Modeling the relationship between scanned rump and 12th-rib fat in young temperate and tropical bovines: Model development and evaluation[1,2]

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ABSTRACT: A decision support tool for predicting subcutaneous fat depths called BeefSpecs, based on the Davis growth model (DGM), has been developed by the Cooperative Research Centre for Beef Genetic Technologies. Currently, the DGM predicts 12th-rib fat thickness (RFT, mm). To allow predictions of fat thickness at the P8 rump (P8FT, mm) site, the standard carcass fat measurement in the Australian beef industry, a relationship was developed between ultrasound RFT and P8FT in steers and heifers from temperate (Angus, Hereford, Shorthorn, and Murray Grey) and tropical (Brahman, Belmont Red, and Santa Gertrudis) breed types. Model development involved fitting various combinations of sex, breed type (BrT), BW, age, and RFT to produce 6 models. The models were challenged with data from 3 independent data sets: 1) Angus steers from 2.4 generations of divergent selection for and against residual feed intake; 2) 2 tropically adapted genotypes [Brahman and tropically adapted composites (combinations of Belmont Red, Charbray, Santa Gertrudis, Senepol, and Brahman breeds)]; and 3) a study using sires from Charolais, Limousin, Belgian Blue, and Black and Red Wagyu breeds and 3 genetic lines of Angus to create divergence in progeny in terms of genetic potential for intramuscular fat percent and retail beef yield. When challenged with data from Angus cattle, the mean biases (MB, mm) for models A to F were −1.23, −0.56, −0.56, −0.02, 0.14, and 0.04, and the root mean square errors of predictions (mm) were 1.53, 0.97, 0.97, 0.92, 0.93, and 0.91, respectively. When challenged with data from Brahman cattle, MB were 0.04, −0.22, −0.14, 0.05, −0.11, and 0.02 and root mean square errors of predictions were 1.30, 1.29, 1.27, 1.23, 1.37, and 1.29, respectively. Generally, model accuracy indicated by MB tended to be less for model E, which contained age rather than BW as a covariate. Models B and C were generally robust when challenged with data from Angus, Brahman, and Tropical Composite cattle as well as crossbred cattle with temperate sires. Model D, which did not contain age, performed the most consistently and was selected for inclusion in the DGM: P8FT, mm = −3.6 (±0.14) + 1.3 (±0.13) × sex + 0.11 (±0.13) × BrT + 0.014 (±4.8E^{-4}) × BW + 0.96 (±0.01) × RFT − 0.73 (±0.08) × sex × BrT − 3.8E^{-3} (±4.2E^{-4}) × sex × BW − 0.09 (±0.01) × sex × RFT + 1.3E^{-3} (±3.7E^{-4}) × BrT × BW + 0.24 (±0.01) × BrT × RFT (adjusted R^2 = 0.86; SE = 0.013). Model D has been implemented in BeefSpecs to predict P8FT.

Key words: beef cattle, heifer, P8 rump fat, steer, temperate, tropical

INTRODUCTION

Market signals have resulted in increased interest in improving carcass and meat quality in the seed stock sector of the beef industry (Johnston et al., 2003). However, genetic selection is slow in altering animal growth and composition (Meszaros, 1999) relative to other means (e.g., managerial and nutritional manipu-

lation; Ball et al., 1997). Phenotypic prediction of fatness in beef cattle has the capacity to assist producers in making decisions to improve compliance with market specifications.

The Davis growth model (**DGM**), a dynamic steer growth model (Oltjen et al., 1986) that predicts accretion (in kg) of total body protein and fat (kg), is currently being used by the Cooperative Research Centre (**CRC**) for Beef Genetic Technologies in Australia to predict 12th-rib fat thickness (**RFT**, mm). The DGM partitions total body fat into 4 fat depots (intermuscular, intramuscular, subcutaneous, and visceral; Sainz and Hasting, 2000) and predicts RFT from subcutaneous fat (McPhee et al., 2008). The P8 rump site (**P8FT**) is the current standard carcass fat measurement for the Australian beef industry. Therefore, a relationship to predict P8FT from model-predicted RFT is required.

Previous studies have shown that breed and sex influence fat partitioning within the subcutaneous depot between rib and rump sites in both cattle (Phillips et al., 1984; Hopkins et al., 1993) and sheep (Clarke et al., 1988). Carcass weight also influences the distribution of fat in the subcutaneous depot (Phillips et al., 1984). Breed types (**BrT**) that are temperate (*Bos taurus*, including Continental) have been the primary focus of these studies, and the relationship between P8FT and RFT has not been elucidated for tropical breeds [e.g., increased or variable (or both) *Bos indicus* content]. Therefore, the objective of this study was to develop a model that describes the relationship between P8FT and RFT in steers and heifers from both temperate and tropical breeds and to validate the relationship by using independent data sets.

MATERIALS AND METHODS

Animal care and use committee approval was not obtained for this study because data were obtained from an existing database (CRC for Beef Genetic Technologies database).

This study developed models that describe the relationship between scanned RFT and P8FT in beef cattle. Evaluation of the models developed was undertaken using 3 independent data sets. Data were collected from experiments conducted within the CRC for Cattle and Beef Quality. Data used during model development were taken from a breeding program that ran from 1993 to 1997 (Robinson, 1995; Upton et al., 2001), and the challenge data sets for model evaluation consisted of 3 independent experiments: Angus steers selected for and against residual feed intake (**RFI**; data set 1; Hegarty et al., 2005); tropically adapted breeds in Northern Australia (data set 2; Burrow et al., 2003; Burrow and Bindon, 2005); and a study of temperate, Continental, and Japanese sire breeds used to create divergence in progeny in terms of genetic potential for intramuscular fat percent and retail beef yield (data set 3; McKiernan et al., 2005).

Model Development Data

Robinson (1995) and Upton et al. (2001) have described the design, management, and operations of the project from which the data used here were generated. In brief, the project was designed as a large progeny test for carcass and meat quality traits of 4 temperate (Angus, Hereford, Shorthorn, and Murray Grey) and 3 tropical (Brahman, Belmont Red, and Santa Gertrudis) BrT (Upton et al., 2001). Animals were allocated to 1 of 2 finishing regimens (pasture or feedlot) for temperate cattle or 3 finishing regimens (pasture, feedlot in Northern Australia, or feedlot in South Australia) for tropical cattle (Johnston et al., 2003).

The traits [age, BW, scanned RFT, and P8FT (mm)] used in this study were taken from heifers and steers 1) on delivery before backgrounding, 2) before finishing just after backgrounding had been completed, and 3) before slaughter, as well as at other intermediate points in time. The RFT was recorded between the 12th and 13th ribs and the P8FT was recorded at the intersection between a line parallel to the spine from the tuber ischium and a line perpendicular to it from the spinous process of the third sacral vertebra (Johnston et al., 2003). All ultrasound measurements were taken by accredited technicians (Upton et al., 1999) with an Aloka 500V real-time ultrasound scanner using a 17-cm transducer (Corometrics Medical Systems Inc., Wallingford, CT), with vegetable oil as the coupling agent, and fat depths were recorded using the calipers built into the scanner (Wolcott et al., 2001). A total of 7,530 animals had on average 3 data recordings taken (i.e., between 1 and 6), resulting in 22,279 observations being used during the model development analysis in this study (Table 1). Unadjusted preslaughter data for age, BW, RFT, and P8FT are shown in Table 1 for the tropical and temperate BrT.

Model Evaluation Data

Three independent data sets were used to challenge the models developed. These data sets are described below.

Data Set 1. The data were taken from an experiment established at the Agricultural Research Centre, Trangie, New South Wales, Australia (Arthur et al., 2001). In brief, 109 Angus steers born in 2001 were the result of an average of 2.4 generations of divergent selection for and against RFI while also maintaining an unselected line (Hegarty et al., 2005). The steers entered the CRC for Cattle and Beef Quality Tullimba Research feedlot (Armidale, New South Wales, Australia) after backgrounding, at approximately 20 mo of age, weighing an average of 462 kg (Hegarty et al., 2005). Eight feedlot pens that contained automated feed intake recorders (Ruddweigh, Guyra, New South Wales, Australia; Bindon, 2001) were used, with each accommodating 12 steers. The steers underwent a stan-

Table 1. Summary of preslaughter data for age, BW, scanned 12th-rib fat thickness (RFT), and P8 rump fat thickness (P8FT) of temperate and tropical cattle types taken from the Cooperative Research Centre straight breeding project (Robinson, 1995; Upton et al., 2001) used for model development

Trait	n	Minimum	Maximum	Mean	SD
Temperate					
Age, d	10,052	216	961	476.44	153.79
BW, kg	10,052	114	792	384.04	120.33
RFT, mm	10,052	0	27	4.70	3.91
P8FT, mm	10,052	1	33	6.06	4.91
Tropical					
Age, d	12,227	163	1,326	586.44	208.77
BW, kg	12,227	85	798	357.53	124.40
RFT, mm	12,227	1	27	3.36	3.02
P8FT, mm	12,227	1	41	5.63	5.35
Overall					
Age, d	22,279	163	1,326	536.81	193.87
BW, kg	22,279	85	798	369.49	123.29
RFT, mm	22,279	0	27	3.96	3.51
P8FT, mm	22,279	1	41	5.83	5.16

dard feedlot induction program, after which the animals were given ad libitum access to a finishing ration. At 3 stages during the experiment, BW was recorded and RFT and P8FT scans were taken. The first was after weaning, the second was before entry into the feedlot, and the third was before slaughter. Animals with missing data or missing birth dates were removed from the data set. Therefore, animals had traits recorded at 1, 2, or 3 of these time points, and the total number of observations available was 292. Additional details are reported by Hegarty et al. (2005). The number of measurements, mean age, BW, RFT, and P8FT are shown in Table 2 for the RFI cattle.

Data Set 2. Data were taken from a project established to examine the possibilities of improving efficiency and product quality without detrimentally affecting breeder herd performance or adaptability in Northern Australian environments (Burrow and Bindon, 2005). This study incorporated 2 tropically adapted genotypes, Brahman and tropically adapted composites (hereafter, Tropical Composites), that were considered to be extreme genotypes for carcass quality, adaptation, and male and female fertility of tropically adapted breeds (Burrow et al., 2003). The Tropical Composites were composed of varying quantities of Belmont Red, Charbray, Santa Gertrudis, Senepol, and Brahman breeds (Corbet et al., 2007).

The progeny were bred on 8 properties throughout Queensland and the Northern Territory. The steer progeny were transferred at weaning to 1 of 5 grow-out properties in central Queensland and New South Wales, before being finished in the CRC for Cattle and Beef Quality Research Tullimba feedlot and slaughtered at an average carcass weight of 320 kg (Burrow et al., 2003). The heifer progeny were allocated to 1 of 4 research stations throughout Queensland after weaning and were mated in large multiple-sire mating groups at approximately 2 yr of age (Corbet et al., 2007). Body weights and scanned RFT and P8FT were taken periodically on the steers up until slaughter and on the heifers until they had reared at least 2 calves to weaning.

Data were used for model evaluation, provided that age, BW, RFT, and P8FT were available for a single measurement time point. Heifer data included only those taken before the first recorded mating date. Animals with missing data or missing birth dates were removed from the data set. Model predictions were made for individual Tropical Composite animals by weighting the BrT coefficient in the prediction models by the estimated proportion of tropical content. Anomalies in the data (e.g., RFT of 35 mm corresponding to P8FT of 1 mm) were also removed by comparison of average differences between RFT and P8FT and the dif-

Table 2. Summary of preslaughter data for age, BW, scanned 12th-rib fat thickness (RFT), and P8 rump fat thickness (P8FT) of Angus cattle selected for and against residual feed intake (Hegarty et al., 2005; data set 1)

Trait	n	Minimum	Maximum	Mean	SD
Age, d	292	193	775	519.08	231.14
BW, kg	292	182	790	435.37	168.72
RFT, mm	292	2	17	6.27	3.73
P8FT, mm	292	2	20	7.48	4.87

Table 3. Summary of preslaughter data for age, BW, scanned 12th-rib fat thickness (RFT), and P8 rump fat thickness (P8FT) of Brahman and Tropical Composite[1] cattle (Burrow et al., 2003; Burrow and Bindon, 2005; data set 2)

Trait	n	Minimum	Maximum	Mean	SD
Brahman					
Age, d	7,873	142	1,046	519.75	193.90
BW, kg	7,873	87	724	305.48	115.93
RFT, mm	7,873	1	15	2.41	2.13
P8FT, mm	7,873	1	25	3.80	3.43
Tropical Composite					
Age, d	8,856	164	1,056	539.56	196.42
BW, kg	8,856	44	774	332.69	128.26
RFT, mm	8,856	1	23	2.52	2.49
P8FT, mm	8,856	1	28	3.59	3.75

[1]Tropical Composite: varying quantities of Belmont Red, Charbray, Santa Gertrudis, Senepol, and Brahman breeds.

ference for a single animal at 1 point in time. Further details of this experiment are available from Burrow et al. (2003) and Burrow and Bindon (2005). The number of measurements, mean age, BW, RFT, and P8FT are shown in Table 3 for Brahman and Tropical Composite cattle.

Data Set 3. An experiment was conducted at 4 locations across southern Australia beginning in 1999 and ending in 2005. Heifer and steer progeny were generated from breeding programs on commercial properties in New South Wales, Victoria, South Australia, and Western Australia (McKiernan et al., 2005). The sires used in the breeding program were selected to create divergence in genetic potential of the progeny for intramuscular fat percent and retail beef yield. The breeds from which sires were drawn included Charolais, Limousin, Belgian Blue, Black and Red Wagyu, and 3 genetic lines of Angus (McKiernan et al., 2005). The breeding program in New South Wales used only Hereford dams, whereas the breeding programs in Victoria and South Australia used both Angus dams and first-cross dams derived from Hereford, Angus, Limousin, Simmental, and some dairy breeds to create crossbred progeny. The Western Australian site used predominantly Angus and Murray Grey cows. For model evaluation, the crossbred progeny were grouped based on sire breed: Temperate (3 genetic lines of Angus), Continental (Charolais, Limousin, and Belgian Blue), and Japanese (Black and Red Wagyu).

Body weights, RFT, and P8FT measurements were taken at strategic times throughout the experiment depending on location. Crossbred animals from New South Wales had BW and scan measurements taken at 2 time points, whereas the crossbred and Angus animals from Victoria and South Australia and the Angus animals from Western Australia had BW and scan measurements taken at 1 time point. Animals with missing data or missing birth dates were removed from the data set. Full details of this experiment were reported by McKiernan et al. (2005). The number of measurements, mean age, BW, RFT, and P8FT from the Angus and crossbred cattle in this experiment are shown in Table 4.

Statistical Analysis

Animals with missing fat measurements and missing birth dates were removed from the development data, leaving 22,279 observations. There were 12,227 and 10,052 observations from tropical and temperate BrT, respectively (Table 1). Of the tropical animals, 5,106 observations were from heifers and 7,121 observations were from steers, whereas 964 and 9,088 observations were from temperate heifers and steers, respectively.

Linear regression analyses were conducted using the linear model procedure in the R statistical package (R Development Core Team, 2008) with P8FT as the dependent variable (Eq. [1]) as follows:

$$\text{P8FT, mm} = \beta_0 + \beta_1\text{sex} + \beta_2\text{BrT} + \beta_3\text{BW} + \beta_4\text{age}$$
$$+ \beta_5\text{RFT} + \text{interactions} + e, \quad [1]$$

where combinations of RFT, age, and BW were fitted as covariates; sex and BrT were fitted as fixed effects, with β_i representing the regression coefficient of each fitted covariate/fixed effect; and e was the residual error. All 2-way interactions were evaluated. The fixed effects were coded as follows: sex (heifer = 0; steer = 1) and BrT (temperate = 0; tropical = 1). The linear regressions were progressively developed, beginning with a model that contained only RFT to a model that included all information sources (i.e., sex, BrT, age, BW, RFT, and significant interactions). The adjusted R^2 $\left(\mathbf{R^2_{adj}}\right)$ and SE were used to assess how well the models fitted the development data. The R^2_{adj} (Eq. [2]) was used to adjust for the different number of parameters fitted in each model during model development:

$$R^2_{adj} = 1 - \left[\frac{SSE(n-1)}{SST(n-p-1)}\right], \quad [2]$$

Table 4. Summary of preslaughter data for age, BW, scanned 12th-rib fat thickness (RFT), and P8 rump fat thickness (P8FT) of Angus and crossbred cattle (grouped by sire genotype: temperate, Continental, and Japanese)[1] with divergence in genetic potential for intramuscular fat percent and retail beef yield (McKiernan et al., 2005; data set 3)

Trait	n	Minimum	Maximum	Mean	SD
Angus cattle					
Age, d	251	289	685	347.30	65.94
BW, kg	251	180	608	290.82	65.84
RFT, mm	251	2	9	3.10	1.20
P8FT, mm	251	2	11	3.59	1.61
Temperate[2]					
Age, d	885	193	703	385.16	143.28
BW, kg	885	112	548	318.46	81.83
RFT, mm	885	1	13	2.64	1.42
P8FT, mm	885	1	13	3.57	2.03
Continental[2]					
Age, d	319	183	711	379.28	143.65
BW, kg	319	168	524	318.59	86.55
RFT, mm	319	1	12	1.98	1.20
P8FT, mm	319	1	12	2.52	1.64
Japanese[2]					
Age, d	362	189	696	381.94	151.52
BW, kg	362	136	479	297.45	84.43
RFT, mm	362	1	9	2.47	1.42
P8FT, mm	362	1	16	3.50	2.12

[1]Temperate: 3 genetic lines of Angus; Continental: Charolais, Limousin, and Belgian Blue; Japanese: Black and Red Wagyu.

[2]Dam genotype varied between sites, ranging from pure Hereford dams to first-cross dams derived from Hereford, Angus, Limousin, Simmental, and dairy breeds.

where SST is the total sums of squares, SSE is the error sums of squares, n is the number of observations, and p is equal to the number of parameters in the model.

Model evaluation was conducted using a customized procedure in the R statistical package (R Development Core Team, 2008). Model predictions of P8FT were evaluated using mean bias (**MB**; Eq. [3]):

$$\frac{\sum\left(O_i - P_i\right)}{n}, \quad [3]$$

where n is the number of scanning data points, O_i is the observed P8FT, and P_i is the predicted P8FT, respectively ($i = 1$ to n). The error of prediction was assessed by the mean square error of prediction (**MSEP**; Eq. [4]):

$$\frac{\sum_{i=1}^{n}\left(O_i - P_i\right)^2}{n}, \quad [4]$$

where the terms are as defined above. The root MSEP (**RMSEP**) was used as a measure of the accuracy of prediction. The MSEP was decomposed into bias, slope, and random components as a proportion of MSEP to assess the error structure, following the method of Tedeschi (2006). The statistical significance of each MB was evaluated using a paired t-test of the mean of the differences between the observed and model-predicted values.

RESULTS

Model Development

The coefficients for the linear regressions of P8FT on RFT are shown in Table 5 when fitting combinations of sex, BrT, age, and BW. The linear regression between RFT and P8FT (model A) demonstrates that RFT accounted for a large proportion of the variation in P8FT $\left(R^2_{adj} = 0.79\right)$, which was not unexpected given the corelationship that exists between these 2 subcutaneous fat depots. Models B and C demonstrate that BrT and sex had significant effects on the relationship between P8FT and RFT ($P < 0.05$ and $P < 0.01$, respectively). Model E demonstrates that when RFT and age were fitted, sex and BrT were significant ($P < 0.01$), but BrT was not significant ($P = 0.33$, 0.32) in models D and F when BW was fitted. However, BrT was found to have strong interactions with sex, RFT, and BW ($P < 0.01$) in model D, but more moderate interactions with BW and age ($P < 0.05$) and strong interactions with sex and RFT ($P < 0.01$) were seen in model F.

The R^2_{adj} and SE shown in Table 5 indicate model A was a poorer descriptor of the relationship between RFT and P8FT than the other models. Model F, which

Table 5. Linear regression coefficients for the prediction of P8 rump fat thickness (mm)

| Model	Equation[1]	R^2_{adj}	SE
A	$0.64_{(0.02)} + 1.31_{(4.5E^{-3})} \times RFT$	0.79	0.016
B	$0.55_{(0.03)} - 0.23_{(0.04)} \times BrT + 1.17_{(5E^{-3})} \times RFT + 0.41_{(8E^{-3})} \times BrT \times RFT$	0.83	0.014
C	$0.48_{(0.09)} \times sex + 0.18_{(0.09)} \times BrT + 1.26_{(0.01)} \times RFT - 0.44_{(0.09)} \times sex \times BrT - 0.09_{(0.01)} \times sex$ $\times RFT + 0.37_{(9E^{-3})} \times BrT \times RFT$	0.83	0.014
D	$-3.6_{(0.14)} + 1.3_{(0.13)} \times sex + 0.11_{(0.13)} \times BrT + 0.014_{(4.8E^{-4})} \times BW + 0.96_{(0.01)} \times RFT - 0.73_{(0.08)} \times sex \times BrT$ $- 3.8E^{-3}_{(4.2E^{-4})} \times sex \times BW - 0.09_{(0.01)} \times sex \times RFT + 1.3E^{-3}_{(3.7E^{-4})} \times BrT \times BW + 0.24_{(0.01)} \times BrT \times RFT$	0.86	0.013
E	$-2.58_{(0.12)} + 1.03_{(0.1)} \times sex - 0.29_{(0.11)} \times BrT + 7.8E^{-3}_{(2.6E^{-4})} \times age + 1.09_{(0.01)} \times RFT - 0.34_{(0.09)} \times sex \times BrT$ $- 1.7E^{-3}_{(2.1E^{-4})} \times sex \times age - 0.091_{(0.01)} \times sex \times RFT - 4.4E^{-4}_{(2.1E^{-4})} \times BrT \times age + 0.27_{(0.01)} \times BrT \times RFT$	0.86	0.013
F	$-3.59_{(0.14)} + 1.26_{(0.13)} \times sex - 0.12_{(0.12)} \times BrT + 8.6E^{-3}_{(7.3E^{-4})} \times BW + 4.4E^{-3}_{(3.9E^{-4})} \times age + 0.99_{(0.02)} \times RFT$ $- 0.50_{(0.09)} \times sex \times BrT - 1.4E^{-3}_{(6.5E^{-4})} \times sex \times BW - 1.5E^{-3}_{(3.2E^{-4})} \times sex \times age - 0.10_{(0.01)} \times sex \times RFT$ $+ 1.5E^{-3}_{(5.9E^{-4})} \times BrT \times BW - 6.6E^{-4}_{(3.3E^{-4})} \times BrT \times age + 0.23_{(0.01)} \times BrT \times RFT$	0.87	0.013

[1]RFT = 12th-rib fat thickness (mm); BrT = breed type (temperate = 0; tropical = 1); BW (kg); sex (heifer = 0; steer = 1).

contained all terms, had the greatest R^2_{adj} and smallest SE (R^2_{adj} = 0.87, SE = 0.013), but models B and C, which contained only BrT, sex, and RFT, had slightly smaller R^2_{adj} and slightly greater SE (R^2_{adj} = 0.83, SE = 0.014; Table 5).

Predictions of P8FT are illustrated in Figure 1 when using simulated RFT for models D and E in comparison with predictions using model A. The BrT and sex differences are clearly demonstrated, with tropical heifers generally having the greatest P8FT predictions across all RFT and temperate steers having the least. Comparison of Figures 1a and 1b illustrates the different patterns of P8FT predictions, with model E producing smaller predictions for heifers of both BrT than model D. The P8FT predictions for steers of both BrT were similar for the 2 models, which resulted in model D accentuating the differences between the sexes.

Model Evaluation

The MB in Table 6 of all models indicates that P8FT was overpredicted for RFI cattle from data set 1, with model C having the least MB. Model E had the smallest RMSEP, followed by models F and D, with models B and C having slightly greater RMSEP, which suggests model E had the greatest accuracy in this data set. Model A, which contained only RFT, was the least accurate predictor of P8FT. Decomposition of the MSEP revealed that most of the error contained in the predictions of all models was of a random nature, except for model A, which had a large proportion of error in the bias component. Although models D and F had the majority of error contained in the random component of MSEP, slightly larger proportions of error were contained in the bias component relative to models B, C, and E. Model C had the largest quantity of error in the slope component of MSEP, although it was relatively small.
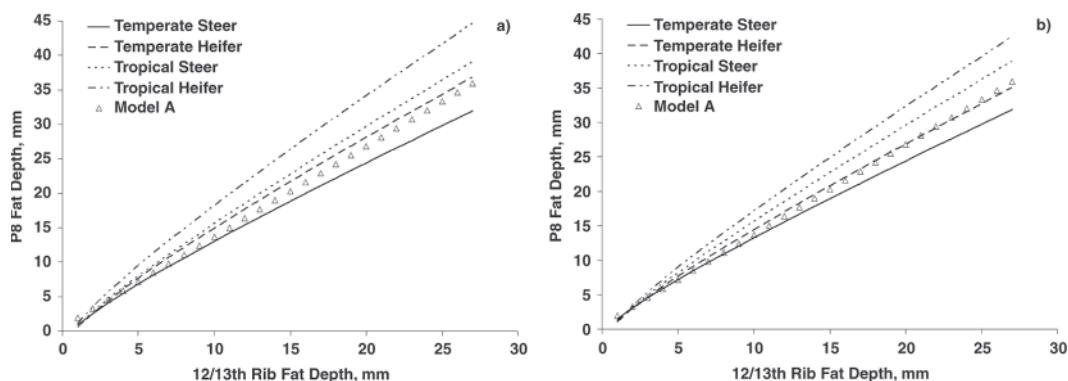
Figure 1. Predictions of P8 fat depth (mm) with 12th-rib fat depth ranging from 1 to 27 mm for temperate and tropical steers and heifers using models D (a) and E (b), which contain BW and age, respectively, in comparison with model A, which contains only 12th-rib fat (taken from Table 5).

Table 6. Model evaluation using data from cattle selected for residual feed intake in data set 1 (Hegarty et al., 2005)

Item	Model					
	A	B	C	D	E	F
Mean observed, mm	7.48	7.48	7.48	7.48	7.48	7.48
Mean predicted, mm	8.88	7.89	7.76	7.96	7.86	7.97
Mean bias, mm	−1.40	−0.41	−0.28	−0.48	−0.38	−0.49
P-value[1]	<0.01	<0.01	<0.01	<0.01	<0.01	<0.01
MSEP[2]						
RMSEP	2.02	1.51	1.51	1.48	1.40	1.47
Bias, %	47.91	7.38	3.44	10.55	7.39	11.31
Slope, %	0.60	3.12	5.76	3.71	1.45	3.43
Random, %	51.49	89.50	90.81	85.74	91.16	85.26

[1]Paired t-test of mean bias.

[2]MSEP = mean square prediction error; bias = MSEP decomposed into error attributable to overall bias of prediction; slope = MSEP decomposed into error attributable to deviation of the regression slope from unity; random = MSEP decomposed into error attributable to the random variation; RMSEP = root MSEP.

When using data for Angus cattle from data set 3, models A, B, and C produced the largest overpredictions of P8FT, whereas models E and F tended to make slight underpredictions, with model D having the smallest MB (Table 7). The RMSEP followed similar patterns, with models A, B, and C having the largest MB, the remaining models being similar, and model F having the smallest MB. Decomposition of MSEP indicated that the majority of error contained in the predictions from models D, E, and F was of a random nature. Models A, B, and C tended to have greater proportions of error contained in the bias component. Models D, E, and F had most of their remaining error in the slope component (Table 7).

The P8FT for Brahman cattle from data set 2 was found to be relatively accurately predicted by all models (Table 8). Model B, which contained BrT and RFT, made the largest overpredictions, with model F making slight underpredictions and having the smallest MB. Models A and D made slightly larger underpredictions, whereas models C and E made smaller overpredictions relative to model B. Model D had the smallest RMSEP, but model E had the largest. Differences in RMSEP between the remaining models were minor, although models B and F had slightly greater RMSEP than model C. Decomposition of the MSEP indicated that the majority of error in all models was of a random nature. The average MB in Table 8 was less than the average MB in Tables 6 and 7. The average RMSEP in Table 8 was intermediate to the average RMSEP in Tables 6 and 7.

Model evaluation for animals composed of more than 1 genotype (crossbred) is demonstrated in Table 9. The MB for crossbred temperate genotypes (Angus sires) from data set 3 (Table 9) indicates that model A tended to overpredict P8FT. Models B and C made smaller overpredictions, whereas the remaining models tended to make underpredictions. The RMSEP suggest that models B and C made the most accurate predictions of P8FT and that model E was the least accurate. Decomposition of MSEP revealed that the majority of error in models B to G was contained in the random component, whereas model A contained a larger proportion of error in the bias component (Table 9). The magnitude of the MB in Table 9 was generally similar to that in

Table 7. Model evaluation using Angus data from data set 3 (McKiernan et al., 2005)

Item	Model					
	A	B	C	D	E	F
Mean observed, mm	3.59	3.59	3.59	3.59	3.59	3.59
Mean predicted, mm	4.81	4.15	4.15	3.61	3.44	3.55
Mean bias, mm	−1.23	−0.56	−0.56	−0.02	0.14	0.04
P-value[1]	<0.01	<0.01	<0.01	0.73	0.01	0.53
MSEP[2]						
RMSEP	1.53	0.97	0.97	0.92	0.93	0.91
Bias, %	64.28	33.42	33.42	0.05	2.37	0.16
Slope, %	3.29	0.26	0.26	19.39	8.17	14.13
Random, %	32.44	66.32	66.32	80.57	89.46	85.71

[1]Paired t-test of mean bias.

[2]MSEP = mean square prediction error; bias = MSEP decomposed into error attributable to overall bias of prediction; slope = MSEP decomposed into error attributable to deviation of the regression slope from unity; random = MSEP decomposed into error attributable to the random variation; RMSEP = root MSEP.

Table 8. Model evaluation using Brahman data from data set 2 (Burrow et al., 2003; Burrow and Bindon, 2005)

Item	Model					
	A	B	C	D	E	F
Mean observed, mm	3.83	3.83	3.83	3.83	3.83	3.83
Mean predicted, mm	3.79	4.05	3.97	3.78	3.94	3.81
Mean bias, mm	0.04	−0.22	−0.14	0.05	−0.11	0.02
P-value[1]	<0.01	<0.01	<0.01	<0.01	<0.01	0.10
MSEP[2]						
RMSEP	1.30	1.29	1.27	1.23	1.37	1.29
Bias, %	0.10	3.03	1.15	0.15	0.60	0.04
Slope, %	9.51	2.62	0.11	7.22	4.21	7.05
Random, %	90.39	94.35	98.73	92.63	95.19	92.91

[1]Paired t-test of mean bias.

[2]MSEP = mean square prediction error; bias = MSEP decomposed into error attributable to overall bias of prediction; slope = MSEP decomposed into error attributable to deviation of the regression slope from unity; random = MSEP decomposed into error attributable to the random variation; RMSEP = root MSEP.

Table 8, but the RMSEP tended to be smaller in magnitude.

The Tropical Composite data from data set 2 tested the transferability of models to tropical and temperate crossbreeds. The MB in Table 10 indicates that all models tended to overpredict P8FT. Model C had the smallest MB, followed by model D, with model E having the largest. Models A, B, and C had the smallest MB but similar RMSEP, suggesting they were the most accurate, whereas models E and F were the least accurate. Decomposition of the MSEP suggested that the majority of error for all models was contained in the random component. Models B, E, and F contained the greatest proportions of error in the bias component, with model A having the greatest amount of error in the slope component, although not dramatically large (Table 10).

The model evaluations presented in Tables 11 and 12 were conducted with BrT that were not present in the model development data set [i.e., crossbreds with Continental (Charolais and Limousin) and Japanese (Red and Black Wagyu) sires] to test the transferability of the regressions to other *B. taurus* BrT. The MB in Table 11 indicates that all models tended to overpredict P8FT, with model A making the largest overpredictions. The RMSEP revealed that models B and C were the most accurate, whereas model E was the least accurate. The decomposition of MSEP revealed that models A, B, and C had a greater proportion of error contained in the bias component, whereas the other 3 models had some error contained in the slope component. The random component of all models contained the largest amount of error.

In contrast to the results presented in Table 11, the MB in Table 12 indicates that most models tended to make underpredictions of P8FT in crossbred animals from Japanese sires. The RMSEP in Table 12 suggests that models E and F were the least accurate and model B had the greatest accuracy. The remaining models had slightly less accuracy than model B. Decomposition of MSEP indicated that most errors in the models were contained in the random component. Models A, D, and

Table 9. Model evaluation using data from crossbred animals with temperate[1] sires from data set 3 (McKiernan et al., 2005)

Item	Model					
	A	B	C	D	E	F
Mean observed, mm	3.57	3.57	3.57	3.57	3.57	3.57
Mean predicted, mm	4.13	3.68	3.66	3.51	3.46	3.45
Mean bias, mm	−0.56	−0.11	−0.09	0.06	0.11	0.12
P-value[2]	<0.01	<0.01	0.01	0.09	<0.01	<0.01
MSEP[3]						
RMSEP	1.16	1.03	1.04	1.11	1.28	1.19
Bias, %	23.47	1.22	0.71	0.32	0.75	1.01
Slope, %	1.44	3.69	6.99	2.20	2.36	3.16
Random, %	75.09	95.09	92.31	97.48	96.89	95.84

[1]Temperate: 3 genetic lines of Angus.

[2]Paired t-test of mean bias.

[3]MSEP = mean square prediction error; bias = MSEP decomposed into error attributable to overall bias of prediction; slope = MSEP decomposed into error attributable to deviation of the regression slope from unity; random = MSEP decomposed into error attributable to the random variation; RMSEP = root MSEP.

Table 10. Model evaluation using Tropical Composite[1] data from data set 2 (Burrow et al., 2003; Burrow and Bindon, 2005)

	Model					
Item	A	B	C	D	E	F
Mean observed, mm	3.63	3.63	3.63	3.63	3.63	3.63
Mean predicted, mm	3.92	3.98	3.83	3.89	4.21	4.07
Mean bias, mm	−0.29	−0.35	−0.20	−0.27	−0.58	−0.44
P-value[2]	<0.01	<0.01	<0.01	<0.01	<0.01	<0.01
MSEP[3]						
RMSEP	1.23	1.22	1.22	1.30	1.59	1.46
Bias, %	5.69	8.38	2.73	4.17	13.52	9.08
Slope, %	5.06	0.99	3.57	3.91	0.94	3.27
Random, %	89.25	90.63	93.69	91.92	85.54	87.66

[1]Tropical Composite: combinations of Belmont Red, Charbray, Santa Gertrudis, Senepol, and Brahman breeds.

[2]Paired t-test of mean bias.

[3]MSEP = mean square prediction error; bias = MSEP decomposed into error attributable to overall bias of prediction; slope = MSEP decomposed into error attributable to deviation of the regression slope from unity; random = MSEP decomposed into error attributable to the random variation; RMSEP = root MSEP.

Table 11. Model evaluation using data from crossbred animals with Continental[1] sires from data set 3 (McKiernan et al., 2005)

	Model					
Item	A	B	C	D	E	F
Mean observed, mm	2.52	2.52	2.52	2.52	2.52	2.52
Mean predicted, mm	3.23	2.99	2.98	2.89	2.76	2.82
Mean bias, mm	−0.71	−0.47	−0.46	−0.37	−0.24	−0.29
P-value[2]	<0.01	<0.01	<0.01	<0.01	<0.01	<0.01
MSEP[3]						
RMSEP	1.30	1.20	1.17	1.25	1.35	1.29
Bias, %	29.76	15.06	15.64	8.57	3.01	5.19
Slope, %	6.98	0.20	0	15.59	14.68	16.63
Random, %	63.26	84.74	84.36	75.84	82.31	78.18

[1]Continental: Charolais, Limousin, and Belgian Blue.

[2]Paired t-test of mean bias.

[3]MSEP = mean square prediction error; bias = MSEP decomposed into error attributable to overall bias of prediction; slope = MSEP decomposed into error attributable to deviation of the regression slope from unity; random = MSEP decomposed into error attributable to the random variation; RMSEP = root MSEP.

Table 12. Model evaluation using data from crossbred animals with Japanese[1] sires from data set 3 (McKiernan et al., 2005)

	Model					
Item	A	B	C	D	E	F
Mean observed, mm	3.50	3.50	3.50	3.50	3.50	3.50
Mean predicted, mm	3.90	3.52	3.50	3.10	3.27	3.13
Mean bias, mm	−0.40	−0.01	0.01	0.40	0.23	0.37
P-value[2]	<0.01	0.80	0.92	<0.01	<0.01	<0.01
MSEP[3]						
RMSEP	1.09	1.05	1.07	1.14	1.19	1.19
Bias, %	13.05	0.02	0	12.48	3.70	9.65
Slope, %	0.17	8.72	10.86	0.51	1.05	1.42
Random, %	86.79	91.26	89.14	87.01	95.26	88.93

[1]Japanese: Black and Red Wagyu.

[2]Paired t-test of mean bias.

[3]MSEP = mean square prediction error; bias = MSEP decomposed into error attributable to overall bias of prediction; slope = MSEP decomposed into error attributable to deviation of the regression slope from unity; random = MSEP decomposed into error attributable to the random variation; RMSEP = root MSEP.

F had greater quantities of error in the bias component, whereas models B and C had slightly greater quantities of error in the slope component.

DISCUSSION

The key to profitability and sustainability of any meat production system is to produce what the consumer demands consistently and cost effectively (Egan et al., 2001; McPhee et al., 2006). In Australia, consumers prefer approximately 2 mm of fat cover when purchasing steaks (Egan et al., 2001) and commonly remove most traces of visible fat before cooking and consuming it (Baghurst, 2004). Japanese consumers purchase meat that has been trimmed to a minimal fat covering (Egan et al., 2001), and US consumers consider leanness an important attribute when purchasing meat (Jacobs et al., 1977; Savell et al., 1989; Killinger et al., 2004). Thus, Australian, Japanese, and US consumers are concerned with the leanness and fat cover of meat, and it has been demonstrated that overfat meat is a difficult product to sell (Egan et al., 2001). Within Australia, beef producers have not generally been effective at meeting the requirements of all consumers; a recent study involving 20,000 animals demonstrated that between 16 and 70% of cattle undergoing either short (100 d on feed) or long (>220 d on feed) feeding programs were unable to meet market specifications, depending on what markets and which specifications were being examined (Slack-Smith et al., 2009).

The influence that BrT and sex have on fat partitioning is well established (Kempster et al., 1976; Seideman et al., 1982; Hopkins et al., 1993) and is supported by the findings of this study. This study found that within sex, tropically adapted cattle had greater P8FT at any given RFT compared with temperate cattle, in agreement with the results of Yokoo et al. (2008). Sex has been shown to have important effects on the quantity of fat deposited in different depots in both sheep (Butterfield et al., 1985; Thompson et al., 1987) and cattle (Jones et al., 1990). Generally, females are expected to be fatter than castrate males at the same BW, which in turn are fatter than intact males (Seideman et al., 1982). This study found in general that within BrT, heifers had greater P8FT at any given RFT compared with steers.

Carcass weight has been found to influence the distribution of fat within the subcutaneous depot (Phillips et al., 1984); thus, a relationship exists between fat depths at the P8 rump and the 12th-13th-rib sites (Hopkins et al., 1993). In this study, the relationship between P8FT and RFT was influenced by BW. In contrast to the results of Phillips et al. (1984), age was found to have significant effects on the relationship between P8FT and RFT when fitted simultaneously with BW and when fitted independently of BW. Breed type was found to be nonsignificant in the regressions that contained BW (models D and F); however, BrT was significant when

age was fitted independently of BW. This finding suggests that age has different effects on the relationship between P8FT and RFT in different BrT, which places limitations on the capacity for age to be used as an indicator of maturity.

Subcutaneous fat has been shown to be more actively mobilized than other fat depots (Butler-Hogg et al., 1985), and given that nutritional supply varies across time, seasonal influences would be considered to have important effects on the relationship between P8FT and RFT. Seasonal influences and, more specifically, nutritional variation across time are one factor that has not been considered in this study but that has been shown to have large effects on measurements within fat depots (Hopkins et al., 1993). These types of effects could also be of greater importance in animals that have been extensively grazed rather than those intensively fed in feedlots, primarily because of the consistency of nutrient supply.

The purpose of this research was to develop a relationship between P8FT and RFT accurate enough to be used for phenotypic prediction. Model evaluation revealed that, in general, models D and B consistently made the most accurate predictions of P8FT. The accuracy of predictions made by model E fluctuated dramatically between evaluations, and thus between BrT. In many cases, the RMSEP were within, or close to, the limits (≤ 1.5 mm) of the proficiency tests used to accredit ultrasound scanners in Australia (Upton et al., 1999). Model A was the major exception when predicting P8FT for RFI cattle from data set 1 and Angus cattle from data set 3, in which the RMSEP were greater than the proficiency test requirements. Model E also had an RMSEP of <1.5 mm when predicting P8FT in Tropical Composite cattle from data set 2.

An interesting outcome from the model evaluation is the less accurate performance of model F, which included all available information concerning sex, breed, BW, age, and RFT. Even though this model had the greatest R^2_{adj} (0.87) and smallest SE (0.013) when fitting the CRC straight breeding data, the presence of both age and BW had negative effects on the accuracy of P8FT predictions for evaluation data sets. This outcome could be a consequence of both BW and age acting as pseudo indicators of animal maturity and having antagonistic effects on P8FT predictions.

Comparison of model evaluation results for RFI cattle from data set 1 and the Angus and temperate crossbred cattle from data set 3 suggests that all models were less accurate for the RFI cattle. A possible explanation could be the genetic background of the RFI cattle. The steers were derived from a population that had been selected for divergence in RFI (Arthur et al., 2001) for 2.4 generations. Positive correlations have been found between RFI and subcutaneous fat deposition in this population after one generation of selection (Richardson et al., 2001), which resulted in different amounts of subcutaneous fat deposition in the selection

lines (McDonagh et al., 2001). Such correlated changes in fat distribution from selection would not have been accounted for in the unselected data used for model development. However, a possible alternative explanation could be that the methane production study conducted by Hegarty et al. (2005), in which these animals were exposed to 15 d of methane sampling, caused the animals to utilize subcutaneous fat from different locations (i.e., rib vs. rump) differentially, possibly because of excessive handling, leading to increased stress.

The accuracy of most models when predicting P8FT of crossbred animals is an encouraging outcome. This result indicates that the models could be used to predict P8FT with a high degree of confidence, particularly for crossbred animals with temperate sires. A tendency existed for all models to make overpredictions for Tropical Composites and for crossbred cattle with Continental sires. Crossbred cattle with Japanese sires were most accurately predicted when only sex and BrT were fitted, in preference to age and BW. However, model evaluation for crossbred animals with sires of Continental and Japanese BrT was conducted using data with small ranges of P8FT and RFT measurements. Thus, caution should be taken when using these models to predict P8FT for these BrT, particularly when RFT is greater than 15 mm.

Breed, sex, and BW were shown to have important influences on the relationship between P8FT and RFT. Model evaluation demonstrated that models B, C, and D, which included combinations of BrT, sex, and BW, consistently had the greatest predictive accuracies and the smallest prediction bias. In most evaluations using independent data sets, these models had RMSEP that were less than the proficiency requirements of ultrasound scanners in Australia. This study has developed and evaluated models for predicting P8FT from RFT in steers and heifers from both temperate and tropical breeds that can be used in the phenotypic prediction of fat deposition.

The models developed in this study can be used to explore the relationships between different sites of subcutaneous fat deposition within animals (i.e., rib vs. rump). The models developed and evaluated in this study have the capacity to be used in association with growth models to predict P8FT from RFT in steers and heifers from both temperate and tropical breeds. The DGM, in conjunction with model D developed in this study, have been used as the driver behind the development of a decision support tool called BeefSpecs (Oddy et al., 2008). BeefSpecs is a practical tool that can be used in the field to predict P8FT at a predetermined slaughter weight and can therefore assist producers in making decisions to help meet specifications for both Australian domestic and other international markets.

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