The Ability of Measures of Carcass Composition to Predict Empty Body Protein and Lipid 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. Scientists with an interest in modeling pig growth and predicting nutrient requirements require accurate esimates of empty body chemical composition. Empty body protein and lipid mass are expensive and difficult to obtain. Actual or predicted measures of fat-free lean are more easily obtained.

The objectives of this study were to evaluate the reliability of predictive measures of carcass composition and to develop a 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 (barrows and gilts), 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).

The ability to accurately predict empty body protein (MTPRO) and lipid mass (MTLIP) from the carcass measures was evaluated by regression analyses. MTPRO data were fit to regression equations including carcass weight (CW) and either the actual or predicted values of fat-free lean mass (FFLM), lipid-free soft tissue (LFSTIS), or dissected lean in the four lean cuts (DL). Empty body lipid mass (MTFAT) data were fit to regression equations including CW and either the actual or predicted values of total carcass fat (TOFAT) and total soft tissue lipid (TLIPID). The predicted values of the alternative measure of carcass composition were predicted from ribbed carcass measurements.

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 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.

Results

Acronyms and definitions of the variables are presented in Table 1. Table 1 also contains overall and sex means for the light and heavy weight data sets. Table 2 contains means for empty body protein and empty body lipid mass, for the two sexes, four weight groups, and seven genetic populations.

Prediction equations for MTPRO are presented in Table 3 and the residual value statistics are presented in Table 4. Equation 1 includes the standard ribbed carcass measurements (CW, 10th rib fat depth [FD10R] and carcass loin eye area [LEA]). The other equations include CW (if significant) and either the actual or predicted value of LFSTIS or FFLM. The predicted values were determined from equations including the ribbed carcass measurements.

Overall, there was no substantial advantage in terms of R^2 or magnitude of biases to favor the use of the actual versus the predicted LFSTIS or FFLM in the prediction of MTPRO. Also, there was no advantage of using one measure of carcass "lean" mass over another in the prediction of MTPRO. Carcass weight was significant for each equation (P<.01), indicating that MTPRO cannot be predicted as a simple linear function of any of the actual or predicted carcass composition measurements. Not including the CW term resulted in significant (P<.01) weight group biases.

LEA was not significant (P=.92) in equation 1 for the light weight data and had marginal impact (P=.17) in the heavy pig data. The MTPRO of genetic population 4 (G₄) was overestimated by each prediction equation. This is likely caused by G₄ having a different ratio of MTPRO to the carcass composition measures than the other genetic populations. G₄ had less visceral protein than the overall mean (3.77 vs. 4.03 lb) and a slightly higher dressing percentage (75.8 vs. 74.8%). For all other genetic populations, the mean absolute value of bias is 1.0 to 1.7% of the mean value. Sex and weight group biases were not significant in the prediction of MTPRO.

Prediction equations for MTLIP are presented in Table 5 and the summary of residual value statistics are presented in Table 6. Overall, the R^2 are higher (.88 to .92) for the prediction equations for MTLIP than MTPRO ($R^2 = .74$ to .82). Overall, the use of actual TOFAT or STLIP data in the prediction of MTLIP resulted in R^2 values of .82 to .93. The inclusion of predicted TOFAT and STLIP of standard carcass measurements resulted in R^2 values of .88. Carcass weight was significant for each equation (P<.001), indicating that MTLIP cannot be predicted as a simple linear function of the actual or predicted values of TOFAT or STLIP. The regression coefficients for the predicted or actual values of TOFAT and STLIP are smaller for the heavy weight data than the light weight data.

There were no significant genetic population (P>.10) or weight group (P>.57) biases in the prediction of MTLIP. The CR values (.97 to .98) indicate that the prediction equations rank the genetic populations correctly. The VR values ranged from 85 to 93%. However, the MTLIP of gilts was over predicted by .73 lb in the light weight and .95 lb in the heavy weight data. With an 8.34 and 10.23 lb difference in MTLIP between the barrows and gilts in the light and heavy weight data (Table 1), the prediction equations account for 80% of the true difference in MTLIP between the barrows and gilts.

Discussion

The mass and growth of MTPRO and MTLIP are primary inputs needed to model nutrient (energy, protein and macromineral) requirements. MTPRO and MTLIP are expensive to obtain on a regular basis; thus, they must be predicted from less costly measurement methods in order to estimate farm-specific nutritional requirements.

It was expected that the measures of carcass composition based on chemical analysis (STLIP and LFSTIS) would result in the most accurate predictions of MTPRO and MTLIP. Standard ribbed carcass measurements (CW, LEA, FD10R) and either the actual or predicted values of LFSTIS or FFLM resulted in MTPRO prediction equations with similar accuracy in terms of RSD, VR, CR and magnitude of biases. Equations including STLIP were slightly more accurate (.01 higher R^2 , .1 to .2 lower RSD) in predicting MTLIP than equations including TOFAT. Equations including the actual STLIP or TOFAT values were more accurate (.04 to .05 higher R^2 , .5 to .7 lb lower RSD) than equations using the predicted values of TOFAT, STLIP or ribbed carcass measurements.

The predicted values of the measures of carcass composition were from equations including CW, FD10R and LEA. These equations were the most accurate in terms of RSD, VR and CR. Using the predicted values from other prediction equations would have resulted in less accurate, more biased prediction of the measures of empty body composition.

Implications

Empty body protein and lipid mass are used to predict daily nutrient requirements. Predicted or actual values of measures of carcass composition or standard carcass measurements can be used to predict empty body protein and lipid in market weight pigs.

References

Gu, Y., A.P. Schinckel, T.G. Martin, J.C. Forrest, C.H. Kuei, and L.E. Watkins. 1992. Genotype and treatment biases in estimation of carcass lean of swine. J. Anim. Sci. 70:1708-1718.

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

			220, 251, an weight g	d 284 lb roups		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	16.7	
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	15.6	85.16	90.32	80.09	19.1	

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	Empty body protein, lb	Empty body lipid, lb
Sex		
Barrows	32.41	82.23
Gilts	35.27	73.63
SE	.25	.88
Significance	.0001	.0001
Weight group		
220	28.22	54.90
251	31.75	67.46
282	35.71	84.44
334	40.56	105.2
SE	.40	1.26
Significance	.0001	.0001
Genetic population		
1	32.63	83.11
2	35.94	70.99
3	34.61	77.16
4	33.73	79.81
5	33.29	80.25
6	33.51	80.69
7	34.39	73.85
SE	.49	1.59
Significance	.001	.0001

Table 2. Least squares means for empty body protein mass and empty body lipid mass in the dissected fat tissue^a.

^aPooled dissected lean or fat tissue from the four lean cuts.

Table 3.	Equations	and	regression	analysis	for	predicting	empty	body	protein	mass	(lb)	using	various	carcass	measurements	and
dissection	data.															

		220,	251, and 282	lb weight	groups ^b (N	=152)	251, 292, and 334 lb weight groups ^b (N=152)					
Eq.	Variable ^a	\mathbb{R}^2	RSD, lb	b_0	bi	Signif ^c	\mathbf{R}^2	RSD, lb	b_0	b_i	Signif ^c	
1	CW LEA FD10R	.75	.93	8.18	.167 (NS) -5.88	.001 .92 .001	.79	1.08	4.06	.170 .307 -5.28	.001 .17 .001	
2	CW LFSTIS	.75	.93	2.05	.0324 .242	.01 .001	.81	1.01	86	.0461 .238	.001 .001	
3	CW PLFSTIS	.74	.95	1.63	.0191 .272	.17 .001	.79	1.08	-1.08	.0415 .248	.001 .001	
4	CW FFLM	.77	.89	3.77	.0578 .224	.001 .001	.81	1.00	1.87	.0851 .212	.001 .001	
5	CW PFFLM	.74	.95	3.61	.0475 .240	.001 .001	.79	1.08	-2.31	.0808 .227	.001 .001	

^a CW = warm carcass weight (lb), LEA = 10^{th} rib loin eye area (in²), FD10R = off-midline 10th rib fat depth (in), LFSTIS = lipid-free soft tissue, PLFSTIS = predicted lipid-free soft tissue mass (lb), and PFFLM = predicted fat-free lean muscle mass (lb). PFFLM and PLFSTIS were predicted using equations which included CW, LEA, and FD10R. ^b b₀ = intercept, b_i = partial regression coefficient of the ith independent variable, R² = coefficient of determination, RSD = residual

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

^c Signif = significance.

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		Ligh (220,	t weight of 251, and	data sets 282 lbs)	Heavy weight data sets (251, 282, and 335 lbs)						
Eq.	Variable	Genetic Population Signif.	Sex Signif.	CR ^b	VR ^b	Genetic Population Signif.	Sex Signif.	CR ^b	VR ^b			
1	CW, LEA, FD10R	.11	.54	.86	.79	.41	.34	.90	.78			
2	CW, LFSTIS	.06	.40	.83	.76	.50	.19	.91	.84			
3	CW, PLFSTIS	.05	.68	.82	.79	.35	.37	.89	.79			
4	CW, FFLM	.15	.62	.88	.78	.29	.38	.93	.90			
5	CW, PFFLM	.05	.68	.83	.79	.34	.38	.89	.79			

Table 4. Significance of residual mean value (biases) for genotype populations and sex subpopulations in the prediction of empty body protein mass.^a

^a CW = warm carcass weight (lb), LEA = 10th rib loin eye area (in²), FD10R = off-midline 10th rib fat depth (in), FFLM = fat-free lean mass (lb), PFFLM = predicted fat-free lean muscle mass (lb), LFSTIS = lipid-free soft tissue mass (lb), PLFSTIS = predicted lipid-free soft tissue mass (lb), DL = dissected lean in the four lean cuts (lb), and PDL = predicted dissected lean mass (lb).

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

Table 5.	Equations	and	regression	analysis	for	predicting	empty	body	lipid	mass	(lb)	using	various	carcass	measurements	and
dissection	data.															

		220,	251, and 282	lb weight	groups ^b (N	=152)	251, 292, and 334 lb weight groups ^b (N=152)					
Eq.	Variable ^a	\mathbb{R}^2	RSD, lb	b_0	b_i	Signif ^c	\mathbf{R}^2	RSD, lb	b_0	b_i	Signif ^c	
1	CW LEA FD10R	.88	2.5	-32.8	.465 -2.06 21.95	.001 .008 .001	.88	3.0	-34.2	.489 -2.36 20.55	.001 .005 .001	
2	CW TOFAT	.92	2.0	-13.7	.134 .834	.001 .001	.92	2.5	-7.1	.133 .749	.001 .001	
3	CW PTOFAT	.88	2.5	-12.6	.108 .890	.001 .001	.88	3.0	-4.6	.0977 .811	.005 .001	
4	CW STLIP	.93	1.9	-5.3	.137 .945	.001 .001	.93	2.3	-8.8	.177 .872	.001 .001	
5	CW PSTLIP	.88	2.5	-4.6	.121 .986	.001 .001	.88	3.0	-8.8	.174 .877	.001 .001	

^a CW = warm carcass weight (lb), LEA = 10^{th} rib loin eye area (in²), FD10R = off-midline 10^{th} rib fat depth (in), TOFAT = total carcass fat mass (lb), PTOFAT = predicted total carcass fat mass (lb), STLIP = soft tissue lipid mass (lb), and PSTLIP = predicted soft tissue lipid mass (lb). PTOFAT and PSTLIP are predicted using equations which included CW, LEA, and FD10R. ^b b₀ = intercept, b_i = partial regression coefficient of the ith independent variable, R² = coefficient of determination, RSD = residual

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

^c Signif = significance.

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		Ligh (220,	t weight of 251, and	lata sets 282 lbs)	Heavy weight data sets (251, 282, and 335 lbs)					
Eq.	Variable	Genetic Population Signif.	Sex Signif.	CR ^b	VR ^b	Genetic Population Signif.	Sex Signif.	CR ^b	VR ^b		
1	CW, LEA, FD10R	.46	.08	.97	.85	.87	.06	.97	.80		
2	CW, TOFAT	.40	.09	.98	.93	.12	.12	.97	.81		
3	CW, PTOFAT	.48	.08	.97	.85	.90	.05	.97	.80		
4	CW, STLIP	.50	.09	.98	.92	.90	.12	.98	.89		
5	CW, PSTLIP	.46	.08	.97	.85	.90	.05	.97	.80		

Table 6. Significance of residual mean value (biases) for genotype populations and sex subpopulations in the prediction of empty body lipid mass.^a

^a CW = warm carcass weight (lb), LEA = 10th rib loin eye area (in²), FD10R = off-midline 10th rib fat depth, TOFAT = total carcass fat tissue mass (lb), PTOFAT = predicted total carcass fat tissue mass (lb), STLIP = soft tissue lipid (lb), and PSTLIP = predicted soft tissue lipid mass (lb). PTOFAT and PSTLIP were predicted using equations 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 means.