Prediction of lean meat content in pork carcasses: genetic effect

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Objectives: The lean meat content (LMC) is one of the criteria used in the breeding evaluation of pigs. The evaluation in the French collective system uses an equation predicting the old definition of the EU LMC from proportions of cuts, established on commercial slaughterpigs (Daumas, 2008). The aim of the study was to develop accurate models on purebred carcasses to predict the new definition of the EU LMC for improving breeding evaluations.

Materials and Methods: The trial was designed for 504 pigs: half of females from three paternal lines and half of uncastrated males from three maternal lines. The paternal lines were two Pietrain lines, either homozygous for the N allele (P_NN) or the n allele (P_ nn) of *RYR1 (halothane)* gene, and a Duroc (Du) line. The maternal lines were Large White (LW), and two Landrace lines (LR and LR_M6). Pigs were raised in a breeding station over 4 batches, distributed in 9 pens of 14 pigs. Feeding was ad libitum in a bi- phase sequence. Fat and muscle thicknesses were measured on the back by ultrasound around 110 kg. Target liveweight for slaughtering was 120 kg. Carcasses were measured with the French Image-Meater method (Blum *et al.*, 2014). The right sides were cut according to a normalized procedure and four cuts (backfat, loin, ham, belly) were weighed. The left carcass sides were scanned by computed tomography. Muscle volume and Lean Meat Content (LMC, %) were calculated according to the procedures described in Daumas and Monziols (2018). Least squares means of LMC were compared within paternal or maternal lines with a Tukey test. Means with a different superscript letter differ significantly with a p-value less than 5%. LMC was regressed on three sets of predictors: one average backfat and one muscle thickness measured on live pigs by ultrasound (US), two fat thicknesses and two muscle thicknesses measured at the splitline of half-carcasses by vision (IM), four cut proportions in half-carcasses (CUT). Genetic effect on the regressions was tested in a general linear model. Non-significant variables were removed before calculating the determination coefficient (R^2) and the root mean square of error (RMSE).

Results and Discussion: Data was validated only for 234 carcasses: 29 LR_M6, 30 LR, 33 Du, 40 P_NN, 46 P_nn and 55 LW. LMC was the lowest in Du (55.6[a]) and LR (57.3[a]), intermediate in LW (59.2[b]), P_NN (61.1[c]), LR_M6 (61.6[c]), and the highest in P_nn (64.2[d]).

The regressions of LMC on the whole sample gave a R^2 of 0.54 for US, 0.63 for IM and 0.82 for CUT, and a RMSE of 2.52 for US,

2.26 for IM and 1.56 for CUT. When adding genetic effect, the R^2 rose to 0.74, 0.73 and 0.93, respectively. For US model, interaction was significant with the mean fat thickness, muscle thickness was not significant, and the RMSE was 1.92. For IM model, genetic effect was only additive and the RMSE was 1.96. For CUT model, all interactions were significant except with % backfat, and the RMSE was 1.07.

Conclusions: As expected, the CUT method, which includes backfat proportion, was more accurate for predicting the new definition of the EU LMC than US and IM methods, which include only fat thicknesses. The genetic effect for the CUT method was important, allowing to reduce the error of more than 30 %. Therefore, it could be worthwhile to consider specific LMP prediction equations based on the cuts proportions per genetic population.

References:

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