Evaluation of Commonly Used Lean Prediction Equations for Accuracy and Biases

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Introduction

A great deal of work has been done on developing equations for estimating fat-free lean mass in pigs (Fahey et al., 1977; Forrest et al., 1989; Orcutt et al., 1990). Most equations are evaluated by statistics such as coefficient of determination (R^2) and residual standard deviation (RSD) for the data set from which they were derived. A better means of evaluating prediction equations is to use the prediction equations on other data sets. This is called an "out of sample" evaluation.

Most equations currently in use have not been evaluated for the extent to which they account for genotype and sex differences in carcass composition. Packers produce pork products from pigs of diverse genotype backgrounds and different sexes. Therefore, any realistic attempt to develop an unbiased evaluation system should account for a high percentage of genotype and sex differences. Also, prediction equations should accurately predict the lean content of carcasses in different weight ranges. The objective of this study was to examine the impact of biases associated with genotype, sex and weight range on prediction of fat-free lean mass in pigs.

Bias

Bias refers to systematic under or overestimation of carcass composition or value that may result from a particular component of an equation or method of evaluation. This may be due to the technology used, differences in composition of carcasses being evaluated, or a combination thereof. Several causes of bias have been hypothesized. They may occur when subpopulations have different:
1. Relationships between dependent and independent variables.
2. Body shapes.
3. Distribution of fat and lean (i.e., different percentage of total lean in each cut).
4. Composition of the fat and lean (i.e., percentage of fat within the lean).

Regression equations follow the format:
$$Y_{ijk} = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_3 x_3 + \ldots + \beta_n x_n + e_{ijk}$$
where Y_{ijk} = the dependent variable (e.g., carcass lean, carcass fat, etc.)
β_0 = intercept
β_1 = regression coefficient for independent variable x_1, β_2 for x_2, etc.
e_{ijk} = residual error
The value of the residual error is the difference between the actual and predicted values.

Genotype and sex biases are the differences between actual and predicted lean content for specific genotypes and sexes. Genotype and sex systematic bias refers to the overestimation or underestimation of carcass composition associated with a characteristic of the genotype-sex subpopulations (Gu et al., 1992; Hicks et al., 1999). For example, the lean mass value of fatter

genotypes may be overestimated and lean genotypes underestimated. This becomes important to producers and packers when processors use this lean mass calculation for pricing carcasses.

Determination of Carcass Fat-Free Lean

To determine the actual fat-free lean mass (FFLM) for a carcass, the total fat tissue mass including connective tissue, water, and ash mass associated with adipose tissue must be taken into account (Fahey et al., 1977, Orcutt, et al., 1990; NPPC, 1994). The lipid percentage of the dissected lean in each of the four major primals and other soft tissue was adjusted to include the mass of the other components of fat tissue (water, protein, and ash). The correction factor was obtained by dividing the percentage of lipid in the dissected lean of each of the four primal cuts and other soft tissue (CL%) by the percentage of lipid in the pooled dissected fat sample (CLT%). Calculation of FFLM of each of the five carcass components (four primal cuts and other soft tissue) was determined with the following equation: FFLM = DL - [DL x (CL%/CLT%)], where DL was dissected lean or other soft tissue mass. Total carcass FFLM was estimated as the sum of the FFLM of each of the four major primal cuts (ham, loin, Boston butt, and picnic) and other soft tissue. This calculation of the undissected fat assumes the lipid percentage of fat tissue contained within the dissected lean of each of the four primal cuts and other soft tissue was similar to the lipid percentage contained within the dissected fat (Fahey et al., 1977).

Three sets of equations were evaluated for their ability to predict fat-free lean mass. These equations had been derived from different data sets. The mean values and standard deviations of each of these data sets were somewhat different (Table 1). The equations are given in Table 2. The first set of equations are derived from the data set used in this study (Hicks et al., 1998), which is described below. Equations 1 and 5 were derived from the light weight pig data, and equations 2 and 6 were based on the heavy weight pig data.

The second set of equations, equations 3 and 7, are the 1991 NPPC equations (NPPC, 1991) derived from the data published in Orcutt et al. (1990). The NPPC 1991 equations predicted lean standardized to contain 5% fat. They were converted to predict fat-free lean by multiplying the equation by a constant of .95 (NPPC, 1994).

The third set of equations used, equations 4 and 8, were the recently published lipid-free lean equations (NPPC, 1999). It is important to realize that although not specified in detail, lipid-free lean is a substantially different means to standardize the lean content than past fat-free lean equations. An example is shown in Table 3. A lean pig has approximately 57.8% total dissected lean containing 7% lipid. This percent lipid includes a fair amount of external and seam fat that cannot be trimmed without cutting into the muscle itself. Typically, dissected lean of lean pigs contains 7% lipid and dissected fat tissue contains 70% lipid (Wagner et al., 1999). In general, the fat of lean pigs contains a lower percent lipid than the 80% found by Fahey et al. (1997) and 75% found by Orcutt et al. (1990). To predict fat-free lean (Fahey et al., 1977; Orcutt et al., 1990; Hicks et al., 1998), the 7% lipid within the dissected loin is divided by .70, and thus the dissected lean is predicted to contain 10% fat tissue. This results in calculated values of 52% fat-free lean and 30% total carcass fat (both dissected fat and the fat tissue within the dissected lean; Wagner et al., 1999).

Lipid-free lean is the total amount of soft tissue minus the analyzed amount of lipid. In this example, the pig contains 61% lipid-free lean and 21% lipid [(57.78% x .07) + (24.22% x .70)]. Thus, in most cases, lipid-free lean is greater than dissected lean, and fat-free lean is always less than dissected lean. This is important when comparing the results of the prediction equations. It is important to realize that nutritional models have been developed in which fat-free lean is used to predict empty body protein accretion and daily lysine requirements (Schinckel and DeLange 1996; Schinckel et al., 1996; NRC, 1998). University and private industry nutritionists have written numerous articles utilizing the relationship of fat-free lean gain to daily lysine requirements.

Methods

Data used were for 219 pigs from seven U.S. genotypes which had considerable variation in carcass composition. The data were divided into two groups: light weight pigs with target weights of 220, 252 and 284 lb (n=168), and heavy weight pigs with target weights of 252, 284 and 334 lb (n=164). The genotypes involved (matings are listed as sire x dam) were:

G_1 = Synthetic hybrid,

G_2 = [Hampshire (H) x Duroc (D)] x [Large White (LW) x Landrace (L)],

G_3 and G_4 = commercial terminal crosses from two different sources,

G_5 = D x (LW x L),

G_6 = L x [Yorkshire (Y) x D] maternal line, and

G_7 = HD x (L x YD) terminal cross.

Measurements taken with the optical probe included fat depth (FAT34, in.) and loin muscle depth (M34, in.) taken approximately 3 inches off-midline at the 3rd to 4th from the last rib. Standard carcass measurements included fat depth measured off-midline at the tenth rib (FD10R, in.) and loin eye area measured at the tenth rib (LEA, in^2). Fat-free lean was also determined for these pigs (actual fat-free lean mass).

The eight equations described above were then used to predict fat-free lean for the 168 light weight and 164 heavy weight pigs in this data set. Relationships among these predictions of fat-free lean were evaluated. Note that the predictions using equations 1 and 5 for the light weight pigs, and equations 2 and 6 for the heavy weight pigs, are "within sample" predictions, as these were the data used to derive those equations. All other predictions are "out of sample."

Results

The means and standard deviations of the predicted values from each equation are given in Table 4 for light weight pigs and Table 5 for heavy weight pigs. Equations derived from the three data sets have nearly identical correlations with fat-free lean mass. Although the data sets have observations with different mean carcass weights and carcass measurements, predicted values of each equation are highly correlated to the actual amount of fat-free lean. The lipid-free equations overestimate the amount of fat-free lean by 14.6 lb for the lighter weight pigs (mean weight = 248 lb) and 17.3 lb for the heavier weight pigs (mean weight = 284 lb).

The predicted values from the equations using the same measurements (carcass measurements or optical probe measurements) are highly correlated with each other (Tables 6 and 7). For all practical purposes, the equations will rank pigs the same.

The values of residual means (biases) and actual means for fat-free lean are presented in Tables 8 and 9. The mean residual values were standardized to an overall mean value of zero. Thus, the values are the residual values remaining after the overall over or underestimation of the specific equation had been accounted for. For biases, positive values indicate that the equation underestimates the actual means and negative values indicate overestimation. The genetic population mean predicted by the specific equation is the actual mean minus the predicted genetic population bias minus the overall bias. The relative fat-free lean content of G_5 pigs was overestimated by every equation. G_4 was overestimated by the majority of the equations. G_3 was underestimated by all six equations. G_2 was underestimated by the majority of the equations. The fact that some genotypes are consistently over or underestimated by the majority of equations indicate that bias is an attribute of the genetic population. The correlations between the actual and predicted means (CR) of the genotype-sex subpopulations indicate that overall the genetic groups were ranked correctly (r >.90). The variance ratios (VR) close to one for the light weight data set indicate that the variance in the predicted means was close to that of the actual means. The variance ratios were smaller (.48 to .75) for the heavier weight pigs, so the predicted values had less spread than the actual pounds of fat-free lean. Equation 7 ranked the subpopulations correctly; however, the predicted genotype-sex means had less spread than the other equations. These equations tended to underestimate the lean mass of the leaner genotype-sex groups and overestimate the lean content of the less lean genotype-sex groups.

The overall and weight group means for the mean residual values of the eight prediction equations are shown when estimating the fat-free lean content of pigs with target weights 220, 252 and 334 lb (Table 10) and the pigs with target weights of 252, 284 and 334 lb (Table 11).

Equations 4 and 8 (NPPC, 1999) overestimate the fat-free lean content of the lighter weight pigs by 14.4 lb for standard carcass measurements (Eq. 4) and 14.7 lbs for the fat-o-meter measurements (Eq. 8). There were significant weight group biases for all equations except equations 1 and 4, which were derived from this data set, and the 1991 NPPC equations (Eq. 3 and 7). Equations 2 and 6 were derived from the heavier pigs in the 1991 lean growth trial. Equations 2 and 6 overestimate the light weight (220 lb) pigs and underestimate the 284 target weight pigs. Equations 4 and 8 had highly significant target weight biases, possibly due to the difference in the method of fat standardization (lipid-free lean versus fat-free lean).

When estimating the fat-free lean content of heavier pigs (target weights of 252, 284 and 334 lb), all prediction equations had large weight biases except equations 2 and 6, which were derived from that data set ("within sample" evaluation). Equations using the data derived from the lighter weight pigs in the 1991 Purdue trial (Eq. 1 and 5) and the 1991 NPPC equations (Eq. 3 and 7) do not estimate the fat-free lean content of the heavier pigs as accurately as equations 2 and 6. Equations derived from light pigs (Eq. 1, 3, 5, and 7) also had larger genotype and sex biases.

Significant weight group biases were previously reported by Orcutt et al. (1990). Weight group biases are due to the fact that at different live weight ranges, the relationships between fat-

free lean mass and other carcass measurements, and relationships among the carcass measurements, change. As carcass weight increases, the regression coefficients change - the regression coefficients for carcass weight decrease and for backfat thickness increase. For this reason, it is desirable that prediction equations be utilized that have close to the same mean and have similar statistical parameters (variances and covariances for the variables) as the pigs which the equation is to used to evaluate. If the fat-free lean content of a specific weight range is to be accurately predicted, the prediction equation must include only pigs of the same liveweight range. For this reason, it is important that "out of sample" evaluations be conducted and the magnitude of biases be evaluated.

It is important that equations be unbiased, so they will accurately predict the amount of lean, regardless of the genetic population, sex, or weight of the pig. If there are genetic population biases, and the equation is used across populations, then the differences between the populations may not be accurate. With weight group biases, the equation will not be able to predict true differences in lean content for pigs of different weights. In addition, biases become important to producers and packers when processors use the equations for pricing carcasses. As profit margins become smaller, it is important to have accurate information for determination of price and for lean growth modeling. Accurate calculations of fat-free lean are needed for producers to determine optimal diets, management strategy, slaughter weights, and marketing strategy.

Implications

The equations will rank the pigs nearly identically. However, the magnitude of overall genotype, sex and weight range biases were substantially different. The new lipid-free lean equations result in calculated values which are approximately 14-18 lb higher for pounds of lean, and 8% higher for percent lean, than the currently used fat-free lean equations. In general, all the equations will rank the genetic populations and sexes correctly. However, all equations produced genotype-sex genetic population biases which had standard deviations of 1.6 to 3.2 lb fat-free lean. These biases limit the accuracy of the prediction equations to precisely estimate differences in lean mass between genetic populations. The majority of equations also had significant biases associated with specific ranges in live weight. Prediction equations must be carefully evaluated with respect to potential genetic population, sex, and weight group biases.

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Table 1. Summary statistics for the data used to derive the prediction equations.

Variable	1991 Purdue[a]		1991 Purdue[b]		1991 NPPC[c]		1999 NPPC[d]	
	Mean	SD	Mean	SD	Mean	SD	Mean	SD
Live weight	248	26	284	34	232	18	290	31
Hot carcass weight (HCWT)	185	22	214	28	171	14	216	25
3/4 fat depth, 10th rib (FD10R)	1.21	.33	1.37	.39	1.16	.31	1.14	.37
Loin eye area (LEA)	5.45	.90	5.94	1.01	4.85	.73	6.56	1.1
Optical probe fat depth (FAT34)	1.03	.30	1.16	.33	1.18	.31	.94	.29
Optical probe muscle depth (M34)	.91	.23	1.98	.26	1.9	.28	2.3	.36

[a] Hicks et al. (1999), 1991 Purdue Lean Growth Trial Data. Data for pigs with target live weights of 220, 252 and 284 lb.

[b] 1991 Purdue Lean Growth Trials Pigs with target live weights of 252, 284 and 334 lb.
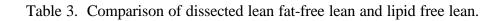
[c] Orcutt et. al. (1990).

[d] NPPC (1999).

Table 2. Prediction equations evaluated.

Equation number	
	Equations using standard carcass measurements:
1	Fat-free Lean, lb = 10.96 + (.431 x HCWT) – (18.82 x FD10R) + (2.358 x LEA)
2	Fat-free Lean, lb = 25.19 + (.3668 x HCWT) – (21.18 x FD10R) + (2.753 x LEA)
3	Lean (5% Fat), lb = 7.231 + (.437 x HCWT) – (18.75 x FD10R) + (3.877 x LEA)
4	Lipid Free Lean, lb = 11.45 + (.5102 x HCWT) – (19.93 x FD10R) + (2.593 x LEA)
	Equations using optical probe measurements:
5	Fat-free Lean, lb = 8.267 + (.46 x HCWT) – (22.96 x FAT34) + (6.16 x M34)
6	Fat-free Lean, lb = 22.72 + (.384 x HCWT) – (25.95 x FAT34) + (8.12 x M34)
7	Lean (5% Fat), lb = 2.83 + (.469 x HCWT) – (18.47 x FAT34) + (9.824 x M34)
8	Lipid-Free Lean, lb = 17.27 + (.545 x HCWT) – (27.93 x FAT34) + (3.547 x M34)

Equations 1 and 4 from Hicks et al. (1999), 1991 Purdue Lean Growth Trial Data. Equations derived from data for pigs with target live weights of 220, 252 and 284 lb.

Equations 2 and 5 from 1991 Purdue Lean Growth Trials Pigs with target live weights of 252, 284 and 334 lb. Mean weight equals 284 lb.

Equations 3 and 7 from Orcutt et. al. (1990), 1991 NPPC equations for lean containing 5% fat.

Equations 4 and 8 from NPPC (1999), lipid-free lean equations.

Table 3. Comparison of dissected lean fat-free lean and lipid free lean.

57.78% Dissected Lean containing 7% Lipid	52% Fat-Free Lean	61% Lipid 52% Fat-Free Lean plus 9% water and protein associated wth Fat tissue
24.22% Dissected FAT containing 70% Lipid	30% Total Carcass FAT tissue (both dissected and within the dissected lean)	21% Lipid
18% Bone and Skin	18% Bone and Skin	18% Bone and Skin

Table 4. Mean predicted values for fat pounds of lean and standard deviation for light weight pigs for each equation[a].

Equation Number and Origin	Fat-Free Lean, lb	
	Mean	SD
1. Purdue, 1991	80.5	11.3
2. Purdue, 1991[b]	82.2	11.0
3. NPPC, 1991	82.0	11.9
4. NPPC, 1999	95.6	13.0
5. Purdue, 1991	80.5	11.1
6. Purdue, 1991[b]	82.6	10.6
7. NPPC, 1991	84.6	10.7
8. NPPC, 1999	95.9	12.9

[a] Actual mean 80.5 lb fat-free lean with a standard deviation of 12.2 lb. The 1991 NPPC equations (3 and 6) were adjusted to predict fat-free lean. NPPC 1999 equations (4 and 8) predict lipid-free lean.
[b] Prediction Equations 2 and 6 were developed from heavy pigs (target weights of 252, 284 and 334 lb, mean weight 284 lb), 1991 Purdue Lean Growth Trial.

Table 5. Mean predicted values for fat pounds of lean and standard deviation for heavy weight pigs for each equation[a].

Equation Number and Origin	Fat-Free Lean, lb	
	Mean	SD
1. Purdue, 1991	91.5	13.0
2. Purdue, 1991[b]	91.1	12.3
3. NPPC, 1991	93.3	13.6
4. NPPC, 1999	108.9	15.0
5. Purdue, 1991	92.4	12.9
6. Purdue, 1991[b]	91.1	11.9
7. NPPC, 1991	96.2	12.7
8. NPPC, 1999	108.6	14.8

[a] Actual mean 91.5 lb fat-free lean with a standard deviation of 13.41 lb. The 1991 NPPC equations (3 and 6) were adjusted to predict fat-free lean. NPPC 1999 equations (4 and 8) predict lipid-free lean.
[b] Prediction Equations 2 and 6 were developed from heavy pigs (target weights of 252, 284 and 334 lb, mean weight 284 lb), 1991 Purdue Lean Growth Trial.

Table 6. Correlations between the predicted values of the equations and actual fat-free lean using light weight pigs (mean live weight = 248 lb).

Origin	Equation	Fat-free Lean	EQ1	EQ2	EQ3
Carcass Measurements:					
Purdue 1991	EQ1	.936			
Purdue 1991[a]	EQ2	.922	.987		
NPPC 1991	EQ3	.934	.998	.989	
NPPC 1999	EQ4	.934	.998	.975	.995

Origin	Equation	Fat-free Lean	EQ5	EQ6	EQ7
Optical Probe Measurements:					
Purdue 1991	EQ5	.920			
Purdue 1991[a]	EQ6	.903	.981		
NPPC 1991	EQ7	.912	.912	.956	
NPPC 1999	EQ8	.918	.998	.977	.986

[a] Prediction Equations 2 and 6 were developed from heavy pigs (target weights of 252, 284 and 334 lb, mean weight 284 lb), 1991 Purdue Lean Growth Trial.

Table 7. Correlations between the predicted values of the equations and actual fat-free lean using heavy weight pigs (mean live weight = 284 lb).

Origin	Equation	Fat-free Lean	EQ1	EQ2	EQ3
Carcass Measurements:					
Purdue 1991	EQ1	.904			
Purdue 1991[a]	EQ2	.917	.985		
NPPC 1991	EQ3	.906	.998	.987	
NPPC 1999	EQ4	.892	.998	.972	.995

Origin	Equation	Fat-free Lean	EQ5	EQ6	EQ7
Optical Probe Measurements:					
Purdue 1991	EQ5	.874			
Purdue 1991[a]	EQ6	.891	.981		
NPPC 1991	EQ7	.851	.992	.954	
NPPC 1999	EQ8	.872	.998	.978	.985

[a] Prediction Equations 2 and 6 were developed from heavy pigs (target weights of 252, 284 and 334 lb, mean weight 284 lb), 1991 Purdue Lean Growth Trial.

Table 8. Residual genotype mean values (biases[a]) for fat-free lean mass in pounds from different equations, for light weight pigs (mean live weight = 248 lb).

| | Genotype | | | | | | | | Sex | | | | | |
	G_1	G_2	G_3	G_4	G_5	G_6	G_7	Sig	G	B	Sig	SD[b]	CR[c]	VR[d]
Means	79.4	90.3	83.9	83.0	76.8	80.5	81.8							
EQ1	.6	1.4	1.4	.36	-2.4	1.3	-1.2	.006	-.2	.2	.55	1.6	.93	.89
EQ2	1.3	-.7	1.0	-1.2	-2.1	1.7	-1.7	.02	-.2	.2	.63	1.6	.97	1.12
EQ3	1.0	1.4	1.3	-2.0	-1.9	1.6	-1.3	.004	-.1	.1	.81	1.7	.94	.94
EQ4	.9	.9	1.5	-2.1	-2.2	1.4	-1.3	.01	-.1	.1	.92	1.7	.94	1.06
EQ5	1.0	.5	1.2	-2.1	-2.1	.4	.3	.10	.5	-.5	.10	1.6	.96	.88
EQ6	1.8	-.4	.7	-1.8	-1.7	.9	0.0	.24	.1	-1.7	.71	1.4	.98	1.10
EQ7	-.2	1.6	1.4	-2.3	-2.1	.5	1.1	.03	.9	-.9	.02	1.9	.96	.68
EQ8	2.2	-.6	1.3	-2.2	-2.1	-.6	-.1	.05	.2	-.2	.62	1.7	.96	1.14

[a] Positive values indicate underestimation, negative values indicate overestimation. Residual values were standardized so the mean equals zero.
[b] SD = standard deviation of the 14 genotype-sex residual mean values.
[c] CR = correlation between the actual and predicted genotype-sex means.
[d] VR = variance of the 14 predicted genotype-sex means divided by the variance of the actual genotype-sex means.

Table 9. Residual genotype mean values (biases[a]) for fat-free lean mass in pounds from different equations, for heavy weight pigs (mean live weight = 284 lb).

| | Genotype | | | | | | | | Sex | | | | | |
	G_1	G_2	G_3	G_4	G_5	G_6	G_7	Sig	G	B	Sig	SD[b]	CR[c]	VR[d]
Means	85.1	99.8	91.6	96.0	85.7	89.1	89.2							
EQ1	-.1	3.2	1.4	-.2	-3.0	.1	-3.1	.005	.85	-.85	.05	2.6	.93	.57
EQ2	1.1	2.6	1.2	-.4	-2.6	1.2	-3.2	.002	.34	.-34	.40	2.4	.93	.75
EQ3	.4	3.3	1.4	-.9	-2.4	1.0	-2.7	.008	.64	-.64	.25	2.5	.93	.68
EQ4	.2	2.9	1.6	-.7	-2.9	1.1	-2.5	.06	.61	-.61	.24	2.4	.93	.65
EQ5	.3	1.7	1.9	.5	-3.4	0.0	-1.4	.13	1.6	-1.6	.001	2.8	.92	.48
EQ6	1.6	.7	1.7	.1	-2.9	.3	-1.8	.11	1.1	-1.1	.02	2.5	.93	.65
EQ7	-1.2	3.0	1.9	.3	-3.2	-.1	-1.0	.10	2.2	-2.2	.002	3.2	.89	.62
EQ8	1.4	.5	2.1	.3	-3.6	.2	-1.5	.21	1.4	-1.4	.03	2.7	.92	.63

[a] Positive values indicate underestimation, negative values indicate overestimation. Residual values were standardized so the mean equals zero.
[b] SD = standard deviation of the 14 genotype-sex residual mean values.
[c] CR = correlation between the actual and predicted genotype-sex means.
[d] VR = variance of the 14 predicted genotype-sex means divided by the variance of the actual genotype-sex means.

Table 10. Overall mean and target weight group (220, 252 and 284 lb) mean residual values (bias[a]).

| Origin | Equation | Mean | Weight Group | | | Prob |
			220	252	284	
Purdue 1991	1[b]	0.0	-.66	.88	-.33	.14
Purdue 1991	2	1.0	-2.4	.75	1.70	.0001
NPPC 1991	3	-.83	-.31	.73	-.45	.31
NPPC 1999	4	-14.4	1.40	.90	-2.30	.0001
Purdue 1991	5[b]	0.0	-1.00	1.49	-.54	.06
Purdue 1991	6	-1.4	-3.23	1.27	1.98	.0001
NPPC 1991	7	-3.6	-.60	1.28	-.71	.07
NPPC 1999	8	-14.7	.63	1.33	-2.07	.0001

[a] Negative residual values designate overestimation, and positive residual values designate underestimation.
[b] Equations 1 and 5 were derived from the same data set being analyzed here ("within sample").

Table 11. Overall mean and target weight group (252, 284 and 334 lb) mean residual values (bias[a]).

| Origin | Equation | Mean | Weight Group | | | Prob |
			252	284	334	
Purdue 1991	1	-.47	1.96	.75	-2.72	.0001
Purdue 1991	2[b]	0.0	-.35	.70	-.34	.53
NPPC 1991	3	-2.24	2.13	.95	-3.28	.0001
NPPD 1999	4	-17.82	4.27	.95	-5.22	.0001
Purdue 1991	5	-1.30	2.28	.74	-3.04	.0001
Purdue 1991	6[b]	0.0	-.33	.50	-.17	.77
NPPC 1991	7	-5.24	2.71	.75	-3.46	.0001
NPPC 1999	8	-17.51	4.28	.77	-5.06	.0001

[a] Negative residual values designate overestimation, and positive residual values designate underestimation.
[b] Equations 2 and 6 were derived from the same data set being analyzed here ("within sample").