

VISION VERSUS REFLECTANCE TECHNOLOGY FOR DEVIATIONS FOR SEX AND HALOTHANE GENOTYPE IN PIG CARCASS CLASSIFICATION

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Abstract – This work aims to compare the systematic deviations for sex and halothane genotype subpopulations between pig classification methods by automatic vision and semi-automatic reflectance. A sample of 209 carcasses, stratified according to sex (50% castrated males and 50% females), was measured by CSB Image-Meater® (IM) and CGM. An ear sample was analysed for halothane gene (Hal). The left sides were cut according to the EU procedure and the four main cuts were weighed and scanned by X-Ray tomography in order to determine lean meat percentage (LMP). For each device the LMP was regressed on the fat and muscle depths included in the official equations. For each equation were calculated the systematic deviations per level of the sex and Hal factors by mean difference between predicted and observed values. The LMP overestimation for castrated males increased from 0.4% with CGM to 0.7% with IM. The LMP overestimation for non-sensitive homozygotes Hal, not significant with CGM, rose to 0.5%. Systematic deviations for sexual types could be cancelled at least by a differentiated offset in the prediction equations.

Key Words – CGM, CSB Image-Meater®, X-Ray tomography.

I. INTRODUCTION

Sex and halothane gene, well known for their effects on carcass composition, are not included in the present EU authorised equations for carcass classification. Consequently, the prediction equations of lean meat percentage (LMP) could suffer from systematic deviations for these subpopulations. Automation of pig classification is expanding. It is accompanied by a change both in the measurement principle and in the location of the measured variables. Until mid-2013, pigs were classified in France by the CGM reflectance method, the name of the semi-automatic device being handled by an operator taking back measures. Since then, the pigs of the large slaughterhouses in the Uniporc West zone are classified by the Image-Meater® (IM) method, an automatic vision apparatus taking measurements at the junction between loin and ham. To determine LMP the Commission Regulation (EC) No 1249/2008 introduced the possibility to use X-ray tomography “provided that it gives satisfactory comparative dissection results”. The LMP measured by X-ray tomography according to the procedure developed by Daumas *et al.* [1] was found to be very close to the LMP measured by dissection. The objective of this work was to quantify the systematic deviations related to sex and halothane genotype factors for CGM and IM classification methods.

II. MATERIALS AND METHODS

A sample of 250 carcasses, stratified by sex, 50% female and 50% castrated male, was selected from three slaughterhouses. All selected carcasses were measured on the slaughter line by the IM and then on a side rail by the CGM manipulated by a skilled operator. The variables are those of the authorized methods [2, 3], namely:

- CGM: thicknesses of fat (G2) and muscle (M2) between the third and fourth last ribs, 6 cm from the dorsal midline and parallel to it;
- IM: two thicknesses of fat (G3 and G4) and two thicknesses of muscle (M3 and M4) on the splitline.

An ear sample was taken on each carcass and then sent to a laboratory for halothane genotyping. After cooling the left half carcasses were transported daily from each slaughterhouse to IFIP facilities in Romillé. The day after the killing, these half carcasses were prepared and cut according to the European procedure [4]. The four main cuts (ham, loin, shoulder and belly) were then weighed and scanned. Acquisition and image analysis were made according to the procedure developed by Daumas *et al.* [5] and reminded by Daumas *et al.* [1], allowing to calculate LMP. The LMP was regressed by ordinary least squares on the one hand on the CGM thicknesses and on the other hand on the IM thicknesses. For each equation were calculated the systematic deviations for each level of the two factors sex and Hal by mean difference between fitted and observed values. All calculations were performed with SAS software version 9.4 [6].

III. RESULTS AND DISCUSSION

Nine carcasses were discarded due to an incorrect identification by the IM apparatus. In addition, a number of samples could not be genotyped. As only two pigs were Hal sensitive homozygotes (nn) they were removed before statistical analysis. In the analysed dataset, comprising 209 pigs, sex-ratio and Hal-ratio were fairly balanced (Table 1). Moreover, the Hal-ratio was rather close to the proportions in the French population, estimated at 45% heterozygotes (Nn) and 55% non-sensitive homozygotes (NN). Table 1 presents the mean observed LMP (X-Ray) and the fitted LMPs per subpopulation. Table 2 shows the mean deviations per classification method and subpopulation.

Table 1. Mean LMP per classification method and per sexual type and Hal genotype

Method	Females	Castrates	Hal Nn	Hal NN
n	106	103	108	101
X-ray tomography	61.7	58.7	60.9	59.5
CGM	61.2	59.1	60.9	59.4
Image-Meater	61.0	59.4	60.3	60.0

Table 2. Mean deviation from the regression of LMP on classification variables per sexual type and Hal genotype

Method	Females	Castrates	Hal Nn	Hal NN
n	105	103	108	100
CGM	-0.41	+0.42	+0.02	-0.03
Image-Meater	-0.70	+0.72	-0.53	+0.55

The LMP overestimation for castrated males increased from 0.4% with CGM to 0.7% with IM. The LMP overestimation for Hal NN, not significant with CGM, rose to 0.6%. The increase in systematic deviations is consistent with the greater error of IM (RMSE = 2.29 vs 1.76) in estimating the LMP. Differences in prediction error (RMSEP) were already observed: 2.35 [2] and 2.20 [7] for IM versus 2.03 for CGM [3].

IV. CONCLUSION

The change from CGM to IM almost doubled the overestimation of castrated males and the underestimation of females, both now reaching 0.7% LMP. It has also made significant and of significant practical importance the effect of halothane genotype. The overestimation of the NN genotype and the underestimation of the Nn genotype increased to about 0.5%. The systematic deviations for the sexual types could be cancelled by a specific offset in the prediction equation. The systematic deviations for the halothane genotypes could be reduced by incorporating a prediction of the halothane status in the equation. These deviations could also be managed commercially.

ACKNOWLEDGEMENTS

We thank FranceAgriMer and Inaporc for their financial contribution to the experimental stage.

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