

## **Influence of Systematic Biases Associated with Genotype and Sex on Prediction of Lean Mass and Carcass Value in U.S. Pigs**

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### **Introduction**

Much work has been done on developing equations for estimating fat-free lean mass and carcass value in pigs (Akridge et al., 1992; and Boland et al., 1995). However, 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 genotypic backgrounds and different sexes. Therefore, any realistic attempt to develop an unbiased evaluation system should account for a high percentage of the genotype and sex differences. Equations for predicting lean mass and carcass value use a variety of evaluation technologies. These include rulers, optical probes, ultrasonic imaging, and electromagnetic scanning. Regression equations are used to convert measurement readings from these technologies into lean mass and carcass value (Forrest et al., 1989). The objective of this study was to examine the influence of biases associated with genotype and sex on prediction of fat free lean mass and carcass value in pigs, and measures that can be put in place to minimize biases.

### **Bias**

Bias refers to under or overestimation of carcass composition or value that may result from a particular system or method of evaluation. This may be due to the technology used, differences in composition of carcasses being evaluated, or a combination thereof. Genotype and sex biases are the differences between actual and predicted genotype and sex values, resulting from prediction equations not including genotype or sex. Genotype and sex systematic bias refers to the overestimation or underestimation of carcass composition or value associated with a characteristic of the genotype-sex subpopulations. 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.

### **Methods**

Data used were for 165 pigs from seven U.S. genotypes which had considerable variation in carcass composition. The genotypes involved (matings are listed as sire x dam) were:

G<sub>1</sub> = Synthetic hybrid,

G<sub>2</sub> = [Hampshire (H) x Duroc (D)] x [Large White (LW) x Landrace (L)],

G<sub>3</sub> and G<sub>4</sub> = commercial terminal crosses from two different sources,

G<sub>5</sub> = D x (LW x L),

G<sub>6</sub> = L x [Yorkshire (Y) x D] maternal line, and

G<sub>7</sub> = HD x (L x YD) commercial cross.

Measurements were taken with the ruler, optical probe (OP), electromagnetic scanning (EMS), and ultrasonic scanning, as well as standard carcass measurements. Values measured included carcass weight (CW), midline backfat at the last rib (BFLR), mean BFLR for the genotype-sex group adjusted for liveweight (XBFLR), loin eye area (LEAT10R) and fat depth (FD10R) measured approximately 3 in. off-midline at the 10<sup>th</sup> rib, fat depth measured approximately 3 in. off-midline at the 3<sup>rd</sup> to 4<sup>th</sup> from the last rib (FAT34), and total body electrical conductivity (PEAK) measured by the TOBEC machine. These were used to predict fat free lean mass and carcass value. Carcass value was the sum of the values of wholesale cuts and byproducts.

## Results

Table 1 presents the coefficients of determination ( $R^2$ ) and residual standard deviations (RSD) for selected equations for fat free lean mass and carcass value prediction. A high  $R^2$  and low RSD mean that the prediction is very accurate. The corresponding values of residual genotype means (biases), as well as actual mean values for fat free lean mass and carcass value as classified by genotype and sex, are presented in Table 2. For biases, positive values indicate that the prediction underestimated the observed means, and negative values indicate an overestimation. The  $R^2$  ranged from .69 to .89 for lean mass and from .82 to .93 for carcass value. Corresponding values of RSD ranged from 7.9 lb to 4.0 lb and from \$6.34 to \$4.41 per pig. Single technology, midline ruler last rib backfat (equation 1) produced the least accurate and most biased equation, an indication that use of single technology may not adequately account for genotype-sex differences. Biases were reduced after including XBFLR (equation 2). The significance of XBFLR indicates that equation 1 resulted in systematic biases. Use of standard ribbed carcass measurements (equation 3) produced almost identical results to the combined technology of OP and EMS (equation 4). These two equations reduced biases by including both a measure of fatness (backfat depth) and a measure of muscle mass (loin eye area or TOBEC PEAK value).

Lean genotypes were consistently underestimated and below average lean genotypes were overestimated for all equations evaluated (Table 2). This was understandable because the regression equation pulls extreme genotypes toward the mean. The variation in the level of biases relative to the true value indicate that equations for estimating lean mass using different carcass measurements may give different results for the same group of carcasses. Gilts were consistently underestimated while barrows were consistently overestimated. The variation in magnitude of bias reflected the variation in carcass composition. With the exception of equations 1 and 2 ( $P < .01$ ), biases were not significant.

## Discussion

Lack of uniformity among packers in regard to recognising and rewarding producers of above average lean genotypes may affect profitability of the pig farm operation. Carcass merit marketing is intended to convey price signals from the consumer back to the producer. Lack of uniformity among packers means that producers of above average lean genotypes will supply packers who can identify the leanness of their pigs and who will pay a premium. Producers of below average lean genotypes will tend to supply packers who are not identifying leanness and who will overpay for their pigs.

The lack of uniformity in carcass composition among genotypes and sexes, and lack of uniformity in technology adoption by packers, make elimination of biases in predicting lean mass and carcass value a difficult task. The use of technically different classification devices within the same market region raises the question of which factors cause biases and influence the level and precision of estimates of lean mass and carcass value. Some problems due to operator error, measurement technique and carcass traits used for estimation may be overcome in the future by new technological innovations and research.

Our data suggest that to reduce biases, new technologies must include both a measure of fatness and muscle mass. Branscheid and Sack (1988) suggested equations for specific genotypes and sexes. However, dissection of carcasses or application of different equations to different genotypes is not practical, because under the conditions of the slaughter line, identifying weight groups, genotypes, and sexes is unreliable and time consuming. Total elimination of biases is not achievable, because the level of bias depends on the distribution of the measured traits, which is partly due to complex factors like genotype-environmental-nutritional interactions. However, several measures can be put in place to minimise biases. These include increased premiums for producers of above average lean genotypes, and scheduling and contract supply to ensure uniform loads of pork products. A periodic reassessment of carcass evaluation systems will be required.

## References

- Akridge, J.T., B.W. Brorsen, L.D. Whipker, J.C. Forrest, C.H. Kuei, and A.P. Schinckel. 1992. Evaluation of alternative techniques to determine pork carcass value. *J. Anim. Sci.* 70:18-28.
- Boland, A.M., K.A. Foster, A.P. Schinckel, J. Wagner, W. Chen, E.P. Berg, and J.C. Forrest. 1995. Alternative pork carcass evaluation techniques: I. Differences in predictions of value. *J. Anim. Sci.* 73:637-644.
- Branscheid, W., and E. Sack. 1988. Comparison of objective grading devices among extremely different breeds. *Pig News and Information.* 2(9):129-135.
- Forrest, J.C., C.H. Kuei, M.W. Orcutt, A.P. Schinckel, J.R. Stouffer, and M.D. Judge. 1989. A review of potential methods of on-line pork carcass evaluation. *J. Anim. Sci.* 67:2164-2170.

Table 1. Coefficients of determination and residual standard deviations from estimated fat free lean mass and carcass value<sup>a</sup>.

Equation	Technology	Variable	N	R <sup>2</sup>	RSD
<u>Lean mass, lb</u>					
1	Ruler	CW, BFLR	151	.69	7.9
2	Ruler	CW, BFLR, XBFLR	151	.71	6.4
3	RIB	CW, LEAT10R, FD10R	151	.87	4.3
4	OP + EMS	CW, FAT34, PEAK	133	.89	4.0
<u>Carcass value, \$/pig</u>					
1	Ruler	CW, BFLR	137	.82	6.34
2	Ruler	CW, BFLR, XBFLR	134	.83	6.34
3	RIB	CW, LEAT10R, FD10R	137	.93	4.41
4	OP + EMS	CW, FAT34, PEAK	136	.92	4.64

<sup>a</sup> N = number of observations.

R<sup>2</sup> = coefficient of determination.

RSD = residual standard deviation, in pounds (lean mass) or dollars (carcass value).

Ruler = midline ruler backfat measurements.

RIB = ribbed carcass measurements.

OP = optical probe.

EMS = electromagnetic scanning.

CW = carcass weight.

BFLR = midline backfat at the last rib.

XBFLR = mean BFLR of the genotype-sex group adjusted for liveweight.

LEAT10R = loin eye area measured off-midline at the 10<sup>th</sup> rib.

FD10R = fat depth measured off-midline at the 10<sup>th</sup> rib.

FAT34 = fat depth at the 3<sup>rd</sup> to 4<sup>th</sup> from the last rib.

PEAK = total body electrical conductivity measured by EMS.

Table 2. Residual genotype mean values (biases<sup>a</sup>) for lean mass in pounds and carcass value in dollars from different equations.

	Genotype <sup>b</sup>							Sex <sup>c</sup>	
	G <sub>1</sub>	G <sub>2</sub>	G <sub>3</sub>	G <sub>4</sub>	G <sub>5</sub>	G <sub>6</sub>	G <sub>7</sub>	F	B
<u>Fat Free Lean Mass, lb</u>									
Mean <sup>d</sup>	79.40	90.28	83.90	83.02	76.76	80.53	81.79	87.45	80.98
<u>Equation</u>									
1	-1.50	1.63	.75	.00	-4.39	.24	1.74	1.83	-2.20
2	.40	1.14	.02	-.66	-4.67	.97	1.61	.90	-1.32
3	.71	1.21	1.56	-1.46	-2.31	1.04	-1.30	.07	-.22
4	.04	.84	1.50	-.38	-2.03	.44	-.72	.07	-.55
<u>Carcass Value, \$/pig</u>									
Mean <sup>d</sup>	138	152	144	150	140	141	144	149	138
<u>Equation</u>									
1	-4.52	.73	-1.51	3.91	-3.39	-.98	2.38	1.30	-2.16
2	-3.76	-1.90	-1.78	4.76	-3.05	-.23	2.48	.63	-1.62
3	-3.20	-.96	-.07	2.06	-.84	.33	.01	-.21	.00
4	-2.62	.80	-.30	3.08	-1.10	-.91	.61	.19	.52

<sup>a</sup> Positive values indicate underestimation, negative values indicate overestimation.

<sup>b</sup> Genotypes (matings are listed as sire x dam):

G<sub>1</sub> = Synthetic hybrid.

G<sub>2</sub> = [Hampshire (H) x Duroc (D)] x [Large White (LW) x Landrace (L)].

G<sub>3</sub> and G<sub>4</sub> = commercial terminal crosses from two different sources.

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G<sub>6</sub> = L x [Yorkshire (Y) x D] maternal line.

G<sub>7</sub> = HD x (L x YD) commercial cross.

<sup>c</sup> Sexes: F = gilts, B = barrows.

<sup>d</sup> Least-squares mean adjusted for liveweight.