Two on-farm data collection methods to determine dynamics of swine compositional growth and estimates of dietary lysine requirements[1]

A. P. Schinckel‡, J. W. Smith, II*, M. D. Tokach*, S. S. Dritz†[2], M. Einstein‡, J. L. Nelssen*, and R. D. Goodband*

*Department of Animal Sciences and Industry and †Food Animal Health and Management Center, Kansas State University, Manhattan 66506-0201 and ‡Department of Animal Sciences, Purdue University, West Lafayette, IN 47907-1151

ABSTRACT: An experiment was conducted to evaluate the use of two real-time ultrasound data-collection methods to develop a dynamic assessment of live weight growth, protein and lipid accretions, and lysine requirement curves on two commercial swine operations. For the first method, pigs (40 barrows and 40 gilts) were weighed (ranging from 18 to 121 kg) and scanned ultrasonically to collect backfat depth and longissimus muscle area measurements every 3 wk in the finishing facility on two farms (serial method). For the second method, pigs (200 gilts and 200 barrows) of similar corresponding ages on the same two farms were weighed and scanned on 1 d (mass scan) at three different times (February, April, and May). Thirty-two pigs/sex were measured at approximately the same ages as with the serial scans. Pigs on farm 1 grew faster and had smaller backfat depths and larger longissimus muscle areas ($P < 0.01$) than those on farm 2, irrespective of method. These measurements were used to predict empty-body protein and lipid contents using nonlinear functions, which then were converted to accretion rates and lysine requirements at each BW. Protein accretion (g/d) and daily lysine requirements increased and then decreased for each sex on each farm and were higher on farm 1 than on farm 2. Data from the individual mass scans had larger standard errors for modeled live weight growth than data from the serial scans. Combining data from the three mass scans yielded growth curves with standard errors similar to those for the curves from the serial scans. For the protein accretion curves, the standard errors of the combined mass scans were approximately 20% lower than the standard errors of the serial scans. The standard errors for the modeled lysine:calorie ratio requirement from the serial scans were approximately 1% of the requirement at each BW. These results indicated that either the serial or mass scan data-collection method is a practical means of determining on-farm growth and daily protein and lipid accretion rates, which can be used to determine the farm-specific lysine requirements of growing-finishing pigs.

Key Words: Growth, Lysine, Modeling, Pigs, Protein Requirement

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Introduction

The lysine requirements for growing-finishing pigs have been examined extensively (NRC, 1998). Researchers have investigated the effects of genotype (Friesen et al., 1994), environment (Stahly et al., 1979; Lopez et al., 1994), and health status (Williams et al., 1997a,b) on dietary lysine requirements. Generally, these experiments have shown that the lysine requirement (g:Mcal ME or % of diet) is greater during growing (20 to 50 kg) than during finishing (50 to 110 kg) or similar when expressed as grams per day. However, the dynamics of the relationship between daily protein accretion rates and lysine requirements were not assessed. This, coupled with the wide variety of estimates for lysine requirements, makes application of these estimates in diet formulation of farm-specific diets difficult.

Researchers have developed models to predict live weight growth and protein and lipid accretion rates to understand the growth and protein deposition of pigs (Black et al., 1986; Schinckel and de Lange, 1996). Also, researchers have improved the mathematical functions

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[2]Correspondence: phone: 785-532-4202; fax: 603-676-5543; E-mail: dritz@vet.ksu.edu.

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that are used to describe live weight growth and body component accretion curves (Whittemore, 1986; Bridges et al., 1992; Schinckel and de Lange, 1996). However, the functions have been evaluated primarily in research scenarios with optimum environments, which typically do not mimic those in commercial swine production units. Usually, the growth and protein accretion rates on commercial farms are much lower than those observed in research environments (Holck et al., 1998). Friesen (1994) laid the foundation for this series of on-farm experiments and proposed that this type of analysis could be used to determine the lysine requirements based on a farm's unique circumstances.

Therefore, our objective was to evaluate two methods of data collection (serial or mass scan) for modeling the dynamics of growth, protein, and lipid accretion rates and estimates of lysine requirements on two commercial swine operations.

Materials and Methods

Data Collection

Animals and Housing. Data were collected concurrently from January to June in two commercial swine operations in southwestern Minnesota (farm 1) and northeastern Kansas (farm 2). All pigs were terminal-cross pigs (PIC, Franklin, KY) ranging in weight from 18 to 121 kg. Pigs were fed and housed in commercial finishing facilities using the standard operating procedures for each operation. Diets and environments were not manipulated by the researchers; however, pigs were fed diets specific for each sex (barrow or gilt) formulated to meet or exceed estimated lysine and energy requirements suggested by NRC (1998) for expected levels of growth performance. Housing was in double curtain-sided barns with 1,200 and 600 pigs and 48 and 24 pens per room (25 pigs/pen) on farms 1 and 2, respectively. Barns consisted of a single room in farm 1 and four rooms per barn in farm 2. Each barn housed 24 pens of each sex in farm 1 and a single sex in farm 2. Pigs were initially 78 and 82 d of age on farms 1 and 2, respectively, and remained in the finishing facility for approximately 17 wk.

On farm 1, total dietary lysine:calorie ratios (g/Mcal ME) fed during the data collection period were 3.9, 3.7, 3.3, 2.9, 2.7, and 2.3 g/Mcal ME for gilts and 3.9, 3.7, 3.1, 2.5, 2.0, and 1.8 for barrows from 12 to 20.5, 20.5 to 34, 34 to 57, 57 to 77, 77 to 95, and 95 kg to market, respectively. On farm 2, total dietary lysine:calorie ratios fed during the data collection period were 3.90, 3.69, 3.38, 2.92, 2.61, and 2.30 g/Mcal ME for the gilts and 3.54, 3.23, 2.76, 2.45, and 2.14 g/Mcal ME for the barrows from 11 to 23, 23 to 36, 36 to 54, 54 to 72.6, 72.6 to 90, and 90 kg to market, respectively. All diets were corn or milo and soybean meal-based, supplemented with 0.15% added L-lysine HCl and, depending on ingredient prices, added dietary fat (6% choice white grease on farm 1 and 5% soy oil on farm 2). The ratio of all other essential amino acids in proportion to lysine were in excess of those suggested by NRC (1998).

Ultrasound Methods. All pigs were individually weighed and scanned ultrasonically by the same National Swine Improvement Federation-certified technician using an Aloka 500v linear array ultrasound unit with a 3.5-MHz, 17-cm linear probe (Corometrics Medical Systems, Wallingford, CT) to obtain measurements of 10th rib backfat depth and longissimus muscle area. The backfat depth was measured from a cross-sectional image at the ¾ point of the longest axis of the loin, opposite the midline, and perpendicular to the skin using the anatomical markers as described by NPPC (2000). Longissimus muscle area was determined from the same image with the aid of computer software (Rib-O-Matic, Critical Vision, Atlanta, GA). One pen from every three contiguously located pens was randomly selected to select individual pigs. Then a subsample of pigs (five per pen for serial and four per pen for mass) were randomly selected from the designated pens.

Data Collection Method 1: Serial Scanning. Eighty pigs (40 barrows and 40 gilts) were ear-tagged, individually weighed, and scanned ultrasonically during the 1st wk after placement in the finishing facilities on each of the two farms. Pens of pigs were selected randomly throughout the entire barn to minimize effects of environmental variation within the barns. The same pigs were serially weighed and scanned using ultrasound at approximately 3-wk intervals until the entire group was marketed (Table 1). No pigs selected for serial scanning were marketed until after the last scan was obtained.

Data Collection Method 2: Mass Scanning. Four hundred pigs (200 barrows and 200 gilts) were individually scanned on 1 d in February, April, and May. On each day 32 pigs per sex and age were weighed and scanned at six ages coinciding with the six ages of the serially scanned pigs. The 40 pigs of each sex used for the serial scans were included in the mass scan portion based on their corresponding week of placement in the finishing barn. In all, six sets of pigs were used for each mass scan to yield the 400 pigs/farm per scan day. The production system on farm 2 prevented the use of six age groups for barrows on scans 2 and 3 and gilts on scan 3. Pigs on farm 2 were moved into the finishing facility over a 2-wk period, which sometimes did not follow the age interval we desired. Also, older pigs (> 175 d) were not readily available on farm 2 because of marketing opportunities at the time of the scan. Rooms were ineligible for selection of mass scan pigs if any pigs had been marketed from the room. Barns from which different ages were selected were not all on the same site in farm 1 but were on farm 2 and were selected from multiple rooms in farm 2. However, within farm 1 and 2 all pigs were managed similarly.

Live weight and accretion curves were generated for each mass scan (400 pigs/farm), and the data from all three scans were combined (1,200 pigs/farm, 600 pigs/sex) to generate overall mass curves. Therefore, four

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Table 1. Mean and standard deviation (SD) of age, body weight (BW), 10th rib backfat depth (BF), and longissimus muscle area (LMA) on each weigh day for the serial and mass data collection methods[a]

	Barrows						Gilts					
	BW		BF		LMA		BW		BF		LMA	
Age, d	kg	SD	cm	SD	cm^2	SD	kg	SD	cm	SD	cm^2	SD
Farm 1												
Serial												
78	25.2	3.9	0.74	0.11	10.7	2.4	26.6	4.1	0.76	0.13	12.3	2.0
99	42.1	6.1	0.97	0.21	17.3	2.8	44.0	5.3	0.91	0.16	18.8	2.5
120	60.1	7.5	1.19	0.31	23.5	3.6	59.2	6.5	1.09	0.21	24.2	3.0
141	78.7	8.1	1.35	0.44	33.1	2.7	75.8	7.7	1.17	0.28	33.2	4.2
162	97.1	8.5	1.80	0.46	36.2	3.8	93.0	9.0	1.45	0.37	40.3	4.0
182	108.9	9.7	1.88	0.55	43.0	6.5	110.5	11.0	1.65	0.45	46.2	5.2
195	119.6	10.6	2.49	0.81	46.8	5.9	119.3	13.8	2.01	0.57	49.9	5.3
Mass 1												
64	21.2	3.6	0.72	0.11	9.0	1.4	18.8	3.7	0.69	0.15	8.0	1.5
99	42.2	6.1	0.97	0.21	17.3	2.8	44.0	5.3	0.93	0.16	18.9	2.5
113	56.1	7.5	1.22	0.28	21.1	3.7	50.3	6.0	1.01	0.18	19.2	3.4
127	73.4	12.0	1.52	0.46	27.3	4.7	75.2	7.6	1.30	0.28	29.6	4.2
162	100.4	8.3	2.16	0.46	37.2	5.3	98.9	11.8	1.65	0.44	40.1	5.4
190	121.4	10.7	2.74	0.55	40.6	5.5	116.7	9.8	2.08	0.55	43.3	5.8
Mass 2												
64	21.1	3.4	0.77	0.14	9.0	1.9	20.8	3.7	0.73	0.12	9.1	1.5
78	32.4	9.9	0.88	0.14	12.8	2.9	31.7	5.8	0.89	0.17	14.6	2.6
99	43.0	6.6	0.93	0.16	18.1	3.6	48.6	5.7	0.96	0.15	22.4	3.5
141	78.7	8.1	1.35	0.44	33.1	2.7	75.8	7.7	1.16	0.28	33.2	4.2
155	79.2	7.9	1.55	0.43	32.0	5.0	83.7	8.5	1.44	0.30	35.5	5.0
169	102.6	12.8	1.80	0.48	38.3	6.6	97.7	10.4	1.44	0.35	39.8	6.1
Mass 3												
62	19.2	2.3	0.72	0.11	9.1	1.6	21.9	3.6	0.77	0.13	10.5	2.3
76	31.0	6.9	0.90	0.19	14.0	2.5	34.3	5.0	0.93	0.12	16.0	2.7
97	46.1	6.6	0.98	0.18	20.4	3.9	45.4	4.6	0.95	0.17	20.3	3.4
118	57.0	7.0	1.15	0.24	24.0	4.6	57.0	5.2	1.09	0.21	25.4	2.9
169	80.5	12.5	1.78	0.54	34.6	5.7	76.8	8.5	1.37	0.28	35.1	6.0
182	108.9	9.7	1.89	0.56	43.1	6.5	110.5	11.0	1.65	0.45	46.2	5.2
Farm 2												
Serial												
82	33.3	4.7	0.89	0.14	13.6	2.5	29.3	2.4	0.81	0.12	13.6	2.0
104	46.4	5.7	1.04	0.27	18.8	4.2	42.4	4.1	0.94	0.23	19.0	2.5
125	63.1	7.0	1.45	0.38	23.4	3.1	58.2	6.2	1.24	0.35	24.3	3.3
146	80.3	7.4	2.01	0.44	29.4	3.6	73.0	7.6	1.50	0.46	29.0	3.8
167	96.3	8.4	2.41	0.61	34.1	4.2	89.0	9.2	1.65	0.57	37.7	4.7
192	115.3	10.7	3.02	0.71	38.1	4.5	106.7	10.5	2.26	0.72	40.7	5.6
203	121.4	12.4	3.40	0.77	40.2	6.1	114.4	10.7	2.57	0.77	44.4	6.4
Mass 1												
84	38.4	4.6	1.06	0.28	15.8	1.8	32.0	5.0	0.88	0.19	14.4	3.1
104	45.1	9.5	1.08	0.26	18.4	4.1	42.4	4.1	0.93	0.23	18.7	2.5
127	64.5	8.2	1.58	0.60	23.9	3.7	59.9	8.4	1.30	0.31	25.2	3.9
138	79.0	7.9	1.92	0.55	29.5	5.1	70.0	7.4	1.40	0.33	28.0	3.6
153	86.1	9.6	2.06	0.57	31.7	5.3	83.1	9.7	1.66	0.50	32.4	4.5
165	96.6	8.0	2.54	0.56	33.2	4.3	103.0	9.9	2.22	0.50	36.5	6.0
Mass 2												
79	30.1	6.7	0.99	0.22	12.5	2.9	33.0	5.3	0.97	0.17	13.9	2.7
106	53.2	12.7	1.28	0.38	21.2	4.6	45.9	6.5	1.18	0.32	18.7	3.8
126	70.0	7.0	1.70	0.55	26.6	4.4	58.5	8.3	1.31	0.33	23.6	4.6
146	80.3	7.4	2.00	0.44	29.4	3.6	73.0	7.6	1.50	0.45	28.9	3.8
169	92.7	11.4	2.26	0.75	31.6	4.5	86.9	8.3	1.76	0.50	32.7	3.5
182	—	—	—	—	—	—	95.4	7.9	1.71	0.59	39.2	6.5
Mass 3												
70	18.9	3.1	.86	0.16	8.2	1.8	23.0	3.4	0.95	0.11	10.7	1.9
103	46.4	7.2	1.29	0.34	19.9	3.2	40.4	5.1	1.22	0.21	16.8	2.6
136	67.4	8.4	1.76	0.38	27.1	4.9	70.6	7.1	1.78	0.53	28.7	4.9
163	96.5	13.2	2.36	0.68	40.2	6.1	97.1	10.3	2.08	0.57	39.6	5.3
203	121.4	12.4	3.40	0.77	40.2	6.1	114.3	10.7	2.57	0.77	44.4	6.4

[a]Serial indicates data were derived from 40 pigs for each farm and sex combination selected on the first weigh date and then data were collected on these same pigs until they were marketed. Mass indicates data were derived from 32 pigs for each farm, sex, and age combination weighed and scanned on 1 d in three different months (mass 1, mass 2, and mass 3).

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mass scan curves for each sex and farm were developed. Thus, the two different data collection methods consisted of serially collecting data on the same pigs (serial) over time or collecting cross-sectional data for similar corresponding ages on different pigs on 1 d (mass).

Statistical Analysis

End Point Analysis. The final live weight and scan data from the serially scanned pigs and each of the three mass scans were used to establish days to 115 kg live weight and adjust fat depth and longisimuss muscle areas to 115 kg live weight using National Swine Improvement Federation recommended standards (Bates et al., 1994), because the final scan occurred on different days for each farm. The PROC GLM procedure of SAS (SAS Inst. Inc., Cary, NC) within each set of scan data then was used on the individual adjusted values to evaluate the effects of sex, farm, and the sex × farm interaction with the residual degrees of freedom used as the error term.

Curve Fitting. Live weight data were fitted to age using ($WT = M(1 - e^{\{-mT^a\}})$) from Bridges et al. (1986) and generalized nonlinear ($WT = M(1 - e^{b_0 + b_1T + b_2T^2})$) functions, where M = an estimate of mature BW, WT = BW – birth weight (1.4 kg), and T is days of age. The PROC NLIN procedure of SAS was used to fit these functions.

Initial analyses indicated that the variation in live weight increased with age. Thus, to reduce the heterogeneity of variance, the variance in live weight at each weigh day was standardized by the equation $STDWT = \overline{WT_j} + ((WT_{ij} - \overline{WT_j})/SD_j)$, where STDWT is the standardized weight, $\overline{WT}_j$ is the mean live weight at the j^{th} weigh day, WT_{ij} is the live weight of the i^{th} pig at the j^{th} weigh day, and SD_j is the standard deviation of live weight for the j^{th} weigh day. This standardization of the variance in BW results in a weighted least squares nonlinear regression analysis, which is needed to account for the increased variation in BW as age increases (Neter et al., 1996).

Prediction equations including live weight and 10th rib backfat depth and longissimus muscle area determined by ultrasound were used to predict empty body protein (**EBP**, kg) and empty body lipid (**EBL**, kg) content. Different equations were used to predict body composition at different weight ranges: 20 to 32, 32 to 40, 40 to 55, 55 to 80, 80 to 100, and 100 to 140 kg. These prediction equations were developed from two studies using five genotypes of pigs that were scanned serially and slaughtered (Thompson et al., 1996; Wagner et al., 1999). Modeled empty body protein content data were fitted to allometric ($EBP = aX^b$), augmented allometric ($EBP = aX^b(700 - X)^c$), and generalized nonlinear ($EBP = M(1 - e^{b_0 + b_1x + b_2x^2})$) functions (x) of live weight (Wagner et al., 1999), where EBP = an estimate of mature body protein content. The generalized nonlinear function was solved by linearizing the function $LN(1 - (EBP/M)) = b_0 + b_1x + b_2x^2$ and identifying the value of M (20, 25, 30, or 35 kg) that resulted in the highest R^2 values. These parameter values were used as initial values for an interactive solution by PROC NLIN in SAS. Modeled empty body lipid content data were fitted to allometric ($EBL = aX^b$), augmented allometric ($EBL = aX^b(700 - X)^c$), and exponential ($EBL = e^{b_0 + b_1x + b_2x^2 + b_3x^2}$) functions (x) of live weight (Wagner et al., 1999). The significance of the c coefficient of the augmented allometric function and b_3 coefficient of the exponential function were evaluated and deleted if $P > 0.10$. The R^2 values were calculated as the squared correlation coefficient between the modeled $\left(\hat{Y}_i\right)$ and observed values (Y_i) for each component. The residual standard deviation (RSD) for all functions was calculated, and the equations with the lowest RSD were used to calculate their respective curves. The RSD was calculated by the equation $RSD = \left(\sum_{i=1}^{n}(e_i)^2/(n - p)\right)^{1/2}$, where e_i is the residual value for the i^{th} observation, n = number of observations, and p = the degrees of freedom of the model. For almost all cases, generalized nonlinear (live weight and EBP) and exponential (EBL) functions minimized the RSD values; as a result, these equations were used for all curves. Daily gain and protein and lipid accretion relative to live weight gain were determined by the derivative of each function. Average daily gain (ADG) was determined as the derivation of the live weight function on time. Daily protein accretion (**PA**) and lipid accretion (**LA**) rates were determined by $\partial C/\partial T = ((\partial C/\partial LW) \times (\partial LW/\partial T))$ (Whittemore et al., 1988; Schinckel and de Lange, 1996), where C is the body component content, LW is live weight, and T is time period.

Feed Intake and Lysine Requirement Calculations. Daily ME requirements (**MER**, Mcal) were estimated based on the energy required for growth and maintenance using the following equation: $MER = 0.25517BW^{0.60} + (8.84 \times PA) + (11.4 \times LA)$, where BW = body weight (kg), PA = empty-body protein accretion (kg/d), and LA = empty-body lipid accretion (kg/d) (Noblet et al., 1999). Maintenance digestible lysine requirement (**MLR**, g/d) was calculated as $MLR = 0.036 \times BW^{0.75}$ (Fuller et al., 1989). Digestible lysine required for lean-gain (**LLG**, g/d) was determined by LLG = (66 × PA)/0.60, where PA = protein accretion (kg/d), 66 = the lysine content of empty body protein (g/kg), and 0.60 = the efficiency of lysine utilization. The majority of experiments have found the lysine content of empty body protein averages 6.6% (Campbell et al., 1988; Batterham et al., 1990; Kyriazakis and Emmans, 1993). The postabsorptive efficiency of lysine utilization generally is accepted to be 55 to 65% (Whittemore, 1983; NRC, 1998; Mohn et al., 2000). Daily total lysine requirements (**TLR**, g/d) were determined by $TLR = (MLR + LLG)/0.88$, where 0.88 = the digestibility of lysine. The lysine digestibility of typical corn-soybean meal diets ranges from 85.5 to 87.5% (depending on the total

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lysine level) using NRC (1998) values for true digestible lysine. When 0.15% L-lysine HCl is used in the diet, the digestibility increases to an average of 87.5 to 88.5%. The daily lysine requirements relative to daily energy requirements or lysine:calorie ratio (**LCR**) were calculated as grams of total dietary lysine:megacalories of ME using the equation LCR = (TLR/MER).

Bootstrapping Procedures. To evaluate the precision of the procedures to predict nutrient requirements it was critical to have a measure of the sampling variances for the protein accretion and lipid accretion curves and subsequent modeled nutrient requirements. The equations to predict the daily protein accretion and lipid accretion rates were determined as the products of the first derivatives of two nonlinear functions. Thus, standard errors could not be calculated using conventional statistical procedures. Subsequently, the standard errors of the modeled nutrient requirements (MER, TLR, and LCR) that are functions of the protein accretion and lipid accretion curves also could not be modeled using conventional procedures. A resampling procedure known as bootstrapping was used to estimate the variation about a statistic to determine the precision of the estimates (Efron, 1982). Bootstrapping procedures can be used to develop the standard errors of the parameters and modeled values of the live weight growth and body component accretion curves (Thompson et al., 1996).

Based on the initial estimates for the parameters and random resampling of the residuals, 100 bootstrap data sets were generated by taking the modeled values from each initial curve and repetitively adding the randomly resampled residual values. The nonlinear functions were fitted to each bootstrap data set. Thus, for each individual genotype by farm data set, 100 bootstrap curves for live weight and lipid and protein accretion were generated. These 100 modeled curves were used to generate 100 modeled nutrient requirement curves. The standard errors of the modeled values of each variable were approximated as the standard deviation of the bootstrap estimates (Efron, 1982; Sokal and Rohlf, 1995). The mean standard errors at each kg of live weight were calculated for the serial scans (n = 4), individual mass scans (n = 4), and combined mass scans (n = 12).

Results

End Point Analysis

Barrows reared on farm 2 required nine additional days to reach 115 kg live weight (198.4 vs 189.4 d, $P < 0.01$) and had greater adjusted backfat depth (3.24 vs 2.38 cm, $P < 0.01$) and smaller adjusted longissimus muscle area (38.9 vs 45.7 cm^2, $P < 0.01$) than barrows reared on farm 1 for the serially measured pigs. Similar results ($P < 0.01$) were obtained for the means of the three mass scans (193.1 vs 187.5 d, 3.20 vs 2.22 cm backfat, and 37.2 vs 41.6 cm^2 longissimus muscle area; $P < 0.01$) in comparisons between barrows from farm 2 and those from farm 1.

Gilts reared on farm 2 required 14.4 additional days to reach 115 kg (203.9 vs 189.5 d, $P < 0.01$) and had greater adjusted backfat depth (2.58 vs 1.94 cm, $P < 0.01$) and smaller adjusted longissimus muscle area (44.6 vs 48.8 cm^2, $P < 0.01$) compared to gilts from farm 1 for serially measured pigs. Similar results were obtained for the means of the three mass scans (199.7 vs 188.4 d, 2.38 vs 1.83 cm backfat , and 42.5 vs 44.7 cm^2 longissimus muscle area; $P < 0.01$) in comparisons between gilts from farm 2 to those from farm 1. Mean ages, BW, backfat, and longissimus muscle area of pigs on each scan date are presented in Table 1.

Live Weight Curve Fitting

The nonlinear functions relating LW to age had similar RSD for the three individual mass, combined mass, and serial scans (Table 2). Modeled growth rate was greater for barrows than for gilts on each farm, and pigs on farm 1 grew faster than pigs on farm 2 (Figure 1). Modeled ADG curves for gilts on both farms had similar shapes. From 150 to 200 d of age, modeled ADG for barrows on both farms was similar and decreased over time; ADG for gilts followed a similar pattern but decreased at a slower rate. The live weight and protein accretion curves for each of the individual mass scans were variable and not consistant with those for the serial scans (data not shown). Modeled live weight curves from scan 1 did not show the same curvilinear response that increased and then decreased for pigs on farm 2. Data from scan 2 did not yield a curvilinear response that increased and then decreased for barrows or gilts on either farm. The modeled live weight and protein accretion curves generated from scan 3 exhibited a quadratic response similar to that observed in the serial scans, but at a much lower magnitude. When the data from all three mass scans were combined, the RSD of the live weight functions decreased dramatically and the resulting live weight curves were very similar to those of the serial scans.

Modeled Protein and Lipid Composition and Lysine Requirements

The RSD for modeled empty body protein and empty body lipid contents from the mass scans were similar to and, in some cases, lower than, those from the serial scans (Table 2). Modeled protein accretion increased and then decreased for all pigs (Figure 2). Pigs on farm 1 had approximately 20 g/d greater modeled protein accretion than pigs on farm 2, but values were similar between sexes on each farm. Modeled lipid accretion increased as weight increased for barrows and gilts on both farms (Figure 3). The modeled lipid accretion were similar for the gilts on both farms and the barrows on farm 1, but the barrows on farm 2 had substantially greater lipid accretion from 50 to 105 kg.

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Table 2. Regression variables for modeled growth and carcass parameters of barrows and gilts from farms 1 and 2

Item and scan[a]	Variable M[b]	β_0	β_1	β_2	β_3	RSD	R^2
Live wt, kg vs age[c]							
Farm 1							
Barrows							
Serial	157.11	0.02116	0.00081	–0.000041	—	7.97	0.992
Overall mass	198.00	–0.00784	–0.00002	–0.000024	—	9.10	0.985
Mass 1	210.94	–0.00257	–0.00007	–0.000023	—	8.50	0.985
Mass 2	340.63	0.00413	–0.00040	–0.000095	—	10.87	0.972
Mass 3	177.76	–0.00149	–0.00029	–0.000027	—	18.49	0.977
Gilts							
Serial	216.32	0.06404	–0.00117	–0.000017	—	8.59	0.992
Overall mass	205.86	–0.00189	–0.00037	–0.000021	—	9.04	0.993
Mass 1	183.32	–0.00407	0.00012	–0.000029	—	8.43	0.989
Mass 2	225.77	0.00157	–0.00066	–0.000015	—	7.40	0.982
Mass 3	239.51	0.00108	–0.00061	–0.000015	—	10.02	0.979
Farm 2							
Barrows							
Serial	155.71	–0.23104	0.00421	–0.000051	—	8.38	0.992
Overall mass	161.02	–0.01781	0.00038	–0.000034	—	8.04	0.994
Mass 1	326.55	0.00033	–0.00050	–0.000897	—	7.64	0.986
Mass 2	127.92	–0.00386	–0.00026	–0.000043	—	8.58	0.982
Mass 3	191.93	–0.00475	0.00006	–0.000021	—	7.10	0.992
Gilts							
Serial	176.58	–0.03614	0.00051	–0.000026	—	7.77	0.991
Overall mass	181.18	–0.00755	–0.00031	–0.000022	—	8.40	0.993
Mass 1	436.31	0.00390	–0.00025	–0.000077	—	7.83	0.985
Mass 2	174.35	0.00167	–0.00110	–0.000018	—	7.50	0.981
Mass 3	192.31	–0.00194	–0.00043	–0.000019	—	8.42	0.984
Empty-body protein, kg vs BW[c]							
Farm 1							
Barrows							
Serial	22.38	–0.03951	–0.00365	–0.00005	—	0.46	0.990
Overall mass	21.10	–0.05710	–0.00354	–0.00006	—	0.38	0.987
Mass 1	24.72	–0.03309	–0.00398	–0.00003	—	0.39	0.985
Mass 2	20.47	–0.06699	–0.00283	–0.00007	—	0.33	0.991
Mass 3	22.04	–0.06864	–0.00258	–0.00006	—	0.35	0.988
Gilts							
Serial	35.68	0.01330	–0.00415	–0.00001	—	0.39	0.993
Overall mass	21.10	–0.05710	–0.00354	–0.00006	—	0.33	0.992
Mass 1	22.67	–0.04951	–0.00373	–0.00005	—	0.33	0.988
Mass 2	24.39	–0.04109	–0.00340	–0.00005	—	0.29	0.993
Mass 3	–22.98	–0.05791	–0.00291	–0.00006	—	0.30	0.992
Farm 2							
Barrows							
Serial	44.65	0.01696	–0.00361	0.00000	—	0.51	0.982
Overall mass	21.11	–0.05702	–0.00354	–0.00007	—	0.49	0.973
Mass 1	20.89	–0.00181	–0.00597	–0.00003	—	0.46	0.991
Mass 2	15.58	–0.17518	–0.00261	–0.00012	—	0.44	0.983
Mass 3	19.25	–0.07763	–0.00315	–0.00007	—	0.58	0.973
Gilts							
Serial	58.71	0.02696	–0.00336	0.00001	—	0.57	0.980
Overall mass	42.23	–0.00794	–0.00354	–0.00000	—	0.47	0.978
Mass 1	38.48	0.00126	–0.00364	–0.00000	—	0.39	0.983
Mass 2	26.97	–0.09870	–0.00409	–0.00003	—	0.45	0.974
Mass 3	18.69	–0.10673	–0.00153	–0.00010	—	0.58	0.969

(continued)

Because the modeled total lysine requirement is based on constants multiplied by protein accretion, the curves are similar in shape to those for protein accretion. The modeled lysine:calorie ratio requirement decreased as live weight increased (Figure 4). The change was more rapid from 30 to 70 kg live weight than from 70 to 110 kg live weight. Gilts had higher modeled lysine:calorie ratio values than bar-

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Table 2. (continued) Regression variables for modeled growth and carcass parameters of barrows and gilts from farms 1 and 2

Item and scan[a]	Variable M[b]	β_0	β_1	β_2	β_3	RSD	R^2
				Empty-body lipid, kg vs BW[d]			
Farm 1							
Barrows							
Serial	—	–0.06181	0.05352	–0.00030	8.2×10.9^{-7}	1.97	0.986
Overall mass	—	0.29190	0.03873	–0.00010	—	1.58	0.984
Mass 1	—	0.26915	0.03955	–0.00011	—	1.80	0.986
Mass 2	—	0.28828	0.03866	–0.00011	—	1.26	0.986
Mass 3	—	0.29068	0.03932	–0.00011	—	1.51	0.982
Gilts							
Serial	—	–0.05164	0.05248	–0.00030	8.4×10^{-7}	1.41	0.987
Overall mass	—	0.29190	0.03873	–0.00010	—	1.22	0.986
Mass 1	—	0.42935	0.03428	–0.00008	—	1.66	0.989
Mass 2	—	0.29367	0.03825	–0.00011	—	1.01	0.983
Mass 3	—	0.34118	0.03709	–0.00010	—	1.12	0.986
Farm 2							
Barrows							
Serial	—	–0.36281	0.06402	–0.00038	9.8×10^{-7}	2.22	0.986
Overall mass	—	0.35605	0.03862	–0.00010	—	1.92	0.977
Mass 1	—	0.53605	0.03204	–0.00005	—	1.88	0.957
Mass 2	—	0.31679	0.03882	–0.00009	—	1.75	0.964
Mass 3	—	0.48556	0.03644	–0.00009	—	2.26	0.988
Gilts							
Serial	—	–0.42199	0.06841	–0.00049	1.6×10^{-6}	2.04	0.985
Overall mass	—	0.32369	0.03796	–0.00010	—	1.70	0.974
Mass 1	—	0.11628	0.04325	–0.00013	—	1.40	0.975
Mass 2	—	0.20379	0.04231	–0.00013	—	1.68	0.963
Mass 3	—	0.40682	0.03726	–0.00010	—	2.02	0.985

[a]Serial indicates data were derived from 40 pigs for each farm and sex combination selected on the first weigh date and then data were collected on these same pigs until they were marketed. Mass indicates data were derived from 32 pigs for each farm, sex, and age combination weighed and scanned on 1 d in three different months (mass 1, mass 2, and mass 3). The overall mass consisted of the data from all three mass collection days.

[b]M = estimate of mature BW or mature empty body protein content, kg.

[c]Live weight and empty-body protein mass were fit as a function to age or live weight (x), respectively: ($Y = M(1 - e^{\beta_0 + \beta_1 x + \beta_2 x^2})$).

[d]Empty-body lipid content was fit as a function to live weight (x): ($EBL_{serial} = e^{b_0 + b_1 x + b_2 x^2 + b_3 x^3}$) and ($EBL_{mass} = e^{b_0 + b_1 x + b_2 x^2}$).

rows, and farm 1 had higher modeled lysine:calorie ratio values than farm 2.

Bootstrap Standard Errors

The standard errors for the modeled daily BW gains were substantially greater with the individual mass scans than with the combined mass and serial scan data (Figure 5). The standard errors of the modeled ADG curves were similar for the combined mass and serial scans. This is likely because standard errors of the combined mass data were reduced by having approximately three times as many observations per analysis than the serial scan data. The standard errors for daily BW growth rates were larger at the lighter and heavier weights, especially within 10 kg of the initial and final weights. The standard errors were approximately two times greater at 25 to 30 kg and three times greater at 110 kg than the standard errors at 50 to 90 kg live weight.

The standard errors for protein accretion were slightly less with the combined mass scans than with the serial scans; both were less than the errors with individual mass scans (Figure 6). The standard errors of the protein accretion curves were related to the standard errors for ADG at each BW and the RSD and number of observations for the functions relating empty body protein to BW. The standard errors for ADG and RSD for the nonlinear function fitting empty body protein to BW were similar for the combined mass and serial scans. However, the combined mass scans included approximately three times as many observations in the analysis fitting empty body protein to BW than the serial scans.

The standard errors for lipid accretion were smaller than the standard errors for protein accretion (Figure 7). The R^2 values of the functions relating empty body protein and empty body lipid were similar. The RSD for the functions relating empty body lipid to BW were

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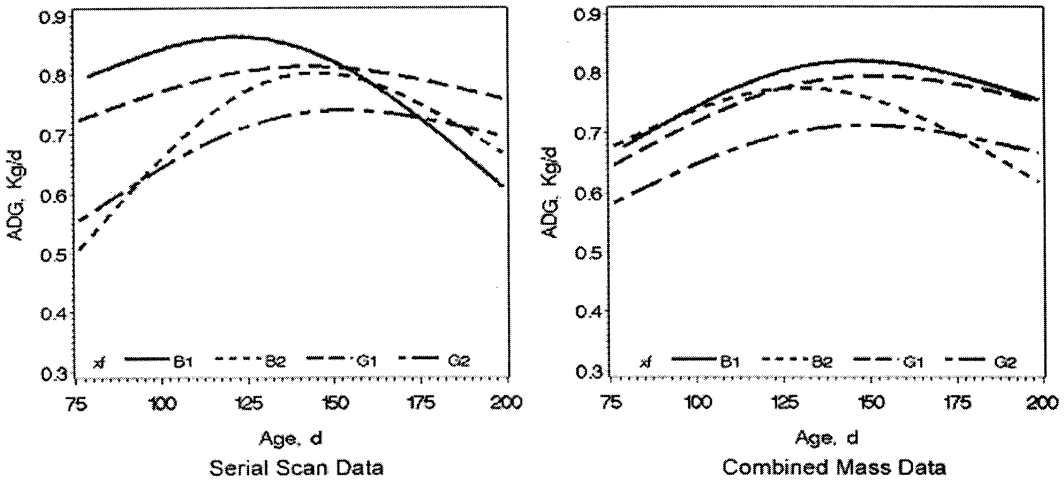

Figure 1. Modeled growth rates (XF = sex-farm group; B = barrows; G = gilts). Live weight on age was modeled using the derivative of the function ($LW = M(1 - e^{\beta_0 + \beta_1 x + \beta_2 x^2})$), where LW = live weight, M = an estimation of mature body weight, and x = day of age.

three to four times greater than the functions relating empty body protein to BW. The least squares solution of the exponential function relating empty body lipid to BW via natural log transformation may be more stable and results in more stable modeled marginal growth rates than the interactive solution of the nonlinear function relating empty body protein to BW. The standard errors for the modeled total lysine requirement followed patterns similar to those of the standard errors for modeled protein accretion (data not shown), because total lysine requirement is based primarily on the modeled protein accretion rates. The standard errors for total lysine requirement were 0.126 times the standard error for modeled protein accretion, as expected based on the equation relating total lysine requirement to protein accretion.

The standard errors for lysine:calorie ratio were 40 to 50% greater for the individual mass scans than for the combined mass scans (Figure 8). The standard errors for the combined mass scans were approximately 20% lower than the standard errors of the serial scans. Standard errors of the lysine:calorie ratio for the serial scans were approximately 1% of the modeled lysine:calorie ratio requirement at each BW.

Discussion

Smith et al. (1992) showed that ultrasound scanning was a practical means of determining carcass merit of pigs. Schinckel and de Lange (1996) indicated that serial ultrasound can be used in "ideal" conditions to determine growth and composition curves for different

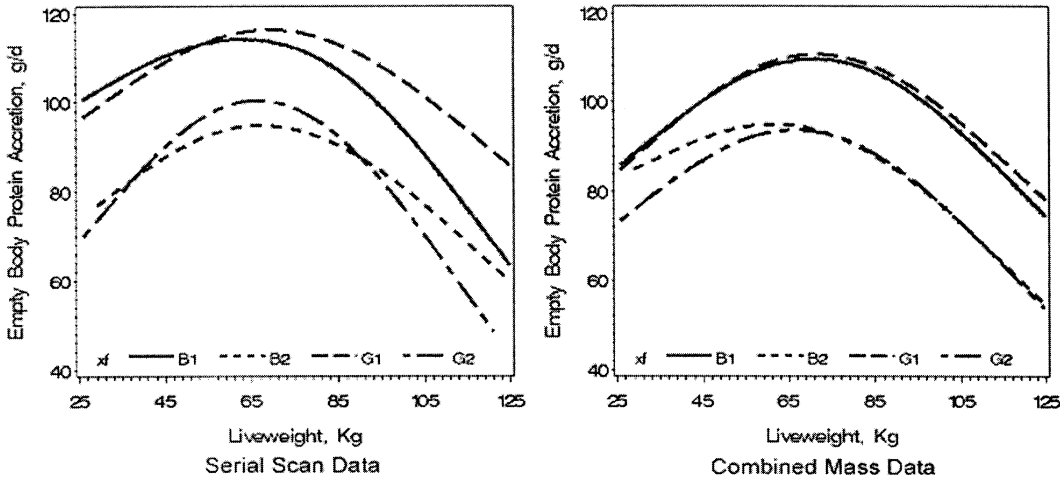

Figure 2. Modeled daily empty body protein accretion rates (XF = sex-farm group; B = barrows; G = gilts). Protein accretion was modeled using the derivative of a generalized nonlinear function: ($EBP = M(1 - e^{b_0 + b_1 x + b_2 x^2})$), where EBP = protein mass, M = an estimation of mature protein content, and x = live weight.

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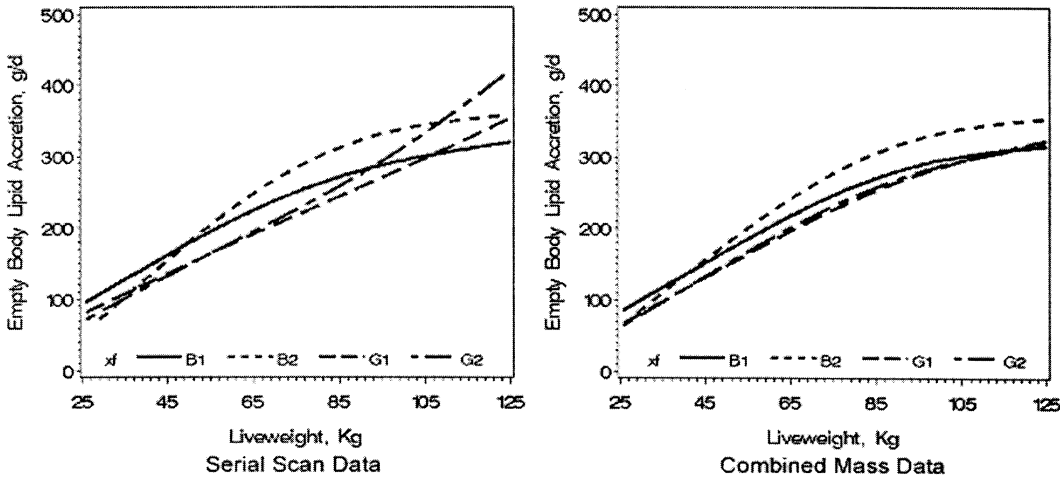

Figure 3. Modeled daily empty-body lipid accretion (XF = sex-farm group; B = barrows; G = gilts). Lipid accretion was modeled using the derivative of a generalized exponential function: ($EBL = (e^{b_0 + b_1 x + b_2 x^2 + b_3 x^3})$), where EBL = empty-body lipid mass and x = live weight.

genetic populations. However, determining growth rates and body composition in ideal conditions does not necessarily replicate performance achieved in commercial operations. Holck et al. (1998) showed that growth rate and protein accretion were approximately 30% lower in pigs raised on commercial operation than in pigs raised in an "ideal" environment. Many factors such as disease, temperature, crowding, and social interactions can influence a pig's growth performance (Whittemore et al., 1988; Schinckel, 1994; Hyun et al., 1998). Several researchers have shown that ADG and protein accretion increase, then decrease, as live weight increases in growing-finishing pigs (Whittemore et al., 1988; Friesen et al., 1996; Schinckel et al., 1996), which agrees with both the serial and mass scan data in this study.

The large difference between the modeled protein accretion and ADG of farms 1 and 2 based on both the serial and mass data initially was unexpected because both farms used similar genetics and nutritional programs. However, environmental and management differences existed between the two operations. Pigs used on farm 1 were all born within 1 wk and were maintained as a group throughout the nursery and finishing facility. Also, all buildings were managed on an all-in all-out (**AIAO**) basis, and the finishing facility housed only the pigs from one group. In contrast, pigs on farm 2 were farrowed over a 2-wk period and were

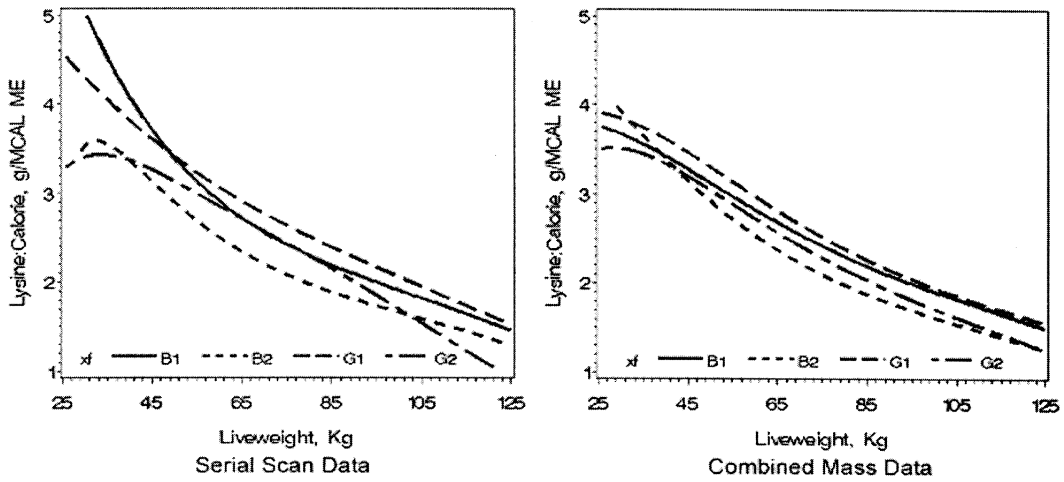

Figure 4. Modeled dietary lysine: calorie ratios from the serial scan data (XF = sex-farm group; B = barrows; G = gilts). Daily total lysine requirements (TLR, g/d) calculated by $((0.036 \times BW^{0.75}) + ((0.066 \times PA) \div 0.60)) \div 0.88 = TLR$. Metabolizable energy requirements (MER, Mcal ME/d) calculated by: $(0.25517[BW]^{0.6}) + (8.84 \times PA) + (11.4 \times LA) = MER$, where BW = body weight, PA = protein accretion, and LA = lipid accretion. Lysine:calorie ratio calculated as TLR/MER.

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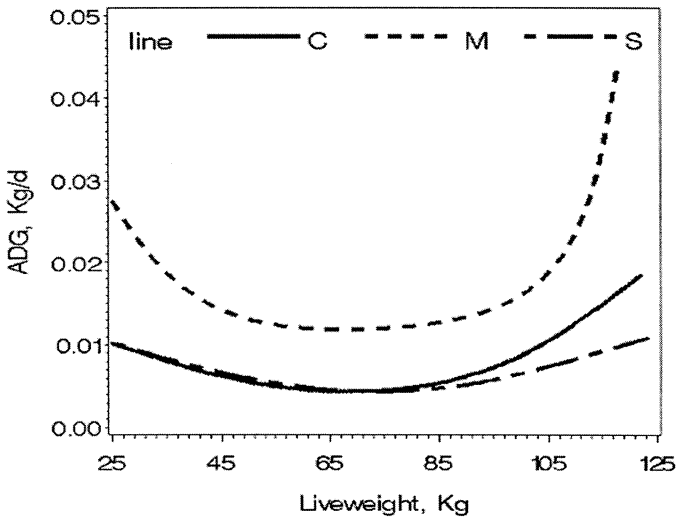

Figure 5. Bootstrap standard errors for the modeled live weight growth rates (kg/d) for serial (S), individual mass (M), and combined mass scans (C). Live weight on age was modeled using the derivative of a generalized nonlinear function: ($WT = M(1 - e^{\beta_0 + \beta_1 x + \beta_2 x^2})$), where WT = live weight, M = an estimation of mature body weight, and x is d of age.

not maintained as a group throughout the nursery and finishing periods. As a result, pigs were commingled between groups and thus did not show the growth performance benefits of AIAO production as described by Scheidt et al. (1995). Buildings on farm 2 contained four rooms of 600 pigs, which may have increased the opportunity to spread growth-influencing diseases from group to group.

The growth differences between the two farms were similar to those for the individual and combined mass scans. The increased bootstrap standard errors observed in the live weight curves from the individual mass scan were likely due to variation in the environmental factors affecting the various age groups of pigs (Figure 1). The standard deviation in BW of pigs of each age group of the individual mass scans was simi-

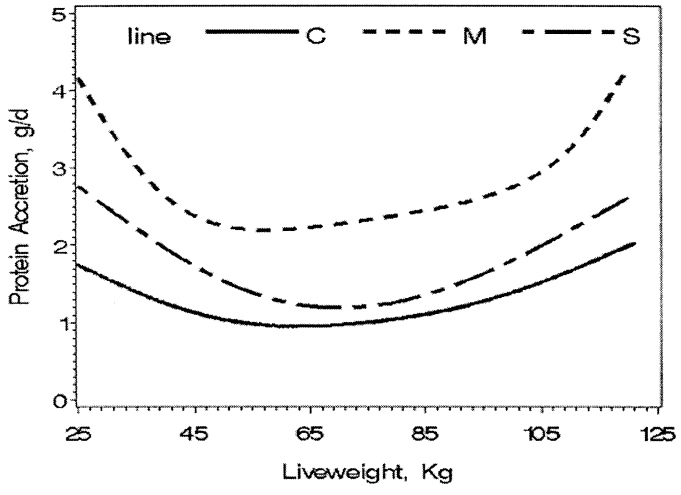

Figure 6. Bootstrap standard errors for the modeled daily empty body protein accretion rate (g/d) for serial (S), individual mass (M), and combined mass (C) scans. Protein accretion was modeled using the derivative of a generalized nonlinear function: ($EBP = M(1 - e^{\beta_0 + \beta_1 x + \beta_2 x^2})$), where EBP = empty body protein content, M = an estimation of mature protein content, and x = live weight.

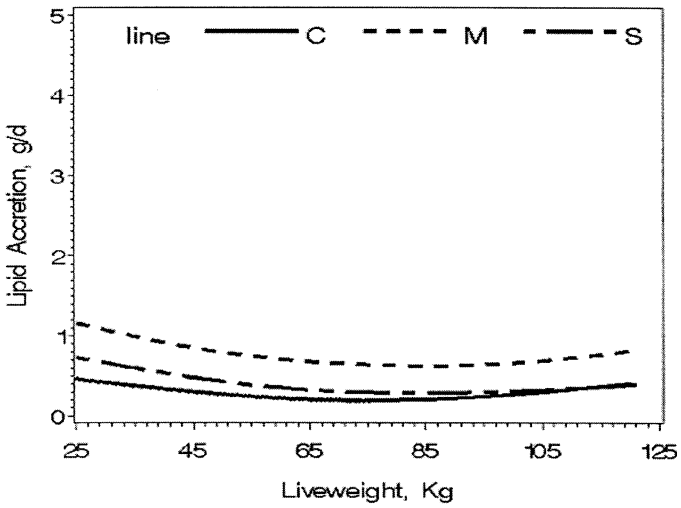

Figure 7. Bootstrap standard errors for the modeled daily empty body lipid accretion rates (g/d) for serial (S), individual mass (M), and combined mass (C) scans. Lipid accretion was modeled using the derivative of a generalized exponential function: ($EBL_{mass} = (e^{b_0 + b_1 x + b_2 x^2})$) and ($EBL_{serial} = (e^{b_0 + b_1 x + b_2 x^2 + b_3 x^3})$), where EBL = empty-body lipid content and x = live weight.

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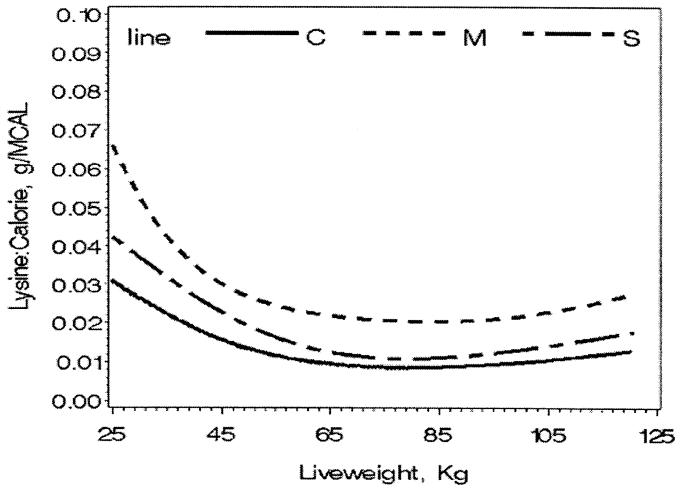

Figure 8. Bootstrap standard errors for the modeled grams of total lysine required per megacalorie of metabolizable energy intake for serial (S), individual mass (M), and combined mass (C) scans. Daily total lysine requirements (TLR, g/d) calculated by: $((0.036 \times BW^{0.75}) + ((0.066 \times PA) \div 0.60)) \div 0.88 = TLR$. Metabolizable energy requirements (MER, Mcal ME/d) calculated by: $(0.25517[BW]^{0.6}) + (8.84 \times PA) + (11.4 \times LA) = MER$, where BW = body weight, PA = protein accretion, and LA = lipid accretion. Lysine:calorie ratio calculated as TLR/MER.

lar to the standard deviation of the pigs sampled on each weigh day of the serial scans. For example, the SD of weight for the youngest group measured was 3.9, 3.6, 3.4, and 2.3 for the serial, mass 1, mass 2, and mass 3 measurements, respectively, from farm 1 (Table 1). Thus, the increased bootstrap standard errors of the mass scan data likely were due to the fact that the pigs sampled at each age were from different groups that had been exposed to different environmental effects. One group of pigs may have had a disease outbreak or an environmental stressor that decreased ADG and resulted in their mean weight being less than expected by the growth function. Additionally, determining pigs' age was imprecise on farm 2. The midpoint of the 2-wk farrowing period was used as the birth date for all pigs to determine age and contributed to the variation in the live weight curves. This problem could have been alleviated if the pigs had been identified at birth. Another potential confounding factor in predicting ADG using the mass scans may be the age intervals of the pigs actually weighed and scanned. The initial intention was to use groups of pigs in 3-wk age intervals; however, because of pig production scheduling on the farms the intervals were somewhat variable (Table 1). By not maintaining the 3-wk age interval, the analysis was less able to accurately assess the dynamic changes in live weight growth rate.

Unlike the live weight curves, the protein and lipid mass curves from individual mass scans had RSD that were very similar to those of the equations from the serial scan data. Also, the differences between farms for protein accretion and lipid accretion relative to live weight were similar for both serial and mass scans. The modeled total lysine requirement requirements differed between the serial and individual mass scans for each farm-sex subclass. The differences between the modeled total lysine requirement values appeared to be due primarily to variation in the live weight growth curves, which affect the daily protein accretion curves. The standard errors of total lysine requirement and protein accretion are dependent on the standard errors of the ADG curves and modeled marginal growth rates of protein accretion to BW gain. Thus, if precise protein accretion and total lysine requirement curves are desired, sampling errors associated with the live weight growth curves should be minimized.

The modeled lysine:calorie ratio requirements were similar for the serial, individual mass scans, and combined mass scans for each sex within farm subgroup. Because the energy and lysine requirements for maintanence are relatively small and the energy cost for lipid and protein growth are similar (11.4 vs 8.84 Mcal/kg, respectively; Noblet et al., 1999), the modeled lysine:calorie ratio requirements are based largely on the proportional growth of protein to the sum of protein and lipid (Bikker et al., 1994). Therefore, the proportional growth of empty body protein and empty body lipid based on the modeled marginal growth rates of empty body protein and empty body lipid to BW can be used to predict lysine:calorie ratio requirements.

Even though most modeled lysine:calorie ratio requirements were similar between the serial and mass scans, one individual mass scan per sex on each farm did not fit with the others. In the case of farm 1, the modeled lysine:calorie ratio requirements from scan 2 were dissimilar to those of the other four predictions. This may have been due to the age intervals of pigs used in that particular scan. The oldest pigs used were only 169 d, whereas the oldest pigs in the serial scan and mass scan 1 and 3 were 195, 190, and 182 d, respectively. On farm 2, the modeled lysine requirements from mass scan 1 for barrows and mass scan 2 for gilts differed from the other modeled lysine:calorie ratio values. The differing prediction for the barrows might have been due to the age of the oldest pigs, similar to the data from the other farm. In the case of the gilts, the oldest gilts scanned were unusually lean (1.71 cm backfat depth), which allowed the protein accretion curves to remain high and yield high modeled lysine:calorie ratio and total lysine requirements.

The accurate prediction of farm-specific lysine requirements requires accurate ultrasonic measurements of backfat depth and longissimus muscle area (Smith et al., 1999). Operator error and consistent location of the measurement are concerns with ultrasonic probe measurements (Sather et al., 1987). Ultrasound technicians should be trained carefully and

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evaluated for their accuracy of measurement (Bates et al., 1994). The live ultrasound measurements should be similar to carcass measurements if well-trained personnel perform them.

These bootstrapping standard errors provide insight as to the number of observations and procotol, including the number of scans and interval between scans needed to achieve the designed levels of precision. Standard errors have not been established for most procedures to either predict or directly evaluate nutrient requirements. Bootstrapping procedures are computationally difficult, especially for variables such as total lysine requirement and lysine:calorie ratio, which are themselves functions of the modeled marginal growth of protein accretion, BW, and lipid accretion. Currently the development of bootstrapping standard errors for each pork producer's growth curve analysis is not practical.

The standard errors of the modeled total lysine requirement and lysine:calorie ratio values increased close to the initial and final BW. Initiating the BW and ultrasonic scanning at lighter weights (less than 25 kg) and carrying pigs to heavier weights (greater than 125 kg) will provide a more precise estimation of lysine requirements for the entire growing-finishing period (Smith et al., 1999). Because stocking density, group size, and pen effects can affect pig growth, the optimal procedure is to provide stocking density and group size similar to those achieved with the usual marketing strategy (Hyun et al., 1998). One procedure is to sample pigs randomly from numerous pens, and then as BW increases, to market pigs not identified for serial scanning at normal market weights. The pigs identified for serial scans can be carried to a pork processor's highest desired weight (125 to 130 kg). With serial scanning, it is important not to continue to include BW data after any identified pigs have been marketed. With mass scanning, it is important to not collect data from groups that have been marketed partially. Simulation has shown that this will substantially bias the ADG, protein accretion, and total lysine requirement downward at the later stages of growth (Schinckel and Einstein, 1995).

The standard errors of the modeled lysine:calorie ratio values were approximately 1% of the modeled value at each BW for the serial scans, slightly lower for the combined mass scan data, and approximately 2% for the individual mass scan data. The greatest standard error for the individual mass scan translates into a 95% confidence interval for total dietary lysine percentage of approximately 0.06%. The modeled lysine:calorie ratio values in this trial assumed that the pigs had average maintenance requirements and were reared in a thermoneutral environment. Pigs reared in environments below thermoneutral temperatures would use energy to maintain their body temperature and have greater actual energy intakes than those modeled by the ME intake prediction equation used in this trial (NRC, 1998).

This trial described one of a number of possible means to predict total lysine requirement and lysine:calorie ratio for growing-finishing pigs. A second method involves obtaining mean fat-free lean growth data, which can be used to develop protein accretion curves (Schinckel et al., 1996; NRC, 1998), and determining on-farm feed-intake curves (de Lange et al., 1993; de Lange and Schruers, 1995). With actual collection and analysis of feed intake information, the assumptions of average maintenance requirements and thermoneutral environmental conditions would not be needed in the prediction of daily energy intakes. However, this method assumes that the feed intake data are collected accurately on enough pigs and BW ranges. In our experience, this has been difficult. Another drawback of this method is that a feed wastage factor needs to be assumed or estimated. Also, this method assumes that the shapes of the protein accretion curves are identical for pigs with similar mean fat-free lean growth reared in production units with different environmental stressors and genetic populations (Schinckel and de Lange, 1996).

A third method to predict lysine:calorie ratio values at each live weight is to establish the relationships between the lysine:calorie ratio values and mean fat-free lean adjusted to a constant carcass or live weight. Data from numerous on-farm trials utilizing serial ultrasound measurements have been used to predict the lysine:calorie ratio values from the fat-free lean percentage at 113 kg live weight (Dritz et al., 1997). Different equations are used for barrows and gilts. The major drawbacks to this method are that a prediction of total lysine requirement is not possible, and it assumes that the relative marginal growth rates of empty body protein and empty body lipid are similar at each live weight for pigs with similar fat-free lean percentages.

These results indicate that live weight and ultrasonic scan data can be used to model dynamics of growth and accretion rates and predict lysine requirements of pigs on commercial farms. However, the procedure used will be based on the objectives of the experiment. If the objective is to compare growth and accretion rates between factors within a farm or determine daily lysine and nutrient requirements, serial weighing and scanning of pigs should be conducted. The lower bootstrap standard errors for the serially collected data compared to the indidual mass scan indicate that sample size could be decreased or confidence bands decreased with similar sample sizes. An example would be to compare the lysine requirements of two genetic lines. The serial method would result in less variation from enviromental factors and more accurately detect differences.

If the objective is to characterize the mean environmental influence within or among farms on modeled requirements, then it appears that a mass scan procedure seems to be more appropriate. However, because of the environmental influences on ADG, a larger num-

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ber of groups will have to be employed to obtain standard errors of the estimates similar to those obtained in a serial scan. Also, if a qualified technician or equipment is not readily accessible, performing mass scan data collection on a single day will be easier and more efficient to implement. This is in contrast to the technician having to make multiple visits to the farm for the serial method. If the objective is simply to determine the LCR requirement for a commercial operation, then pigs can be either serially or mass scanned to determine the relative protein and lipid accretion curves.

Implications

Live weight growth and rates of protein and lipid accretion differ among farms, resulting in different lysine requirements. As swine operations become more system-oriented and information-driven, pork producers will demand farm-specific nutrient recommendations. These requirements can be modeled using real-time ultrasound measurements using either serially or mass collected cross-sectional data on specific farms. Either serial measurements within a group or mass-collected measurements across several groups of different ages can be used, depending on the objective of the measurement.

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