

## Genomic selection in pig breeding for improved meat quality

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**ABSTRACT:** A total of 4,576 Norsvin Landrace and 3,408 Norsvin Duroc test station boars, with records on intramuscular fat (IMF) from August 2008 to January 2014, were used for this study. A group of these animals, 1,538 and 1,014 Landrace and Duroc boars, respectively, were also genotyped with the Porcine 60K Illumina SNP chip as part of an ongoing breeding program. Traditional quantitative genetic analyses gave estimated heritabilities of 0.43 and 0.69 for Landrace and Duroc, respectively. With the use of these parameters, the accuracies of traditional selection and genomic selection were tested by comparing phenotype predictions with real phenotypes in a group of young selection candidates. Compared with traditional selection, the results show a large improvement in the accuracies of breeding values (from 0.36 to 0.63 in averages for three validations on two breeds) with the use of genomic selection, and we conclude that the entry of genomic selection in pig breeding programs will help facilitate breeding for meat quality.

**Keywords:** Meat quality; Intramuscular fat; Pig breeding; Genomic selection

### Introduction

An increased consumer's awareness of eating quality has forced pig breeding companies to pay more attention to meat quality, and some have included quality traits as an integral part of the breeding programs.

The breeding programs for the Norwegian Landrace and Duroc have been operated by Norsvin, Norway, for 55 and 22 years, respectively. Norsvin is the pig breeding association in Norway and has a long tradition of selection towards improved carcass and meat quality. By the 1960s, research on intramuscular fat (IMF) in pig meat was conducted at the Norwegian University of Life Sciences with the importance of IMF for juiciness and taste of the pig meat being emphasized (Vold (1969)). In the breeding goal anno 1987, IMF was included in the breeding goal for Norsvin Landrace, but the laboratory method was costly and not sufficiently accurate to detect the variation in this breed. Therefore, IMF was replaced by other meat quality traits such as pH and colour.

The Duroc pigs imported to Norway in 1992 were rather fat and the strength of this breed was an exceptionally good meat quality. Due to years of well-organized selection, this breed has changed dramatically. The current Norsvin Duroc breed is now very efficient with respect to

lean meat growth, and the original high meat quality for Duroc is maintained. This has been possible by giving the IMF and water holding capacity high economic values in the breeding goal. Subsequently, looking back at the adjustments of the breeding scheme, the meat quality has been weighted from 0% to 11% and from 19% to 41% in the breeding goals for Norsvin Landrace and Norsvin Duroc, respectively.

Several R&D projects on meat quality have been performed in Norsvin together with collaborators the last two decades. For example, a large experimental population with meat quality recording was established and genome scan performed in mid-90s. Significant QTLs for IMF and some fatty acids were detected, and comprehensive evaluation of eating quality was performed (Grindflek et al. (2001)). Furthermore, more recent studies demonstrated that it is possible to establish simple laboratory routines and high-quality rapid analyses of meat- and fat quality traits at a research abattoir. The methods established require low labor and enables large-scale measuring, but still the methods could provide high heritabilities for several meat and fat quality traits. For example, a NIR (Near Infrared Spectroscopy) analysis of IMF gave heritabilities of 0.50 and 0.62 for Norsvin Landrace and Norsvin Duroc, respectively (Gjerlaug-Enger et al. (2010)).

The IMF is unfavorably genetically correlated to pig production efficiency, e.g. feed efficiency and particularly lean meat percentage. In 2008, the Computed tomography (CT) scanning of boars became a part of the test program at the Norsvin boar testing station. Images from the CT scanner made it possible to obtain an accurate carcass composition from live pigs. Since these young boars are selection candidates for AI elite boars, this information substantially improves the accuracy of the selection for carcass traits (Gjerlaug-Enger et al. (2012)). Therefore, the Norsvin R&D team is now searching for a way to acquire a higher accuracy for the breeding values of meat quality traits for the living selection candidates, to improve the balanced selection between pig production efficiency and meat quality.

Two alternative strategies with different technologies are investigated. The first strategy is based on an *in vivo* analysis of IMF using Computed Tomography (Kongsro et al. (2013)) or using Real-time Ultrasound (Newcom et al. (2002)), since a phenotype of IMF on the selection candidate itself would be of high value because of the high heritability of the trait. The second strategy is

based on genomic selection (Meuwissen et al. (2001)), as genomic predictions can be applied early in life. Genomic selection is therefore particularly useful for meat quality traits, and this paper will be devoted to Norsvin's experience in increase of accuracy for IMF breeding values due to genomic selection.

## Materials and Methods

**Animals.** The data presented in this paper were obtained from boars tested from August 2008 to January 2014 at the Norsvin's boar testing station in southeastern Norway. In total, 4,576 Norsvin Landrace and 3,408 Norsvin Duroc boars with phenotypes on IMF were included. All animals entering the test after August 2011 were genotyped. Altogether, 1,538 Landrace and 1,149 Duroc boars had both phenotypes and genotypes in this study. Additionally, 3,275 and 1,878 relatives from the Landrace and Duroc populations, respectively, were also genotyped. The genotyping of the 60 K porcine SNP array was performed using the iScan platform (Illumina, San Diego, CA, USA), with 39,046 and 41,010 segregating SNP used for the Norsvin Landrace and Duroc breeds, respectively.

Boars were kept in single-breed groups of 12 pigs per pen, and fed ad libitum on conventional concentrates. The boars were entering the test at ~35 kg and ended the test at 120 kg. The boars were selection candidates to be AI elite boars based on estimated breeding values (EBV) and genetic uniqueness, and 100 young elite boars were selected annually out of the ~3,000 boars tested. In addition, Norsvin regularly exports Landrace and Duroc boars to several customers and subsidiaries. However, annually ~1,800 boars were slaughtered after test, and recordings for meat and fat quality were collected for the on going breeding program.

**The trait.** A FOSS FoodScan<sup>™</sup> near-infrared spectrophotometer was used for the determination of IMF in *M. longissimus dorsi*. Loin chops were trimmed for fat and homogenized, and the scanning region was 850 to 1050 nm (Gjerlaug-Enger et al. (2010)).

**Statistical analyses.** Initial computations were separately performed on each breed using SAS Proc GLM to evaluate non-genetic factors to be included in the model. For the analyzed traits, the fixed effects were herd x year, birth month, mother's parity number, the fixed regression of the number of littermates and the slaughter weight of the pig.

**The genomic relationship matrix.** The LDMIP software was used to calculate the genomic relationship matrix (G-matrix) by imputing missing genotypes and genotype probabilities for ungenotyped animals with the use of linkage disequilibrium analysis (Meuwissen and Goddard, 2010). Based on these genotypes, a genomic relationship matrix was calculated at each of the marker positions and averaged over the positions, using the methods in Van-

Raden (2008). These G-matrixes, including both genotyped and ungenotyped ancestors, contained 9,745 Landrace and 6,653 Duroc animals in the analyses used in this study.

**Quantitative genetic analyses.** The DMU software package (Madsen and Jensen (2010)) was used in the estimation of genetic parameters. The genetic parameters were estimated with the traditional relationship matrix only, while the BLUE and the BLUP values were estimated with use of an traditional relationship (I) or a combined relationship matrix, combining the traditional and the genomic relationship (II) in a one-step analysis (Legarra et al. (2009)). BLUP values for the effect of the animal from the first analysis was named EBV, while BLUP values from the second analysis were named GEBV, fitting into the genomic selection methodology (Meuwissen et al. (2001)).

**Validation of EBV vs. GEBV.** For a comparison of the two methods, traditional selection and genomic selection, the accuracy of EBV and GEBV was evaluated analytically and validated by correlating predictions to phenotype in a group of young selection candidates. In this study, the youngest boars of each breed had their phenotypes masked for this purpose, and the predictions were calculated from the BLUE and the BLUP values for each animal.

Accuracies are calculated as: accuracy = correlation/square root ( $h^2$ ), because breeding values cannot predict the environmental noise of the phenotypes.

## Results and Discussion

**Heritabilities.** Table 1 shows the genetic parameters estimated with traditional quantitative genetic methods. The heritabilities estimated for IMF were high and in good agreement with previously reported estimates obtained from chemical analyses of IMF (Hovenier et al. (1992); Suzuki et al. (2005)), as well as from other NIR measurements of IMF (Hermesch et al. 2000). As shown in Table 1, Duroc has a higher heritability, a higher phenotypic level and a larger variation observed for IMF compared with Landrace. This is also previously reported by Gjerlaug-Enger et al. (2010).

**Table 1. Heritabilities ( $h^2$ ) for intramuscular fat (IMF) with standard errors (SE), genetic and phenotypic standard deviations ( $\sigma_a$ ,  $\sigma_p$ ) in Norsvin Landrace and Norsvin Duroc.**

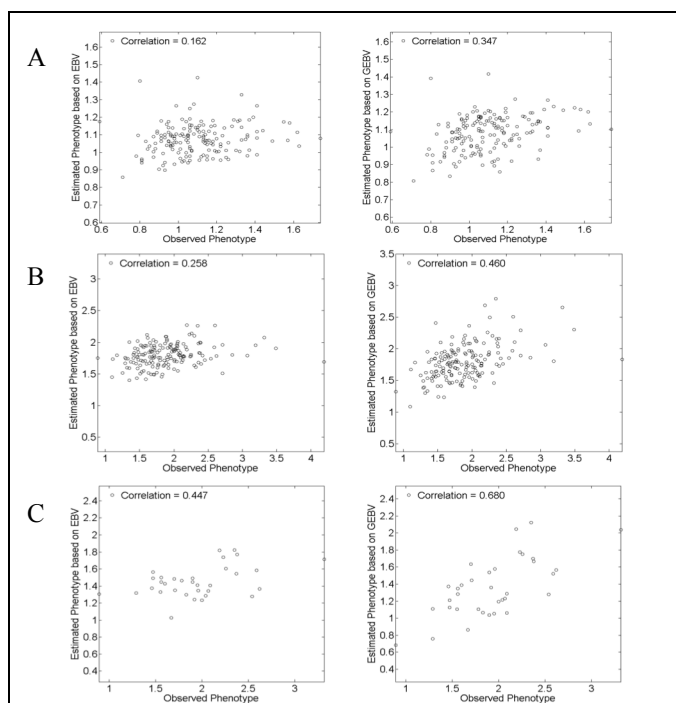
BREED	$h^2$	SE	$\sigma_a$	$\sigma_p$
Norsvin Landrace	0.43	0.05	0.12	0.18
Norsvin Duroc	0.69	0.06	0.40	0.48

**Validation.** The correlations between predicted phenotypes and actual phenotypes for IMF in Norsvin Landrace and Duroc breeds are presented in Figure 1, and accuracies for the EBVs and GEBVs are presented in Table 2. For both breeds, predictions based on GEBVs show much higher correlations to the phenotypes compared to

predictions based on EBVs. Furthermore, the accuracies of GEBVs were significantly better compared with the accuracies for EBVs, where the improvement ranges from 0.24 to 0.28 for the three examples shown in this paper.

The family structure of the validated animals was of importance for this result as well. Circumstances such as the number of animals from different half-sib groups representing the training animal, in addition to the number of animals representing the reference population, can influence the result. The accuracy of estimated breeding values will always increase as the tested half-sib group and the number of other tested relatives increases. Therefore, a large number of animals with masked phenotypes makes the validation test more complicated (Figure 1, A and B), compared with a test with a low number of animals (Figure 1, C). Example C is closer to the situation of boar selection from the boar test station at Norsvin, compared with example A and B. A certain size of half-sibs tested is preferred before the young boars are selected for AI.

IMF can be measured with high accuracy at slaughtered animals, but it is not perfect for breeding purposes. A higher accuracy for IMF breeding values on the live selection candidates would be highly beneficial. This study clearly shows that genomic selection can solve this problem. An improvement in accuracy for estimated breeding values of 0.27 on the selection candidates is convincing, and genomic selection will help facilitate breeding for meat quality.



**Figure 1.** The plots show the predicted phenotype with the EBV<sup>1</sup> or the GEBV<sup>2</sup> plotted against the observed phenotype for boars with masked phenotype. **A: 166 Landrace, B: 170 Duroc and C: 43 Duroc.**

EBV<sup>1</sup>: Estimated breeding values from pedigree relationship matrix

GEBV<sup>2</sup>: Estimated breeding values from genomic relationship matrix for single-step analysis using both pedigree and genomic information

**Table 2. Correlations between predicted phenotypes and actual phenotypes and accuracies for EBV<sup>1</sup> and GEBV<sup>2</sup> in Norsvin Landrace and Norsvin Duroc.**

BREED	N masked	r <sub>EBV,P</sub> <sup>3</sup>	r <sub>GEBV,P</sub> <sup>4</sup>	Acc <sub>EBV</sub> <sup>5</sup>	Acc <sub>GEBV</sub> <sup>6</sup>
Norsvin Landrace	166	0.16	0.35	0.25	0.53
Norsvin Duroc	170	0.26	0.46	0.31	0.55
Norsvin Duroc	34	0.45	0.68	0.54	0.82
Average values		0.29	0.50	0.36	0.63

EBV<sup>1</sup> and GEBV<sup>2</sup>: See Figure 1 for abbreviation definitions.

r<sub>EBV,P</sub><sup>3</sup>: Correlation between predicted phenotypes and actual phenotypes for IMF using traditional selection.

r<sub>GEBV,P</sub><sup>4</sup>: Correlation between predicted phenotypes and actual phenotypes for IMF using genomic selection.

Acc<sub>EBV</sub><sup>5</sup>: Accuracy for EBV = correlation/square root (h<sup>2</sup>).

Acc<sub>GEBV</sub><sup>6</sup>: Accuracy for GEBV = correlation/square root (h<sup>2</sup>).

with the same h<sup>2</sup> for both EBV and GEBV, estimated with traditional breeding value estimation.

Trait for all analyses: intramuscular fat (IMF).

## Conclusion

Compared with traditional selection, the results shows that there was a significant improvement in the accuracy of estimated breeding values for meat quality in young boar tested selection candidates when using genomic selection.

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