

**Genomic Relationships Give Improved Prediction Ability for a Selection of Traits in Norsvin Landrace and Duroc**

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**ABSTRACT:** To increase the genetic gain in our breeding program, Norsvin has implemented genomic selection for all traits in both the Landrace and Duroc breeds. Here we present some of our results leading to the decision of full implementation. In a cross validation study for different traits, with a variety of heritabilities, we observe that utilization of genomic relationship gives improved prediction ability. Precise ranking of animals is a key tool for efficient selection, and will increase the genetic progress in Norsvin’s breeding program.

**Keywords:** Genomic selection; One-step; genomic relationship

**Introduction**

Genomic selection (Meuwissen et al., (2001)) holds great promise for more efficient pig breeding (Tribout et al., (2013)), especially for traits that are not recorded on the selection candidates before selection (Lillehammer et al., (2011)). This includes traits that are not registered on the selection candidates themselves, e.g. intra muscular fat percent (IMF; Gjerlaug-Enger et al., (2010)) and mortality prior to 3 weeks of age (mortality) and traits that are expensive to measure (e.g. osteochondrosis scored by computed tomography (OCT; Aasmundstad et al., (2013))).

The one-step approach (Christensen and Lund, (2010); Legarra et al., (2009)) allows genomic prediction using information of genotyped and non-genotyped animals simultaneously and is found to outperform other GBLUP methods with regards to reliabilities (Gao et al., (2012)). In this study, we have analyzed how genomic estimated breeding values (GEBV) based on one-step approach deviates from the traditional estimated breeding values (EBV).

**Materials and Methods**

**Genomic relationships.** Genotyping of the 60 K porcine SNP array was performed using the iScan platform (Illumina, San Diego, CA, USA). Genotyped animals were included in the genomic relationship matrix if SNP markers passed quality thresholds of minor allele frequency, call frequency and Parent-Child Mendelian errors. The LDMIP

program (Meuwissen and Goddard, (2010)) was used to estimate the genotypes of the ancestors of the genotyped animals to avoid bias in the relationships (Ødegård et al., (2013)). The genomic relationship matrix (G-matrix) was calculated (VanRaden, (2008)) and a small number (0.001) was added to the diagonal elements to guarantee a positive definite matrix. Further, the G-matrix was scaled to have the same diagonal and off-diagonal averages as the corresponding traditional relationship matrix, using G-ADJUST in DMU (Madsen and Jensen, (2013)). Breeding values were predicted by DMU in a one-step approach (Christensen and Lund, (2010); Legarra et al., (2009)) as well as by traditional methods using pedigree based relationship matrices (Lynch and Walsh, (1998)).

**Statistical models.** For IMF, the fixed effects were herd x year, birth month and parity of sow while fixed regressions were the number of live born littermates and the slaughter weight of the pig. The random effects were the genetic effect of animal and the residual effect. The statistical model fitted for OCT included fixed effects of parity of the dam, herd x year and technicians scoring OC. The random effects included in the model were the pen in boar test, animal genetic effect and residual effect. For the trait “mortality”, a repeatability model was used. This was measured as a maternal ability trait, with number of records corresponding to number of parities of the sow. The fixed effects included the animal’s and the mother’s parity number, herd x year, season and the litter’s breed/crossbreed x year. Fixed regressions were correcting for the age and age squared of the sow within parity. Random effects were common litter effect, permanent environmental effect of the animal, animal genetic effect and residual effect. The number of animals with phenotypes and genotypes are shown in Table 1.

**Cross validation.** To examine the effect of improved relationship estimates, we used cross validation and compared the one-step approach for genomic selection with traditional breeding value estimation. Variance components were estimated, using the pedigree relationship matrix in DMU. Thereafter the observed phenotypes of a selection (Table 1) of young genotyped animals were

**Table 1. Essential statistics for the models and the cross validation test for the different traits.**

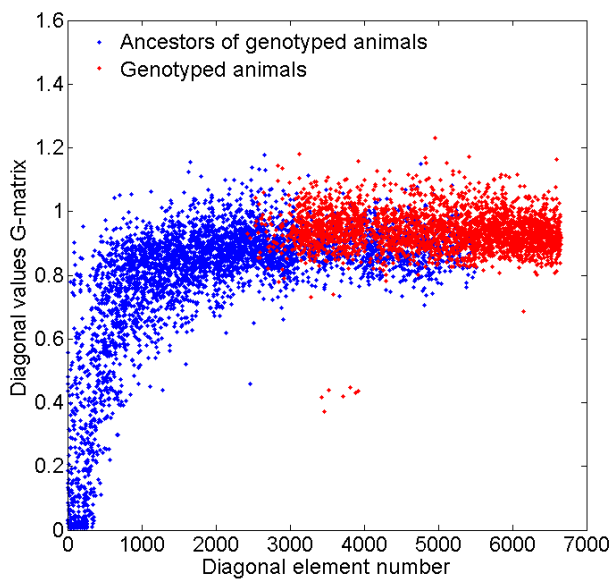
Trait	Breed	#* in GM	# in PR	# in GM&PR	# in test set	h <sup>2</sup>	Corr. OP-EP(EBV)	Corr. OP-EP(GEBV)
IMF	Landrace	9745	4410	1372	166	0.43	0.16	0.35
IMF	Duroc	6653	3373	979	170	0.69	0.25	0.46
OCT	Duroc	6653	1881	1648	200	0.27	0.32	0.38
Mortality	Landrace	9499	49406	4410	199	0.07	0.20	0.22

\*Hash (#): number of animals; GM: Genomic relationship matrix; PR: Phenotype recordings; h<sup>2</sup>: heritability; Corr.: correlation; OP: Observed phenotypic value; EP: Estimated phenotypic value.

masked and the mixed model equations were solved, giving estimates of breeding values and fixed, random and regression effects. These estimates were summed together, giving a phenotypic prediction for the masked animals, and compared with actual observed phenotypes.

## Results and Discussion

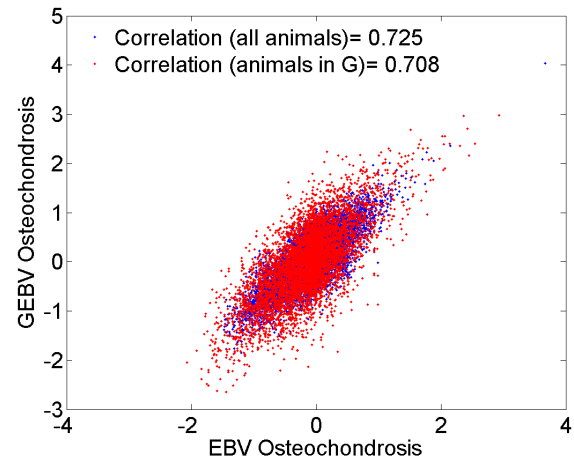
The use of genomic information alters the relationship matrix; it changes the ranking of animals and lead to improved statistical models. The raw genomic relationship matrices (example shown in Figure 1) had lower average values, but larger variance than pedigree relationship matrices. Some of the off-diagonal elements are even negative, which is not possible in the pedigree based relationship matrix. Among all traits in the Norsvin breeding scheme, OCT was the phenotype with largest deviation between EBV and GEBV, see Figure 2. This might be because this trait is measured only on a few individuals (2081 Duroc boars). As shown in Figure 2, the correlation is lower for the genotyped animals than for the remaining animals. This indicates that genotyping the selection candidates can strongly change the ranking of animals. Furthermore, a low correlation between EBV's and GEBV's indicates that there is a substantial potential by implementing genomic selection for the trait. On the other hand, a high correlation would indicate minor potential/risk for transition of the breeding methods.



**Figure 1: Diagonal element values of G-matrix for Duroc breed**

The traits studied here had a variety of heritabilities ranging from 0.07 to 0.69 (see Table 1.) and the GEBV led to improved prediction compared with EBV for all traits. The statistical models of traits with high heritability, e.g. IMF in Duroc (Figure 3), seem to improve prediction ability more than traits with medium and low heritability (e.g. mortality prior to 3 weeks of age, in Figure

4). The low increase of prediction ability of this maternal trait might also be because of the relatively small number of genotyped animals compared with the number of ungenotyped animals (see Table 1). The correlations between observed phenotype and estimated phenotype are sensitive to the number of animals masked and what animals that are masked. However, the differences in correlations of the estimated phenotype based on EBV or GEBV shows improved prediction ability of the genome based statistical models.



**Figure 2: Genomic vs. traditional breeding values for osteochondrosis for Duroc breed. Breeding values for animals contained in the G-matrix (6653 animals) is shown in red, the remaining (~115000) animals in blue.**

## Conclusion

Improved relationship estimates, based on genotyping data, changes the ranking of animals and increases the prediction ability of statistical models for animal breeding. Genotyping of selection candidates is therefore an important action for increasing the genetic progress of Norsvin breeds.

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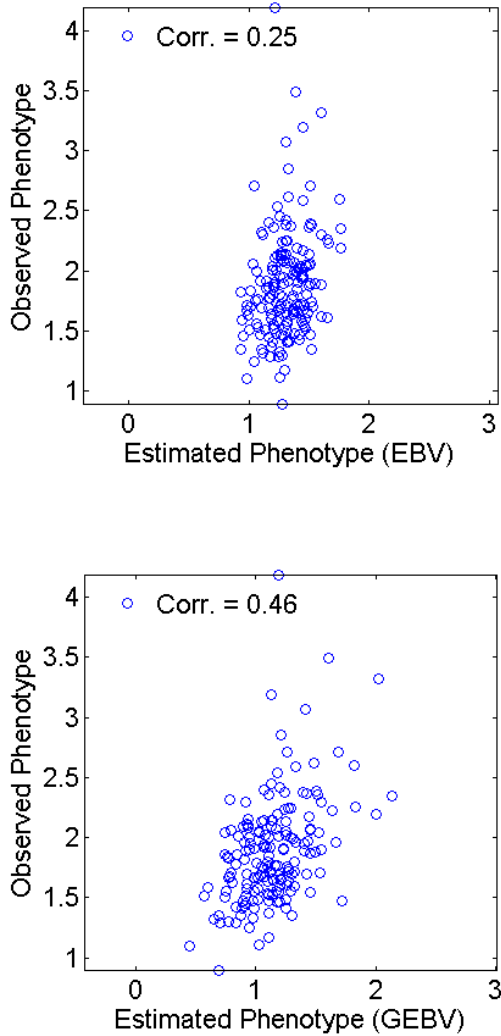
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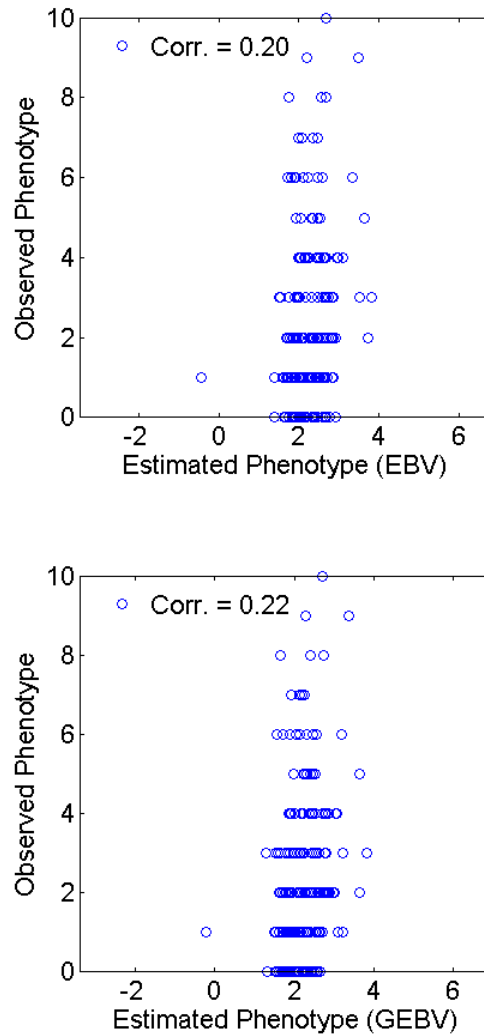
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**Figure 3:** Estimated intramuscular fat percent for Norsvin Duroc based on EBV (upper) and GEBV (lower) vs. the observed phenotype for the same animals.



**Figure 4:** Estimated number of dead piglet from birth to 3 weeks based on EBV (upper) and GEBV (lower) vs. the observed phenotype for the same Norsvin Landrace animals.