Genetic and phenotypic parameters for carcass and meat quality traits in commercial crossbred pigs[1]

Y. Miar,* G. S. Plastow,* S. S. Moore,*† G. Manafiazar,* P. Charagu,‡ R. A. Kemp,§ B. Van Haandel,‡ A. E. Huisman,# C. Y. Zhang,* R. M. McKay,‖ H. L. Bruce,* and Z. Wang*[2]

* Livestock Gentec Centre, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, T6G 2P5, Canada; †Centre for Animal Science, Queensland Alliance for Agriculture & Food Innovation, University of Queensland, St Lucia, Queensland 4072, Australia; ‡Hypor Inc., Regina, SK, S4N 6E1, Canada; §Genesus Genetics, Oakville, MB, R0H 0Y0, Canada; #Research and Technology Centre, Hendrix Genetics, P.O. Box 114, 5830 AC Boxmeer, The Netherlands; and ‖McKay GENSTAT Consultants Inc., Brandon, MB, R7B 3H2, Canada

ABSTRACT: Pork quality and carcass characteristics are now being integrated into swine breeding objectives because of their economic value. Understanding the genetic basis for these traits is necessary for this to be accomplished. The objective of this study was to estimate phenotypic and genetic parameters for carcass and meat quality traits in 2 Canadian swine populations. Data from a genomic selection study aimed at improving meat quality with a mating system involving hybrid Landrace × Large White and Duroc pigs were used to estimate heritabilities and phenotypic and genetic correlations among them. Data on 2,100 commercial crossbred pigs for meat quality and carcass traits were recorded with pedigrees compromising 9,439 animals over 15 generations. Significant fixed effects (company, sex, and slaughter batch), covariates (cold carcass weight and slaughter age), and random additive and common litter effects were fitted in the models. A series of pairwise bivariate analyses were implemented in ASReml to estimate phenotypic and genetic parameters. Heritability estimates (±SE) for carcass traits were moderate to high and ranged from 0.22 ± 0.08 for longissimus dorsi muscle area to 0.63 ± 0.04 for trimmed ham weight, except for firmness, which was low. Heritability estimates (±SE) for meat quality traits varied from 0.10 ± 0.04 to 0.39 ± 0.06 for the Minolta b* of ham quadriceps femoris muscle and shear force, respectively. Generally, most of the genetic correlations were significant ($P < 0.05$) and ranged from low (0.18 ± 0.07) to high (–0.97 ± 0.35). There were high negative genetic correlations between drip loss with pH and shear force and a positive correlation with cooking loss. Genetic correlations between carcass weight (both hot and cold) with carcass marbling were highly positive. It was concluded that selection for increasing primal and subprimal cut weights with better pork quality may be possible. Furthermore, the use of pH is confirmed as an indicator for pork water-holding capacity and cooking loss. The heritabilities of carcass and pork quality traits indicated that they can be improved using traditional breeding methods and genomic selection, respectively. The estimated genetic parameters for carcass and meat quality traits can be incorporated into the breeding programs that emphasize product quality in these Canadian swine populations.

Key words: carcass merit, crossbred, genetic parameter, meat quality, swine

J. Anim. Sci. 2014.92:2869–2884
doi:10.2527/jas2014-7685

INTRODUCTION

Meat quality and carcass yield are growing in importance for meat processors, packers, and consumers because of their high economic value. Processors are normally paid for the weight of the carcass and not for the weight of each primal cut. More recently, the pork industry is moving towards using a grading system meeting the demands of processors, packers, and consumers

---

[1] The authors acknowledge the financial support from Natural Sciences and Engineering Research Council of Canada (NSERC), Hypor Inc., and Genesus Genetics. We would like to extend thanks to the companies for providing the possibility and the facilities to collect the data. We also acknowledge the staff at University of Alberta's Meat Science Laboratory and Livestock Gentec Centre for their help. Z. Wang is grateful for support from Alberta Innovates Bio Solutions.

[2] Corresponding author: Zhiquan@ualberta.ca

Received January 31, 2014.
Accepted April 9, 2014.

based on different primal cut weights (van Wijk et al., 2005). Specific goals of breeding strategies are changed because of alterations in the price of each component of the carcass. However, assessing meat quality on a routine basis is difficult and expensive for processors.

Anecdotally, many pork producers have been particularly attentive to lean meat content as well as to marbling and quality grade to better meet consumer demands. Consequently, carcass and meat quality traits are of increasing relevance for the pig industry. This has led to the development of breeding objectives that include pork quality traits where increasing muscle tissue and decreasing fat are 2 major objectives of swine breeding programs. Meat quality traits are low to moderately heritable while carcass composition traits are highly heritable (Ciobanu et al., 2011).

Genetic improvement of meat and carcass quality in swine breeding program requires estimating the genetic and phenotypic parameters of these traits. Estimates of heritabilities for meat quality and carcass characteristics and genetic correlations between these economically important traits are limited but have received attention recently (Newcom et al., 2002; van Wijk et al., 2005). Study of genetic parameters for pork quality and carcass characteristics is required for Canadian swine populations to implement selection programs that emphasize product quality. The objectives of this study were 1) to estimate heritabilities for various carcass and pork quality traits and 2) to estimate phenotypic and genetic correlations between them in commercial crossbred pigs.

MATERIALS AND METHODS

The hogs used in this study were cared for according to the Canadian Council on Animal Care (Olfert et al., 1993) guidelines.

Animals and Management

The commercial crossbred pigs used in this study were a combination of full and half sib progeny groups representing a multigeneration family structure drawn from breeding populations (Hypor Inc., Regina, SK, Canada, and Genesus Genetics, Oakville, MB, Canada). These pigs were progeny from 139 Duroc boars bred to 429 F_1 hybrid Landrace × Large White sows. These breeds are representative of a large proportion of the Canadian pork production herd. Duroc is being increasingly used for its increased marbling and pH and darker color (redness) of the meat as a result of retailer demand for improved meat quality (Plastow et al., 2005). Pedigree information of 15 ancestral generations comprising 9,439 individuals was available.

Slaughter and Carcass Evaluation

Approximately half of the pigs were born and raised in a farm managed by Hypor in Regina, SK, Canada, and rest of them in a farm managed by Genesus Genetics in Oakville, MB, Canada. Piglets were born and raised under commercial finishing conditions with ad libitum access to a canola, wheat, barley, and soybean diet and water. Males were castrated at 3 to 5 d after birth. The pigs were grown to a final test weight of 115 kg. All pigs were shipped to a provincial abattoir near Brandon, MB, Canada, on the Wednesday of each week after they completed their test period. Average slaughter weight was 124 kg live weight, and the average age at slaughter was 160 d. Animals were shipped to the slaughter plant on a weekly basis with the Hypor slaughter groups ranging from 20 to 35 pigs and the Genesus slaughter groups ranging from 20 to 25 pigs. Pigs were housed overnight at the abattoir with *ad libitum* access to water. All animals in a batch were slaughtered the following morning and the carcass traits were collected within 24 h postmortem. Slaughter date was recorded for all animals, and this was used to assign a slaughter batch ($n = 88$).

Hot carcass weight, which was defined as the weight of the carcass including the head, leaf fat, and kidneys on the carcass, was recorded on the kill floor immediately after animals were stunned, exsanguinated, scalded, dehaired, and dressed and the carcass was split. Following an 18- to 24-h chill, the cold carcass weight (**CCW**) and the carcass length (**CLEN**) were recorded. At this point, the carcasses were broken into the primal cuts (ham, shoulder, belly, and loin). The loin was further broken into the front (anterior portion), a 3-rib sample, a 3-cm chop, a 4-rib sample, and a back (posterior portion). The 3-rib and 4-rib segments were frozen in preparation for shipping to the University of Alberta's Meat Science Laboratory (Edmonton, AB, Canada). The chop was removed at the level of the third and fourth last rib (which corresponded to the Canadian grading site) and was used to determine 1) the area of the longissimus dorsi muscle (**LEA**); 2) subcutaneous backfat depth (**FD**) and loin depth (**LD**); 3) texture score (**TEXS**) measured as a tactile rating that assessed the degree of firmness and exudation or weeping of the longissimus dorsi muscle on a subjective 5-point scale (1 = extremely soft and weeping and 5 = very firm and dry, with a score of 3 being normal) to determine if the loin was pale, soft, and exudative; and 4) subjective carcass marbling score (**CMAR**; 1 to 6, with 0 = devoid, 1 = practically devoid, 2 = trace amount of marbling, 3 = slight, 4 = small, 5 = moderate, and 6 = abundant) as determined by the National Swine Improvement Federation marbling charts (NSIF, 1997).

Primal cuts of ham, loin, shoulder, and belly were weighed and further dissected into trimmed subprimal cuts. The weights of the untrimmed ham, subdivisions of the loin (front, 3-rib sample, chop, 4-rib sample, and back), shoulder, and belly were combined to determine the untrimmed side weight (**USW**). Hams with foot attached or untrimmed (untrimmed ham weight [**UHAM**]) and untrimmed shoulders (untrimmed shoulder weight [**USH**]) were removed from the side weight. Belly (untrimmed belly weight [**UBEL**]) and loin (untrimmed loin weight [**ULOIN**]) were separated from each other and weighed. Hams were processed to a bone-in ham without fat cover and with the foot and tail bone (trimmed ham weight [**THAM**]). The commercial fat trim of the loin was obtained by a commercial trim of the front and back portions and, using that percentage to estimate the trimmed weight on the chop and the 3-rib and 4-rib samples, these were then combined with the trimmed weights of the front and back to obtain the trimmed weight of the entire loin (trimmed loin weight [**TLOIN**]). The neck bones and jowl were removed from the shoulder, and the picnic (trimmed picnic shoulder weight [**PICN**]) and butt (butt shoulder weight [**BUTT**]) were separated. The square cut bellies were trimmed (trimmed belly weight [**TBEL**]) and the ribs (ribs weight [**RIBS**]) were removed.

Meat Quality Measurements

Meat quality measurements were taken in both the slaughterhouse and University of Alberta's Meat Science Laboratory and measurements were performed on both loin and ham. At the slaughterhouse, the front or anterior portion of the loin (longissimus dorsi muscle) was used in determining Minolta color and ultimate pH (**PHU**) or 24-h pH. Loin Minolta L*, a*, and b* (**LOINL**, **LOINA**, and **LOINB**) were taken on 4 sites on the fresh cut surface of a loin chop from the boneless center cut loin using a Minolta CR 310 colorimeter set at C illuminant (Minolta, Osaka, Japan). An PHU measurement was taken in the loin muscle at 2 locations at 24 h postmortem. Meat quality measurements taken on the ham included Minolta L*, a*, and b* values on the fresh cut surface of the inside ham muscle on the gluteus medius (ham gluteus medius Minolta L* [**HGML**], ham gluteus medius Minolta a* [**HGMA**], and ham gluteus medius Minolta b* [**HGMB**]), quadriceps femoris (ham quadriceps femoris Minolta L* *[***HQFL***],* ham quadriceps femoris Minolta a* [**HQFA**], and ham quadriceps femoris Minolta b* [**HQFB**]), and iliopsoas muscles (ham iliopsoas Minolta L* [**HILL**], ham iliopsoas Minolta a* [**HILA**], and ham iliopsoas Minolta L* [**HILB**]). Drip loss (**DL**) determination at the abattoir involved weighing the 3-cm defatted and deboned loin chop and placing it on a stainless steel grid within a container for 48 h at 4°C. At the end of the 48 h, the meat samples were lightly blotted dry with a soaker pad and weighed. The difference in weight was expressed as a percentage of the initial weight to determine DL.

At 4 d postmortem, frozen 3-rib and 4-rib samples of the loin of each carcass were packed in coolers and transported by overnight courier to Meat Science Laboratory at the University of Alberta for further meat quality analyses. Before analysis, the pork loin was removed from frozen storage and allowed to thaw at 4°C for 61 h. Each thawed pork loin was removed from the vacuum package bag and was weighed and recorded as whole loin weight (**WLW**), defined as the weight of 3-rib and 4-rib samples of the loin received at University of Alberta containing meat, fat, and bone. The thick backfat was taken from the loin and was weighed and recorded as backfat weight (**BFW**). Then, rib eye was removed from the loin and its weight was recorded as rib eye weight (**REAW**), and it was used for the meat quality assays. A 3-cm chop was removed from the tail end of the loin section and refrigerated at 4°C for 1 h. Rib eye area Minolta L*, a*, and b* (**REAL**, **REAA**, and **REAB**) values were taken on 3 sites of the chop using a commercial color meter (CR400; Konica-Minolta, Osaka, Japan) on a D 65 light setting that mimics daylight. To measure cooking loss (**CL**), a 200-g roast was cooked in a 71°C water bath and weighed before and after cooking and CL was recorded as the percentage of weight change divided by the initial weight multiplied by 100. Shear force (**SHF**) was the mean of six 1-cm^2 cores cut from the roast that had been cooked and then refrigerated overnight at 4°C. The remainder of the pork loin section was physically dissected into muscle and fat, recorded as rib trim weight (**RTW**), and bone, recorded as bone weight (**BOW**).

Statistical and Genetic Analyses

There were 2,100 pigs with meat quality and carcass data. The significance of the fixed effects and covariates were determined for each trait using the GLM procedure of SAS (SAS Inst., Inc., Cary, NC), and different significant ($P < 0.1$) fixed factors for each trait were remained in the subsequent mixed model analyses. Likelihood ratio test was used to determine the significance of different random terms in the mixed model analysis using ASReml 3.0 (Gilmour et al., 2009). By comparing twice the difference in logarithmic likelihoods between the full and reduced models with χ^2 having degrees of freedom equal to the number of parameters tested, it was confirmed that the effects of common litter were not significant ($P > 0.05$) for meat quality and carcass traits, except for HCW, CCW, LEA, PHU, and DL. Maternal genetic effects were tested in a similar manner and were shown to be not significant ($P > 0.05$).

Genetic and phenotypic (co)variances were estimated for commercial crossbred populations using a pairwise bivariate animal model using ASReml 3.0 software (Gilmour et al., 2009). The animal model included random additive polygenic effects in the final model for all traits and random litter effect for some traits. Birth weight, WLW received at Meat Science Laboratory, CCW, and slaughter age were included in the model as linear covariates. Company, sex, and slaughter batch were included in the model as fixed effects. The model is given by

$$\begin{bmatrix}\mathbf{y}_1\\ \mathbf{y}_2\end{bmatrix}=\begin{bmatrix}\mathbf{X}_1 & 0\\ 0 & \mathbf{X}_2\end{bmatrix}\begin{bmatrix}\mathbf{b}_1\\ \mathbf{b}_2\end{bmatrix}+\begin{bmatrix}\mathbf{Z}_1 & 0\\ 0 & \mathbf{Z}_2\end{bmatrix}\begin{bmatrix}\mathbf{a}_1\\ \mathbf{a}_2\end{bmatrix}+\begin{bmatrix}\mathbf{Z}_3 & 0\\ 0 & \mathbf{Z}_4\end{bmatrix}\begin{bmatrix}\mathbf{c}_1\\ \mathbf{c}_2\end{bmatrix}+\begin{bmatrix}\mathbf{e}_1\\ \mathbf{e}_2\end{bmatrix}$$

in which $\mathbf{y}_1$ and $\mathbf{y}_2$ are the vectors of phenotypic measurements for traits 1 and 2, respectively; $\mathbf{X}_1$ and $\mathbf{X}_2$ are the incidence matrices relating the fixed effects to vectors $\mathbf{y}_1$ and $\mathbf{y}_2$, respectively; $\mathbf{b}_1$ and $\mathbf{b}_2$ are the vectors of fixed effects for traits 1 and 2, respectively; $\mathbf{Z}_1$ and $\mathbf{Z}_2$ are the incidence matrices relating the phenotypic observations to the vector of polygenic (**a**) effects for traits 1 and 2, respectively; $\mathbf{Z}_3$ and $\mathbf{Z}_4$ are the incidence matrices relating the phenotypic observations to the vector of common litter (**c**) effects for traits 1 and 2, respectively; and $\mathbf{e}_1$ and $\mathbf{e}_2$ are the vectors of random residuals for the traits 1 and 2, respectively.

It was assumed that random effects were independent. In particular, the variances were assumed to be $V(a)=\mathbf{A}\sigma_a^2$, $V(c)=\mathbf{I}\sigma_c^2$, and $V(e)=\mathbf{I}\sigma_e^2$, in which $\mathbf{A}$ is the numerator relationship matrix, $\mathbf{I}$ is the identity matrix, σ_a^2 is a direct additive genetic variance, σ_c^2 is a common litter effect variance, and σ_e^2 is a residual variance. Heritability was estimated using variance components obtained from the bivariate analyses, and the average estimates of corresponding pairwise bivariate analyses were reported as the heritabilities:

$$h^2=\sigma_a^2/\left(\sigma_a^2+\sigma_e^2\right).$$

A preliminary univariate animal model for each trait was performed to obtain initial values of variance parameters that were then used in subsequent bivariate analyses. The initial values of covariance parameters between traits were obtained by multiplying their standard deviations by their phenotypic or genetic correlations. Pairwise bivariate analyses were performed separately for carcass and meat quality traits. The 2-trait animal model used to estimate (co)variance components, phenotypic and genetic correlations as well as the heritabilities was implemented in ASReml 3.0 (Gilmour et al., 2009).

RESULTS AND DISCUSSION

Means and Standard Deviations

Most of the traits were recorded on all individuals within group. Means, standard deviations, number of measurements per trait, and minimum and maximum for each carcass and meat quality trait are given in Table 1. There are a total of 19 carcass and 24 meat quality traits analyzed in this study. Most of the carcass traits had 2,084 observations except for TBEL with 1,663 and HCW and CCW with 2,086 observations. Most of the meat quality traits had 2,067 to 2,084 observations except for DL with 1,418 observations available for the analysis (Table 1). Furthermore, relevant fixed and random effects fitted in the mixed model analysis for carcass and meat quality traits are presented in Table 2.

Heritability Estimates

Heritability estimates with their standard errors are presented in Tables 3 and 4 (diagonal elements). Several factors influence the heritability estimates, which may include the end-point adjustment such as age or weight adjustment, sampling, population size, effect of heterosis on crossbred populations, and the completeness of pedigree (Miar et al., 2014). Although a total of 43 heritabilities for carcass (*n* = 19) and meat quality (*n* = 24) traits were presented in Tables 3 and 4 for completeness, we will mainly focus here on those new and rarely reported traits. Heritabilities for some traits reported extensively elsewhere will not be discussed unless it is useful to compare them with the present study.

Heritability estimates (±SE) for carcass traits were moderate to high except for firmness that was low, and ranged from 0.22 ± 0.08 for LEA to 0.63 ± 0.04 and 0.63 ± 0.06 for THAM and ULOIN, respectively. Carcass traits generally have been reported as moderate to high heritable traits in previous studies. Primal and subprimal cuts weights were more heritable (0.51 on average) than subjective marbling score (0.23 ± 0.05). Heritability estimates for UBEL (0.49 ± 0.06) and TBEL (0.53 ± 0.06) were nearly identical. Heritability estimate for ULOIN was more heritable (0.63 ± 0.06) than TLOIN (0.52 ± 0.07). This was different for the UHAM, which was less heritable (0.46 ± 0.06) compared to THAM (0.63 ± 0.04). The heritability estimates obtained for carcass traits are among the highest heritabilities estimated in this study. The high values of heritability for the carcass traits would indicate the significant potential for improving carcass merit traits in commercial crossbred pigs.

The heritability estimates for HCW and CCW were 0.28 ± 0.08, and 0.29 ± 0.08, respectively. Zumbach et al. (2008) reported low to moderate heritability of 0.14 and 0.28 for carcass weight in environments without and with heat stress, respectively, and this is the only literature available at the present. The moderate heritabilities for HCW and CCW indicate that genetic improvement for these traits is achievable through selection. Heritability estimates for basic carcass yield component traits were 0.31 ± 0.06, 0.41 ± 0.06, and 0.51 ± 0.07 for FD, LD, and CLEN, respectively. Backfat depth is the most studied trait among all carcass merit traits as it is related to overall carcass yield (Marcoux

Table 1. The descriptive statistics for carcass and meat quality traits: abbreviations, number of animals per trait (*n*), means, SD, minimum (Min.), and maximum (Max.) values

Trait	Abbreviation	*n*	Mean	SD	Min.	Max.
Carcass trait						
Hot carcass weight, kg	HCW	2,086	93.12	9.13	64.60	130.00
Cold carcass weight, kg	CCW	2,086	80.58	8.02	55.50	115.30
Backfat depth, mm	FD	2,084	14.42	4.00	6.00	32.00
Loin depth, mm	LD	2,084	68.46	5.50	52.00	88.00
Carcass length, cm	CLEN	2,084	83.43	2.78	52.30	92.40
Longissimus dorsi muscle area, cm^2	LEA	2,084	53.20	5.91	35.00	74.50
Texture score	TEXS	2,084	3.02	0.37	1.00	4.00
Carcass marbling score	CMAR	2,084	2.91	1.03	1.00	6.00
Untrimmed side weight, kg	USW	2,084	39.85	3.98	27.25	57.01
Untrimmed ham weight, kg	UHAM	2,084	11.04	0.97	8.41	15.09
Untrimmed loin weight, kg	ULOIN	2,084	14.56	5.07	7.12	29.37
Untrimmed shoulder weight, kg	USH	2,084	9.49	1.82	5.23	15.98
Untrimmed belly weight, kg	UBEL	2,084	8.29	1.38	4.39	12.71
Trimmed ham weight, kg	THAM	2,084	8.29	1.38	4.39	12.71
Trimmed loin weight, kg	TLOIN	2,084	7.53	3.70	1.52	13.51
Trimmed belly weight, kg	TBEL	1,663	11.33	2.92	6.24	18.76
Trimmed picnic shoulder weight, kg	PICN	2,084	7.02	2.53	1.76	14.40
Butt shoulder weight, kg	BUTT	2,084	4.30	0.51	2.77	6.53
Ribs weight, kg	RIBS	2,084	3.04	1.10	1.05	5.84
Meat quality trait						
Whole loin weight,[1] kg	WLW	2,067	1.53	0.24	0.15	2.61
Rib eye weight,[1] kg	REAW	2,077	0.60	0.10	0.25	0.99
Backfat weight,[1] kg	BFW	2,074	0.35	0.11	0.04	1.41
Rib trim weight,[1] kg	RTW	2,071	0.35	0.07	0.17	0.87
Bone weight,[1] kg	BOW	2,077	0.17	0.03	0.08	0.36
Cooking loss,[1] %	CL	2,073	26.69	3.26	11.65	53.74
Rib eye area Minolta L*[1]	REAL	2,075	44.45	2.84	30.55	56.85
Rib eye area Minolta a*[1]	REAA	2,075	7.81	1.21	3.39	11.94
Rib eye area Minolta b*[1]	REAB	2,075	2.81	1.21	–1.54	7.48
Shear force, N[1]	SHF	2,074	49.02	1.29	21.62	118.00
Loin Minolta L*	LOINL	2,084	48.42	2.84	39.83	60.50
Loin Minolta a*	LOINA	2,084	6.18	1.60	2.00	12.43
Loin Minolta b*	LOINB	2,084	15.07	2.03	9.10	22.35
Ultimate pH	PHU	2,084	5.73	0.18	5.28	6.36
Ham gluteus medius Minolta L*	HGML	2,084	45.35	2.40	37.80	54.20
Ham gluteus medius Minolta a*	HGMA	2,084	6.75	1.24	2.40	10.90
Ham gluteus medius Minolta b*	HGMB	2,084	13.78	1.20	9.60	17.70
Ham quadriceps femoris Minolta L*	HQFL	2,084	50.06	3.38	36.30	62.30
Ham quadriceps femoris Minolta a*	HQFA	2,084	4.69	1.59	0	17.70
Ham quadriceps femoris Minolta b*	HQFB	2,084	13.91	1.60	9.20	19.50
Ham iliopsoas Minolta L*	HILL	2,084	42.79	2.80	32.60	54.90
Ham iliopsoas Minolta a*	HILA	2,084	19.72	1.80	12.00	25.80
Ham iliopsoas Minolta b*	HILB	2,084	16.99	1.70	11.30	22.20
Drip loss, %	DL	1,418	1.49	0.19	0.72	2.14

[1] All information is from the rib eye muscle received at the University of Alberta's Meat Science Laboratory (Edmonton, AB, Canada).

et al., 2007). For FD, the estimate in this study (0.31 ± 0.06) was lower than the average heritability (0.43) of many previous studies reported by Ciobanu et al. (2011). Heritability estimate of LD in the present study (0.41 ± 0.06) was close to the average (0.47) of many previous studies reported by Stewart and Schinckel (1991). For CLEN, the estimate of heritability in this study (0.51 ± 0.07) was in agreement with the average (0.56 and 0.57) of all studies reviewed by Stewart and Schinckel (1991) and Ducos (1994), respectively. These moderate to high heritabilities would be expected because pig breeders have known that these carcass traits are easy to change by selection.

Table 2. Significance of the fixed and random effects included in the models for the analysis of carcass and meat quality traits

	Fixed effects						Random effects		
Trait	Company	Sex	Batch	Age	WLW[1]	CCW[2]	Dam	Litter	Animal
Carcass traits									
Hot carcass weight	**	**	**	**	–	–	NS[3]	**	✓
Cold carcass weight	**	**	**	**	–	–	NS	**	✓
Backfat depth	NS	**	*	NS	–	–	NS	NS	✓
Loin depth	**	**	**	NS	–	–	NS	NS	✓
Carcass length	**	**	**	**	–	–	NS	NS	✓
Longissimus dorsi muscle area	**	**	**	**	–	–	NS	**	✓
Texture score	**	NS	**	–	–	–	NS	NS	✓
Carcass marbling score	NS	**	**	–	–	–	NS	NS	✓
Untrimmed side weight	**	**	**	**	–	–	NS	NS	✓
Untrimmed ham weight	**	NS	**	**	–	–	NS	NS	✓
Untrimmed loin weight	**	**	**	**	–	–	NS	NS	✓
Untrimmed shoulder weight	**	**	**	**	–	–	NS	NS	✓
Untrimmed belly weight	**	**	**	**	–	–	NS	NS	✓
Trimmed ham weight	**	NS	**	**	–	–	NS	NS	✓
Trimmed loin weight	**	NS	**	**	–	–	NS	NS	✓
Trimmed belly weight	**	**	**	**	–	–	NS	NS	✓
Trimmed picnic shoulder weight	**	**	**	**	–	–	NS	NS	✓
Butt shoulder weight	**	**	**	**	–	–	NS	NS	✓
Ribs weight	*	*	**	**	–	–	NS	NS	✓
Meat quality traits									
Whole loin weight	**	**	**	–	–	**	NS	NS	✓
Rib eye weight	NS	**	**	–	**	–	NS	NS	✓
Backfat weight	**	**	**	–	**	–	NS	NS	✓
Rib trim weight	**	**	**	–	**	–	NS	NS	✓
Bone weight	**	**	**	–	**	–	NS	NS	✓
Cooking loss	**	**	**	–	–	–	NS	NS	✓
Minolta L* rib eye area	*	**	**	–	–	–	NS	NS	✓
Minolta a* rib eye area	**	**	**	–	–	–	NS	NS	✓
Minolta b* rib eye area	**	**	**	–	–	–	NS	NS	✓
Shear force	NS	**	**	–	–	–	NS	NS	✓
Minolta L* loin	NS	*	**	–	–	–	NS	NS	✓
Minolta a* loin	*	**	**	–	–	–	NS	NS	✓
Minolta b* loin	**	**	**	–	–	–	NS	NS	✓
pH ultimate	**	NS	**	–	–	–	NS	**	✓
Minolta L* ham *gluteus medius*	NS	NS	**	–	–	–	NS	NS	✓
Minolta a* ham *gluteus medius*	NS	**	**	–	–	–	NS	NS	✓
Minolta b* ham *gluteus medius*	**	**	**	–	–	–	NS	NS	✓
Minolta L* ham *quadriceps femoris*	**	NS	**	–	–	–	NS	NS	✓
Minolta a* ham *quadriceps femoris*	**	NS	**	–	–	–	NS	NS	✓
Minolta b* ham *quadriceps femoris*	**	NS	**	–	–	–	NS	NS	✓
Minolta L* ham *iliopsoas*	**	**	**	–	–	–	NS	NS	✓
Minolta a* ham *iliopsoas*	**	NS	**	–	–	–	NS	NS	✓
Minolta b* ham *iliopsoas*	**	**	**	–	–	–	NS	NS	✓
Drip loss	**	NS	**	–	–	–	NS	**	✓

[1] WLW = whole loin weight (received at the University of Alberta [Edmonton, AB, Canada]).

[2] CCW = cold carcass weight.

[3] NS = nonsignificant.

$^{**}P < 0.05$; $^{*}P < 0.1$.

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

Trait[1]	HCW	CCW	FD	LD	CLEN	LEA	TEXS	CMAR	USW
HCW	**0.28 ± 0.08**[2]	**0.32 ± 0.02**	**0.50 ± 0.04**	**0.37 ± 0.04**	**0.63 ± 0.02**	**0.30 ± 0.02**	**0.38 ± 0.05**	**0.44 ± 0.04**	**0.98 ± 0.00**
CCW	**0.64 ± 0.22**	**0.29 ± 0.08**	**0.47 ± 0.04**	**0.39 ± 0.04**	**0.59 ± 0.02**	**0.32 ± 0.02**	**0.37 ± 0.05**	**0.44 ± 0.05**	**0.99 ± 0.00**
FD	**0.39 ± 0.15**	**0.35 ± 0.16**	**0.31 ± 0.06**	**–0.37 ± 0.02**	0.01 ± 0.03	**–0.38 ± 0.02**	**–0.14 ± 0.02**	**0.33 ± 0.02**	**0.33 ± 0.03**
LD	**0.77 ± 0.24**	**0.78 ± 0.21**	**–0.34 ± 0.12**	**0.41 ± 0.06**	**0.11 ± 0.03**	**0.70 ± 0.01**	–0.04 ± 0.03	**–0.22 ± 0.03**	**0.22 ± 0.03**
CLEN	**0.89 ± 0.06**	**0.77 ± 0.15**	0.19 ± 0.12	0.14 ± 0.11	**0.51 ± 0.07**	**0.35 ± 0.05**	–0.01 ± 0.03	–0.00 ± 0.03	**0.61 ± 0.02**
LEA	**0.70 ± 0.26**	**0.63 ± 0.26**	–0.24 ± 0.13	**0.78 ± 0.05**	**0.47 ± 0.14**	**0.22 ± 0.08**	**0.30 ± 0.06**	0.13 ± 0.08	**0.43 ± 0.04**
TEXS	**–0.61 ± 0.27**	**–0.63 ± 0.26**	0.15 ± 0.23	**–0.40 ± 0.20**	–0.09 ± 0.19	**–0.56 ± 0.28**	**0.09 ± 0.04**	**–0.11 ± 0.02**	**–0.18 ± 0.03**
CMAR	**0.63 ± 0.22**	**0.59 ± 0.21**	**0.33 ± 0.14**	0.01 ± 0.15	0.03 ± 0.14	0.05 ± 0.20	0.04 ± 0.24	**0.23 ± 0.05**	**0.16 ± 0.03**
USW	**0.99 ± 0.00**	**0.99 ± 0.00**	**0.28 ± 0.11**	**0.37 ± 0.10**	**0.80 ± 0.05**	**0.72 ± 0.12**	**–0.48 ± 0.18**	**0.35 ± 0.13**	**0.55 ± 0.06**
UHAM	**0.99 ± 0.02**	**0.99 ± 0.01**	0.07 ± 0.13	**0.49 ± 0.09**	**0.71 ± 0.06**	**0.75 ± 0.12**	**–0.56 ± 0.17**	0.22 ± 0.14	**0.93 ± 0.02**
ULOIN	**0.70 ± 0.07**	**0.73 ± 0.07**	0.16 ± 0.19	**0.53 ± 0.16**	**0.56 ± 0.09**	**0.66 ± 0.13**	–0.32 ± 0.27	0.02 ± 0.14	**0.62 ± 0.04**
USH	**0.99 ± 0.01**	**0.98 ± 0.02**	**0.28 ± 0.11**	**0.29 ± 0.10**	**0.69 ± 0.06**	**0.57 ± 0.13**	**–0.47 ± 0.17**	**0.42 ± 0.12**	**0.90 ± 0.02**
UBEL	**0.96 ± 0.0**	**0.96 ± 0.03**	**0.30 ± 0.11**	0.17 ± 0.11	**0.69 ± 0.06**	**0.50 ± 0.17**	–0.25 ± 0.19	0.19 ± 0.13	**0.78 ± 0.04**
THAM	**0.92 ± 0.12**	**0.91 ± 0.11**	0.10 ± 0.09	**0.24 ± 0.09**	**0.31 ± 0.07**	**0.42 ± 0.13**	**–0.38 ± 0.17**	**0.29 ± 0.11**	**0.52 ± 0.06**
TLOIN	**0.88 ± 0.08**	**0.88 ± 0.08**	0.00 ± 0.13	**0.44 ± 0.10**	**0.56 ± 0.08**	**0.79 ± 0.12**	–0.28 ± 0.19	–0.06 ± 0.14	**0.57 ± 0.06**
TBEL	**0.42 ± 0.17**	**0.41 ± 0.17**	0.15 ± 0.11	–0.10 ± 0.11	0.12 ± 0.10	–0.01 ± 0.16	–0.13 ± 0.19	0.11 ± 0.13	**0.22 ± 0.09**
PICN	**0.70 ± 0.16**	**0.70 ± 0.16**	0.02 ± 0.12	0.06 ± 0.11	0.17 ± 0.10	0.27 ± 0.16	–0.23 ± 0.19	0.18 ± 0.13	**0.39 ± 0.09**
BUTT	**0.78 ± 0.13**	**0.82 ± 0.13**	–0.15 ± 0.14	**0.31 ± 0.12**	**0.36 ± 0.11**	**0.69 ± 0.16**	**–0.61 ± 0.21**	0.22 ± 0.15	**0.60 ± 0.08**
RIBS	**0.71 ± 0.13**	0.17 ± 0.38	–0.23 ± 0.16	0.27 ± 0.15	**0.52 ± 0.11**	**0.56 ± 0.19**	**–0.49 ± 0.23**	0.15 ± 0.17	**0.61 ± 0.09**

Trait	UHAM	ULOIN	USH	UBEL	THAM	TLOIN	TBEL	PICN	BUTT	RIBS
HCW	**0.63 ± 0.02**	**0.67 ± 0.01**	**0.63 ± 0.01**	**0.58 ± 0.01**	**0.56 ± 0.02**	**0.60 ± 0.01**	**0.46 ± 0.04**	**0.45 ± 0.04**	**0.40 ± 0.04**	**0.35 ± 0.05**
CCW	**0.67 ± 0.02**	**0.70 ± 0.01**	**0.66 ± 0.02**	**0.61 ± 0.01**	**0.58 ± 0.02**	**0.63 ± 0.01**	**0.47 ± 0.04**	**0.46 ± 0.04**	**0.41 ± 0.04**	**0.43 ± 0.03**
FD	**0.12 ± 0.03**	**0.38 ± 0.05**	**0.32 ± 0.03**	**0.31 ± 0.03**	**0.09 ± 0.03**	0.03 ± 0.03	**0.14 ± 0.03**	0.03 ± 0.03	–0.01 ± 0.03	0.01 ± 0.03
LD	**0.32 ± 0.03**	**0.41 ± 0.05**	**0.11 ± 0.03**	**0.12 ± 0.03**	**0.22 ± 0.03**	**0.35 ± 0.03**	0.01 ± 0.03	**0.13 ± 0.03**	**0.19 ± 0.03**	**0.17 ± 0.03**
CLEN	**0.52 ± 0.02**	**0.53 ± 0.04**	**0.50 ± 0.02**	**0.51 ± 0.02**	**0.36 ± 0.03**	**0.52 ± 0.03**	**0.16 ± 0.03**	**0.24 ± 0.03**	**0.29 ± 0.03**	**0.39 ± 0.03**
LEA	**0.46 ± 0.03**	**0.45 ± 0.04**	**0.35 ± 0.05**	**0.39 ± 0.05**	**0.40 ± 0.04**	**0.51 ± 0.03**	**0.31 ± 0.06**	**0.35 ± 0.05**	**0.35 ± 0.04**	**0.33 ± 0.05**
TEXS	**–0.13 ± 0.03**	**–0.17 ± 0.03**	**–0.14 ± 0.03**	**–0.15 ± 0.03**	**–0.07 ± 0.03**	**–0.15 ± 0.03**	**–0.07 ± 0.02**	**–0.07 ± 0.02**	**–0.07 ± 0.02**	**–0.11 ± 0.03**
CMAR	0.04 ± 0.03	**0.08 ± 0.04**	**0.22 ± 0.03**	**0.12 ± 0.03**	**0.07 ± 0.03**	–0.04 ± 0.03	**0.06 ± 0.02**	0.02 ± 0.02	0.03 ± 0.02	**0.08 ± 0.03**
USW	**0.88 ± 0.01**	**0.75 ± 0.01**	**0.86 ± 0.01**	**0.83 ± 0.01**	**0.62 ± 0.02**	**0.70 ± 0.02**	**0.29 ± 0.03**	**0.42 ± 0.03**	**0.47 ± 0.02**	**0.48 ± 0.03**
UHAM	**0.46 ± 0.06**	**0.66 ± 0.03**	**0.70 ± 0.02**	**0.74 ± 0.01**	**0.70 ± 0.01**	**0.63 ± 0.02**	**0.24 ± 0.03**	**0.39 ± 0.03**	**0.43 ± 0.02**	**0.43 ± 0.03**
ULOIN	**0.77 ± 0.12**	**0.63 ± 0.06**	**0.44 ± 0.03**	**0.74 ± 0.01**	**0.07 ± 0.02**	**0.91 ± 0.01**	**0.13 ± 0.03**	**0.22 ± 0.03**	**0.26 ± 0.03**	**0.42 ± 0.03**
USH	**0.83 ± 0.04**	0.15 ± 0.11	**0.55 ± 0.06**	**0.56 ± 0.02**	**0.60 ± 0.02**	**0.36 ± 0.03**	**0.21 ± 0.03**	**0.42 ± 0.03**	**0.49 ± 0.02**	**0.39 ± 0.03**
UBEL	**0.71 ± 0.05**	**0.83 ± 0.03**	**0.44 ± 0.08**	**0.49 ± 0.06**	**0.29 ± 0.03**	**0.72 ± 0.02**	**0.33 ± 0.03**	**0.33 ± 0.03**	**0.36 ± 0.03**	**0.47 ± 0.03**
THAM	**0.59 ± 0.05**	**–0.26 ± 0.08**	**0.57 ± 0.04**	0.02 ± 0.08	**0.63 ± 0.04**	**0.21 ± 0.03**	**0.21 ± 0.03**	**0.31 ± 0.03**	**0.34 ± 0.03**	**0.32 ± 0.04**
TLOIN	**0.53 ± 0.08**	**0.96 ± 0.01**	0.15 ± 0.10	**0.87 ± 0.03**	**0.18 ± 0.07**	**0.52 ± 0.07**	**0.09 ± 0.03**	**0.21 ± 0.03**	**0.28 ± 0.03**	**0.44 ± 0.03**
TBEL	**0.21 ± 0.10**	–0.02 ± 0.09	**0.18 ± 0.09**	**0.21 ± 0.09**	**0.18 ± 0.07**	–0.06 ± 0.10	**0.53 ± 0.06**	**0.67 ± 0.02**	**0.40 ± 0.02**	**0.50 ± 0.03**
PICN	**0.38 ± 0.09**	0.15 ± 0.10	**0.36 ± 0.09**	**0.28 ± 0.10**	**0.21 ± 0.06**	0.09 ± 0.10	**0.91 ± 0.07**	**0.44 ± 0.06**	**0.49 ± 0.02**	**0.51 ± 0.03**
BUTT	**0.66 ± 0.08**	**0.33 ± 0.10**	**0.47 ± 0.09**	**0.48 ± 0.10**	**0.28 ± 0.09**	**0.42 ± 0.11**	**0.63 ± 0.08**	**0.75 ± 0.06**	**0.29 ± 0.05**	**0.42 ± 0.02**
RIBS	**0.61 ± 0.10**	**0.43 ± 0.11**	**0.49 ± 0.11**	**0.56 ± 0.10**	**0.32 ± 0.11**	**0.58 ± 0.12**	**0.82 ± 0.06**	**0.75 ± 0.07**	**0.80 ± 0.08**	**0.32 ± 0.06**

[1] CCW = cold carcass weight; FD = backfat depth; LD = loin depth; CLEN = carcass length; LEA = area of the *longissimus dorsi* muscle; TEXS = texture score; CMAR = carcass marbling score; USW = untrimmed side weight; UHAM = untrimmed ham weight; ULOIN = untrimmed loin weight; USH = untrimmed shoulder weight; UBEL = untrimmed belly weight; THAM = trimmed ham weight; TLOIN = trimmed loin weight; TBEL = trimmed belly weight; PICN = trimmed picnic shoulder weight; BUTT = butt shoulder weight; RIBS = ribs weight.

[2] The significant correlations are highlighted in bold ($P < 0.05$).

For LEA, the heritability estimate in the present study (0.22 ± 0.08) was lower than estimates by Suzuki et al. (2005) for ultrasound measurements of LEA in Duroc (0.41) and average estimate (0.47) of previous studies by Stewart and Schinckel (1991). The differences with previous studies may be due to using carcass measurement in the current study compared to ultrasound measurements in the previous studies. In addition to differences in measurement techniques, sample size and statistical models used for (co)variance estimation were also different from previous studies. Marbling is an estimate of intramuscular fat, which has been associated with increased sensory acceptance in cooked pork (Brewer et al., 2001). The moderate heritability of CMAR in this study (0.23 ± 0.05) suggested that genetic improvement of marbling might be possible. Intramuscular fat content can also influence sensory quality. Generally, as intramuscular fat content increases, the sensory chewiness

Table 4. Estimates of genetic (below diagonal) and phenotypic (above diagonal) correlations, heritabilities (diagonal), and their standard error of estimates among meat quality traits

Trait[1]	WLW	REAW	BFW	RTW	BOW	CL	REAL	REAA
WLW	**0.28 ± 0.08**[2]	**–0.14 ± 0.03**	**–0.24 ± 0.03**	**0.12 ± 0.03**	**0.17 ± 0.03**	**0.10 ± 0.03**	–0.03 ± 0.03	**0.04 ± 0.02**
REAW	0.16 ± 0.16	**0.31 ± 0.06**	**–0.46 ± 0.02**	**0.09 ± 0.03**	–0.02 ± 0.03	**0.12 ± 0.03**	**–0.10 ± 0.02**	**0.23 ± 0.08**
BFW	–0.19 ± 0.14	**–0.88 ± 0.07**	**0.38 ± 0.06**	**–0.27 ± 0.03**	**–0.22 ± 0.03**	**–0.15 ± 0.03**	**0.06 ± 0.03**	**0.29 ± 0.07**
RTW	0.17 ± 0.18	0.29 ± 0.17	**–0.69 ± 0.12**	**0.22 ± 0.06**	**0.16 ± 0.03**	**0.07 ± 0.03**	**–0.04 ± 0.02**	**0.26 ± 0.08**
BOW	0.23 ± 0.20	0.17 ± 0.21	**–0.48 ± 0.18**	**0.97 ± 0.21**	**0.12 ± 0.05**	0.03 ± 0.03	–0.03 ± 0.03	**0.27 ± 0.07**
CL	–0.02 ± 0.18	**0.49 ± 0.15**	**–0.43 ± 0.15**	**0.41 ± 0.19**	0.16 ± 0.24	**0.20 ± 0.05**	**0.13 ± 0.03**	–0.00 ± 0.03
REAL	–0.01 ± 0.16	0.09 ± 0.16	0.12 ± 0.14	0.08 ± 0.18	–0.37 ± 0.20	0.10 ± 0.18	**0.28 ± 0.06**	**–0.19 ± 0.03**
REAA	–0.11 ± 0.14	–0.27 ± 0.16	0.07 ± 0.16	–0.26 ± 0.19	0.24 ± 0.23	–0.14 ± 0.19	**–0.36 ± 0.16**	**0.26 ± 0.09**
REAB	–0.02 ± 0.16	–0.01 ± 0.15	0.14 ± 0.14	–0.10 ± 0.17	–0.15 ± 0.21	–0.03 ± 0.18	**0.60 ± 0.10**	**0.59 ± 0.16**
SHF	0.11 ± 0.15	0.00 ± 0.15	0.38 ± 0.35	0.09 ± 0.17	0.12 ± 0.20	**0.58 ± 0.13**	**–0.33 ± 0.14**	–0.15 ± 0.16
LOINL	0.13 ± 0.16	0.15 ± 0.16	–0.13 ± 0.15	0.20 ± 0.18	–0.03 ± 0.22	0.27 ± 0.18	0.20 ± 0.16	–0.21 ± 0.17
LOINA	–0.08 ± 0.15	–0.16 ± 0.15	–0.14 ± 0.14	0.28 ± 0.16	0.14 ± 0.21	0.14 ± 0.53	**–0.30 ± 0.15**	**0.76 ± 0.16**
LOINB	0.25 ± 0.18	0.07 ± 0.18	–0.16 ± 0.17	0.34 ± 0.20	–0.02 ± 0.26	**0.38 ± 0.19**	–0.10 ± 0.18	0.32 ± 0.19
PHU	–0.15 ± 0.22	–0.38 ± 0.23	0.04 ± 0.21	0.14 ± 0.24	0.50 ± 0.27	**–0.62 ± 0.26**	–0.02 ± 0.21	0.33 ± 0.31
HGML	–0.16 ± 0.18	**0.35 ± 0.17**	–0.28 ± 0.16	**0.40 ± 0.19**	0.04 ± 0.24	0.32 ± 0.20	**0.35 ± 0.17**	–0.29 ± 0.18
HGMA	–0.24 ± 0.14	0.05 ± 0.14	0.06 ± 0.13	–0.17 ± 0.17	–0.02 ± 0.20	0.14 ± 0.17	–0.19 ± 0.14	**0.43 ± 0.16**
HGMB	–0.21 ± 0.21	**0.40 ± 0.20**	–0.14 ± 0.20	0.29 ± 0.23	–0.03 ± 0.28	**0.46 ± 0.22**	0.23 ± 0.21	0.13 ± 0.23
HQFL	–0.21 ± 0.18	0.28 ± 0.17	–0.03 ± 0.17	0.09 ± 0.20	0.10 ± 0.24	**0.38 ± 0.19**	**0.40 ± 0.17**	–0.28 ± 0.20
HQFA	–0.08 ± 0.16	–0.21 ± 0.16	0.13 ± 0.15	–0.24 ± 0.18	0.18 ± 0.22	–0.05 ± 0.18	**–0.40 ± 0.15**	**0.69 ± 0.18**
HQFB	–0.14 ± 0.23	0.10 ± 0.23	0.13 ± 0.21	0.01 ± 0.26	0.38 ± 0.29	0.43 ± 0.25	0.04 ± 0.23	0.19 ± 0.23
HILL	–0.01 ± 0.16	0.02 ± 0.15	0.21 ± 0.14	–0.09 ± 0.18	–0.18 ± 0.22	0.11 ± 0.18	0.16 ± 0.16	0.03 ± 0.17
HILA	–0.20 ± 0.19	–0.01 ± 0.19	0.08 ± 0.18	–0.17 ± 0.21	0.03 ± 0.26	–0.09 ± 0.22	–0.21 ± 0.19	0.16 ± 0.20
HILB	–0.02 ± 0.17	–0.01 ± 0.16	**0.35 ± 0.15**	–0.20 ± 0.19	–0.13 ± 0.23	0.08 ± 0.19	0.12 ± 0.17	0.03 ± 0.18
DL	–0.31 ± 0.19	**0.39 ± 0.18**	**–0.44 ± 0.16**	0.09 ± 0.22	–0.18 ± 0.26	**0.52 ± 0.20**	**0.57 ± 0.21**	0.04 ± 0.30

Trait	REAB	SHF	LOINL	LOINA	LOINB	PHU	HGML	HGMA	HGMB
WLW	0.02 ± 0.02	–0.03 ± 0.03	0.01 ± 0.03	–0.02 ± 0.03	0.02 ± 0.03	**0.09 ± 0.04**	–0.00 ± 0.03	**–0.07 ± 0.03**	0.01 ± 0.03
REAW	**–0.16 ± 0.03**	**0.08 ± 0.03**	–0.02 ± 0.03	**–0.09 ± 0.03**	**–0.06 ± 0.03**	**0.12 ± 0.06**	0.01 ± 0.03	–0.03 ± 0.03	–0.01 ± 0.03
BFW	**0.10 ± 0.03**	**–0.13 ± 0.03**	0.03 ± 0.03	0.04 ± 0.03	**0.06 ± 0.03**	**0.13 ± 0.06**	–0.04 ± 0.03	**0.04 ± 0.02**	0.00 ± 0.03
RTW	–0.02 ± 0.03	0.04 ± 0.03	–0.01 ± 0.03	–0.00 ± 0.03	–0.02 ± 0.03	**0.20 ± 0.07**	**0.04 ± 0.02**	–0.04 ± 0.03	0.00 ± 0.03
BOW	–0.02 ± 0.03	**0.08 ± 0.03**	–0.03 ± 0.03	0.05 ± 0.03	0.01 ± 0.03	**0.20 ± 0.08**	–0.02 ± 0.03	–0.00 ± 0.03	–0.02 ± 0.02
CL	**0.09 ± 0.03**	**0.29 ± 0.03**	**0.14 ± 0.03**	**0.07 ± 0.03**	**0.12 ± 0.03**	**–0.16 ± 0.03**	**0.08 ± 0.03**	**0.07 ± 0.03**	**0.09 ± 0.03**
REAL	**0.65 ± 0.02**	**–0.18 ± 0.03**	**0.23 ± 0.03**	0.03 ± 0.03	**0.15 ± 0.03**	**–0.12 ± 0.03**	**0.22 ± 0.03**	0.02 ± 0.03	**0.18 ± 0.03**
REAA	**0.43 ± 0.04**	**–0.09 ± 0.03**	0.01 ± 0.03	**0.37 ± 0.03**	**0.19 ± 0.04**	**–0.06 ± 0.03**	–0.02 ± 0.03	**0.25 ± 0.04**	**0.10 ± 0.05**
REAB	**0.31 ± 0.06**	**–0.19 ± 0.03**	**0.17 ± 0.03**	**0.19 ± 0.03**	**0.21 ± 0.03**	**–0.13 ± 0.03**	**0.16 ± 0.03**	**0.13 ± 0.03**	**0.18 ± 0.03**
SHF	**–0.35 ± 0.13**	**0.39 ± 0.06**	**–0.06 ± 0.03**	0.00 ± 0.03	–0.03 ± 0.03	–0.05 ± 0.03	**–0.07 ± 0.03**	0.05 ± 0.03	–0.05 ± 0.03
LOINL	–0.03 ± 0.16	–0.12 ± 0.15	**0.31 ± 0.06**	**0.23 ± 0.03**	**0.77 ± 0.01**	**–0.37 ± 0.02**	**0.34 ± 0.02**	0.04 ± 0.03	**0.30 ± 0.02**
LOINA	0.19 ± 0.14	0.22 ± 0.14	**–0.40 ± 0.15**	**0.36 ± 0.06**	**0.72 ± 0.01**	**–0.30 ± 0.03**	0.02 ± 0.03	**0.42 ± 0.02**	**0.18 ± 0.03**
LOINB	0.11 ± 0.18	–0.01 ± 0.17	**0.51 ± 0.12**	**0.46 ± 0.13**	**0.20 ± 0.06**	**–0.44 ± 0.02**	**0.22 ± 0.03**	**0.24 ± 0.03**	**0.31 ± 0.02**
PHU	0.14 ± 0.19	0.20 ± 0.21	**–0.65 ± 0.21**	**–0.37 ± 0.16**	**–0.64 ± 0.16**	0.15 ± 0.09	**–0.23 ± 0.03**	**–0.14 ± 0.03**	**–0.22 ± 0.02**
HGML	0.03 ± 0.17	–0.20 ± 0.16	**0.45 ± 0.15**	**–0.42 ± 0.16**	–0.06 ± 0.20	**–0.49 ± 0.23**	**0.22 ± 0.05**	0.04 ± 0.03	**0.80 ± 0.01**
HGMA	0.14 ± 0.14	**0.35 ± 0.13**	**–0.30 ± 0.14**	**0.55 ± 0.11**	0.13 ± 0.17	0.01 ± 0.20	**–0.42 ± 0.15**	**0.38 ± 0.06**	**0.48 ± 0.02**
HGMB	0.32 ± 0.21	0.09 ± 0.20	0.33 ± 0.19	0.03 ± 0.21	0.39 ± 0.21	**–0.65 ± 0.33**	**0.56 ± 0.14**	**0.34 ± 0.17**	**0.12 ± 0.05**
HQFL	0.06 ± 0.29	–0.30 ± 0.17	**0.66 ± 0.14**	–0.18 ± 0.18	0.28 ± 0.20	**–0.60 ± 0.26**	**0.74 ± 0.15**	–0.20 ± 0.17	0.36 ± 0.22
HQFA	0.09 ± 0.16	**0.45 ± 0.14**	–0.16 ± 0.16	**0.53 ± 0.13**	0.19 ± 0.18	–0.11 ± 0.22	–0.18 ± 0.18	**0.52 ± 0.12**	0.24 ± 0.21
HQFB	0.27 ± 0.21	–0.05 ± 0.21	**0.67 ± 0.17**	0.19 ± 0.21	**0.71 ± 0.19**	**–0.98 ± 0.35**	**0.70 ± 0.22**	0.05 ± 0.21	**0.87 ± 0.25**
HILL	0.03 ± 0.15	–0.00 ± 0.15	**0.39 ± 0.14**	–0.15 ± 0.15	0.30 ± 0.17	–0.17 ± 0.21	0.24 ± 0.16	–0.06 ± 0.14	**0.36 ± 0.18**
HILA	–0.13 ± 0.19	0.07 ± 0.17	0.06 ± 0.19	**0.43 ± 0.16**	**0.44 ± 0.19**	–0.39 ± 0.27	–0.34 ± 0.20	**0.58 ± 0.15**	0.11 ± 0.25
HILB	–0.01 ± 0.16	0.01 ± 0.16	**0.31 ± 0.15**	–0.00 ± 0.16	**0.48 ± 0.17**	**–0.48 ± 0.23**	0.13 ± 0.18	0.04 ± 0.15	**0.46 ± 0.18**
DL	0.23 ± 0.19	**–0.38 ± 0.18**	**0.55 ± 0.24**	**0.42 ± 0.19**	0.40 ± 0.24	**–0.99 ± 0.49**	0.30 ± 0.21	0.06 ± 0.18	0.26 ± 0.24

Table 4. (cont.)

Trait	HQFL	HQFA	HQFB	HILL	HILA	HILB	DL
WLW	**–0.06 ± 0.03**	0.00 ± 0.03	–0.02 ± 0.03	–0.03 ± 0.03	–0.03 ± 0.03	–0.04 ± 0.03	**0.16 ± 0.08**
REAW	0.03 ± 0.03	–0.03 ± 0.03	0.00 ± 0.03	**–0.05 ± 0.02**	0.00 ± 0.03	–0.04 ± 0.03	**0.25 ± 0.08**
BFW	–0.00 ± 0.03	0.02 ± 0.03	0.02 ± 0.03	0.02 ± 0.03	**–0.05 ± 0.02**	0.03 ± 0.03	**0.20 ± 0.10**
RTW	–0.01 ± 0.03	–0.01 ± 0.03	0.00 ± 0.03	–0.01 ± 0.03	0.02 ± 0.03	–0.00 ± 0.03	**0.27 ± 0.08**
BOW	0.02 ± 0.03	0.04 ± 0.03	0.03 ± 0.02	–0.02 ± 0.03	0.01 ± 0.03	–0.02 ± 0.03	**0.28 ± 0.08**
CL	**0.12 ± 0.03**	0.05 ± 0.03	**0.12 ± 0.02**	**0.07 ± 0.03**	0.03 ± 0.03	**0.06 ± 0.03**	**0.14 ± 0.03**
REAL	**0.18 ± 0.03**	–0.00 ± 0.03	**0.14 ± 0.03**	**0.12 ± 0.03**	–0.01 ± 0.03	**0.10 ± 0.03**	**0.27 ± 0.03**
REAA	0.00 ± 0.03	**0.23 ± 0.03**	**0.11 ± 0.04**	0.02 ± 0.03	**0.11 ± 0.03**	0.06 ± 0.04	**0.06 ± 0.03**
REAB	**0.15 ± 0.03**	**0.11 ± 0.03**	**0.17 ± 0.03**	**0.08 ± 0.03**	0.02 ± 0.03	**0.08 ± 0.03**	**0.25 ± 0.03**
SHF	–0.05 ± 0.03	**0.06 ± 0.03**	–0.00 ± 0.03	–0.00 ± 0.03	0.05 ± 0.03	–0.00 ± 0.03	**–0.10 ± 0.03**
LOINL	**0.30 ± 0.02**	–0.01 ± 0.03	0.24 ± 0.02	**0.24 ± 0.03**	**0.06 ± 0.03**	**0.23 ± 0.03**	**0.26 ± 0.03**
LOINA	**0.08 ± 0.03**	**0.29 ± 0.03**	**0.17 ± 0.03**	0.04 ± 0.03	**0.19 ± 0.03**	**0.11 ± 0.03**	**0.24 ± 0.03**
LOINB	**0.24 ± 0.02**	**0.13 ± 0.03**	**0.26 ± 0.02**	**0.20 ± 0.03**	**0.14 ± 0.03**	**0.24 ± 0.03**	**0.30 ± 0.03**
PHU	**–0.17 ± 0.03**	**–0.08 ± 0.03**	**–0.18 ± 0.02**	**–0.17 ± 0.03**	**–0.12 ± 0.03**	**–0.19 ± 0.03**	**–0.16 ± 0.03**
HGML	**0.31 ± 0.02**	–0.01 ± 0.03	**0.24 ± 0.02**	**0.24 ± 0.03**	–0.04 ± 0.03	**0.18 ± 0.03**	**0.16 ± 0.03**
HGMA	**0.09 ± 0.03**	**0.32 ± 0.03**	**0.19 ± 0.03**	**0.12 ± 0.03**	**0.26 ± 0.02**	**0.21 ± 0.03**	**0.14 ± 0.03**
HGMB	**0.25 ± 0.02**	**0.13 ± 0.03**	**0.29 ± 0.02**	**0.26 ± 0.02**	**0.10 ± 0.02**	**0.30 ± 0.02**	**0.19 ± 0.03**
HQFL	**0.19 ± 0.05**	–0.03 ± 0.03	**0.74 ± 0.01**	**0.24 ± 0.03**	0.03 ± 0.03	**0.19 ± 0.03**	**0.16 ± 0.03**
HQFA	**–0.46 ± 0.17**	**0.27 ± 0.06**	**0.53 ± 0.02**	**–0.06 ± 0.03**	**0.23 ± 0.02**	**0.06 ± 0.03**	**0.10 ± 0.03**
HQFB	**0.67 ± 0.13**	0.20 ± 0.21	**0.10 ± 0.04**	**0.13 ± 0.03**	**0.12 ± 0.02**	**0.18 ± 0.02**	**0.16 ± 0.03**
HILL	0.09 ± 0.18	–0.18 ± 0.16	0.10 ± 0.22	**0.32 ± 0.06**	**0.17 ± 0.03**	**0.83 ± 0.01**	**0.13 ± 0.03**
HILA	0.01 ± 0.22	**0.38 ± 0.17**	0.21 ± 0.26	–0.29 ± 0.19	**0.16 ± 0.05**	**0.52 ± 0.02**	**0.08 ± 0.03**
HILB	0.04 ± 0.19	–0.11 ± 0.17	0.31 ± 0.39	**0.92 ± 0.03**	0.00 ± 0.21	**0.26 ± 0.06**	**0.15 ± 0.03**
DL	0.36 ± 0.22	0.08 ± 0.19	0.41 ± 0.26	0.16 ± 0.20	0.09 ± 0.23	0.24 ± 0.21	**0.21 ± 0.09**

[1] WLW = whole loin weight; REAW = rib eye weight; BFW = backfat weight; RTW = rib trim weight; BOW = bone weight; CL = cooking loss; REAL = rib eye area Minolta L*; REAA = rib eye area Minolta a*; REAB = rib eye area Minolta b*; SHF = shear force; LOINL = loin Minolta L*; LOINA = loin Minolta a*; LOINB = loin Minolta b*; PHU = ultimate pH; HGML = ham gluteus medius Minolta L*; HGMA = ham gluteus medius Minolta a*; HGMB = ham gluteus medius Minolta b*; HQFL = ham quadriceps femoris Minolta L*; HQFA = ham quadriceps femoris Minolta a*; HQFB = ham quadriceps femoris Minolta b*; HILL = ham iliopsoas Minolta L*; HILA = ham iliopsoas Minolta a*; HILB = ham iliopsoas Minolta b*; DL = drip loss.

[2] The significant correlations are highlighted in bold ($P < 0.05$).

score decreases, especially in pork with normal pH values (Lonergan et al., 2007). It appears that the estimate of CMAR in this study is within the range of previous reports. Most studies (Lo et al., 1992; Gibson et al., 1998; Sonesson et al., 1998; van Wijk et al., 2005) estimated a low to moderate (0.13–0.31) heritability for CMAR. The estimated heritability of TEXS in this study was 0.09 ± 0.04, indicating the presence of a small additive genetic effect on TEXS. The difference (0.09 vs. 0.20) between this study and van Wijk et al. (2005) may be due to the existence of heterosis in this crossbred population, different subjective measurement of firmness, and different statistical models used for (co)variance estimation.

Heritability estimates for primal and subprimal cuts weight were 0.55 ± 0.06, 0.46 ± 0.06, 0.63 ± 0.06, 0.55 ± 0.06, 0.49 ± 0.06, 0.63 ± 0.04, 0.52 ± 0.07, 0.53 ± 0.06, 0.44 ± 0.06, 0.29 ± 0.05, and 0.32 ± 0.06, for USW, UHAM, ULOIN, USH, UBEL, THAM, TLOIN, TBEL, PICN, BUTT, and RIBS, respectively. These heritabilities are among the highest in this study and were within the range of previous reports (Newcom et al., 2002; van Wijk et al., 2005), which presented a range of 0.40 to 0.57 for UHAM, 0.29 to 0.51 for ULOIN, 0.39 to 0.76 for THAM, 0.51 to 0.72 for TLOIN, and 0.51 for UBEL. However, limited studies on heritability estimation of primal and subprimal traits, especially for USW, USH, UBEL, TBEL, PICN, BUTT, and RIBS, make it difficult to compare these results with literature values. The estimated heritabilities of these traits were moderate or high indicating great opportunities to improve these traits in swine breeding programs.

Heritability estimates (±SE) for meat quality traits varied from 0.10 ± 0.04 for HQFB to 0.39 ± 0.06 for SHF. The heritability estimates for the traits related to water-holding capacity were low to moderate including DL, PHU, and CL (0.21 ± 0.09, 0.15 ± 0.09, and 0.20 ± 0.05, respectively). Different measurements of REAW had a moderate heritability and ranged from 0.22 ± 0.06 for RTW to 0.38 ± 0.06 for BFW, except for the BOW of rib eye, which was low (0.12 ± 0.05).

Ultimate pH is the most studied trait among all meat quality traits because it is associated with pork color, DL, and water-holding capacity and so it is a significant economic indicator (Bendall and Swatland, 1988). The estimated heritability of PHU in this study (0.15 ± 0.09) was within the range (0.07–0.39) reported previously (Cameron, 1990; De Vries et al., 1994; Hermesch et al., 2000a; Andersen and Pedersen, 2000; van Wijk et al., 2005; Ciobanu et al., 2011). This was close to the average estimate (0.21) of 33 studies reviewed by Ciobanu et al. (2011). Ultimate pH in this study and van Wijk et al. (2005) were corrected for common litter environmental effects in contrast to the other studies. The heritability estimate for DL (0.21 ± 0.09) was within the range (0.01 to 0.31) of literature reports (De Vries et al., 1994; Sonesson et al., 1998; Hermesch et al., 2000a; van Wijk et al., 2005; Ciobanu et al., 2011), and it is close to the average estimate (0.16) of 10 studies reviewed by Ciobanu et al. (2011). For CL, the estimate in this study (0.20 ± 0.05) was in agreement with the average (0.16) of all studies reviewed by Ciobanu et al. (2011). Shear force, which evaluates the degrees of tenderness, had the highest heritability estimate (0.39 ± 0.06) among meat quality traits. Although the current estimate was higher than estimates (0.17 and 0.20) reported by Lo et al. (1992) and De Vries et al. (1994), respectively, it is close to the average (0.30) of all studies reviewed by Ciobanu et al. (2011).

Among the technological meat quality traits, color had the highest heritability and ranged from 0.10 ± 0.05 to 0.38 ± 0.06 (average = 0.25). Generally, the estimated heritabilities for the lightness of loin (0.31 ± 0.06) and rib eye area (0.28 ± 0.06) were in agreement with the average estimate (0.28) found in previous studies (Cameron, 1990; Hermesch et al., 2000a; van Wijk et al., 2005; Ciobanu et al., 2011). The estimated heritabilities for the redness of loin (0.36 ± 0.06) and rib eye area (0.26 ± 0.09) were lower than the range of published estimates (0.52 and 0.57) by Sonesson et al. (1998) and Andersen and Pedersen (2000), respectively. This might be due to different population structure and statistical models used for variance component estimations. For LOINB and REAB, the estimated heritabilities in this study (0.20 ± 0.06 and 0.31 ± 0.06, respectively) were higher than the estimate of redness of loin (0.15) published by van Wijk et al. (2005). It might be due to their adjustment for CCW, which was not significant in the current study. Furthermore, the estimate of heritability for REAB was higher than the estimate of heritability for LOINB in this study. This can be explained by the differences in the average measurement of REAB, which was smaller than the average measurement of LOINB (2.81 vs. 15.07). This might be due to measuring of LOINB before freezing and early postmortem and measuring of REAB after freezing and late postmortem. The average estimated heritabilities for the lightness of ham (0.20) were close but higher than the estimate (0.11) by van Wijk et al. (2005). The average estimated heritabilities (0.27) for the redness of ham were in agreement with the estimate (0.26) published by van Wijk et al. (2005). For yellowness of ham, the average (0.12) estimate in this study was the same as reported by van Wijk et al. (2005). Heritability estimates for Minolta color traits measured on different muscles of ham were 0.22 ± 0.05, 0.38 ± 0.06, 0.12 ± 0.05, 0.19 ± 0.05, 0.27 ± 0.06, 0.10 ± 0.04, 0.32 ± 0.06, 0.16 ± 0.05, and 0.26 ± 0.06 for HGML, HGMA, HGMB, HQFL, HQFA, HQFB, HILL, HILA, and HILB, respectively. To our knowledge, no heritability estimates for Minolta color traits measured on the gluteus medius, quadriceps femoris, and iliopsoas muscles were previously available for comparison and would be worth further investigation. Heritability estimates for different weights of rib eye area were 0.28 ± 0.06, 0.31 ± 0.06, 0.38 ± 0.06, 0.22 ± 0.06, and 0.12 ± 0.05 for WLW, REAW, BFW, RTW, and BOW, respectively. Again, these estimates are new in the present study, and no estimates were available in literature, and warrant further investigation. Low to moderate heritabilities of pork quality indicate opportunities to improve these traits through genomic selection.

Correlations among Traits

The phenotypic and genetic correlations and their standard errors are reported in Tables 3, 4, 5, and 6. Generally, almost all of the phenotypic correlations and most of the genetic correlations were significant ($P < 0.05$). Although presented for completeness, phenotypic correlations will not discussed because they are of little interpretive value.

Correlations Among Carcass Traits. The phenotypic and genetic correlations among carcass traits are presented in Table 3. Almost all of the phenotypic and most of the genetic correlations among carcass traits were significant ($P < 0.05$). Generally, high genetic correlations were found between HCW and primal and subprimal weights and other carcass traits except for FD (0.39 ± 0.15) and TBEL (0.42 ± 0.17), which were moderate. A strong negative genetic correlation was observed between HCW and TEXS (–0.61 ± 0.27). Cold carcass weight had high average (0.81) genetic correlations with primal, subprimal, and carcass traits. Cold carcass weight had negative genetic correlation only with TEXS (–0.63 ± 0.26), which was similar to that of HCW. Unfortunately, no genetic correlations were available for comparisons in the literature for HCW and CCW and suggest a need for further validation.

Backfat depth was moderately correlated with LD (–0.34 ± 0.12), CMAR (0.33 ± 0.14), USW (0.28 ± 0.11), USH (0.28 ± 0.11), and UBEL (0.30 ± 0.11). Loin depth was highly correlated with LEA (0.78 ± 0.05) and ULOIN (0.53 ± 0.16) but moderately correlated with TLOIN (0.44 ± 0.10). Moderate genetic correlations were found between LD with TEXS (–0.40 ± 0.20), USW (0.37 ± 0.10), UHAM (0.49 ± 0.09), and BUTT (0.31 ± 0.12), but the correlations between LD with USH (0.29 ± 0.10) and THAM (0.24 ± 0.09) were in a low range. Carcass

Table 5. Estimates of phenotypic correlations and their standard error of estimates between meat quality and carcass traits

Traits[1]	HCW	CCW	FD	LD	CLEN	LEA	TEXS	CMAR	USW	UHAM
WLW	**0.39 ± 0.05**	**0.35 ± 0.05**	0.02 ± 0.03	0.04 ± 0.03	–0.01 ± 0.03	**0.32 ± 0.06**	**–0.04 ± 0.02**	–0.03 ± 0.03	**–0.11 ± 0.04**	**–0.14 ± 0.03**
REAW	**0.40 ± 0.05**	**0.40 ± 0.05**	**–0.22 ± 0.03**	**0.21 ± 0.03**	**0.10 ± 0.03**	**0.31 ± 0.05**	0.03 ± 0.02	**–0.08 ± 0.03**	**0.08 ± 0.03**	**0.13 ± 0.03**
BFW	**0.40 ± 0.05**	**0.40 ± 0.05**	**0.42 ± 0.02**	**–0.17 ± 0.03**	**–0.07 ± 0.03**	**0.30 ± 0.06**	–0.04 ± 0.03	**0.11 ± 0.03**	**0.09 ± 0.03**	–0.02 ± 0.03
RTW	**0.40 ± 0.05**	**0.41 ± 0.05**	**–0.20 ± 0.03**	**0.10 ± 0.03**	0.03 ± 0.03	**0.31 ± 0.06**	–0.02 ± 0.03	–0.04 ± 0.03	–0.02 ± 0.03	0.01 ± 0.03
BOW	**0.40 ± 0.05**	**0.41 ± 0.05**	**–0.11 ± 0.03**	0.01 ± 0.03	**0.09 ± 0.03**	**0.32 ± 0.06**	**–0.07 ± 0.02**	–0.03 ± 0.03	0.02 ± 0.03	0.03 ± 0.03
CL	**0.28 ± 0.06**	**0.27 ± 0.06**	**–0.07 ± 0.03**	0.03 ± 0.03	–0.01 ± 0.03	**0.22 ± 0.05**	–0.05 ± 0.02	–0.05 ± 0.03	–0.01 ± 0.02	0.00 ± 0.03
REAL	**0.29 ± 0.06**	**0.28 ± 0.06**	–0.03 ± 0.03	0.03 ± 0.03	**–0.06 ± 0.03**	**0.21 ± 0.06**	**–0.13 ± 0.02**	–0.01 ± 0.03	–0.02 ± 0.03	–0.01 ± 0.03
REAA	0.00 ± 0.03	0.00 ± 0.03	**0.08 ± 0.03**	–0.03 ± 0.03	0.01 ± 0.033	**–0.06 ± 0.03**	0.08 ± 0.07	**0.17 ± 0.04**	0.02 ± 0.03	0.04 ± 0.05
REAB	0.02 ± 0.03	0.01 ± 0.03	0.00 ± 0.03	0.01 ± 0.03	–0.03 ± 0.03	–0.01 ± 0.03	**–0.13 ± 0.02**	**0.07 ± 0.03**	0.02 ± 0.03	0.02 ± 0.03
SHF	–0.05 ± 0.03	–0.04 ± 0.03	–0.02 ± 0.03	–0.03 ± 0.03	0.01 ± 0.03	–0.01 ± 0.03	**0.08 ± 0.03**	–0.04 ± 0.03	–0.04 ± 0.03	–0.05 ± 0.03
LOINL	**0.12 ± 0.03**	**0.11 ± 0.03**	**0.12 ± 0.03**	**0.07 ± 0.03**	–0.11 ± 0.03	**0.07 ± 0.03**	**–0.39 ± 0.02**	**0.09 ± 0.03**	**0.11 ± 0.03**	**0.07 ± 0.03**
LOINA	0.04 ± 0.03	0.04 ± 0.03	**0.19 ± 0.03**	**–0.07 ± 0.03**	–0.05 ± 0.03	**–0.12 ± 0.03**	**–0.30 ± 0.02**	**0.17 ± 0.03**	0.04 ± 0.03	–0.03 ± 0.03
LOINB	**0.12 ± 0.03**	**0.11 ± 0.03**	**0.18 ± 0.03**	0.03 ± 0.03	**–0.09 ± 0.03**	–0.00 ± 0.03	**–0.44 ± 0.02**	**0.15 ± 0.03**	**0.11 ± 0.03**	0.05 ± 0.03
PHU	0.02 ± 0.03	0.02 ± 0.03	0.00 ± 0.03	**–0.10 ± 0.03**	**0.12 ± 0.03**	**–0.05 ± 0.02**	**0.19 ± 0.03**	**0.06 ± 0.03**	0.03 ± 0.03	0.04 ± 0.03
HGML	0.03 ± 0.03	0.04 ± 0.03	**–0.10 ± 0.03**	**0.15 ± 0.03**	–0.01 ± 0.03	**0.12 ± 0.03**	**–0.18 ± 0.02**	–0.03 ± 0.03	0.03 ± 0.03	**0.08 ± 0.03**
HGMA	–0.04 ± 0.03	–0.05 ± 0.03	**0.09 ± 0.03**	–0.04 ± 0.03	–0.05 ± 0.03	–0.05 ± 0.03	**–0.12 ± 0.02**	0.05 ± 0.03	–0.05 ± 0.03	–0.04 ± 0.03
HGMB	0.03 ± 0.03	0.03 ± 0.03	–0.01 ± 0.03	**0.09 ± 0.03**	–0.04 ± 0.03	**0.07 ± 0.03**	**–0.22 ± 0.02**	0.03 ± 0.02	0.02 ± 0.03	**0.06 ± 0.03**
HQFL	0.05 ± 0.03	**0.06 ± 0.03**	0.02 ± 0.03	0.03 ± 0.03	–0.01 ± 0.03	0.02 ± 0.03	**–0.20 ± 0.02**	0.05 ± 0.03	**0.06 ± 0.03**	**0.12 ± 0.03**
HQFA	–0.01 ± 0.03	–0.00 ± 0.03	0.02 ± 0.03	0.02 ± 0.03	0.01 ± 0.03	0.00 ± 0.03	**–0.09 ± 0.02**	–0.00 ± 0.03	–0.00 ± 0.03	**–0.10 ± 0.03**
HQFB	**0.08 ± 0.03**	**0.09 ± 0.03**	0.01 ± 0.03	**0.05 ± 0.02**	0.03 ± 0.03	0.05 ± 0.03	**–0.20 ± 0.02**	**0.04 ± 0.02**	**0.08 ± 0.03**	**0.07 ± 0.03**
HILL	–0.01 ± 0.03	–0.01 ± 0.03	0.00 ± 0.03	0.03 ± 0.03	–0.02 ± 0.03	0.01 ± 0.03	**–0.11 ± 0.02**	–0.02 ± 0.03	–0.00 ± 0.03	**0.07 ± 0.03**
HILA	–0.02 ± 0.03	–0.02 ± 0.03	–0.01 ± 0.03	0.01 ± 0.03	–0.02 ± 0.03	0.00 ± 0.03	**–0.07 ± 0.02**	–0.03 ± 0.03	–0.0 ± 0.03	–0.02 ± 0.03
HILB	0.02 ± 0.03	0.02 ± 0.03	0.03 ± 0.03	0.03 ± 0.03	–0.02 ± 0.03	–0.01 ± 0.03	**–0.14 ± 0.02**	–0.00 ± 0.03	0.02 ± 0.03	**0.06 ± 0.03**
DL	0.01 ± 0.03	0.01 ± 0.03	0.01 ± 0.03	0.02 ± 0.03	–0.03 ± 0.03	0.01 ± 0.03	**–0.23 ± 0.06**	**0.07 ± 0.03**	0.03 ± 0.03	**0.06 ± 0.04**
Traits	ULOIN	USH	UBEL	THAM	TLOIN	TBEL	PICN	BUTT	RIBS	
WLW	–0.03 ± 0.03	–0.03 ± 0.03	–0.01 ± 0.03	0.01 ± 0.03	**–0.07 ± 0.03**	**0.40 ± 0.02**	**0.37 ± 0.03**	**0.33 ± 0.03**	**0.20 ± 0.03**	
REAW	0.03 ± 0.03	**0.08 ± 0.03**	–0.01 ± 0.03	**0.12 ± 0.03**	**0.10 ± 0.03**	**–0.06 ± 0.03**	**0.11 ± 0.03**	**0.20 ± 0.03**	**0.14 ± 0.03**	
BFW	**0.09 ± 0.03**	0.03 ± 0.03	**0.16 ± 0.03**	–0.04 ± 0.03	–0.02 ± 0.03	**0.25 ± 0.03**	0.04 ± 0.03	**–0.12 ± 0.03**	**–0.11 ± 0.03**	
RTW	0.00 ± 0.03	0.01 ± 0.02	**–0.08 ± 0.03**	0.01 ± 0.03	0.04 ± 0.03	–0.05 ± 0.03	0.02 ± 0.03	**0.11 ± 0.03**	**0.06 ± 0.03**	
BOW	–0.01 ± 0.03	**0.07 ± 0.03**	–0.03 ± 0.03	0.03 ± 0.03	0.03 ± 0.03	**–0.08 ± 0.03**	0.03 ± 0.03	**0.09 ± 0.03**	**0.08 ± 0.03**	
CL	**0.06 ± 0.03**	–0.04 ± 0.03	0.00 ± 0.03	**–0.06 ± 0.03**	**0.07 ± 0.03**	**–0.06 ± 0.03**	–0.03 ± 0.03	0.03 ± 0.03	0.01 ± 0.03	
REAL	0.02 ± 0.03	–0.02 ± 0.03	–0.01 ± 0.03	–0.03 ± 0.03	0.02 ± 0.03	0.01 ± 0.03	–0.00 ± 0.03	–0.02 ± 0.03	–0.03 ± 0.03	
REAA	0.04 ± 0.04	0.05 ± 0.05	**0.10 ± 0.05**	0.04 ± 0.05	0.05 ± 0.05	**0.14 ± 0.05**	**0.13 ± 0.07**	**0.15 ± 0.07**	**0.23 ± 0.07**	
REAB	0.05 ± 0.03	0.00 ± 0.03	0.04 ± 0.03	–0.02 ± 0.03	0.04 ± 0.03	**0.08 ± 0.03**	0.04 ± 0.03	0.01 ± 0.03	0.04 ± 0.03	
SHF	–0.02 ± 0.03	–0.03 ± 0.03	–0.04 ± 0.03	–0.03 ± 0.03	–0.01 ± 0.03	**–0.12 ± 0.03**	**–0.09 ± 0.03**	–0.04 ± 0.03	–0.03 ± 0.03	
LOINL	**0.19 ± 0.03**	**0.07 ± 0.03**	**0.13 ± 0.03**	**–0.07 ± 0.03**	**0.17 ± 0.03**	0.01 ± 0.03	0.03 ± 0.03	0.05 ± 0.03	–0.01 ± 0.03	
LOINA	**0.18 ± 0.03**	–0.01 ± 0.03	**0.08 ± 0.03**	**–0.13 ± 0.03**	**0.12 ± 0.03**	–0.02 ± 0.03	–0.01 ± 0.03	–0.00 ± 0.03	**0.07 ± 0.03**	
LOINB	**0.28 ± 0.03**	0.03 ± 0.03	**0.16 ± 0.03**	**–0.14 ± 0.03**	**0.24 ± 0.03**	0.02 ± 0.03	0.04 ± 0.03	0.05 ± 0.03	**0.06 ± 0.03**	
PHU	**–0.07 ± 0.03**	**0.08 ± 0.03**	0.03 ± 0.03	**0.08 ± 0.03**	**–0.09 ± 0.03**	**0.08 ± 0.03**	0.05 ± 0.03	**0.07 ± 0.03**	0.06 ± 0.04	
HGML	–0.02 ± 0.03	0.03 ± 0.03	0.00 ± 0.03	**0.09 ± 0.03**	0.05 ± 0.03	–0.00 ± 0.03	0.00 ± 0.03	0.02 ± 0.03	0.03 ± 0.03	
HGMA	0.00 ± 0.03	**–0.09 ± 0.03**	–0.01 ± 0.03	–0.05 ± 0.03	–0.04 ± 0.03	**–0.06 ± 0.03**	**–0.07 ± 0.03**	**–0.10 ± 0.03**	0.01 ± 0.03	
HGMB	**0.06 ± 0.03**	–0.02 ± 0.03	0.04 ± 0.03	0.00 ± 0.03	**0.08 ± 0.03**	–0.02 ± 0.03	–0.01 ± 0.03	–0.02 ± 0.03	0.04 ± 0.03	
HQFL	0.02 ± 0.03	0.04 ± 0.03	0.05 ± 0.03	**0.06 ± 0.03**	0.02 ± 0.03	0.01 ± 0.03	0.01 ± 0.03	–0.00 ± 0.03	0.02 ± 0.03	
HQFA	**0.06 ± 0.03**	–0.01 ± 0.03	0.01 ± 0.03	**–0.08 ± 0.03**	0.05 ± 0.03	0.01 ± 0.03	–0.02 ± 0.03	–0.04 ± 0.03	0.00 ± 0.03	
HQFB	**0.13 ± 0.03**	0.05 ± 0.03	**0.10 ± 0.03**	–0.01 ± 0.03	**0.12 ± 0.03**	0.03 ± 0.03	0.03 ± 0.03	0.02 ± 0.03	0.04 ± 0.03	
HILL	–0.03 ± 0.03	–0.03 ± 0.03	0.01 ± 0.03	0.04 ± 0.03	–0.04 ± 0.03	–0.00 ± 0.03	–0.02 ± 0.03	**–0.06 ± 0.03**	–0.01 ± 0.03	
HILA	0.05 ± 0.03	**–0.07 ± 0.03**	0.03 ± 0.03	–0.05 ± 0.03	**0.07 ± 0.03**	–0.02 ± 0.03	–0.04 ± 0.03	–0.05 ± 0.03	0.01 ± 0.03	
HILB	**0.06 ± 0.03**	–0.03 ± 0.03	**0.06 ± 0.03**	–0.01 ± 0.03	0.05 ± 0.03	–0.00 ± 0.03	–0.02 ± 0.03	**–0.06 ± 0.03**	–0.00 ± 0.03	
DL	0.03 ± 0.03	0.06 ± 0.04	0.04 ± 0.04	0.07 ± 0.04	0.04 ± 0.04	–0.05 ± 0.04	0.03 ± 0.05	**0.12 ± 0.06**	**0.19 ± 0.07**	

[1]CCW = cold carcass weight; FD = backfat depth; LD = loin depth; CLEN = carcass length; LEA = area of the *longissimus dorsi* muscle; TEXS = texture score; CMAR = carcass marbling score; USW = untrimmed side weight; UHAM = untrimmed ham weight; WLW = whole loin weight; REAW = rib eye weight; BFW = backfat weight; RTW = rib trim weight; BOW = bone weight; CL = cooking loss; REAL = rib eye area Minolta L*; REAA = rib eye area Minolta a*; REAB = rib eye area Minolta b*; SHF = shear force; LOINL = loin Minolta L*; LOINA = loin Minolta a*; LOINB = loin Minolta b*; PHU = ultimate pH; HGML = ham *gluteus medius* Minolta L*; HGMA = ham *gluteus medius* Minolta a*; HGMB = ham *gluteus medius* Minolta b*; HQFL = ham *quadriceps femoris* Minolta L*; HQFA = ham *quadriceps femoris* Minolta a*; HQFB = ham *quadriceps femoris* Minolta b*; HILL = ham *iliopsoas* Minolta L*; HILA = ham *iliopsoas* Minolta a*; HILB = ham *iliopsoas* Minolta b*; DL = drip loss; ULOIN = untrimmed loin weight; USH = untrimmed shoulder weight; UBEL = untrimmed belly weight; THAM = trimmed ham weight; TLOIN = trimmed loin weight; TBEL = trimmed belly weight; PICN = trimmed picnic shoulder weight; BUTT = butt shoulder weight; RIBS = ribs weight.

[2]The significant ($P < 0.05$) correlations are highlighted in bold.

Table 6. Estimates of genetic correlations and their standard error of estimates between meat quality and carcass trait

Traits[1]	HCW	CCW	FD	LD	CLEN	LEA	TEXS	CMAR	USW	UHAM
WLW	–0.32 ± 0.21	**–0.54 ± 0.16**	–0.00 ± 0.15	0.01 ± 0.14	0.02 ± 0.13	0.15 ± 0.19	–0.06 ± 0.23	–0.07 ± 0.16	–0.08 ± 0.13	–0.13 ± 0.13
REAW	**0.40 ± 0.19**	**0.39 ± 0.19**	**–0.31 ± 0.13**	**0.40 ± 0.12**	0.06 ± 0.13	**0.57 ± 0.17**	–0.18 ± 0.23	0.12 ± 0.16	**0.24 ± 0.12**	**0.33 ± 0.12**
BFW	0.13 ± 0.18	0.07 ± 0.18	**0.60 ± 0.10**	**–0.22 ± 0.10**	–0.03 ± 0.12	**–0.35 ± 0.17**	–0.18 ± 0.21	–0.00 ± 0.15	0.07 ± 0.12	–0.05 ± 0.12
RTW	0.11 ± 0.22	0.19 ± 0.21	**–0.41 ± 0.14**	**0.26 ± 0.12**	0.09 ± 0.13	0.22 ± 0.19	**–0.39 ± 0.19**	–0.10 ± 0.16	0.09 ± 0.13	0.11 ± 0.13
BOW	**0.60 ± 0.27**	**0.63 ± 0.27**	–0.24 ± 0.17	–0.04 ± 0.16	**0.30 ± 0.15**	0.16 ± 0.24	–0.24 ± 0.27	0.22 ± 0.19	**0.31 ± 0.15**	**0.35 ± 0.16**
CL	–0.06 ± 0.24	–0.05 ± 0.22	–0.10 ± 0.16	–0.10 ± 0.15	–0.01 ± 0.14	0.07 ± 0.21	–0.35 ± 0.24	–0.03 ± 0.18	–0.01 ± 0.14	0.02 ± 0.15
REAL	–0.04 ± 0.21	–0.08 ± 0.20	–0.04 ± 0.14	0.05 ± 0.13	–0.12 ± 0.12	0.17 ± 0.19	–0.20 ± 0.22	–0.12 ± 0.16	–0.02 ± 0.12	0.05 ± 0.12
REAA	–0.02 ± 0.29	–0.02 ± 0.28	–0.04 ± 0.15	0.02 ± 0.14	–0.06 ± 0.13	0.10 ± 0.26	–0.08 ± 0.22	0.14 ± 0.16	–0.03 ± 0.13	–0.06 ± 0.13
REAB	0.08 ± 0.12	0.07 ± 0.12	–0.12 ± 0.14	0.17 ± 0.13	–0.07 ± 0.12	0.20 ± 0.13	–0.26 ± 0.21	–0.03 ± 0.16	0.09 ± 0.12	0.14 ± 0.12
SHF	–0.09 ± 0.12	–0.07 ± 0.11	0.17 ± 0.13	**–0.24 ± 0.12**	–0.07 ± 0.11	–0.12 ± 0.13	0.08 ± 0.22	**0.30 ± 0.14**	–0.07 ± 0.12	–0.16 ± 0.12
LOINL	0.01 ± 0.12	0.03 ± 0.12	**–0.25 ± 0.12**	**0.36 ± 0.12**	**–0.29 ± 0.11**	**0.42 ± 0.12**	**–0.38 ± 0.19**	–0.12 ± 0.16	0.01 ± 0.12	0.09 ± 0.13
LOINA	**–0.21 ± 0.10**	–0.17 ± 0.12	0.02 ± 0.14	0.08 ± 0.13	**–0.24 ± 0.12**	–0.02 ± 0.13	0.09 ± 0.22	–0.03 ± 0.15	–0.17 ± 0.12	**–0.24 ± 0.12**
LOINB	–0.10 ± 0.14	–0.08 ± 0.14	–0.27 ± 0.16	**0.38 ± 0.14**	**–0.32 ± 0.13**	**0.35 ± 0.15**	–0.37 ± 0.21	–0.13 ± 0.17	–0.08 ± 0.14	–0.05 ± 0.14
PHU	–0.35 ± 0.40	–0.37 ± 0.38	0.21 ± 0.21	**–0.66 ± 0.17**	**0.38 ± 0.17**	**–0.78 ± 0.28**	0.05 ± 0.31	0.22 ± 0.21	0.22 ± 0.18	0.18 ± 0.18
HGML	0.14 ± 0.14	0.15 ± 0.13	**–0.39 ± 0.14**	**0.37 ± 0.13**	–0.04 ± 0.13	**0.30 ± 0.13**	–0.36 ± 0.22	0.11 ± 0.17	0.10 ± 0.14	**0.26 ± 0.13**
HGMA	**–0.21 ± 0.10**	**–0.21 ± 0.10**	0.06 ± 0.13	0.06 ± 0.12	**–0.26 ± 0.11**	0.05 ± 0.13	0.10 ± 0.20	0.11 ± 0.15	**–0.22 ± 0.11**	**–0.22 ± 0.10**
HGMB	0.01 ± 0.18	0.01 ± 0.18	–0.33 ± 0.19	**0.41 ± 0.17**	–0.27 ± 0.17	**0.37 ± 0.18**	–0.21 ± 0.28	0.12 ± 0.21	–0.04 ± 0.18	0.09 ± 0.17
HQFL	0.06 ± 0.14	0.07 ± 0.13	–0.16 ± 0.16	**0.28 ± 0.14**	**–0.26 ± 0.12**	0.16 ± 0.15	**–0.61 ± 0.19**	0.01 ± 0.17	0.08 ± 0.14	**0.24 ± 0.12**
HQFA	0.02 ± 0.13	0.02 ± 0.13	0.24 ± 0.14	0.06 ± 0.13	–0.10 ± 0.12	0.08 ± 0.13	0.16 ± 0.23	0.15 ± 0.16	0.01 ± 0.13	–0.12 ± 0.12
HQFB	0.17 ± 0.17	0.19 ± 0.17	–0.07 ± 0.19	**0.39 ± 0.16**	–0.21 ± 0.17	**0.34 ± 0.17**	**–0.55 ± 0.23**	0.10 ± 0.21	0.18 ± 0.16	0.26 ± 0.16
HILL	0.06 ± 0.12	0.05 ± 0.12	–0.17 ± 0.13	**0.27 ± 0.12**	–0.07 ± 0.12	0.19 ± 0.12	–0.27 ± 0.21	–0.17 ± 0.15	0.04 ± 0.12	0.12 ± 0.12
HILA	–0.15 ± 0.14	–0.15 ± 0.14	–0.05 ± 0.15	0.03 ± 0.15	**–0.26 ± 0.13**	–0.01 ± 0.15	–0.14 ± 0.23	–0.15 ± 0.17	–0.15 ± 0.14	–0.12 ± 0.14
HILB	0.07 ± 0.13	0.06 ± 0.13	–0.07 ± 0.15	**0.27 ± 0.13**	–0.13 ± 0.13	0.17 ± 0.14	–0.22 ± 0.23	–0.18 ± 0.16	0.06 ± 0.13	0.12 ± 0.13
DL	0.27 ± 0.32	0.22 ± 0.31	0.01 ± 0.17	0.15 ± 0.16	–0.25 ± 0.16	0.30 ± 0.31	**–0.72 ± 0.26**	–0.06 ± 0.19	0.02 ± 0.15	0.05 ± 0.15
Traits	ULOIN	USH	UBEL	THAM	TLOIN	TBEL	PICN	BUTT	RIBS	
WLW	0.15 ± 0.12	–0.03 ± 0.13	0.12 ± 0.13	–0.04 ± 0.10	0.01 ± 0.13	**0.74 ± 0.07**	**0.80 ± 0.07**	**0.74 ± 0.08**	**0.57 ± 0.13**	
REAW	0.08 ± 0.12	**0.26 ± 0.12**	0.04 ± 0.13	**0.23 ± 0.09**	0.18 ± 0.13	–0.16 ± 0.12	0.15 ± 0.13	**0.34 ± 0.13**	**0.34 ± 0.16**	
BFW	0.14 ± 0.11	–0.07 ± 0.11	**0.26 ± 0.11**	–0.08 ± 0.09	–0.00 ± 0.12	**0.38 ± 0.09**	0.10 ± 0.11	**–0.32 ± 0.13**	**–0.24 ± 0.15**	
RTW	0.14 ± 0.12	0.11 ± 0.12	–0.01 ± 0.13	0.03 ± 0.10	0.15 ± 0.14	–0.10 ± 0.13	0.07 ± 0.13	**0.39 ± 0.14**	**0.38 ± 0.16**	
BOW	–0.01 ± 0.15	**0.44 ± 0.15**	0.13 ± 0.16	0.22 ± 0.13	0.16 ± 0.17	–0.10 ± 0.15	**0.32 ± 0.16**	**0.57 ± 0.16**	**0.74 ± 0.16**	
CL	0.13 ± 0.13	–0.05 ± 0.14	0.09 ± 0.14	–0.12 ± 0.12	0.19 ± 0.15	**–0.26 ± 0.13**	–0.18 ± 0.14	0.02 ± 0.15	0.28 ± 0.18	
REAL	0.16 ± 0.11	–0.06 ± 0.12	–0.03 ± 0.13	–0.07 ± 0.09	0.10 ± 0.12	0.04 ± 0.12	–0.03 ± 0.13	–0.00 ± 0.13	–0.05 ± 0.16	
REAA	–0.06 ± 0.12	–0.03 ± 0.12	0.08 ± 0.13	–0.07 ± 0.10	–0.03 ± 0.13	0.14 ± 0.12	0.04 ± 0.13	0.01 ± 0.14	**0.35 ± 0.15**	
REAB	**0.20 ± 0.10**	0.00 ± 0.12	0.09 ± 0.12	–0.05 ± 0.10	0.16 ± 0.12	**0.20 ± 0.10**	0.15 ± 0.12	0.14 ± 0.14	**0.31 ± 0.15**	
SHF	–0.07 ± 0.11	0.01 ± 0.12	–0.01 ± 0.11	–0.07 ± 0.09	–0.13 ± 0.12	–0.11 ± 0.11	–0.16 ± 0.12	–0.06 ± 0.13	0.05 ± 0.16	
LOINL	**0.25 ± 0.11**	–0.07 ± 0.12	0.09 ± 0.12	**–0.20 ± 0.10**	**0.34 ± 0.12**	–0.15 ± 0.12	–0.05 ± 0.12	0.15 ± 0.14	–0.24 ± 0.15	
LOINA	**0.22 ± 0.10**	**–0.25 ± 0.11**	0.07 ± 0.12	**–0.36 ± 0.09**	**0.23 ± 0.11**	–0.15 ± 0.12	–0.02 ± 0.12	0.15 ± 0.13	0.16 ± 0.15	
LOINB	**0.55 ± 0.10**	**–0.29 ± 0.13**	**0.28 ± 0.13**	**–0.52 ± 0.10**	**0.67 ± 0.11**	–0.11 ± 0.14	0.08 ± 0.14	**0.34 ± 0.15**	0.05 ± 0.18	
PHU	**–0.42 ± 0.19**	**0.44 ± 0.16**	–0.03 ± 0.19	**0.45 ± 0.15**	**–0.68 ± 0.23**	0.28 ± 0.19	0.12 ± 0.19	0.05 ± 0.20	0.05 ± 0.24	
HGML	–0.17 ± 0.12	0.22 ± 0.13	–0.12 ± 0.14	**0.32 ± 0.11**	–0.00 ± 0.15	–0.09 ± 0.14	–0.01 ± 0.14	0.22 ± 0.15	–0.01 ± 0.17	
HGMA	–0.06 ± 0.11	**–0.29 ± 0.11**	–0.11 ± 0.11	–0.13 ± 0.09	–0.15 ± 0.12	–0.11 ± 0.11	**–0.25 ± 0.12**	–0.13 ± 0.13	0.08 ± 0.15	
HGMB	0.10 ± 0.17	–0.15 ± 0.17	0.06 ± 0.18	–0.04 ± 0.15	0.20 ± 0.19	–0.12 ± 0.18	–0.13 ± 0.17	0.13 ± 0.18	0.08 ± 0.22	
HQFL	–0.01 ± 0.13	0.05 ± 0.13	–0.03 ± 0.14	**0.21 ± 0.10**	0.12 ± 0.15	–0.14 ± 0.14	–0.12 ± 0.14	–0.05 ± 0.15	–0.15 ± 0.17	
HQFA	0.05 ± 0.12	0.04 ± 0.12	–0.01 ± 0.13	–0.07 ± 0.10	–0.01 ± 0.13	0.03 ± 0.13	–0.03 ± 0.13	0.02 ± 0.14	0.24 ± 0.16	
HQFB	**0.33 ± 0.15**	0.03 ± 0.16	0.21 ± 0.17	–0.02 ± 0.15	**0.42 ± 0.17**	–0.08 ± 0.17	–0.09 ± 0.17	0.10 ± 0.18	0.14 ± 0.21	
HILL	–0.00 ± 0.11	–0.03 ± 0.12	0.01 ± 0.12	0.10 ± 0.09	0.02 ± 0.13	0.09 ± 0.12	0.09 ± 0.12	–0.10 ± 0.13	–0.04 ± 0.15	
HILA	0.09 ± 0.12	**–0.28 ± 0.13**	0.00 ± 0.14	–0.17 ± 0.11	0.20 ± 0.14	–0.13 ± 0.13	**–0.24 ± 0.12**	–0.16 ± 0.15	–0.13 ± 0.18	
HILB	**0.25 ± 0.12**	–0.15 ± 0.13	0.19 ± 0.13	–0.07 ± 0.11	**0.29 ± 0.13**	0.08 ± 0.13	0.00 ± 0.14	–0.16 ± 0.15	–0.10 ± 0.18	
DL	–0.07 ± 0.14	0.09 ± 0.14	–0.09 ± 0.15	0.08 ± 0.12	–0.07 ± 0.16	**–0.46 ± 0.14**	**–0.36 ± 0.15**	–0.09 ± 0.16	0.03 ± 0.19	

[1] CCW = cold carcass weight; FD = backfat depth; LD = loin depth; CLEN = carcass length; LEA = area of the *longissimus dorsi* muscle; TEXS = texture score; CMAR = carcass marbling score; USW = untrimmed side weight; UHAM = untrimmed ham weight; WLW = whole loin weight; REAW = rib eye weight; BFW = backfat weight; RTW = rib trim weight; BOW = bone weight; CL = cooking loss; REAL = rib eye area Minolta L*; REAA = rib eye area Minolta a*; REAB = rib eye area Minolta b*; SHF = shear force; LOINL = loin Minolta L*; LOINA = loin Minolta a*; LOINB = loin Minolta b*; PHU = ultimate pH; HGML = ham gluteus medius Minolta L*; HGMA = ham gluteus medius Minolta a*; HGMB = ham gluteus medius Minolta b*; HQFL = ham quadriceps femoris Minolta L*; HQFA = ham quadriceps femoris Minolta a*; HQFB = ham quadriceps femoris Minolta b*; HILL = ham iliopsoas Minolta L*; HILA = ham iliopsoas Minolta a*; HILB = ham iliopsoas Minolta b*; DL = drip loss; ULOIN = untrimmed loin weight; USH = untrimmed shoulder weight; UBEL = untrimmed belly weight; THAM = trimmed ham weight; TLOIN = trimmed loin weight; TBEL = trimmed belly weight; PICN = trimmed picnic shoulder weight; BUTT = butt shoulder weight; RIBS = ribs weight.

[2] The significant ($P < 0.05$) correlations are highlighted in bold.

length was moderately to highly correlated with LEA (0.47 ± 0.14), USW (0.80 ± 0.05), UHAM (0.71 ± 0.06), ULOIN (0.56 ± 0.09), USH (0.69 ± 0.06), UBEL (0.69 ± 0.06), THAM (0.31 ± 0.07), TLOIN (0.56 ± 0.08), BUTT (0.36 ± 0.11), and RIBS (0.52 ± 0.11). A negative genetic correlation was found between LEA and TEXS (–0.56 ± 0.28) indicating the adverse effect of selection for LEA on pork quality. Moderate to high genetic correlations were estimated between LEA with USW (0.72 ± 0.12), UHAM (0.75 ± 0.12), ULOIN (0.66 ± 0.13), USH (0.57 ± 0.13), UBEL (0.50 ± 0.17), THAM (0.42 ± 0.13), TLOIN (0.79 ± 0.12), BUTT (0.69 ± 0.16), and RIBS (0.56 ± 0.19).

Texture score is used to assess the degree of firmness and exudation or weeping of the longissimus dorsi muscle and was negatively correlated with most of the primal and subprimal cut weights including HCW (–0.61 ± 0.27), CCW (–0.63 ± 0.26), LD (–0.40 ± 0.20), LEA (–0.56 ± 0.28), USW (–0.48 ± 0.18), UHAM (–0.56 ± 0.17), USH (–0.47 ± 0.17), THAM (–0.38 ± 0.17), BUTT (–0.61 ± 0.21), and RIBS (–0.49 ± 0.23). These results showed that deterioration of pork quality may have occurred over many generations through the selection for increasing carcass weight. In addition, unfavorable genetic correlations between TBEL and PICN subprimal cuts with DL indicated adverse effect on water-holding capacity. Carcass marbling, which is associated with eating quality and consumer demand (Brewer et al., 2001), was correlated with HCW (0.63 ± 0.22), CCW (0.59 ± 0.21), FD (0.33 ± 0.14), USW (0.35 ± 0.13), USH (0.42 ± 0.12), and THAM (0.29 ± 0.11) but there was no correlation with LD (0.01 ± 0.15), CLEN (0.03 ± 0.14), LEA (0.05 ± 0.20), TEXS (0.04 ± 0.24), and the remainder of the subprimal weights (0.14 on average).

The primal and subprimal cut weights were moderately to highly correlated with each other and ranged from (0.32 ± 0.11) between THAM and RIBS to (0.96 ± 0.01) between TLOIN and ULOIN, with a few correlations being exceptions with low and nonsignificant ($P > 0.05$) correlations. Untrimmed side weight had a moderate to high correlation with all of the primal and subprimal cuts except with TBEL, which was low (0.22 ± 0.09). Both primal cuts for loin and ham were highly correlated with their subprimal cuts, although the correlation between ULOIN and TLOIN was higher (0.96 ± 0.01) than the correlation between UHAM and THAM (0.59 ± 0.05), which might be due to differences in fat deposition in hams and loins. These results were in agreement with van Wijk et al. (2005) who reported the genetic correlations of 0.60 between ULOIN and TLOIN and 0.61 between UHAM and THAM. Newcom et al. (2002) showed high genetic correlations between UHAM and THAM (0.89) and between ULOIN and TLOIN (0.90). In contrast, UBEL had a low (0.21 ± 0.09) genetic correlation with TBEL, which might be due to more fat deposition in belly. Untrimmed ham weight had moderate to high genetic correlations with all of the subprimal cuts (0.64 on average), excepting with TBEL, which had a low correlation (0.21 ± 0.10). A few reports presented genetic correlations between ham and loin primal and subprimal cuts but no genetic correlations were available in the literature for others (Newcom et al., 2002; van Wijk et al., 2005).

The valuable subprimal cuts of the carcass are the hams and loins and so their weights are most important to overall carcass value. A high genetic correlation was found between UHAM and ULOIN (0.77 ± 0.12), and it was higher than the correlation observed between THAM and TLOIN (0.18 ± 0.07). This result showed that selection for high ham yield (UHAM) would lead to high loin yield (ULOIN). However, selection for high trimmed ham (THAM) may not necessarily increase high trimmed loin (TLOIN) due to their low genetic correlation. In addition, ULOIN was correlated with UBEL (0.83 ± 0.03), BUTT (0.33 ± 0.10), and RIBS (0.43 ± 0.11). The high genetic correlation between ULOIN and UBEL confirmed that selection for loin weight would increase belly yield. There were moderate to high genetic correlations between USH with UBEL (0.44 ± 0.08), THAM (0.57 ± 0.04), PICN (0.36 ± 0.09), BUTT (0.47 ± 0.09), and RIBS (0.49 ± 0.11) and a low genetic correlation was found with TBEL (0.18 ± 0.09). A high genetic correlation was observed between UBEL and TLOIN (0.87 ± 0.03). Genetic correlation between TBEL and PICN was high (0.91 ± 0.07). Ribs weight and BUTT had moderate to high genetic correlations with those primal and subprimal weights. Genetic correlations among primal and subprimal cuts were limited in the literature, most likely because these traits are difficult and expensive to measure.

Correlations among Meat Quality Traits. The phenotypic and genetic correlations among meat quality traits are presented in Table 4. Most of the phenotypic and genetic correlations among meat quality traits were significant ($P < 0.05$). Strong negative genetic correlations were found between PHU with CL (–0.62 ± 0.26) and DL (–0.99 ± 0.49). Ciobanu et al. (2011) reported the genetic correlations of –0.68 between PHU and CL and –0.71 between PHU and DL as the average correlations of many previous studies, which were in good agreement with our estimates. These high genetic correlations were in the range of –0.82 to –0.45 for between PHU and CL and –0.99 to –0.50 between PHU and DL (De Vries et al., 1994; Sellier, 1998; Gibson et al., 1998; Hermesch et al., 2000b). This substantiates evidence of the value of muscle pH as an indicator trait for DL and CL in crossbred pig genetic improvement programs to improve pork quality traits and reduce the cost of DL and CL measurement.

Estimated genetic correlations between DL with LOINL (0.55 ± 0.24) and LOINA (0.42 ± 0.19) were moderate to high, whereas corresponding correlations between DL and Minolta L* and a* measurements of ham muscles were not significant (0.27 and 0.08, respectively, on average). Sellier (1998) and van Wijk et al. (2005) reported moderate genetic correlations between DL and LOINL (0.49 and 0.38, respectively), which were in agreement with this study. No genetic correlation between DL and color of ham was found, which might be due to the measurement of DL on loin. Drip loss had positive high correlation with CL (0.52 ± 0.20) but negative correlation with SHF (–0.38 ± 0.18). A high genetic correlation between DL and CL was reported by Sellier (1998), which was in agreement with this study (0.66).

Shear force assesses the degree of toughness and was highly correlated with CL (0.58 ± 0.13). This result suggested that genetic improvement for CL by selecting for reduced CL may result in more tender meat. Shear force was positively correlated with the Minolta A* measurements of ham including HGMA (0.35 ± 0.13) and HQFA (0.45 ± 0.14), and was negatively correlated with the Minolta measurements of rib eye area including REAL (–0.33 ± 0.14) and REAB (–0.35 ± 0.13). No information was found for Minolta color traits measured on the gluteus medius, quadriceps femoris, and iliopsoas muscles in literature. The Minolta color measurements on the loin were moderately to highly correlated with the corresponding measurements on the ham (gluteus medius, quadriceps femoris, and iliopsoas) muscles except for the Minolta b* between LOINB and HGMB. No literature values were found for these traits and to our awareness this is the first report for these traits. Minolta L* were negatively correlated with the Minolta a* measurements for both ham and loin and ranged from (–0.36 ± 0.16) between REAL and REAA to (–0.46 ± 0.17) between HQFL and HQFA. The Minolta L* for both ham and loin were highly correlated with Minolta b* values and ranged from (0.51 ± 0.12) between LOINL and LOINB to (0.92 ± 0.03) between HILL and HILB and were in good agreement with the average estimate of 0.81 reported by van Wijk et al. (2005).

Minolta a* of ham muscle on the gluteus medius was negatively correlated with LOINL (–0.30 ± 0.14); however, HQFA and HILA were not correlated with LOINL. The correlations between PHU and the color measurements showed a moderate to high negative genetic correlations and ranged from (–0.37 ± 0.16) with LOINA to (–0.98 ± 0.35) with HQFB. This substantiates evidence of the value of PHU as an indicator trait for color measurements on either loin or ham.

Correlations between Carcass and Meat Quality Traits. The phenotypic and genetic correlations between carcass and pork quality traits are presented in Tables 5 and 6, respectively. Generally, some of the phenotypic and genetic correlations were significant ($P < 0.05$). Low negative genetic correlations were estimated for HCW and CCW with meat redness of loin and ham gluteus medius. No correlation was found for FD with both DL and PHU. The estimated correlations for FD with pork lightness of loin and ham gluteus medius were of favorable low to moderate magnitude (–0.25 ± 0.12 and –0.39 ± 0.14, respectively). These indicated that pork quality was not negatively affected by selection against FD. There was a low correlation between LD and SHF (–0.24 ± 0.12). In addition, LD and LEA were similarly and highly correlated with PHU (–0.66 ± 0.17 and –0.78 ± 0.28, respectively). Moderate correlations were observed between LD and LEA with lightness of loin (0.36 ± 0.12 and 0.42 ± 0.12) and ham (0.31 and 0.22 on average, respectively). This indicates that single-trait selection on LD and loin eye area may lead to undesirable lower pH pork with paler color.

Favorable low to moderate negative genetic correlations were obtained for CLEN with both lightness of loin and ham (–0.29 ± 0.11 and –0.12 on average) and PHU (0.38 ± 0.17). Firmness was moderately to highly correlated with lightness of loin and ham (–0.38 ± 0.19 and –0.42 on average) and DL (–0.72 ± 0.26). This indicates the value of subjective TEXS as an indicator trait for meat water-holding capacity. Carcass marbling was lowly correlated with all of the meat quality traits. Low to moderate correlations were estimated for PHU and DL with most of the primal and subprimal cuts except for TLOIN, which was highly correlated with PHU (–0.68 ± 0.23). In addition, the correlations for the color traits with most of the primal and subprimal cuts were of favorable moderate to high magnitude. Untrimmed loin weight and TLOIN were lowly to moderately correlated with LOINL (0.25 ± 0.11 and 0.34 ± 0.12), respectively, which were higher than correlations of UHAM and THAM with lightness of ham (both averaging 0.21). The Minolta color measurements were also lowly to moderately and favorably correlated with most of the primal and subprimal cut weight, except for HQFB, which was found to be unfavorably correlated with TLOIN. Primal and subprimal weights were favorably and lowly correlated with DL, except for TBEL and PICN, which were found to be unfavorably correlated with DL (–0.46 ± 0.14 and –0.36 ± 0.15, respectively).

To our knowledge, no literature was found presenting correlations of primal and subprimal cuts except for loin and somewhat ham with pork quality traits. This study showed that pork quality traits had favorable genetic relationships with the primal and subprimal weights. This indicated that selection for primal and subprimal cut weight would not negatively affect pork quality. van Wijk et al. (2005) is the only literature that presented genetic relationships between loin and ham primal and subprimal cuts with pork quality traits, which were similar to this study. Our study confirmed the results by van Wijk et al. (2005) that favorable correlations between cut weight and meat quality traits are in contrast to the general perception.

Some of the estimates herein are new contributions to the genetic parameters for carcass and pork quality traits, especially on ham traits. Novel results of this study show the significance of genetic selection for various carcass weight traits including hot carcass, cold carcass, rib eye, and primal and subprimal cuts weights in the swine breeding programs due to their moderate to high heritabilities. However, firmness and color measurements of gluteus medius, quadriceps femoris, and iliopsoas muscles had low to moderate heritabilities indicating the opportunities for new genomic selection to improve them. The results of this study confirm the value of pH as an indicator trait for pork water-holding capacity. Novel genetic correlations in this study indicate the value of carcass and ham weight as good indicator traits for indirect selection of primal, subprimal, and carcass traits. However, unfavorable genetic correlation was found between both carcass weight and loin eye area with TEXS but favorable genetic relationship was found between ham weight and TEXS. These results could indicate that deterioration of pork quality may have occurred over many generations through the selection for increasing carcass weight and especially for loin weight. It was concluded that single-trait selection on loin traits might lead to increased belly weight and undesirable lower pH pork with paler color. Therefore, selection for ham weight can be valuable for increasing both carcass weight and primal and subprimal cuts weights without adverse consequences on pork quality. In addition, color of ham muscles had moderate to high genetic correlations with corresponding measurements on the loin indicating that selection can be made on ham. Lightness and yellowness reflectance of ham are highly positively correlated to each other and negatively to pH. Favorable correlation between FD and pork lightness of ham showed that selection for leanness over many generations was not as adverse as selection for loin weight traits. Although novel genetic parameter estimates are valuable for the design of a breeding program in Canadian swine populations, further studies are needed to investigate the genetic relationships of carcass and meat quality traits with growth and performance traits.

Implications

Measurement of carcass and meat quality traits is difficult, expensive, can only be performed postmortem, and is destructive to the sample. Therefore, selection of purebreds based on crossbred performance for these traits would be useful to help improving pure lines of pigs to produce improved pork quality from commercial crossbred pigs without the need of measurements on pure lines. Estimates of genetic parameters for carcass and meat quality traits in crossbred pigs will provide not only insight into the biological basis of these traits but also a valuable reference to develop efficient genetic improvement programs for these traits. Genetic parameters obtained herein are valuable for the design of a breeding program emphasizing product quality in Canadian swine populations, especially with the new parameters for traits that have not previously been studied. Furthermore, the use of pH is suggested as an effective indicator for DL and CL of meat. It was concluded that selection for increasing primal and subprimal cut weights with better pork quality may be possible. In addition, moderate to high heritability of carcass traits would indicate the good opportunity of improving carcass merit traits in commercial crossbred pigs. In addition, the high cost of data collection and low to moderate heritability of meat quality traits provide the opportunities to improve them through genomic efforts.

LITERATURE CITED

Andersen, S., and B. Pedersen. 2000. Genetic parameters for colour traits and pH and correlations to production traits. In: Proceedings of EAAP, Zurich, Switzerland. Publ. 100. p. 129–133.

Bendall, J. R., and H. J. Swatland. 1988. A review of the relationships of pH with physical aspects of pork quality. Meat Sci. 24:85–126.

Brewer, M. S., L. G. Zhu, and F. K. McKeith. 2001. Marbling effects on quality characteristics of pork loin chops: Consumer purchase intent, visual and sensory characteristics. Meat Sci. 59:153–163.

Cameron, N. D. 1990. Genetic and phenotypic parameters for carcass traits, meat and eating quality traits in pigs. Livest. Prod. Sci. 26:119–135.

Ciobanu, D., S. M. Lonergan, and E. J. Huff-Lonergan. 2011. Genetics of meat quality and carcass traits. In: M. F. Rothschild and A. Rubinsky, editors, The genetics of the pigs. CAB Int., New York. p. 355–389.

De Vries, A. G., P. G. van der Wal, T. Long, G. Eikelenboom, and J. W. M. Merks. 1994. Genetic parameters of pork quality and production traits in Yorkshire populations. Livest. Prod. Sci. 40:277–289.

Ducos, A. 1994. Paramètres génétiques des caractères de production chez le porc. Mise au point bibliographique. (In French.) Techni-porc 17:35–67.

Gibson, J. P., C. Aker, and R. Ball. 1998. Levels of genetic variation for growth, carcass and meat quality traits of purebred pigs. In: Proc. 6th World Cong. Genet. Appl. Livest. Prod., Armidale, Australia. p. 499–502.

Gilmour, A. R., B. J. Gogel, B. R. Cullis, and R. Thompson. 2009. ASReml user guide release 3.0. VSN International Ltd., Hemel Hempstead, UK.

Hermesch, S., B. G. Luxford, and H. U. Graser. 2000a. Genetic parameters for lean meat yield, meat quality, reproduction and feed efficiency traits for Australian pigs 1. Description of traits and heritability estimates. Livest. Prod. Sci. 65:239–248.

Hermesch, S., B. G. Luxford, and H. U. Graser. 2000b. Genetic parameters for lean meat yield, meat quality, reproduction and feed efficiency traits for Australian pigs. 2. Genetic relationships between production, carcass and meat quality traits. Livest. Prod. Sci. 65:249–259.

Lo, L. L., D. G. McLaren, F. K. McKeith, F. L. Fernando, and J. Novakofski. 1992. Genetic analysis of growth, real time ultrasound, carcass and pork quality traits in Duroc and Landrace pigs: II. Heritabilities and correlations. J. Anim. Sci. 70:2357–2396.

Lonergan, S. M., K. J. Stalder, E. Huff-Lonergan, T. J. Knight, R. N. Goodwin, K. J. Prusa, and D. C. Beitz. 2007. Influence of lipid content on pork sensory quality within pH classification. J. Anim. Sci. 85:1074–1079.

Marcoux, M., C. Pomar, L. Faucitano, and C. Brodeur. 2007. The relationship between different pork carcass lean yield definitions and the market carcass value. Meat Sci. 75:94–102.

Miar, Y., G. S. Plastow, H. L. Bruce, S. S. Moore, O. N. Durunna, J. D. Nkrumah, and Z. Wang. 2014. Estimate of genetic and phenotypic parameters for ultrasound and carcass merit traits in crossbred beef cattle. Can. J. Anim. Sci. (in press).

National Swine Improvement Federation (NSIF). 1997. Guidelines for uniform swine improvement programs. www.nsif.com/guidel/guidelines.htm (Accessed on April 1, 2014)

Newcom, D. W., T. J. Baas, J. W. Mabry, and R. N. Goodwin. 2002. Genetic parameters for pork carcass components. J. Anim. Sci. 80:3099–3106.

Olfert, E. D., B. M. Cross, and A. A. McWilliams, editors. 1993. Guide to the care and use of experimental animals. Vol. 1. Canadian Council on Animal Care, Ottawa, Ontario, Canada.

Plastow, G. S., D. Carrión, M. Gil, J. A. Garcia-Regueiro, M. Font i Furnols, M. Gispert, M. A. Oliver, A. Velarde, M. D. Guàrdia, M. Hortós, M. A. Rius, C. Sárraga, I. Díaz, A. Valero, A. Sosnicki, R. Klont, S. Dornan, J. M. Wilkinson, G. Evans, C. Sargent, G. Davey, D. Connolly, B. Houeix, C. M. Maltin, H. E. Hayes, V. Anandavijayan, A. Foury, N. Geverink, M. Cairns, R. E. Tilley, P. Mormède, and S. C. Blott. 2005. Quality pork genes and meat production. Meat Sci. 70:409–421.

Sellier, P. 1998. Genetics of meat and carcass traits. In: M. F. Rothschild and A. Ruvinsky, editors, The Genetics the pig. CAB Int., Wallingford, UK. p. 463–510.

Sonesson, A. K., K. H. de Greef, and T. H. E. Meuwissen. 1998. Genetic parameters and trends of meat quality, carcass composition and performance traits in two selected lines of large white pigs. Livest. Prod. Sci. 57:23–32.

Stewart, T. S., and A. P. Schinckel. 1991. Genetic parameters for swine growth and carcass traits. In: L. D. Young, editor, Genetics of swine. USDA-ARS, Roman L. Hruska U.S. Meat Animal Research Center, Clay Center, NE. p. 77–79.

Suzuki, K., M. Irie, H. Kadowaki, T. Shibata, M. Kumagai, and A. Nishida. 2005. Genetic parameter estimates of meat quality traits in Duroc pigs selected for average daily gain, longissimus muscle area, backfat thickness, and intramuscular fat content. J. Anim. Sci. 83:2058–2065.

van Wijk, H. J., D. J. G. Arts, J. O. Matthews, M. Webster, B. J. Ducro, and E. F. Knol. 2005. Genetic parameters for carcass composition and pork quality estimated in a commercial production chain. J. Anim. Sci. 83:324–333.

Zumbach, B., I. Misztal, S. Tsuruta, J. P. Sánchez, M. Azain, W. Herring, J. Holl, T. Long, and M. Culbertson. 2008. Genetic component of heat stress in finishing pigs: Parameter estimation. J. Anim. Sci. 86:2076–2081.