

COMPUTED TOMOGRAPHY FOR COMPARING THE LEAN MEAT CONTENT OF DIFFERENT GENOTYPES OF ENTIRE MALE PIGS

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I. INTRODUCTION

In the framework of pig carcass classification a new EU regulation applying from July 2018 makes compulsory the use of a new reference. It is a lean meat percentage (LMP) based on total dissection (LMPtd) of a half-carcass. Manual dissection can be replaced by an unbiased computed tomography (CT) procedure. Daumas *et al.* [1] developed a pan-European CT procedure for determining this LMP. The hypothesis is such a procedure could be applied on very lean carcasses, issued from entire males of purebred used as terminal sires in production. The aim of this paper is to test this CT procedure to assess the LMP differences between several lean genetic groups and the three halothane genotypes.

II. MATERIALS AND METHODS

The study is based on LMP analysis with computed tomography (CT) of 2,471 entire male pigs from 13 genetic types, gathered in 3 groups: purebred Pi train-like breeds (P), crossbred Pi train x Large-White types (X) and crossbred fattening pigs (T). Halothane genotype was either determined or deduced. Table 1 gives the number of pigs by genetic group crossed with halothane genotype.

Table 1 Number of pigs by genetic group and halothane genotype

Genetic group	NN	Nn	nn	Total
Purebred Pi�train-like breeds (P)	308	133	346	787
Crossbred Pi�train x Large-White types (X)	328	538	0	866
Crossbred fattening pigs (T)	388	430	0	818
Total	1024	1101	346	2471

Half-carcasses were CT scanned with 3 mm slice thickness. LMPct was calculated according to Daumas *et al.* [1] and then multiplied by 0.965 to be scaled with manual dissection [1], giving LMPtd/ct.

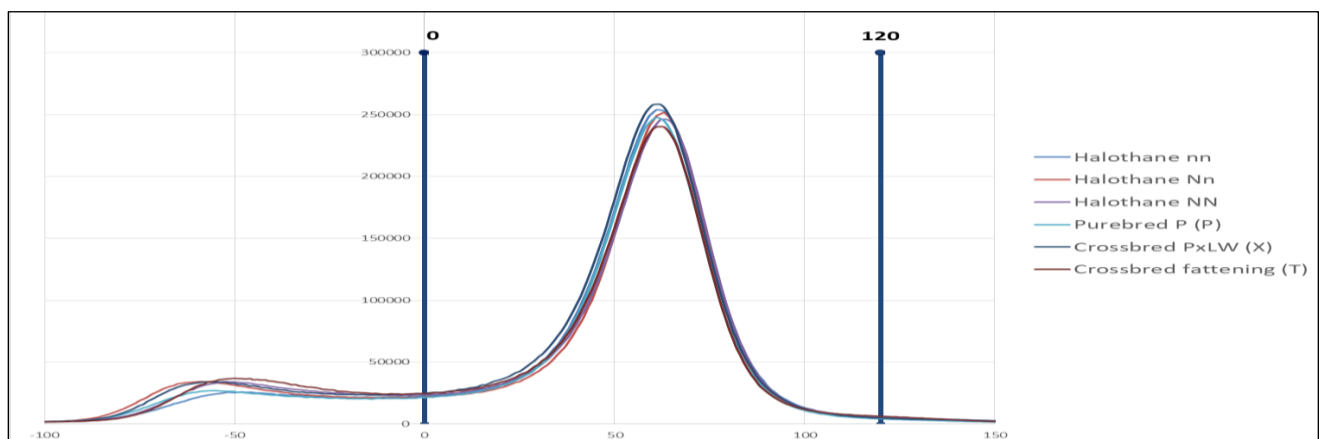


Figure 1. Histograms of HU values of six pigs: one for each level of genetic group and halothane genotype

To check the distribution of muscle volume six pigs were selected: one for each genetic group and one for each halothane genotype. In each category was chosen the pig which LMP was the nearest to the average of the category. Figure 1 shows the number of voxels for each Hounsfield Unit (HU) between -100 and +150 for each of the six selected pigs. The histograms showed no deviation from 60 HU for the muscle peak as well as from the 0-120 range for the muscle volume. Moreover, there was no visual abnormality on the processed images (not shown).

Genetic effects were tested by variance analysis in a linear model. Genetic group and halothane genotype were included as fixed effects; carcass weight was tested as covariable.

III. RESULTS AND DISCUSSION

Genetic group and halothane genotype as well as the covariable carcass weight were highly significant ($P < 0.0001$). Least square means are reported in Table 2. The main LMP difference (2.7) was observed between nn and NN. Heterozygotes were closer to NN (1.0) than to nn (1.7). Purebred animals were leaner (+1.3) than crossbred Piétrain x Large-White types themselves leaner (+1.0) than crossbred fattening pigs.

Table 2 Least Square Means of lean meat content (%) by genetic type and halothane genotype

	Genetic group			Halothane genotype		
	P	X	T	nn	nN	NN
LMPtd/ct	64.9 ^a	63.6 ^b	62.6 ^c	65.1 ^x	63.4 ^y	62.5 ^z

Values with different superscript in genetic group or in halothane genotype are significantly different ($P < 0.0001$)

Most of authors [2, 3, 4] reported higher differences between nn and Nn than between Nn and NN, conversely to Gispert *et al.* [5]. Salmi *et al.* [6] reported in a meta-analysis a random effects estimation of the least squares mean difference for lean % of -1.0 between NN and Nn genotypes with a 95% confidence interval of -1.3, -0.6. Nevertheless, the definition of lean % was not detailed. In fact, it was heterogeneous between studies, with different estimation methods, which might affect the mean differences.

IV. CONCLUSION

The use of the CT procedure developed by Daumas *et al.* [1] for determining the LMP of pig half-carcasses seems also useful for entire males. A specific thresholding of rind seems not be necessary. This procedure has allowed to quickly quantify genetic differences of LMP on about 2,500 pigs. Results, both between halothane genotype and genetic groups were consistent with the literature.

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