Evaluation of procedures to predict fat-free lean in swine carcasses[1,2]

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ABSTRACT: The objectives were to develop equations for predicting fat-free lean in swine carcasses and to estimate the prediction bias that was due to genetic group, sex, and dietary lysine level. Barrows and gilts (n = 1,024) from four projects conducted by the National Pork Board were evaluated by six procedures, and their carcass fat-free lean was determined. Pigs of 16 genetic groups were fed within weight groups one of four dietary regimens that differed by 0.45% in lysine content and slaughtered at weights between 89 and 163 kg. Variables in equations included carcass weight and measures of backfat depth and LM. Fat-free lean was predicted from measures of fat and muscle depth measured with the Fat-O-Meater (FOM), Automated Ultrasonic System (AUS), and Ultrafom (UFOM) instruments, carcass 10th-rib backfat and LM area (C10R), carcass last-rib backfat (CLR), and live animal scan of backfat depth and LM area with an Aloka 500 instrument (SCAN). Equations for C10R (residual standard deviation, RSD = 2.93 kg) and SCAN (RSD = 3.06 kg) were the most precise. The RSD for AUS, FOM, and UFOM equations were 3.46, 3.57, and 3.62 kg, respectively. The least precise equation was CLR, for which the RSD was 4.04 kg. All procedures produced biased predictions for some genetic groups ($P < 0.01$). Fat-free lean tended to be overestimated in fatter groups and underestimated in leaner ones. The CLR, FOM, and AUS procedures overestimated fat-free lean in barrows and underestimated it in gilts ($P < 0.01$), but other procedures were not biased by sex. Bias due to dietary lysine level was assessed for the C10R, CLR, FOM, and SCAN procedures, and fat-free lean in pigs fed the low-lysine dietary regimen was overestimated by CLR, FOM, and SCAN ($P < 0.05$). Positive regressions of residuals (measured fat-free lean minus predicted fat-free lean) on measured fat-free lean were found for each procedure, ranging from 0.204 ± 0.013 kg/kg for C10R to 0.605 ± 0.049 kg/kg for UFOM, indicating that all procedures overestimated fat-free lean in fat pigs and underestimated it in lean pigs. The pigs evaluated represent the range of variation in pigs delivered to packing plants, and thus the prediction equations should have broad application within the industry. Buying systems that base fat-free lean predictions on measures of carcass fat depth and muscle depth or area will overvalue fat pigs and undervalue lean pigs.

Key Words: Body Lean Mass, Methodology, Pigs, Prediction, Statistical Bias

 J. Anim. Sci. 2004. 82:2428–2441

Introduction

In most markets, percentage of fat-free lean predicted from carcass weight and measures of backfat depth and LM determines the value of pork carcasses. Procedures to predict fat-free lean, based on methods first described by Fahey et al. (1977) are described in the *National Pork Board Handbook* (NPB, 2000).

Packers use various instruments for backfat and LM measurements, and the site where measurements are made varies. Each packer applies a unique procedure to estimate carcass fat-free lean for all pigs delivered to that market. Predictions of fat-free lean, however, may be biased when one equation is used across pigs of different genetic groups and sexes, or pigs treated with ractopamine hydrochloride (Gu et al., 1992; Hicks et al., 1998; Schinckel et al., 2003). The precision of

[1]Published as paper No. 14214, Journal Ser., Nebraska Agric. Res. Div., Univ. Nebraska, Lincoln 68583-0908.

[2]This research was supported in part by the National Pork Producers Council and the National Pork Board.

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Received August 8, 2003.

Accepted April 12, 2004.

procedures used by different packers to predict carcass fat-free lean and possible bias due to weight, genetic group, and management are not well documented. This information is needed for pork producers to understand pricing matrices used by packers and to develop effective marketing strategies.

The National Pork Board (formerly the National Pork Producers Council) conducted four experiments during the years 1996 through 2000 in which backfat and LM measurements of 1,024 pigs were evaluated by six procedures and their carcass composition was determined. The pigs were barrows and gilts of 16 genetic groups that were fed diets differing in lysine content and slaughtered at live weights between approximately 89 and 163 kg. These data were analyzed to 1) develop fat-free lean prediction equations for pork carcasses evaluated by each procedure and to compare the relative precision of various procedures and 2) determine whether procedures are biased for certain genetic groups, weight classes, or carcass fat-free lean classes.

Experimental Procedures

Carcasses of 1,024 pigs from four National Pork Board (**NPB**) projects were evaluated. Pigs in two projects were grown at the Minnesota Swine Evaluation Station and those in the other two projects were grown in the swine testing station at New Hampton, IA. All pigs were slaughtered at Quality Pork Processors packing plant in Austin, MN. Half of each carcass was transported to Geneva Meats, Geneva, MN, where it was dissected, and tissue samples were collected for lipid analyses.

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.

National Swine Improvement Federation-certified technicians obtained real-time ultrasonic measurements of backfat depth (**SCANBF**) and LM area (**SCANLMA**) on live pigs within 3 d of slaughter. Measurements were taken with an Aloka 500-V real-time ultrasound instrument equipped with a 3.5-MHz, 12.5-cm linear transducer (Corometrics Medical Systems Inc., Wallingford, CT). The transducer was placed vertically between the 10th and 11th ribs encompassing the cross section of the LM from the medial end near the vertebral column to the lateral boundary.

Hot carcasses were evaluated at Quality Pork Processors with a ruler, the Fat-O-Meater (SFK Technology A/S, Herlev, Denmark), the Animal Ultrasound Services Carcass Value Technology System (Animal Ultrasound Services [**AUS**] Inc., Ithaca, NY), and an Ultrafom 300 (SFK Technology A/S).

The ruler was used to record fat depth, including skin, on the midline of the split carcass at the last rib (**LRBF**). The Fat-O-Meater is an optical probe that measures the difference in light reflectance every 0.5 mm as it passes through fat and muscle tissue and records the depth of each tissue. Fat-O-Meater measurements of backfat (**FOMBF**) and LM depth (**FOMLD**) were made perpendicular to the muscle between the third and fourth from the last ribs. The AUS Carcass Value Technology System is an automated and computerized real-time ultrasound system that measures backfat (**AUSBF**) and LM depth (**AUSLD**). The image equipment consisted of an Aloka 500-V (Corometrics Medical Systems) ultrasound system equipped with a 3.5-MHz body composition transducer (Aloka model UST-5044-3.5) that was 12.6 cm long. Measurements were made with the transducer placed longitudinally between the 10th and last rib approximately 6.4 cm off the midline of the carcass. Interpretation of the images was by AUSKey, a computer software package for measuring fat and muscle depth from real time ultrasonic images. The UltraFom 300 is a hand-held, real-time ultrasound probe with the same measuring capabilities as the Fat-O-Meater. It consists of 64 sensor elements that send sound pulses into the carcass to measure backfat (**UFOMBF**) and LM depth (**UFOMLD**). Measurements were made with the transducer held longitudinally at the same location where AUS measurements were made.

After chilling, carcasses were cut between the 10th and 11th ribs to expose the exterior fat covering the LM and the muscle itself. Backfat depth (**BF10**) was measured at a point three-fourths the distance from the medial boundary of the longest axis of the LM perpendicular to the outer edge of the skin. Longissimus muscle (**LMA**) area was recorded.

The six procedures are designated as 1) **C10R**, prediction of fat-free lean from hot carcass weight, BF10, and LMA; 2) **CLR**, prediction from hot carcass weight and LRBF; 3) **FOM**, prediction from hot carcass weight, FOMBF, and FOMLD; 4) **AUS**, prediction from hot carcass weight, AUSBF, and AUSLD; 5) **UFOM**, prediction from hot carcass weight, UFOMBF, and UFOMLD; and 6) **SCAN**, prediction from hot carcass weight, SCANBF, and SCANLMA. Although the live weight of all pigs was recorded, nearly all markets in the United States use carcass weight in predictions of fat-free lean. Therefore, prediction equations including only carcass weight were developed.

National Pork Board Projects

Pigs came from four NPB projects: 1) the 1996 National Barrow Show sire progeny test (**NBS96**), 2) the Quality Lean Growth Modeling project (**QLGM**) conducted during 1996 and 1997, 3) the Genetics of Lean Efficiency project (**GLE**) conducted during 1999 and 2000, and 4) the 2000 National Barrow Show sire progeny test (**NBS00**).

NBS96. Purebred and crossbred barrows and gilts were submitted to the National Barrow Show progeny test in sire groups to test sires for growth and carcass traits. Pigs were grown at the New Hampton, IA, test station. Tamworth, Yorkshire, Duroc, Hampshire, Spot,

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

			Lysine, %			
ME, kcal/kg	Pig weight, kg	Added fat, %	Diet 1	Diet 2	Diet 3	Diet 4
3,524	41 to 63.5	5	1.25	1.10	0.95	0.80
3,440	64 to 86.5	3	1.10	0.95	0.80	0.65
3,310	87 to 108.5	0	0.95	0.80	0.65	0.50
3,312	109 to 149.5	0	0.80	0.65	0.50	0.35

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 45 to 113 kg (Table 2) 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. Data from this subset of pigs were used only in the C10R and CLR analyses. The UFOM technology was not available for the project and the pigs were not scanned live for BF and LMA. In addition, because this was the first experience with FOM and AUS procedures, data for these procedures in this subset of carcasses were not included in analyses.

QLGM. The QLGM project was conducted in three replications. The objective was to determine genetic line, dietary lysine level, and sex effects and their interactions on lean growth. A total of 1,588 barrows and gilts was 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 U.S.A., 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 commingled following segregated early-weaning procedures. They were moved to a grower barn at the Minnesota Swine Testing Station at approximately 18 kg, and to experimental facilities at approximately 45 kg. Pigs received a common diet to weight of 45 kg and one of four diets (Table 1) to a weight of either 113, 131.5, or 150 kg. The UFOM instrument was not available for this project; pigs were evaluated with the other five procedures.

GLE. The GLE project included purebred Duroc and Yorkshire barrows and gilts tested in two replicates. 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 six to eight pigs per sire family to the Minnesota Swine Evaluation Station for testing from approximately 45 kg to weights of 113 or 131.5 kg. Pigs were fed Diet 2 (Table 1) throughout the test period. A total of 230 carcasses were evaluated and dissected. Pigs in this and the NBS00 projects were evaluated by all six procedures.

NBS00. The NBS00 had the same objective and procedures as NBS96. Although pigs were grown at the New Hampton, IA, test station, the project overlapped with the GLE project and pigs were slaughtered on the same days as the GLE Rep. 2 pigs. A total of 94 pigs was evaluated and dissected.

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 meal form with particle size less than 750 (m. Added fat was choice white grease.

There were 35 pens with approximately 16 pigs of one genetic group per pen in each replication of the

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

Weight range, kg	NBS96	QLGM	GLE	NBS00	Total
<97.5	1	—	3	—	4
97.5 to 104	1	1	1		3
104.3 to 110.7	30	28	8	38	104
111.1 to 117.5	40	138	81	52	311
117.9 to 124.3	1	57	21	4	83
124.7 to 131.1	—	100	36	—	136
131.5 to 137.9	—	109	70	—	179
138.3 to 144.7	—	54	10	—	64
145.1 to 151.5	—	101	—	—	101
151.9 to 158.3	—	36	—	—	36
≥158.7	—	3	—	—	3
Total	73	627	230	94	1,024

[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 group evaluated by each procedure in each project[a]

	Genetic group[b]																
Method[c]	T	Y	D	H	S	C	P	B	L	X	BX	DB	M	DX	NH	HX	Total
	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
UFOM	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
FOM	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
AUS	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
SCAN	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
	QLGM																
C10R	—	—	—	—	—	—	—	—	—	—	92	105	125	96	76	131	625
CLR	—	—	—	—	—	—	—	—	—	—	92	106	126	96	76	131	627
UFOM	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
FOM	—	—	—	—	—	—	—	—	—	—	82	92	112	89	66	114	555
AUS	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
SCAN	—	—	—	—	—	—	—	—	—	—	91	105	121	94	74	125	610
	GLE																
C10R	—	113	116	—	—	—	—	—	—	—	—	—	—	—	—	—	229
CLR	—	114	116	—	—	—	—	—	—	—	—	—	—	—	—	—	230
UFOM	—	23	31	—	—	—	—	—	—	—	—	—	—	—	—	—	54
FOM	—	106	104	—	—	—	—	—	—	—	—	—	—	—	—	—	210
AUS	—	83	94	—	—	—	—	—	—	—	—	—	—	—	—	—	177
SCAN	—	113	116	—	—	—	—	—	—	—	—	—	—	—	—	—	229
	NBS00																
C10R	—	16	12	1	7	6	35	9	8	—	—	—	—	—	—	—	94
CLR	—	16	12	1	7	6	35	9	8	—	—	—	—	—	—	—	94
UFOM	—	12	10	1	5	6	28	3	7	—	—	—	—	—	—	—	72
FOM	—	15	7	1	7	4	28	8	8	—	—	—	—	—	—	—	78
AUS	—	12	9		7	4	26	9	4	—	—	—	—	—	—	—	71
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 = Miscellaneous crossbreds; BX = Berkshire-sired crosses; DB = Danbred USA; M = Monsanto Choice Genetics; DX = Duroc-sired crossbreds; NH = Newsham Hybrids; and HX = Hampshire-sired crossbreds.

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

QLGM project. Pens of pigs were randomly assigned to one of the dietary regimens. There were 8 to 10 pens per regimen in each replication. A total of 25 to 27 pens per regimen were represented in the 627 QLGM pigs in which fat-free lean was determined. Diet 2 was used throughout the trial in the GLE project, and Diet 3 was used in the NBS96 and NBS00 projects.

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.

Genetic Groups of Pigs. The genetic groups 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. Pigs were tested with the HAL-1843 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. Because there were so few heterozygous pigs, stress gene genotype was not considered in the analyses.

Carcass Separation Procedures. Across projects, pigs were slaughtered on 55 d. Project leaders provided supervision of data collection on each slaughter day. The numbers of observations by each procedure applied to pigs of each genetic group in each project are in Table 3. All procedures were not used in all projects, leading to variation in the number of pigs evaluated by each procedure. In addition, preliminary analyses indicated results of AUS data from the QLGM project were unreliable. 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.

Determination of fat-free lean content and the dissection of carcasses were carried out under a protocol established in 1996 by an NPB advisory committee of producers, industry representatives, meat scientists, and public officials. Carcasses were separated according

to the standards of the Institutional Meat Purchase Specification (**IMPS**) for fresh pork products, Series 400 (http://www.ams.usda.gov/lsg/imps/imps400.pdf). Half of each carcass was separated into 10 end points for weights of primal and subprimal cuts, skin, and bone. All meat, fat, and other soft tissue of each end point were coarsely ground, and a random sample of each ground end point was collected and analyzed for total lipid content by the method described by Folch et al. (1957). Each carcass half was skinned and separated into the following: 1) soft tissue in the jowl (IMPS 419); 2) soft tissue in the spare rib (IMPS 416) and belly (IMPS 408); 3) inside ham muscle (IMPS 402F); 4) outside ham muscle (IMPS 402E); 5) other soft tissue in the ham; 6) ham knuckle muscle (the quadriceps femoris); 7) LM (IMPS 410); 8) tenderloin muscle (IMPS 415) plus other soft tissue in the loin; 9) soft tissue in the boneless picnic (IMPS 405), boneless butt (IMPS 407), and shoulder (IMPS 403); and 10) the total of fatback, ham external fat, ham seam fat, loin external fat, picnic external fat, and butt external fat. Each component was weighed, ground and mixed, and sampled for determination of lipid percentage. Weight of fat-free lean in each other component was calculated from the percentage of lipid in Component 10 in the manner described by other researchers (Fahey et al., 1977; Wagner et al., 1999). The equation used was

$$\text{Component weight of fat-free lean} = \text{component weight} - (\text{component weight} \times [\text{component lipid \%} \div \text{component 10 lipid \%}])$$

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

Data Analyses

Prediction Equations. The SAS software (SAS Inst. Inc., Cary, NC) was used for all statistical analyses. Weight of carcass fat-free lean and percentage fat-free lean were fitted in separate models for carcasses evaluated by each procedure. The objective was to find best-fitting regression equations to predict fat-free lean across genetic groups, 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, LM measurement, and hot carcass weight and the cross product of the linear variables. Final models were developed with backward elimination to remove regression variables for which probabilities that regression coefficients equaled 0 were greater than 0.10. First, cross product terms were deleted from models if they were not significant, then quadratic terms, and finally nonsignificant linear terms were deleted. 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 $P \leq 0.10$. Final regression equations were those for which probabilities for all regression coefficients were at level $P \leq 0.10$.

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 = weight or percentage of fat-free lean, SLDATE = random effect of slaughter date, BF10 = 10th-rib carcass backfat depth, LMA = 10th-rib LM area, CWT = hot carcass weight, b_0 = intercept, b_i = regression coefficient on each variable, and e = residual error. The final model after elimination of nonsignificant 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, σ^2_{GRP}, and to residual error, σ^2_R, were calculated in final models and used to assess the precision of the prediction equation. Residuals, the difference between measured and predicted fat-free lean, or between measured and predicted percentage fat-free lean, were calculated for each procedure. The variance of these residuals is the sum of the variance components due to slaughter day and to residual error ($\sigma^2_{Res} = \sigma^2_{GRP} + \sigma^2_R$). Precision was expressed as the square root of the variance of residuals and defined as the residual standard deviation (**RSD** = σ_{Res}).

Evaluation of Bias. Residual weight and percentage of fat-free lean were calculated for each pig from the final equation for each procedure. Bias was assessed by fitting the residuals to a model that included the fixed effects of project, genetic group within project, sex, and diet within project. Because of the poor connection of genetic groups and diets across projects, these effects were nested within project. Mean residuals and their standard errors for each subclass were calculated, and means were tested to determine whether they differed from zero.

To test whether prediction equation biases by each procedure were related to the measured variables, residuals were regressed on carcass weight and the independent variables in each equation. Significant regressions indicate that additional terms, such as cubic or higher order cross product terms, would improve the fit of the equations across subclasses. The model included the fixed effect of project and the linear regression of the variables measured by each procedure. In addition, to determine whether there was systematic bias related to measured fat-free lean in the carcass, residuals for weight of fat-free lean were regressed on measured fat-free lean and residuals for percentage fat-free lean were regressed on percentage fat-free lean. The model included the fixed effect of project and the regression on measured values.

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

Trait[a]	No.	Mean	SD	Min	Max
FFL, kg	1,024	45.3	6.9	23.6	69.8
FFL%	1,024	48.5	5.2	31.7	61.8
LWT, kg	1,024	126.0	13.9	89.3	163.3
CWT, kg	1,024	93.5	11.3	63.0	127.0
LRBF, mm	1,024	29.7	7.4	10.2	55.9
BF10, mm	1,021	27.4	8.4	7.6	58.4
LMA, cm^2	1,021	41.3	7.1	18.7	77.4
UFOMBF, mm	126	20.0	5.9	10.1	36.3
UFOMLD, mm	126	48.5	7.3	32.8	65.1
FOMBF, mm	843	24.2	6.6	8.0	52.0
FOMLD, mm	843	57.3	9.3	23.0	88.0
AUSBF, mm	248	22.4	6.7	9.9	42.6
AUSLD, mm	248	63.7	10.7	39.0	97.0
SCBF, mm	931	25.7	7.6	8.9	58.4
SCLMA, cm^2	931	41.8	6.8	17.7	66.5

[a]FFL = kg fat-free lean; FFL% = percentage fat-free lean; LWT = preslaughter live weight; CWT = hot carcass weight; LRBF = last rib backfat depth; BF10 = 10th-rib backfat depth; LMA = 10th-rib LM area, UFOMBF = backfat depth measured with Ultrafom; UFOMLD = LM depth measured with Ultrafom; FOMBF = backfat depth measured with Fat-O-Meater; FOMLD = LM depth measured with Fat-O-Meater; AUSBF = backfat depth measured with Automated Ultrasonic System; AUSLD = LM depth measured with Automated Ultrasonic System; SCBF = live pig backfat depth measured at 10th rib with Aloka 500; and SCLMA = live pig LM area measured at 10th rib with Aloka 500.

Comparison of Procedures. No exact statistical test to compare equations for the different procedures exists. Nevertheless, variances of residuals and Akaike's information criterion (**AIC**) statistic are useful to compare alternative models. The AIC statistic is a log likelihood value that is used to evaluate the appropriate covariance structure among alternative models. It depends on the number of parameters estimated and on the number of records in the data set. Therefore, AIC statistics should be compared only when different models are fitted to the same data. The model that produces an AIC value closest to zero and with the least RSD is considered most desirable.

Final models for each equation were fitted to the subset of data with the largest number of carcasses that were evaluated by all procedures being compared. 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 proce-

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

	Method[b]					
Variable[c]	C10R, mm	CLR	UFOM	FOM	AUS	SCAN
N	1021	1024	126	843	248	931
b_0	2.61	5.6	20.76	16.89	1.59	–0.46
BF	–0.543	–0.44	–1.04	0.18	–0.36	–0.60
BF × BF	0.006	—	0.015	–0.015	0.0077	0.011
BF × BF × BF	—	—	—	0.00028	—	—
LM	—	—	—	0.06	0.20	—
CWT	0.61	0.56	0.41	0.17	0.48	0.70
CWT × CWT	—	—	—	0.0025	—	—
BF × LM	0.0087	—	—	—	–0.0062	0.0084
BF × CWT	–0.0055	—	—	–.0059	—	–0.0085
σ^2_{GRP}	0.71	1.54	0.40	1.99	2.21	1.01
σ^2_R	7.85	14.81	12.67	10.76	9.77	8.36
RSD	2.93	4.04	3.62	3.57	3.46	3.06

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

[b]C10R = 10th-rib backfat depth, mm and LM area, cm^2; CLR = last-rib backfat depth, mm; UFOM = ultrafom backfat depth, mm and loin depth, mm; FOM = Fat-O-Meater backfat depth, mm and loin depth, mm; AUS = Automated Ultrasound System backfat depth, mm and loin depth, mm; SCAN = live animal backfat depth, mm and LM area, cm^2 at 10th rib.

[c]b_o = intercept; BF = backfat depth, mm; LM = LM area, cm^2 (C10R and SCAN) or LM depth, mm (UFOM, FOM, and AUS); CWT = hot carcass weight, kg; σ^2_{GRP} = variance component for group (project/slaughter-date subclass); σ^2_R= residual error variance component, RSD = residual standard deviation.

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

	Method[b]					
Variable[c]	C10R	CLR	UFOM	FOM	AUS	SCAN
N	1021	1024	126	843	248	931
b_o	45.34	62.4	37.48	77.83	21.18	61.09
BF	–0.65	–0.73	0.85	–0.36	–0.40	–1.13
BF × BF	0.0041	—	—	–0.016	.0092	0.011
BF × BF × BF	—	—	—	0.00030	—	—
LM	0.62	—	0.59	0.069	0.74	—
LM × LM	–0.0046	—	—	—	—	—
CWT	—	—	–0.11	–0.44	0.32	0.086
CWT × CWT	—	—	—	0.00024	—	—
BF × LM	—	—	–0.027	—	–0.0076	0.0085
BF × CWT	—	0.0028	—	—	—	–0.0036
LM × CWT	—	—	—	—	–0.0056	—
σ^2_{GRP}	0.86	2.1	0.66	2.24	2.88	1.19
σ^2_R	8.89	16.6	17.23	11.78	12.27	9.15
RSD	3.12	4.32	4.23	3.74	3.89	3.22

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

[b]C10R = 10th-rib backfat depth (mm) and LM area (cm^2); CLR = last-rib backfat depth (mm); UFOM = ultrafom backfat depth (mm) and loin depth (mm); FOM = Fat-O-Meater backfat depth (mm) and loin depth (mm); AUS = Automated Ultrasound System backfat depth (mm) and loin depth (mm); SCAN = live animal backfat depth (mm) and LM area (cm^2) at 10th rib.

[c]b_o = intercept; BF = backfat depth, mm; LM = LM area, cm^2 (C10R and SCAN) or LM depth, mm (UFOM, FOM, and AUS); CWT = hot carcass weight, kg; σ^2_{GRP} = variance component for group (project/slaughter-date subclass); σ^2_R= residual error variance component, RSD = residual standard deviation.

dures. Models for FOM, AUS, and UFOM procedures were added in that order until all procedures were compared.

Results

Statistics describing the data are in Table 4. Standard deviations of all traits were very large relative to the mean owing in large part to the wide range of slaughter weights.

Prediction Equations. Final equations to predict weight and percentage of fat-free lean by each procedure are in Tables 5 and 6, respectively. The best-fitting equations for each procedure included various combinations of linear, quadratic, cubic, and cross product terms among independent variables. Within procedure, the variables included in equations to predict weight and percentage of fat-free lean differed.

All final equations to predict weight of fat-free lean except the CLR equation contained a quadratic term for the respective fat depth measurement, and the FOM equation contained a cubic term for fat depth. The measure of LM entered the FOM and AUS equations as a linear term and the C10R, AUS, and SCAN equations as a cross product with the respective measure of fat depth. No equation contained a measure of LM as a quadratic term. The linear effect of hot carcass weight was included in every equation, the quadratic effect in the FOM equation, and the cross product of hot carcass weight with fat depth entered the C10R, FOM, and SCAN equations. The cross product term of fat depth and LM area or depth entered the C10R, AUS, and SCAN equations.

All final equations to predict the percentage fat-free lean contained the linear effect of fat depth. The quadratic effect of fat depth was included in all equations except the CLR and UFOM equations, and as for prediction of weight of fat-free lean, the FOM equation included the cubic effect of fat depth. The linear effect of LM area or depth entered the C10R, UFOM, FOM, and AUS equations, and the quadratic term was included in the C10R equation. Percentage of fat-free lean was calculated as weight of fat-free lean divided by hot carcass weight and thus is adjusted for carcass weight. Nevertheless, hot carcass weight entered the UFOM, FOM, AUS, and SCAN equations as a linear effect, the FOM equation as a quadratic effect, and the CLR, AUS, and SCAN equations as a cross product term with fat depth or muscle depth. The cross product term of fat depth and LM depth entered the UFOM, AUS, and SCAN equations.

The residual variance for weight of fat-free lean ranged from 8.56 kg^2 (C10R, RSD = 2.93 kg) to 16.35 kg^2 (CLR, RSD = 4.04 kg) and from 9.75%^{2} (C10R, RSD = 3.12%) to 18.70%^{2} (CLR, RSD = 4.32%) for percentage of fat-free lean. The random effect of the combination of project and slaughter date accounted for a significant proportion of the variation for all methods, ranging from 3.1% of the total for prediction of weight of fat-free lean for the UFOM procedure to 18.5% for the AUS procedure.

Comparison of Procedures. Table 7 shows slaughter day and within-slaughter day variance components and values of AIC for best-fitting models for each procedure. Degrees of freedom in models differed because the number of regression variables depended on the procedure.

Table 7. Comparisons of equations to predict weight of fat-free lean (kg)

Procedure[a]	df	σ^2_{grp}[b]	σ^2_R[b]	AIC[c]
	C10R and CLR (n = 1,021)			
C10R	6	0.72	7.85	5,104.6
CLR	3	1.57	14.82	5,722.7
	C10R, CLR, and SCAN (n = 928)			
C10R	6	0.66	8.00	4,659.2
CLR	3	1.54	15.07	5,217.3
SCAN	6	1.03	8.36	4,710.9
	C10R, CLR, SCAN, and FOM (n = 823)			
C10R	6	0.66	8.02	4,139.2
CLR	3	1.40	14.97	4,620.6
SCAN	6	1.10	8.37	4,185.7
FOM	8	2.06	10.65	4,413.9
	C10R, CLR, SCAN, FOM, and AUS (n = 216)			
C10R	6	1.76	6.68	1,085.1
CLR	3	3.13	12.04	1,182.4
SCAN	6	1.41	6.87	1,086.8
FOM	8	3.89	8.96	1,166.0
AUS	6	2.13	9.53	1,152.5
	All methods (n = 57)			
C10R	6	1.38	7.30	309.8
CLR	3	5.07	14.55	326.7
SCAN	6	0.30	6.21	298.7
FOM	8	2.48	9.12	330.6
AUS	6	4.56	10.61	328.8
UFOM	4	2.18	13.46	326.3

[a]C10R = carcass 10th-rib equation; CLR = carcass last-rib equation; SCAN = equation from live animal scan measurements; FOM = Fat-O-Meater equation; AUS = Automated Ultrasonic System equation; and UFOM = Ultrafom equation.
[b]σ^2_{grp} = Variance component due to combination of project and slaughter day; σ^2_R = within slaughter day variance component.
[c]Akaike's information criterion statistic.

Numbers of observations also differ from those in Tables 5 and 6 because different pigs were missing observations from different procedures.

In all comparisons, AIC and residual variance statistics were least for C10R and SCAN equations, indicating that they produced the best fit, whereas CLR equations had the poorest fit. In the entire data set and in larger subsets of the data, both total variance and AIC values for C10R were less than for SCAN, indicating that the C10R equation was more precise. However, overall, the difference between these procedures was relatively small. Equations for FOM and AUS produced similar fits, but were less precise than either SCAN or C10R equations. The UFOM technology was used on relatively few carcasses that also were evaluated by other procedures. Thus, comparisons of UFOM precision relative to other procedures should be made with caution. Comparisons of procedures to predict percentage fat-free lean are not shown because rankings of procedures and relative differences in accuracy were very similar to those for weight of fat-free lean.

Bias. Probability values from analyses of variance are in Table 8. Because *P*-values in the ANOVA for weight and percentage of fat-free lean were very similar, only results for prediction of the weight of fat-free lean are presented. Every procedure produced biased predictions for some subclasses. Significant bias that was due to genetic group occurred with every procedure. Equations for C10R, UFOM, and SCAN were not biased by sex; however, bias due to sex was significant for the other procedures. Bias due to dietary regimen could be assessed only in the QLGM project and only for the C10R, CLR, FOM, and SCAN procedures. Predictions by CLR, FOM, and SCAN were biased by dietary regimen, whereas predictions by C10R were not.

Estimates of mean bias for genetic groups are in Table 9. A negative sign on the estimate means that on average the procedure overestimated fat-free lean of carcasses in that subclass, and a positive estimate means that weight of fat-free lean was underestimated. The direction of bias across projects was consistent for some groups, whereas for others the sign on the estimate varied across projects. Average fat-free lean in Berkshire and Berkshire crosses was overestimated by every procedure in every project. Weight of fat-free lean in Duroc, Duroc cross, and Poland China pigs also tended to be overestimated. Weight of fat-free lean in Danbred and Newsham Hybrid pigs in the QLGM project and in Yorkshire pigs in all projects was underestimated by all procedures.

Estimates of bias by each procedure due to sex, averaged across projects, are in Table 10. The CLR equation

Table 8. Degrees of freedom (df) and probabilities (*P*) from ANOVA for models of residuals for weight of fat-free lean (calculated minus predicted weight of fat-free-lean, kg) by each procedure[a]

	C10R		CLR		UFOM		FOM		AUS		SCAN	
Item	df	*P*	df	*P*	df	*P*	df	*P*	df	*P*	df	*P*
Project	3	0.03	3	<0.01	1	0.16	2	<0.01	1	0.40	2	<0.01
Genetic group (project)	22	<0.01	22	<0.01	8	<0.01	13	<0.01	7	<0.01	13	<0.01
Sex	1	0.54	1	<0.01	1	0.81	1	<0.01	1	<0.01	1	0.52
Diet	3	0.15	3	<0.01	—	—	3	<0.01	—	—	3	0.03

[a]C10R = carcass 10th-rib equation; CLR = carcass last-rib equation; UFOM = Ultrafom equation; FOM = Fat-O-Meater equation; AUS = Automated Ultrasonic System equation; and SCAN = equation from live animal scan measurements.

Table 9. Mean (û) and standard error (se) for residual (fat-free lean minus predicted fat-free lean, kg) by procedure for each genetic group within project[a,b,c]

	C10R		CLR		UFOM		FOM		AUS		SCAN	
Genetic group	û	se	û	se	û	se	û	se	û	se	û	se
	QLGM											
BX	–0.93	0.30	–3.43	0.37	—	—	–2.60	0.36	—	—	–1.52	0.32
DB	0.65	0.28	1.85	0.34	—	—	0.14	0.35	—	—	0.38	0.29
MCG	0.03	0.26	0.07	0.31	—	—	0.11	0.31	—	—	–0.56	0.27
DX	–0.98	0.29	–1.44	0.36	—	—	–0.84	0.35	—	—	–1.04	0.30
NH	0.79	0.33	1.75	0.40	—	—	0.17	0.41	—	—	0.80	0.34
HX	0.28	0.25	1.90	0.31	—	—	0.65	0.31	—	—	–0.12	0.26
	NBS96											
T	–0.94	2.25	–0.35	3.50	—	—	—	—	—	—	—	—
Y	1.53	0.58	1.01	0.90	—	—	—	—	—	—	—	—
D	–2.62	1.12	–1.92	1.75	—	—	—	—	—	—	—	—
H	–1.19	0.92	0.68	1.43	—	—	—	—	—	—	—	—
–S	–3.05	1.60	–6.29	2.48	—	—	—	—	—	—	—	—
CW	–1.08	0.71	–4.45	1.11	—	—	—	—	—	—	—	—
PC	–2.14	1.01	–2.55	1.57	—	—	—	—	—	—	—	—
B	–1.94	0.91	–3.38	1.43	—	—	—	—	—	—	—	—
L	1.31	0.54	0.86	0.85	—	—	—	—	—	—	—	—
MX	–1.22	0.87	–0.65	1.33	—	—	—	—	—	—	—	—
	GLE											
Y	1.06	0.28	1.49	0.33	1.12	0.72	1.53	0.32	0.36	0.36	1.35	0.28
D	–0.37	0.27	0.75	0.33	0.93	0.59	1.45	0.32	–0.14	0.33	0.02	0.27
	NBS00											
Y	0.85	0.65	0.36	0.88	2.32	0.96	0.16	0.85	1.83	0.94	1.26	0.73
D	–0.30	0.78	–0.63	1.01	0.39	1.06	0.93	1.25	0.35	1.09	0.51	0.85
S	–0.36	2.64	–3.30	3.50	0.44	3.30	–1.67	3.30			–0.54	2.93
CW	0.09	1.00	–1.71	1.32	–0.79	1.51	–0.65	1.25	1.64	1.23	1.31	1.11
PC	–1.99	1.07	–2.65	1.43	–0.49	1.34	–1.70	1.65	0.77	1.62	0.40	1.20
B	–0.85	0.45	–3.90	0.59	–2.76	0.63	–1.92	0.62	–2.18	0.63	–0.31	0.50
L	0.75	0.89	–0.09	1.17	0.06	1.90	–1.06	1.17	0.24	1.08	0.87	1.04
MX	1.27	0.93	–0.63	1.24	0.50	1.24	–0.20	1.17	1.20	1.62	1.00	1.11

[a]C10R = carcass 10th-rib equation; CLR = carcass last rib equation; UFOM = Ultrafom equation; FOM = Fat-O-Meater equation; AUS = Automated Ultrasonic System equation; and SCAN = equation from live animal scan measurements.

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

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

overestimated fat-free lean in barrows by 1.20 ± 0.24 kg, whereas the FOM and AUS procedures underestimated lean in gilts by 0.46 ± 0.24 and 1.03 ± 0.36 kg, respectively.

Estimates of bias due to dietary regimen are in Table 11. The C10R, CLR, FOM, and SCAN procedures all produced overestimates of fat-free lean in pigs fed Diet 4, the low-lysine regimen. Differences in bias among

Table 10. Mean (û) and standard error (se) for residual (fat-free lean minus predicted fat-free lean, kg) by procedure for each sex across projects[a]

	C10R		CLR		UFOM		FOM		AUS		SCAN	
Sex[b]	û	se	û	se	û	se	û	se	û	se	û	se
B	–0.29	0.19	–1.20	0.24	0.41	0.45	–0.24	0.24	–0.37	0.32	0.24	0.20
G	–0.18	0.20	0.18	0.24	0.57	0.54	0.46	0.24	1.03	0.36	0.36	0.21

[a]C10R = carcass 10th-rib equation; CLR = carcass last-rib equation; UFOM = Ultrafom equation; FOM = Fat-O-Meater equation; AUS = Automated Ultrasonic System equation; and SCAN = equation from live animal scan measurements.

[b]B = barrow; G = gilt.

Table 11. Mean (û) and standard error (se) for residual (fat-free lean minus predicted fat-free lean, kg) by procedure for dietary regimens in the Quality Lean Growth Modeling Project[a]

	C10R		CLR		FOM		SCAN	
Diet[b]	û	se	û	se	û	se	û	se
D1	0.03	0.25	0.60	0.30	–0.10	0.30	–0.19	0.25
D2	0.00	0.24	0.60	0.29	0.03	0.29	–0.27	0.24
D3	0.28	0.23	0.30	0.28	–0.16	0.28	0.01	0.23
D4	–0.42	0.22	–1.04	0.27	–1.36	0.27	–0.94	0.23

[a]C10R = carcass 10th-rib equation; CLR = carcass last-rib equation; FOM = Fat-O-Meater equation; and SCAN = equation from live animal scan measurements.
[b]See Table 1 for description of dietary regimens.

dietary regimens were not significant for the C10R equation, but were for each of the other procedures. Overestimates of the amount of fat-free lean in pigs fed Diet 4 by the CLR, FOM, and SCAN procedures ranged from 0.94 ± 0.23 to 1.36 ± 0.27 kg.

The results of analyses in which residuals were regressed on variables in the prediction equation are not shown because only the regression on AUSLD in the AUS equation was significant ($P < 0.05$). None of the other regression coefficients differed from zero for any procedure ($P > 0.10$). However, significant, positive regressions of residuals on measured fat-free lean were found for every procedure (Table 12). The regression coefficients ranged from 0.204 ± 0.013 kg/kg for the C10R equation to 0.605 ± 0.049 kg/kg for the UFOM equation. The proportion of the variation in residuals (R2) explained by the model that included project and the linear regression on measured fat-free lean ranged from 0.20 for the C10R equation to 0.58 for the UFOM equation.

Discussion

The procedure used herein to estimate fat-free lean in the carcass was first described by Fahey et al. (1977). Amount of fat-free lean was calculated by adjusting weight of dissected lean tissue to a fat-free basis with the ratio of percentage of lipid in lean tissue to percentage of lipid in fat tissue. An assumption held is that equal lipid percentages in dissected fat tissue and in fat depots remaining within dissected lean tissue are equal. Another procedure that has been used produces an estimate that is often called *fat-free lean* in the literature but is more correctly an estimate of lipid-free lean. In that procedure, the percentage of lipid-free lean is calculated from the weight of dissected lean and the percentage of lipid in this tissue. The two procedures produce different estimates because, in addition to adipose tissue, the dissected fat contains cytoplasmic fluids, water, and ash (Allen et al., 1976) and because the percentage of lipid in the dissected fat tissue and different fat depots within the carcass varies (Higbie et al., 2002). The fat-free lean procedure was used herein because most packer buying systems are based on procedures that predict fat-free lean.

Although estimates of fat-free lean and lipid-free lean have substantial differences (Schinckel et al., 2001), Schinckel et al. (2003) reported that the correlation between weights and percentages of these two components were 0.97 and 0.96, respectively. Schinckel et al. (2003) reported only minor differences in the ranking of R^2 and RSD statistics for prediction of fat-free and lipid-free lean with the same independent variables and estimates of bias due to ractopamine hydrochloride treatment were very similar for both variables. Therefore, in the discussion that follows, to avoid the redundancy of having to explicitly define the method used in work cited by others, prediction by both procedures will be referred to as fat-free lean.

Considerable research to develop prediction equations to estimate weight or percentage of fat-free lean (Fahey et al., 1977; Forrest et al., 1989; Orcutt et al.,

Table 12. Regression coefficients (b) ± standard error (se) of residuals (fat-free lean minus predicted fat-free lean) regressed on fat-free lean

Procedure	b ± se (kg/kg)	R^2
1. Carcass 10th-rib backfat and LM area, and hot carcass weight (C10R)	0.204 ± 0.013**	0.20
2. Live scan of 10th-rib backfat and LM area, and hot carcass weight (SCAN)	0.224 ± 0.014**	0.24
3. Fat-O-Meater backfat and LM depth and hot carcass weight (FOM)	0.283 ± 0.016**	0.31
4. Carcass last rib backfat depth and hot carcass weight (CLR)	0.380 ± 0.016**	0.39
5. Automated Ultrasonic System backfat and LM depth and hot carcass weight (AUS)	0.405 ± 0.031**	0.41
6. Ultrafom backfat and LM depth and hot carcass weight (UFOM)	0.605 ± 0.049**	0.58

**$P < 0.01$.

1990; Gu et al., 1992; Hicks et al., 1998; Higbie et al., 2002, and Schinckel et al., 2003) or lipid-free lean (Grisdale et al., 1984; Gresham et al., 1994; Cisneros et al., 1996; Berg et al., 1999) has been done. Others have focused on procedures to predict weight of closely trimmed retail cuts (Terry et al., 1989; Gresham et al.; 1992). The main differences between our experiment and previous research are in the sample size, variation in the sample of pigs used, and in statistical procedures. The experiments reported by Forrest et al. (1989) and Orcutt et al. (1990) included 412 and 361 pigs, respectively. All other experiments cited above contained 200 or fewer pigs. Our sample of pigs included a broader range of genetic groups and greater variation in weight than any other experiment. Gu et al. (1992) and Schinckel et al. (2003) estimated the effect of feeding diets with and without the feed additive ractopamine hydrochloride on the precision of fat-free lean prediction. In a similar way, we assessed the effects of lysine levels in the diet on the precision of predictions, whereas a standard diet for all pigs was used in most other experiments. In addition, we considered the quadratic effects of independent variables and possible interactions among independent variables in the statistical analyses, whereas most other reports considered only linear effects. Therefore, equations presented here have application broader than those from other studies.

Estimates of fat-free lean obtained by the C10R and SCAN procedures were more precise than by the CLR procedure; accuracy of C10R and SCAN equations were similar. Residual standard deviations for predicting weight of fat-free lean for C10R, SCAN, and CLR were 2.93, 3.06, and 4.04 kg, and RSD for percentage fat-free lean were 3.12, 3.22, and 4.32%, respectively. Although residual standard deviations tended to be larger than those reported in the literature, the ranking of these procedures is consistent with that in several other reports. As examples, residual standard deviations for prediction of fat-free lean from carcass weight and measures of 10th-rib fat and muscle depth ranged from 1.16 kg (Higbie et al., 2002) to 2.31 kg (Gu et al., 1992). Other researchers also have found that inclusion of a measure of LM along with a measure of fat depth improves the precision of predicting fat-free lean and that off-midline measures of fat depth provide greater precision than midline measurements (Gu et al., 1992; Berg et al., 1999; Hicks et al., 1998; Schinckel et al., 2003). Several researchers also have found that ultrasound scan measures of fat depth and muscle area or depth in live animals are less precise than carcass measures of these traits but that the difference is not large (Gresham et al., 1994; Cisneros et al., 1996; Hicks et al., 1998; Higbie et al., 2002; Schinckel et al., 2003).

The FOM procedure was less precise in prediction of fat-free lean than either the C10R or SCAN procedure. No direct comparison of the FOM with other procedures used here was found in the literature. However, a finding of lower precision for optical probes than direct carcass measurements is consistent with reports of other experiments that used optical probe procedures. Forrest et al. (1989) used an optical grading probe (PG 100 Pork Grader; Anitech Inc., Markham, Ontario) to measure fat and muscle depth at the 10th rib. The RSD for prediction of fat-free lean was 2.19 kg compared with an RSD of 2.07 for direct carcass measurements. Hicks et al. (1998) used an electronic probe (HgP4; Hennessy Grading Probe, Hennessy and Chong, Auckland, New Zealand) to measure fat and muscle depth between the third and fourth ribs anterior from the last rib. They obtained an RSD of 2.16 kg in prediction of fat-free lean compared with an RSD of 1.95 kg for direct carcass measurements.

The AUS and UFOM are ultrasound procedures that measure fat and muscle depth. The precision of these procedures and FOM was very similar. The RSD for these three procedures when applied across all pigs for which each procedure was used ranged from 3.46 to 3.62 kg and AIC values from analyses with the same carcasses were very similar (Table 7). Results in the literature for AUS and UFOM were not found, but comparison of other ultrasound measurements of fat and muscle depth with direct carcass measurements produced similar results (Forrest et al., 1989).

Gu et al. (1992) evaluated bias in the prediction of fat-free lean in genetic groups of pigs that included a synthetic line and four crossbred groups of the Duroc, Hampshire, Yorkshire, and Landrace breeds. Prediction equations based on midline fat depth were biased by genetic group ($P < 0.001$), but bias due to genetic group was not found for the equation based on off-midline measures of carcass fat depth and LM area ($P = 0.65$) or the equation based on optical probe of fat and muscle depth ($P = 0.41$). Variation in fat-free lean among genetic groups in that study was not large. Mean fat-free lean ranged from 38.5 to 41.4 kg. Hicks et al. (1998) investigated bias due to genetic group in predictions of fat-free lean in a sample that included seven genetic groups with greater variation among them (range in fat-free lean averaged across sexes was 35.9 to 41.1 kg) and found that all equations produced biased predictions for some groups. Our results in which significant bias due to genetic group occurred for every procedure are consistent with the findings of Hicks et al. (1998). All procedures that we evaluated tended to overestimate fat-free lean in Berkshire and Duroc and in crosses of these breeds with other breeds. Amount of fat-free lean in pigs sired by the Danbred terminal sire line and Newsham Hybrid crosses tended to be underestimated. In general agreement with these results, Hicks et al. (1998) found that fat-free lean in pigs by Duroc sires and Large White × Landrace cross mothers and F_1 Duroc × Hampshire pigs was consistently overestimated, whereas fat-free lean in a terminal cross hybrid and in pigs by Landrace sires and Large White × Duroc mothers was consistently underestimated.

Significant bias due to sex occurred for the CLR, FOM, and AUS procedure, but sex did not bias other

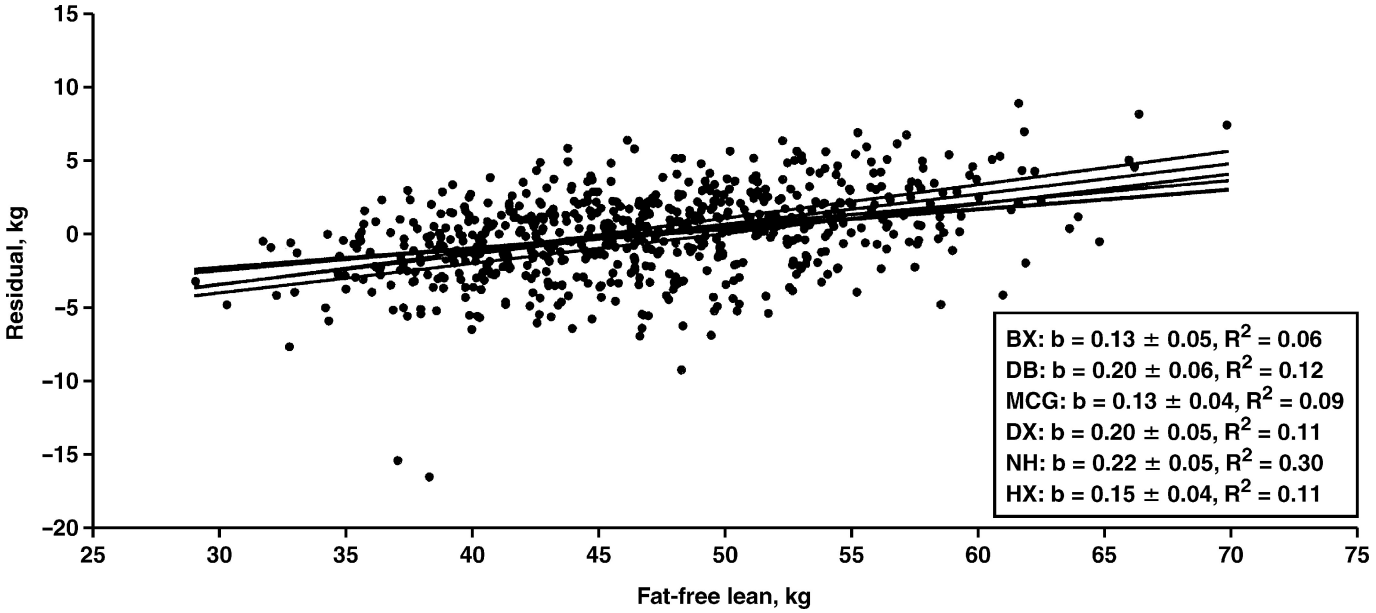

Figure 1. Regressions of residuals (fat-free lean minus predicted fat-free lean, kilograms) for the C10R equation applied to Quality Lean Growth Modeling data (BX = Berkshire cross; DB = Danbred; MCG = Monsanto Choice Genetics; DX = Duroc cross; NH = Newsham Hybrid; and HX = Hampshire cross).

procedures ($P > 0.50$). The CLR, FOM, and AUS procedures overestimated fat-free lean in barrows and underestimated it in gilts. Grisdale et al. (1984) found that sex class influenced regressions incorporating last-rib measurements in predicting fat-free lean, and Hicks et al. (1998) reported significant overestimation of fat-free lean in barrows and underestimation in gilts for every procedure evaluated, including procedures similar to the C10R and SCAN procedures used herein. Models fitted by Hicks et al. (1998) included only linear effects of independent variables, whereas quadratic and cross product terms were considered in models used herein. Addition of these terms may have accounted for sex differences in our analyses.

The bias due to dietary regimen was assessed for the C10R, CLR, FOM, and SCAN procedures, and they all overestimated fat-free lean in pigs fed Diet 4, although the effect was not significant for the C10R procedure ($P = 0.15$) but was for each other procedure ($P < 0.05$). Feeding diets with inadequate dietary lysine to meet lean growth potential reduces the rate of lean growth (Figueroa et al., 2002, 2003). Diet 4, with 0.8% lysine during early stages of growth and stepped down to 0.35% at later stages, provided insufficient lysine to meet lean growth potential of many pigs in this project. Mean fat-free lean adjusted for carcass weight and averaged across genetic groups and sexes for pigs in the QLGM project was 47.6, 47.2, 47.3, and 44.8 kg for pigs fed Diets 1 to 4, respectively. Diet seemingly affected where and how much fat was deposited and direct carcass measurements of fat depth and LM area at the 10th rib, the C10R procedure, detected these differences due to Diet 4 better than the measurements made with the CLR, FOM, and SCAN procedures. No reports of experiments in which the effect of dietary lysine on prediction of fat-free lean were found. However, fat-free lean in pigs fed the feed additive ractapomine hydrochloride was underestimated by all procedures in the experiments reported by Gu et al. (1992) and Schinckel et al. (2003).

All procedures evaluated herein produced biased predictions of fat-free lean for at least some classes, but the least bias occurred for predictions with the C10R equation. Gu et al. (1992) proposed adjusting independent variables for mean differences among subclasses to remove the effects of bias but found that this procedure only marginally improved the precision of predicting fat-free lean. Bias also was not related to hot carcass weight or to the measurements of backfat and LM made by any procedure evaluated herein, indicating that more complex models of these traits will not remove bias. Regressions of differences between predicted and measured fat-free lean revealed that bias was related to amount of fat-free lean in carcasses. All procedures tended to overestimate the amount of fat-free lean in fat pigs and underestimate it in lean pigs. This relationship is illustrated for the pigs in the QLGM project evaluated by the C10R equation in Figure 1 and for the FOM procedure in Figure 2. The difference between measured and predicted amounts increased linearly with greater deviation from the mean fat-free lean of the population, and the relationship was similar for all genetic groups. However, the relationship of residuals with measured fat-free lean was not strong. The percentage of within-genetic group variation in residuals explained by regression on measured fat-free lean ranged from 6 to 30% for C10R and from 11 to 31% for FOM. Other investigations of bias in predicting fat-free

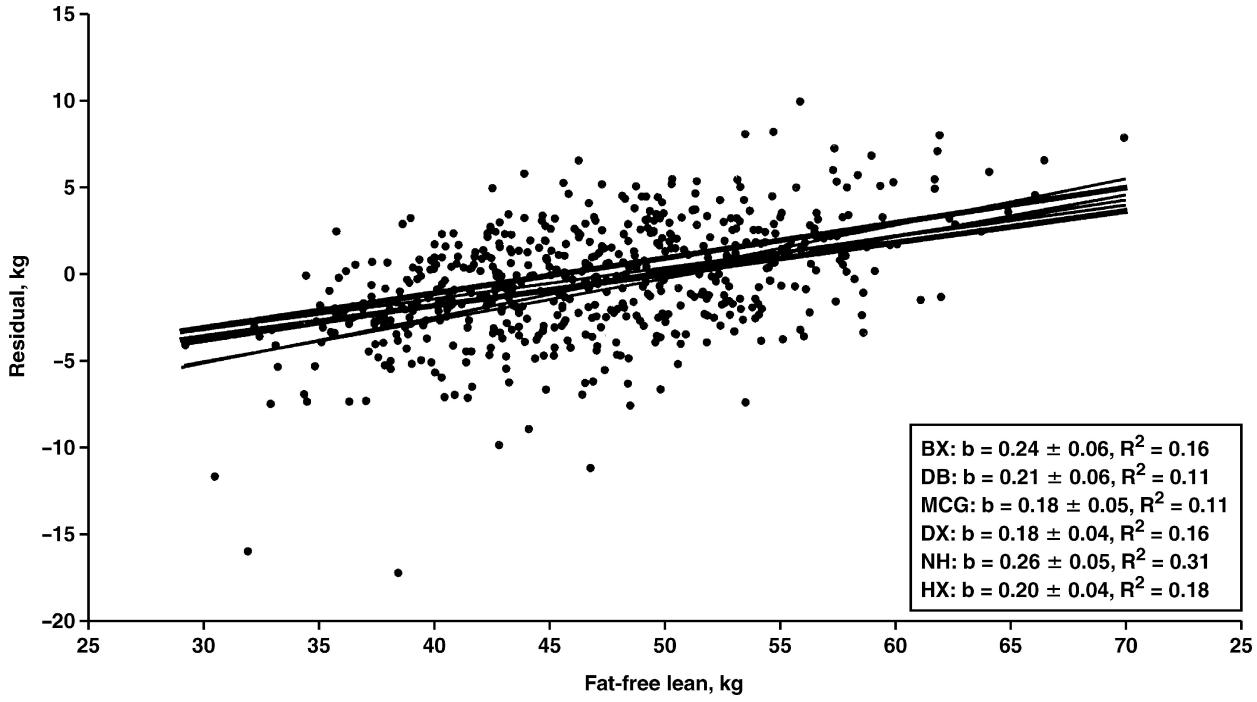

Figure 2. Regressions of residuals (fat-free lean minus predicted fat-free lean, kilograms) for the FOM equation applied to Quality Lean Growth Modeling data (BX = Berkshire cross; DB = Danbred; MCG = Monsanto Choice Genetics; DX = Duroc cross; NH = Newsham Hybrid; HX = Hampshire cross).

lean have found very similar results (Gu et al., 1992; Cisneros et al., 1996; Hicks et al., 1998; Schinckel et al., 2003).

The investigations of bias reported herein and those of the researchers cited above indicate that there are differences in fat-free lean among genetic groups, sexes, or dietary treatments that are not detected by procedures that measure fat depth and LM. Hicks et al. (1998) discuss strategies that could be used to minimize bias. These include evaluation of carcasses with electromagnetic scanners to measure total body electrical conductivity (**TOBEC**), which has been found to more accurately predict carcass fat-free lean than procedures that measure fat depth and muscle depth or area (Gu et al., 1992; Hicks et al., 1998; Higbie et al., 2002) and to have less bias than these procedures. Other strategies include combining technologies and developing breed/sex/treatment-specific prediction equations. However, these strategies may be unrealistic because genetic group and rearing background of pigs delivered to packers are often not known. Furthermore, selection within breeds, changes in use of breeds in crossbreeding systems, and on-going modifications in feeding/rearing environments cause continuous changes in type of pigs delivered to plants. There remains a need for improved technologies or additional traits that can be measured at line speeds to improve the precision of predicting fat-free lean in pork carcasses.

Other reports in which the variation between predicted and measured fat-free lean was partitioned into that between and within slaughter day were not found. Herein, variation due to slaughter day was least for the UFOM procedure, explaining 3.7% of the total variation, and greatest for the AUS procedure, explaining 19% of the variation. However, the estimate for UFOM is less reliable than the others because it was used on fewer pigs evaluated on fewer days. Slaughter-day variation also was low for the C10R procedure. Slaughter day variation is due to random variation among days in estimation of fat-free lean and in measurements of independent variables. The relative values of between- and within- slaughter day variance components when procedures were applied to the same carcasses (Table 7) were similar to those when the maximum data were used to develop equations for each procedure (Table 6). Thus, the differences among procedures in the variance components due to slaughter day are due to random variation among days in measurement of independent variables. Technicians seemingly were more consistent from day to day in applying the UFOM and C10R procedures than other procedures.

Implications

Equations for predicting fat-free lean by six procedures were derived from a sample of barrows and gilts representing the total range of genetic groups and variation in weight of pigs normally delivered to packers. Equations including carcass weight and off-midline 10th-rib fat depth and longissimus muscle area are recommended because this procedure produced the most precise, least-biased predictions. Equations using car-

cass midline fat depth at the last rib are not recommended. Use of ultrasound and optical probe instruments to measure fat and muscle depth off the midline were more reliable than a single measure of fat depth at the last rib. Prediction equations from easily obtainable measures of fat depth and muscle depth or area were biased across all genetic groups, sexes, and dietary regimens. Research is needed to develop new procedures and/or additional variables that can be measured at normal line speeds of packing plants to decrease the bias in prediction that is due to different subclasses.

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