Evaluation of Alternative Measures of Pork Carcass Composition

A.P. Schinckel, J.R. Wagner, J.C. Forrest, and M.E. Einstein
Department of Animal Sciences and Elanco Animal Health, Indianapolis

Introduction

Research has been conducted to evaluate effects of experimental treatments, to model pig growth, and to evaluate pork production systems (Schinckel and de Lange, 1996). Alternative endpoints include physical carcass dissection, fat-free or fat-standardized lean mass, mass of trimmed retail cuts, and empty body chemical composition. Carcass composition endpoints should be accurately and economically predicted from easily obtained carcass measurements. The prediction equations should be carefully evaluated for their ability to account for the differences due to genetic population, sex and weight. The objectives of this study were to evaluate the alternative methods of defining pork carcass composition and develop a further understanding of the interrelationships among various pork carcass and empty body composition endpoints.

Materials and Methods

Experimental Animals and Slaughter Procedures

Data from 203 pigs, representing seven genotypes and two sexes (gilts and barrows) were used (Hicks et al., 1998). The pigs were removed individually from the research trial at their predetermined target slaughter weight of 220, 251, 282, or 334 lbs. Pigs were weighed (on farm) and live animal B-mode ultrasound (Aloka Model 500V) measurements were taken for backfat depth, 2.8 in. off-midline, at the 10^{th} rib (UBF) and last rib (UBFL). Ultrasonic measurements of the loin eye area were also taken at the 10^{th} rib (ULEA). The pigs were transported to the Purdue University Meat Laboratory for slaughter and carcass dissection. At approximately 45 min after exsanguination, the right side of each carcass was probed 2.8 in. from midline with an optical probe (HGP4, Hennessy Grading Probe) between the third and fourth ribs anterior from the last rib.

The right sides were then placed in a 35°F chilling unit for 24 hours before carcass measurements were taken. Midline backfat thickness was measured at the last rib. Loin eye area and fat depth measurements (three-quarters of the length of the transverse section of the exposed longissimus muscle) were taken between the 10^{th} and 11^{th} ribs.

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). The second method, based largely on chemical analysis, partitions the soft tissue into lipid-free soft tissue (LFSTIS) and soft tissue lipid (STLIP).

Fat-free lean mass (FFLM) is a measure of dissected carcass lean muscle after accounting for the predicted amount of fat tissue remaining in the dissected lean. To determine FFLM, the

total fat tissue mass including connective tissue, water, and ash mass associated with adipose tissue must be taken into account. Calculation of FFLM of each of the five carcass components (four lean cuts and other soft tissue) was determined with the following equation: FFLM = DL [1-(CL%/CLT%)], where DL was dissected lean or other soft tissue mass, CL% was the percentage of lipid in the dissected lean of the four lean cuts and other soft tissue, and CLT% was the percentage of lipid in the pooled dissected fat sample. Total carcass FFLM is the sum of the FFLM of each of the four lean cuts and other soft tissue. Total carcass fat (TOFAT) is the fat tissue contained within the carcass soft tissue. TOFAT is the sum of the dissected fat plus the predicted amount of undissected fat (CL%/CLT%) within each of the four lean cuts and other soft tissue.

Lipid-free soft tissue mass (LFSTIS) is the sum of the lipid-free mass of each of the six carcass components (dissected lean of the four primal cuts, other soft tissue, and pooled disssected fat sample). Carcass soft tissue lipid mass (STLIP) was calculated as the sum of the lipid mass of each of the six carcass components. Both sets of carcass composition variables sum to soft tissue mass. LFSTIS includes FFLM plus the lipid-free (water, protein and ash) mass associated with the carcass fat tissue, both within the dissected fat and dissected lean tissue.

Statistical Analysis

Least squares means were calculated with a model consisting of sex, weight group, genetic population, their interactions, and slaughter weight deviation (a covariate used to adjust each pig's slaughter weight to the actual mean of the target weight group). Regression equations for predicting the mass of the carcass composition endpoint measures were developed using the GLM procedure of SAS (1992). Independent variables were grouped according to the type of measurements used (i.e., midline ruler, optical probe, ribbed carcass, and live ultrasonic scanning). Accuracy of each prediction equation was evaluated by R^2, which is the multiple coefficient of determination, and the residual standard deviation (RSD).

Least squares means of the residual values for the genetic population, sex, and target weight subclasses were evaluated as estimates of subpopulation biases (Gu et al., 1992). The correlation coefficients (CR) between the 14 predicted and observed genotype-sex means were used as measures of genotype bias. The proportion of variation among genotypes accounted for by each equation was determined by the variance ratio (VR), which is the variance of predicted genotype-sex means divided by the variance of observed means.

Weight group ($P<.001$), genetic population x weight group ($P<.01$), and sex x weight group ($P<.05$) biases were found to be significant. Thus, 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).

Results

Acronyms and definitions for the variables are presented in Table 1. Table 1 also contains the overall and sex means for the light and heavy weight data sets. LFSTIS was 17.4 lbs greater than FFLM (98.3 vs. 80.9 lbs) in the light weight data set and 20.5 lbs greater (111.6 vs. 91.1 lbs) in the heavy weight data set. LFSTIS percentage was 9.5 units greater than FFLM percentage in

both the light and heavy weight data. Overall, gilts had 7.9 lbs (9.7%) greater FFLM and 6.9 lbs (6.8%) greater LFSTIS than barrows. Also, gilts had less TOFAT, NLFAT, and STLIP than barrows.

Prediction equations for FFLM and LFSTIS are presented in Tables 2 and 3. Summary statistics describing biases associated with genetic population, sex and weight group are presented in Table 6. The highest RSD values were produced by a combination of carcass weight and midline last rib measurements (Equation 1). The equations based on ribbed carcass measurements (CW, LEA and FD10R; Equation 3) were slightly more accurate than the equations based on live weight and live-animal ultrasonic measurements (Equation 4).

Overall, equations predicting LFSTIS had higher R^2 values and lower RSD values than equations predicting FFLM. The LFSTIS equations had RSD's averaging 4.6% of the mean LFSTIS. The RSD's of the FFLM prediction equations averaged 6.5% of the mean FFLM value.

For the same prediction equation and weight range of the data, the majority (7 of 8) of the LFSTIS equations had larger regression coefficients for CW or LW and smaller regression coefficients for the measures of backfat (the sum of the UBF and UBFL coefficients for Equation 4) than the FFLM equations.

All equations overestimated the FFLM and LFSTIS of the barrows and underestimated the lean content of the gilts. However, the magnitude of the sex biases were substantially smaller for Equations 3 and 4, which included loin eye area measurements (LEA or ULEA). Overall, the prediction equations ranked the genetic populations correctly for the three measures of carcass "lean" mass, as CR ranged from .88 to .97. However, Equation 1 had substantially smaller VR values (.32 to .43) than the other prediction equations (.72 to .96).

Prediction equations for TOFAT and TLIPID are presented in Tables 4 and 5. Equation 3 (ribbed carcass measurements) was most accurate followed by Equation 4 (live animal ultrasound and LW), Equation 2 (optical probe) and Equation 1 (CW and BFLR). Summary statistics describing biases associated with the prediction of TOFAT and STLIP are presented in Table 6. All equations overestimated the TOFAT and STLIP of the gilts and underestimated the barrows. In general, the prediction equations ranked the genetic populations properly (CR = .87 to .97). However, Equation 1 (VR = .38 to .59) and Equation 2 (VR = .72 to .80) predicted less variation for the genetic population-sex means than the actual variation in genetic population-sex means.

Discussion

The primary objective of this study was to evaluate the two alternative methods used to define pork carcass composition. The first method results in the carcass soft tissue being divided into two tissue fractions, fat-tissue-free lean and total carcass fat. Numerous researchers have adjusted dissected carcass lean mass to a fat-tissue-free basis (Fahey et al., 1977; Wagner et al., 1999). Other researchers, based on chemical analysis, have separated soft tissue into LFSTIS and STLIP. Essentially the measurements of lean mass account for either the fat tissue contained within the muscle tissue (FFLM) or the percent lipid within the soft tissue (both muscle and fat).

LFSTIS includes the FFLM and the mass of the non-lipid components (water, protein and ash) of the carcass fat tissue. The difference between TOFAT and STLIP is also NLFAT. NLFAT was affected by genetic population, sex, weight group, and genetic population by weight interactions. Because LFSTIS includes both FFLM and NLFAT, the absolute and percentage differences between FFLM and LFSTIS will differ for specific genetic populations, sexes and experimental treatments. Treatment, genotype or sex differences for FFLM will tend to have smaller actual and predicted differences for LFSTIS growth. For example, from 220 to 334 lbs live weight, gilts have a 12.9% greater FFLM gain than barrows (32.8 vs. 29.1 lb, Table 3) and 12.1% greater protein accretion (14.3 vs. 13.0 lb), but only a 4.4% greater LFSTIS gain (42.1 vs. 40.3 lb) than barrows. Thus, if the objective of an experiment is to specifically measure muscle growth or protein accretion, FFLM should be used.

FFLM gain has been extensively used to predict lysine requirements (Schinckel and de Lange, 1996; NRC, 1998). Muscle tissue has high concentrations of lysine and other essential amino acids. Muscle growth accounts for approximately 70% of the total body lysine accretion. NLFAT gain contains approximately 11.7% crude protein and is low in lysine and other essential acids. For this reason, predicted daily lysine requirements are proportional to daily FFLM gain.

From a practical perspective, biases occur when different subpopulations – genetic populations, sexes, weight groups or treatments – have different values of the dependent variable (Y) at identical values of the independent variables (Gu et al., 1992; Wagner et al., 1993). Subpopulation differences in the distribution of lean and fat tissues and the chemical composition of the fat and lean tissues are partially responsible for subpopulation biases.

Implications

Fat-free lean mass is a more precise measurement of muscle mass and essential amino acid requirements than lipid-free soft tissue. Lipid-free soft tissue is a less expensive measurement of carcass composition than fat-free lean mass. Measures of carcass composition must be clearly and consistently defined.

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

Acronym	Definition of variable and unit of measurement	220, 251, and 284 lb weight groups				251, 284, and 334 lb weight groups			
		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	16.7
NLFAT	Non-lipid carcass fat tissue mass, lb	17.4	17.81	16.98	3.5	20.57	21.43	19.71	5.5
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
FD10R	Fat depth at 10^{th} 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 10^{th} 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 10^{th} rib loin eye area, $in.^2$	6.00	5.74	6.26	.85	6.64	6.35	6.89	.93
UBF	Ultrasonic backfat 10^{th} 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

Table 2. Equations and regression analysis for predicting fat-free lean mass (lb) using measurements from various technologies.

		220, 251, and 282 lb weight groups[b]						251, 282, and 335 lb weight groups[b]					
Eq.	Variable[a]	n	R^2	RSD, lb	b_0	b_i	Signif[c]	n	R^2	RSD, lb	b_0	b_i	Signif[c]
1	CW	154	.68	6.86	21.4	.478	.001	153	.66	7.85	42.8	.410	.001
	BFLR					-25.1	.001					-31.5	.001
2	CW	153	.84	4.78	8.02	.460	.001	152	.79	6.12	22.7	.385	.001
	MD34					6.27	.001					8.12	.001
	FD34					-23.07	.001					-25.93	.001
3	CW	154	.87	4.32	11.00	.434	.001	153	.84	5.40	25.2	.367	.001
	LEA					2.39	.001					2.75	.001
	FD10R					-18.93	.001					-21.10	.001
4	LW	142	.85	4.78	1.39	.324	.001	138	.83	5.69	24.4	.218	.001
	UBF					3.58	.09					-4.00	.10
	UBFL					-17.58	.001					-18.53	.001
	ULEA					3.85	.001					4.91	.001

[a] CW = warm carcass weight (lb), BFLR = last rib midline backfat thickness (in), FD34 = optical probe off-midline fourth rib 3/4 fat depth (in), MD34 = optical probe fourth rib muscle depth (in), LEA = 10^{th} rib loin eye area (in^2), FD10R = off-midline 10^{th} rib fat depth (in), LW = live weight, UBFL = ultrasonic backfat at last rib (in), ULEA = ultrasonic 10^{th} rib loin eye area (in^2), and UBF = ultrasonic backfat at the 10^{th} rib (in).

[b] b_0 = intercept, b_i = partial regression coefficient of the i^{th} independent variable, n = number of observations used in the model, R^2 = coefficient of determination, and RSD = residual standard deviation.

[c] Signif = significance.

Table 3. Equations and regression analysis for predicting lipid-free soft tissue mass (lb) using measurements from various technologies.

		220, 251, and 282 lb weight groups[b]						251, 282, and 335 lb weight groups[b]					
Eq.	Variable[a]	n	R^2	RSD, lb	b_0	b_i	Signif[c]	n	R^2	RSD, lb	b_0	b_i	Signif[c]
1	CW	154	.79	5.88	26.8	.533	.001	153	.78	7.05	33.5	.524	.001
	BFLR					-23.5	.001					-27.4	.001
2	CW	153	.89	4.12	13.0	.511	.001	152	.90	4.94	12.5	.498	.001
	MD34					6.21	.001					9.63	.001
	FD34					-20.1	.001					-22.9	.001
3	CW	154	.91	3.75	16.2	.481	.001	153	.92	4.30	18.1	.491	.001
	LEA					2.36	.001					2.49	.001
	FD10R					-16.1	.001					-19.4	.001
4	LW	142	.90	4.08	3.8	.385	.001	138	.91	4.70	15.5	.345	.001
	UBF					-6.10	.01					-4.98	.05
	UBFL					-11.9	.001					-16.4	.001
	ULEA					3.34	.001					3.80	.001

[a] CW = warm carcass weight (lb), BFLR = last rib midline backfat thickness (in), FD34 = optical probe off-midline fourth rib 3/4 fat depth (in), MD34 = optical probe fourth rib muscle depth (in), LEA = 10^{th} rib loin eye area (in^2), FD10R = off-midline 10^{th} rib fat depth (in), LW = live weight, UBFL = ultrasonic backfat at last rib (in), ULEA = ultrasonic 10^{th} rib loin eye area (in^2), and UBF = ultrasonic backfat at the 10^{th} rib (in).

[b] b_0 = intercept, b_i = partial regression coefficient of the i^{th} independent variable, n = number of observations used in the model, R^2 = coefficient of determination, and RSD = residual standard deviation.

[c] Signif = significance.

Table 4. Equations and regression analysis for predicting total carcass fat mass (lb) using measurements from various technologies.

		220, 251, and 282 lb weight groups[b]						251, 282, and 335 lb weight groups[b]					
Eq.	Variable[a]	n	R^2	RSD, lb	b_0	b_i	Signif[c]	n	R^2	RSD, lb	b_0	b_i	Signif[c]
1	CW	154	.71	8.24	-33.9	.359	.001	153	.81	8.99	-56.8	.432	.001
	BFLR					31.85	.001					38.86	.001
2	CW	153	.85	5.89	-21.4	.379	.001	152	.87	7.58	-35.2	.460	.001
	MD34					-5.35	.02					-7.67	.004
	FD34					25.14	.001					31.19	.001
3	CW	154	.89	5.20	-23.6	.395	.001	153	.89	6.86	-38.1	.467	.001
	LEA					-2.13	.004					-2.35	.007
	FD10R					25.14	.001					26.48	.001
4	LW	142	.87	5.36	-33.7	.327	.001	138	.88	7.05	-50.0	.425	.001
	UBF					7.28	.02					8.90	.02
	UBFL					27.8	.001					19.6	.001
	ULEA					-1.96	.02					-3.46	.001

[a] CW = warm carcass weight (lb), BFLR = last rib midline backfat thickness (in), FD34 = optical probe off-midline fourth rib 3/4 fat depth (in), MD34 = optical probe fourth rib muscle depth (in), LEA = 10^{th} rib loin eye area (in^2), FD10R = off-midline 10^{th} rib fat depth (in), LW = live weight, UBFL = ultrasonic backfat at last rib (in), ULEA = ultrasonic 10^{th} rib loin eye area (in^2), and UBF = ultrasonic backfat at the 10^{th} rib (in).

[b] b_0 = intercept, b_i = partial regression coefficient of the i^{th} independent variable, n = number of observations used in the model, R^2 = coefficient of determination, and RSD = residual standard deviation.

[c] Signif = significance.

Table 5. Equations and regression for predicting soft tissue lipid mass (lb) using measurements from various technologies.

		220, 251, and 282 lb weight groups[b]						251, 282, and 335 lb weight groups[b]					
Eq.	Variable[a]	n	R^2	RSD, lb	b_0	b_i	Signif[c]	n	R^2	RSD, lb	b_0	b_i	Signif[c]
1	CW	154	.73	3.18	-39.5	.304	.001	153	.79	3.54	-21.6	.317	.001
	BFLR					30.29	.001					6.20	.001
2	CW	153	.86	2.28	-26.4	.328	.001	152	.88	2.66	-25.1	.347	.001
	MD34					-5.32	.001					-9.18	.001
	FD34					26.43	.001					28.17	.001
3	CW	154	.89	2.02	-28.7	.348	.001	153	.91	2.35	-31.1	.343	.001
	LEA					-2.11	.001					-2.09	.002
	FD10R					22.29	.001					24.69	.001
4	LW	142	.88	2.03	-35.9	.265	.001	138	.90	2.38	-41.2	.299	.001
	UBF					9.80	.001					9.86	.001
	UBFL					13.38	.001					17.36	.001
	ULEA					-1.45	.04					-2.35	.002

[a] CW = warm carcass weight (lb); BFLR = last rib midline backfat thickness (in); FD34 = optical probe off-midline fourth rib 3/4 fat depth (in); MD34 = optical probe fourth rib muscle depth (in); LEA = 10^{th} rib loin eye area (in^2); FD10R = off-midline 10^{th} rib fat depth (in); LW = live weight; UBFL = ultrasonic backfat at last rib (in); LEA = ultrasonic 10^{th} rib loin eye area (in^2); and UBF = ultrasonic backfat at the 10^{th} rib (in).

[b] b_0 = intercept, b_i = partial regression coefficient of the i^{th} independent variable, n = number of observations used in the model, R^2 = coefficient of determination, and RSD = residual standard deviation.

[c] Signif = significance.

Table 6. Evaluation of biases for genotype populations, sex, and weight group subpopulations in the prediction of the carcass component mass.

		Light weight data sets (220, 251, and 282 lbs)				Heavy weight data sets (251, 282, and 334 lbs)			
Eq.	Variables[a]	Genetic population Signif.	Sex Signif.	CR[b]	VR[b]	Genetic population Signif.	Sex Signif.	CR[b]	VR[b]
FFLM - Fat-free lean mass, lb									
1	CW, BFLR	.01	.001	.88	.35	.001	.018	.89	.48
2	CW, FD34, MD34	.10	.11	.96	.92	.09	.013	.94	.72
3	CW, FD10R, LEA	.008	.53	.96	.93	.001	.40	.94	.79
4	LW, UBF, UBFL, ULEA	.001	.23	.88	.98	.001	.25	.90	.89
LFSTIS - lipid-free soft tissue mass, lb									
1	CW, BFLR	.02	.001	.89	.39	.001	.04	.88	.49
2	CW, FD34, MD34	.64	.20	.96	.87	.55	.08	.97	.81
3	CW, FD10R, LEA	.20	.65	.97	.85	.40	.81	.97	.87
4	LW, UBF, UBFL, ULEA	.002	.37	.96	.97	.004	.81	.93	.96
TOFAT - Total carcass fat mass, lb									
1	CW, BFLR	.02	.001	.38	.38	.32	.007	.94	.59
2	CW, FD34, MD34	.03	.03	.72	.72	.34	.001	.93	.78
3	CW, FD10R, LEA	.03	.21	.81	.81	.008	.06	.94	.84
4	LW, UBF, UBFL, ULEA	.004	.36	.82	.82	.001	.10	.93	1.00
STLIP - Soft tissue lipid mass, lb									
1	CW, BFLR	.02	.001	.87	.43	.07	.01	.94	.58
2	CW, FD34, MD34	.10	.04	.97	.76	.53	.003	.96	.80
3	CW, FD10R, LEA	.22	.28	.98	.85	.21	.20	.97	.88
4	LW, UBF, UBFL, ULEA	.005	.49	.97	.86	.01	.39	.95	1.02

[a] CW = warm carcass weight (lb), BFLR = midline backfat thickness at last rib (in), FD34 = optical probe off-midline fourth rib 3/4 fat depth (in), MD34 = optical probe fourth rib muscle depth (in), LEA = 10^{th} rib loin eye area (in^2), FD10R = off-midline 10^{th} rib fat depth, LW = live weight, ULEA = ultrasonic 10^{th} rib loin eye area (in^2), UBF = ultrasonic backfat at 10^{th} rib (in), and UBFL = ultrasonic fat depth at last rib (in).

[b] CR and VR are the correlations and variance ratios, respectively, between the predicted and observed genetic population-sex means.