THE MEASUREMENT OF PIG CARCASS LEAN MEAT PERCENTAGE WITH X-RAY COMPUTED TOMOGRAPHY

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Introduction

The physical dissection of pig carcasses is presently the official reference method for the determination of the real lean meat content of pig carcasses in the European Community. But it is a very expensive and time consuming procedure. The results of a joint European project (EUPIGCLASS) recommended the inclusion in the future of scanning by CT as an alternative to the physical dissection method (Dobrowolski *et al.*, 2004). Consequently, the German authorities provided a CT at the Federal Research Centre for Nutrition and Food, Location Kulmbach, with the objective of having the facilities for more regular tests of the grading systems in Germany. In this paper, we present the scanning protocol adopted, and the results of an evaluation of the accuracy of the CT method. In particular, we propose a spectral analysis of X-ray attenuation data by partial least squares (PLS) regression, refined by a smoothing of the PLS calibration model.

Materials and Methods

Carcasses were selected according to a sampling scheme stratified by fat depth, carcass weight, and sex (for details, see Judas *et al.*, 2005). Left half-carcasses were selected at the slaughter line for grading and dissection. The chilled carcasses were transported to the Institute of Meat Production and Market Research in Kulmbach, and were prepared according to the requirements of EC Council Regulation (EEC) № 3220/84. Dissection was carried out by expert technicians of the institute between one and four days *post mortem* and immediately after CT scanning. All cuts except the head were dissected. Lean meat weight (LMW) was determined with tendons and coarse fasciae removed.

A Siemens *Somatom Plus 4* spiral computer tomograph was used for scanning. Scanning parameters were 140 kV tube voltage, 146 mA tube current, a rotation time of 1 sec with pitch 1. Reconstruction algorithm AB50 was applied. Slice thickness was 10 mm with a 460 mm squared field of view at a resolution of 512x512 pixels. Scanning was performed in 2–3 spirals per carcass and lasted 15–30 min.

CT scanning produces a series of images that show tissues in shades of grey according to their density (Figure 1, left). Each pixel of an image represents a voxel with a constant volume, in this case 8.1 mm³. Each grey value is the visualization of the variation in X-ray attenuation measured in Hounsfield units (HU). The total volume per HU value has specific bi-modal distributions that differ between carcasses (Figure 1, right). Peaks around -70 HU represent adipose tissue, peaks around +70 HU represent muscle tissue.

A problem in the interpretation and analysis of the image information stems from mixed voxels which embody both adipose and muscle tissue, or muscle and bone tissue, or tissue and air. Therefore, a calibration with dissection LMW is required.

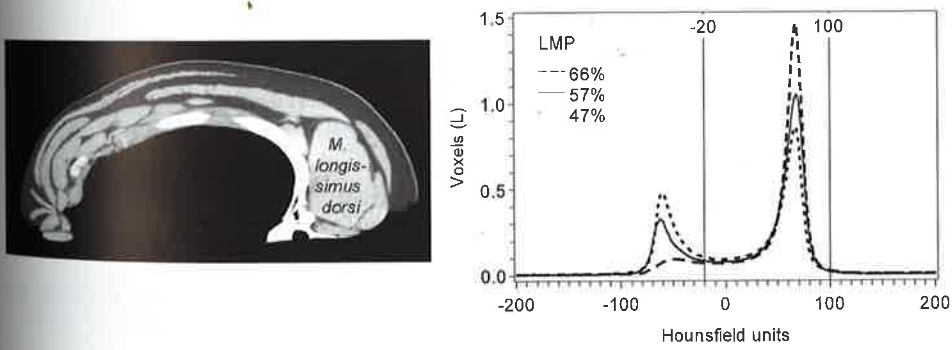

Figure 1: Left: Transversal grey-scale CT image of loin/belly. Right: Distribution of voxel-volume for discrete X-ray attenuation values (for three half-carcasses of 51 kg each, but with different LMP; the range -20 – 100 HU is optimal for the calibration of the PLS-model).

PLS is a regression method especially suited for the analysis of spectral data, and the distributions of voxel-volume vs. HU values can be treated as such. In this study, both cross-validation and test-set-validation have been used to identify an optimum model. For PLS, variables (i.e. volume per carcass per HU value) are centered and standardized. For the computation of estimated LMW from HU spectra, re-transformed unweighted regression coefficients have to be used (Figure 2, left).

Results and Discussion

The optimum fit was obtained when the range of HU values was restricted to -20 – 100 (Figure 2). Extending the range to lower or higher values increased the validation-RMSE determined by cross-validation. Values around 70 HU had the most influence on predicting LMW. But values of 85–90 HU had the highest raw correlation coefficients, which reflects their higher density. Negative regression coefficients at the extremes (<0 HU, >90 HU) stabilize the PLS predictions. This model proved also the best for an independent test data set, for which a sample of 19 carcasses was chosen (Figure 2, right). These test sample carcasses had been used for an initial evaluation of CT scanning parameters. They were selected from the same abattoir and with a similar stratification as the calibration data set.

The PLS regression coefficients display some erratic variation in the lower half and at the upper end of HU values (Figure 2, left). This is an expression of too little differentiation of HU spectra in these ranges, and of insufficient information from the sample to produce a continuous distribution that is to be expected theoretically. But this erratic result can easily be smoothed without any loss of prediction accuracy (Figure 2).

Lean meat percentage (LMP) was computed from LMW in relation to the weights of the dressed half-carcasses. There was a good fit between LMP from dissection and from CT analysis: the absolute RMSE was 0.5%-points, which corresponds to a relative RMSE of 0.9% of average dissection LMP (58.1%). Thus, the accuracy of determination of lean meat percentage with a CT is practically the same as with the reference dissection method (Nissen *et al.*, 2006).

Conclusions

High resolution CT scanning is suited to differentiation of carcass tissues with high precision. We conclude that CT scanning with a defined protocol, combined with well-calibrated PLS-regression, provides an applicable alternative to manual dissection. Smoothing of the PLS model allows the formulation of a general, robust relationship between Hounsfield spectra and lean meat content of carcasses.

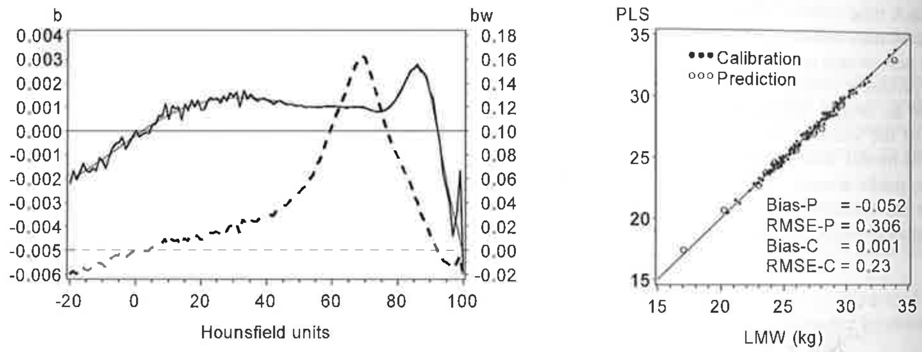

Figure 2: Left: PLS-model for -20 – 100 HU with 4 PC axes. The PLS model is optimized for centered and standardized data and produces weighted regression coefficients *bw* (dashed). The re-transformed raw regression coefficients *b* can be smoothed (solid curves). Right: Fit of the smoothed PLS model for the calibration data set (n=136) and the test data set (n=19); *LMW* — lean meat weight from dissection; diagonal — target line (identity).

References

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