Ractopamine Treatment Biases in the Prediction of Fat-free Lean Mass

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Introduction

Numerous research trials have been conducted which have evaluated the impact of ractopamine (RAC) to alter carcass composition. In the majority of these trials, carcass composition of the control and RAC fed pigs was predicted from equations including standard carcass measurements. Substantial biases have been found in the prediction of the fat-free lean mass of pigs fed RAC (Gu et al., 1992). The objectives of this study were 1) to evaluate the effect of RAC and dietary lysine and crude protein (CP) on the prediction of alternative carcass composition endpoints; and 2) to evaluate the ability of prediction equations that include partial carcass dissection or chemical analyses to minimize prediction biases.

Materials and Methods

The 45 barrows used were part of an experiment designed to evaluate the effects of dietary lysine and crude protein levels while feeding RAC (Paylean™, Elanco Animal Health) on growth performance and carcass traits (Herr et al., 2000). Barrows (PIC 337 sires by C22 dams) were allotted at 153 lb body weight to three dietary treatments. The treatments were: 1) 16% CP (0.82% lysine) control diet (CON); 2) 16% CP (0.82% lysine) with 20 ppm RAC (RAC16); and 3) a phase feeding sequence containing 20 ppm RAC (RAC-P) consisting of 18% CP (1.08% lysine) during weeks one and four, 20% CP (1.22% lysine) during weeks two and three, 16% CP (0.95% lysine) during week five, and 16% CP (0.82% lysine) during week six.

Slaughter procedures. Pigs were removed when the mean of their experimental block reached 240 lbs. The afternoon prior to slaughter, pigs were weighed (on farm) and live animal B-mode ultrasound (Aloka Model 500V Real-Time Ultrasound, Corometrics Medical Systems, Wallingford, CT) measurements were taken for backfat depth, 3 in. off-midline, at the 10^{th} rib (UBF) and last rib (UBFL). Ultrasonic measurements of the loin eye area were also taken at the 10^{th} rib (ULEA). Fifteen pigs per treatment were transported to the Purdue University Meat Science Laboratory. The pigs were stunned, immediately exsanguinated, and then scalded and mechanically dehaired.

The both sides were placed in a 35.5°F chilling unit for 24 h before further carcass measurements were taken. Backfat thickness, including skin, was measured with a ruler over the midline opposite the last rib. The right side of each carcass was ribbed between 10^{th}- and 11^{th}-rib positions prior to fabrication. Loin eye area and fat depth measurements (three-quarters of the length of the transverse section of the exposed longissimus muscle) were taken between the 10^{th} and 11^{th} ribs.

The right side of each carcass was fabricated into trimmed wholesale cuts. The ham, loin, Boston butt, and picnic were individually dissected into lean, fat, bone, and skin. The dissected lean and fat tissue from the other cuts (belly, spare ribs, jowl, neckbone, tail, and lean and fat trimmings) were pooled. A 1 lb fat tissue sample was obtained from the other cuts (belly, spare ribs, jowl, neckbone, tail) proportional to their weight. The lipid content of the dissectible lean from the four lean cuts (ham, loin, picnic and Boston butt), pooled dissected fat, other cut soft tissue, and other cut fat sample were determined.

The percentage of inseparable fat tissue in the dissected lean of the four lean cuts and other cut soft tissue was predicted by dividing the percentage of lipid in the dissected lean of the four lean cuts and other cut soft tissue (CL%) by the percentage of lipid in the pooled dissected fat sample (CLT%) or other cut fat sample. Calculation of fat-free lean mass (FFLM) of each of the two carcass components (dissected lean from the four lean cuts and other cut soft tissue) was determined with the following equation: FFLM = DLM [1 - (CL% / CLT%)], where DLM was dissected lean or other soft tissue mass. Total carcass FFLM was estimated as the sum of the FFLM of each of the four lean cuts and other cut soft tissue.

Statistical analysis. Least squares means were calculated with the GLM procedure of SAS (SAS Inst. Inc., Cary, NC) for each dietary treatment. Regression equations for predicting the mass of the carcass composition end point measures were developed using the GLM procedure of SAS. Independent variables, included in multiple regression equations, were grouped according to the type of measurements used (i.e., midline ruler, ribbed carcass, live ultrasonic scanning and partial dissection).

The accuracy of each prediction equation was evaluated by the multiple coefficient of determination (R^2) and by the residual standard deviation (RSD). Least squares means of the residual values for the three treatments yield estimates of subpopulation biases (Gu et al., 1992). The residual values are the actual minus predicted value of the carcass component mass for each observation. Therefore, overprediction of a carcass component mass was indicated by negative residual values and underprediction was indicated by positive residual values.

Results

Acronyms, definitions for variables, overall means, and diet treatment means are given in Table 1. The standard deviations for live weight and carcass weight (10.7 and 9.2 lbs) are smaller than in past pork carcass composition trials, as termination occurred when a mean block weight of 240 lbs was achieved.

The dietary RAC and lysine treatments significantly affected the carcass FFLM and FFL%. The RAC-P barrows had the greatest FFLM, the RAC16 pigs were intermediate and the CON pigs had the least amount of FFLM. The RAC-P barrows had lower percent lipid in the other cut soft tissue than the CON and RAC16 barrows. Also, percent lipid in the dissected lean was less for the RAC-P barrows than for the RAC16 and CON barrows. However, the SD for FFL% (3.60%) is greater than the SD for LFSTIS% (3.23%) or DL% (2.91%). The CON pigs had a lower TOFAT% (24.86% vs. 33.27%) and LFSTIS% (16.44 vs. 29.86%) than 251 lb barrows of seven U.S. genetic populations evaluated 10 years ago (Wagner et al., 1999; Schinckel et al., 2001). The RAC-P barrows had less ultrasonic last rib, ultrasonic 10^{th} rib, and carcass 10^{th} rib backfat thickness than the CON and RAC16 barrows, which had similar values for each of the variables. There were no treatment differences for midline last rib backfat thickness.

Prediction equations for FFLM are presented in Table 2 with corresponding summary statistics describing biases (residual values) associated with RAC treatment. As expected, partial regression coefficients for measures of backfat thickness were negative, whereas the coefficients for carcass weight, live weight, loin muscle area, and dissected loin and ham lean were positive. The highest RSD values were produced by a combination of carcass weight (CW) and midline last rib backfat measurements (Equation 2). The mean residual values and predicted values indicated that Equation 2 only predicted 5% of the true difference between the RAC16 and CON treatments and 32% of the true difference between the CON and RAC-P treatments. For fat-free lean mass, approximately 50% of the residual variance of Equation 2 was accounted for by the RAC treatment. Equation 3, based on ribbed carcass measurements (CW, loin eye area, and 10^{th}

rib backfat depth), had slightly smaller RSD's than equations based on live weight and live animal ultrasonic measurements (Equation 1). Equation 1 predicted 53% of the increased FFLM produced by the RAC treatments. Equation 3 predicted 49% of the increased FFLM produced by RAC.

Inclusion of dissected loin lean or dissected ham lean increased the accuracy of the prediction equations. Equation 4 predicted 62% of the true difference between the RAC (RAC16 and RAC-P) and CON treatments for fat-free lean mass. Equation 5 predicted 76.4% and Equation 6 predicted 88.5% of the true difference between the RAC and CON treatments.

The inclusion of the PLIPOC with FD10R and CW improved the accuracy of prediction for FFLM. Equation 7 predicted 63.3% of the true differences between the RAC and control treatments for fat-free lean mass.

Equation 8 for FFLM included CW, percent lipid in the other cuts, dissected ham lean, dissected ham fat, 10^{th} rib fat depth, and loin eye area. The inclusion of 10^{th} rib fat depth and loin eye area were not significant for predicted FFLM when the other four variables were included. Equation 8 accounted for 78% of the difference between the CON and RAC16 treatments and 92% of the difference between the CON and RAC-P treatments for FFLM.

Discussion

The first objective of this research was to evaluate the magnitude of prediction biases of alternative carcass composition endpoints when RAC was fed. From a practical perspective, biases occur when different subpopulations have different values of lean mass at the same values of the independent variables (Gu et al., 1992; Hicks et al., 1998). Subpopulation differences in the proportional mass of lean and fat tissues and the chemical composition of the lean and fat tissues are partially responsible for subpopulation biases (Gu et al., 1992; Schinckel et al, 2001). Prediction biases will likely cause producers marketing RAC pigs to only receive partial payment of the increased carcass cut out value produced by RAC. Also, prediction biases will add additional "measurement method" variation on the predicted carcass value of RAC-fed pigs.

Research should not be targeted to identify a constant value that should be added for "RAC-fed" pigs. The impact of RAC to alter carcass composition is dependent on the RAC level fed, the duration of use, and the dietary lysine level fed. The economic return for increased leanness of the producers' pigs will determine the optimal RAC and lysine level used.

Fat-free lean gain has been extensively used to predict lysine requirements (Schinckel and DeLange, 1996). The use of ribbed carcass or live animal ultrasound measurements in equations predicted approximately 50% of the increased FFLM produced by RAC. Prediction equations developed from pigs not fed RAC would have underpredicted the FFLM of the RAC-P pigs by 7.4 lb based on real-time ultrasound measurements and 7.2 lb based on standard ribbed carcass measurements. These equations underpredicted FFLM gain by approximately 0.19 lb/day. Essentially, the use of either real-time ultrasound or ribbed carcass measurements would predict approximately 50% of the increase in daily FFLM gain. This would result in diets being fed which would be expected to only allow approximately 50% of the RAC response to increase FFLM to be achieved.

Researchers whose objective is to accurately evaluate the impact of RAC on carcass component mass and growth should consider additional measurements based on partial dissection or chemical analyses. The incorporation of dissected ham lean had a slightly greater impact than dissected loin lean to reduce prediction biases. The only other means found to precisely predict

the response to RAC is the use of total body electrical conductance (TOBEC) in combination with carcass weight and a measure of 10^{th} rib backfat depth (Gu et al., 1992).

Implications

Prediction equations from easily obtained carcass measures will only partially predict the true effect of RAC to increase carcass leanness. The dietary lysine and crude protein levels fed affected the magnitude of the ractopamine response and biases. Researchers wanting to accurately predict compositional growth of RAC-fed pigs should consider some partial carcass dissection, chemical analyses or alternative technologies. Marketing systems utilizing carcass measurements to predict lean mass will only partially account for the increased lean mass and value of RAC fed pigs.

References

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Table 1. Overall and treatment carcass means for pigs fed ractopamine and different lysine levels

				Treatment LS means			
	Acronym	**Mean**	**SD**	**Control**	**RAC16**	**RAC-P**	**SE**
Live weight, lb	LW	25.18	10.69	248.8	250.9	253.5	2.6
Carcass weight, lb	CW	192.9	9.23	190.2[a]	191.2[a]	197.4[b]	2.2
Fat-free lean mass, lb	FFLM	94.3	8.8	86.8[a]	93.56[b]	102.5[c]	1.5
Fat-free lean percentage	FFL%	48.85	3.60	45.67[a]	48.91[b]	51.96[c]	0.65
Lipid free soft tissue percentage	LFSTIS%	56.97	3.23	54.08[a]	57.10[b]	57.73[c]	0.59
Total carcass fat percentage	TOFAT%	23.51	3.09	24.86[a]	24.48[a]	21.21[b]	0.68
Ultrasonic last rib backfat depth, in	UBFL	0.56	0.11	0.61[a]	0.58[a]	0.50[b]	0.03
Ultrasonic 10^{th} rib backfat depth, in	UBF	0.68	0.16	0.71[a]	0.74[a]	0.59[b]	0.04
Ultrasonic 10^{th} rib loin muscle area, in^2	ULEA	6.84	0.63	6.48[a]	6.94[b]	7.09[b]	0.15
Fat depth, 10^{th} rib, in	FD10R	0.66	0.17	0.74[a]	0.64[b]	0.61[b]	0.04
Loin muscle area, 10^{th} rib, in^2	LEA	7.44	0.809	7.04[a]	7.37[a]	7.92[b]	0.26
Midline last rib backfat thickness, in	BFLR	0.82	0.14	0.83	0.84	0.78	0.04
Dissected ham lean, one side, lb	DHAML	15.34	1.56	13.89[a]	15.35[b]	16.49[c]	0.28
Dissected loin lean, one side, lb	DLOINL	12.1	1.27	11.31[a]	12.04[a]	12.94[b]	2.8
Dissected lean percentage	DL%	41.13	2.91	38.43[a]	41.69[b]	43.28[c]	0.55
Dissected ham fat, one side, lb	DHAMF	4.25	0.88	4.20	4.34	3.77	0.20
Dissected loin fat, one side, lb	DLOINF	5.45	0.97	5.32[a]	5.49[ab]	5.00[b]	0.24
Percent lipid in other cut soft tissue	PLIPOC	26.93	5.27	29.40[a]	27.94[a]	23.44[b]	1.20
Percent lipid in the dissected fat	%LIPFAT	62.89	0.89	63.05[ab]	64.97[a]	60.64[b]	0.96
Percent lipid in the dissected lean	%LIPDL	5.03	4.13	5.26[a]	5.39[a]	4.44[b]	0.21

[abc]Treatment means with different superscripts are different, $P < 0.05$.

Table 2. Prediction equations, mean residual values, and predicted values for fat-free lean mass (FFLM, lb)[a]

							Mean residual value[d] / Predicted value			
Equation	**Variable[b]**	**R^2**	**RSD / RSD_R[c]**	**b_0[c]**	**b_i[c]**	**Sign**	**Control**	**RAC16**	**RAC-P**	**Sign**
1	LW	0.599	5.78	3.61	0.331	0.004	-3.48	-0.42	3.92	0.0005
	ULEA		4.76		4.56	0.005	90.30	93.98	98.59	
	UBFL				-29.6	0.001				
2	CW	0.490	6.44	-2.45	0.580	0.0001	-5.69	.66	5.03	0.001
	BFLR		4.54		-18.4	0.01	92.51	92.88	97.49	
3	CW	0.620	5.62	-24.2	0.643	0.0001	-3.64	-.07	-3.57	0.0006
	FD10R		4.63		-21.4	0.001	90.46	93.5	98.94	
	LEA				1.16	0.14				
4	CW	0.741	4.63	-20.06	0.402	0.0003	-2.84	-0.030	2.89	0.001
	FD10R		3.88		-9.35	0.09	89.66	93.61	99.63	
	DLOINL				3.56	0.0001				
5	CW	0.751	4.54	-9.24	0.316	0.006	1.26	1.34	2.6	0.015
	FD10R		4.06		-9.74	0.06	88.05	94.91	99.91	
	DHAML				3.19	0.0001				
6	CW	0.839	3.66	-8.24	0.131	0.09	-.85	-1.19	2.05	0.018
	DLOINL		3.26		2.96	0.0001	87.68	94.75	100.46	
	DHAML				2.70	0.0001				
7	CW	0.798	4.14	-3.06	0.654	0.0001	-2.73	1.06	1.65	0.002
	FD10R		3.48		-9.80	0.05	89.57	92.48	100.86	
	PLIPOC				-.831	0.0001				
8	CW	0.903	2.95	-11.93	0.485	0.0001	-1.21	.24	.97	0.08
	PLIPOC		2.65		-0.417	0.0022	88.03	93.30	101.54	
	DHAML				2.49	0.0001				
	DHAMF				-3.36	0.0006				

[a]N = 45 pigs.

[b] Variable definitions and acronyms are listed in Table 1.

[c] b_0 = intercept; b_i = partial regression coefficient of the ith independent variable; RSD = residual standard deviation; RSD_R = the residual standard deviation after accounting for remaining treatment effects.

[d]Negative residual values indicate overprediction and positive residual values indicated underprediction of the body component mass.