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Predicting carcass composition of terminal sire sheep using X-ray computed tomography

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Abstract

The best means to utilize X-ray computed tomography (CT) and ultrasound to predict carcass lean, fat and bone weights *in vivo* in terminal sire sheep were tested. Data on 160 lambs from three breeds were considered: 50 Suffolk males, 50 Suffolk females, 40 Texel males and 20 Charollais males. One-fifth of the lambs within each breed and sex group were slaughtered at each of 14, 18 and 22 weeks of age and the remaining two-fifths at 26 weeks. Carcasses were dissected into lean, fat and bone weights. Prior to slaughter all lambs were CT scanned, with cross-sectional scans taken at seven sites along the body (ischium, hip, mid shaft of femur, 2nd and 5th lumbar vertebrae and 6th and 8th thoracic vertebrae), and ultrasound scanned at the 3rd lumbar vertebra and 13th rib. A set of three CT scans that reliably predicted carcass lean, fat and bone weights was identified which included a scan in each of the three main carcass regions: ischium in the hind leg, 5th lumbar vertebra in the loin and 8th thoracic vertebra in the shoulder. Breed and sex affected the intercepts of the prediction equations but not their slopes. Therefore, a minimal set of equations is likely to be sufficient to predict tissue weights, at least within terminal sire sheep breeds. Equations derived showed high degrees of fit to the data with R^2 values of 0.924, 0.978 and 0.830 for lean, fat and bone weights, respectively, when predicted using CT alone, and 0.589 and 0.857 for lean and fat weights, respectively, when predicted using ultrasound alone. Using live weight in addition to CT information only improved prediction accuracy slightly for lean (0.966) and fat (0.986) although more substantially for bone (0.925). Where live and tissue weights are considered contemporaneously in genetic evaluations, excluding live weight from prediction may therefore be preferable to avoid collinearity among weight measures.

Keywords: carcass composition, computed tomography, prediction, scanning, sheep.

Introduction

The well documented decline in lamb consumption in many western countries in the past few decades has been attributed in part to consumer perception of lamb as an excessively fat meat (Kempster, 1983; Ward *et al.*, 1995) with lamb fat perceived as being greasy and unpalatable (Woodward and Wheelock, 1990). Consumers prefer leaner meat than that provided by the average lamb carcass, a preference thought to be due to taste, wastage and health concerns (Woodward and Wheelock, 1990).

Ultrasound scanning has been used widely in sheep breeding programmes to address the problem of over-fatness in lamb by genetically improving the rate of lean tissue growth (Simm, 1994; Stanford *et al.*, 1998). X-ray computed tomography (CT) scanning can provide more accurate information on body composition in sheep *in vivo* than ultrasound (Sehested, 1984; Young *et al.*, 1996 and 2001)

and thus has the potential to improve rates of genetic gain from selection by as much as 50% when used in combination with ultrasound scanning (Simm and Dingwall, 1989; Jopson *et al.*, 1995). Opportunities offered by CT have in fact been incorporated into sheep breeding programmes in New Zealand, the UK and Norway where information from CT has been included in genetic evaluations (Nicoll *et al.*, 1997; Young *et al.*, 2001; Vangen *et al.*, 2003).

Although more accurate, CT scanning has disadvantages relative to ultrasound scanning. Firstly, CT is much more expensive than ultrasound. Secondly, CT scanning units are typically situated at fixed locations, requiring transport of animals to and from the CT facility, whereas ultrasound is readily portable. Therefore, CT is likely to be most economically beneficial to the sheep industry when applied in a two-stage selection programme where initial screening of selection candidates is done using ultrasound

(Jopson *et al.*, 1995 and 1997; Lewis and Simm, 2002). To design a two-stage selection programme of this type requires information on the accuracy of both ultrasound and CT scanning in predicting carcass composition in the breed types to be selected (Jopson *et al.*, 1995).

CT scanning can produce large amounts of information since cross-sectional scans can be collected at many anatomical positions along the body of each animal. However, collection and interpretation of CT images is costly. Therefore, in order for CT scanning to be used economically in selection programmes, a scanning protocol is needed that utilizes as few scans as possible without compromising the accuracy of prediction of carcass tissue weights. It is also important to consider which measures should be included in a prediction equation. Live weight is strongly related to carcass weight; in combination with CT or ultrasound scan information, live weight is therefore useful for predicting weights of carcass components, namely lean, fat and bone (Lambe *et al.*, 2003; Jones *et al.*, 2004). However, if live weight is included together with predicted tissue weights in a genetic evaluation, the collinearity among such measures may confuse or limit their interpretation (McCullagh and Nelder, 1989). Since tissue weights are used in genetic evaluations it was of interest to use CT to predict tissue weights rather than proportions although tissue proportions are a useful measure of carcass composition.

This study aimed to determine the 'best' set of cross-sectional CT scans to predict carcass lean, fat and bone weights in terminal sire (meat) sheep and generate equations that use CT information to predict carcass tissue weights. In doing so, we considered the value of ultrasound scan information either in addition to or instead of CT for predicting tissue weights. In these analyses the hypothesis that a single equation was adequate to predict tissue weights in different breeds, sexes and genetic selection lines was tested. In addition, the value of including live weight in predictions was evaluated.

Material and methods

Animals and management

An experiment was conducted at the Scottish Agricultural College (SAC) in 1997 where lambs of three breeds were subject to serial slaughter and dissection to obtain detailed information on carcass composition at 14, 18, 22 and 26 weeks of age. There were 50 male Suffolk and 50 female Suffolk, 40 male Texel and 20 male Charollais lambs. The Suffolk lambs were obtained from the SAC Suffolk flock and consisted of equal numbers from a line selected on an index to improve 'lean tissue growth' (LTG) and from a line that was unselected (control). An equal number of male and female lambs were considered from each line. Suffolk lambs used reflected gains from 9 years of selection, in which time the LTG line had diverged from the control line by +4.9 kg in live weight, -1.1 mm in ultrasound fat depth and +2.8 mm in ultrasound muscle depth. Further details of the SAC Suffolk flock are given by Simm *et al.* (2002). Texel lambs came from the ANTUR flock at the Institute of Rural Sciences,

Aberystwyth and consisted of equal numbers from its LTG and high leg conformation (HC) lines. Lambs of the HC line were expected to have 0.4 kg more lean in the carcass side and higher lean:bone ratio and carcass lean proportion than LTG line lambs at a constant slaughter weight. Further details of the ANTUR flock are given by Wolf *et al.* (2001). Charollais lambs came from two commercial pedigree flocks that were members of the Charollais sire referencing scheme. Selection in the Charollais scheme was based on a LTG index.

Suffolk lambs were born at the Woodhouselee SAC farm near Penicuik, Scotland and weaned at 8 weeks of age. For 1 to 2 weeks prior to weaning they had been offered *ad libitum* access to a high quality pelleted food with 12.4 MJ metabolizable energy and 178 g crude protein per kg dry matter. Texel and Charollais lambs were purchased at around 8 weeks of age, transferred to Woodhouselee and gradually introduced to the same food whilst also having *ad libitum* access to hay during the adjustment period. Lambs were penned in groups by breed and sex. Further details about the animals used in this study and their management are given by Jones *et al.* (2002b).

Slaughter procedure and measurements

Combinations of breed, sex and genetic line were used to define seven groups of animals as shown in Table 1. One-fifth of the lambs in each of the seven groups were slaughtered at each of 14, 18 and 22 weeks of age and the remaining two-fifths at 26 weeks of age. Prior to slaughter all lambs were weighed and scanned using ultrasound and CT. After slaughter, carcasses were chilled for 24 h and then weighed before being split longitudinally into two carcass sides. The carcass sides (excluding kidney knob, channel and thoracic fat) were then frozen. Following thawing, the left carcass side was separated into eight joints as described by Cuthbertson *et al.* (1972): leg, chump, loin, breast, best end, middle neck, shoulder and neck. Each joint was then dissected into lean, fat (subcutaneous and intermuscular), bone (vertebral and other) and waste.

Ultrasound measurements

All lambs were ultrasound scanned 24 to 72 h prior to slaughter on their right side at two sites (3rd lumbar vertebrae and 13th rib) using a Vetscan real-time B-mode ultrasonic scanner with a 3.5 MHz transducer. Muscle depth was measured vertically at the deepest point at each site. Four fat depths were measured on each scan: the first above the boundary between *m. longissimus thoracis et lumborum* and the vertebral spinous process, and the others at progressively lateral intervals of 1.88 cm. This resulted in fat depths that, for most animals, spanned the *longissimus* muscle. Measurement resolution of the ultrasound scanner was 1 mm.

X-ray computed tomography measurements

Lambs scheduled for slaughter at each age point were CT scanned 24 to 72 h prior to slaughter. Two longitudinal topograms (Figure 1a) were taken to identify anatomical

Predicting carcass composition using CT scanning

Table 1 Mean live weights and their standard deviations (kg) for lambs of each breed, sex and line group slaughtered at each age

Breed	Sex [†]	Line [§]	Age at slaughter [†]							
			14		18		22		26	
			Mean	s.d.	Mean	s.d.	Mean	s.d.	Mean	s.d.
Charollais	M		36.3	5.82	47.0	1.96	56.5	3.99	66.5	6.48
Suffolk	F	C	34.0	5.45	43.5	11.53	58.9	8.43	63.4	8.26
Suffolk	F	LTG	36.4	9.08	50.7	5.69	67.7	4.09	73.0	7.36
Suffolk	M	C	40.3	4.67	46.9	4.34	61.1	1.28	68.4	7.53
Suffolk	M	LTG	46.6	4.18	60.5	4.34	63.5	6.13	84.1	5.00
Texel	M	HC	24.9	9.08	44.1	5.21	42.3	7.96	50.0	6.93
Texel	M	LTG	31.7	5.86	41.1	7.86	51.6	7.08	54.4	6.35

[†] There were five lambs in each Suffolk group, and four lambs in each Texel and Charollais group, at each of 14, 18 and 22 weeks. At 26 weeks there were 10 lambs in each Suffolk group, and eight lambs in each Texel and Charollais group, totalling 160 lambs across all groups and ages.

[‡] M refers to male lambs and F to female lambs.

[§] Line refers to the genetic selection line. The Charollais were all selected on a lean tissue growth index (LTG). Within the Suffolk, LTG is the lean tissue growth rate selection line and C is the control line for this selection programme. Within the Texel, HC is the high leg conformation selection line and LTG is the lean tissue growth rate selection line.

locations for the seven sites along the body (ischium, femur, hip, 5th and 2nd lumbar vertebrae (LV5 and LV2, respectively) and 8th and 6th thoracic vertebrae (TV8 and TV6, respectively) where cross-sectional tomograms were taken (Figure 1b). A full description of the scanning protocol is given in Jones *et al.* (2002a). Images obtained using the CT scanner were analysed using the Sheep Tomogram Analysis Routines software (STAR, version 0.6), which was developed jointly by Biomathematics and Statistics Scotland (BioSS) and SAC. This was used to determine total areas

of fat, lean and bone in each image, with a measurement resolution of 2 mm.

Statistical methods

Mean live weights for the seven groups at each age are shown in Table 1. Within each age group in the experiment the average coefficient of variation was 13.2%. Considerable overlap in live weight between contiguous age groups, also noted by Jones *et al.* (2002b), led us to ignore age in

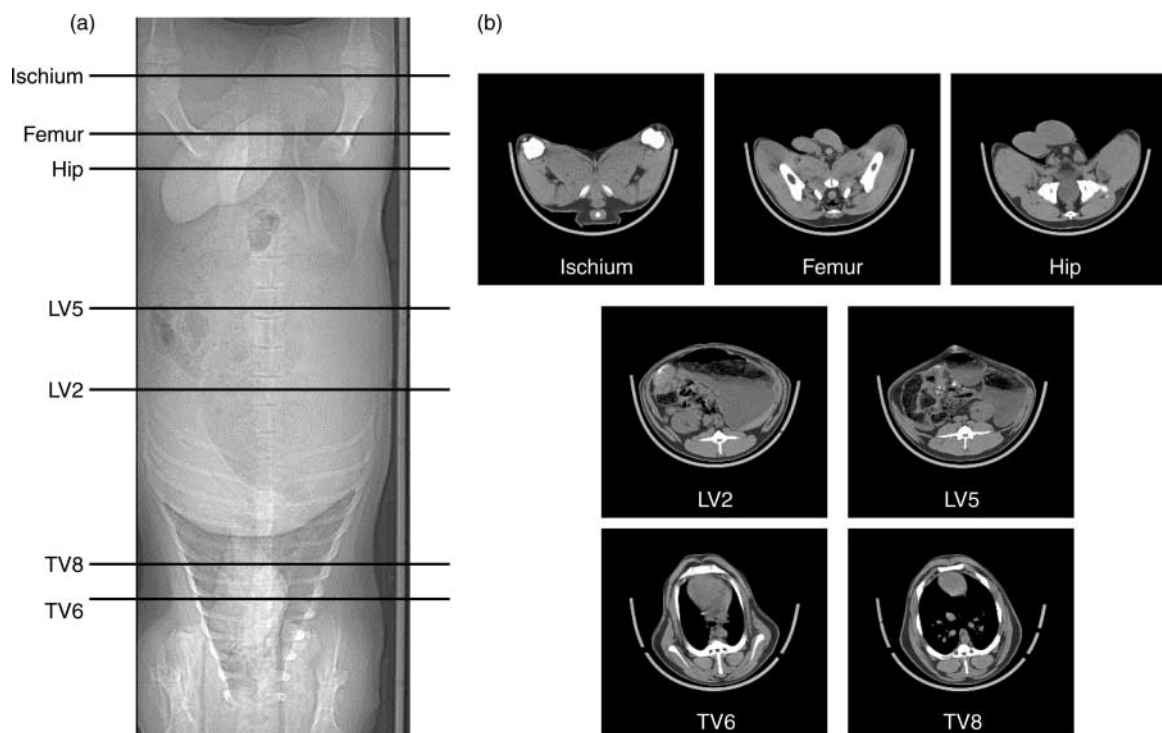


Figure 1 (a) Longitudinal X-ray computed tomography (CT) scan (topogram) showing the dorso-ventral view of the skeleton with positions marked for the seven cross-sectional tomograms; ischium, femur, hip, 5th and 2nd lumbar vertebrae (LV5 and LV2) and 8th and 6th thoracic vertebrae (TV8 and TV6). (b) The seven cross-sectional CT scans taken. Fat areas are shown as dark grey, lean as light grey, bone as white and air as black.

all analyses and use only live weight as a possible predictor. To describe the data, means for each group of lambs were calculated for live weight, carcass weight and tissue weights (Table 2). Overall means of tissue areas in each of the seven cross-sectional CT scans and ultrasonically determined muscle and fat depths were also calculated (Table 3).

All measurements were log transformed using natural logarithms (\log_e). This equalized variances across the range of the data and made relationships between variables more nearly linear (example shown in Figure 2). An added advantage of using the log transformation is that the residual standard deviation (r.s.d.) of a regression equation is a proportional measure.

Statistical analysis was conducted in four stages. Firstly muscle and fat depths from ultrasound scanning were used, both with and without live weight, to predict dissected carcass lean and fat weights. Secondly, lean, fat and bone areas from the CT scans, both with and without live weight, were used to predict corresponding dissected tissue weights. Thirdly, we compared effectiveness of ultrasound *versus* CT in predicting carcass tissue weights. Lastly, usefulness of adding ultrasound information to CT information in predicting carcass tissue weights was tested.

The general model used in the analyses was:

$$y_{ij} = a + g_j + \beta_j \mathbf{D}_{ij} + c_j LW_{ij} + \varepsilon_{ij} \quad (1)$$

where y_{ij} is the log of dissected weight of tissue in the carcass for lamb i ($i = 1, 2, 3, \dots, 160$) that was in group g ($j = 1, 2, \dots, 7$), a the intercept, β a vector of the linear regression coefficients for the logs of predictor variables for group j , \mathbf{D} a matrix of the logs of predictor variables appropriate to the analysis, c the regression coefficient of the log of live weight for group j , LW the log of live weight, when included, and ε the residual error. Predictor variables included in matrix \mathbf{D} will be specified below at each stage of the analysis.

Initial analysis was performed excluding the effect of group. Group effects were then included in the model as (i) an effect on the intercept only or (ii) an effect on both intercept and slope. Live weight was also included or excluded as a predictor among these permutations. The different models were compared for their goodness-of-fit using adjusted R -squared (R^2) values and r.s.d.

Predicting tissue weights using ultrasound scanning. Logs of carcass fat and lean weights were regressed on logs of ultrasound fat and muscle depths respectively using model 1. This was done for each tissue, defining the \mathbf{D} matrix to include each ultrasound scan site separately, the two scan sites simultaneously, or the average of the two scan sites.

Regression of log tissue weight on log of the scan site average provided the best fit, and thereafter that average, defined as ultrasound, was used as the predictor in the \mathbf{D} matrix in model 1. The effect of including the log of live weight as a predictor in addition to ultrasound was then tested without including the effect of group. Subsequently, group effect was also fitted in the model with firstly the intercept being allowed to differ for the seven different groups, and secondly with both intercept and slope being allowed to differ for the seven different groups. Scenarios including and excluding live weight as a predictor were considered.

When fitting the effect of the seven groups significantly improved model fit, additional analyses were undertaken to determine which breed, sex and genetic line within the group effect explained its significance. This was done by considering subsets of the data: the effect of sex was tested using only data on Suffolk lambs (100 lambs) and the effect of breed was tested using only data on male lambs (110 lambs). There were no significant effects of genetic line in prediction of carcass tissue weights from ultrasound. Group effects, where present, affected only the value of the intercept of the prediction equation and not the slope.

To generate a set of equations to predict carcass tissue weights from the ultrasound data, a regression was run for each tissue using data for all lambs and including only group effects that had been significant in previous analyses for that tissue. This was done both with and without live weight. Coefficients for predictor variables, a general intercept and breed and/or sex effects were obtained from this regression to construct the prediction equations.

Predicting tissue weights using CT scanning. Correlations between tissue areas in the seven reference scans were calculated for each of lean, fat and bone. Kendall's coefficient of concordance values were also calculated between the seven measurements of each tissue (Genstat 6 Committee, 2002). Only tissue areas corresponding to the specific tissue being considered were used to predict a tissue weight, e.g. only fat areas were used to predict fat

Table 2 Group means of live weight, carcass weight and dissected carcass tissue weights for the whole carcass (kg) (mean age of 21.2 weeks)

Breed	Sex [†]	Line [†]	Live		Carcass		Lean		Fat		Bone	
			Mean	s.d.	Mean	s.d.	Mean	s.d.	Mean	s.d.	Mean	s.d.
Charollais	M		54.6	12.94	26.9	7.54	14.9	3.16	7.65	3.75	4.16	0.837
Suffolk	F	C	52.6	14.51	23.9	7.08	11.9	2.81	8.37	3.63	3.44	0.686
Suffolk	F	LTG	60.2	16.09	26.9	8.34	13.7	3.52	8.65	4.11	4.31	0.905
Suffolk	M	C	57.0	12.86	25.8	6.27	13.6	2.57	8.18	3.30	3.89	0.589
Suffolk	M	LTG	67.7	15.51	30.8	7.74	16.4	3.29	9.29	3.93	4.89	0.830
Texel	M	HC	42.3	11.60	20.1	6.00	12.8	3.34	4.18	2.11	2.95	0.697
Texel	M	LTG	46.7	11.03	22.6	5.76	14.4	3.26	4.47	2.00	3.51	0.657

[†] As explained in Table 1.

Predicting carcass composition using CT scanning

Table 3 Means of ultrasound muscle (lean) and fat depths (mm) at the 3rd lumbar vertebra (3) and 13th rib (13) and X-ray computed tomography (CT)-determined lean, fat and bone areas (mm²) in each of the seven cross-sectional scans (mean age of 21.2 weeks)

	Lean		Fat		Bone	
	Mean	s.d.	Mean	s.d.	Mean	s.d.
Ultrasound						
3	28.0	3.69	5.89	2.61		
13	31.0	4.38	5.46	2.34		
CT [†]						
Ischium	29838	4242	9113	4242	3626	640
Femur	29327	4412	8256	4238	5249	1432
Hip	25876	4258	6550	3438	4921	1175
LV5	12373	2188	6354	3419	1098	214
LV2	12596	2306	6554	3569	1061	251
TV8	13254	2250	10729	5625	4573	991
TV6	16140	2747	12161	5668	4705	962

[†] The seven cross-sectional CT scans were positioned according to skeletal landmarks of ischium, femur, hip, 5th and 2nd lumbar vertebrae (LV5 and LV2) and 8th and 6th thoracic vertebrae (TV8 and TV6).

weight. Best subsets regression was performed to determine which single, pair and trio of the seven CT scans were most useful in predicting each tissue weight (Genstat 6 Committee, 2002).

It is sensible in practice to have a single set of CT scans to predict all three tissues. It is also sensible to have a small number of CT scans to reduce time and costs associated with the scanning procedure and image analysis. Therefore, using the results of the best subsets regression, a subset of scans was chosen for use in formulating prediction equations for all three tissues. The criteria used to choose those three scan sites were: (i) they were good predictors of the three tissue weights, and (ii) collectively they represent all of the main carcass areas (hind leg, loin and shoulder). The scans chosen were ischium (in the hind leg), LV5 (in the loin area) and TV8 (in the shoulder area). These

scans were the same three as found best in a preliminary analysis of the same data (Young *et al.*, 2001) and have been used in other CT scanning experiments with meat sheep at the SAC-BioSS CT scanning unit in Edinburgh.

Regressions without group effects were run for the logs of lean, fat and bone weight, with the **D** matrix in model 1 including the respective tissue areas from the three chosen CT scans. These were repeated adding log of live weight to the model. The effect of group was then tested by allowing firstly, the intercept to differ between groups, and secondly, both the intercept and slope to differ between groups. Where fitting the effect of the seven groups significantly improved fit of the regression, the effect of sex was tested using only Suffolk data, and the effect of breed tested using only male data. There were no significant effects of line on prediction of carcass tissue weight from CT information. As with ultrasound, where group effects were identified, only intercepts differed significantly between groups.

To generate a minimum set of equations that could be used to predict carcass tissue weights from the CT data, a regression was run for each tissue using the data for all lambs and including the effects that had been significant in previous analyses for that tissue. This was done both with and without live weight. Coefficients for tissue areas in the ischium, LV5 and TV8 scans and for live weight, a general intercept and breed and/or sex effects were obtained from this regression to derive the prediction equation. Predicted tissue weights on a log scale were compared with the log of actual dissected tissue weights. Additionally, antilogs were taken of predicted tissue weights and compared with actual dissected tissue weights on a linear scale.

Comparing the effectiveness of ultrasound and CT in prediction of dissected tissue weights. Firstly, adjusted R^2 and r.s.d. values from the best prediction equations formulated for lean and fat weights using ultrasound and CT

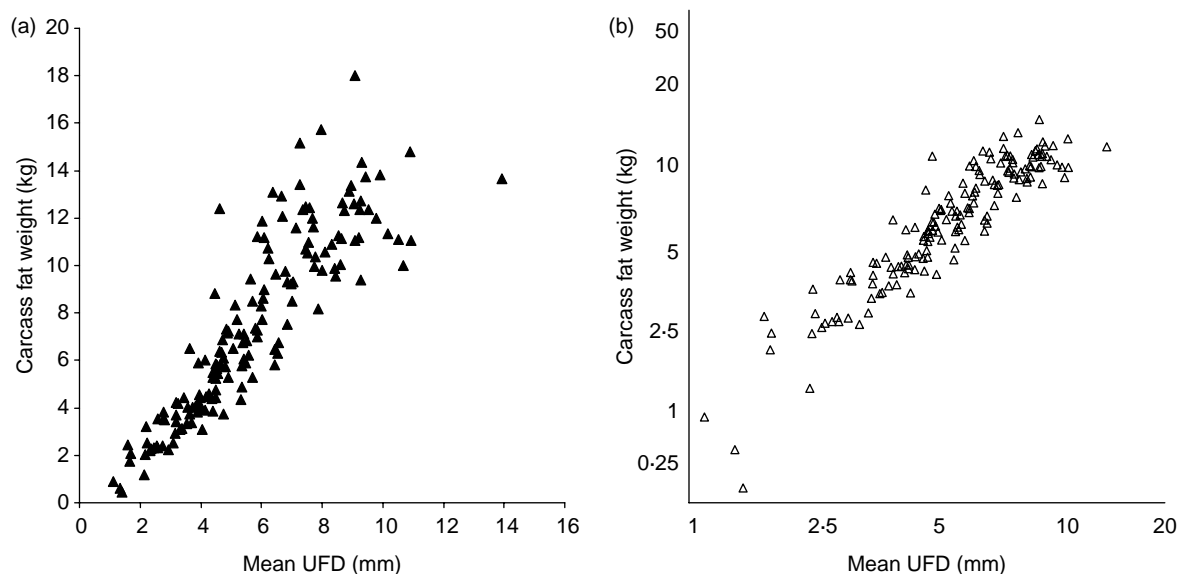


Figure 2 Relationship between carcass fat weight and ultrasound fat depth on (a) linear scales and (b) log scales showing how the log transformations equalized variances across the range of the data.

were compared. Secondly, improvement in prediction of lean and fat weights by adding mean ultrasound lean and fat depths to the CT information was examined by formulating a prediction equation including both ultrasound and CT information; adjusted R^2 and r.s.d. obtained from these analyses were then compared with those when tissue weights were predicted from CT alone.

Results

Using ultrasound to predict tissue weights

Muscle depths and weights. Ultrasound muscle depths at the 3rd lumbar vertebra (UMD3) and 13th rib (UMD13) were used to predict carcass muscle weight. The difference between using each of the two measurements alone (R^2 0.456, r.s.d. 0.209 for UMD13 v. R^2 0.409, r.s.d. 0.218 for UMD3) was small. Using both was better than either of the single measurements alone, although not by much (adjusted R^2 0.491, r.s.d. 0.202 for both). Using the mean of the two muscle depths gave an R^2 of 0.494 (r.s.d. 0.201).

Using mean ultrasound muscle depth, the importance of including group and live weight to predict muscle weight was tested (Table 4). Allowing the intercept to differ between groups increased R^2 from 0.494 to 0.589, and reduced r.s.d. from 0.201 to 0.181. Allowing different slopes did not significantly improve fit. Within the Suffolk lambs, males had a higher intercept than females ($P < 0.01$). Within the male lambs, Suffolks had a lower intercept than the Charollais or Texels ($P < 0.01$), as shown in Figure 3.

Using live weight alone to predict carcass lean weight gave an R^2 of 0.804 and an r.s.d. of 0.125. Using both live weight and mean ultrasound muscle depth gave an R^2 of 0.810, and an r.s.d. of 0.123. Allowing different intercepts for groups significantly increased R^2 (0.942) and reduced r.s.d. (0.0681); allowing different slopes gave no significant further improvement. As shown in Table 4, Suffolk lambs had a higher intercept than the Charollais or Texel ($P < 0.001$); there was no significant difference between male and female Suffolk lambs.

Fat depths and weights. Measures of ultrasound fat depth at 3rd lumbar vertebra (UFD3) and 13th rib (UFD13) were used to predict carcass fat weight (Table 4). There was little

difference between using either measure (R^2 0.833, r.s.d. 0.265 for UFD3 v. R^2 0.820, r.s.d. 0.275 for UFD13). Using both measures increased prediction accuracy slightly (adjusted R^2 0.856, r.s.d. 0.246). Using their mean of gave an R^2 of 0.857 (r.s.d. 0.245).

The mean of the two ultrasound fat depths was used to test the importance of group effects and live weight in prediction of fat weight. There were no substantial differences between the seven groups in their intercepts or slopes (Figure 4; Table 4). Adding live weight increased R^2 to 0.956 and reduced r.s.d. to 0.136 but there were still no significant differences between the seven groups. Using live weight alone to predict carcass fat weight gave an R^2 of 0.910 and r.s.d. of 0.194.

Using CT to predict tissue weights

Kendall's coefficients of concordance between the seven CT scan area measurements were 0.871 for lean, 0.974 for fat and 0.521 for bone.

Correlations between fat areas in the different CT scans were large, positive and very highly significant, with an average value of 0.975 (s.d. 0.0119). Highest correlations were between fat areas of adjacent scan sites (0.984); the strength of the correlation decreased slightly with increasing distance between the scans with a lowest value of 0.945.

Correlations between lean areas in different scans were all positive and very highly significant. The average correlation was 0.862 (s.d. 0.0445) with the highest correlations between adjacent scan sites (0.957). The correlations between tissue areas did not differ in a consistent way for scans that were two to six scan sites apart (range of 0.894 to 0.794).

Correlations between bone areas in different scans were all positive and very highly significant. The average correlation was 0.472 (s.d. 0.125). In contrast to fat and lean tissue areas, the highest correlations were between bone tissue areas at the scan sites that were furthest apart, the ischium and the 6th thoracic vertebra (0.652). Apart from this value, the average correlations between bone areas in different scans did not vary consistently with distance between scan sites (range of 0.589 to 0.281).

Table 4 Intercepts and coefficients (s.e. in parentheses) for equations to predict carcass fat and lean weights from the mean of ultrasound muscle or fat depths (as appropriate) at 3rd lumbar vertebra and 13th rib with and without live weight (LW); all variables as log values (where significant group effects exist, adjustments to the intercepts for the groups that differ significantly are shown)

LW included	Tissue	Intercept	Coefficients		Adjustments to intercept [†]		R^2	r.s.d.
			Tissue depth	LW	Suffolk	Female		
No	Lean	-2.8220 (0.3740)	1.6380 (0.1130)				0.589	0.1810
No	Fat	-0.2218 (0.0693)	1.2588 (0.0407)				0.857	0.2450
Yes	Lean	-1.9120 (0.1430)	0.4538 (0.0569)	0.7871 (0.0248)			0.942	0.0681
Yes	Fat	-4.0120 (0.2040)	0.5597 (0.0433)	1.2446 (0.0658)	-0.2252 (0.0120)	-0.1054 (0.0365)	0.956	0.1360

[†] Adjustments to the intercept shown should be added to the general intercept for the prediction equation for a lamb in a given category. For example, a Suffolk lamb would have an intercept of $-2.8220 + -0.1169 = -2.9389$. If the lamb was a female Suffolk, the intercept would be $-2.8220 + -0.1169 + -0.1054 = -3.0443$.

Predicting carcass composition using CT scanning

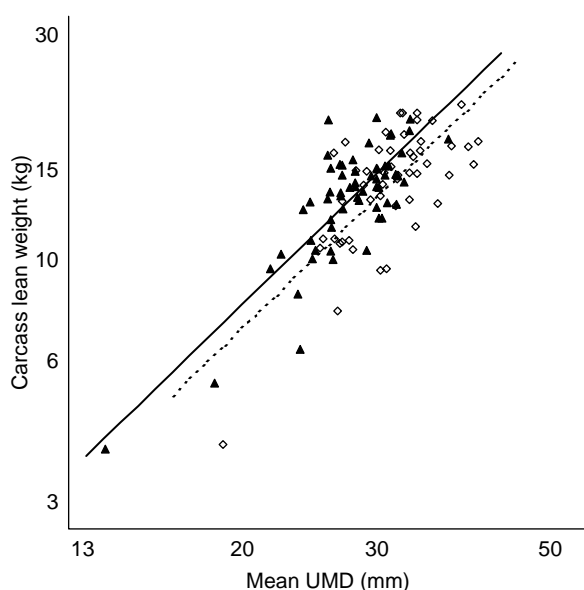


Figure 3 Relationship between carcass muscle weight and the average of ultrasound muscle depth (UMD) at the 3rd lumbar vertebra and 13th rib for male lambs; Suffolk (data \diamond , regression \cdots) and other two breeds (data \blacktriangle , regression —) shown separately.

As expected, higher correlations were found generally between tissue areas in scans grouped in the same region of the body, for example among the ischium, femur and hip scans in the hind leg.

Choice of CT scan sites. Of the lean areas in the seven CT scans, the best single predictor of carcass lean weight was lean area in the ischium scan (R^2 0.890). The best pair of predictors was the lean areas in the ischium and in the femur (R^2 0.920). The best set of three predictors included the lean areas in the ischium, femur and LV5 scans (R^2 0.926). Addition of more predictors did not significantly improve fit. When all seven scans were included in a regression to predict lean weight, only the lean areas of the ischium, femur, LV5 and TV6 scans contributed significantly to the prediction.

Of the seven CT scan fat areas, the best single predictor of carcass fat weight was fat area in the TV8 scan (R^2 0.964). The best pair of predictors was the fat areas in the TV8 and LV5 (R^2 0.967) and the best set of three predictors was those in the TV8, LV5 and TV6 scans (R^2 0.969). Addition of more predictors did not significantly increase R^2 . With all seven scans included in the regression only the fat areas in the LV5, TV8 and TV6 scans contributed significantly.

Of the seven CT scan bone areas, the best single predictor of carcass bone weight was bone area in the TV6 scan (R^2 0.674). The best pair of predictors was those in the TV6 and hip (R^2 0.747) and the best set of three predictors was those in the TV6, hip and ischium scans (R^2 0.783). Inclusion of more predictors added little to the fit, and when all seven scans were included in a regression to predict bone weight only bone areas in the ischium, hip, LV5, TV8 and TV6 scans contributed significantly.

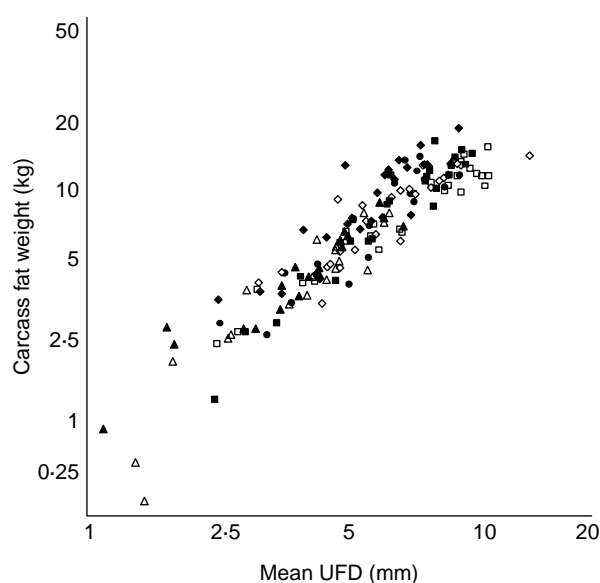


Figure 4 Relationship between carcass fat weight and the average of ultrasound fat depth (UFD) on log scales at 3rd lumbar vertebra and 13th rib (Charollais \bullet , Suffolk control line female \square , Suffolk control line male \diamond , Suffolk selection line female \blacksquare , Suffolk selection line male \blacklozenge , Texel high leg conformation line \triangle and Texel lean tissue growth selection line \blacktriangle).

Based on these results, and the selection criteria defined earlier, the ischium, LV5 and TV8 scans were chosen as the set of three scans for predicting tissue weights.

Group differences. When predicting tissue weights from CT tissue areas in the three chosen scans, for all three tissues, the intercept differed between groups while the slopes did not (Table 5). For lean weight, Texel lambs had a lower intercept than the other two breeds ($P < 0.001$); when this effect was included, R^2 increased from 0.902 to 0.924 and the r.s.d. fell from 0.0886 to 0.0778. For fat weight, the female lambs had a lower intercept ($P < 0.001$). Including the sex effect increased R^2 from 0.968 to 0.978 and reduced the r.s.d. from 0.116 to 0.0969. For bone weight, Texel lambs had the lowest intercept ($P < 0.001$). Including this effect increased R^2 from 0.751 to 0.830 and reduced the r.s.d. from 0.130 to 0.107.

Adding live weight to CT prediction of carcass composition. Including live weight, along with CT tissue areas in the chosen set of three CT scans increased R^2 for all three tissues (Table 5). For carcass lean weight R^2 increased from 0.902 to 0.958 and the r.s.d. fell from 0.0886 to 0.0582. Fitting group as well further increased R^2 to 0.966 and reduced the r.s.d. to 0.0524. The group effect was exclusively due to Suffolk lambs. Within the males, the Suffolk lambs had a lower intercept than the other two breeds; within the Suffolks, the females had a higher intercept. For carcass fat weight R^2 increased from 0.968 to 0.986 and the r.s.d. reduced from 0.116 to 0.0770. There was no effect of group ($P > 0.10$). For carcass bone weight R^2 increased from 0.751 to 0.905 and the r.s.d. fell from 0.130 to 0.0800. Including a group effect as well further increased R^2 to 0.925 and reduced the r.s.d. to 0.0714. Within Suffolk lambs females had a lower intercept than

Table 5 Intercepts and coefficients (s.e. in parenthesis) for equations to predict carcass lean, fat and bone weights from their respective tissue areas in X-ray computed tomography (CT) scans at the ischium, LV5 and TV8 with and without live weight (LW); all variables as log values (where significant group effects exist, adjustments to the intercepts for the groups that differ significantly are shown)

LW included	Tissue	Intercept	Coefficients					Adjustments to intercept [†]					R ²	r.s.d.
			Ischium	LV5	TV8	LW	Texel	Suffolk	Female					
No	Lean	-14.233 (0.463)	1.0570 (0.1110)	0.5790 (0.0881)	0.0563 (0.0701)	-0.1042 (0.0151)							0.924	0.0778
No	Fat	-7.047 (0.166)	0.1731 (0.0638)	0.2623 (0.0586)	0.5632 (0.0667)								0.978	0.0969
No	Bone	-8.276 (0.431)	0.3293 (0.0634)	0.3789 (0.0582)	0.5134 (0.0510)	-0.1839 (0.0214)							0.830	0.1070
Yes	Lean	-8.087 (0.558)	0.3994 (0.0879)	0.2839 (0.0607)	0.2100 (0.0498)	0.4934 (0.0338)							0.966	0.0524
Yes	Fat	-6.790 (0.132)	0.0734 (0.0513)	0.2016 (0.0463)	0.3883 (0.0547)	0.6827 (0.0487)							0.986	0.0770
Yes	Bone	-4.586 (0.409)	0.1856 (0.0439)	0.1698 (0.0431)	0.1523 (0.0427)	0.4992 (0.0356)	-0.1039 (0.0169)						0.925	0.0713

[†]As in Table 4.

males; within male lambs, Texels had a lower intercept than Charollais and Suffolks.

The relationship between the lean tissue weight measured by dissection and that predicted from CT information alone, using the relevant equation in Table 5, is shown in Figure 5 for both log transformed and linear scales. Figure 6 shows the same relationships, where live weight was included in the predictions. For fat, R^2 for the relationship between actual and CT predicted fat weights on the linear scale was 0.974 when live weight was not included and 0.985 when it was. The R^2 of the relationship between actual and CT predicted bone weights on the linear scale was 0.805 when live weight was not included and 0.918 when it was.

Comparing the effectiveness of ultrasound and CT to predict tissue weights

Lean and fat weights were predicted more accurately using CT than ultrasound whether live weight was also included in the prediction equation or not.

Considering ultrasound in addition to CT to predict tissue weights

Given tissue area information from the chosen three CT scans, adding ultrasound scan information did not significantly improve prediction of tissue weight for lean (R^2 0.902, r.s.d. 0.0886 with CT alone v. R^2 0.911, r.s.d. 0.0844 including ultrasound) or fat (R^2 0.968, r.s.d. 0.116 with CT alone v. 0.968, r.s.d. 0.115 including ultrasound). This was also the case when live weight was included as a predictor.

Discussion

In the sheep industry, CT scanning is used in breeding programmes to improve lean tissue growth rate and carcass composition, particularly in terminal sires. In the United Kingdom, these breeds contribute approximately 30% of the genes to the slaughter generation (Simm, 1987). The three breeds used here were representative of animals to be scanned commercially in terminal sire breeding programmes. The prediction equations generated therefore will cover the range of live weights and carcass composition typically found in lambs scanned.

Common prediction equations applied to the different genetic selection lines within a breed indicating that the equations generated will be relevant as carcass composition changes for the foreseeable future. Where breed or sex differences in the prediction equations were present only the intercepts and not the slopes differed. The equations developed are therefore applicable across breeds and sexes of terminal sire sheep; adjustments to the intercepts are required only in some cases.

Choice of CT scan positions

The set of three CT scan positions chosen as predictors for carcass tissue weights (ischium, LV5 and TV8) met the two

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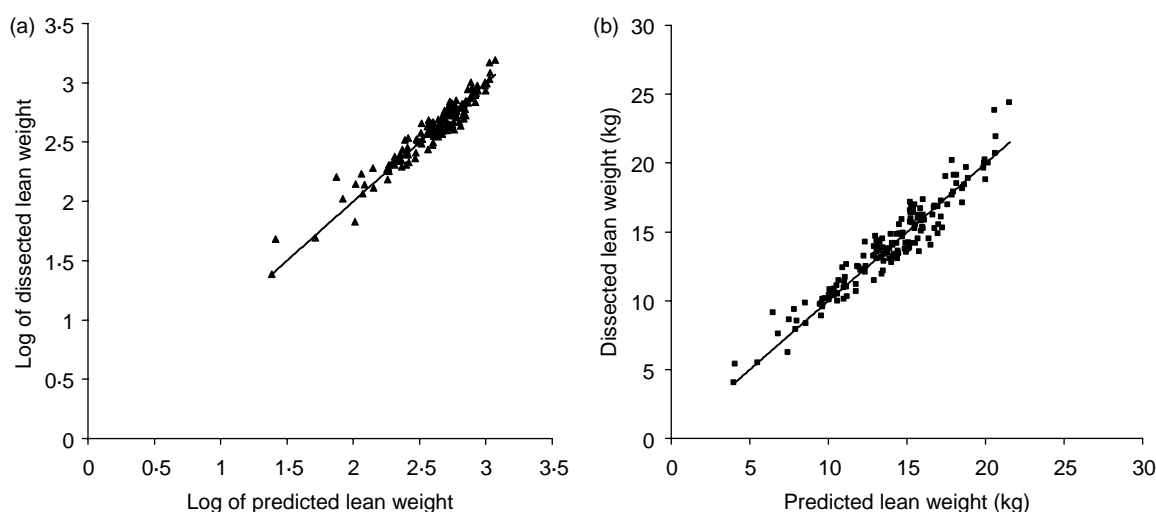


Figure 5 (a) Relationship for all animals between log actual carcass lean weight and log lean weight predicted from X-ray computed tomography (CT) information using the CT prediction equation not including live weight (Table 5). The regression line shown is $y = 0.9903x$ (s.e. 0.0109); $R^2 = 0.924$. (b) Relationship between actual carcass lean weight and lean weight predicted from X-ray computed tomography (CT) information for all animals. Predicted lean weight was calculated as the anti-log of the outcome of using the CT prediction equation not including live weight (Table 5). The regression line shown is $y = 0.9988x$ (s.e. 0.00555); $R^2 = 0.912$.

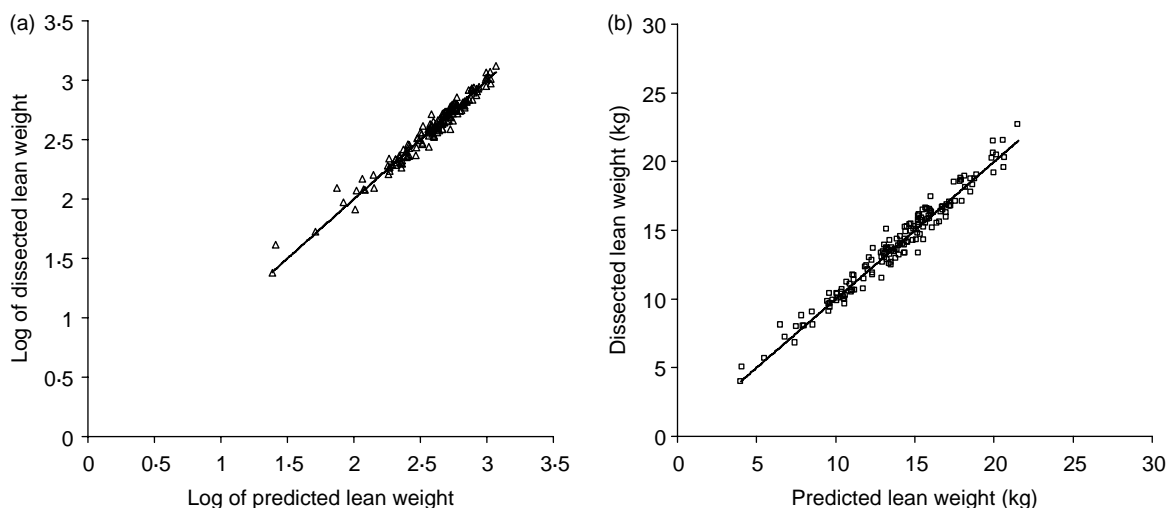


Figure 6 (a) Relationship, for all animals, between log actual carcass lean weight and log lean weight predicted from X-ray computed tomography (CT) information and live weight using the CT prediction equation including live weight (Table 5). The regression line shown is $y = 0.9904x$ (s.e. 0.0112); $R^2 = 0.966$. (b) Relationship between actual carcass lean weight and lean weight predicted from X-ray computed tomography (CT) information and live weight for all animals. Predicted lean weight was calculated as the anti-log of the outcome of using the CT prediction equation including live weight (Table 5). The regression line shown is $y = 0.9991x$ (s.e. 0.00357); $R^2 = 0.964$.

criteria of having a small number of CT scans while being useful to predict all three tissues. The chosen scans include one scan in each of the main carcass areas: the ischium scan in the hind leg, the LV5 scan in the loin and the TV8 scan in the chest/shoulder region. The set includes the 'best' predictors of lean and fat, ischium and TV8, respectively. The LV5 scan was included as it was useful for all tissues and provided a scan in the loin area.

For bone, neither of the two 'best' predictors was included in the chosen set. Accurate prediction of bone weight was of lower priority than lean and fat weights since bone is not

included in the lean tissue growth index. The best single scan for predicting bone weight was TV6. However, the TV8 scan was chosen instead because it was the best predictor of fat weight as well as being useful for bone. Further examination of the effect of the choice of TV8 over TV6 showed that in fact TV6 was not significantly better at predicting bone weight than TV8 given that the ischium and LV5 scans were also included in the prediction equation. In addition, the TV8 scan is less influenced by animal posture. In CT scanning the animal may move slightly, which can cause substantial changes in the orientation of the bones seen in the TV6 scan. There is relatively less change for the

TV8 scan and, as a result, it is subject to fewer errors associated with bones moving in and out of the scan plane due to animal movement (Lambe *et al.*, 2003).

Although the chosen set of scans was not the same as the best set for each tissue, differences in prediction accuracy were very small. For example, as the femur scan was important only for predicting lean weight, it was excluded from the chosen set. However, this resulted in little loss in prediction accuracy when predicting lean weight (R^2 0.930, r.s.d. 0.0750 for chosen set of scans *v.* R^2 0.939, r.s.d. 0.699 with addition of femur scan). As the femur scan is more affected by animal posture than the other scans in the hind leg (Lambe *et al.*, 2003), this is further justification for its exclusion.

It was interesting that scans through the hind leg provided little valuable predictive information about fat weight. This is likely due to fat areas in the hind leg scans defining a smaller proportion of the total carcass tissue area in the scan (20%) than fat areas in the loin (32%) and shoulder (35%) region scans.

Data transformations

All measurements were log transformed. This resulted in residuals that were closer to being normally distributed. Other advantages of using the log transformation were that variances were equalised across the range of the data, relationships between variables became more nearly linear, and r.s.d. became a proportional measure of prediction error. This avoids the problem inherent to absolute R^2 values, which are dependent on the intrinsic variation of a particular experiment or set of conditions. Using the log transformation meant that the predicted tissue weights were on the log scale and required transformation back to the linear scale for use in carcass evaluation. Figures 5b and 6b show that there is still a very close relationship between actual and predicted lean tissue weights when transformed back to the linear scale. The R^2 values of the regressions of actual on predicted tissue weights were similar on both scales. Slopes of the regression lines were not significantly different from unity on either scale.

Since measurements made on the lambs differ in dimension, it was postulated these measurements required transformation to bring them onto geometrically equivalent scales. Initially, all measurements were transformed to the cubic dimension with linear measurements cubed, area measurements raised to the $3/2$ power, and weights not transformed. However, statistical analysis of the data when transformed in this way showed that the residuals of the regressions were not normally distributed. These problems did not occur with the log transformations.

Accuracy of prediction

Ultrasound. Accuracies of prediction of carcass tissue weights from ultrasound tissue depths in this study were higher than the 50 to 70% reported by Alliston (1983) and Simm (1987). They were also slightly higher than prediction accuracies achieved by Young *et al.* (1996) in Dorset Down lambs of up to 83% for lean weight and 63% for fat weight

and those reported by Bishop (1994) in Scottish Blackface lambs (73% for lean weight and 80% for fat weight). In both of those studies live weight was included along with ultrasound tissue depths. The high accuracy of prediction with ultrasound found here reflected the range of breeds and ages used. Even within breed-age subsets of data, R^2 was still higher than in other reports. For example, for Suffolk lambs at 26 weeks predicting lean weight using ultrasound muscle depth and live weight gave an R^2 (%) of 86.6 and r.s.d. of 0.0633. For fat weight predicted using ultrasound fat depth and live weight R^2 (%) was 83.0 and r.s.d. was 0.0926.

In this study all lambs were kept under the same conditions for the duration of the trial and ultrasound scans were all carried out by one very experienced operator with a great deal of care taken in scan positioning and tissue depth measurements on scans. This may have led to less measurement error than in previous studies, which might explain the higher than expected accuracy of prediction of lean and fat. In addition, we used the average of tissue depths from ultrasound scans at two different sites rather than from a single site. This would be expected to increase the accuracy of prediction compared with single measurements, although benefits may be only slight (Simm *et al.*, 2002). In this study, R^2 values were slightly lower for the single sites. Bishop (1994) used the average of four measurements since this resulted in lower error variance than fitting all four separately.

Prediction of tissue weights using only live weight gave R^2 values of 0.804, 0.910 and 0.858 for lean, fat and bone respectively. These are higher than those in several studies reviewed by Simm (1987) and those found by Young *et al.* (1996) when using live weight to predict tissue weights estimated by the Cavalieri CT scanning technique. Addition of ultrasound measurements to live weight did not explain much more variation in tissue weights. This may partially account for the higher than expected prediction accuracy achieved for ultrasound when live weight was also included. When ultrasound measures alone were used to predict tissue weights, prediction accuracies were more similar to those achieved in other studies.

X-ray computed tomography. Sehested (1984) showed that lamb carcass composition could be predicted by CT with accuracies of 92 to 94% in agreement with the 92 to 98% found more recently by Vangen and Jopson (1996). In Dorset Down ewe lambs, R^2 values of 93%, 94% and 73% for fat, lean and bone, respectively, were found using four CT scans and live weight to predict the tissue weights that were estimated using the Cavalieri CT scanning method (Young *et al.*, 1996). Prediction accuracies achieved in the present study when live weight was included were close to those found in other studies for fat and lean weights, but higher for bone weight, perhaps reflecting the more variable data used.

Use of live weight in prediction equations

Live weight is generally considered the most important single predictor of many carcass traits (Lawrence and

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Fowler, 2002), although using it can cause problems with correlation among tissue weights and with live weight (Jones *et al.*, 2004). In multi-trait genetic evaluations where predicted tissue weights and live weights may be considered jointly, colinearity may inflate estimates of co-variances among such measures. Consequently, estimating breeding values or selection indices derived using such co-variances may be less reliable. Prediction equations were thus generated both with and without live weight.

Including live weight increased accuracy of prediction of carcass tissues compared with either ultrasound or CT information alone. The gain in prediction accuracy was moderate with ultrasound and small with CT in agreement with Lambe *et al.* (2003). When information from three CT scans but not live weight was used to predict lean, fat, and bone weight by Lambe *et al.* (2003), R^2 values were 81.4%, 98.6% and 56.1%, respectively; addition of live weight in the prediction equation only explained significant extra variation for lean weight. In the present study, reduction in R^2 when excluding live weight was small for both lean and fat weights but larger for bone weight. Since the reduction in prediction accuracy is generally small, it may be better to use tissue weights predicted without live weight information if they are to be used in a selection index or breeding objective including live weight. It is necessary to examine the effects on estimates of genetic parameters of excluding live weight when predicting tissue weights, as compared with including live weight (Jones *et al.*, 2004). There are other situations where it is also highly undesirable to use live weight as a predictor of tissue weights, for example when it is of interest to identify animals that differ from the average fat to live weight ratio.

Utility of CT scanning

Tissue weights were more accurately predicted with CT than with ultrasound, particularly when live weights are excluded from the prediction. With CT scanning, fat can be accurately measured in all depots, whereas ultrasound provides information only on subcutaneous fat. Selection for reduced subcutaneous fat will reduce overall fatness because genetic correlations between fat in different depots are positive and moderately high (Wolf *et al.*, 1981). However, selection on CT measurements should allow for more rapid progress in reducing overall carcass fatness (Simm and Dingwall, 1989; Lewis and Simm, 2002) and could help remove excess fat from intermuscular fat depots that are difficult to trim during meat processing. In addition, CT can provide information on other traits affecting carcass quality that cannot be measured easily by other means, for example muscularity (Jones *et al.*, 2002a) and fat distribution and partitioning (Young *et al.*, 2001).

The information provided here can be used to design economically viable two-stage selection strategies in terminal sire breeds, where most animals would be scanned ultrasonically with only those of higher genetic merit scanned by CT (Jopson *et al.*, 1995, 1997 and 2004; Lewis and Simm, 2002). A suitable set of three CT scans to predict carcass lean, fat and bone weights in terminal sire lambs has been identified, which saves on time and costs for CT scanning.

The set includes a scan in each of the three main carcass regions: ischium, LV5 and TV8. These CT scan positions are now in use by major UK sire referencing schemes in meat breeds.

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