Evaluation of Procedures to Predict Fat-free Lean in Pork Carcasses

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Introduction

Marketing is a major challenge for pork producers. In most markets, carcass weight and predicted amount of fat-free lean in the carcass are used to determine value. Lean is usually predicted from measures of carcass weight, backfat and *longissimus* muscle area or muscle depth. However, procedures to measure these traits vary greatly among packers. Optimum weight and leanness in different packer grids also vary. Because of this variation, producers do not know whether pigs are fairly evaluated on a particular packer grid. Information on accuracy of procedures to predict lean is needed for producers to understand different matrices and to develop effective marketing strategies.

Many pork producers are becoming involved in producer-owned packing plants and cooperative marketing groups. These producers need unbiased information about variation in lean meat yield of pigs that differ by weight, sex and genetic type in order to plan meat sales.

History

In 1990, approximately 25 percent of U. S. market hogs were purchased on a carcass merit system that differentiated price based on lean content. The differentials varied, and data to indicate whether the price spread was sufficient between good and poor quality pigs were scarce.

A checkoff-funded task force in 1990 recommended that procedures be established to determine value of pigs based on pounds of quality lean in the carcass. Knife separable lean from whole carcass dissection was recommended as the standard, but this endpoint is subject to cutting style and workmanship differences. Since then, carcass separation followed by chemical analysis for total lipids has become the standard for prediction of Fat Free Lean.

In 1993, the National Pork Producers Council's (NPPC) Lean Value Task Force, funded by the National Pork Board (NPB) and in cooperation with the Pork Committee of the American Meat Institute, developed the Uniform Lean Information Project. In it, the Fat-Free Lean Index, (FFLI) was developed. The intent of the FFLI was to permit pork producers to compare the lean content of their pigs over time and with the pigs of other producers, even though each producer may be marketing to different processors using different technology to estimate carcass lean content. The original FFLI equations were based on carcass separation data collected in

university trials from 1970 to 1985 from pigs weighing between 200 and 250 lb. Since then, pigs have been made leaner through genetic selection and market weights have increased greatly.

Delegates to the 1995 NPPC Annual Meeting reaffirmed the commitment to value-based marketing by calling for continued producer support of research and equipment to more accurately measure carcass composition, muscle quality and other factors that may affect consumer preferences. The delegates challenged packers to provide accurate, objective and standardized information to producers and asked for information about possible third-party oversight of post-slaughter evaluation. Delegates to the 1996 NPPC Annual Meeting called for all pork processors to report the FFLI to producers. In addition, the swine nutrition committee of The National Research Council (NRC) in 1998 adopted FFLI as the accepted predictor of lean to be used in diet formulation programs. As a result of these actions, evaluation of carcasses by several procedures and collection of detailed carcass lean separation data were included in projects being conducted by NPB staff and program committees. These data were used to develop new FFL prediction equations for different evaluation procedures.

NPB Database

Carcasses of 1,024 pigs from four NPB projects were evaluated. In each project, pigs were grown at the MN Swine Evaluation station and slaughtered at Quality Pork Processors packing plant in Austin, MN. One-half of each carcass was transported to Geneva Meats, Geneva, MN, where it was dissected and tissue samples were collected for lipid analyses.

Project Objectives

Data from these projects were analyzed to 1) develop fat-free lean prediction equations for pork carcasses evaluated by several different procedures, 2) determine whether procedures differ in accuracy, and 3) determine whether procedures are biased for certain genetic types, weight classes, or carcass lean classes.

Carcass Evaluation Methods

Carcasses were evaluated by six procedures. Four procedures were applied to hot carcasses, one was used in chilled carcasses, and one was used in live pigs before slaughter. Hot carcasses were all evaluated with instruments that Quality Pork Processors installed at the end of their slaughter floor. These instruments were a Fat-O-Meat'r ™ (FOM), an Animal Ultrasound Services (AUS) system, an Ultrafom (UFOM) system and a ruler (RULER).

The Ruler was used to record fat depth, including skin, on the midline of the split carcass at the last rib (LRBF). The FOM, an optical probe, measures both backfat (FOMBF) and *longissimus* muscle depth (FOMLD) perpendicular to the muscle between the 3rd and 4th from

the last ribs. The Carcass Value Technology System (AUS; Animal Ultrasound Services, Inc, Ithaca, NY), an automated and computerized ultrasonic system, measures backfat (AUSBF) and *longissimus* muscle depth (AUSLD) longitudinally between the 10th and last rib approximately 2 in off the midline of the carcass. The UFOM, a real-time ultrasonic scanning instrument, measures backfat (UFOMBF) and *longissimus* muscle depth (UFOMLD) longitudinally at the same location as the AUS measurement.

After chilling, carcasses were ribbed between the 10th and 11th ribs. Backfat depth (BF10) and *longissimus* muscle (LMA) area of chilled carcasses were measured at the ¾ distance along the *longissimus* muscle from the edge of the muscle and perpendicular to the outer edge of the skin.

National Swine Improvement Federation Certified Technicians obtained real-time ultrasonic measurements of backfat depth (SCANBF) and loin muscle area (SCANLMA) at the 10th rib on pigs within three days of slaughter. Measurements were taken with an A-mode instrument (Aloka 500) with the probe placed approximately at the 10th rib 2.5 in off the midline and perpendicular the skin surface.

These procedures were all applied to the same carcasses allowing direct comparisons of accuracy of the procedures. In the following discussion, the six procedures are designated as 1) C10R, prediction of lean from carcass weight, BF10, and LMA; 2) CLR, prediction from carcass weight and LRBF; 3) FOM, prediction from carcass weight, FOMBF, and FOMLD; 4) AUS, prediction from carcass weight, AUSBF, and AUSLD; 5) UFOM, prediction from carcass weight, UFOMBF, and UFOMLD; and 6) SCAN, prediction from carcass weight, SCANBF, and SCANLMA.

Dissection of carcasses at Geneva Meats and determination of lean content were by a protocol established in 1996 by an NPB advisory committee of producers, industry representatives, meat scientists and public officials. One-half of each carcass was separated into ten endpoints for weights of primal and sub-primal cuts, skin, and bone. All meat, fat and other soft tissue of each endpoint was coarsely ground, and a random sample of each ground endpoint was collected and submitted to the Iowa State University Meat Laboratory to determine total lipid content by the Fulch method.

The projects from which data came were:

1996 National Barrow Show Sire Progeny Test (NBS96). Purebred barrows and gilts were submitted to the National Barrow show progeny test in sire groups to test specific boars for growth and carcass traits. Tamworth, Yorkshire, Duroc, Hampshire, Spot, Chester White, Poland China, Berkshire, and Landrace pigs and crossbred pigs by purebred sires were included.

Pigs were fed Diet 3 (Table 1) from approximately 100 to 250 lb and processed at Quality Pork Processors packing plant. Seventy-three carcasses were dissected at Geneva Meats and used to train Quality Pork Processor staff on carcass measurement protocols for the instruments described above and to train staff at Geneva Meats on carcass dissection protocols. Because this was the first experience with FOM, AUS and UFOM procedures, data for these procedures in this subset of carcasses were not included in analyses.

Quality Lean Growth Modeling Project (QLGM). The QLGM project was funded by NPPC checkoff funds and was conducted in three replications during 1996 and 1997. The objective was to determine genetic line, dietary protein, and sex effects and their interactions on lean growth. A total of 1,588 barrows and gilts were included. Carcass dissection was performed in a sample of 627 carcasses.

Crossbred pigs sired by purebred Berkshire, Duroc and Hampshire boars and by boars of Danbred USA, Newsham Hybrid, and Monsanto Choice Genetics sire lines were included. Managers of the populations selected the pigs. Pigs were weaned at 8 to 19 d of age, placed in a common nursery, and co-mingled following SEW procedures. They were moved to a grower house at the MN Swine Testing Station at approximately 40 lb, and to experimental facilities at approximately 100 lb. Pigs received a common diet to weight of 100 lb and one of four diets (Table 1) to a weight of either 250, 290, or 330 lb.

Genetics of Lean Efficiency Project GLE). The GLE was conducted in 1999 and 2000 and included purebred Duroc and Yorkshire barrows and gilts. The objective was to provide data for estimation of genetic parameters for meat quality and relationships of meat quality with rate and composition of growth. Breeders submitted purebred pigs to the MN Swine Evaluation Station for testing from approximately 100 lb to weights of 250 or 290 lb. Pigs were fed Diet 2 (Table 1) throughout the test period. Populations were sampled to represent many sires with 6 to 8 pigs per sire family. Pigs were tested in two replicates. A total of 230 carcasses were evaluated and dissected.

2000 National Barrow Show Sire Progeny Test (NBS00). The NBS00 had the same objective and procedures as NBS96. It overlapped with the GLE project and pigs were slaughtered on the same days as the GLE, REP 2 pigs. A total of 94 pigs were dissected and evaluated.

Diets

Diets fed to pigs within a weight range had constant energy, minerals and vitamins, but differed in amount of lysine, depending on project (Table 1). Lysine was supplied by corn and soybean meal. Diets were fed in ground form with particle size less than 750 microns. Added fat was choice white grease. Pens of pigs within genetic type in the QLGM project were

randomly assigned to a diet. Diet 2 was used throughout the trial in the GLE project and Diet 3 in the NBS96 and NBS00 projects.

Table 1. Energy, fat, and lysine levels in diets fed pigs of different weight ranges

Metabolized Energy, Kcal/lb	Weight range, lb	Added fat %	Lysine levels, %			
			Diet 1	Diet 2	Diet 3	Diet 4
1598	90-140	5	1.25	1.10	.95	.80
1560	141-190	3	1.10	.95	.80	.65
1501	191-240	0	.95	.80	.65	.50
1502	241-290	0	.80	.65	.50	.35
1502	291-330	0	.80	.65	.50	.35

Distribution of Pig Weights at Slaughter

Target slaughter weights differed across projects. Only carcasses with even carcass splits were chosen for separation. The distribution of live pig weights at slaughter by project is in Table 2.

Table 2. Distribution of live weight at slaughter by project[a].

Weight range, lb	NBS96	QLGM	GLE	NBS00	Total
< 215	1		3		4
215 – 229	1	1	1		3
230 – 244	30	28	8	38	104
245 – 259	40	138	81	52	311
260 – 274	1	57	21	4	83
275 – 289		100	36		136
290 – 304		109	70		179
305 – 319		54	10		64
320 – 334		101			101
335 – 349		36			36
≥ 350		3			3
Total	73	627	230	94	1024

[a]NBS96 = National Barrow Show 1996 Progeny Test, QLGM = Quality Lean Growth Modeling, GLE = Genetics of Lean Efficiency, NBS00 = National Barrow Show 2000 Progeny Test.

Table 3. Number of carcasses of each genetic type evaluated by each procedure in each project[a]

Method[c]	Breed or cross[b]																Total
	T	Y	D	H	S	C	P	B	L	X	BX	DB	M	DX	NH	HX	
NBS96																	
C10R	1	15	4	6	2	10	5	6	17	7							73
CLR	1	15	4	6	2	10	5	6	17	7							73
QLGM																	
C10R											92	105	125	96	76	131	625
CLR											92	106	126	96	76	131	627
FOM											82	92	112	89	66	114	555
AUS																	
UFOM																	
SCAN											91	105	121	94	74	125	610
GLE																	
C10R		113	116														229
CLR		114	116														230
FOM		106	104														210
AUS		83	94														177
UFOM		23	31														54
SCAN		113	116														229
NBS00																	
C10R		16	12		1	7	6	35	9	8							94
CLR		16	12		1	7	6	35	9	8							84
FOM		15	7		1	7	4	28	8	8							78
AUS		12	9			7	4	26	9	4							67
UFOM		12	10		1	5	6	28	3	7							65
SCAN		16	12		1	7	6	35	8	7							92

[a]NBS96 = National Barrow Show 1996 Progeny Test, QLGM = Quality Lean Growth Modeling, GLE = Genetics of Lean Efficiency, NBS00 = National Barrow Show 2000 Progeny Test.

[b]T = Tamworth, Y = Yorkshire, D = Duroc, H = Hampshire, S = Spot, C = Chester White, P = Poland China, B = Berkshire, L = Landrace, X = Misc. crossbreds, BX = Berkshire-sired crosses, DB = Danbred USA, M = Monsanto Choice Genetics, DX = Duroc-sired crossbreds, NH = Hewsham Hybrids, and HX = Hampshire-sired crossbreds.

[c]Evaluations of fat-free lean by carcass 10th rib backfat and *longissimus* muscle area (C10R), carcass last rib backfat (CLR), Fat-O-Meat'r ™ (FOM), Automated Ultrasonic System (AUS), Ultrafom (ULFOM), and live animal scans of 10th rib backfat and *longissimus* area (SCAN).

Genetic Types of Pigs

The genetic types of pigs evaluated by each procedure in each project are listed in Table 3. Purebred and crossbred pigs broadly representing the genetic variation in the industry were sampled. The projects were not designed to compare populations so such comparisons are not made here. Pigs were tested for the HAL 1843 genotype by the licensed DNA test. Of the 1,024 pigs on which fat-free lean was determined, 964 were homozygous for the non-stress allele, and 60 were heterozygous.

Across projects, pigs were slaughtered on 55 different days. Dr. Eric Berg, University of Missouri, trained and supervised the meat cutters during data collection for the NBS96 and QLGM Rep 1 (1996) projects. Each day after 1996, staff of the Texas A&M University Meats Laboratory, directed by Dr. Rhonda Miller, supervised carcass separation. The number of observations by each procedure applied to pigs of each breed or cross in each project is in Table 3.

Carcass Separation Endpoints. Each carcass half was skinned and separated into ten endpoints: 1) soft tissue in the jowl, 2) soft tissue in the spare rib and belly, 3) inside ham muscle, 4) outside ham muscle, 5) other soft tissue in ham, 6) ham knuckle muscle, 7) *longissimus* muscle, 8) tenderloin muscle plus other soft tissue in loin, 9) soft tissue in boneless picnic, boneless butt and shoulder, and 10) the total of fatback , ham external fat, ham seam fat, loin external fat, picnic external fat, and butt external fat. The percentage of total lipid in each component was determined. Percentage of lipid in Component 10 was used to calculate weight of fat-free lean in each other component as: Component weight of fat-free lean = Component weight – (Component weight*Component lipid %/Component 10 lipid %).

Total carcass fat-free lean was calculated as the sum of fat-free lean in Components 1 to 9. Percentage fat-free lean was calculated as total weight expressed as a percentage of carcass weight.

Data analyses

Calculation of prediction equations. Pounds of total carcass fat-free lean and percentage fat-free lean were fitted in separate models to data for each procedure. The objective was to find best-fitting regression equations to predict fat-free lean across genetic types, weight ranges, sexes and diets. Mixed model procedures were used. Effect of slaughter date within project (with a maximum of 55 subclasses) was fitted as a random effect in all models. Regression variables in preliminary models included linear and quadratic effects of backfat depth, *longissimus* muscle area or depth, and carcass weight and the cross product of linear variables. Final models were developed with backward elimination to remove regression variables for which regression

coefficients did not differ from zero at $P > 0.10$. First, cross product terms were eliminated if they were not significant, then quadratic terms, and finally non-significant linear terms were eliminated. Third order terms, e.g., BF10*BF10*BF10, were included in models for which quadratic terms were significant and were left in final models if they were important at $P < 0.10$. Best fitting regression equations were those from final models in which all regression coefficients were significant.

As an example of this procedure, analyses to develop an equation of C10R measurements began with the model:

$$FFL = SLDATE + b_0 + b_1*BF10 + b_2*BF10*BF10 + b_3*LMA + b_4*LMA*LMA + b_5*CWT + b_6*CWT*CWT + b_7*BF10*LMA + b_8*BF10*CWT + b_9*BF10*LMA + e,$$

where

FFL = pounds or percentage of fat-free lean, SLDATE = random effect of slaughter date, BF10 = 10^{th} rib carcass backfat depth, LMA = 10th rib *longissimus* muscle area, CWT = carcass weight, b_0 = intercept, b_i = regression coefficient on each variable, and e = residual error.

The final model after elimination of non-significant variables was:

$$FFL = SLDATE + b_0 + b_1*BF10 + b_2*BF10*BF10 + b_3* CWT + b_4*BF10*LMA + b_5*BF10*CWT + e.$$

Variance components due to slaughter date and to residual were calculated in final models and used to assess precision of the prediction equation.

Pigs in the QLGM project were evaluated by the AUS procedure; however, preliminary analyses indicated results of AUS data from the project were unreliable as residual error variances were approximately 50% greater than when QLGM data were deleted. Therefore, final equations for AUS were developed with data from only the GLE and NBS00 projects.

Evaluation of bias. A predictor is biased if for pigs in some fixed classes such as breed or diet it consistently overestimates or underestimates actual fat-free lean. For each predictor the residual for each pig was calculated as the difference between that pig's predicted and actual weight of fat-free lean or predicted percentage and actual percentage fat-free lean. A positive residual occurred when the predicted value was greater than the actual, an overestimate of FFL. A negative residual occurred when actual fat-free lean was underestimated.

Bias was assessed by fitting the residuals for each procedure within project to a model that included the fixed effects of breed, sex, and diet. A predictor is unbiased for that subclass if

the average residual is zero. Mean residuals and their standard errors for each subclass were calculated and means were tested to determine whether they differed from zero.

It is also possible that predictors on average are unbiased, but are biased at extreme values of the regression variable. For example, a predictor may overestimate fat-free lean in light carcasses, and underestimate lean in heavy carcasses, but be unbiased at intermediate weights. If this occurs, additional variables in regression equations may be necessary. To test whether there was a relationship of residuals with measured variables, residuals were fitted to a model that included the fixed effect of project and the regression coefficient of residuals on the variables measured by that procedure. For example, residuals from the prediction equation based on C10R measurements were fitted to the model:

$$\text{Residual FFL} = \text{project} + b_1*\text{BF10} + b_2*\text{LMA} + b_3*\text{CWT} + e.$$

Regression coefficients that did not differ significantly from zero indicated that bias was unrelated to the variables that were measured.

Lastly, it is important to know whether prediction equations are biased when applied to data for pigs with extreme leanness or fatness. To test this possible bias, residuals for predicted weight of fat free lean were regressed on actual fat-free lean and residuals for percentage fat-free lean were regressed on actual percentage fat-free lean. The model included only the fixed effect of project and the regression on actual value. A regression coefficient not significantly different from zero indicates predictions are unbiased.

Comparison of procedures. Final equations for each procedure were compared to determine whether they differed in precision in prediction of pounds or percentage of fat-free lean. This was accomplished by fitting final models for each equation to the data for the largest subset of carcasses that were evaluated by both procedures. First, the procedures used to evaluate the largest number of carcasses (C10R and CLR) were compared. Then, equations for C10R, CLR, and SCAN were compared with data from carcasses evaluated by all three procedures. The process was repeated by adding FOM, AUS, and UFOM procedures in that order until comparisons had been made among all procedures. Variances of residuals and the Akaike's Information Criterion statistic were used to make comparisons.

Results

Statistics describing the data used in the analyses are in Table 4. Standard deviations of all traits were very large relative to the mean due in large part to the wide range of slaughter weights. This measure of variation should be used only to describe variation in the sample of pigs in this analysis and not to describe variation in other populations or samples.

Table 4. Number of observations (N), mean, standard deviation (SD), minimum (Min), and maximum (Max) values for each trait for pigs used in analyses

Trait[a]	N	Mean	SD	Min	Max
FFL, lb	1024	99.90	15.17	52.09	153.99
FFL%	1024	48.53	5.20	31.65	61.84
LWT, lb	1024	277.82	30.60	197.00	360.00
CWT, lb	1024	206.17	25.01	139.00	280.00
LRBF, in	1024	1.17	0.29	0.40	2.20
BF10, in	1021	1.08	0.33	0.30	2.30
LMA, in^2	1021	6.40	1.10	2.90	12.00
UFOMBF, mm	126	20.02	5.90	10.10	36.30
UFOMLD, mm	126	48.50	7.25	32.80	65.10
FOMBF, mm	853	24.20	6.62	8.00	52.00
FOMLD, mm	843	57.30	9.34	23.00	88.00
AUSBF, mm	248	22.39	6.66	9.87	42.63
AUSLD, mm	248	63.66	10.68	39.01	97.00
SCBF, in	931	1.01	0.30	0.35	2.30
SCLMA, in^2	945	6.48	1.05	2.74	10.30

[a]FFL = lb fat-free lean, FFL% = percentage fat-free lean, LWT = pre-slaughter live weight, CWT = carcass weight, LRBF = last rib backfat depth, BF10 = 10^{th} rib backfat depth, LMA = 10^{th} rib *longissimus* muscle area, UFOMBF = backfat depth measured with Ultrafom, UFOMLD = *longissimus* muscle depth measured with Ultrafom, FOMBF = backfat depth measured with Fat-O-Meat'r™, FOMLD = *longissimus* muscle depth measured with Fat-O-Meat'r™, AUSBF = backfat depth measured with Automated Ultrasonic System, AUSLD = *longissimus* muscle depth measured with Automated Ultrasonic System, SCBF = live pig backfat depth measured at 10^{th} rib with Aloka 500, and SCLMA = live pig *longissimus* muscle area measured at 10^{th} rib with Aloka 500.

Final prediction equations

Final equations to predict pounds and percentage of fat-free lean by each procedure are in Tables 5 and 6, respectively. The best-fitting equations across procedures included various combinations of linear, quadratic, and cross products of backfat, *longissimus* muscle measurements, and carcass weight. Total variance, the sum of that due to slaughter day and the residual variance, ranged from 41.65 lb^2 for C10R to 79.52 for CLR for prediction of pounds of fat-free lean, and from 9.45 $\%^2$ for C10R to 18.7 $\%^2$ for CLR for prediction of percentage fat-free lean. The square root of these variances is the standard deviation of difference between predicted and actual values across all samples in the study. Therefore, the equation for C10R with the lowest variance on average predicted lean within ± 6.45 lb and ± 3.07 % of actual, and

the equation for CLR with the greatest variance predicted lean within ± 8.91 lb and 4.32 % of actual. These traits are considered to be normally distributed and thus predicted values by the C10R equation of approximately 68% of the carcasses will be within ± 6.45 lb and ± 3.07 % of actual values and predictions for approximately 95% of carcasses will be within ± 12.90 lb and ± 6.14 % of actual values. Similar intervals can be constructed for other procedures.

Table 5. Final regression equations to predict fat-free lean (lb)[a]

	Method[b]					
Variable[c]	Carcass 10R	Carcass LR	UFOM	FOM	AUS	SCAN
N	1021	1021	126	853	248	931
b_o	5.76	12.41	35.83	37.23	3.51	-1.01
BF	-30.38	-24.57	-2.02	0.40	-0.80	-33.54
BF*BF	8.54		0.029	-0.032	0.017	15.66
BF*BF*BF				0.00062		
LMA			0.14	0.14	0.45	
LMA*LMA			0.41			
CWT	0.61	0.56		0.17	0.48	0.70
CWT*CWT				0.0011		
BF*LMA	3.13				-0.014	3.03
BF*CWT	-0.14			-.0059		-0.21
σ^2_{GRP}	3.50	7.50	1.21	9.66	10.76	4.91
σ^2_R	38.15	72.02	61.74	52.32	47.94	40.63

[a]Model: Fat-free lean = Project/slaughter-date group + x variables (group fitted as random effect) in SAS PROC MIXED.

[b]Carcass 10R = 10th rib backfat (in) and longissimus muscle area (in^2); Carcass LR = last rib backfat (in); UFOM = ultrafom backfat depth (mm) and loin depth (mm); FOM = Fat-O-Meat'r™ backfat depth (mm) and loin depth (mm); AUS = automated ultrasound system backfat depth (mm) and loin depth (mm); SCAN = live animal backfat depth (in) and longissimus muscle area (in^2) at 10th rib.

[c]b_o = intercept; BF = backfat depth, in; LMA = longissimus muscle area, in^2 (carcass 10R and SCAN) or *longissimus* muscle depth, mm (UFOM, FOM, and AUS); CWT = carcass weight, lb; σ^2_{GRP} = variance component for group (project-slaughter-date subclass); σ^2_R = residual variance component.

Table 6. Final regression equations to predict percentage fat-free lean by each procedure[a]

	Method[b]					
Variable[c]	Carcass 10R	Carcass LR	UFOM	FOM	AUS	SCAN
N	1021	1021	126	853	248	931
b_o	45.34	62.39	37.49	77.83	21.18	61.09
BF	-16.50	-18.61	0.85	-0.36	-0.40	-.28.62
BF*BF	2.66			-0.02	.0092	7.37
BF*BF*BF				.00030		
LMA	4.01		0.59	0.69	0.74	
LMA*LMA	-0.19					
CWT			-0.05	-0.20	0.14	0.04
CWT*CWT				.00049		
BF*LMA			-0.03		-0.0076	1.40
BF*CWT		0.03195				-0.042
LMA*CWT					-0.0026	
σ^2_{GRP}	.86	2.0565	.66	2.24	2.88	1.19
σ^2_R	8.89	16.64	17.23	11.78	12.27	9.15

[a]Model: Fat-free lean % = Project/slaughter-date group + x variables (group fitted as random effect) in SAS PROC MIXED.

[b]Carcass 10R = 10th rib backfat (in) and longissimus muscle area (in^2); Carcass LR = last rib backfat (in); UFOM = ultrafom backfat depth (mm) and loin depth (mm); FOM = Fat-O-Meat'r™ backfat depth (mm) and loin depth (mm); AUS = automated ultrasound system backfat depth (mm) and loin depth (mm); SCAN = live animal backfat depth (in) and longissimus muscle area (in^2) at 10th rib.

[c]b_o = intercept; BF = backfat depth, in; LMA = longissimus muscle area, in^2 (carcass 10R and SCAN) or *longissimus* muscle depth, mm (UFOM, FOM, and AUS); CWT = carcass weight, lb; σ^2_{GRP} = variance component for group (project-slaughter-date subclass); σ^2_R = residual variance component.

Comparison of procedures

There is no exact statistical test to compare equations for the different procedures. Table 7 contains results when parameters for best-fitting equations were estimated for each procedure in combinations with the same data. Degrees of freedom in models differed because the number of regression variables depended on the procedure. Models with the lowest total variance, the sum of the group and residual variance components, are most precise. However, when variances

differ little among models, it is not clear if this represents real differences in fit or if the difference is due to random variation in this sample. Additional evidence comes from comparing –2 Res log likelihood ratios and Aikaike's Information Criterion. Without explaining the theory, the closer to zero both of these values are, the better the model fits the data. One can compare these values only from two models that were fitted to the same data because a property of these values is that they automatically decrease as the number of observations analyzed decreases. Thus, comparisons of the fit when C10R and CLR models were compared with data from 1,021 carcasses with those for FOM fitted to 823 carcasses are not appropriate.

In all comparisons, C10R equations produced the best fit and CLR equations produced the poorest fit. SCAN equations fitted the data nearly as well as C10R equations. Standard deviations of residuals differed very little between C10R and SCAN. Equations for FOM and AUS produced similar fits, but appear to be less precise than either SCAN or C10R equations. Very few carcasses were evaluated by UFOM and other procedures and thus a fair assessment of its precision relative to other procedures is not possible. The data for comparison of procedures to predict percentage fat-free lean are not shown because the results were very similar to those in Table 6.

Bias

Because of the poor connection of breeds and diets across projects, models of residuals to assess bias were fitted separately within each project. Probability values from analyses of variance are in Table 8, and mean bias for breeds, sexes, and diets for each procedure are in Appendix Tables 1 to 6. Only results for prediction of pounds of fat-free lean are shown.

Every procedure produced biased predictions for some subclasses. Significant bias due to breed occurred with every procedure in several projects. This means that inherent differences in fat-free lean exists among breeds that are not related to the measures of backfat, *longissimus* muscle area or depth, or carcass weight that were included in the prediction equations. Equations for C10R were not biased by sex; however, bias due to sex was significant in at least one project for all other procedures. Bias due to diet could be assessed only in the QLGM project and only for the C10R, CLR, FOM, and SCAN procedures. Both the C10R and SCAN procedures produced predictions that were not biased by diet.

The final equation for each procedure over estimated actual pounds of fat-free lean in Berkshire and Berkshire cross carcasses in every project and most estimates were significantly different from zero (Appendix Tables 1 to 6). Pounds of lean in Duroc and Duroc cross carcasses also was overestimated in many projects and several estimates were significant. Most procedures underestimated pounds of fat-free lean in Danbred USA and Newsham Hybrid

Table 7. Comparisons[a] of equations to predict pounds of fat-free lean

Procedure[b]	Num df	σ^2_{grp}	σ^2_R	-2 Res Log l	AIC
		C10R and CLR (n = 1021)			
C10R	9	3.76	38.15	6660.6	-3332.3
CLR	7	2.71	72.0	7278.9	-3641.4
		C10R, CLR & SCAN (n = 928)			
C10R	9	3.42	38.90	6070.0	-3037.4
CLR	6	2.48	73.12	6630.6	-3317.3
SCAN	9	3.77	40.72	6113.3	-3058.6
		C10R, CLR, SCAN & FOM (n = 823)			
C10R	9	3.39	38.98	5383.6	-2693.8
CLR	6	1.90	72.56	5868.6	-2936.4
SCAN	9	3.80	40.71	5419.8	-2711.9
FOM	11	5.85	51.80	5675.4	-2839.7
		C10R, CLR, SCAN, FOM & AUS (n = 216)			
C10R	6	8.65	32.42	1395.9	-690.0
CLR	3	6.41	58.34	1497.2	-750.6
SCAN	6	7.65	33.35	1378.6	-691.3
FOM	8	12.63	43.35	1487.2	-743.6
AUS	6	10.58	46.40	1478.3	-741.1
		All methods (n = 58)			
C10R	6	6.68	35.48	348.4	-176.2
CLR	3	0	67.93	390.0	-196.0
SCAN	6	2.81	30.26	338.8	-171.4
FOM	8	1.90	44.22	401.4	-202.7
AUS	6	0	53.01	397.6	-199.8
UFOM	6	12.78	69.13	410.2	-207.1

[a]Num df = degrees of freedom in numerator of model (corresponds with number of regression coefficients in prediction equation), σ^2_{grp} and σ^2_R are variance components due to slaughter date and to residual, respectively, -2 Res log l = -2 times log likelihood ratio, and AIC = Akaike's Information Criterion.

[b]C10R = Carcass 10th rib equation, CLR = carcass last rib equation, SCAN = equation from live animal scan measurements, FOM = Fat-O-Meat'r™ equation, AUS = Automated Ultasonic System equation, and UFOM = Ultrafom equation.

Table 8. Probabilities of tests of differences in bias (predicted minus actual pounds of fat-free-lean) among breeds, sexes, and diets in each project[a] by each procedure

	QLGM	NBS96	GLE	NBS00	QLGM	NBS96	GLE	NBS00
	Carcass 10th Rib (C10R)				Carcass Last Rib (CLR)			
Breed	<0.0001	<0.0005	<0.0002	0.14	<0.0001	<0.0001	0.07	<0.0009
Sex	0.66	0.38	0.27	0.09	0.0002	0.06	<0.0001	0.96
Diet	0.17				<0.0001			
	Fat-O-Meat'r ™ (FOM)				Automated Ultrasonic System (AUS)			
Breed	<0.0001		0.83	0.27			0.32	0.0036
Sex	0.29		0.0002	0.88			0.005	0.059
Diet	0.0004							
	Ultrafom (UFOM)				Live Scan (SCAN)			
Breed			0.39	0.002	< 0.0001		< 0.0006	0.47
Sex			0.06	0.18	0.60		0.15	0.04
Diet					0.29			

[a]NBS96 = National Barrow Show 1996 Progeny Test, QLGM = Quality Lean Growth Modeling, GLE = Genetics of Lean Efficiency, NBS00 = National Barrow Show 2000 Progeny Test.

crosses and in purebred Yorkshire and estimates for these groups in several projects differed significantly from zero. There was less consistency in bias for other breeds and crosses across projects and procedures.

There was a tendency for all equations to predict more lean than actual in barrow carcasses and less in gilts. Bias due to sex was not significant in any project for the C10R equation. Significant bias due to sex did occur for other procedures, although the pattern of the bias was not consistent across projects.

Diet pigs were fed produced significantly biased predictions by all procedures except C10R. Generally, bias was not significant when equations were applied to carcasses of pigs fed Diets 1 to 3, but most equations, including the C10R equation, predicted more lean in carcasses of pigs fed Diet 4, the low protein diet, than they actually possessed.

The equations for all procedures tended to predict more lean than actual in fatter pigs (Berkshire and Berkshire crosses, barrows, and pigs fed low-protein diets) and less lean than actual in lean pigs. To determine whether the observed bias was related to the measured variables, residuals were regressed on the backfat and *longissimus* muscle measurements in each equation and on carcass weight. None of these regressions differed from zero for any procedure

(P > 0.10). Therefore, inclusion of additional coefficients of higher order variables is not expected to produce unbiased equations. However, significant, negative regressions of residuals on actual fat-free lean were found for every procedure (Table 9). Residuals tended to be positive in pigs with small amount of fat-free lean and as actual fat-free lean increased the difference between predicted and actual values decreased, becoming zero around the population mean and decreasing to larger negative values in lean pigs. Pounds of fat-free lean tended to be overestimated in pigs with less fat-free lean than average and underestimated in pigs with greater than average amount of lean. The general nature of these relationships is illustrated in Figures 1 and 2 for predictions from the C10R equation and in Figure 3 for predictions from the AUS equation. These equations were selected to illustrate the relationship because they represent equations with the most and the least bias, excluding the UFOM equation that was based on very few data points.

Table 9. Regression coefficients (b) ± standard error (se) of residuals (predicted pounds fat-free lean – actual) regressed on actual fat-free lean

Procedure	b ± se
1. Carcass 10th Rib backfat and *longissimus* area, and carcass weight (C10R)	-0.204 ± 0.013**
2. Live scan of 10th rib backfat and *longissimus* area, and carcass weight (SCAN)	-0.224 ± 0.014**
3. Fat-O-Meat'r ™ backfat and *longissimus* muscle depth and carcass weight (FOM)	-0.285 ± 0.016**
4. Carcass last rib backfat depth and carcass weight (CLR)	-0.380 ± 0.016**
5. Automated Ultrasonic System backfat and *longissimus* muscle depth and carcass weight (AUS)	-0.409 ± 0.030**
6. Ultrafom backfat and *longissimus* muscle depth and carcass weight (UFOM)	-0.594 ± 0.050**

**P < 0.01.

Summary. Equations to predict pounds of fat-free lean (FFL) by six procedures were derived from evaluation of 1,024 carcasses of barrows and gilts of a wide range of breeds and breed crosses. Variables in the equations included carcass weight and measurements of backfat and *longissimus* muscle depth with 1) Fat-O-Meat'r™ (FOM), 2) Automated Ultrasonic System (AUS), or 3) Ultrafom (UFOM) instruments, 4) 10th rib backfat and *longissimus* muscle (C10R), 5) last rib carcass backfat (CLR), and 6) live animal scan of backfat depth and *longissimus* muscle area with an Aloka 500 instrument (SCAN). Equations for C10R and SCAN procedures were most precise and predicted FFL within ± 6.45 lb and 3.1% (C10R) and 6.75 lb and 3.2%

(SCAN). Precision of equations for AUS, FOM and UFOM were similar and predicted FFL within ± 7.66, 7.87, and 7.93 lb, respectively. The least precise equation was CLR for which the average error was 8.80 lb.

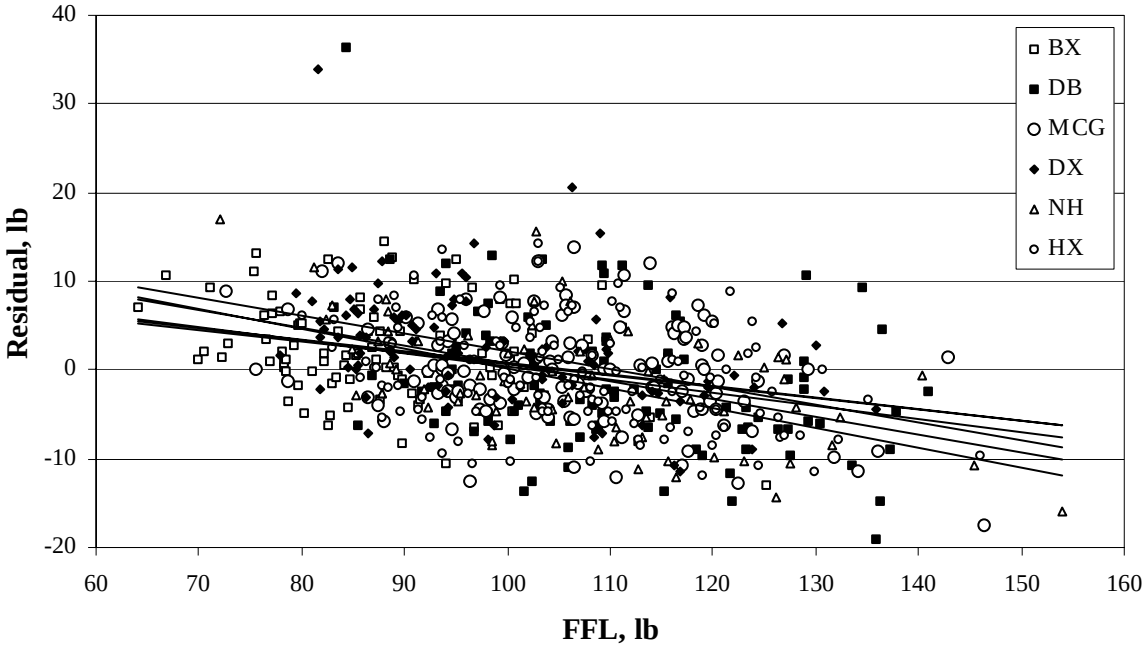


Figure 1. Residuals predicted from C10R equation (predicted - actual) plotted against FFL for QLGM project. Lines are slopes for each breed cross and illustrate similar response for all groups.

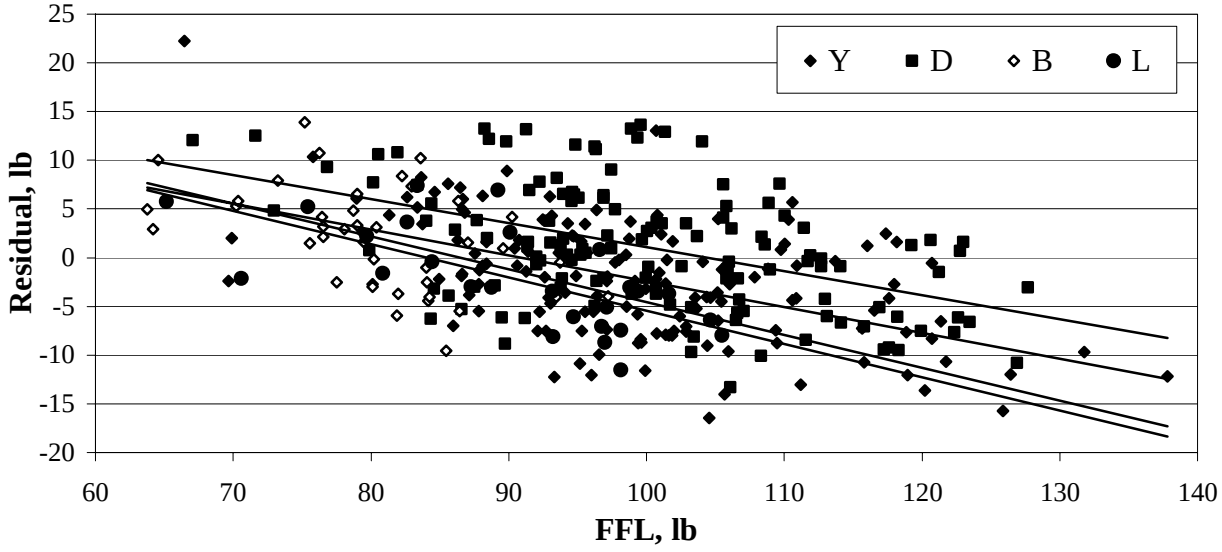
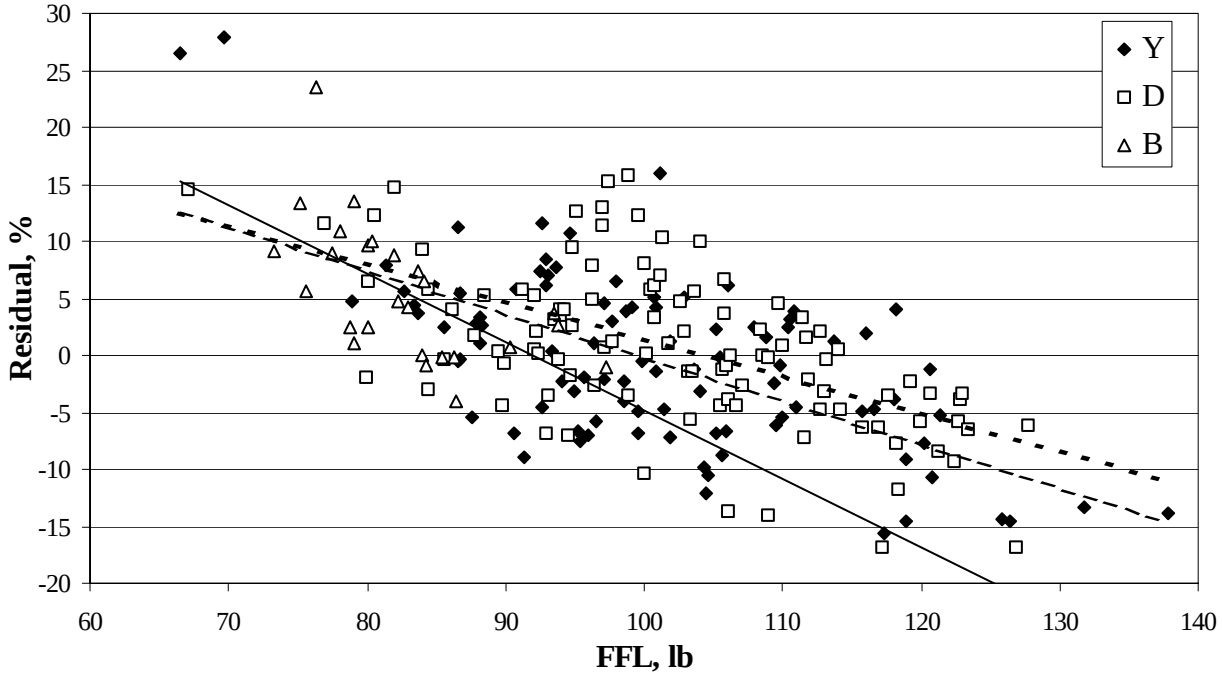


Figure 2. Residuals from prediction of FFL from C10R equation (predicted - actual) plotted against FFl for Yorkshire (Y), Duroc (D), Berkshire (B), and Landrace (L): Projects NBS96, GLE, and NBS2000. Parallel lines show similar regressions for each breed.

Figure 3. Residuals from AUS equation (predicted - actual) plotted against FFL for Yorkshire (Y), Duroc (D), and Berkshire (B) for GLE, NBS96, and NBS00 projects. Lines illustrate similar relationship for all breeds.



Bias in predictions for breed, sex and amount of protein in diets pigs were fed was assessed. All equations produced biased predictions for at least some classes, but the least bias occurred for predictions with the C10R equation. Bias was not related to carcass weight or to measurements of backfat and muscle depth or area. Regressions of differences between predicted and actual fat-free lean revealed that bias was related to actual fat-free lean in carcasses. All procedures tended to overestimate the amount of lean in fat pigs and underestimate it in lean pigs. The average difference between predicted and actual amounts increased with greater deviation from the mean fat-free lean of the population.

No procedure with measurements used in this study to eliminate bias was identified. Inherent differences among breeds in amount of fat-free lean that are unrelated to carcass weight, backfat thickness, and *longissimus* muscle area or depth exist. The procedures used do not detect these differences among carcasses.

Appendix

Table 1. Average bias in prediction of pounds of fat-free lean from carcass 10th rib measurements (predicted fat-free lean minus actual fat-free lean)[a,b]

	QLGM			NBS96			GLE			NBS00		
	û	se	Pr	û	Se	Pr	û	se	Pr	û	se	Pr
						Breed						
BX	2.19	0.66	0.001									
DB	-1.30	0.62	0.037									
MCG	0.05	0.57	0.923									
DX	2.28	0.65	0.001									
NH	-1.61	0.73	0.030									
HX	-0.48	0.56	0.387									
T				2.19	4.95	0.661						
Y				-3.26	1.27	0.013	-2.22	0.61	0.000	-1.78	1.47	0.230
D				5.87	2.48	0.021	0.93	0.59	0.117	0.76	1.72	0.660
H				2.74	2.02	0.180						
S				6.84	3.53	0.057				0.91	5.82	0.877
CW				2.48	1.57	0.120				-0.09	2.20	0.967
PC				4.84	2.23	0.034				4.49	2.36	0.061
B				4.39	2.01	0.032				2.00	0.99	0.047
L				-2.79	1.20	0.023				-1.54	1.96	0.434
MX				2.80	1.91	0.148				-2.70	2.05	0.192
						Sex						
B	0.30	0.36	0.399	3.17	0.99	0.002	-0.17	0.55	0.761	-0.86	1.15	0.459
G	0.08	0.37	0.836	2.04	1.05	0.056	-1.11	0.65	0.087	1.37	1.15	0.236
						Diet						
D1	0.06	0.55	0.910									
D2	0.13	0.52	0.803									
D3	-0.49	0.50	0.328									
D4	1.06	0.49	0.032									

[a]NBS96 = National Barrow Show 1996 Progeny Test, QLGM = Quality Lean Growth Modeling, GLE = Genetics of Lean Efficiency, NBS00 = National Barrow Show 2000 Progeny Test.

[b]T = Tamworth, Y = Yorkshire, D = Duroc, H = Hampshire, S = Spot, C = Chester White, P = Poland China, B = Berkshire, L = Landrace, X = Misc. crossbreds, BX = Berkshire- sired crosses, DB = Danbred USA, M = Monsanto Choice Genetics, DX = Duroc-sired crossbreds, NH = Hewsham Hybrids, and HX = Hampshire-sired crossbreds.

Table 2. Average bias in prediction of pounds of fat-free lean from carcass last rib measurements (predicted fat-free lean minus actual fat-free lean)[a,b]

	QLGM			NBS96			GLE			NBS00		
	Û	se	P	Û	se	P	Û	se	P	Û	se	P
						BREED						
BX	7.59	0.82	<.0001									
DB	-4.08	0.77	<.0001									
MSG	–0.16	0.70	0.821									
DX	3.19	0.81	<.000									
NH	-3.77	0.91	<.000									
HX	-4.12	0.69	<.000									
T	0.71	6.44	0.913									
Y				-2.20	1.66	0.190	-3.57	0.72	<.0001	-0.19	1.84	0.920
D				4.20	3.22	0.200	-1.76	0.71	0.013	2.44	2.17	0.263
H				-1.50	2.62	0.568						
S				13.94	4.59	0.004				5.73	7.32	0.436
CW				9.79	2.05	<.0001				4.45	2.77	0.111
PC				5.59	2.90	0.058				5.86	2.97	0.052
B				7.47	2.61	0.006				9.01	1.25	<.0001
L				-1.86	1.56	0.236				-0.66	2.47	0.790
MX				1.50	2.48	0.548				1.00	2.58	0.699
						SEX						
B	0.99	0.44	0.027	5.35	1.29	0.0001	0.22	0.66	0.738	3.41	1.45	0.021
G	-1.43	0.46	0.002	2.18	1.36	0.115	-5.56	0.77	<.0001	3.50	1.44	0.017
						DIET						
1	-1.24	0.68	0.066									
2	-1.28	0.64	0.047									
3	-0.66	0.62	0.288									
4	2.29	0.61	0.0002									

[a]NBS96 = National Barrow Show 1996 Progeny Test, QLGM = Quality Lean Growth Modeling, GLE = Genetics of Lean Efficiency, NBS00 = National Barrow Show 2000 Progeny Test.

[b]T = Tamworth, Y = Yorkshire, D = Duroc, H = Hampshire, S = Spot, C = Chester White, P = Poland China, B = Berkshire, L = Landrace, X = Misc. crossbreds, BX = Berkshire- sired crosses, DB = Danbred USA, M = Monsanto Choice Genetics, DX = Duroc-sired crossbreds, NH = Hewsham Hybrids, and HX = Hampshire-sired crossbreds.

Table 3. Average bias in prediction of pounds of fat-free lean (predicted – actual) from FOM measurements[a,b]

	QLGM			GLE			NBS00		
	û	SE	P	Û	SE	P	û	SE	P
Breed									
BX	5.63	0.76	<.0001						
DB	-0.51	0.72	0.478						
MCG	-0.42	0.65	0.514						
DX	1.71	0.73	0.019						
NH	-0.42	0.85	0.621						
HX	-1.51	0.64	0.019						
Y				-3.77	0.82	<.0001	-0.25	1.65	0.879
D				-3.53	0.83	<.0001	-1.89	2.41	0.437
S							2.91	6.37	0.649
CW							1.61	2.41	0.508
PC							3.33	3.19	0.299
B							4.27	1.21	0.0007
L							1.90	2.27	0.406
MX							0.17	2.24	0.9396
Sex									
B	1.06	0.41	0.009	-1.44	0.76	0.059	1.62	1.38	0.242
G	0.43	0.43	0.314	-5.85	0.89	<.0001	1.39	1.28	0.284
Diet									
1	0.16	0.62	0.800						
2	-0.19	0.61	0.754						
3	0.18	0.57	0.753						
4	2.83	0.55	<.0001						

[a]QLGM = Quality Lean Growth Modeling, GLE = Genetics of Lean Efficiency, NBS00 = National Barrow Show 2000 Progeny Test.

[b]T = Tamworth, Y = Yorkshire, D = Duroc, H = Hampshire, S = Spot, C = Chester White, P = Poland China, B = Berkshire, L = Landrace, X = Misc. crossbreds, BX = Berkshire- sired crosses, DB = Danbred USA, M = Monsanto Choice Genetics, DX = Duroc-sired crossbreds, NH = Hewsham Hybrids, and HX = Hampshire-sired crossbreds.

Table 4. Average bias in prediction of pounds of fat-free lean from Automated Ultrasonic System (AUS) (predicted fat-free lean minus actual fat-free lean)[a,b]

	GLE			NBS00		
	û	se	Pr	û	se	Pr
			Breed			
Y	-0.47	0.80	0.5595	-3.78	1.98	0.0608
D	0.63	0.75	0.4057	-0.55	2.29	0.8117
C				-2.84	2.50	0.2613
P				-0.98	3.28	0.7650
B				5.39	1.29	<.0001
L				-0.08	2.24	0.9727
X				-2.31	3.28	0.4841
			SEX			
M	1.66	0.75	0.0276	0.95	1.16	0.4163
F	-1.50	0.81	0.0644	-2.42	1.40	0.0891

[a]GLE = Genetics of Lean Efficiency, NBS00 = National Barrow Show 2000 Progeny Test.

[b]Y = Yorkshire, D = Duroc, C = Chester White, P = Poland China, B = Berkshire, L = Landrace, X = Misc. crossbreds.

Table 5. Average bias in prediction of pounds of fat-free lean from Ultrafom (UFOM) (predicted fat-free lean minus actual fat-free lean)[a,b]

	GLE			NBS00		
	û	se	Pr	û	se	Pr
			Breed			
Y	-3.63	1.60	0.028	-4.53	2.08	0.033
D	-1.88	1.25	0.138	-0.30	2.32	0.898
S			|	-1.88	7.19	0.794
C				2.47	3.32	0.460
P				1.28	2.91	0.661
B				6.60	1.37	<.0001
L				-1.03	4.13	0.803
X				-1.55	2.70	0.568
			Sex			
M	-0.76	1.18	0.5218	-1.13	1.53	0.465
F	-4.75	1.70	0.0073	1.39	1.64	0.399

[a]GLE = Genetics of Lean Efficiency, NBS00 = National Barrow Show 2000 Progeny Test.

[b]Y = Yorkshire, D = Duroc, S = Spot, C = Chester White, P = Poland China, B = Berkshire, L = Landrace, X = Misc. crossbreds.

Table 6. Residuals (predicted – actual) for FFL, lb, predicted from Live SCAN measurements and Carcass Weight

	û	se	P	Û	se	P	û	se	P
	QLGM			GLE			NBS00		
				Breed					
BX	3.32	0.69	<.0001						
DB	-0.85	0.64	0.185						
M	1.21	0.60	0.043						
DX	2.26	0.68	0.0009						
NH	-1.78	0.77	0.021						
HX	0.24	0.59	0.680						
Y				-3.11	0.62	<.0001	-2.25	1.43	0.119
D				-0.10	0.60	0.874	-0.18	1.68	0.913
S							-0.29	5.66	0.959
C							-2.29	2.14	0.287
P							-0.90	2.30	0.697
B							1.02	0.97	0.292
L							-2.66	2.01	0.191
X							-2.42	2.13	0.259
				Sex					
M	0.87	0.38	0.020	-0.98	0.56	0.084	-2.56	1.12	0.026
F	0.59	0.39	0.125	-2.23	0.66	0.0009	0.07	1.13	0.954
				Diet					
1	0.39	0.57	0.489						
2	0.56	0.54	0.300						
3	-0.05	0.52	0.919						
4	2.03	0.51	<.0001						

[a]QLGM = Quality Lean Growth Modeling, GLE = Genetics of Lean Efficiency, NBS00 = National Barrow Show 2000 Progeny Test.

[b]T = Tamworth, Y = Yorkshire, D = Duroc, H = Hampshire, S = Spot, C = Chester White, P = Poland China, B = Berkshire, L = Landrace, X = Misc. crossbreds, BX = Berkshire- sired crosses, DB = Danbred USA, M = Monsanto Choice Genetics, DX = Duroc-sired crossbreds, NH = Hewsham Hybrids, and HX = Hampshire-sired crossbreds.