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Investigating genetic parameters for primal lean and fat content via dual energy x-ray absorptiometry in crossbred pigs

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Introduction

Carcass lean and fat yield are economically important traits in commercial swine production, with carcass value in Canada largely determined by weight and lean yield (%). Predicted lean yield is routinely estimated from optical probe measurements of loin muscle and backfat depth during grading (Pomar and Marcoux, 2003), based on prediction equations developed from the 1992 Canadian National Cutout Study (CPC, 1994). Backfat thickness is the primary driver of predicted lean yield, accounting for up to 90% of trait variability (Fredeen and Bowman, 1968; Barducci *et al.*, 2020). Although carcass cutout studies are the gold standard for evaluating tissue composition, their cost and labor requirements limit their routine use in selection programs. Newer approaches, such as dual energy x-ray absorptiometry (DEXA), offer scalable insights into lean, fat and bone content and may be suitable for integration into genomic selection programs. Furthermore, interest in customizing market-specific primal composition has highlighted the need to optimize tissue distribution to maximize carcass value. Consequently, the objectives of this study were to estimate genetic parameters for carcass and primal-specific DEXA-derived lean and fat traits and to quantify their genetic relationships with predicted lean yield, to assess their applicability to swine genetic improvement programs.

Materials & Methods

Data and editing. All experimental procedures were approved by the Agriculture and Agri-Food Canada Lacombe Research and Development Centre (AAFC-LRDC) Animal Care Committee (#202204; Mozduri *et al.*, 2025). Animals were raised under standard commercial production practices and slaughtered at the federally inspected AAFC-LRDC abattoir. Carcass records were available for 2,464 crossbred pigs (1,118 females and 1,346 males) from 8 Duroc sires and 145 Landrace × Yorkshire F1 dams (Genesus Genetic Technologies Inc., Richmond, Canada). Animals were slaughtered across 89 kill dates from 2021 to 2024 at an average (± standard deviation) age of 162.5 ± 12.6 days and live weight of 121.8 ± 8.2 kg.

At grading, hot carcass weight (HCWT, kg) was taken, and lean and fat depth of the *longissimus dorsi* (mm) were measured using a PG-100 Destron optical probe (Anitech Information Systems Inc., Markham, Canada) at the standardized grading site (7 mm from the midline between the 3rd and 4th last rib; Pomar and Marcoux, 2003). Carcass lean yield was then predicted using the standard equation (CPC, 1994). The cooled carcass sides were broken into primals (loin, belly, butt, picnic, and ham) according to the Institutional Meat Purchase Specifications for pork (IMPS, 2014). Individual primals were scanned using DEXA to quantify lean, fat, and bone content (%; Soladoye *et al.*, 2016). Total lean and fat content were calculated as the sum of tissues across all primals. Additional details on data collection are provided in Mozduri *et al.* (2025).

Data editing and quality control were conducted using R (v4.5.1; R Core Team, 2025). Records with incomplete information, slaughter dates with fewer than 10 carcasses, and trait values

exceeding three standard deviations from the mean were excluded. The final dataset included 2,418 carcass records.

Genotypes. Blood samples were collected at slaughter and genotyped using SkimSEEK™, a low-pass sequencing platform with imputation to whole-genome sequence (36,566,734 SNP; Neogen®, Edmonton, AB). Genotype quality control was conducted in PLINK v2.00a3.6 (Purcell *et al*., 2007; Chang *et al.*, 2015), excluding variants and samples with minor allele frequency <0.01, variant or sample genotyping rate <0.10, or deviation from Hardy–Weinberg equilibrium (p < 1e-6). After quality control, variants were filtered using VCFTOOLS (v3; Danecek *et al*., 2011) and a custom pipeline to retain 54,230 autosomal SNP corresponding to a custom Affymetrix Axiom Porcine Genotyping Array (Affymetrix, Santa Clara, CA). Additional quality control was performed in R using the ASRgenomics package (v1.1.5; Gezan *et al.*, 2022). Following all filtering steps, genotypes for 908 pigs across 52,560 SNP remained.

Statistical analyses. (Co)variance components (± standard errors) were estimated using bivariate single-step GBLUP animal models implemented in WOMBAT (Meyer, 2007). Heritability estimates represent the mean estimate across all analyses for each trait. All models included sex as a fixed effect, HCWT as a covariate, and random effects of litter (dam × birth date), contemporary group (slaughter date), and animal, and were specified as follows (Eq. 1):

$$\begin{pmatrix}\mathbf{y_1}\\ \mathbf{y_2}\end{pmatrix} = \begin{pmatrix}\mathbf{X_1} & 0\\ 0 & \mathbf{X_2}\end{pmatrix}\begin{pmatrix}\mathbf{b_1}\\ \mathbf{b_2}\end{pmatrix} + \begin{pmatrix}\mathbf{Z_1} & 0\\ 0 & \mathbf{Z_2}\end{pmatrix}\begin{pmatrix}\mathbf{a_1}\\ \mathbf{a_2}\end{pmatrix} + \begin{pmatrix}\mathbf{W_1} & 0\\ 0 & \mathbf{W_2}\end{pmatrix}\begin{pmatrix}\mathbf{c_1}\\ \mathbf{c_2}\end{pmatrix} + \begin{pmatrix}\mathbf{CE_1} & 0\\ 0 & \mathbf{CE_2}\end{pmatrix}\begin{pmatrix}\mathbf{l_1}\\ \mathbf{l_2}\end{pmatrix} + \begin{pmatrix}\mathbf{e_1}\\ \mathbf{e_2}\end{pmatrix} \quad (1)$$

Where: subscripts 1 and 2 refer to the first and second trait in each bivariate analysis; **y** are vectors of phenotypic observations; **b, a**, **c, l,** and **e** are vectors of fixed, animal additive genetic, contemporary group, litter and residual effects, respectively; and **X, Z, W** and **CE** are design matrices relating observations to the fixed, additive genetic, contemporary group, and litter effects, respectively. The following (co)variance structures were assumed for random effects: $\begin{pmatrix}\mathbf{a_1}\\ \mathbf{a_2}\end{pmatrix} \sim N(0, \mathbf{H} \otimes \begin{pmatrix}\boldsymbol{\sigma}^2_{a1} & \boldsymbol{\sigma}_{a1,a2}\\ \boldsymbol{\sigma}_{a1,a2} & \boldsymbol{\sigma}^2_{a2}\end{pmatrix}$, where **H** is a hybrid relationship matrix combining both pedigree (**A**) and genomic (**G**) relationships (Legarra *et al.*, 2009) created in WOMBAT with default parameters (Meyer, 2007), $\begin{pmatrix}\mathbf{c_1}\\ \mathbf{c_2}\end{pmatrix} \sim N(0, \mathbf{I} \otimes \begin{pmatrix}\boldsymbol{\sigma}^2_{c1} & \boldsymbol{\sigma}_{c1,c2}\\ \boldsymbol{\sigma}_{c1,c2} & \boldsymbol{\sigma}^2_{c2}\end{pmatrix}$, $\begin{pmatrix}\mathbf{l_1}\\ \mathbf{l_2}\end{pmatrix} \sim N(0, \mathbf{I} \otimes \begin{pmatrix}\boldsymbol{\sigma}^2_{l1} & \boldsymbol{\sigma}_{l1,l2}\\ \boldsymbol{\sigma}_{l1,l2} & \boldsymbol{\sigma}^2_{l2}\end{pmatrix}$, and $\begin{pmatrix}\mathbf{e_1}\\ \mathbf{e_2}\end{pmatrix} \sim N(0, \mathbf{I} \otimes \begin{pmatrix}\boldsymbol{\sigma}^2_{e1} & \boldsymbol{\sigma}_{e1,e2}\\ \boldsymbol{\sigma}_{e1,e2} & \boldsymbol{\sigma}^2_{e2}\end{pmatrix}$, where **I** are identity matrices.

Results & Discussion

Heritability. Descriptive statistics, additive genetic variances and heritability estimates are presented in Table 1. Heritability estimates were moderate for all traits, ranging from 0.27 ± 0.05 (loin lean) to 0.42 ± 0.06 (picnic lean). The heritability estimates for DEXA-derived total lean (0.35 ± 0.06) and predicted lean yield (0.34 ± 0.05) were similar; however, the DEXA-derived trait exhibited greater genetic variance, suggesting potential advantages for inclusion in selection programs. These results align with estimates previously reported for DEXA primal fat traits by Mozduri *et al.* (2025) using an earlier dataset from this ongoing research (0.46 ± 0.15 for loin fat to 0.55 ± 0.08 for picnic fat).

Genetic correlations. The genetic correlations (r_g; Table 2) between predicted lean yield and DEXA-derived total lean (0.78 ± 0.06) and fat (-0.80 ± 0.05) were strong, but differed from one, indicating that the predicted trait does not fully capture variation in carcass lean and fat content. The nearly inverse relationship between total lean and total fat (-0.99 ± 0.01) was expected due to minimal variation in the bone mass across carcasses. Genetic correlations

observed among primal-specific DEXA traits ranged from 0.82 ± 0.05 to 0.94 ± 0.02 for lean traits and 0.84 ± 0.04 to 0.93 ± 0.02 for fat traits (data not shown).

Table 1. Trait means, additive genetic variances and heritability estimates.

	Trait	n[1]	Mean ± SD	σ_A^2	h^2 ± SE
Carcass Traits	Predicted Lean Yield (%)[2]	2,414	59.4 ± 1.8	0.95	0.34 ± 0.05
	Total Lean (%)	2,174	58.2 ± 3.4	3.33	0.35 ± 0.06
	Total Fat (%)	2,171	32.2 ± 3.6	3.87	0.37 ± 0.06
Primal Traits	Loin Lean (%)	2,174	52.8 ± 4.7	4.83	0.27 ± 0.05
	Belly Lean (%)	2,171	66.1 ± 3.8	5.09	0.39 ± 0.06
	Ham Lean (%)	2,167	63.7 ± 2.9	2.17	0.30 ± 0.06
	Picnic Lean (%)	2,174	65.1 ± 3.2	3.67	0.42 ± 0.06
	Butt Lean (%)	2,171	57.9 ± 4.2	5.47	0.37 ± 0.06
	Loin Fat (%)	2,170	34.9 ± 4.7	6.33	0.35 ± 0.06
	Belly Fat (%)	2,171	33.3 ± 3.8	5.16	0.39 ± 0.06
	Ham Fat (%)	2,169	28.3 ± 2.9	2.26	0.35 ± 0.06
	Picnic Fat (%)	2,174	27.1 ± 3.3	3.39	0.38 ± 0.06
	Butt Fat (%)	2,169	38.2 ± 4.3	5.71	0.39 ± 0.06

[1] n: number of observations, SD: standard deviation, σ_A^2: additive genetic variance, h^2: heritability estimate, SE: standard error.
[2] Predicted carcass lean yield from the grading probe measurements, subsequent traits were DEXA-derived.

Predicted lean yield is derived based on estimates of loin muscle and fat depth, which are strongly associated with overall leanness (Fredeen and Bowman, 1968; Pomar and Marcoux, 2003). Interestingly, there were some differences in the genetic correlations between predicted lean yield and the individual DEXA-derived primal traits (Table 2; $|r_g|$ = 0.62 to 0.83). The strongest correlations were with the loin traits, as expected, because predicted lean yield is based on loin measures, while the weakest correlations were with the ham traits. Correlations between the individual primals with total lean and fat were stronger ($|r_g| \geq 0.88$). These findings indicate that incorporating DEXA data into genetic improvement programs could enhance selection for primal-specific tissue composition.

Table 2. Genetic correlations (± standard error) between whole carcass and primal traits.

	Predicted Lean Yield (%)[1]	Total Lean (%)	Total Fat (%)
Total Lean (%)	0.78 ± 0.06	-	-
Total Fat (%)	-0.80 ± 0.05	-0.99 ± 0.01	-
Loin Lean (%)	0.83 ± 0.05	0.98 ± 0.01	-0.98 ± 0.01
Belly Lean (%)	0.73 ± 0.06	0.94 ± 0.02	-0.93 ± 0.02
Ham Lean (%)	0.62 ± 0.09	0.91 ± 0.03	-0.88 ± 0.04
Picnic Lean (%)	0.72 ± 0.07	0.92 ± 0.02	-0.90 ± 0.03
Butt Lean (%)	0.77 ± 0.06	0.96 ± 0.01	-0.97 ± 0.01
Loin Fat (%)	-0.82 ± 0.05	-0.96 ± 0.01	0.98 ± 0.01
Belly Fat (%)	-0.73 ± 0.06	-0.94 ± 0.02	0.94 ± 0.02
Ham Fat (%)	-0.65 ± 0.08	-0.92 ± 0.02	0.92 ± 0.02
Picnic Fat (%)	-0.71 ± 0.07	-0.91 ± 0.03	0.91 ± 0.03
Butt Fat (%)	-0.77 ± 0.06	-0.96 ± 0.01	0.97 ± 0.01

[1] Predicted carcass lean yield from the grading probe measurements, subsequent traits were DEXA-derived.

Conclusions

This study presents genetic parameters for DEXA-derived lean and fat content traits in a large commercial crossbred swine population. The DEXA-derived traits had higher additive genetic variance and similar heritability estimates compared to predicted lean yield. Correlations for DEXA-derived total and primal-specific lean and fat with predicted lean yield were moderate to high, but significantly different from one. The results suggest potential to enhance selection for primal-specific tissue composition using DEXA technology. Ongoing work will expand data collection, evaluate correlations to performance and pork quality traits, and support the implementation of routine genomic evaluations for these traits.

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