A genetic evaluation of growth, ultrasound, and carcass traits at alternative slaughter endpoints in crossbred heavy lambs[1]

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ABSTRACT: Genetic parameters were estimated for growth, ultrasound, and carcass traits in a Canadian crossbred heavy lamb population. Traits analyzed included birth, weaning, post-weaning, and ultrasound scanning weights; pre- and post-weaning average daily gain; ultrasonically measured eye muscle and fat depths; hot carcass weight; fat depth at the GR site (110 mm from the midline on the 12th rib); carcass conformation scores; saleable meat yield; price grid value; and total carcass value. The impact of three alternative slaughter endpoints (slaughter age, carcass weight, and carcass fatness) on genetic parameter estimates was also evaluated. In general, carcass traits were found to be moderately heritable, with heritability estimates ranging from 0.17 ± 0.02 for hot carcass weight at a constant slaughter age to 0.34 ± 0.02 for average carcass conformation score at a constant carcass weight. Heritability estimates were similar when observations were adjusted to alternative slaughter endpoints, but for some traits, phenotypic variance and genetic correlation estimates differed. Genetic correlations between carcass traits and growth and ultrasound traits were typically favorable. Ultrasonically measured eye muscle depth and fat depth were found to be moderately to strongly positively correlated with hot carcass weight (0.33 ± 0.15 to 0.71 ± 0.19) and fat depth at the GR site (0.38 ± 0.14 to 0.74 ± 0.12), respectively, reaffirming the usefulness of selection on ultrasound traits to improve carcass yield and quality. Genetic correlations among carcass traits were generally favorable, with the exception of moderate unfavorable positive genetic correlations between fat depth at the GR site and primal cut carcass conformation scores (0.31 ± 0.05 to 0.60 ± 0.05). Overall, the results of this research suggest that there is potential to improve carcass yield and quality through genetic selection and provides the population-specific genetic parameter estimates needed for the genetic evaluation of carcass traits in the Canadian sheep population. Nevertheless, the optimal endpoint for carcass trait genetic evaluations will need to be further investigated, considering both the current findings and additional information on production practices in the industry.

Key words: carcass, genetic parameters, growth, lamb, sheep, ultrasound

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INTRODUCTION

The Canadian sheep industry faces many challenges in providing a consistent supply of high-quality lamb. Improved production efficiency and lamb quality are critical to meet the domestic demand for Canadian lamb products (Gooch et al., 2006). The Canadian Sheep Genetic Evaluation System (**CSGES**) provides genetic evaluations for reproduction, growth, and ultrasound traits. Animals are also ranked for six selection indexes designed to meet various Terminal and Maternal economic breeding objectives, as proposed by Quinton et al. (2014). However, genetic evaluations for carcass traits, which have a major impact on the profitability of meat lamb production, are currently unavailable. Lambs marketed at the ideal weight, age, and fatness level are of increased value to processors and yield greater producer profit under a price grid classification system. Carcass traits, such as carcass weight, fat depth, and conformation, have been considered economically important traits for many years in the CSGES (Tosh and Wilton, 2002; Quinton et al., 2014), but infrequent phenotyping has prevented their genetic evaluation.

Since 2007, all heavy lambs in the province of Quebec (lambs under 1 yr of age with a carcass weight of at least 16.4 kg) have been marketed through the Heavy Lamb Sales Agency (**HLSA**). Producer payment through the HLSA utilizes a price grid classification system, thus rewarding producers that meet target weight, muscularity, and fatness levels and providing the phenotypes needed for the genetic evaluation of these traits (Les Éleveurs d'ovins du Québec, 2017). Although genetic parameters have not been previously estimated for these traits in a Canadian sheep population, published genetic parameter estimates suggest that carcass traits are moderately heritable (Safari et al., 2005) and carcass trait genetic evaluations have been successfully implemented in other national sheep breeding programs (Beef + Lamb New Zealand Genetics, 2017; Swan et al., 2017). Nonetheless, population-specific genetic parameter estimates are needed for the implementation of carcass trait genetic evaluations in the Canadian sheep industry.

A slaughter endpoint is a criterion used to decide when to market animals for slaughter. The choice of slaughter endpoint is often regionally dependent, with slaughter age, carcass weight, and carcass fatness level being common decision support criteria. The Canadian sheep industry is highly decentralized and production practices vary greatly by flock size and geographical region (Quinton et al., 2014), thus it is unknown which slaughter endpoint(s) would be the most suitable for the genetic evaluation of carcass traits in the CSGES. The slaughter endpoint used in genetic evaluations may have implications for the genetic correlations between traits (Pollott et al., 1994), and consequently, influence the selection response achieved through the use of multiple-trait selection indexes. Thus, it is important to evaluate the impact of alternative slaughter endpoints to ensure that proposed carcass trait genetic evaluations are representative of diverse breeding objectives among commercial sheep producers. Breeding objectives utilized to derive existing CSGES selection indexes (Quinton et al., 2014) assumed that rail-graded lambs were marketed at a constant slaughter age. Quinton et al. (2014) noted that producers typically aim to market lambs at a constant weight but commercial data demonstrated a wide range of weight and age endpoints. The effect of alternative slaughter endpoints on carcass trait genetic parameter estimates has been studied more extensively in beef cattle, as reviewed by Ríos-Utrera and Van Vleck (2004), but, to the best of our knowledge, evaluation of all three slaughter endpoints in sheep is limited to studies by Pollott et al. (1994) and Conington et al. (1998). These studies utilized a sample of animals from designed experiments in British sheep populations and differed from the present study with respect to the breeds, production systems, and traits analyzed. Furthermore, the genetic parameter estimates presented by Pollott et al. (1994) and Conington et al. (1998) typically had large standard errors, which limited the interpretation of genetic correlation results. Thus, it is unclear if the results presented by Pollott et al. (1994) and Conington et al. (1998) would be applicable to the breeds and production practices in the Canadian sheep industry.

Consequently, the objectives of this research were 1) to estimate the first genetic parameters for carcass traits in a Canadian crossbred heavy lamb population; 2) to estimate the correlations between carcass, growth, and ultrasound traits; and 3) to evaluate the impact of alternative slaughter endpoints on carcass trait genetic parameter estimates.

MATERIALS AND METHODS

Animals

Data used in this research were obtained from commercial producer and abattoir records, thus, animal care approval was not required. As part of the routine grading procedures of the HLSA, carcass yield and quality measurements on over 80,000 heavy lambs raised under commercial conditions were recorded between January 2011 and August 2013. Animal identification (tattoo number) was used to link carcass measurements to pedigree and management records of 16,565 lambs enrolled in the CSGES. Consistent with the Canadian sheep population, approximately 29% of the lambs with carcass records were purebred, while in the total dataset approximately 60% of animals were purebred. The breeds represented included Polled Dorset (**DP**; 26%), Rideau Arcott (**RI**; 22%), Romanov (**RV**; 21%), Suffolk (**SU**; 13%), Polypay (**PO**; 8%), Canadian Arcott (**CD**; 4%), Hampshire (**HA**; 3%), and rare breeds and unknown crosses (3%). The major breeds are typical of the Canadian sheep population and included highly prolific Maternal breeds (RV, RI, PO), Maternal or Maternal sire breeds (DP), and Terminal sire breeds (SU, HA, CD).

Data

Management information (sex, date of birth, breed composition, age at weighing, flock identification, and producer-defined management group) and growth and ultrasound trait measurements were retrieved from the CSGES for all animals with carcass records and their relatives. Contemporary groups were defined as management group within year and flock. Abattoir identification was unavailable, but slaughter groups were formed as unique month-year combinations of slaughter date to account for seasonal or market differences that may have influenced carcass characteristics. The difference between birth and slaughter dates was used to calculate slaughter age (**SAGE**, days). Lambs used in this research were an average of 172.0 ± 40.9 d of age at slaughter and ranged from 54 to 353 d of age. Only carcasses that met the heavy lamb classification criteria (**HCW** $\geq$ 16.4 kg and SAGE $\leq$ 365 d) and animals with growth trait records that were within the CSGES trait limits, as per Schaeffer and Szkotnicki (2015), were retained.

Traits analyzed in this research included growth, ultrasound, and carcass traits. Birthweight (**BWT**, kg) was measured within 24 h of birth, while records for weaning weight (**WWT**, kg), post-weaning weight (**PWWT**, kg), and ultrasound scanning weight (**WTUS**, kg) were measured at an average age of 54.5 ± 9.8, 97.5 ± 11.5, and 97.8 ± 11.8 d, respectively. Adjusted 50-d and 100-d weights were used to calculate pre-weaning average daily gain (**ADG50**, kg) and post-weaning average daily gain (**ADG100**, kg), assuming linear growth during each period (Schaeffer and Szkotnicki, 2015). Eye muscle depth (**EMDUS**, mm), a measure of the longissimus dorsi muscle and average fat depth (**FATUS**, mm) were measured by accredited ultrasound technicians at a site halfway between the last rib and the hip bone between the third and fourth lumbar vertebrae. Hot carcass weight (HCW, kg) was recorded after the carcass was dressed, following the specifications for Canadian lamb processing (Government of Canada, 1992). Carcass fat depth (**FATGR**, mm) was measured as the total tissue depth at the GR site (110 mm from the midline on the 12th rib) (Kirton and Johnson, 1979). Carcass conformation scores, ranging from 1 (poor muscling) to 5 (excellent muscling), were used to assess the muscularity of carcasses in three primal cuts: shoulder (**SHOUL**), loin (**LOIN**), and leg (**LEG**). Primal cut conformation scores were then averaged and rounded to the nearest whole number to calculate an average carcass conformation score (**AVGCONF**). Saleable meat yield (**SMY**, % of HCW) was predicted from FATGR and AVGCONF using equations derived by Jones et al. (1996). Price grid value (**CINDEX**) was derived from price grid class (20.0 to 24.0 kg and <20.0 or >24.0 kg), FATGR, and AVGCONF measurements, as per the Heavy Lamb Sales Agency Producer's Guide (Les Éleveurs d'ovins du Québec, 2017). Total carcass value (**PRICE**, $CAD) was estimated based on CINDEX and HCW, assuming a base price per kilogram of HCW of $7.85 (Les Éleveurs d'ovins du Québec, 2017).

Both R (R Core Team, 2017) and SAS (SAS Institute Inc., 2013) statistical software were used for preliminary data editing. Animals with an unknown dam, contemporary group with fewer than three animals, or that were cross-fostered or bottle-fed were excluded from the final dataset. Fixed-effects models, as described in Table 1, were used to adjust the observations for each trait and any animal with a residual more than 3 SDs from the mean was further excluded to remove potential outliers. There were 29,923 animals with records in the final dataset, including 14,441 animals with carcass records.

Pedigree

The *pedigree* package (Coster, 2013) was used to trim branches of the full CSGES pedigree without carcass trait data. The final pedigree contained 37,885 animals over 21 generations. Due to the editing procedure, dam information was known for all

Table 1. Fixed and random effects fitted in the genetic parameter estimation models for various trait groups[1]

	Growth traits					Ultrasound traits		Carcass traits		
Effect	BWT	WWT	PWWT	ADG50; ADG100	WTUS	Age constant	Weight constant	Age constant	Weight constant	Fat constant
	Fixed categorical effects									
Sex	+	+	+	+	+	+	+	+	+	+
Dam age at parity	+	+	+	+	+	+	+	+	+	+
Birth type	+	–	–	–	–	–	–	–	–	–
Birth-rearing type	–	+	+	+	+	+	+	+	+	+
Slaughter group	–	–	–	–	–	–	–	+	+	+
	Fixed covariate effects									
Breed composition	+	+	+	+	+	+	+	+	+	+
SAGE	–	–	–	–	–	–	–	+	–	–
HCW	–	–	–	–	–	–	–	–	+	–
FATGR	–	–	–	–	–	–	–	–	–	+
Age at weaning	–	+		–	–	–	–	–	–	–
Age at post-weaning	–	–	+	–	–	–	–	–	–	–
Age at ultrasound	–	–	–	–	+	+	–	–	–	–
Weight at ultrasound	–	–	–	–	–	–	+	–	–	–
	Random effects									
Additive genetic	+	+	+	+	+	+	+	+	+	+
Contemporary group	+	+	+	+	+	+	+	+	+	+
Maternal genetic	+	+	+	+	+	–	–	–	–	–
Maternal permanent environmental	+	+	+	+	+	–	–	–	–	–

[1] ADG50 = pre-weaning average daily gain; ADG100 = post-weaning average daily gain; BWT = birthweight; FATGR = fat depth at the GR site; HCW = hot carcass weight; PWWT = post-weaning weight; SAGE = age at slaughter; WTUS = scanning weight; WWT = weaning weight.

animals with records, but sire identification information was missing for about 19% of animals with records, consistent with the common sheep production practice of group mating. Animals with records were the progeny of 2,760 known sires and 17,451 dams, and had an average pedigree depth of 10.4 generations. Known sires and dams had an average of 8.8 and 1.7 progeny with records, respectively.

Statistical Analyses

The MEANS and GLM procedures of SAS (SAS Institute Inc., 2013) were used to estimate descriptive statistics (Table 2) and test the significance of fixed effects, respectively. (Co)variance components were estimated using mixed linear animal models in the ASReml statistical software (Gilmour et al., 2015). The fixed and random effects included in the models for the various trait groups are summarized in Table 1 and described below. Univariate analyses were used to estimate the heritability of each trait, while genetic and phenotypic correlations were estimated from bivariate analyses. For the purposes of comparison, the heritability estimates were categorized as low (<0.15), moderate (0.15 to 0.30), or high (>0.30), while genetic correlations were categorized as being weak (<0.30), moderate (0.30 to 0.70), or strong (>0.70). Phenotypic correlations between growth and carcass traits are presented in Supplementary Tables S1 to S3. Preliminary descriptive analysis and genetic parameter estimates for a subset of the traits studied were initially presented in Massender et al. (2018).

Fixed effects. The final model for each trait (Table 1) included fixed effects of sex (male or female), dam age at parity (1, 2, …, 7), birth (single, twin, or triplet or more) or birth-rearing type (born as single raised as single, born as multiple raised as single, born as twin raised as twin, born as triplet or more and raised as twin, and born as triplet or more and raised as triplet or more), and linear covariates of fractional breed composition for the seven major breeds (DP, RV, RI, SU, PO, CD, and HA). Analyses of WWT, PWWT, and WTUS included age of the animal at measurement as a linear covariate. Ultrasound measurements were adjusted to either a fixed age or WTUS. Slaughter group was included in all carcass trait models and the effect of slaughter endpoint on genetic parameter estimates was evaluated by modeling carcass traits at each of three alternative slaughter endpoints (age

Table 2. Trait abbreviations and descriptive statistics[1]

Trait	Abbreviation	*n*	Mean ± SD	Range	CV (%)
Growth traits					
Birthweight, kg	BWT	22,494	4.3 ± 1.1	1.2–8.0	25.6
50-d weaning weight, kg	WWT	29,082	19.8 ± 6.0	3.5–40.0	30.5
100-d post-weaning weight, kg	PWWT	26,763	33.0 ± 8.1	8.0–65.0	24.5
Pre-weaning average daily gain, kg	ADG50	29,082	0.3 ± 0.1	0.0–1.1	31.4
Post-weaning average daily gain, kg	ADG100	26,693	0.3 ± 0.1	0.0–1.5	31.4
Scanning weight, kg	WTUS	1,299	38.1 ± 8.1	15.4–64.0	21.1
Ultrasound traits					
Ultrasonic eye muscle depth, mm	EMDUS	1,299	26.8 ± 3.8	10.6–36.6	14.2
Ultrasonic fat depth, mm	FATUS	1,299	3.8 ± 1.4	0.9–10.8	36.9
Carcass traits					
Hot carcass weight, kg	HCW	14,441	23.2 ± 2.3	16.4–31.7	9.9
Carcass fat depth at the GR site, mm	FATGR	14,441	11.0 ± 3.3	1.0–19.0	30.0
Slaughter age, days	SAGE	14,441	172.0 ± 40.9	54.0–353.0	23.8
Predicted saleable meat yield, %	SMY	14,441	77.2 ± 1.5	72.0–82.0	2.0
Leg conformation, score	LEG	14,441	2.9 ± 0.5	1.0–4.0	18.2
Loin conformation, score	LOIN	14,441	3.5 ± 0.6	2.0–5.0	16.8
Shoulder conformation, score	SHOUL	14,441	3.0 ± 0.6	1.0–5.0	21.5
Average carcass conformation, score	AVGCONF	14,441	3.1 ± 0.6	2.0–4.0	17.8
Carcass price grid value, score	CINDEX	14,441	101.8 ± 3.5	85.0–106.0	3.4
Total carcass value, $CAD	PRICE	14,441	184.4 ± 16.5	124.1–218.6	9.0

[1] CV (%) = coefficient of variation; *n* = number of records; SD = standard deviation.

at slaughter, carcass weight, and carcass fat depth).

Random effects. Random effects in each model included contemporary group and animal additive genetic effect (Table 1). Contemporary groups were assumed to be uncorrelated, but the covariance between traits due to the contemporary group effect was fitted in the bivariate analyses. As maternal additive genetic and maternal permanent environmental effects were significant ($P < 0.01$), both effects were retained in the final growth trait models, with no covariance assumed between the direct and maternal genetic effects. Some ultrasound and carcass traits have been found to be weakly to moderately influenced by maternal effects (e.g., Mortimer et al., 2010; Einarsson et al., 2015); however, the structure of data used in this research was inadequate to estimate these effects.

RESULTS AND DISCUSSION

Descriptive Statistics

The number of observations varied from 1,299 for ultrasound measurements and WTUS to 29,082 for WWT and ADG50 (Table 2). Ultrasound measurements are recorded infrequently in Canada due to their cost and lack of access to ultrasound technicians. This suggests that the genetic evaluation of carcass trait records generated through rail-graded marketing systems may be a promising method to improve carcass quality. However, ultrasound traits remain valuable indicators of carcass quality because rail-graded marketing systems are uncommon outside of Quebec and carcass traits cannot be measured directly on breeding candidates. According to the HLSA, the ideal carcass is between 20.0 and 24.0 kg with high muscularity scores (4 to 5) and a target FATGR measurement between 7 and 12 mm (Les Éleveurs d'ovins du Québec, 2017). In this dataset, average HCW (23.2 ± 2.3) and FATGR (11.0 ± 3.3) were on the high end of the ideal range, while the average AVGCONF (3.1 ± 0.6) was low (Table 2). Approximately 56%, 61%, and 23% of observations were within the ideal ranges for HCW, FATGR, and AVGCONF, respectively.

Phenotypic Variation and Heritability

Growth traits. Direct heritability estimates for growth traits were generally moderate, with maternal heritability and maternal permanent environmental variance ratio estimates decreasing and direct heritability estimates increasing as age at measurement increased (Table 3), consistent with results presented by Tosh and Kemp (1994) and Boareki (2017) in purebred Canadian sheep populations. Maternal heritability and maternal permanent environmental variance ratio were the largest for BWT (0.15 ± 0.01 and 0.10 ± 0.01, respectively) and the smallest for ADG100 (0.02 ± 0.01 and 0.03 ± 0.01, respectively) (Table 3). Although significant maternal effects have been reported for carcass traits in other populations (e.g., Mortimer et al., 2010; Einarsson et al., 2015), the low maternal effect estimates observed for PWWT and ADG100 suggest that maternal effects are likely to be small for ultrasound and carcass traits.

Direct heritability of BWT was estimated to be 0.18 ± 0.01 and was similar to published estimates (Table 3), which range from 0.07 ± 0.03 in an Australian Maternal crossbred population (Ingham et al., 2007) to 0.22 ± 0.04 in Australian Merino sheep (Mortimer et al., 2017a). Birthweight has generally been found to be less heritable in Canadian sheep populations (Tosh and Kemp, 1994; Boareki, 2017), with published heritability estimates ranging from 0.07 for RV sheep to 0.39 for HA sheep (Tosh and Kemp, 1994). The direct heritability estimate for WWT (0.23 ± 0.01; Table 3) was consistent with literature estimates, which varied from 0.09 ± 0.05 in a multi-breed New Zealand Terminal and Dual-Purpose crossbred population (Payne et al., 2009) to 0.40 ± 0.03 in Australian Merino sheep (Huisman and Brown, 2008). However, WWT is often measured at a later age in other countries and lower heritability estimates (0.05 to 0.21) have been reported for WWT and adjusted WWT in Canadian sheep populations (Tosh and Kemp, 1994; Boareki, 2017). Direct heritability for PWWT was estimated to be 0.25 ± 0.01 (Table 3). Post-weaning weight is measured at a wide range of ages (100 to 180 d), but, Maxa et al. (2007a) reported a lower direct heritability for PWWT (0.17 ± 0.04) for a population of SU sheep and Terminal crosses from the Czech Republic at a similar age. The direct heritability estimates reported by Tosh and Kemp (1994) and Boareki (2017) for PWWT and adjusted PWWT in Canadian populations ranged from 0.14 to 0.39. The heritability of WTUS (0.30 ± 0.06; Table 3) was found to be similar to recent literature results (Brito et al., 2017; Mortimer et al., 2017a). Direct heritability estimates for ADG50 and ADG100 were 0.21 ± 0.01 and 0.15 ± 0.01, respectively (Table 3). The direct heritability estimate for ADG100 was similar to the estimate of 0.16 ± 0.03 by Maximini et al. (2012) in a multi-breed Austrian sheep population.

Ultrasound traits. Ultrasound traits were found to be moderately to highly heritable (0.16 ± 0.06 to 0.35 ± 0.06; Table 3). Direct heritability estimates for EMDUS in the literature have ranged from 0.32 ± 0.02 in Lleyn sheep (Ceyhan et al., 2015) to 0.40 ± 0.05 in Scottish Blackface sheep (Karamichou et al., 2007) and 0.20 ± 0.06 (Mortimer et al., 2017a) to 0.42 in an Icelandic sheep population (Einarsson et al., 2015) for age- and weight-constant EMDUS, respectively. Direct heritability estimates ranging from 0.23 ± 0.01

Table 3. Phenotypic variance (σ_p^2), ratio of contemporary group effect variance to phenotypic variance (g^2), maternal permanent environmental effect variance ratio (c^2), direct heritability (h_d^2), maternal heritability (h_m^2), and total heritability (h_t^2) estimates for growth and ultrasound traits[1]

Trait[2]	σ_p^2	g^2	c^2	h_d^2	h_m^2	h_t^2
Growth traits						
BWT	0.62	0.19 ± 0.01	0.10 ± 0.01	0.18 ± 0.01	0.15 ± 0.01	0.26 ± 0.01
WWT	19.23	0.30 ± 0.01	0.05 ± 0.01	0.23 ± 0.01	0.05 ± 0.01	0.26 ± 0.01
PWWT	37.08	0.34 ± 0.01	0.03 ± 0.01	0.25 ± 0.01	0.05 ± 0.01	0.27 ± 0.01
WTUS	39.68	0.29 ± 0.04	–	0.30 ± 0.06	–	0.30 ± 0.06
ADG50	0.01	0.33 ± 0.01	0.05 ± 0.01	0.21 ± 0.01	0.06 ± 0.01	0.24 ± 0.01
ADG100	0.01	0.45 ± 0.01	0.03 ± 0.01	0.15 ± 0.01	0.02 ± 0.01	0.15 ± 0.01
Ultrasound traits						
EMDUSa	10.92	0.28 ± 0.04	–	0.16 ± 0.06	–	0.16 ± 0.06
EMDUSw	6.26	0.32 ± 0.04	–	0.35 ± 0.06	–	0.35 ± 0.06
FATUSa	2.16	0.49 ± 0.04	–	0.22 ± 0.05	–	0.22 ± 0.05
FATUSw	1.60	0.56 ± 0.03	–	0.22 ± 0.05	–	0.22 ± 0.05

[1] Parameter estimates are followed by their approximate standard error.

[2] ADG50 = pre-weaning average daily gain; ADG100 = post-weaning average daily gain; BWT = birthweight; EMDUS = ultrasonically measured eye muscle depth; FATUS = ultrasonically measured fat depth; PWWT = post-weaning weight; WTUS = scanning weight; WWT = weaning weight. Ultrasound eye muscle and fat depth measurements adjusted to a constant age (EMDUSa, FATUSa) or scanning weight (EMDUSw, FATUSw).

in a crossbred Australian population (Walkom and Brown, 2016) to 0.37 ± 0.02 (Ceyhan et al., 2015) and 0.12 ± 0.07 in Danish Shropshire sheep (Maxa et al., 2007b) to 0.42 (Einarsson et al., 2015) have been reported for age- and weight-constant FATUS, respectively.

Greater phenotypic variation was observed for age-constant EMDUS (10.92 mm^2) compared to weight-constant EMDUS (6.26 mm^2) (Table 3), while additive genetic variance estimates remained similar, leading to higher direct heritability estimates for weight-constant EMDUS (0.35 ± 0.06 vs. 0.16 ± 0.06). However, the direct heritability estimates for FATUS were the same at alternative endpoints (0.22 ± 0.05), due to similar phenotypic and additive genetic variation in the weight- and age-constant analyses. Higher phenotypic variation for age-constant EMDUS was also reported by Fernandes et al. (2004) in a Canadian sheep population, although they reported higher direct heritability estimates from age-constant analyses. Fernandes et al. (2004) concluded that both weight- and age-adjusted ultrasound measurements were useful because they provide information on proportionality of the carcass and growth rate, respectively. Mortimer et al. (2014) found that adjusting ultrasound trait measurements to a constant weight and age reduced phenotypic variation, resulting in higher direct heritability estimates from the weight- and age-adjusted analyses when compared to age-adjusted analyses. Although the genetic parameter estimates must be interpreted cautiously due to the small sample size in the present research, these results suggest that the covariate used in ultrasound genetic evaluations could have an impact on their usefulness as indicators of carcass yield and quality.

Carcass traits at alternative slaughter endpoints. There were considerable differences in the phenotypic variance of some traits when observations were adjusted to alternative slaughter endpoints (Table 4). Reduced phenotypic variation could make it more difficult to identify superior individuals, thus, the phenotypic variance of traits may be of interest in determining appropriate slaughter endpoint(s) for carcass trait genetic evaluations. Pollott et al. (1994) also noted that traits highly dependent on a particular endpoint were less variable than when adjusted to the other endpoints, for example, conformation traits that were adjusted to a constant fatness. Phenotypic variance for most traits was the highest when observations were adjusted to a constant SAGE, in agreement with the results reported by Pollott et al. (1994). This trend makes sense given that animals often differ in growth rate and maturation, likely leading to greater variability in carcass traits at a constant age.

Direct heritability estimates for carcass traits ranged from 0.17 ± 0.02 for HCW at a constant SAGE to 0.34 ± 0.02 for AVGCONF at a constant carcass weight (Table 4). Heritability estimates generally differed by less than the standard errors of the estimates between alternative slaughter endpoints with the exception of FATGR and the carcass conformation traits where differences between 0.03 to 0.05 were observed between analyses. There was a trend for direct heritability estimates at a

Table 4. Phenotypic variance (σ_p^2), ratio of contemporary group effect variance to phenotypic variance (g^2), and direct heritability (h_d^2) estimates for carcass traits at alternative slaughter endpoints[1]

	Slaughter endpoint								
	Slaughter age			Carcass weight			Carcass fatness		
Trait[2]	σ_p^2	g^2	h_d^2	σ_p^2	g^2	h_d^2	σ_p^2	g^2	h_d^2
HCW	4.87	0.33 ± 0.02	0.17 ± 0.02	–	–	–	4.54	0.35 ± 0.02	0.18 ± 0.02
FATGR	9.54	0.21 ± 0.01	0.30 ± 0.02	8.44	0.19 ± 0.01	0.33 ± 0.03	–	–	–
SMY	2.13	0.17 ± 0.01	0.26 ± 0.02	1.96	0.15 ± 0.01	0.28 ± 0.02	0.25	0.11 ± 0.01	0.26 ± 0.02
LEG	0.25	0.12 ± 0.01	0.32 ± 0.02	0.24	0.12 ± 0.01	0.33 ± 0.02	0.23	0.10 ± 0.01	0.30 ± 0.02
LOIN	0.28	0.17 ± 0.01	0.27 ± 0.02	0.27	0.16 ± 0.01	0.29 ± 0.02	0.24	0.12 ± 0.01	0.24 ± 0.02
SHOUL	0.35	0.14 ± 0.01	0.31 ± 0.02	0.34	0.14 ± 0.01	0.32 ± 0.02	0.30	0.11 ± 0.01	0.28 ± 0.02
AVGCONF	0.26	0.14 ± 0.01	0.32 ± 0.02	0.24	0.13 ± 0.01	0.34 ± 0.02	0.23	0.10 ± 0.01	0.30 ± 0.02
CINDEX	11.72	0.08 ± 0.01	0.23 ± 0.02	11.31	0.07 ± 0.01	0.22 ± 0.02	8.27	0.09 ± 0.01	0.22 ± 0.02
PRICE	236.91	0.28 ± 0.01	0.19 ± 0.02	53.36	0.10 ± 0.01	0.20 ± 0.02	243.45	0.29 ± 0.01	0.18 ± 0.02

[1] Parameter estimates are followed by their approximate standard error.

[2] AVGCONF = average carcass conformation score; CINDEX = carcass price grid value; FATGR = fat depth at the GR site; HCW = hot carcass weight; LEG = leg carcass conformation score; LOIN = loin carcass conformation score; PRICE = total carcass value; SHOUL = shoulder conformation score; SMY = predicted saleable meat yield.

constant fatness and constant carcass weight to be the lowest and the highest, respectively. The lower direct heritability estimates for carcass traits at a constant fatness could indicate that adjusting for fatness removes more of the additive genetic variation in the traits compared to the other two endpoints. These trends were in agreement with results reported by Pollott et al. (1994) and Conington et al. (1998); however, Pollott et al. (1994) generally reported larger differences in direct heritability estimates between alternative slaughter endpoints. Overall, the small differences in the direct heritability estimates of the carcass traits at alternative slaughter endpoints are likely to be of little practical significance.

The direct heritability of HCW was estimated to be 0.17 ± 0.02 and 0.18 ± 0.02 when observations were adjusted to a constant age and fatness, respectively (Table 4). Published direct heritability estimates for HCW adjusted to a constant SAGE have ranged from 0.20 ± 0.05 (Payne et al., 2009) to 0.59 in a multi-breed Australian Merino and Terminal crossbred population (Daetwyler et al., 2012). Carcass fat depth was found to be highly heritable (0.30 ± 0.02 to 0.33 ± 0.03; Table 4), in agreement with most literature estimates (Mortimer et al., 2010; Brito et al., 2017). Direct heritability estimates for FATGR adjusted to a constant carcass weight have ranged from 0.20 ± 0.02 (Brito et al., 2017) in a New Zealand Terminal crossbred population to 0.47 ± 0.08 (Ingham et al., 2007) in the literature. Direct heritabilities estimated with age and weight (Mortimer et al., 2010) or age (Mortimer et al., 2017b) slaughter endpoints have also been reported in Australian multi-breed and Merino populations (0.50 ± 0.05 and 0.23 ± 0.11, respectively). Direct heritability estimates for carcass conformation traits ranged from 0.24 ± 0.02 to 0.34 ± 0.02 (Table 4) and were consistent with published estimates, which ranged from 0.14 ± 0.05 (Karamichou et al., 2007) to 0.45 ± 0.05 (Maxa et al., 2007b), assessed on a range of European sheep breeds graded using the EUROP classification system (Meat and Livestock Commercial Services Ltd., n.d.). The composite traits (SMY, CINDEX, and PRICE) were all found to be moderately heritable (0.18 ± 0.02 to 0.28 ± 0.02; Table 4). Published direct heritability estimates have ranged from 0.19 ± 0.06 (Karamichou et al., 2007) to 0.23 ± 0.10 in Scottish Blackface sheep (Conington et al. 1998) for PRICE with observations adjusted to a constant age, and 0.32 ± 0.12 for observations adjusted to a constant fatness (Conington et al. 1998). Published direct heritability estimates for SMY ranged from 0.29 ± 0.11 (Mortimer et al., 2017b) to 0.32 (Daetwyler et al., 2012) and are similar to the estimates presented here (0.26 ± 0.02 to 0.28 ± 0.02).

Genetic Correlations

Growth traits. Consistent with literature estimates, body weight traits were all moderately to strongly correlated (0.46 ± 0.04 to 0.89 ± 0.01; Table 5), with weights measured at closer ages having stronger phenotypic and genetic correlations than those measured at more distant ages (Fischer et al., 2006; Ingham et al., 2007; Huisman and Brown, 2008; Boareki, 2017). Positive genetic correlations between WWT, PWWT, and WTUS (0.82 ± 0.06 to 0.89 ± 0.01; Table 5) were favorable, as selection for these traits would be expected to increase production efficiency. However, it is well reported that the positive genetic correlations between BWT and other weight traits are concerning due to the potential for reduced lambing ease or number of lambs born as BWT increases (Brown, 2007; Li and Brown, 2016; Boareki, 2017). Quinton et al. (2014) and Boareki (2017) concluded that utilizing selection indexes is important to balance the effects of selection for reproductive and growth traits. Where estimable, moderate to strong positive genetic correlations were generally observed between body weight traits and pre- and post-weaning average daily gain (0.27 ± 0.05 to 0.89 ± 0.01; Table 5), although the correlations were weaker than those reported by Maximini et al. (2012) between WTUS and average daily gain (0.96 ± 0.01).

Ultrasound traits. Genetic correlation estimates among EMDUS and FATUS adjusted to either age- or weight-constant endpoints (−0.13 ± 0.16 to 0.42 ± 0.16; Table 5) were generally positive and weak to moderate in magnitude with large standard errors, suggesting that selection on EMDUS to improve carcass conformation may result in unfavorable increases in FATUS. These results contrast with those described by Fernandes et al. (2004), who found a weak negative correlation between the traits when adjusted to a constant weight (−0.17).

Carcass traits. An unfavorable weak positive genetic correlation between HCW and FATGR at a constant age was identified (0.15 ± 0.07; Table 6), although this correlation was weaker than some literature estimates (Ingham et al., 2007; Brito et al., 2017). Hot carcass weight had a strong positive genetic correlation with PRICE at both age

Table 5. Genetic and phenotypic correlations among growth and ultrasound traits[1,2]

	BWT	WWT	PWWT	WTUS	ADG50	ADG100	EMDUSa	EMDUSw	FATUSa	FATUSw
BWT		0.36 ± 0.01	0.31 ± 0.01	0.28 ± 0.03	0.35 ± 0.01	0.10 ± 0.01	0.15 ± 0.04	−0.07 ± 0.04	0.13 ± 0.04	−0.02 ± 0.04
WWT	0.50 ± 0.04		0.77 ± 0.01	0.71 ± 0.02	NC[3]	0.11 ± 0.01	0.42 ± 0.03	−0.11 ± 0.04	0.39 ± 0.03	0.04 ± 0.04
PWWT	0.46 ± 0.04	0.89 ± 0.01		NC	0.75 ± 0.01	0.69 ± 0.01	0.64 ± 0.02	−0.01 ± 0.04	0.52 ± 0.03	0.03 ± 0.05
WTUS	0.57 ± 0.12	0.82 ± 0.06	NC		0.69 ± 0.02	0.62 ± 0.02	0.66 ± 0.02	−0.02 ± 0.04	0.52 ± 0.03	−0.05 ± 0.05
ADG50	0.49 ± 0.04	NC	0.89 ± 0.01	0.77 ± 0.06		0.11 ± 0.01	0.41 ± 0.03	−0.11 ± 0.04	0.38 ± 0.03	0.03 ± 0.04
ADG100	0.27 ± 0.05	0.49 ± 0.04	0.82 ± 0.02	0.56 ± 0.09	0.51 ± 0.04		0.44 ± 0.03	0.00 ± 0.04	0.32 ± 0.04	−0.01 ± 0.05
EMDUSa	0.38 ± 0.18	0.36 ± 0.12	0.54 ± 0.08	0.40 ± 0.14	0.34 ± 0.13	0.22 ± 0.14		NC	0.41 ± 0.03	0.10 ± 0.04
EMDUSw	−0.17 ± 0.13	−0.41 ± 0.11	−0.28 ± 0.11	−0.47 ± 0.15	−0.37 ± 0.11	−0.25 ± 0.11	NC		0.06 ± 0.04	0.11 ± 0.04
FATUSa	0.21 ± 0.15	0.47 ± 0.10	0.63 ± 0.08	0.58 ± 0.10	0.40 ± 0.10	0.25 ± 0.12	0.42 ± 0.16	−0.13 ± 0.16		NC
FATUSw	−0.16 ± 0.14	0.02 ± 0.12	−0.02 ± 0.11	−0.07 ± 0.15	−0.03 ± 0.12	−0.03 ± 0.12	0.29 ± 0.19	0.32 ± 0.13	NC	

[1] Phenotypic and genetic correlation estimates are presented above and below the diagonal, respectively, and are followed by their approximate standard error.

[2] ADG50 = pre-weaning average daily gain; ADG100 = post-weaning average daily gain; BWT = birthweight; EMDUS = ultrasonically measured eye muscle depth; FATUS = ultrasonically measured fat depth; PWWT = post-weaning weight; WTUS = scanning weight; WWT = weaning weight. Ultrasound eye muscle and fat depth measurements adjusted to a constant age (EMDUSa, FATUSa) or scanning weight (EMDUSw, FATUSw).

[3] NC: Model did not converge.

Table 6. Phenotypic and genetic correlation estimates for carcass traits adjusted to a fixed slaughter age endpoint[1,2]

	HCW	FATGR	SMY	LEG	LOIN	SHOUL	AVGCONF	CINDEX	PRICE
HCW		0.35 ± 0.01	−0.30 ± 0.01	0.23 ± 0.01	0.23 ± 0.01	0.18 ± 0.01	0.22 ± 0.01	−0.19 ± 0.01	0.88 ± 0.01
FATGR	0.15 ± 0.07		−0.94 ± 0.01	0.24 ± 0.01	0.39 ± 0.01	0.37 ± 0.01	0.35 ± 0.01	−0.54 ± 0.01	0.13 ± 0.01
SMY	−0.15 ± 0.07	−0.94 ± 0.01		−0.02 ± 0.01	−0.21 ± 0.01	−0.13 ± 0.01	−0.09 ± 0.01	0.62 ± 0.01	−0.04 ± 0.01
LEG	0.03 ± 0.07	0.31 ± 0.05	−0.03 ± 0.06		0.36 ± 0.01	0.38 ± 0.01	0.62 ± 0.01	0.10 ± 0.01	0.27 ± 0.01
LOIN	0.00 ± 0.07	0.58 ± 0.05	−0.38 ± 0.06	0.57 ± 0.05		0.45 ± 0.01	0.57 ± 0.01	−0.01 ± 0.01	0.22 ± 0.01
SHOUL	0.08 ± 0.07	0.53 ± 0.05	−0.26 ± 0.06	0.63 ± 0.04	0.65 ± 0.04		0.77 ± 0.01	0.02 ± 0.01	0.19 ± 0.01
AVGCONF	0.04 ± 0.07	0.48 ± 0.05	−0.19 ± 0.06	0.83 ± 0.02	0.75 ± 0.03	0.89 ± 0.02		0.10 ± 0.01	0.26 ± 0.01
CINDEX	−0.24 ± 0.08	−0.59 ± 0.05	0.69 ± 0.04	0.08 ± 0.07	−0.07 ± 0.07	−0.04 ± 0.07	0.01 ± 0.07		0.23 ± 0.01
PRICE	0.87 ± 0.02	−0.17 ± 0.07	0.18 ± 0.07	0.04 ± 0.07	−0.06 ± 0.07	0.01 ± 0.07	0.00 ± 0.07	0.24 ± 0.07	

[1] Phenotypic and genetic correlation estimates are presented above and below the diagonal, respectively, and are followed by their approximate standard error.

[2] AVGCONF = average carcass conformation score; CINDEX = carcass price grid value; FATGR = fat depth at the GR site; HCW = hot carcass weight; LEG = leg carcass conformation score; LOIN = loin carcass conformation score; PRICE = total carcass value; SHOUL = shoulder conformation score; SMY = predicted saleable meat yield.

and fatness endpoints (0.87 ± 0.02 to 0.90 ± 0.02; Tables 6 and 8), whereas FATGR and PRICE had favorable weak to moderate (−0.53 ± 0.05 to −0.17 ± 0.07; Tables 6 and 8) negative correlations at both age and fatness endpoints. These results were in agreement with those reported by Karamichou et al. (2007) and indicate that total price was more strongly associated with carcass yield than carcass quality. Thus, genetic selection to increase HCW would be expected to favorably increase carcass value independent of the endpoint used in the analysis. Among the carcass conformation traits, moderate to strong positive genetic correlations were observed at all endpoints (0.54 ± 0.05 to 0.89 ± 0.02; Tables 6 to 8), suggesting that selection for AVGCONF could be beneficial to simultaneously improve all primal cut conformation traits. Unfavorable moderate positive genetic correlations between FATGR and carcass conformation scores at age and weight endpoints (0.31 ± 0.05 to 0.60 ± 0.05; Tables 6 and 7) indicate that selection to reduce FATGR will reduce muscularity. Similarly, Einarsson et al. (2015) identified a moderate positive genetic correlation (0.38) between FATGR and EUROP carcass conformation score. Adjusting AVGCONF to a constant weight or age resulted in weak unfavorable negative correlations (−0.18 ± 0.06 and −0.19 ± 0.06, respectively) with SMY, while at a constant fatness, the traits were strongly positively correlated (0.96 ± 0.01), due to the fact that SMY is predicted based on AVGCONF and FATGR (Tables 6 to 8). The endpoint used in the analysis was found to have an influence on both the magnitude and direction of some genetic correlations. Furthermore, the unfavorable correlations observed between some traits underscore the importance of using selection indexes for balanced carcass trait genetic improvement.

Growth and ultrasound traits. Weight and gain traits were generally found to be positively correlated with age-constant EMDUS and FATUS, with correlation estimates ranging from 0.22 ± 0.14 to 0.54 ± 0.08 and 0.21 ± 0.15 to 0.63 ± 0.08, respectively (Table 5). In contrast, correlations between weight traits and weight-constant EMDUS and FATUS were generally negative and ranged from −0.47 ± 0.15 to −0.17 ± 0.13 and −0.16 ± 0.14 to 0.02 ± 0.12 (Table 5). Most estimates of EMDUS and FATUS found in the literature were adjusted to a constant weight, and negative correlations between weight traits and EMDUS and FATUS have been previously identified (Maximini et al., 2012; Mortimer et al., 2014). Mortimer et al. (2014) found that genetic correlations between weight traits and age-constant EMDUS and FATUS were positive while negative correlations were found when adjusting EMDUS and FATUS observations to a constant age and weight.

Growth and carcass traits. Most genetic correlations between growth and carcass traits were weak to moderate in strength (Tables 9 to 11). Hot carcass weight was generally positively correlated with all growth traits at both age and fatness slaughter endpoints (0.07 ± 0.07 to 0.38 ± 0.05; Tables 9 and 11), indicating that current selection for weight and gain traits is expected to indirectly improve HCW. Thus, indirect genetic improvement for carcass yield remains achievable for commercial producers that market on a live-weight basis without the use of ultrasound measures. Interestingly, correlations between HCW and WWT and HCW and PWWT were not considerably different at either

Table 7. Phenotypic and genetic correlation estimates for carcass traits adjusted to a fixed carcass weight endpoint[1,2]

	FATGR	SMY	LEG	LOIN	SHOUL	AVGCONF	CINDEX	PRICE
FATGR		−0.93 ± 0.01	0.18 ± 0.01	0.35 ± 0.01	0.32 ± 0.01	0.30 ± 0.01	−0.52 ± 0.01	−0.42 ± 0.01
SMY	−0.94 ± 0.01		0.05 ± 0.01	−0.16 ± 0.01	−0.08 ± 0.01	−0.03 ± 0.01	0.60 ± 0.01	0.48 ± 0.01
LEG	0.31 ± 0.05	−0.04 ± 0.06		0.33 ± 0.01	0.34 ± 0.01	0.60 ± 0.01	0.15 ± 0.01	0.13 ± 0.01
LOIN	0.60 ± 0.05	−0.40 ± 0.06	0.58 ± 0.05		0.42 ± 0.01	0.55 ± 0.01	0.03 ± 0.01	0.04 ± 0.01
SHOUL	0.51 ± 0.05	−0.24 ± 0.06	0.64 ± 0.04	0.64 ± 0.04		0.76 ± 0.01	0.06 ± 0.01	0.05 ± 0.01
AVGCONF	0.48 ± 0.05	−0.18 ± 0.06	0.84 ± 0.02	0.75 ± 0.03	0.89 ± 0.02		0.15 ± 0.01	0.13 ± 0.01
CINDEX	−0.56 ± 0.05	0.67 ± 0.04	0.09 ± 0.06	−0.06 ± 0.07	−0.02 ± 0.07	0.02 ± 0.06		0.85 ± 0.01
PRICE	−0.53 ± 0.05	0.58 ± 0.05	0.03 ± 0.07	−0.08 ± 0.07	−0.09 ± 0.07	−0.06 ± 0.07	0.93 ± 0.02	

[1] Phenotypic and genetic correlation estimates are presented above and below the diagonal, respectively, and are followed by their approximate standard error.

[2] AVGCONF = average carcass conformation score; CINDEX = carcass price grid value; FATGR = fat depth at the GR site; LEG = leg carcass conformation score; LOIN = loin carcass conformation score; PRICE = total carcass value; SHOUL = shoulder conformation score; SMY = predicted saleable meat yield.

Table 8. Phenotypic and genetic correlation estimates for carcass traits adjusted to a fixed carcass fatness endpoint[1,2]

	HCW	SMY	LEG	LOIN	SHOUL	AVGCONF	CINDEX	PRICE
HCW		0.11 ± 0.01	0.14 ± 0.01	0.10 ± 0.01	0.08 ± 0.01	0.12 ± 0.01	−0.01 ± 0.01	0.91 ± 0.01
SMY	−0.09 ± 0.07		0.62 ± 0.01	0.52 ± 0.01	0.67 ± 0.01	0.75 ± 0.01	0.36 ± 0.01	0.22 ± 0.01
LEG	−0.03 ± 0.07	0.86 ± 0.02		0.30 ± 0.01	0.32 ± 0.01	0.59 ± 0.01	0.28 ± 0.01	0.23 ± 0.01
LOIN	−0.18 ± 0.08	0.71 ± 0.04	0.54 ± 0.05		0.36 ± 0.01	0.50 ± 0.01	0.27 ± 0.01	0.18 ± 0.01
SHOUL	−0.07 ± 0.07	0.86 ± 0.02	0.61 ± 0.05	0.54 ± 0.05		0.74 ± 0.01	0.29 ± 0.01	0.17 ± 0.01
AVGCONF	−0.09 ± 0.07	0.96 ± 0.01	0.83 ± 0.03	0.68 ± 0.04	0.87 ± 0.02		0.38 ± 0.01	0.24 ± 0.01
CINDEX	−0.20 ± 0.08	0.56 ± 0.06	0.42 ± 0.06	0.55 ± 0.06	0.47 ± 0.06	0.49 ± 0.06		0.34 ± 0.01
PRICE	0.90 ± 0.02	0.03 ± 0.07	0.07 ± 0.07	−0.03 ± 0.08	0.03 ± 0.07	0.02 ± 0.07	0.21 ± 0.08	

[1] Phenotypic and genetic correlation estimates are presented above and below the diagonal, respectively, and are followed by their approximate standard error.

[2] AVGCONF = average carcass conformation score; CINDEX = carcass price grid value; HCW = hot carcass weight; LEG = leg carcass conformation score; LOIN = loin carcass conformation score; PRICE = total carcass value; SHOUL = shoulder conformation score; SMY = predicted saleable meat yield.

age (0.38 ± 0.05 versus 0.38 ± 0.05; Table 9) or fatness (0.21 ± 0.06 versus 0.18 ± 0.05; Table 11) endpoints, indicating that selection on WWT is likely adequate for HCW genetic improvement. However, Brito et al. (2017) reported a much stronger genetic correlation of 0.92 ± 0.02 between HCW and liveweight at 180 d in a New Zealand sheep population, and Australian research has indicated that WWT and PWWT are both moderately to strongly correlated with HCW, with genetic correlation estimates above 0.60 in many studies (Ingham et al., 2007; Greeff et al., 2008; Mortimer et al., 2010). Thus, it may be beneficial to examine the genetic correlation between a weight trait measured more closely to SAGE to allow for better indirect selection to improve HCW in the Canadian sheep population. With the exception of moderate negative genetic correlations between FATGR and BWT (−0.36 ± 0.06 to −0.35 ± 0.06), weak negative genetic correlations were observed between growth traits and FATGR (−0.16 ± 0.14 to −0.09 ± 0.05; Tables 9 and 10). Published genetic correlation estimates between FATGR and liveweights have varied widely. Most genetic correlation estimates between these traits have been positive when FATGR was unadjusted (Brito et al., 2017) or adjusted to a constant weight (Ingham et al., 2007; Greeff et al., 2008), although Mortimer et al. (2010) reported a moderate negative correlation when FATGR was adjusted to a constant weight. In general, conformation traits had weak negative correlations with the growth traits (−0.27 ± 0.06 to −0.08 ± 0.06; (Tables 9 to 11), indicating that selection on growth traits alone is not expected to substantially increase carcass muscularity. Overall, genetic correlations between growth and carcass traits were generally favorable, with the exception of unfavorable negative genetic correlations between growth traits and carcass conformation traits.

Ultrasound and carcass traits. Hot carcass weight and PRICE were generally found to be positively correlated with EMDUS (0.31 ± 0.22 to 0.73 ± 0.18; Tables 9 to 11), with the strongest correlations being observed when observations were adjusted to a constant age. The moderately strong positive genetic correlations between HCW and EMDUS were in agreement with published estimates (Brito et al., 2017; Mortimer et al., 2017b). Genetic correlations between FATGR and FATUS were moderate to strong at all endpoints (0.38 ± 0.14 to 0.74 ± 0.12; Tables 9 and 11) and were within the range of published estimates (Brito et al., 2017; Mortimer et al., 2017b), suggesting that FATUS is a good indicator of GR site carcass fatness. Most measures of carcass muscularity and quality (LEG, LOIN, SHOUL, AVGCONF, SMY, CINDEX) had weak to moderate genetic correlations with the ultrasound traits (Tables 9 to 11). Carcass conformation traits were generally found to be positively correlated with both EMDUS (−0.08 ± 0.19 to 0.48 ± 0.14) and FATUS (0.13 ± 0.14 to 0.55 ± 0.15) at all slaughter endpoints (Tables 9 to 11). Similarly, Einarsson et al. (2015) reported a moderate genetic correlation between EUROP carcass conformation score and EMDUS (0.53). The genetic correlations between EMDUS and the carcass conformation traits, and FATGR and FATUS, were found to be the strongest in the weight-constant ultrasound analyses (Tables 9 to 11), suggesting that ultrasound traits should continue to be

Table 9. Genetic correlations between growth traits, ultrasound traits, and carcass traits adjusted to a fixed slaughter age endpoint[1,2]

	BWT	WWT	PWWT	ADG50	ADG100
HCW	0.07 ± 0.07	0.38 ± 0.05	0.38 ± 0.05	0.37 ± 0.05	0.21 ± 0.06
FATGR	−0.36 ± 0.06	−0.09 ± 0.05	−0.11 ± 0.05	−0.09 ± 0.05	−0.09 ± 0.06
SMY	0.34 ± 0.07	0.03 ± 0.05	0.04 ± 0.05	0.05 ± 0.06	0.04 ± 0.06
LEG	−0.14 ± 0.06	−0.12 ± 0.05	−0.18 ± 0.05	−0.12 ± 0.05	−0.17 ± 0.05
LOIN	−0.26 ± 0.06	−0.19 ± 0.05	−0.19 ± 0.05	−0.18 ± 0.05	−0.15 ± 0.06
SHOUL	−0.25 ± 0.06	−0.18 ± 0.05	−0.20 ± 0.05	−0.18 ± 0.05	−0.12 ± 0.05
AVGCONF	−0.24 ± 0.06	−0.17 ± 0.05	−0.22 ± 0.05	−0.16 ± 0.05	−0.19 ± 0.05
CINDEX	0.22 ± 0.07	−0.11 ± 0.06	−0.13 ± 0.06	−0.12 ± 0.06	−0.10 ± 0.06
PRICE	0.12 ± 0.07	0.28 ± 0.05	0.27 ± 0.05	0.26 ± 0.05	0.16 ± 0.06
	WTUS	EMDUSa	EMDUSw	FATUSa	FATUSw
HCW	0.23 ± 0.16	0.71 ± 0.19	0.44 ± 0.15	0.24 ± 0.17	0.10 ± 0.17
FATGR	−0.13 ± 0.15	0.25 ± 0.19	0.36 ± 0.14	0.49 ± 0.14	0.74 ± 0.12
SMY	0.01 ± 0.17	−0.18 ± 0.21	−0.18 ± 0.16	−0.47 ± 0.15	−0.62 ± 0.14
LEG	−0.26 ± 0.13	0.17 ± 0.17	0.39 ± 0.12	0.16 ± 0.14	0.41 ± 0.13
LOIN	−0.22 ± 0.15	0.03 ± 0.19	0.22 ± 0.14	0.25 ± 0.16	0.54 ± 0.15
SHOUL	−0.16 ± 0.15	0.36 ± 0.19	0.46 ± 0.13	0.33 ± 0.16	0.55 ± 0.15
AVGCONF	−0.17 ± 0.14	0.19 ± 0.18	0.34 ± 0.12	0.31 ± 0.14	0.53 ± 0.13
CINDEX	0.00 ± 0.17	0.16 ± 0.22	0.18 ± 0.16	−0.06 ± 0.18	−0.11 ± 0.17
PRICE	0.23 ± 0.17	0.73 ± 0.18	0.54 ± 0.14	0.20 ± 0.17	0.07 ± 0.17

[1] Correlation coefficients are followed by their approximate standard error.

[2] ADG50 = pre-weaning average daily gain; ADG100 = post-weaning average daily gain; AVGCONF = average carcass conformation score; BWT = birthweight; CINDEX = carcass price grid value; EMDUS = ultrasonically measured eye muscle depth; FATGR = fat depth at the GR site; FATUS = ultrasonically measured fat depth; HCW = hot carcass weight; LEG = leg carcass conformation score; LOIN = loin carcass conformation score; PRICE = total carcass value; PWWT = post-weaning weight; SHOUL = shoulder conformation score; SMY = predicted saleable meat yield; WTUS = scanning weight; WWT = weaning weight. Ultrasound eye muscle and fat depth measurements adjusted to a constant age (EMDUSa, FATUSa) or scanning weight (EMDUSw, FATUSw).

Table 10. Genetic correlations between growth traits, ultrasound traits, and carcass traits adjusted to a fixed carcass weight endpoint[1,2]

	BWT	WWT	PWWT	ADG50	ADG100
FATGR	−0.35 ± 0.06	−0.14 ± 0.05	−0.16 ± 0.05	−0.14 ± 0.05	−0.12 ± 0.05
SMY	0.33 ± 0.06	0.08 ± 0.05	0.09 ± 0.05	0.08 ± 0.05	0.06 ± 0.06
LEG	−0.13 ± 0.06	−0.14 ± 0.05	−0.20 ± 0.05	−0.13 ± 0.05	−0.18 ± 0.05
LOIN	−0.25 ± 0.06	−0.22 ± 0.05	−0.22 ± 0.05	−0.21 ± 0.05	−0.16 ± 0.05
SHOUL	−0.27 ± 0.06	−0.25 ± 0.05	−0.27 ± 0.05	−0.25 ± 0.05	−0.17 ± 0.05
AVGCONF	−0.24 ± 0.06	−0.21 ± 0.05	−0.27 ± 0.05	−0.21 ± 0.05	−0.22 ± 0.05
CINDEX	0.24 ± 0.07	−0.05 ± 0.06	−0.07 ± 0.06	−0.06 ± 0.06	−0.06 ± 0.06
PRICE	0.13 ± 0.07	−0.13 ± 0.06	−0.13 ± 0.06	−0.12 ± 0.06	−0.07 ± 0.06
	WTUS	EMDUSa	EMDUSw	FATUSa	FATUSw
FATGR	−0.16 ± 0.14	0.05 ± 0.19	0.20 ± 0.14	0.38 ± 0.14	0.64 ± 0.12
SMY	0.06 ± 0.16	0.03 ± 0.21	−0.02 ± 0.15	−0.38 ± 0.15	−0.55 ± 0.14
LEG	−0.26 ± 0.13	0.10 ± 0.17	0.32 ± 0.12	0.14 ± 0.14	0.39 ± 0.13
LOIN	−0.24 ± 0.14	−0.08 ± 0.19	0.13 ± 0.14	0.18 ± 0.15	0.48 ± 0.15
SHOUL	−0.21 ± 0.14	0.24 ± 0.19	0.40 ± 0.13	0.25 ± 0.15	0.51 ± 0.14
AVGCONF	−0.20 ± 0.13	0.10 ± 0.17	0.28 ± 0.12	0.25 ± 0.14	0.50 ± 0.13
CINDEX	0.04 ± 0.18	0.29 ± 0.22	0.27 ± 0.16	−0.01 ± 0.18	−0.11 ± 0.17
PRICE	−0.03 ± 0.17	0.31 ± 0.22	0.32 ± 0.16	0.00 ± 0.18	0.00 ± 0.17

[1] Correlation coefficients are followed by their approximate standard error.

[2] ADG50 = pre-weaning average daily gain; ADG100 = post-weaning average daily gain; AVGCONF = average carcass conformation score; BWT = birthweight; CINDEX = carcass price grid value; EMDUS = ultrasonically measured eye muscle depth; FATGR = fat depth at the GR site; FATUS = ultrasonically measured fat depth; LEG = leg carcass conformation score; LOIN = loin carcass conformation score; PRICE = total carcass value; PWWT = post-weaning weight; SHOUL = shoulder conformation score; SMY = predicted saleable meat yield; WTUS = scanning weight; WWT = weaning weight. Ultrasound eye muscle and fat depth measurements adjusted to a constant age (EMDUSa, FATUSa) or scanning weight (EMDUSw, FATUSw).

Table 11. Genetic correlations between growth traits, ultrasound traits, and carcass traits adjusted to a fixed carcass fatness endpoint[1,2]

	BWT	WWT	PWWT	ADG50	ADG100
HCW	0.11 ± 0.07	0.21 ± 0.06	0.18 ± 0.05	0.20 ± 0.06	0.11 ± 0.06
SMY	−0.14 ± 0.07	−0.19 ± 0.05	−0.22 ± 0.05	−0.18 ± 0.05	−0.15 ± 0.06
LEG	−0.08 ± 0.06	−0.10 ± 0.05	−0.17 ± 0.05	−0.09 ± 0.05	−0.16 ± 0.05
LOIN	−0.19 ± 0.07	−0.19 ± 0.05	−0.19 ± 0.05	−0.18 ± 0.06	−0.14 ± 0.06
SHOUL	−0.22 ± 0.06	−0.23 ± 0.05	−0.24 ± 0.05	−0.22 ± 0.05	−0.15 ± 0.06
AVGCONF	−0.19 ± 0.06	−0.18 ± 0.05	−0.24 ± 0.05	−0.18 ± 0.05	−0.21 ± 0.05
CINDEX	−0.08 ± 0.07	−0.20 ± 0.06	−0.23 ± 0.06	−0.21 ± 0.06	−0.17 ± 0.06
PRICE	0.06 ± 0.07	0.09 ± 0.06	0.06 ± 0.06	0.09 ± 0.06	0.03 ± 0.06
	WTUS	EMDUSa	EMDUSw	FATUSa	FATUSw
HCW	0.13 ± 0.16	0.50 ± 0.21	0.33 ± 0.15	0.01 ± 0.17	−0.11 ± 0.16
SMY	−0.22 ± 0.14	0.20 ± 0.18	0.41 ± 0.13	0.16 ± 0.15	0.38 ± 0.15
LEG	−0.25 ± 0.14	0.17 ± 0.18	0.38 ± 0.13	0.13 ± 0.14	0.35 ± 0.14
LOIN	−0.24 ± 0.16	−0.04 ± 0.20	0.16 ± 0.15	0.15 ± 0.17	0.41 ± 0.16
SHOUL	−0.21 ± 0.15	0.35 ± 0.21	0.48 ± 0.14	0.21 ± 0.17	0.43 ± 0.16
AVGCONF	−0.19 ± 0.14	0.17 ± 0.19	0.34 ± 0.13	0.25 ± 0.15	0.46 ± 0.14
CINDEX	−0.09 ± 0.15	0.20 ± 0.19	0.30 ± 0.14	0.18 ± 0.16	0.28 ± 0.16
PRICE	0.12 ± 0.17	0.69 ± 0.19	0.56 ± 0.14	0.12 ± 0.18	0.03 ± 0.17

[1] Correlation coefficients are followed by their approximate standard error.

[2] ADG50 = pre-weaning average daily gain; ADG100 = post-weaning average daily gain; AVGCONF = average carcass conformation score; BWT = birthweight; CINDEX = carcass price grid value; EMDUS = ultrasonically measured eye muscle depth; FATUS = ultrasonically measured fat depth; HCW = hot carcass weight; LEG = leg carcass conformation score; LOIN = loin carcass conformation score; PRICE = total carcass value; PWWT = post-weaning weight; SHOUL = shoulder conformation score; SMY = predicted saleable meat yield; WTUS = scanning weight; WWT = weaning weight. Ultrasound eye muscle and fat depth measurements adjusted to a constant age (EMDUSa, FATUSa) or scanning weight (EMDUSw, FATUSw).

evaluated with observations adjusted to a constant weight in the CSGES to provide the best indication of their corresponding carcass trait measures. The results of this study reaffirm the usefulness of ultrasound measurements as indicators of carcass yield and quality in Canadian sheep breeding programs. In the future, genetic correlations should be re-estimated with a larger ultrasound trait dataset to clarify the optimal ultrasound trait endpoint to maximize indirect response in carcass quality traits.

Alternative Slaughter Endpoints

The ideal slaughter endpoint to use in genetic evaluations will depend on a producer's current breeding objective, which is in turn contingent on local production and marketing systems. Age, weight, and fatness slaughter endpoints each have their own advantages and disadvantages from a practical standpoint and further industry consultation is necessary to determine the optimal endpoint(s) for genetic evaluations. The aim of age-constant carcass trait genetic evaluations is to improve growth rate and production efficiency, but it may result in greater carcass variability, as indicated by the larger phenotypic variance observed when observations were adjusted to a constant SAGE. Nevertheless, an age endpoint may be useful for annual lambing systems where overwintering is expensive. Using weight as the endpoint in genetic evaluations would allow improvements to carcass uniformity and quality without increasing weight. However, the strong positive correlations between HCW and PRICE suggest that increasing HCW is economically advantageous under the current HLSA price grids. Marketing lambs at heavier weights was found to be common in the dataset with over 35% of carcasses having a HCW greater than the HLSA's ideal weight of 24.0 kg. Marketing animals at a constant fatness threshold aims to improve uniformity, carcass quality, and saleable meat production. However, fatness is expensive to objectively measure via ultrasound, the genetic correlation between producer-measured subjective fat scores and FATGR are unknown in the Canadian sheep population, and heritability and phenotypic variance estimates tended to be the lowest in the fat-constant analyses. Given the diverse range of production practices, it is unlikely that a single endpoint would be ideal for all Canadian sheep producers. Consequently, it may be optimal to design two alternative Terminal sire selection indexes that are optimized for SAGE and carcass weight endpoints to target extensive and intensive producers, respectively. This would increase flexibility and allow Canadian sheep producers to evaluate the current performance of their flocks in order to determine whether selection for greater production efficiency or carcass quality would be optimal.

CONCLUSIONS

The consistency and quality of Canadian lamb carcasses has been previously identified as a barrier to the expansion of the Canadian lamb industry. This study presents the first genetic parameter estimates for carcass traits in a Canadian heavy lamb population and provides the parameters necessary for their genetic evaluation. Carcass traits were found to be moderately to strongly heritable, indicating that there is considerable potential to improve carcass yield and quality through genetic selection. Alternative slaughter endpoints had little impact on carcass trait heritability estimates, but genetic correlations were sensitive to the endpoint used to derive the estimates and further industry consultation is necessary to determine the ideal slaughter endpoint(s) for genetic evaluations. Growth and ultrasound traits were generally found to be favorably correlated with carcass traits, which suggests that current genetic selection practices should have a beneficial impact on carcass yield and quality. Future research will evaluate the relative efficiency of direct and indirect carcass trait selection as well as the value of including carcass traits into new Terminal sire selection indexes for the Canadian sheep industry.

SUPPLEMENTARY DATA

Supplementary data are available at *Journal of Animal Science* online.

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