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GENETIC ANALYSIS OF LONGISSIMUS DORSI FROM CT-SCANNED PIGS

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I. INTRODUCTION

Over the past 17 years, Topigs Norsvin has computed tomography (CT)-scanned approximately 80,000 nucleus boars at 120 kg, generating high-resolution 3D data. This valuable resource has been instrumental in developing new phenotypes for pig breeding. Since 2011, a semi-automatic algorithm has been employed to produce carcass cut phenotypes on live selection candidates, with the process becoming fully automated in 2019. To enhance economic profitability in swine breeding, it is essential to optimize each part of the carcass to align with market value, while adhering to biological constraints and animal welfare standards. In this study, we present a more detailed in silico partitioning of the pig anatomy, using convolutional neural network-based model. Additionally, we demonstrate how traits derived from this anatomical model can be utilized to breed for both the quantity and quality of specific muscles, exemplified by the Longissimus Dorsi (LD) muscle.

II. MATERIALS AND METHODS

As a part of Topigs Norsvin's breeding program, all test-boars are sedated and CT-scanned at 120 kg. Each scan consists of about 1200 images (dependent on the animals' length) with mm resolution. A subset of animals was labelled through an active learning procedure initiated with predictions from three different segmentation models, one for bones, one for heart and lungs and one for LD, constituting 29 different anatomical classes, together (Figure 1). These predictions were combined in in DarwinV7 (https://docs.v7labs.com/) and used to train 2D convolutional neural network (cnn) Resnet model (He et al., 2016). Then an iterative procedure was started, by alternately training Resnet models on all available labels, running inference on new animals, and manual corrections of labels in ITK-SNAP (http://www.itksnap.org/). A total of 36 animals with full segmentations, consisting of 63,295 images. Of all images, 33% were rotation augmentations to get more relevant variance related to positioning of the animal. A train/validation split of 0.75/0.25 trained the model until it reached a plateau at 60 iterations, yielding a validation F1-score of 0.94. Afterwards, the model was trained for 60 iterations, with all data in training set, yielding a final training F1-score of 0.97. The trained segmentation model was applied to a set of 14490 Duroc pigs, and for each of the anatomical 29 classes, the weight of mean and standard deviation of Hounsfield units (HU) values was calculated. In addition, intramuscular fat (IMF) content was measured using Near-Infrared Reflectance (NIR) spectroscopy, assessing the IMF levels in the LD muscle of the Duroc pigs after slaughter (Gjerlaug-Enger et al., 2010). CT-based phenotypes related to the LD class were extracted and corrected for "live weight at CT scanning" and "herd-year-season" in a subsequent genetic analysis, using ASReml (https://vsni.co.uk/software/asreml-r/). IMF was analyzed in a model with "herd-year-season" and "slaughter-weight" as fixed effect, for 7920 Duroc boars with this meat quality trait.

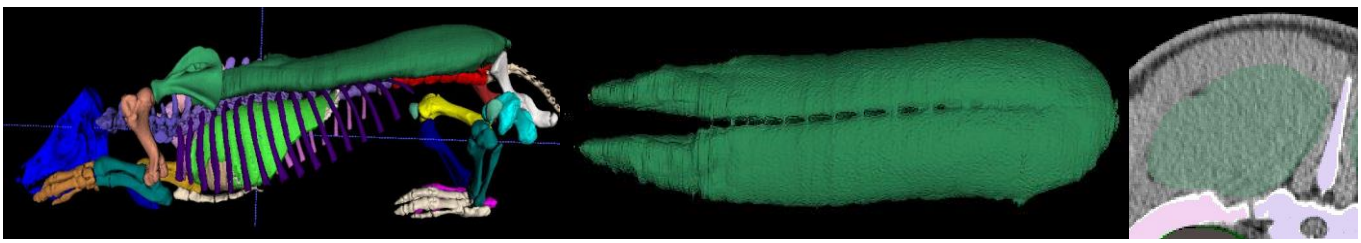


Figure 1 - 29-class segmentation model: AnatomicAI. Volume and cross section of Longissimus Dorsi muscle.

III. RESULTS AND DISCUSSION

The basic statistics of the LD traits (IMF, weight LD, mean and standard deviation of HU values, LD) are presented in Table 1. For the LD traits examined in this study, the estimated heritability's are moderate to high, with relatively small standard errors (Table 2). Additionally, phenotypic correlations between the traits are presented in Table 3.

Table 1 – Number of animals, mean, standard deviation of means, minimum, and maximum for traits measured on the Longissimus Dorsi muscle

Trait	n	Mean	Std	Min	Max
IMF (%)	7920	1.8	0.5	0.7	5.5
Weight (kg)	14490	6.6	0.5	4.3	9.1
Mean HU	14490	54.3	1.9	44.2	62.7
Std HU	14490	28.2	2.9	19.2	73.9

Table 2 - Heritability (h^2) with standard error (SE), phenotypic and genetic standard deviation (StdP and StdA)

Trait	h^2	SE	StdP	StdA
IMF (%)	0.67	0.03	0.45	0.37
Weight (kg)	0.76	0.02	0.42	0.37
Mean HU	0.65	0.02	1.71	1.39
Std HU	0.12	0.02	2.59	0.89

Table 3 - Phenotypic correlations (below diagonal) and genetic correlations (above diagonal; s.e. between brackets) for traits in Longissimus Dorsi muscle

	IMF	Weight	Mean HU	Std HU
IMF		-0.465	-0.602	0.075
Weight	-0.446 (0.034)		0.402	-0.054
Mean HU	-0.688 (0.029)	0.457 (0.026)		0.037
Std HU	0.150 (0.073)	-0.117 (0.063)	-0.147 (0.066)	

The phenotypic relationship between different traits in the LD muscle demonstrates that NIR predicted IMF is negatively correlated to both the weight and the mean HU of LD, and slightly positively correlated to standard deviation of HU values. A larger muscle is more likely to contain a higher proportion of type IIA fibers, as these muscle fibers are larger than type I fibers. Type IIA fibers, which are glycolytic, have less IMF compared to type I fibers. This explains the negative correlation between LD weight and IMF. Additionally, a negative correlation between IMF and muscle density (measured in Hounsfield units, HU) suggests that as fat content increases, muscle density decreases. Fat tissue may replace or fill spaces within muscle tissue, thereby reducing overall density. Fat has low HU values, typically between -120 and -90, which is significantly lower than the HU values for water (0 HU) and average muscle tissue (HU 54 in this study). Such fat tissue can appear as visible marbling and will also increase the variation between pixels measuring fat tissue and muscle fibers within the muscle. This accounts for the positive (though not significant) correlation between the standard deviation of HU and IMF.

IV. CONCLUSION

Integrating advanced CT imaging into pig breeding programs can significantly enhance genetic selection. High-resolution 3D data and convolutional neural network models enable precise anatomical segmentation and development of novel phenotypes, like muscle weight, density, and variation of HU values.
These traits show moderate to high heritability and significant phenotypic correlations to meat quality traits in breeding programs, like IMF. This allows for precise, cost-effective, automated phenotyping, optimizing both muscle quantity and quality in the breeding program. This exemplifies how non-invasive measurement methods represent a major advancement in swine breeding.

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