

Computed tomography for comparing the lean meat content of different genotypes of entire male pigs



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From July 2018 the EU reference for pig grading is the lean meat percentage (LMP) based on total dissection of a half-carcass. Dissection can be replaced by an unbiased computed tomography (CT) procedure. Daumas et Monziols (2018) 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.

Material & Methods

Material

- Sample of 2471 carcasses from entire male pigs
- Originated from 3 genetic groups
 - purebred Piétrain-like breeds (P)
 - crossbred Piétrain x Large-White types (X)
 - G4 crossbred fattening pigs (T)
- Determination or deduction of halothane genotype: NN (normal), Nn (heterozygous), nn (sensitive)

Methods

- Scan of half-carcass (3 mm slices)
- Calculation of LMP (Lean Meat Percentage)
 - Tissue segmentation on the Hounsfield scale: [0, 120] for muscle
 - Application of an average tissue density: 1.04 for muscle
 - Conversion into percentage
 - Scaling with dissection by multiplying by 0.965
- Estimation of Least Squares Means (LSmeans) of LMP by variance analysis
 - Fixed effects: genetic group & halothane genotype
 - Covariable: carcass weight

Results

- Significant effects ($P < 0.0001$) of halothane genotype, genetic group and carcass weight
- Main difference (2.7) between nn and NN
- Nn closer to NN (1.0) than to nn (1.7)

Reference: Daumas, G. & Monziols, M. (2018). Towards a pan-European computed tomography procedure for determining the new EU lean meat content of pigs. In Proceedings 64th International Congress of Meat Science and Technology, in press, 12-17 August 2017, Melbourne, Australia.

Conclusion

- The use of the CT procedure developed by Daumas & Monziols (2018) for determining the LMP of pig half-carcasses seems also useful for entire males. 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.

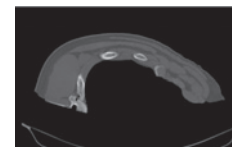
Material & Methods

Number of pigs by genetic group and halothane genotype

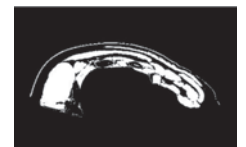
Genetic group	NN	Nn	nn	Total
Purebred Piétrain-like breeds (P)	308	133	346	787
Crossbred Piétrain x Large-White types (X)	328	538	0	866
Crossbred fattening pigs (T)	388	430	0	818
Total	1 024	1 101	346	2 471



CT acquisition (3 mm slices)



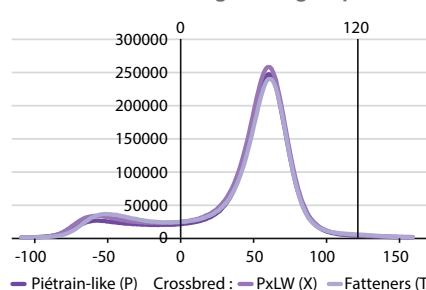
Raw image (middle)



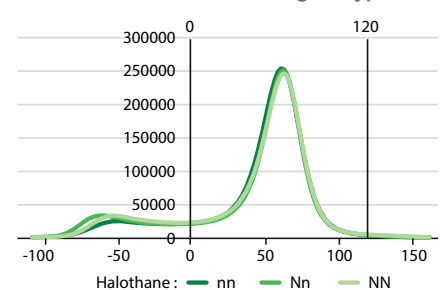
Thresholded image (middle)

Image analysis

HU histograms of 3 pigs having mean LMP in the 3 genetic groups

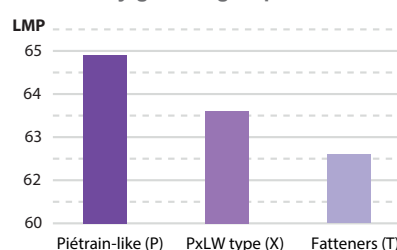


HU histograms of 3 pigs having mean LMP in the 3 halothane genotypes



Results

LSmeans of LMP by genetic group



LSmeans of LMP by halothane status

