Relationship of Alternative Measures of Pork Carcass Composition

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Introduction

Pork carcass and empty body composition research has been conducted to evaluate effects of experimental treatment, to model pig growth, and to evaluate pork production systems. Alternative endpoints included physical carcass dissection, fat-free or fat-standardized dissected lean mass, mass of trimmed retail cuts, and empty body chemical composition. Scientists with an interest in modeling pig growth and predicting nutrient requirements require accurate predictions of empty body chemical composition (Schinckel and de Lange, 1996).

In past research, dissected lean in the four lean cuts was measured for its strong relationship to carcass value. Recently, two methods of separating the soft tissue components have been used: (1) to adjust dissected lean to a fat-free tissue or fat-standardized basis, and (2) to adjust carcass soft tissue mass for the chemically determined lipid content. These two methods of determining and measuring carcass composition appear to be quite similar, but may result in substantially different outcomes when utilized in lean growth modeling and in determining nutrient requirements.

The objectives of this study were to evaluate the alternative methods of defining pork carcass composition and develop further understanding of the interrelationships among various pork carcass and empty body composition endpoints.

Materials and Methods

Data from 203 pigs, representing seven genotypes and two sexes (gilts and barrows), were used to evaluate relationships among different measures of carcass composition. Details of the experimental design and data are presented in Schinckel et al. (2000). Pigs were slaughtered at four target weights: 220, 251, 282, or 334 lbs. The data were analyzed as two separate data sets: a light weight data set (target weights of 220, 251, and 282 lbs) and a heavy weight data set (target weights of 251, 282, and 334 lbs).

Determination of the Mass of Soft Tissue Components

Two methods were used to divide the carcass soft tissue into two measures of carcass composition. The first method is to partition the soft tissue mass into fat-free lean mass (FFLM) and total carcass fat tissue (TOFAT). Fat-free lean mass (FFLM) is a measure of the dissected carcass lean muscle after accounting for the predicted amount of fat tissue remaining in the dissected lean. Lipid-free soft tissue mass (LFSTIS) was calculated as the sum of the lipid-free mass of each of the carcass components (Schinckel et al., 2000). LFSTIS is the total lipid-free mass of the carcass soft tissue.

Carcass soft tissue lipid mass (STLIP) was calculated as the sum of the lipid mass of each of the six carcass components. The non-lipid mass of the total carcass fat tissue (NLFAT) was evaluated, as it provides a direct evaluation of the difference between LFSTIS and FFLM and the difference between TOFAT and STLIP.

The ability to predict the mass of each measure of carcass composition from the actual or predicted mass of the alternative similar component (LFSTIS versus FFLM; TOFAT versus STLIP) was evaluated with regression analysis. The measures of carcass composition (FFLM, LFSTIS, TOFAT and STLIP) were fit to equations including CW and either each variable's alternative actual measure of carcass composition or the predicted value of the alternative measure calculated from ribbed carcass measurements. Accuracy of each prediction equation was evaluated by R^2 and residual standard deviation (RSD). Least squares means of the residual values for the genetic population, sex, and target weight subclasses were used to estimate subpopulation biases (Gu et al., 1992).

The correlation coefficient (CR) between the 14 predicted and observed genotype-sex means for lean mass was used as an overall approximate measure of genotype bias. The proportion of variation among genotypes accounted for by the equation was determined by the variance ratio (VR), which is the variance of predicted genotype-sex means divided by the variance of observed means. Simple correlation coefficients (r) were computed to determine the level of association between dependent and independent variables.

Results

Acronyms and definitions for the variables are given in Table 1. Table 1 also contains the overall and sex means for the light weight data and the heavy weight data. The standard deviations for live weight were greater (34.4 vs. 26.5 lb) for the heavy pig data than for the light pig data. The standard deviations of the majority of the variables are also greater for the heavy weight data, likely due to the increased variation in live weight or carcass weight.

The correlations among the carcass composition mass and carcass percentage measures are presented in Table 2. The three measures of lean mass (FFLM, LFSTIS, and DL) were highly correlated with each other (r = .93 to .97). The three measures of lean mass (FFLM, LFSTIS, and DL) had similar correlations with MTPRO in the light weight data. In the heavy weight data, LFSTIS had a slightly higher correlation with MTPRO (r = .89) than FFLM or DL (r = .82 and .86, respectively). Only LFSTIS had a lower correlation with NLFAT in the light weight data (r = .24) than in the heavy weight data (r = .46).

TOFAT and STLIP were highly correlated with each other (r = .98 and .97, light and heavy weight pig data). The correlation of TOFAT with %LIPFAT was higher in the light weight data (r = .55) than in the heavy weight data (r = .27). The results suggest that pigs with a greater amount of dissected fat tissue have a higher percentage lipid in fat tissue and that the relationship is stronger in lighter weight pigs. Overall, the correlations of TOFAT with %TOFAT (r = .89 and .87) and STLIP with %STLIP (r = .90 and .88) were higher than the correlations of FFLM with FFL% (r = .59 and .56), LFSTIS with %LFSTIS (r = .37 and .38), and DL with %DL (r = .53 and .52).

MTLIP had identical correlations with TOFAT and STLIP (r = .95). MTLIP was positively correlated with NLFAT (r = .46 and .63 in light and heavy weight data). This indicates that pigs with a greater mass of empty body lipid also have more mass of the non-lipid (water, protein, and ash) components associated with the fat tissue.

NLFAT% was negatively correlated with FFL% (r = -.44 and -.50) and DL% (r = -.26 and -.32) while having a positive relationship with TOFAT% (r = .41 and .52 in light and heavy weight data). NLFAT% was also negatively correlated to %LIPFAT (r = -.62).

Correlations between the carcass composition mass and carcass percentage measures with the carcass and live ultrasound measurements are presented in Table 3. Carcass and live ultrasonic loin muscle area measurements were more closely related (r = .75 to .85) with the three measures of carcass lean mass (FFLM, LFSTIS, and DL) than with carcass weight (r = .66 to .79), muscle depth (r = .32 to .46), and off-midline backfat depth measurements (r = -.19 to -.46).

LFSTIS had a slightly higher correlations with CW (r = .79 and .78) than FFLM (r = .70 and .60) or DL (r = .71 and .64) in the light and heavy weight data. LFSTIS had smaller negative relationships with the measures of off-midline backfat (r = -.19 to -.27) than either FFLM or DL (r = -.24 to -.46). This is due to the fact that LFSTIS includes NLFAT, which had a positive relationship to the off-midline measures of fat depth (r = .34 to .39).

NLFAT and STLIP, the two components of TOFAT, have different relationships with CW and the carcass measurements. NLFAT has a weaker relationship with CW (r = .39 and .64 for light and heavy weight data) than STLIP (r = .71 and .74 for light and heavy weight data). NLFAT has a weaker relationship with off-midline measures of fat depth (r = .34 to .39) than STLIP (r = .79 to .84). NLFAT% also had substantially smaller correlations with the measures of off-midline backfat depth measurements (r = .13 to .29) than STLIP% (r = .87 to .90).

The percent lipid in the dissected fat (%LIPFAT) was positively correlated with LW and CW in the light pig data (r = .42 and .43), but not significantly correlated in the heavy weight data (r = .09 and .10). In general, pigs with greater backfat depths had higher percent lipid within the dissected fat (r = .46 to .56) and lean tissue (r = .34 to .49).

MTPRO was positively related to LW (r = .72 and .77), CW (r = .74 and .78), LEA (r = .57 and .62), ULEA (r = .69 and .74), and MD34 (r = .32 and .45). MTPRO had small negative relationships with the off-midline measures of backfat depth (r = -.02 to -.18). MTLIP was positively related to LW (r = .78 and .82), CW (.78 and .82), and off-midline measures of backfat depth (r = .69 to .75).

Results of the regression analyses fitting each measure of carcass composition (FFLM and LFSTIS, TOFAT and STLIP) to the actual and predicted values of the similar alternative measurement are presented in Table 4. The summary of the residual value statistics are presented in Tables 5 and 6. The alternative similar measures of carcass composition mass (FFLM versus LFSTIS; TOFAT versus STLIP) were accurately predicted (R^2 = .89 to .96) from the actual values of alternative similar measurements. Carcass weight was significant (P<.02) for all of the equations relating FFLM to LFSTIS. Also, carcass weight was significant (P<.08) for one of the four light weight and all four of the heavy weight equations relating TOFAT to STLIP. This indicates that the relative growth rates of the similar alternative measurements were different, such that the ratio of one measurement to the other changed as CW increased. The prediction equations utilizing the predicted values of the alternative similar measurements were less accurate ($R^2 = .84$ to .92) than equations including the actual data ($R^2 = .88$ to .96). Equations including the predicted value of the alternative similar measure and CW had similar accuracy and magnitude of biases as prediction equations using the ribbed carcass measurements. The regression coefficients for CW were larger in the heavy weight data than the light weight data. The equations predicting FFLM from predicted values of LFSTIS had significant biases ($P<.05$) associated with genetic populations. Sex by weight group and genetic population by weight group biases were significant ($P<.10$) in the prediction of FFLM or LFSTIS in the heavy weight data.

Discussion

Past research trials have published the actual or predicted values of only one set of carcass composition measures (FFLM and TOFAT versus LFSTIS and STLIP). Measures of carcass composition were accurately predicted from values of the alternative similar measurements and carcass weight. However, the prediction equations had significant biases associated with genetic population. The genetic population biases are likely caused by the ratio of the similar alternative variables being different for the genetic populations due to differences in either the ratio of FFLM to LFSTIS or %LIPFAT, and the ratio of STLIP to TOFAT. The sex by weight group and genotype by weight group biases ($P<.10$) in the heavy weight data are likely caused by variation between the genotypes and sexes in both the amount and the relative growth rates of the similar alternative measures of composition.

Implications

The different measures of carcass composition have different relative growth rates and have different relationships with carcass and live measurements. Although the alternative measurements of lean mass are highly related to each other (high linear correlations), the relationships among the variables cannot be modeled as simple linear regression equations.

References

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Table 1. Overall barrow and gilt means for the light and heavy pig data sets.

		220, 251, and 284 lb weight groups				251, 284, and 334 lb weight groups			
Acronym	Definition of variable and unit of measurement	Overall mean	Barrows	Gilts	SD	Overall mean	Barrows	Gilts	SD
LW	Live weight, lb	247.70	247.60	247.80	26.5	284.20	284.60	283.80	34.4
CW	Warm carcass weight, lb	185.01	187.20	185.70	22.5	214.62	214.83	214.4	27.8
FFLM	Fat-free lean mass, lb	80.93	77.00	84.75	12.1	90.10	86.42	95.46	13.4
TOFAT	Total carcass fat tissue mass, lb	65.05	73.34	64.97	15.2	84.81	90.79	78.93	20.5
LFSTIS	Lipid-free soft tissue mass, lb	98.34	94.82	101.70	12.3	111.55	107.87	115.17	15.0
STLIP	Carcass soft tissue lipid mass, lb	51.68	55.53	40.02	13.4	64.24	69.36	59.22	18.7
NLFAT	Non-lipid carcass fat tissue mass, lb	17.4	17.81	16.98	3.5	20.57	21.43	19.71	5.5
DL	Dissected lean in the four lean cuts, lb	32.94	31.17	34.73	4.6	36.95	35.30	38.58	5.4
FFL%	Fat-free lean, %	43.87	41.94	45.70	4.6	42.60	40.44	44.73	5.2
TOFAT%	Total carcass fat, %	37.17	39.57	34.88	5.8	39.21	41.92	36.54	6.3
LFSTIS%	Lipid-free soft tissue, %	53.31	51.65	54.89	4.2	52.13	50.36	53.88	4.6
STLIP%	Soft tissue lipid, %	27.72	29.86	25.69	5.3	29.68	32.00	27.39	5.6
NLFAT%	Non-lipid fat, %	9.44	9.71	9.19	1.7	9.53	9.91	9.14	2.0
DL%	Dissected lean, %	39.13	37.44	40.74	4.0	38.10	36.35	39.83	4.3
MTPRO	Empty body protein, lb	31.92	30.62	33.25	4.0	35.67	34.13	37.26	5.1
MTLIP	Empty body lipid, lb	68.94	73.24	64.90	15.7	85.16	90.32	80.09	19.1
FD10R	Fat depth at 10th rib, in.	1.23	1.36	1.10	.33	1.38	1.53	1.74	.38
BFLR	Midline backfat thickness at last rib, in.	1.14	1.20	1.09	.23	1.26	1.36	1.16	.26
LEA	Loin eye area at 10th rib, in.^{2}	5.45	5.06	5.82	.90	5.94	5.56	6.31	1.0
FD34	3/4 last rib fat depth, in.	1.04	1.15	.93	.30	1.17	1.28	1.06	.33
MD34	3/4 last rib muscle depth, in.	1.92	1.84	1.99	.23	1.99	1.94	2.04	.26
ULEA	Ultrasonic 10th rib loin eye area, in.^{2}	6.00	5.74	6.26	.22	6.64	6.35	6.89	.93
UBF	Ultrasonic backfat 10th rib, in.	1.34	1.48	1.20	.36	1.51	1.69	1.35	.39
UBFL	Ultrasonic fat depth at last rib, in.	1.09	1.21	.98	.28	1.21	1.35	1.08	.31
%LIPFAT	% lipid in dissected fat	74.28	75.15	73.41	4.7	75.46	76.17	74.75	4.5
%LIPDL	% lipid in dissected lean	7.57	7.92	7.24	1.5	8.02	8.55	7.49	1.7

Table 2. Correlation among the carcass composition mass and carcass composition percentage measures.[a]

	FFLM	TOFAT	LFSTIS	STLIP	NLFAT	DL	MTPRO	MTLIP	% LIPFAT	% LIPDL	FFL %	TOFAT %	LFSTIS %	STLIP %	NLFAT %	DL %
FFLM		.03	.96	.05	-.05	.97	.85	.15	.08	-.25	.59	-.49	.44	-.37	-.51	.49
TOFAT	-.02		.20	.98	.59	.05	.19	.95	.55	.51	-.76	.84	-.78	.86	.16	-.77
LFSTIS	.93	.26		.16	.24	.96	.86	.28	-.01	-.17	.43	-.33	.37	-.27	-.27	.37
STLIP	-.05	.97	.17		.41	.04	.19	.95	.71	.51	-.73	.81	-.82	.90	-.03	-.77
NLFAT	.09	.74	.46	.56		.06	.10	.46	-.32	.28	-.50	.53	-.22	.31	.80	-.37
DL	.97	.10	.96	.03	.26		.85	.14	-.01	-.14	.55	-.46	.45	-.37	-.39	.53
MTPRO	.82	.33	.89	.27	.40	.86		.26	.13	-.13	.34	-.29	.22	-.19	-.38	.28
MTLIP	.10	.95	.32	.95	.63	.17	.38		.63	.44	-.66	.73	-.73	.80	-.00	-.71
%LIPFAT	-.16	.27	-.31	.47	-.43	-.26	.36	.36		.30	-.38	.44	-.68	.69	-.62	-.52
%LIPDL	-.26	.62	-.08	.62	.41	-.11	-.01	.56	.26		-.56	.57	-.55	.56	.19	-.41
FFL%	.56	-.82	.29	-.82	-.54	.44	.16	-.73	-.32	-.64		-.96	.92	-.89	-.44	.94
TOFAT%	-.49	.87	-.22	.86	.58	-.37	-.12	.77	.33	.37	-.97		-.89	.95	.41	-.91
LFSTIS%	.53	-.73	.38	-.82	-.23	.48	.19	-.70	-.64	.32	.92	-.88		-.94	-.07	.94
STLIP%	-.47	.82	-.29	.88	.34	.41	-.14	.77	.60	.64	-.92	.95	-.95		.12	-.91
NLFAT%	-.25	.47	.11	.27	.88	-.07	.03	.31	-.62	.32	-.50	.52	-.13	.23		-.26
DL%	.56	-.76	.35	-.80	-.38	.52	.21	-.71	-.46	-.51	.95	-.95	.95	-.92	-.33	

[a] The 220, 251 and 282 lb target weight groups are above the diagonal (N=154). The 251, 282 and 334 lb target weight groups are below the diagonal (N=153).

Variable definitions and acronyms are given in Table 1.

For |r| ≥ .15, $P<.05$.

For |r| ≥ 0.21, $P<.01$.

For |r| ≥ .26, $P<.001$.

Table 3. Correlations of carcass composition mass and carcass percentage measures with carcass and live animal ultrasound measurements.[a]

	FFLM	TOFAT	LFSTIS	STLIP	NLFAT	DL	MTPRO	MTLIP	% LIPFAT	% LIPDL	FFL %	TOFAT %	LFSTIS %	STLIP %	NLFAT %	DL %
<u>220, 251, and 282 lb weight groups</u>																
LW	.67	.73	.77	.72	.41	.67	.72	.78	.42	.20	-.18	.26	-.29	.35	-.21	-.25
CW	.70	.72	.79	.71	.39	.70	.74	.78	.43	.19	-.15	.24	-.27	.34	-.23	-.22
BFLR	-.12	.69	-.05	.72	.24	-.15	-.02	.67	.53	.34	-.61	.65	-.70	.71	-.00	-.66
FD10R	-.34	.81	-.22	.82	.37	-.37	-.17	.75	.55	.40	-.84	.88	-.86	.89	.19	-.89
LEA	.75	-.18	.72	-.19	-.02	.78	.57	-.10	-.18	-.25	.61	-.55	.55	-.50	-.29	.61
UBF	-.24	.80	-.21	.82	.34	-.25	-.09	.75	.56	.39	-.79	.82	-.83	.87	.13	-.83
UBFL	-.33	.79	-.19	.80	.38	-.35	-.18	.72	.52	.36	-.82	.85	-.83	.88	.21	-.87
ULEA	.81	.08	.81	.07	.08	.84	.69	.17	-.00	-.10	.46	-.38	.38	-.31	-.32	.45
FAT34	-.35	.77	-.24	.78	.34	-.37	-.17	.69	.53	.40	-.82	.84	-.84	.86	.18	-.86
MD34	.44	-.18	.42	-.20	-.03	.32	.32	-.18	-.16	-.21	.43	-.37	.42	-.36	-.15	.47
<u>251, 282, and 334 lb weight groups</u>																
LW	.57	.79	.76	.74	.65	.64	.77	.82	.09	.33	-.34	.39	-.29	.36	.23	-.30
CW	.60	.78	.77	.74	.64	.66	.78	.82	.10	.33	-.33	.37	-.28	.35	.21	-.28
BFLR	-.27	.73	-.08	.75	.42	-.19	.02	.67	.38	.51	-.74	.77	-.72	.77	.28	-.72
FD10R	-.38	.80	-.19	.84	.39	-.35	-.06	.75	.49	.48	-.88	.87	-.89	.90	.26	-.91
LEA	.77	-.07	.75	-.13	.15	.80	.62	-.01	-.31	-.23	.50	-.43	.54	-.47	-.06	.57
UBF	-.43	.73	-.26	.79	.34	-.41	-.08	.69	.48	.46	-.83	.83	-.86	.87	.25	-.86
UBFL	-.46	.74	-.27	.80	.38	-.38	-.13	.69	.46	.45	-.86	.86	-.88	.89	.29	-.89
ULEA	.81	.07	.81	.01	.20	.85	.74	.14	-.22	-.07	.39	-.33	.42	-.36	-.08	.46
FAT34	-.38	.76	-.19	.80	.37	-.33	-.04	.69	.46	.49	-.83	.84	-.85	.86	.26	-.86
MD34	.52	-.03	.54	-.10	.19	.56	.45	-.03	-.31	-.19	.32	-.27	.40	-.33	.06	.40

[a] N=154 for 220, 251 and 282 lb weight groups. N=153 for 251, 282 and 334 lb weight groups.
Variable definitions and acronyms are given in Table 1.
For |r| ≥ .15, P<.05.
For |r| ≥ .21, P<.01.
For |r| ≥ .26, P<.001.

Table 4. Equations and regression analysis for predicting fat-free lean, lipid-free soft tissue, total carcass fat, and soft tissue lipid mass (lb) from the actual or predicted value of the similar alternative measure of carcass composition.

Dependent Variable /		220, 251, and 282 lb weight groups[b] (N=154)					251, 282, and 334 lb weight goups[b] (N=153)				
	Variable[a]	R^2	RSD, lb	b_0	b_i	Signif[c]	R^2	RSD, lb	b_0	b_i	Signif[c]
FFLM											
	CW	.93	3.3	-7.00	-.085	.001	.89	4.4	6.79	-.145	.020
	LFSTIS				1.06	.001				1.03	.037
	CW	.88	4.2	-8.33	-.120	.001	.84	5.3	5.42	-.171	.001
	PLFSTIS				1.13	.001				1.10	.001
LFSTIS											
	CW	.95	2.9	8.13	.131	.001	.93	3.7	-1.96	.186	.001
	FFLM				.814	.001				.809	.001
	CW	.91	3.7	7.39	.106	.001	.92	4.2	-4.94	.156	.001
	PFFLM				.880	.001				.912	.001
TOFAT											
	CW	.96	3.1	7.89	.0319	.054	.96	4.4	-5.27	.0999	.001
	STLIP				1.07	.001				1.07	.001
	CW	.89	5.1	10.74	NS	.59	.89	6.8	-4.85	.0940	.001
	PSTLIP				1.12	.001				1.08	.004
STLIP											
	CW	.95	12.9	-7.89	NS	.43	.95	3.7	.710	-.0319	.078
	TOFAT				.863	.001				.830	.001
	CW	.89	4.4	-9.50	NS	.58	.91	5.1	4.49	-.0869	.001
	PTOFAT				.888	.001				.924	.001

[a] CW = warm carcass weight (lb), FFLM = fat-free lean muscle (lb), PFFLM = predicted fat-free lean muscle mass (lb), LFSTIS = lipid-free soft tissue (lb), PLFSTIS = predicted lipid-free soft tissue mass (lb), TOFAT = total carcass fat tissue mass (lb), PTOFAT = predicted total carcass fat tissue mass (lb), STLIP = soft tissue lipid mass (lb), and PSTLIP = predicted soft tissue mass (lb). PSTLIP, PTOFAT, PFFLM and PLFSTIS were predicted from ribbed carcass measurements (FD10R, CW, and LEA).

[b] b_0 = intercept, b_i = partial regression coefficient of the ith independent variable, R^2 = coefficient of determination, and RSD = residual standard deviation.

[c] Signif = significance.

Table 5. Significance of residual mean value (biases) for genotype populations and sex subpopulations in the prediction of fat-free lean mass (lb) and lipid-free soft tissue mass (lb) when predicted from the alternative measures of lean mass[a].

	Light weight data sets (220, 251, and 282 lbs)				Heavy weight data sets (251, 282, and 334 lbs)			
Dependent Variable / Variable	Genetic Population Signif.	Sex Signif.	CR[b]	VR[b]	Genetic Population Signif.	Sex Signif.	CR[b]	VR[b]
FFLM								
CW, LFSTIS	.19	.20	.98	.90	.04	.05	.98	.80
CW, PLFSTIS	.007	.76	.96	.87	.001	.41	.94	.79
LFSTIS								
CW, FFLM	.27	.46	.99	.84	.013	.81	.97	.87
CW, PFFLM	.20	.71	.98	.85	.36	.81	.98	.86

[a] CW = warm carcass weight (lb), FFLM = fat-free lean mass (lb), PFFLM = predicted fat-free lean mass (lb), LFSTIS = lipid-free soft tissue (lb), and PLFSTIS = predicted lipid-free soft tissue (lb). PFFLM and PLFSTIS were predicted using an equation which included CW, LEA and FD10R.

[b] CR and VR are the correlations and variance ratios, respectively, between the predicted and observed genetic population-sex mean values. Negative residual values indicate overestimation and positive residual values indicate underestimation of the actual value of the dependent variable.

Table 6. Significance of residual mean value (biases) for genotype populations and sex subpopulations in the prediction of total carcass fat mass and soft tissue lipid mass when predicted from the alternative measure of lipid or fat tissue mass[a].

	Light weight data sets (220, 251, and 282 lbs)				Heavy weight data sets (251, 282, and 334 lbs)			
Dependent Variable / Variable	Genetic Population Signif.	Sex Signif.	CR[b]	VR[b]	Genetic Population Signif.	Sex Signif.	CR[b]	VR[b]
TOFAT								
CW, STLIP	.23	.40	.99	.89	.03	.18	.98	.93
CW, PSTLIP	.01	.31	.99	.92	.001	.06	.94	.84
STLIP								
CW, TOFAT	.28	.57	.99	.95	.01	.53	.99	.86
CW, PTOFAT	.24	.18	.98	.84	.20	.20	.97	.88

[a] CW = warm carcass weight (lb), STLIP = soft tissue lipid mass (lb), PSTLIP = predicted soft tissue lipid mass (lb), TOFAT = total carcass fat tissue mass (lb), and PTOFAT = predicted total carcass fat tissue mass (lb). PTOFAT and PSTLIP were predicted using an equation which included CW, LEA and FD10R.

[b] CR and VR are the correlations and variance ratios, respectively, between the predicted and observed genetic population-sex mean values. Negative residual values indicate overestimation and positive residual values indicate underestimation of the actual value of the dependent variable.