Beef carcass composition assessed by X-ray computed tomography scanning of primal joints

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Introduction X-ray computed tomography (CT) measurements of live sheep have been used to predict carcass composition very accurately (Macfarlane *et al*., 2006). The utilisation of spiral CT scans (SCTS) for quantifying muscle volumes and weights, using automatic image analysis procedures has also been shown to be very accurate in sheep (Navajas *et al.,* 2006). Although the limiting size of the CT gantry prevents CT scanning of live beef cattle, beef primal joints are small enough to be scanned. Hence, SCTS could be used to quantify beef carcass composition, and provide valuable information for breeding programmes including composition faster than by anatomical dissection. The objective of this study was to develop a CT image analysis procedure to assess fat, muscle and bone weights of beef carcasses and to evaluate its accuracy.

Materials and methods Data used in this study were recorded on 7 Aberdeen Angus (AAx) and 15 Limousin (LIMx) crossbred steers that were slaughtered in 2006 (average carcass weight: AAx, 354 kg; LIMx, 360 kg). The left carcass sides were split into 20 primals 48 hours after slaughter and vacuum packed. Individual SCTS of each primal, containing contiguous cross-sectional images (slices) which were 8 mm thick, were collected. Later, primals were fully dissected into fat, muscle and bone. The first step for the image analysis was to estimate the thresholds of CT density for each tissue based on the frequency distribution of pixel values in all primals, in the range -256 HU upwards, and their dissection data. The estimated thresholds were those that minimised the prediction errors. The weights of muscle, fat and bone were calculated based on tissue areas and densities and the thickness of slices in the SCTS: Tissue weight = Σ tissue area x slice thickness x weighted average density of tissue, where weighted average density = Σ (area x tissue density)/ Σ area. Tissue densities were calculated for fat and muscle using the equation: Tissue density (g/cm^3) = (CT tissue density in HU x 0.00106) + 1.00062 (Fullerton, 1980). Bone density used in these calculations was 1.55 g/cm^3. Carcass composition was calculated by adding the tissue weights of all primals measured by CT or dissection. CT and dissection weights of fat, muscle and bone of primals and carcasses were compared using linear regression analysis (model y = ßx) with an intercept of zero because predictions were derived assuming a 1:1 association between CT (y) and dissection values (x).

Results The associations between the predicted composition of beef primals and their dissection values, and the accuracy (R^2) are presented in Table 1. Estimated regression slopes for the three tissues ranged between 0.99 and 1.01 and were not significantly different from one (P>0.05) for fat and bone. The R^2 values for the primal composition were high (0.91 to 0.99). They are similar to the accuracy of predicting sheep carcass composition from *in vivo* CT reference scans (Macfarlane *et al.*, 2006) and SCTS (Navajas *et al.*, 2006).

Table 1 Beef primals composition: associations between CT and dissection

Tissue	Estimated slope (± s.e.)	R^2	r.s.d
Fat	0.997 ± 0.006	0.91	0.26
Muscle	1.007 ± 0.003	0.99	0.32
Bone	0.994 ± 0.004	0.96	0.16

s.e.: standard error of estimates; r.s.d.: residual standard deviation

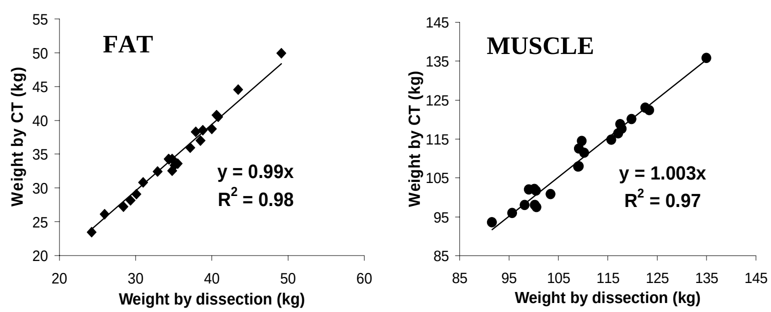

Figure 1 Total fat and muscle weights of beef carcasses by dissection and predicted by CT

The total carcass composition was also predicted with high accuracy by CT (Figure 1). In the case of carcass bone weight, the R^2 value was 0.96. The tissue thresholds estimated in this study will be independently validated in other datasets.

Conclusions Results of this study suggest that it is possible to quantify the weights of fat, muscle and bone of beef primals and of the carcass, with high accuracy, using CT. Procedures developed for image analysis and data management allow fast processing of a significant number of carcasses. This technique may reduce costs and time of assessing carcass composition in a large number of animals, as required for the estimation of genetic parameters and in breeding programmes, including progeny tests for carcass quality.

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References

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