

## Accuracy of virtual partial dissection by computed tomography as predictor of beef carcass composition

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**Introduction** Dissection is the reference method to measure carcass composition, which is one of the attributes that defines carcass value. Full carcass dissection is an expensive and time-consuming procedure, and therefore only suitable for a limited number of applications such as research trials involving a relatively small number of animals. Partial dissection using a sample joint was one of the first methods to be considered to reduce costs and increase the number of carcasses to be assessed. X-ray computed tomography (CT) is a non-invasive method recently evaluated as a predictor of beef carcass composition. Carcass tissue weights were assessed with  $R^2$  values between 0.96 and 0.97 based on the CT scanning of all primal cuts (Navajas *et al.*, 2009). The aim of this study was to compare the potential of the compositions of a forerib sample joint measured by CT and dissection as predictors of beef carcass composition.

**Materials and methods** Data were recorded on 30 Aberdeen Angus and 43 Limousin crossbred heifers and steers that were slaughtered with average (standard deviation) age and hot carcass weight of 584 (26.2) days and 342 (30.0) kg, respectively. At 48 h after slaughter, left carcass sides were split into 20 primal cuts (Navajas *et al.*, 2009), each small enough to pass through the CT scanner, and vacuum packed. Spiral CT scans (SCTS) were collected for each primal cut. After scanning, carcass side (CS) tissue weights were computed based on the fully dissection of all primal cuts into fat, muscle and bone. The weights of muscle, fat and bone of the foreribs (FR) were predicted by CT based on tissue areas and densities and the thickness of slices in the SCTS: Tissue weight =  $\Sigma$  tissue area x slice thickness x weighted average density of tissue, where weighted average density =  $\Sigma$  (area x tissue density) /  $\Sigma$  area. Tissue densities were calculated for fat and muscle using the equation: Tissue density ( $\text{g}/\text{cm}^3$ ) = (CT tissue density in HU x 0.00106) + 1.0062 (Fullerton, 1980). Bone density assumed in these calculations was  $1.55 \text{ g}/\text{cm}^3$ . The prediction equations for tissue weights in the CS were estimated from the composition of the FR using general linear models. The models fitted were: (i) simple regression models to analyse the association between the composition of the FR assessed by dissection and CT methods and CS calculated after dissection, i.e.  $\text{CSF}_D = a + b \text{FRF}_{CT} + e$ , where,  $\text{CSF}_D$  is the carcass side fat weight,  $a$  is the intercept,  $\text{FRF}_{CT}$  is the fat weight in the forerib by CT,  $b$  the regression coefficient and  $e$  is the residual error, and (ii) full model fitting breed (B), sex (S), CS weight (CSWT), FR weight (FRWT) and the weights of the other tissues in the FR, as suggested by Fisher (1990). For example, for  $\text{CSF}_D$ , the model was:  $\text{CSF}_D = a + B + S + b\text{CSWT} + c\text{FRWT} + d\text{FRF}_D + f\text{FM}_D + g\text{FB}_D + e$ , where  $\text{FRF}_D$ ,  $\text{FRM}_D$  and  $\text{FRB}_D$  were the weights of fat, muscle and bone of the FR measured by dissection, respectively; and  $b$  to  $g$  were regression coefficients.  $B$  and  $S$  were fitted as classificatory effects. In (ii), for each carcass tissue weight measured, all possible combinations of predictors were fitted separately by method (dissection or CT) using backward stepwise regression. Final model terms were chosen within method. Models were compared using adjusted coefficient of determination ( $\text{adj-R}^2$ ) and root mean square error (RMSE, kg).

**Results** Accuracies of the prediction models are presented in Table 1. Single regression models with the weights of fat, muscle or bone in the FR measured by CT as the only predictors to estimate fat, muscle or bone of the CS showed  $\text{adj-R}^2$  of 0.77, 0.60 and 0.52, respectively. By adding  $B$ ,  $S$ ,  $\text{CSWT}$  and  $\text{FRWT}$  to FR composition by CT improved the prediction accuracy of carcass fat and muscle weights significantly to  $\text{adj-R}^2$  values of 0.89 and 0.94, respectively, whilst the highest value for carcass

**Table 1** Fitted effects and accuracy of the models for each carcass tissue measured by dissection or predicted by CT

| Models & accuracy                      | Dissection |        |      | CT   |        |      |
|--|------------|--------|------|------|--------|------|
|  | Fat        | Muscle | Bone | Fat  | Muscle | Bone |
| (i) Forerib tissue weight as predictor |            |        |      |      |        |      |
| Adj-R <sup>2</sup>                     | 0.71       | 0.54   | 0.61 | 0.77 | 0.60   | 0.52 |
| RMSE                                   | 3.78       | 8.18   | 1.84 | 3.40 | 7.64   | 2.02 |
| (ii) Full model                        |            |        |      |      |        |      |
| Adj-R <sup>2</sup>                     | 0.87       | 0.95   | 0.84 | 0.89 | 0.94   | 0.80 |
| RMSE                                   | 2.56       | 2.82   | 1.17 | 2.34 | 2.89   | 1.33 |

bone weight was 0.80. In general, equations derived using CT data had slightly lower  $\text{adj-R}^2$  values for bone but similar or better accuracies for fat and muscle compared to those obtained using the FR composition by dissection.

**Conclusions** Virtual partial dissection by CT using the forerib as sample joint provides accurate predictions of CS tissue weights. It could be considered as a very accurate and fast alternative method to assess beef carcass composition, with minimum depreciation of the primals, that could be very useful for breeding programmes and research studies involving large number of animals, including the calibration of other indirect methods (e.g. *in vivo* and carcass video image analysis). Future cross-validation analysis is recommended.

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**References** Fisher AV 1990. Reducing Fat in Meat Animals. 155-343.

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