

ESTIMATION BY VISION OF PORK CUTS COMPOSITION FOR SEX AND HALOTHANE GENOTYPE SUBPOPULATIONS

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Abstract – This work aims to quantify the systematic deviations for sex and halothane genotype subpopulations in the estimation by automatic vision of pork cuts composition. A sample of 208 carcasses, stratified according to sex (50% castrated males and 50% females), was measured on line by the classification method CSB Image-Meater® (IM). 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 CT scanned in order to determine the lean meat percentage (LMP) in each cut. These LMPs were regressed on six IM potential predictors and the carcass weight. 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 absolute deviation per sexual types was the lowest (0.5%) in ham and the highest (1.4%) in belly. The deviations per Hal genotype ranged from 0.3% in shoulder to 0.8% in belly. In all models females and Hal heterozygotes were underestimated and vice-versa. The deviations per Hal genotype were about the half than per sex. The deviations per sex could be removed by at least a different intercept in the prediction equations.

Key Words – CSB Image-Meater®, lean meat percentage, scanner.

I. INTRODUCTION

The meat industry is interested in the prediction of the cuts yields in order to drive the cutting as efficiently as possible. Data from the EU compulsory pig classification give a good opportunity for such predictions. Automation of pig classification is expanding. Vision technology was chosen in particular in France.

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 (LM%) in the carcass and in the cuts suffer from systematic deviations for these subpopulations. The aim of this work is to quantify these deviations in the estimation by automatic vision of pork cuts composition. In case they would be considered important, this work would give the basis to discuss how to take into account sex and halothane gene.

II. MATERIALS AND METHODS

A sample of 250 pigs was selected in three abattoirs and stratified according to sex (50% castrated males and 50% females). Carcasses were measured on line by the CSB Image-Meater® (IM) classification device [1]. An ear sample was analysed for halothane gene (Hal). After overnight chilling the left sides were cut according to the EU procedure [2]. The four main cuts – ham, shoulder, loin and belly – were CT scanned in order to determine LM% according to the procedure developed by Daumas *et al.* [3]. Four dependent variables were studied: the LM% in each cut. From the 16 raw IM variables was built a pool of 6 potential predictors: 3 fat depths, 2 muscle depths and 1 length (Figure 1). Carcass weight was added as predictor. Regression models were selected by using the PRESS statistic in the GLMSELECT procedure of SAS software [4]. For each equation were calculated the systematic deviations per level of the sex and Hal factors by mean difference between predicted and observed values.

III. RESULTS AND DISCUSSION

Because essentially of missing values for Hal analyses the complete dataset comprised 208 observations. The proportions in the sample of Nn and NN genotypes, respectively 52% and 48%, were close to the proportions in the French population. The proportions of Hal genotypes intra-sex were well balanced too. The average LM% in each cut is presented per sexual type and Hal genotype in Table 1. These averages ranged from 55.3% in belly for castrated males to 74.5% in ham for females. Table 2 gathers the mean deviations of LM% with a similar layout.

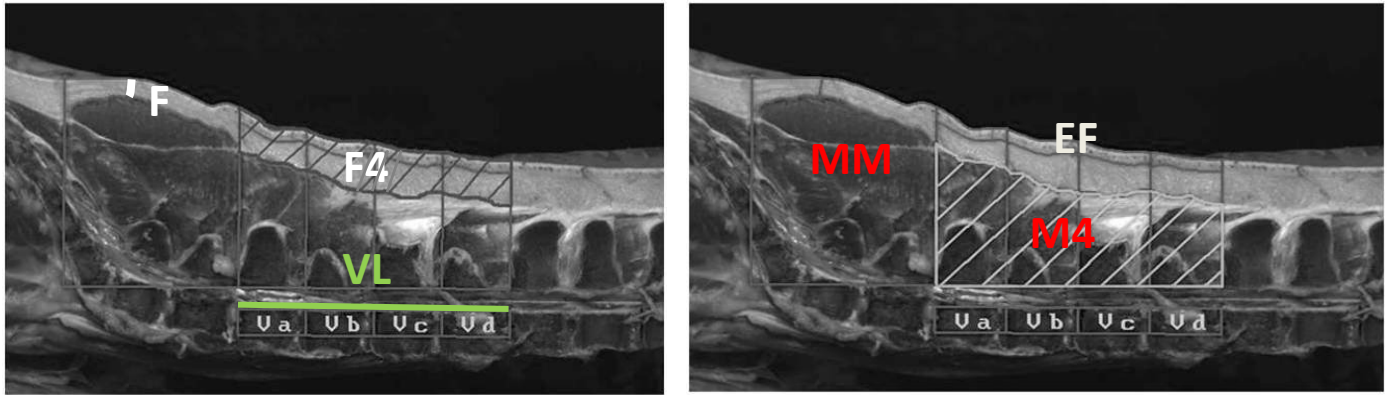


Figure 1. The six pre-selected predictors measured by the CSB Image-Meater® (IM)

F: minimal fat depth over *gluteus medius*, F4: average fat depth over 4 lumbar vertebra (Va-Vd), VL: average vertebra length of Va-Vd, EF: average external fat layer depth over Va-Vd, M4: average muscle depth over Va-Vd, MM: average depth of *gluteus medius* and lumbar muscle.

Table 1. Mean cut's LM% per sexual type and Hal genotype

Cut	Females	Castrates	Hal Nn	Hal NN
n	105	103	108	100
Ham	74.5	72.2	74.0	72.7
Shoulder	70.4	67.6	69.5	68.5
Loin	63.2	58.8	62.0	59.9
Belly	59.9	55.3	58.7	56.5

Table 2. Mean deviation from the regression of cut's LM% on IM per sexual type and Hal genotype

Cut	Females	Castrates	Hal Nn	Hal NN
n	105	103	108	100
Ham	-0.48	+0.49	-0.32	+0.36
Shoulder	-0.73	+0.74	-0.27	+0.29
Loin	-1.13	+1.16	-0.57	+0.62
Belly	-1.32	+1.35	-0.71	+0.76

In all models females and Nn genotypes were underestimated while castrates and NN genotypes were overestimated. The lowest absolute deviation per sex was in ham (0.5%) and the highest in belly (1.4%). The deviations per Hal genotype were lower than per sex, about the half, except in ham. They ranged from 0.3% in shoulder to 0.8% in belly.

IV. CONCLUSION

There was a systematic underestimation of the LM% in all cuts (ham, shoulder, loin and belly) for females and Hal Nn genotypes by the vision method CSB Image-Meater®; conversely, castrated males and NN genotypes were overestimated. The deviations per sex could be removed by at least a different intercept in the prediction equations. Hal genotype being generally unknown on line we recommend to analyse it during the body composition experiments. In case of important deviations, when the estimates of the proportions in population are available and differ from the proportions in the sample, the prediction equations could be calculated by weighed regression.

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