewhere (Koch et al., 1976; Koch et al., 1978; Wheeler et al., 2005). British breeds also had lower BTLean, RulerLean, and DissLean than Continental breeds at all end points (Table 5). However, Angus and Hereford breed solutions were considerably greater for BTLean than for DissLean (Table 5). This indicates that BTLean overestimates DissLean for these breeds relative to Charolais. Angus and Hereford also had greater breed solutions for RulerLean than for DissLean (Table 5). However, RulerLean solutions for Limousin and Blonde d'Aquitaine were considerably lower than corresponding DissLean solutions. This likely reflects the fact that RulerLean does not exceed 65% and thus underestimates actual carcass lean percentage in late maturing or heavily muscled cattle. At least one pair of Continental breeds changed ranks for RulerLean, BTLean, and DissLean when moving among slaughter age, HCW, carcass fat depth, and marbling score constant end points. Similarly, Wheeler et al. (2005) also observed that Angus, Hereford, Simmental, Charolais, Gelbvieh, and Limousin breeds ranked differently for yield grade than for dissected retail product percentage and that breeds ranked differently for both traits when moving among slaughter age, HCW, fat depth, and marbling score constant end points. The carcass lean meat percentage trait and slaughter end points chosen will clearly impact breed solutions and consequently influence across-breed EPD.

### *Preweaning Herd of Origin Effects and Heritabilities*

Herd of origin effects remaining at the end of the postweaning bull test period accounted for 4 to 7% of the phenotypic variance in lean percentage estimated from live ultrasound measurements (Table 6). Similar results were shown in Schenkel et al. (2004) and Bergen et al. (2005b) for individual seedstock ultrasound indicator traits. Preweaning herd of origin should be considered in genetic evaluation of yearling bull traits measured in centralized bull test stations. Heritabilities for scan-age-constant yearling bull lean percentage estimates (Table 6) ranged from 0.26 (Eq. 4) to 0.42 (C-5U), and were representative of the heritabilities of their respective component traits (Bergen et al., 2005b). Heritabilities of lean percentage estimates involving weight and growth traits (C-5U and PRPRD1) were greater than the remaining estimates, which were based only on ultrasound fat depth and LM size. Genetic correlations calculated among the various live animal lean percentage estimates were high (not shown). With the exception of equation C-5U, genetic correlations ranged from 0.90 (Eq. 5 vs. PRPRD1) to 0.99 (Eq. 4 vs. USLean). In contrast, genetic correlations involving equation C-5U ranged from 0.68 (Eq. 4) to 0.90 (PRPRD1). Results of a previous study also indicated that equation C-5U had weaker correlations with the remaining estimates (Bergen et al., 2005a). The same potential sires will likely be selected regardless of which ultrasound lean percentage equation is used, with the possible exception of equation C-5U.

Steer carcass traits had moderate heritability estimates at all end points (Table 6). Hot carcass weight had the highest heritability; marbling score, LM area, BTLean, and DissLean had intermediate heritabilities; and carcass fat depth and RulerLean had the lowest heritabilities regardless of the slaughter end point chosen. These results are in agreement with Shanks et al. (2001), Devitt and Wilton (2001), and Minick et al. (2004). Carcass lean percentage traits tended to have slightly greater heritabilities at slaughter age than at HCW and marbling score constant end points, and heritabilities for all carcass lean percentage traits were numerically lowest at a fat depth constant end point (Table 6).

### *Genetic Correlations Between Yearling Bull and Steer Carcass Indicator Traits with Dissected Steer Carcass Lean Percentage at Alternative Slaughter End Points*

The value of a given live yearling bull or steer carcass indicator trait depends on its heritability as well as the strength of its genetic correlation with the economically relevant trait (steer carcass lean percentage). Genetic correlations between indicator traits with DissLean are shown in Table 7. The correlations between yearling bull growth and ultrasound traits with steer carcass

**Table 6.** Phenotypic variance, contemporary group by phenotypic variance ratio, and heritability ( $\pm$ SE) estimates for carcass lean meat yield estimates in live yearling bulls (ultrasound scan-age-constant), and carcass traits of finished feedlot steers evaluated at different slaughter end points

Trait	End point	Phenotypic variance	Contemporary group by phenotypic variance ratio	Heritability
Live ultrasound lean meat yield percentage estimates in yearling bulls				
C-5U, <sup>1</sup> %	Scan age, d	2.32 $\pm$ 0.09	0.05 $\pm$ 0.03	0.42 $\pm$ 0.09
PRPRD1, <sup>1</sup> %	Scan age, d	3.28 $\pm$ 0.13	0.06 $\pm$ 0.03	0.36 $\pm$ 0.09
USLean, <sup>1</sup> %	Scan age, d	3.77 $\pm$ 0.15	0.05 $\pm$ 0.03	0.34 $\pm$ 0.09
Eq. 4, <sup>1</sup> %	Scan age, d	3.74 $\pm$ 0.14	0.04 $\pm$ 0.03	0.26 $\pm$ 0.08
Eq. 5, <sup>1</sup> %	Scan age, d	4.44 $\pm$ 0.17	0.06 $\pm$ 0.03	0.28 $\pm$ 0.08
Eq. 6, <sup>1</sup> %	Scan age, d	4.45 $\pm$ 0.17	0.07 $\pm$ 0.03	0.30 $\pm$ 0.08
Steer carcass traits				
HCW, kg	Slaughter age, d	1,014.3 $\pm$ 56.7		0.58 $\pm$ 0.10
	Fat depth, mm	1,380.9 $\pm$ 73.6		0.46 $\pm$ 0.10
	Marbling score, <sup>2</sup> units	1,472.7 $\pm$ 79.4		0.51 $\pm$ 0.10
12–13th rib grade fat depth, mm	Slaughter age, d	3.6 $\pm$ 0.2		0.24 $\pm$ 0.08
	HCW, kg	3.5 $\pm$ 0.2		0.22 $\pm$ 0.08
	Marbling score, units	3.7 $\pm$ 0.2		0.19 $\pm$ 0.08
12–13th rib LM area, cm <sup>2</sup>	Slaughter age, d	88.5 $\pm$ 4.6		0.35 $\pm$ 0.09
	HCW, kg	63.9 $\pm$ 3.3		0.41 $\pm$ 0.09
	Fat depth, mm	99.5 $\pm$ 5.1		0.34 $\pm$ 0.09
	Marbling score, units	99.3 $\pm$ 5.1		0.36 $\pm$ 0.09
12–13th rib marbling score <sup>2</sup>	Slaughter age, d	0.34 $\pm$ 0.02		0.43 $\pm$ 0.09
	HCW, kg	0.35 $\pm$ 0.02		0.46 $\pm$ 0.10
	Fat depth, mm	0.35 $\pm$ 0.02		0.37 $\pm$ 0.09
BTLean, <sup>1,3</sup> %	Slaughter age, d	5.19 $\pm$ 0.28		0.44 $\pm$ 0.10
	HCW, kg	5.19 $\pm$ 0.27		0.42 $\pm$ 0.10
	Fat depth, mm	2.56 $\pm$ 0.13		0.36 $\pm$ 0.09
	Marbling score, units	5.17 $\pm$ 0.27		0.41 $\pm$ 0.10
RulerLean, <sup>4</sup> %	Slaughter age, d	2.99 $\pm$ 0.14		0.14 $\pm$ 0.07
	HCW, kg	3.00 $\pm$ 0.14		0.14 $\pm$ 0.07
	Fat depth, mm	1.27 $\pm$ 0.06		0.05 $\pm$ 0.06
	Marbling score, units	3.10 $\pm$ 0.14		0.13 $\pm$ 0.07
DissLean, <sup>5</sup> %	Slaughter age, d	11.29 $\pm$ 0.59		0.39 $\pm$ 0.10
	HCW, kg	11.34 $\pm$ 0.58		0.34 $\pm$ 0.09
	Fat depth, mm	9.97 $\pm$ 0.50		0.30 $\pm$ 0.09
	Marbling score, units	11.04 $\pm$ 0.57		0.37 $\pm$ 0.10

<sup>1</sup>Equations described in Table 1.

<sup>2</sup> $\leq 3.0$  = devoid; 3.1 to 4.0 = traces; 4.1 to 5.9 = slight; 6.0 to 7.0 = small to moderate; and  $\geq 7.0$  = slightly abundant to abundant.

<sup>3</sup>Carcass lean meat yield predicted from HCW, fat depth, and LM area. BTLean = Blue Tag lean percentage.

<sup>4</sup>Carcass lean meat yield predicted from carcass fat depth and LM depth and width using the Canadian beef grading ruler. Equation described in text. RulerLean = ruler lean percentage.

<sup>5</sup>Carcass lean meat yield based on dissection of the 10–11–12th rib section. DissLean = dissected lean percentage.

lean percentage were generally no larger than their SE (Table 7). This might suggest that the population genetic correlations do not differ from zero. Alternatively, this might reflect the relatively low number of tested bulls with progeny carcass data. The following discussion assumes that the magnitudes of the genetic correlations are appropriate, and that the SE would decline if additional data were available. Age-constant DissLean had moderate genetic correlations with yearling bull postweaning gain ( $r_g = 0.31$ ), ultrasound fat depth ( $r_g = -0.34$ ), and LM area ( $r_g = 0.21$ ) in the current study. Crews and Kemp (2001) also reported moderate genetic correlations between DissLean and yearling weight ( $r_g = 0.10$ ), ultrasound fat depth ( $r_g = -0.14$ ), and LM area ( $r_g = 0.60$ ). Compared with the current study, Reverter et al. (2000) reported greater genetic correlations between HCW constant retail product per-

centage in steers with age-constant bull ultrasound fat depth ( $-0.74$  to  $-0.81$ ) and similar correlations with ultrasound LM area (0.19 to 0.49).

Genetic correlations between indicator traits with carcass lean percentage evaluated at different slaughter end points have not been reported previously. Changing the slaughter end point changed the magnitude but usually not the direction of the genetic correlation between any given indicator trait with DissLean (Table 7). Scan-age-constant postweaning gain in yearling bulls was associated with DissLean ( $r_g = 0.26$  to 0.36) at all end points (Table 7). In contrast, scan-age-constant yearling bull ultrasound fat depth had greater associations with DissLean at slaughter age and HCW ( $r_g = -0.34$  and  $-0.25$ , respectively) than at fat depth or marbling score constant end points ( $r_g -0.02$  and  $-0.03$ , respectively; Table 7).

**Table 7.** Genetic correlations among live ultrasound estimates of lean meat yield evaluated in yearling beef bulls on a scan-age-constant basis and steer carcass traits with dissected 10–11–12th rib steer lean meat yield percentage (DissLean) evaluated at different slaughter end points

Trait	Correlation with DissLean adjusted to different slaughter end points <sup>1</sup>			
	Slaughter age	HCW	Carcass fat depth	Marbling score
Live yearling bull traits				
Weight, kg	0.30	0.38	0.42	0.18
Postweaning gain, kg	0.31	0.36	0.33	0.26
Hip height, cm	0.06	0.16	0.16	-0.03
12–13th rib subcutaneous fat depth, mm	-0.34	-0.25	-0.02	-0.03
12–13th rib intramuscular fat content, %	0.14	0.20	0.38	0.44
12–13th rib LM area, cm <sup>2</sup>	0.21	0.23	0.23	0.11
12–13th rib LM method 1 depth, mm	0.12	0.10	0.03	0.01
12–13th rib LM method 1 width, mm	0.38	0.47	0.56	0.08
12–13th rib LM method 2 depth, mm	-0.17	-0.22	-0.38	-0.18
12–13th rib LM method 2 width, mm	NC <sup>2</sup>	NC	NC	0.91
C-5U, <sup>3</sup> %	0.24	0.16	0.10	0.05
PRPRD1, <sup>3</sup> %	0.34	0.25	0.07	0.06
USLean, <sup>3</sup> %	0.39	0.33	0.13	0.08
Eq. 4, <sup>3</sup> %	0.41	0.33	0.10	0.02
Eq. 5, <sup>3</sup> %	0.48	0.40	0.11	0.11
Eq. 6, <sup>3</sup> %	0.25	0.16	-0.08	-0.03
Steer carcass traits <sup>4</sup>				
HCW, kg	-0.02		0.26	0.04
12–13th rib carcass grade fat depth, mm	<b>-0.64</b>	<b>-0.60</b>		<b>-0.60</b>
12–13th rib carcass LM area, cm <sup>2</sup>	<b>0.53</b>	<b>0.59</b>	<b>0.59</b>	<b>0.48</b>
12–13th rib visual carcass marbling score, units	-0.21	-0.14	-0.06	
BTLean <sup>3,5</sup>	<b>0.72</b>	<b>0.71</b>	<b>0.56</b>	<b>0.69</b>
RulerLean <sup>6</sup>	<b>0.70</b>	<b>0.66</b>	0.61	<b>0.67</b>

<sup>1</sup>SE values were similar across end points and ranged from 0.25 to 0.28 (yearling weight, postweaning gain and hip height), 0.32 to 0.39 (ultrasound fat depth and intramuscular fat percentage), 0.33 to 0.48 (ultrasound LM size traits), 0.32 to 0.41 (ultrasound lean meat yield estimates), 0.14 to 0.20 (carcass weight, fat depth, LM area and marbling score), 0.11 to 0.16 (BTLean), and 0.17 to 0.36 (RulerLean). Significant ( $P \leq 0.05$ ) correlations ( $t$ -test) are shown in bold.

<sup>2</sup>NC: bivariate model did not converge.

<sup>3</sup>Equations described in Table 1.

<sup>4</sup>In each column, carcass traits and DissLean are adjusted to the same end point.

<sup>5</sup>Carcass lean meat yield percentage predicted from HCW, fat depth and LM area. BTLean = Blue Tag lean percentage.

<sup>6</sup>Carcass lean meat yield percentage predicted from carcass fat depth and LM depth and width using the Canadian beef grading ruler. Equation described in text. RulerLean = ruler lean percentage.

Bergen et al. (2005a) suggested that yearling bull hip height and ultrasound intramuscular fat percentage might also be valuable predictors of carcass lean percentage. In the current study, yearling bull hip height had weak to moderate genetic associations with DissLean ( $r_g = -0.03$  to 0.16). Yearling bull ultrasound intramuscular fat percentage was positively correlated with DissLean at all end points ( $r_g = 0.14$  to 0.44). An earlier study found that ultrasound marbling score collected using a different technology had a strong, negative association with dissected whole side lean percentage in yearling bulls (Bergen et al., 2005a). Age-constant bull ultrasound intramuscular fat percentage also had a positive genetic correlation ( $r_g = 0.49$ ) with slaughter age-constant steer carcass fat depth in this data set (Bergen et al., 2005b). Consequently, the positive genetic correlation between yearling bull ultrasound intramuscular fat percentage and

steer DissLean observed in the current study was unexpected. Reverter et al. (2000) reported that age-constant (500 d) Hereford bull ultrasound intramuscular fat percentage was positively correlated ( $r_g = 0.40$ ) with weight-constant retail beef yield of commercial cattle even though carcass intramuscular fat percentage and retail beef yield were negatively correlated ( $r_g = -0.57$ ). In the same study, Reverter et al. (2000) found that both age-constant (465 d) Angus bull ultrasound and weight-constant steer carcass intramuscular fat percentage were negatively correlated with weight-constant carcass retail beef yield ( $r_g = -0.31$  and  $-0.37$ , respectively). The unexpected results obtained in the current study, and the conflicting results obtained by Reverter et al. (2000) in Angus and Hereford cattle suggest that the relationship between bull ultrasound intramuscular fat percentage with steer carcass lean percentage merits further study.

Scan-age-constant yearling bull ultrasound LM area was moderately correlated with DissLean ( $r_g = 0.11$  to  $0.23$ ) at all slaughter end points (Table 7). Similar results were observed for method 1 LM size measurements. Method 2 LM depth was negatively associated with DissLean at all end points ( $r_g = -0.17$  to  $-0.40$ ). This result was not unexpected, given that this trait was also negatively correlated with carcass LM area in a previous study (Bergen et al., 2005b). Bivariate animal models involving method 2 width with DissLean failed to converge at 3 out of 4 end points (Table 7). Similar convergence issues in a previous study (Bergen et al., 2005b) were attributed to the low heritability of method 2 LM width. However, LM method 2 width had a stronger association with marbling score constant DissLean than did LM area ( $r_g = -0.91$  and  $0.11$ , respectively; Table 7). Yearling bull LM shape and area warrant further study as indicator traits for steer DissLean.

Genetic relationships between age-constant lean percentage phenotypes calculated for live yearling bulls with steer carcass lean percentage have not been previously reported. Equation 5 had the strongest genetic correlation with DissLean at slaughter age and HCW constant end points ( $r_g = 0.48$  and  $0.40$ , respectively), Eq. 4, USLean, and PRPRD1 were intermediate, and C-5U and Eq. 4 had the lowest genetic correlations with DissLean ( $r_g = 0.16$  to  $0.24$ ). As noted previously, scan-age-constant yearling bull ultrasound fat depth had a low genetic correlation with DissLean at carcass fat depth and marbling score constant end points. Because ultrasound fat depth is the primary determinant of lean percentage phenotype, low genetic correlations among lean percentage estimates obtained on yearling bulls with dissected 10–11–12th rib lean percentage of finished steers at carcass fat depth and marbling score constant end points were not surprising (Table 7). The low genetic correlations between live yearling bull ultrasound lean percentage (particularly Eq. 6) with steer carcass DissLean carcass fat depth or marbling score end points indicate that multiple trait selection for steer carcass lean percentage using across breed EPD for individual live yearling bull ultrasound traits may be more effective than selection based on EPD for live yearling bull ultrasound lean percentage.

As expected, carcass fat depth ( $r_g = -0.60$  to  $-0.64$ ) and LM area ( $r_g = 0.48$  to  $0.59$ ) were strong predictors of DissLean at all end points. Weaker genetic correlations with DissLean were observed for HCW ( $r_g = -0.02$  to  $0.26$ ) and marbling score ( $r_g = -0.06$  to  $-0.21$ ). DissLean had stronger associations with RulerLean and BTLean ( $r_g = 0.66$  to  $0.70$  and  $0.69$  to  $0.72$ , respectively) at slaughter age, HCW, and marbling score constant end points than at a fat constant end point ( $r_g = 0.61$  and  $0.56$ , respectively). Again, this is not surprising given the large role that carcass fat depth plays in determining RulerLean and BTLean.

RulerLean estimates are currently used for carcass price settlement in Canada. However, ongoing advances in individual animal identification and compu-

terized carcass grading may facilitate routine estimation of carcass BTLean (Cannell et al., 2002). Genetic correlations between RulerLean and BTLean were calculated to be  $0.88 \pm 0.07$  (slaughter age-constant),  $0.90 \pm 0.07$  (HCW constant),  $0.59 \pm 0.02$  (fat depth constant), and  $0.87 \pm 0.08$  (marbling score constant), suggesting that these traits are not genetically identical. It is important to be aware that selection for carcass yield grade or estimated retail product percentage is not the same as selecting for dissected carcass lean percentage; neither BTLean ( $r_g = 0.56$  to  $0.72$ ) nor RulerLean ( $r_g = 0.61$  to  $0.70$ ) are perfectly correlated with DissLean (Table 7). Since DissLean is unlikely to be evaluated on individual carcasses in a commercial packing plants in the foreseeable future, genetic evaluations aimed at improving carcass composition will therefore need to combine seedstock ultrasound measurements with commercial carcass RulerLean or BTLean estimates as separate but correlated indicator traits for DissLean.

## IMPLICATIONS

Carcass lean percentage should respond to selection. Opportunities exist to switch from reporting genetic evaluations for individual age-constant ultrasound or carcass indicator traits to reporting genetic evaluations for the economically relevant trait (dissected steer lean percentage) at a more economically relevant end point (carcass weight, fat depth, or marbling score). Discussions between seedstock organizations, feedlot operators, packing plants, and retailers are needed to determine the most commercially desirable end point. Moderate to strong genetic correlations and variation in the sign of these correlations indicate that ultrasound muscle depth and width measurements from yearling bulls may provide valuable information regarding dissected steer lean percentage in addition to that provided by yearling bull ultrasound muscle area. Multiple trait analyses combining seedstock ultrasound with carcass data will produce the fastest genetic improvement in carcass lean percentage.

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