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Predicting tissue distribution and partitioning in terminal sire sheep using x-ray computed tomography[1]

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ABSTRACT: The utility of x-ray computed tomography (CT) scanning in predicting carcass tissue distribution and fat partitioning in vivo in terminal sire sheep was examined using data from 160 lambs representing combinations of 3 breeds (Charollais, Suffolk, and Texel), 3 genetic lines, and both sexes. One-fifth of the lambs were slaughtered at each of 14, 18, and 22 wk of age, and the remaining two-fifths at 26 wk of age. The left side of each carcass was dissected into 8 joints with each joint dissected into fat (intermuscular and subcutaneous), lean, and bone. Chemical fat content of the LM was measured. Tissue distribution was described by proportions of total carcass tissue and lean weight contained within the leg, loin, and shoulder regions of the carcass and within the higher-priced joints. Fat partitioning variables included proportion of total carcass fat contained in the subcutaneous depot and intramuscular fat content of the LM. Before slaughter, all lambs were CT scanned at 7 anatomical positions (ischium, midshaft of femur, hip, second and fifth lumbar vertebrae, sixth and eighth thoracic vertebrae). Areas of fat, lean, and bone (mm^2) and average fat and lean density (Hounsfield units) were measured from each cross-sectional scan. Areas of intermuscular and subcutaneous fat were measured on 2 scans (ischium and eighth thoracic vertebra). Intramuscular fat content was predicted with moderate accuracy (R^2 = 56.6) using information from only 2 CT scans. Four measures of carcass tissue distribution were predicted with moderate to high accuracy: the proportion of total carcass (R^2 = 54.7) and lean (R^2 = 46.2) weight contained in the higher-priced joints and the proportion of total carcass (R^2 = 77.7) and lean (R^2 = 55.0) weight in the leg region. Including BW in the predictions did not improve their accuracy ($P > 0.05$). Although breed-line-sex combination significantly affected fit of the regression for some tissue distribution variables, the values predicted were changed only trivially. Within terminal sire type animals, using a common set of prediction equations is justified. Tissue distribution and fat partitioning affect eating satisfaction and efficiency of production and processing; therefore, including such carcass quality measures in selection programs is increasingly important, and CT scanning appears to provide opportunities to do so.

Key words: fat partitioning, intramuscular fat, prediction, sheep, tissue distribution, x-ray computed tomography

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INTRODUCTION

Consumption of lamb has declined due to concerns over excess dietary fat, waste from trimming, and taste (Ward et al., 1995). Breeding schemes in terminal sire sheep are increasingly tailored to meet consumer demand for lean lamb. It has been found that x-ray computed tomography (**CT**) can accurately measure carcass traits in vivo (muscularity, Jones et al., 2002; tissue weights, Macfarlane et al., 2006). However, other traits such as fat partitioning and tissue distribution may also influence carcass value.

Carcass fat is partitioned among subcutaneous, intermuscular, and intramuscular depots. Unlike subcutaneous fat, intermuscular fat is difficult to trim, risking

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Table 1. Number of lambs of each genotype (breed-line) and sex group slaughtered at each age

	Genotype			Age at slaughter				
Group	Breed	Line[1]	Sex[2]	14 wk	18 wk	22 wk	26 wk	Total
1	Charollais	LTG	M	4	4	4	8	20
2	Suffolk	C	F	5	5	5	10	25
3	Suffolk	LTG	F	5	5	5	10	25
4	Suffolk	C	M	5	5	5	10	25
5	Suffolk	LTG	M	5	5	5	10	25
6	Texel	HC	M	4	4	4	8	20
7	Texel	LTG	M	4	4	4	8	20

[1] Line refers to the genetic line. In the Charollais, selection is on a lean tissue growth index (LTG; Simm and Dingwall, 1989). Within the Suffolk, LTG is the lean tissue growth rate selection line and C is its control line (Simm et al., 2002). Within the Texel, HC is the high leg conformation selection line (Wolf et al., 2001) and LTG is the lean tissue growth rate selection line.

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

fatty meat being presented to consumers (Woodward and Wheelock, 1990). However, a minimum of 3% intramuscular fat is needed for acceptable meat tenderness and juiciness (Savell and Cross, 1988); thus, indiscriminate selection to decrease overall carcass fatness may diminish eating quality (Karamichou et al., 2006). If fat depots could be accurately distinguished in vivo using CT, then differential selection would be possible.

Lamb carcass joints differ in value (MLC, 2005). Wolf (1982) reported high heritability for proportion of carcass lean in higher-priced joints. If the proportion of total carcass weight (or lean) in individual joints could be discriminated, higher-value carcasses could be favored in selection.

Cross-sectional CT images measure body tissues and lean tissue density, with lean of less density perhaps indicating more intramuscular fat. Moreover, scans of different body regions may characterize weight distribution. Our objectives were to assess the accuracy of predicting (i) fat partitioning among different carcass depots and (ii) distribution of total weight and lean across the carcass. Carcasses from animals over a wide range in BW and age were used to derive prediction equations and to test the adequacy of general prediction equations to describe these variables in the relevant range of terminal sire sheep.

MATERIALS AND METHODS

The Animal Experiment Committee at Scottish Agricultural College (**SAC**) approved all procedures and protocols used in the experiment.

Animals and Management

Data from an experiment conducted at SAC in 1997 were used for this study. These data were first described by Jones et al. (2002), who reported the potential of CT scan measurements to predict muscularity, and were also used by Macfarlane et al. (2006), who reported the potential of CT scan data to predict total carcass tissue weights. In this study, the same data on the same animals will be used to examine different objectives: the potential of CT scan data to predict both fat partitioning and tissue distribution across different regions of the carcass. The experiment is described only briefly here, because more detailed information is available in the 2 previous articles (Jones et al., 2002; Macfarlane et al., 2006). Lambs (n = 160) of 3 terminal sire breeds (Charollais, Suffolk, and Texel) were used. Texel and Charollais lambs were all male with Texel lambs selected from 2 different genetic lines. Suffolk lambs were selected from 2 genetic lines and from both sexes. These 7 genotype (breed-line) and sex groups represent the kinds of terminal sire sheep predominant in the United Kingdom industry. By 8 wk of age, all lambs were weaned, group-penned according to breed and sex, and given ad libitum access to a high-quality pelleted feed (12.4 MJ of ME per kg of DM; 178 g of CP per kg of DM) and hay.

Slaughter Procedure and Measurements

One-fifth of the lambs in each of the 7 groups were slaughtered at each of 14, 18, and 22 wk of age, and the remaining two-fifths at 26 wk of age (Table 1). The mean BW for each of the 7 groups at each slaughter age are shown in Macfarlane et al. (2006; Table 1). After slaughter, carcasses were chilled for 24 h and then weighed before being split longitudinally into 2 carcass sides. The carcass sides (excluding the kidney, and the kidney, pelvic, heart, and thoracic fat) were frozen and retained for dissection.

After thawing, the left carcass side was separated into the 8 joints (leg, chump, loin, breast, best-end, middle neck, shoulder, and neck) described by Cuthbertson et al. (1972). Each joint was dissected into lean, fat (subcutaneous and intermuscular), bone (vertebral and other), and waste. The LM was separated during dissection of the loin joint and ground, mixed, and 2 grab samples were taken for chemical analysis. Dry matter of each of the 2 grab samples from the ground LM

Table 2. Abbreviations for both the dependent variables of fat partitioning and tissue distribution (total carcass and carcass lean) and the independent variables [computed tomography (CT) scans, tissue areas, and densities]

Variable	Description
CT scans	
ISC	Cross-sectional CT scan through the ischium
FEM	Cross-sectional CT scan through the midshaft of the femur
HIP	Cross-sectional CT scan through the hip
LV2	Cross-sectional CT scan through the second lumbar vertebra
LV5	Cross-sectional CT scan through the fifth lumbar vertebra
TV6	Cross-sectional CT scan through the sixth thoracic vertebra
TV8	Cross-sectional CT scan through the eighth thoracic vertebra
Tissue areas and densities	
SCFA	Subcutaneous fat area in a given CT scan
ITMFA	Intermuscular fat area in a given CT scan
FA	Total fat area in a given CT scan
LA	Total lean area in a given CT scan
BA	Total bone area in a given CT scan
FD	Average density of fat tissue in a CT scan
LD	Average density of lean tissue in a CT scan
Fat partitioning	
FPART	Subcutaneous fat weight as a proportion of total fat weight in carcass
IAMF	Chemically determined intramuscular fat content of musculus longissimus dorsi
Tissue partitioning: total carcass	
WHPJ	Proportion of total carcass weight contained in higher-priced joints
WLEG	Proportion of total carcass weight contained in leg region
WLOIN	Proportion of total carcass weight contained in loin region
WSHLD	Proportion of total carcass weight contained in shoulder region
Tissue partitioning: carcass lean	
LHPJ	Proportion of total carcass lean weight contained in higher-priced joints
LLEG	Proportion of total carcass lean weight contained in leg region
LLOIN	Proportion of total carcass lean weight contained in loin region
LSHLD	Proportion of total carcass lean weight contained in shoulder region

was determined by freeze-drying to constant weight, and the DM was analyzed for protein (6.25 N) by a micro-Kjeldahl procedure and for ash by burning in a muffle furnace at 550°C. The GE of the DM was determined by adiabatic bomb calorimetry. Proportion of fat in each sample was determined using gross GE and N (Kyriazakis and Emmans, 1992) as

$$\text{lipid (g/g of DM)} = (\text{GE } \{\text{kJ/g of DM}\} - \{23.8 \times [6.25 \times \text{N (g/g of DM)}]\})/39.6,$$

assuming energy content of protein and lipid are 23.8 and 39.6 kJ/g, respectively. The mean of the 2 samples was taken. Sum of water, ash, protein, and fat was on average 98.21% (SD = 0.320), which is within acceptable limits.

X-Ray CT Measurements

Protocols for collection and measurement of x-ray CT scans were as described previously by Jones et al. (2002) and Macfarlane et al. (2006). Briefly, lambs were weighed and CT scanned before slaughter. Cross-sectional CT scans were taken at 7 anatomical locations along the body [ischium (**ISC**), femur, hip, fifth and second lumbar vertebrae (**LV5** and **LV2**, respectively), and eighth (**TV8**) and sixth thoracic vertebrae].

Dependent variables were determined in each image using STAR software (Mann et al., 2003). These were total areas (mm^2) of fat (**FA**), lean, and bone, and mean densities (Hounsfield units) of fat and lean. Areas of subcutaneous and intermuscular fat were assessed in ISC and TV8 images; only these images provide a clear distinction between the 2 fat depots (K. McLean, SAC, Edinburgh, UK, personal communication). Abbreviations for CT scan variables are composed of scan abbreviation and then tissue area or density abbreviation, for example, ISC_FA as shown in Table 2. Mean tissue areas and densities across all 7 CT scans are shown in Table 3 for each genotype-sex group.

Derived Variables

Dissection and chemical analysis data were used to derive variables to describe fat partitioning and tissue distribution for each animal. These are the independent variables; abbreviations for these are shown in Table 2, and means and SD for each genotype-sex group are shown in Table 4.

Fat Partitioning. Carcass fat was dissected into intermuscular and subcutaneous depots; subcutaneous fat as a proportion of total fat, and intermuscular fat as a proportion of total fat, therefore sum to 1. The proportion of total carcass fat that was subcutaneous

Table 3. Means for the independent variables from computed tomography (CT) scans [total fat area (FA), lean area (LA), bone area (BA), subcutaneous fat area (SCFA), intermuscular fat area (ITMFA), lean density (LD), and fat density (FD)] averaged across the available scans for each genotype (breed-line) and sex group adjusted for age together with standard error of the difference (SED) and overall maximum and minimum values

	Group										
Item	1	2	3	4	5	6	7	SED	*P*-value	Maximum	Minimum
FA, mm^2	7,822	9,674	9,048	9,250	9,245	3,814	3,975	652	<0.001	18,857	546
LA, mm^2	20,419	17,021	18,949	18,618	21,890	19,154	20,600	572	<0.001	28,082	9,229
BA, mm^2	3,677	3,244	3,719	3,421	4,176	3,020	3,394	131	<0.001	5,791	1,858
SCFA, mm^2	5,128	6,795	6,192	6,140	5,848	2,312	2,474	490	<0.001	12,698	368
ITMFA, mm^2	3,954	4,486	4,338	4,556	4,938	2,167	2,262	329	<0.001	9,470	370
FD, Hounsfield units	135	134	134	134	135	137	137	0.31	<0.001	140	132
LD, Hounsfield units	90	85	88	86	90	93	94	0.75	<0.001	97	79

fat was calculated for each animal to provide a measure of partitioning of carcass fat between subcutaneous and intermuscular depots (**FPART**). Percentage of intramuscular fat in the LM was also available for each animal (**IAMF**).

Tissue Distribution. Distributions of total weight, and of lean weight across the carcass, were considered. First, the proportion of total carcass weight (**WHPJ**) and total carcass lean weight (**LHPJ**) that was contained in the higher-priced joints (leg, chump, loin, and best-end) was calculated for each animal. This classification was based on the retail prices for each joint (MLC, 2005). Second, proportions of total carcass weight and total carcass lean weight contained in each of the 3 main carcass regions were calculated: hind leg (**WLEG**, **LLEG**), loin (**WLOIN**, **LLOIN**), and shoulder (**WSHLD, LSHLD**). The hind leg region was comprised of the leg and chump joints, the loin region of the loin joint only, and the shoulder region of the shoulder and best-end joints.

Statistical Methods

Derived variables were regressed on possible predictors from CT scan information using a best-subsets regression procedure (Genstat 7, Adept Scientific, Herts, UK) that included only those predictors that contributed significantly ($P < 0.05$) to the explained proportion of variation in the dependent variable, and addition of any further independent variable did not contribute significantly to the variation explained.

Possible predictors considered for FPART were lean area and FA in each of the 7 CT scans, with fat areas for the ISC and TV8 scans split into subcutaneous fat area and intermuscular fat area. Possible predictors for IAMF included both areas and densities of lean and fat in each of the 7 CT scans. Possible predictors for WHPJ and LHPJ included lean, fat, and bone areas in each of the 7 CT scans. This set of possible predictors was also used for weight and lean proportion contained in the leg, loin, and shoulder regions.

Table 4. Means for derived dependent variables describing fat partitioning and tissue distribution (as proportions), for each genotype (breed-line) and sex group adjusted for age, together with standard error of the difference (SED) and overall maximum and minimum values[1]

	Group										
Item	1	2	3	4	5	6	7	SED	*P*-value	Maximum	Minimum
FPART[2]	0.581	0.578	0.577	0.577	0.556	0.540	0.555	0.0123	0.002	0.652	0.453
IAMF[2]	0.039	0.037	0.038	0.042	0.037	0.030	0.029	0.0021	<0.001	0.066	0.009
WHPJ[2]	0.494	0.506	0.497	0.504	0.491	0.501	0.503	0.0041	0.005	0.539	0.442
WLEG[2]	0.319	0.324	0.319	0.326	0.319	0.341	0.337	0.0039	<0.001	0.377	0.264
WLOIN[2]	0.108	0.113	0.111	0.110	0.107	0.100	0.104	0.0023	<0.001	0.130	0.086
WSHLD[2]	0.281	0.278	0.271	0.272	0.274	0.275	0.270	0.0023	<0.001	0.301	0.249
LHPJ[2]	0.542	0.575	0.558	0.569	0.552	0.550	0.548	0.0041	<0.001	0.597	0.485
LLEG[2]	0.363	0.388	0.372	0.385	0.370	0.383	0.375	0.0036	<0.001	0.411	0.314
LLOIN[2]	0.112	0.117	0.119	0.117	0.118	0.107	0.111	0.0023	<0.001	0.132	0.089
LSHLD[2]	0.265	0.254	0.253	0.251	0.256	0.260	0.255	0.0026	<0.001	0.290	0.226
BW, kg	53.3	49.0	57.2	52.7	64.3	39.9	45.3	2.3	<0.001	95.6	15.7

[1] FPART = subcutaneous fat weight as a proportion of total fat weight in carcass; IAMF = chemically determined intramuscular fat content of musculus longissimus dorsi; WHPJ = proportion of total carcass weight contained in higher-priced joints; WLEG = proportion of total carcass weight contained in leg region; WLOIN = proportion of total carcass weight contained in loin region; WSHLD = proportion of total carcass weight contained in shoulder region; LHPJ = proportion of total carcass lean weight contained in higher-priced joints; LLEG = proportion of total carcass lean weight contained in leg region; LLOIN = proportion of total carcass lean weight contained in loin region; LSHLD = proportion of total carcass lean weight contained in shoulder region.

[2] All tissue distribution and partitioning variables are proportions.

Using the data described in this study, Young et al. (2001) and Macfarlane et al. (2006) reported that accurate prediction of total carcass tissue weights using CT scan information can be achieved using information from only 3 CT scans (ISC, LV5, and TV8). It was of interest to determine whether tissue distribution and fat partitioning variables could be predicted with similar accuracy using information from only these 3 scans (reference set), compared with information from all 7 scans. The best subsets regression procedure was repeated for each derived variable, but using only the tissue areas and densities from the ISC, LV5, and TV8 scans as possible predictors.

It was also of interest to determine whether the proportions of total weight and total lean contained within leg, loin, and shoulder regions could be predicted with similar accuracy using CT scan information only from the relevant carcass areas as opposed to all possible scans. A similar procedure to that described above was used with possible predictors for the leg region being tissue areas in the ISC, femur, and hip CT scans. Possible predictors for the loin region were tissue areas in the LV2 and LV5 scans, whereas possible predictors for the shoulder region were tissue areas in the sixth thoracic vertebrae and TV8 CT scans.

The best-subsets regression procedure did not provide estimated values of the regression coefficients. Therefore, once the best set of predictors was chosen, a linear regression of the derived variable on the chosen set of predictors (model 1) was fitted (Genstat 7, Adept Scientific) as

$$y_i = a + \boldsymbol{\beta}\mathbf{D}_i + \varepsilon_i, \qquad [1]$$

where y_i = the derived variable for lamb i (i = 1, 2, 3, ..., 160), a = the intercept; $\boldsymbol{\beta}$ = a vector of the linear regression coefficients for the predictor variables; $\mathbf{D}$ = a matrix of the predictor variables appropriate to the analysis; and ε = the error.

Three alternative more comprehensive models were also fitted. First, the linear regression of BW on the derived variable was added to model 1. Second, a genotype-sex group effect was added to model 1 allowing different intercepts (a_j) for each group. Lastly, a group effect on both the intercept (a_j) and linear coefficients ($\boldsymbol{\beta}_\mathbf{j}$) was added to model 1. Goodness of fit of these more comprehensive models was assessed by changes in residual SD (**RSD**) and adjusted R^2 values (shown as a percentage).

A central reason to predict tissue distribution and partitioning using CT is to include such in vivo measures as selection criteria or goal traits in breeding programs. Typically, genetic evaluations are conducted within breeds, with sex effects (often as part of the contemporary group) accounted for in the statistical model fitted. Thus, even if important, genotype-sex effects on the intercept of CT prediction equations would not bias breeding value estimates if ignored, unless they were due to genetic line. Excluding genotype-sex effects would allow more parsimonious (model 1) and general prediction equations to be used in practice. The importance of genetic line, and its potential interaction with sex, on the accuracy of CT predictions was tested in the Suffolk where data from 2 genetic lines and both sexes were available. The regressions of WHPJ, LHPJ, and LLEG on CT scan information were fitted, allowing line, sex, and their interaction to affect the intercept. These 3 variables were chosen because they were the most accurately predicted using CT.

RESULTS

Adjusted R^2 and RSD for the best set of CT predictors for each derived variable are shown in Table 5 when BW and group effects are either excluded or included in the model fitted. When fitting a more comprehensive model (i.e., BW or group effects) improved goodness of fit ($P < 0.05$), this is specified in the text. Coefficients are shown in the appendix in Tables A1 and A2 for prediction equations derived using the best set of predictors when BW and group effects were not fitted (model 1). Figures 1 and 2 show the effect on accuracy (adjusted R^2) when using a reduced set of potential predictors to describe the tissue distribution variables.

FPART

It was found that FPART was poorly predicted using CT scanning data (R^2 = 6.5, RSD = 0.0392; Table 5). The subset of scans chosen to predict FPART with the best-subsets regression procedure, namely, ISC, LV5, and TV8, were those in the reference set; thus, both the full and reduced set of scans result in the same very low accuracy of prediction.

IAMF

Of the possible predictors of IAMF, 2 gave an R^2 of 56.6 (RSD = 0.00608), and no further CT predictors were significant. When information was available only from the reference scans, prediction accuracy was only slightly less (R^2 = 55.3, RSD = 0.0617; data not shown).

Distribution of Weight Across Carcass

WHPJ. The WHPJ was predicted with moderate accuracy (R^2 = 54.7, RSD = 0.0110) using CT data alone. Of the alternative models, only when adding a group effect on the intercept did prediction accuracy improve slightly ($P = 0.015$). When using only the reference set, prediction accuracy was less (R^2 = 46.1, RSD = 0.0120; Figure 1), but again, goodness of fit improved when including group effects on the intercept ($P < 0.001$, R^2 = 51.4, RSD = 0.0114; data not shown).

WLEG. The WLEG was predicted with moderate to high accuracy using CT information alone (R^2 =

Table 5. Adjusted R^2 and residual SD (RSD) for prediction of fat partitioning, and weight and lean distribution, using the best set of predictors from all 7 computed tomography (CT) scans alone[1]

						Plus group effects			
				Plus BW		a_j		a_j and $\boldsymbol{\beta}_\mathbf{j}$	
Variable[2]	Best set of predictors[3]	R^2	RSD	R^2	RSD	R^2	RSD	R^2	RSD
FPART	ISC_LA, ISC_SCFA	6.5[4]	0.0392	6.0	0.0393	8.5	0.0388	4.8	0.0396
IAMF	LV2_LD, LV2_FA	56.5[4]	0.00608	56.3	0.00610	58.0	0.00598	57.1	0.00605
WHPJ	ISC_FA, FEM_LA, HIP_FA, LV5_FA, TV8_BA, TV8_FA, TV6_FA, TV6_LA	54.7	0.0110	55.3	0.0110	57.6[4]	0.0107	60.0	0.0104
WLEG	ISC_LA, HIP_FA, LV2_LA, LV5_FA, TV8_LA, TV8_BA, TV6_FA	77.7[4]	0.00927	78.0	0.00921	77.9	0.00923	81.7	0.00841
WLOIN	ISC_LA, FEM_FA, FEM_LA, HIP_FA, LV2_LA, TV6_LA	36.0	0.00710	35.6	0.00712	40.5[4]	0.00688	40.2	0.00691
WSHLD	ISC_FA, FEM_BA, LV2_LA, TV8_LA, TV6_FA	19.0	0.00719	19.0	0.00718	28.8[4]	0.00674	24.8	0.00692
LHPJ	ISC_LA, FEM_BA, HIP_FA, LV5_FA, TV6_LA, TV8_LA, TV8_BA	46.2	0.0127	46.4	0.0126	58.6[4]	0.0111	61.4	0.0107
LLEG	ISC_LA, FEM_BA, LV5_LA, TV8_LA, TV8_BA	55.0	0.0103	55.9	0.0102	60.6[4]	0.00968	65.1	0.0910
LLOIN	ISC_FA, FEM_FA, FEM_BA, HIP_FA, HIP_BA, LV2_FA, LV2_LA, TV6_LA	34.0	0.00684	33.8	0.00685	40.8[4]	0.00648	42.7	0.00638
LSHLD	ISC_FA, FEM_BA, LV2_LA, TV8_LA, TV8_BA	36.5	0.00788	37.2	0.00786	44.0[4]	0.0074	41.7	0.00755

[1] These statistics are also shown once adding BW, once adding genotype (breed-line) and sex groups as effects on the intercept (a_j), and once adding individual group effects on both the intercept and the coefficients (a_j and $\boldsymbol{\beta}_\mathbf{j}$).

[2] FPART = subcutaneous fat weight as a proportion of total fat weight in carcass; IAMF = chemically determined intramuscular fat content of musculus longissimus dorsi; WHPJ = proportion of total carcass weight contained in higher-priced joints; WLEG = proportion of total carcass weight contained in leg region; WLOIN = proportion of total carcass weight contained in loin region; WSHLD = proportion of total carcass weight contained in shoulder region; LHPJ = proportion of total carcass lean weight contained in higher-priced joints; LLEG = proportion of total carcass lean weight contained in leg region; LLOIN = proportion of total carcass lean weight contained in loin region; LSHLD = proportion of total carcass lean weight contained in shoulder region.

[3] ISC = ischium; LA = total area of lean; SCFA = areas of subcutaneous fat; LV2 = second lumbar vertebrae; LD = mean density of lean; FA = total area of fat; FEM = femur; HIP = hip; LV5 = fifth lumbar vertebrae; TV8 = eighth thoracic vertebrae; BA = total area of bone; TV6 = sixth thoracic vertebrae.

[4] The best model for each variable.

77.7, RSD = 0.00927), which decreased only slightly with the reference set ($R^2 = 75.4$, RSD = 0.00975; Figure 1). When WLEG was predicted using CT scans in the leg region only, accuracy was less ($R^2 = 64.2$, RSD = 0.0118; Figure 1); this improved slightly when including BW in the prediction equation ($P = 0.005$, $R^2 = 67.0$, RSD = 0.0113).

WLOIN. The WLOIN was predicted with low to moderate accuracy using CT data alone ($R^2 = 36.0$, RSD = 0.00710), which improved when fitting a group effect on the intercept ($P = 0.002$). When only information from the reference set was used, prediction accuracy was less ($R^2 = 27.4$, RSD = 0.00756; Figure 1) and only one predictor was useful (LV5_FA, $P = 0.019$). Including group effects on both intercept and coefficients improved fit ($P = 0.031$, $R^2 = 34.5$, RSD = 0.00718). When exclusively using CT scans from the loin region, only LV5_FA was useful for predicting WLOIN as when the full set of scans was available.

WSHLD. The WSHLD was poorly predicted using CT data alone ($R^2 = 19.0$, RSD = 0.00719). Although including group effects on the intercept improved fit ($P < 0.001$), prediction remained inaccurate ($R^2 = 28.8$). Using information only from the reference set led to even less prediction accuracy ($R^2 = 12.3$, RSD = 0.00748; Figure 1), which was improved upon by including a group effect on the intercept in the model fitted ($P < 0.001$, $R^2 = 24.6$, RSD = 0.00693). When using information from the 2 CT scans in the shoulder/chest region, prediction accuracy was even poorer ($R^2 = 5.6$, RSD = 0.00776; Figure 1), with some improvement when including BW ($P = 0.002$, $R^2 = 10.7$, RSD = 0.00754) and group effects on the intercept ($P < 0.001$, $R^2 = 22.0$, RSD = 0.00705).

Distribution of Lean Across the Carcass

LHPJ. The LHPJ was moderately well predicted using only CT information ($R^2 = 46.2$, RSD = 0.0127). Including group effects on the intercept ($P < 0.001$) substantially increased prediction accuracy ($R^2 = 58.6$). When only information from the reference set was used, prediction of LHPJ was less accurate ($R^2 = 37.7$, RSD = 0.0136; Figure 2); it was improved with addition of group effects on the intercept ($P < 0.001$, $R^2 = 53.7$, RSD = 0.0118).

LLEG. The LLEG was moderately well predicted using CT data alone ($R^2 = 55.0$, RSD = 0.0103). Inclusion of BW ($P = 0.049$) and group effects on the intercept ($P < 0.001$) increased prediction accuracy. For the reference scans, prediction accuracy was decreased slightly (R^2 = 51.3, RSD = 0.0108; Figure 2); it improved when including group effects on both intercept and coefficients ($P = 0.04$, R^2 = 57.5, RSD = 0.0101). Using information only from scans in the leg region led to a large reduction in prediction accuracy (R^2 = 25.2, RSD = 0.0133; Figure 2). By adding group effects on the intercept to the model, prediction accuracy improved substantially to R^2 38.1 ($P < 0.001$, RSD = 0.0121), although it remained considerably less than when information was used from CT scans across the rest of the body.

LLOIN. The LLOIN was predicted with low to moderate accuracy (R^2 = 34.0, RSD = 0.00684). Adding group effects to the intercept increased prediction accuracy to R^2 = 40.8 ($P = 0.001$). When using the reference set alone, prediction accuracy was decreased (R^2 = 17.6, RSD = 0.00765; Figure 2) yet was greatly increased by fitting group effects on the intercept ($P <$ 0.001, R^2 = 34.6, RSD = 0.00681). With information limited to CT scans in the loin region alone, LLOIN was poorly predicted (R^2 = 9.5, RSD = 0.00801, Figure 2). Group effects on both intercept and coefficients were significant ($P = 0.013$), but prediction accuracy remained low (R^2 = 26.0, RSD = 0.00726).

LSHLD. The LSHLD was predicted with low to moderate accuracy (R^2 = 36.5, RSD = 0.00788). Group effects on the intercept were important ($P < 0.001$). When using information only from the reference set, LSHLD could be predicted almost as accurately (R^2 = 32.5, RSD = 0.00812; Figure 2) with a slight improvement from including BW ($P = 0.044$, R^2 = 33.9, RSD = 0.00804). Fitting a group effect on the intercept improved prediction accuracy substantially ($P < 0.001$, R^2 = 43.9, RSD = 0.00741). When using information only from CT scans in the shoulder-chest region, prediction accuracy was markedly less (R^2 = 12.4, RSD = 0.00926), and including BW increased prediction accuracy only slightly ($P = 0.012$, R^2 = 15.3, RSD = 0.00912). However, the addition of an effect of group on both intercept and coefficients improved prediction accuracy considerably ($P < 0.001$, R^2 = 25.0, RSD = 0.00856).

Within Suffolk, for WHPJ, LHPJ, and LLEG, neither genetic line effect nor its interaction with sex improved the fit of the regression ($P > 0.05$) when included with the best set of predictors. Sex did explain significant variation in all 3 variables.

DISCUSSION

Breeding programs for terminal sire sheep in the United Kingdom select for lean tissue growth rate using an index including BW, lean weight, and fat weight (Simm et al., 2001). Although carcass size and composition are the main traits affecting carcass value, tissue distribution and fat partitioning may affect consumer satisfaction, efficiency of production, and processing and, thus, indirectly, overall value (Young et al., 2001). Inclusion of fat partitioning and tissue distribution in selection goals could help to improve carcass quality for the retailer and consumer. An accurate method of predicting these traits in the live animal is needed for this to be possible. This study shows that CT scanning using a limited number of cross-sectional scans can provide predictions in the live animal for some of these quality traits but not for others.

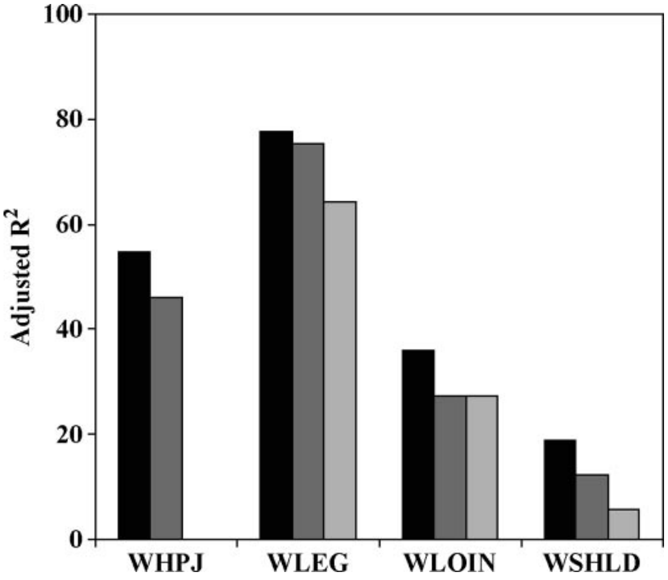

Figure 1. Comparison of adjusted R^2 values for proportion of carcass weight contained in higher-priced joints (WHPJ) and in leg (WLEG), loin (WLOIN), and shoulder (WSHLD) regions, predicted using the best predictors from the full set of 7 computed tomography (CT) scans (ischium, femur, hip, fifth lumbar vertebrae, second lumbar vertebrae, eighth thoracic vertebrae, sixth thoracic vertebrae; black bar), the 3 CT scans in the reference set (ischium, fifth lumbar vertebrae, eighth thoracic vertebrae; dark gray bar), and CT scans only from the region being predicted (light gray bar).

Fat Partitioning

Prediction of partitioning of carcass fat between subcutaneous and intermuscular depots with CT was poor. If used along with weights of fat and lean in the carcass, a measure of fat partitioning might have allowed selection to decrease intermuscular fat. However, very low prediction accuracy, coupled with the low heritability for this trait (Wolf, 1982; Conington et al., 1998), indicate that CT prediction of fat partitioning would not be a useful criterion for selection. There are 2 possible reasons for the poor prediction accuracy for this measure of fat partitioning. First, there may be a narrow range of values for fat partitioning, even among different breeds or sizes of animals. Previous analyses of these data, however, suggest there is some variation in fat partitioning among the genotypes, at least over the range of BW considered (Macfarlane, 2006); furthermore, the coefficient of variation for fat partitioning did not differ greatly from that for tissue distribution variables in these data. Second, there may be error with measurement of subcutaneous and intermuscular fat weight by CT scan tissue areas or dissection, or both.

Of these, it is more likely that the CT measurements did not accurately reflect variability in fat partitioning across the entire carcass; in only 2 of the 7 CT scans (ISC and TV8) could these fat depots be clearly delineated.

The intramuscular fat content in the LM was moderately well predicted with CT and thus could be included as a selection criterion in a breeding program. Intramuscular fat content of over 3% has been shown to be sufficient for meat quality characteristics such as tenderness and juiciness (Savell and Cross, 1988). From previous analyses of these data, some lambs, particularly Suffolk and Texel male lambs selected for lean tissue growth, had intramuscular fat content less than 3% at commercial slaughter weights of 40 kg (Macfarlane, 2006). With continued selection to decrease carcass fatness in these breeds, it will be necessary to monitor intramuscular fat content to ensure that it does not become too low, thereby compromising meat quality; such has proven to be a problem in pigs (Barton-Gade, 1990; Schwörer et al., 1995).

There is a strong positive relationship between dissectible carcass fat and intramuscular fat content (Kempster et al., 1986; Wood, 1990). Selection for decreased carcass fatness may therefore lead to decreased intramuscular fat, with potentially detrimental consequences on meat quality, an issue highlighted by results reported by Karamichou et al. (2006) in Scottish Blackface sheep and by Macfarlane (2006) in terminal sire breeds of sheep using the same data as in the present study. An independent measure of intramuscular fat content that can be included in selection strategies is a necessary counterbalance. The prediction equation derived in this study includes both lean density and carcass fat area in the LV2 scan. Using lean density alone may provide a more independent measure of intramuscular fat content. However, when attempted, prediction accuracy was substantially poorer. A better measure of lean density than that available in these data may improve prediction accuracy. Lean density in CT scan images may be influenced by mixed pixels, those composed of both lean and fat tissue, and may thus be difficult to characterize as either lean or fat. Lean tissue density in an entire CT scan therefore may not reflect the density of lean tissue alone. By analyzing images of specific muscles, or by using a more sophisticated analysis of pixels in the range of tissue density covering lean tissue, a better, more autonomous prediction of intramuscular fat may be possible.

Tissue Distribution

Computed tomography scanning can provide highly accurate predictions of carcass tissue weights in terminal sire sheep (Young et al., 1996, 2001; Macfarlane et al., 2006, all using the same data as in this study) and hill sheep (Lambe et al., 2003), as well as weights of tissues in different parts of the carcass (Kvame et al., 2004). However, the high accuracy of prediction of tissue weights in individual joints may simply reflect variation among animals in total tissue weight in the carcass; there may still be little variation among animals in the proportion of a tissue contained within a given joint. Our interest was to investigate the ability to predict the proportion of total carcass weight or lean contained within different parts of the carcass. The decreased prediction accuracies obtained as compared with those for weights of tissues in different joints by Kvame et al. (2004) likely reflect this different approach. Despite this, proportions of weight contained in the higher-priced joints and proportion of weight and lean contained in the leg region were still predicted with moderate to high accuracy. Proportions of weight and lean in other parts of the carcass were less well predicted, in particular in the shoulder region. Including a measure of the proportion of carcass or lean weight contained in higher-priced joints, or in the leg region in particular, along with overall carcass tissue weights in a selection index, may enable targeted improvement in distribution of lean or weight in the carcass. Because weight of lean in the higher-priced cuts shows a high heritability (Wolf, 1982), and prediction accuracies of weight and lean in higher-priced cuts are moderate to high, especially in the leg region, there is likely to be opportunity for genetic change in these traits.

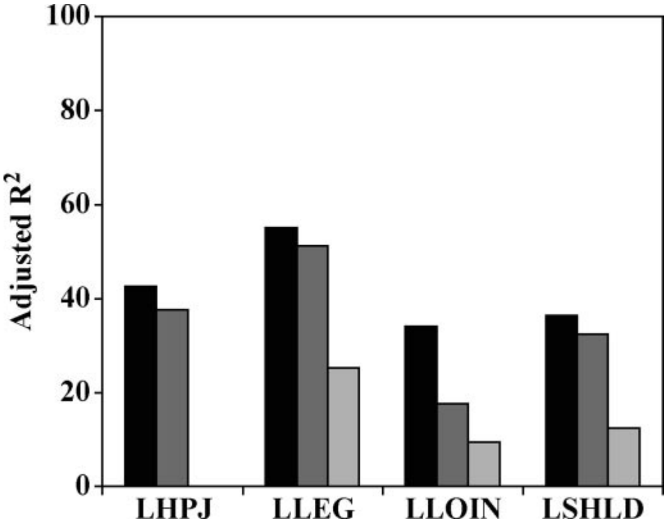

Figure 2. Comparison of adjusted R^2 values for proportion of carcass lean contained in higher priced joints (LHPJ) and in leg (LLEG), loin (LLOIN), and shoulder (LSHLD) regions, predicted using the best predictors from the full set of 7 computed tomography (CT) scans (ischium, femur, hip, fifth lumbar vertebrae, second lumbar vertebrae, eighth thoracic vertebrae, sixth thoracic vertebrae; black bar), the 3 CT scans in the reference set (ischium, fifth lumbar vertebrae, eighth thoracic vertebrae; dark gray bar), and CT scans only from the region being predicted (light gray bar).

Interestingly, the weight of lean contained within the shoulder region was better predicted than the total weight contained within the shoulder region. For the other regions, total weight was better predicted than lean weight. This is possibly due to the bone and fat in the shoulder region being more variable, which might be a function of the more complex shape of the skeleton and fat depots compared with lean tissue in this region.

This work has shown that most tissue distribution variables were predicted nearly as well based on the 3 CT scans from the reference set, which are collected as the standard in the commercial scanning service in the United Kingdom, as when using all 7 available CT scans. However, for proportion of lean contained within the loin, using the decreased set of scans gave a substantially worse prediction than when all 7 scans were used. If this measure was of interest, extra scans would be needed to achieve an accurate prediction. Because prediction accuracies are less for tissue distribution variables than for tissue weights (Macfarlane et al., 2006), it may be prudent to collect more CT scans to improve the quality of prediction. However, such a decision would need to balance the costs and benefits of collecting and interpreting additional scans.

In most cases, limiting the CT scans used for prediction to those from the carcass region being considered decreased prediction accuracy considerably. It is possible that use of information from more scans helped to overcome any measurement errors associated with individual scans. Additionally, where there was greater variation between animals in a tissue area at scan sites outside the carcass region being predicted, this predictor could still be usefully included. Because correlations between tissue areas in different scans are high (Macfarlane et al., 2006), such predictors provide further information on the carcass of an animal.

Accounting for BW does not improve prediction accuracy for most of the measures of tissue distribution and fat partitioning, and where it does, the increase is small. Predictions independent of BW are desirable to avoid collinearity if predicted tissue distribution or partitioning variables are included along with BW in a multitrait genetic evaluation or selection index. Most cases in which the inclusion of BW improved prediction accuracy were with the decreased set of CT scans. The additional variation explained by BW could instead be addressed by including more CT information in the prediction equation.

Prediction accuracy was improved for some variables by fitting an effect of genotype-sex group on the intercept of the regression equation, but not generally on the linear coefficients. However, the improvement in accuracy is not sufficient to justify the complexity of having separate prediction equations for different kinds of terminal sire sheep. This is particularly so because of the small size of the groups of animals used to test whether prediction equations were robust across different types of terminal sire sheep. In a genetic evaluation, ignoring group effects would affect predicted values, but not the ranking of animals based on estimated breeding values. Genetic evaluations are often conducted within breeds, typically with an adjustment for sex. Our analyses have shown that within a breed (Suffolk), genetic line had trivial effect on prediction and thus need not be accounted for directly. Therefore, across breed types like those used in this study, it is likely safe to use common prediction equations.

A more comprehensive spiral CT scanning technology is now available, which is not restricted to a limited number of cross-sectional CT scans at fixed anatomical landmarks within a given time period. Spiral CT scanning captures a large quantity of information along the full length of the body by collecting contiguous cross-sectional scans of a known thickness. Data from this can then be used to reconstruct 3-dimensional images. Using this method, more accurate predictions of tissue distribution are likely to be obtained, because it is possible to measure lean tissue mass in different carcass areas (Navajas et al., 2006), rather than using measurements of tissue areas in a limited number of cross-sectional scans.

In New Zealand, meat yield in the different regions of the carcass is becoming a more common measurement in abattoirs (Jopson et al., 2005), with payment schemes beginning to reflect distribution of weight and tissue across the carcass. In the future, it is likely that classification and grading schemes in the United Kingdom will include measurements of tissue weight in different regions of the carcass. In that case, there may be demand for selection tools that allow breeders to identify animals with more desirable distribution of weight or lean across the carcass. Because some lambs in terminal sire breeds are already being CT scanned as part of industry breeding programs, prediction of tissue distribution and intramuscular fat content could be done at little extra cost.

This study has shown that it is possible to obtain moderately to highly accurate predictions of intramuscular fat content and some tissue distribution variables (WHPJ, LHPJ, WLEG, LLEG), although variables related to the shoulder and loin were less well predicted. Use of the smaller set of 3 reference scans only decreased accuracy slightly. Developments in scanning and image analysis techniques will likely provide even more accurate methods of predicting tissue distribution and intramuscular fat. Genetic parameters and economic values for these traits in the relevant breeds will be required before tissue distribution and intramuscular fat can be formally incorporated into breeding programs. Still, this study demonstrates the potential of CT scanning to improve eating quality and tissue distribution of sheep meats.

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APPENDIX

Table A1. Coefficients of equations for predicting fat partitioning (FPART), intramuscular fat content of musculus longissimus dorsi (IAMF), proportion of carcass weight contained in the higher-priced joints (WHPJ) and in leg (WLEG), loin (WLOIN), and shoulder (WSHLD) regions using information from computed tomography (CT) scans[1]

	FPART		IAMF		WHPJ		WLEG		WLOIN		WSHLD	
Item	Coefficient	SE	Coefficient	SE	Coefficient	SE	Coefficient	SE	Coefficient	SE	Coefficient	SE
Intercept[2]	0.605	0.0227	0.04211	0.00838	0.532	0.00635	0.363	0.00575	0.0999	0.00434	0.276	0.00377
ISC_LA	−0.2056	0.0837	—	—	—	—	0.229	0.0489	−0.112	0.0457	—	—
ISC_FA	—	—	—	—	−0.222	0.0933	—	—	—	—	−0.135	0.0476
FEM_LA	—	—	—	—	0.200	0.0462	—	—	0.121	0.0381	—	—
FEM_FA	—	—	—	—	—	—	—	—	−0.135	0.0659	—	—
FEM_BA	—	—	—	—	—	—	—	—	—	—	0.113	0.0426
HIP_FA	—	—	—	—	0.541	0.134	0.298	0.0940	0.277	0.0825	—	—
LV5_FA	—	—	—	—	−0.404	0.127	−0.360	0.0937	—	—	—	—
LV2_LA	—	—	—	—	—	—	−0.155	0.0755	0.1429	0.0566	−0.195	0.0462
LV2_LD	—	—	−37.8	18.3	—	—	—	—	—	—	—	—
LV2_FA	—	—	0.1726	0.0168	—	—	—	—	—	—	—	—
TV8_LA	—	—	—	—	−0.2984	0.0799	−0.214	0.0715	—	—	0.102	0.0471
TV8_FA	—	—	—	—	0.360	0.116	—	—	—	—	—	—
TV8_SCFA	0.438	0.125	—	—	—	—	—	—	—	—	—	—
TV8_BA	—	—	—	—	−0.684	0.127	−0.646	0.116	—	—	—	—
TV6_LA	—	—	—	—	−0.247	0.0637	—	—	−0.113	0.0477	—	—
TV6_FA	—	—	—	—	−0.421	0.0954	−0.226	0.0592	—	—	0.128	0.0356
R^2, RSD[3]	6.5	0.0392	56.5	0.0608	54.7	0.0110	77.7	0.00927	36.0	0.00710	19.0	0.00719

[1] Coefficients and SE for CT scan tissue areas and densities are all $\times 10^{-5}$.

[2] ISC = ischium; LA = total area of lean; SCFA = areas of subcutaneous fat; LV2 = second lumbar vertebrae; LD = mean density of lean; FA = total area of fat; FEM = femur; HIP = hip; LV5 = fifth lumbar vertebrae; TV8 = eighth thoracic vertebrae; BA = total area of bone; TV6 = sixth thoracic vertebrae.

[3] RSD = residual SD.

Table A2. Coefficients of equations for predicting proportion of carcass lean weight contained in the higher-priced joints (LHPJ) and in leg (LLEG), loin (LLOIN), and shoulder (LSHLD) regions using information from computed tomography (CT) scans[1]

	LHPJ		LLEG		LLOIN		LSHLD	
Item	Coefficient	SE	Coefficient	SE	Coefficient	SE	Coefficient	SE
Constant[2]	0.594	0.00780	0.420	0.00602	0.107	0.00361	0.254	0.00422
ISC_LA	0.355	0.0643	0.376	0.0547	—	—	—	—
ISC_FA	—	—	—	—	0.220	0.0645	−0.1007	0.0180
FEM_LA	—	—	—	—	—	—	—	—
FEM_BA	−0.241	0.0767	−0.228	0.065	−0.127	0.0488	0.1083	0.0472
FEM_FA	—	—	—	—	−0.220	0.0707	—	—
HIP_FA	—	—	—	—	0.320	0.0918	—	—
HIP_BA	—	—	—	—	0.150	0.0590	—	—
LV5_LA	—	—	−0.242	0.0945	—	—	—	—
LV5_FA	−0.305	0.113	—	—	—	—	—	—
LV2_LA	—	—	—	—	0.157	0.0466	−0.4225	0.0555
LV2_FA	—	—	—	—	−0.238	0.0575	—	
TV8_LA	−0.288	0.135	−0.524	0.0742	—	—	0.3063	0.0502
TV8_BA	−1.117	0.158	−1.01	0.126	—	—	0.3822	0.0917
TV6_LA	−0.319	0.124	—		−0.124	0.0378	—	
R^2	46.2		55.0		34.0		36.5	
RSD[3]	0.0127		0.0103		0.00684		0.00788	

[1] Coefficients and SE for CT scan tissue areas are all $\times 10^{-5}$.

[2] ISC = ischium; LA = total area of lean; SCFA = areas of subcutaneous fat; LV2 = second lumbar vertebrae; LD = mean density of lean; FA = total area of fat; FEM = femur; HIP = hip; LV5 = fifth lumbar vertebrae; TV8 = eighth thoracic vertebrae; BA = total area of bone; TV6 = sixth thoracic vertebrae.

[3] RSD = residual SD.