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Implementation of genomic selection in Norsvin genetic program; genetic gain in production and maternal traits in Norsvin Landrace

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ABSTRACT: Genomic estimated breeding values and traditional estimated breeding values were compared regarding to selection differences. Data from altogether 9745 genotyped Norsvin Landrace boars and Norsvin Landsvin sows were included in the genomic relationship matrix and combined with the pedigree relationship matrix using a single-step procedure. The GEBV's increases the selection difference for litter size and maternal ability traits between 26% and 67% compared to traditional EBV's. Correspondingly, for the production traits the selection differences increased between 8% and 34% using the GEBV. In January 2014 genomic selection was fully implemented within the breeding program for Norsvin Landrace and for Norsvin Duroc.
Key words: Genomic selection; Pig breeding; Genetic gain

Introduction

Genomic selection has the potential to increase the genetic progress substantially. Genomic selection enables through information from DNA testing a more accurate prediction of the animals' EBV due to a more accurate estimate of relationship between animals. Breeding values can be accurately estimated without phenotypic records of the selection candidates by using genomic selection (Meuwissen et al., 2001). In Norsvin Landrace, maternal traits and production traits are weighted 50% and 20%, respectively, in the total breeding goal (http://www.norsvin.no). At the boar test station recordings of production traits is obtained before selection of boars. For maternal traits, limited data is available on the boar tested selection candidates. Traditional breeding values gives low accuracy of these traits since boars are not progeny tested (Robinson and Buhr, 2005). Genomic selection could increase the genetic gain through increased selection intensity without increasing the generation interval. Norsvin's utilization of genomic selection is founded on our traditional breeding methods by modifying the relationship matrices in the current evaluation system. This is done by a single-step procedure which includes both the genomic relationship matrix (genotyped animals and close relatives) and the pedigree relationship matrix (un-genotyped animals). The aim of this study was to compare selection intensity using GEBV and traditional EBV for production traits and maternal traits.

Materials and Methods

Animal material and phenotypes. Genotyping of the 60 K porcine SNP array was performed using the iScan platform (Illumina, San Diego, CA, USA). In the EBV estimation of production traits and maternal traits, 9191 animals were included in the genomic relationship matrix. Production traits since 2008 from the boar test station were provided from the Norsvin data bank. Maternal traits since 2004 from nucleus and multiplying herds were provided from Ingris (national recording scheme). Traits, number of records, means and standard deviations (SD) are shown in table 1 and table 2. Selection candidates considered were 5 to 8 month old boars (316 boars) and 5% of these were selected (16 boars).

Table 1. Production traits. No. obs, mean and standard deviation (SD)

Trait	No. obs	Mean	SD
Age at 40kg	9049	84.6	6.7
Days from 40kg to 120kg	8799	77.2	7.0
Kg feed from 40kg to 120 kg	8665	177.6	12.5
Lean meat percentage	8026	68.1	3.7
Carcass percentage	8027	71.9	3.6

Table 2. Maternal traits. No. obs, mean and standard deviation (SD)

Trait	No. obs	Mean	SD
Total born	203533	13.7	6.7
Stillborn	203547	1.3	7.0
Piglet mortality	61222	1.46	12.5
Litter weight	127498	70.9	3.7
SD individual weight at 3 weeks within litter	127389	1.2	3.6

Statistical analysis. The LDMIP software was used to calculate the genomic relationship matrix by imputing missing genotypes and genotype probabilities for ungenotyped animals with the use of linkage disequilibrium analysis (Meuwissen and Goddard, 2010). The genomic relationship matrix was estimated at each of the marker positions and averaged over the positions using the methods of VanRaden (2008).

A multitrait animal model was used for both production traits and maternal traits. The models for each production trait include fixed effect of herd x year, month of birth and pen, and random effect of common litter and genetic effect of the animal. The repitability models for each maternal trait include fixed effects of parity, mother's parity, herd x year, season, breed of the litter x year and random effect of litter, permanent effect of the animal and genetic effect of the animal. The traits, litter weight at 21 days and SD of the individual piglet weight within litter, also include fixed effects of number of piglets at

weaning. All traits include regression of age and squared age of the sow within parity and litter weight and SD of the individual piglet weight within litter also include the regression of age and squared age at weaning.

The same models and DMU software (Madsen and Jensen (2013)) were used for estimation of GEBV's with using a traditional relationship matrix combined with the genomic relationship matrix using a one-step analysis (Legarra et al. (2009). Estimation of the EBV's including a traditional relationship matrix, only. The (Co)variance components, used for both calculation of GEBV and of EBV, were estimated with the traditional relationship matrix.

Results and discussion

Number of boars, means and SD of the breeding values and the selection difference for GEBV and EBV for total born as an example, is shown in Table 3. The selection gain for total born increase from 0.58 to 0.97 (67%) by using GEBV compared to using EBV in selection of boars.

Table 3. Genomic breeding value (GEBV) and traditional bredding value (EBV) for total born. No. of boars, mean and standard deviation (SD)

Total born	No.of boars	Mean	SD
GEBV, selected boars (5%)	16	1.77	0.32
GEBV, selection candidates	316	0.80	0.47
EBV, selected boars (5%)	16	1.40	0.14
EBV, selection candidates	316	0.82	0.29
Selection diff. GEBV		0.97	
Selection diff. EBV		0.58	

The increase in selection differences are shown in Table 4 for the production traits and maternal traits. All traits have a greater selection difference for the estimated GEBV compared to traditional EBV. The increase of selection intensities using GEBV's were larger for the maternal traits compared to production traits which agree with the result of Lillehammer et al. (2013). Current genotyped animals are already pre-selected boars, based on the parents average EBV. The accuracy of the GEBV is expected to increase even further if all selected sows in the nucleus herds are genotyped.

Table 4. Increase in selection diff. for production traits and maternal traits using a GEBV compared to EBV in selection of boars

Trait	Percentage Increase of selection diff.
Age at 40kg	15.8
Days from 40kg to 120kg	20.8
Kg feed from 40kg to 120 kg	9.8
Lean meat percentage	8.1
Carcass percentage	33.7
Total born	67.0
Stillborn	47.0
Piglet mortality	34.5
Litter weight	26.3
SD individual weight at 3 weeks within litter	58.8

Conclusion

Genomic selection has increase the genetic gain for traits in the breeding goals for Norsvin Landrace and Norsvin Duroc. Especially, maternal traits increase the genetic progress due to more accurately estimated breeding values. An advantage of genetic selection is that GEBV increase the accuracy of selection without phenotypic records on the selection candidates.

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