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Estimation of genetic parameters and accuracy of genomic prediction for production traits in Duroc pigs

*Bryan Irvine Lopez[1], Vanessa Viterbo[1,2], Choul Won Song[1], Kang Seok Seo[1]**

[1]*Department of Animal Science and Technology, Sunchon National University, Suncheon, Republic of Korea*

[2]*Department of Animal Science, College of Agriculture, Central Luzon State University, Science City of Muńoz, Republic of the Philippines*

**Corresponding author: sks@sunchon.ac.kr*

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Abstract: Genetic parameters and accuracy of genomic prediction for production traits in a Duroc population were estimated. Data were on 24 828 purebred Duroc pigs born in 2000–2016. After quality control procedures, 30 263 single nucleotide polymorphism markers and 560 animals remained that were used to predict the genomic breeding values of individuals. Accuracies of predicted breeding values for average daily gain (ADG), backfat thickness (BF), loin muscle area (LMA), lean percentage (LP) and age at 90 kg (D90) between pedigree-based and single-step methods were compared. Analyses were carried out with a multivariate animal model to estimate genetic parameters for production traits while univariate analyses were performed to predict the genomic breeding values of individuals. Heritability estimates from pedigree analysis were moderate to high. Heritability estimates and standard error for ADG, BF, LMA, LP and D90 were 0.35 ± 0.01, 0.35 ± 0.11, 0.24 ± 0.04, 0.42 ± 0.11 and 0.37 ± 0.03, respectively. Genetic correlations of ADG with BF and LP were low and negative. Genetic correlations of LMA with ADG, BF, LP and D90 were –0.37, –0.27, 0.48 and 0.31, respectively. High correlations were observed between ADG and D90 (–0.98), and also between BF and LP (–0.93). Accuracies of genomic breeding values for ADG, BF, LMA, LP and D90 were 0.30, 0.33, 0.38, 0.40 and 0.28, respectively. Corresponding accuracies using pedigree-based method were 0.29, 0.32, 0.38, 0.39 and 0.27, respectively. The results showed that the single-step method did not show significant advantage compared to the pedigree-based method.

Keywords: genetic improvement; genomic breeding value; production traits; swine

Genetic improvement is an integral part of many pig development programs. Selecting animals with high production potential based on their genetic value has been carried out in genetic improvement of herds. The advances in computing capacity and the development of animal mixed models using Restricted Maximum Likelihood procedures have all resulted in numerous studies estimating genetic parameters (Chen et al. 2002; Akanno et al. 2013). The estimation of genetic parameters for production traits is important to optimize breeding programs and to improve the sustainability of pig production in economical view (Kapell et al. 2009).

In the last decade, large amount of genomic information has become available regarding animal production and has been integrated in practical breeding programs. In particular, genomic

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selection that is based on the prediction of the genomic estimated breeding value (GEBV) of each individual using dense molecular markers has been implemented in many species. This breeding technology has been very successful in cattle, pig, chicken and other species because it provides additional information for selection and/or allows for a strong reduction in the generation interval (Boichard et al. 2016; Samore and Fontanesi 2016). Use of appropriate methods and models in prediction of the genetic merit of individual animals is the most reliable way of making use of genomic information in selection. Several methods and models to predict GEBV have been presented. Single-step methodology has been widely used in predicting GEBV in pigs (Christensen et al. 2012; Lourenco et al. 2016). One of the advantages of the single-step method is the capability to combine genotyped and non-genotyped animals in the same model. Pig industries usually genotype a limited number of animals because of the cost, where the single-step method becomes more cost effective.

Production traits such as average daily gain (ADG), backfat thickness (BF), loin muscle area (LMA), lean percentage (LP) and age at 90 kg (D90) are the main breeding goal traits in purebred Duroc population in Korea. Due to high importation of Duroc in Korea in recent years, genetic parameters must be investigated in the population. Estimates of genetic parameters may vary between populations and environments. Therefore, the objective of this study is to estimate the genetic parameters for production traits in Duroc population. Moreover, the potential of using genomic information in selection of future breeding stock is evaluated.

MATERIAL AND METHODS

Data were on 24 828 purebred Duroc pigs born from 2000 to 2016. The data included the performance traits, pedigree information for each animal, contemporary group, breed, date of birth, sex and parity number. Traits analyzed in this study were average daily gain (ADG), backfat thickness (BF), loin muscle area (LMA), lean percentage (LP) and age at 90 kg (D90). Performance tests for all animals were performed in accordance with pig testing standards of the Korean Animal Improvement Association.

The data were collected when the animals reached 70 to 110 kg body weight. The ADG was obtained from the difference between final weight and initial weight divided by the days fed. The body weight was measured at the time of testing. Backfat thickness (BF) was measured on live with A-mode scanners (PIGLOG 105) at the shoulder (on the 4th thoracic vertebrae), midback (last thoracic vertebrae) and loin (last lumbar vertebrae) averaged and adjusted to 90 kg using the formula:

$$BF = \text{Average BF} + \frac{(90\text{ kg} - \text{Test end weight}) \times \text{Average BF}}{(\text{Test end weight} - 11.34)}$$

The loin eye area (LMA) is a measurement of the large muscle in the pigs back. The loin eye is measured with the same probe that measures backfat. Eye muscle area was scanned at 5 cm ventrally to the dorsal point of the last thoracic vertebrae, then calculated using the following equation:

$$LMA = \text{LMA measurement} + + \frac{(90\text{ kg} - \text{Test end weight}) \times \text{LMA measurement}}{(\text{Test end weight} - 11.34)}$$

Lean meat percentage (LP) was acquired also from A-mode scanner by the function embedded and used for analyses without body weight adjustment. Days to reach 90 kg body weight (D90) were calculated according to Korean Swine Performance Recording Standards which assume body weight at birth as 1 kg.

$$D90 = \frac{(90\text{ kg} - \text{Test end weight}) \times (\text{Age at the test in days} - 38)}{\text{Test end weight}}$$

A total of 565 female pigs were genotyped using the Illumina PorcineSNP60 BeadChip that includes approximately 62 000 markers. After quality control procedures, there were 30 263 effective single nucleotide polymorphism (SNP) markers and 560 of the animals remaining that were used to predict the breeding values of individuals. In quality control analysis, SNP were retained if the marker was mapped to an autosome, the minor-allele frequency was greater than 0.05, and departures from Hardy–Weinberg equilibrium (0.15). Parent–progeny pairs were tested for conflicts. Remaining animals had a call rate greater than 0.95.

Preliminary computations were performed using the GLM procedure of SAS (Version 9.4) to evaluate non-genetic factors, that is, fixed effects to be included in the model. Variance and covariance components were estimated using the AIREMLF90 program of Misztal et al. (2014). The

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following multi-trait animal model was fitted to estimate genetic parameters:

$$y_t = \mathbf{X}b + \mathbf{Z}u + e$$

where:

y_t = vector of observation
t = five different traits
b = vector of fixed effects including contemporary group (herd-year-week of farrowing), sex and parity
u = vector of random animal effects
e = vector of random residual effects
X, Z = indices matrices

The variance-covariance matrices for the random additive genetic and residual effects were:

$$\text{var}[a] = \mathbf{G} \otimes \mathbf{A}, \text{ var}[e] = \mathbf{R} \otimes \mathbf{I}$$

where:

A = numerator relationship matrix among the animals
I = identity matrix

The pedigree was traced back to 1999, comprising 99 015 animals.

Here, the single-step method proposed by Aguilar et al. (2010) from marker and pedigree information was applied to predict breeding values of individuals. Univariate analyses were conducted using the same model described above, with the exception that the inverse of **A** was replaced by the inverse of the unified relationship matrix **H**. The inverse **H** matrix combines **A** with **G** defined as follows:

$$\mathbf{H}^{-1} = \mathbf{A}^{-1} + \begin{bmatrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{G}^{-1} - \mathbf{A}_{22}^{-1} \end{bmatrix}$$

where:

$\mathbf{G}^{-1}$ = inverse of the genomic relationship matrix as constructed by Gianola et al. (2009)
$\mathbf{A}_{22}^{-1}$ = inverse of the matrix of pedigree relationships among genotyped animals

The data set was split into training and validation data sets to examine the predicting abilities of the two methods. The birthdate January 1, 2014 was selected as the cutoff date for this split. The training and validation data sets consisted of 18 237 and 6 591 animals, respectively. The validation of breeding values was based on the method proposed by Legarra et al. (2008), whereas the phenotypes of the animals in the validation data set were removed and calculated using the formula:

$$\text{acc} = \frac{corr[GEBV, y_c]}{\sqrt{h_{yc}^2}}$$

where:

y_c = phenotype adjusted for fixed effects
h_{yc}^2 = heritability of adjusted phenotypes

Adjusted phenotypes were estimated using the full data. The linear regression of on GEBV was made to assess possible inflation of prediction in which the regression coefficient was expected to be close to 1.

RESULTS AND DISCUSSION

Phenotypic records for animals used in this study are described in Table 1. The average ADG, BF, LMA, LP and D90 with corresponding standard deviation were 652.48 ± 64.05 g/day, 12.84 ± 2.58 mm, 27.30 ± 2.86 cm^2, 57.90 ± 3.04% and 141.70 ± 10.96 days, respectively.

The additive variance, residual variance and heritability estimates, and their corresponding standard errors from a multi-trait animal model using the whole data set are shown in Table 2. The heritability estimates for each trait were found to be moderate to highly heritable ranging from 0.24 to 0.42. These estimates clearly indicate that these traits would be expected to respond to selection. The ADG and D90 had moderate heritability estimate of 0.35 and 0.37, respectively. These results were consistent with Su et al. (2012) observing 0.357 to 0.397 for ADG in Danish Duroc. However, higher estimates of 0.58 for ADG were obtained by Chang et al. (2017) from a Duroc population in Taiwan. Heritability for D90 was comparable to estimates reported by Kim et al. (2004) and Choi et al. (2013) but higher than the estimates of 0.28 reported by Akanno et al. (2013).

Heritability estimates for BF, LMA and LP were 0.35, 0.24 and 0.42, respectively. These estimates

Table 1. Descriptive statistics of phenotypic records

Trait	No. of records	Min	Max	Mean	SD
ADG (g/day)	24 828	390.86	904.23	652.48	64.05
BF (mm)	24 828	6.38	28.54	12.84	2.58
LMA (cm^2)	24 719	17.82	44.78	27.30	2.86
LP (%)	24 640	34.00	66.20	57.90	3.04
D90 (days)	24 828	109.00	221.00	141.70	10.96

SD = standard deviation, ADG = average daily gain, BF = backfat thickness, LMA = loin muscle area, LP = lean percentage, D90 = days to 90 kg

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Table 2. Estimate of variance components and heritability (SE) for the traits investigated

Trait	Additive variance	Residual variance	Heritability
ADG	1032.90 (38.94)	1893.00 (62.24)	0.35 (0.01)
BF	1.39 (0.05)	2.56 (0.08)	0.35 (0.11)
LMA	1.58 (0.08)	5.10 (0.11)	0.24 (0.04)
LP	2.34 (0.07)	3.25 (0.12)	0.42 (0.11)
D90	29.75 (1.09)	50.30 (1.78)	0.37 (0.03)

ADG = average daily gain, BF = backfat thickness, LMA = loin muscle area, LP = lean percentage, D90 = days to 90 kg

are lower in the study of Cabling et al. (2015) in 690 finishing Duroc pigs (0.65, 0.41 and 0.73 for BF, LMA and LP, respectively). Moreover, Do et al. (2013) and Dube et al. (2014) reported an estimate of heritability of 0.54 and 0.48 for BF, respectively. However, Guo et al. (2016) estimated the heritability for BF ranging from 0.30 to 0.32. The estimates for LMA and LP in this study were in agreement with those reported by Choy et al. (2015), using records from different pig farms in South Korea. Furthermore, the heritability estimates in this study were lower, higher or comparable to meta-analysis study of Akanno et al. (2013) in exotic swine breeds which include Duroc with an estimate of 0.46, 0.49. 0.42 for BF, LMA and LP, respectively. Differences in measurement, weight adjustment, sampling, population size and other factors could lead to various estimates of heritabilities in different literature.

Estimates of genetic and phenotypic correlations among production traits are presented in Table 3. ADG was estimated to have low negative genetic and phenotypic correlations with BF and LP. It was also found to have moderate negative correlations with LMA (–0.37) and high negative correlations with D90 (–0.98). Correlations between ADG and BF from various literature were quite variable. Imboonta et al. (2007) and Chang et al. (2017) reported negative genetic correlations of –0.05 and –0.19 between ADG and BF, respectively. However, Hoque et al. (2009) reported a positive genetic correlation of ADG with BF of 0.36. Furthermore, Akanno et al. (2013) reported a genetic correlation ranging from –0.21 to –0.47 between ADG and BF. The genetic correlation between ADG and BF depends on how tightly couples the traits are with the feed intake versus the ability to partition energy intake to lean tissue growth (Rothschild and Ruvinsky 2011). The genetic correlations of D90 with BF, LMA and LP were 0.04, 0.31 and 0.02, respectively. Chen et al. (2002) reported a genetic correlation of days to 113.5 kg with BF and LMA of –0.10 and 0.08, respectively. The genetic correlations of BF with LMA and LP were –0.27 and –0.93, respectively. These estimates were in the range of genetic correlations reported by Akanno et al. (2013).

The accuracies and bias of the predictions obtained for the production traits in this study are summarized in Table 4. The single-step methods have little gain compared to the pedigree-based method. The prediction accuracies using the pedigree-based method for ADG, BF, LMA, LP and D90 were 0.29, 0.32, 0.38, 0.39 and 0.27, respectively. The corresponding accuracies using single-step method for ADG, BF, LMA, LP and D90 were 0.30, 0.33, 0.38, 0.40 and 0.28, respectively. Jiao et al. (2014) reported in Duroc pigs an accuracy of 0.241 and 0.365 for ADG and BF, respectively. Moreover, Christensen et al. (2012) predicted an accuracy of 0.19 and 0.23 for ADG in Danish Duroc pigs using pedigree-based and single-step method, respectively. Single-step methods did

Table 3. Estimate of genetic (below diagonal) and phenotypic (upper diagonal) correlations between traits investigated

Trait	ADG	BF	LMA	LP	D90
ADG	1	–0.11	–0.28	–0.02	–0.98
BF	–0.05	1	–0.08	–0.60	0.10
LMA	–0.37	–0.27	1	0.37	0.25
LP	–0.03	–0.93	0.48	1	0.02
D90	–0.98	0.04	0.31	0.02	1

ADG = average daily gain, BF = backfat thickness, LMA = loin muscle area, LP = lean percentage, D90 = days to 90 kg

Table 4. Prediction accuracies and regression coefficients

Trait	Ped	Reg	GEBV	Reg
ADG	0.29	0.57	0.30	0.62
BF	0.32	0.81	0.33	0.83
LMA	0.38	0.88	0.38	0.89
LP	0.39	0.89	0.40	0.90
D90	0.27	0.54	0.28	0.59

ADG = average daily gain, BF = backfat thickness, LMA = loin muscle area, LP = lean percentage, D90 = days to 90 kg, GEBV = genomic breeding values, Ped = pedigree-based method, Reg = regression coefficients

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not show clear superiority over the pedigree-based method in this study maybe due to very few genotyped animals in both training and validation data set. Moreover, there were only few direct progeny of the genotyped females in the validation data set. The accuracy of prediction is affected by the size of the training population on which the SNP allele effects are estimated (Habier et al. 2007; Simianer 2009). Furthermore, Christensen et al. (2012) and Akanno et al. (2014) implied the choice of genotyped animals is more critical in prediction accuracy than the total number of genotyped animals.

The bias of the predictions was measured as the regression coefficients of y_c on EBV or GEBV as shown in Table 4. The biasness was investigated whether the regression coefficient was close to one. Regression coefficients in all traits were significantly different from 1, which indicated the predictions were generally biased. Regression coefficients of y_c on EBV were 0.57, 0.81, 0.88, 0.89 and 0.59 for ADG, BF, LMA, LP and D90, respectively. The corresponding regression coefficients of y_c on GEBV for ADG, BF, LMA, LP and D90 were 0.62, 0.83, 0.89, 0.90 and 0.59, respectively. Predictions for BF, LMA and LP were generally less biased than those of ADG and D90.

CONCLUSION

Our results showed that the heritabilities for production traits in purebred Duroc population were moderate to high ranging from 0.24 to 0.42. Genetic and phenotypic correlations among traits show that selection to improve LMA is likely to be associated with favourable changes in LP, but unfavourable changes in ADG and D90. In the accuracy of genomic prediction, results showed that the single-step method has little gain compared to the pedigree-based prediction in the accuracy of estimated breeding value. The implication is that it is crucial to determine which animals should be genotyped in genomic prediction.

REFERENCES

Aguilar I., Misztal I., Johnson D.L., Legarra A., Tsuruta S., Lawlor T.J. (2010): Hot topic: A unified approach to utilize phenotypic, full pedigree, and genomic information for genetic evaluation of Holstein final score. Journal of Dairy Science, 93, 743–752.

Akanno E.C., Schenkel F.S., Quinton V.M., Friendship R.M., Robinson J.A.B. (2013): Meta-analysis of genetic parameter estimates for reproduction, growth and carcass traits of pigs in the tropics. Livestock Science, 152, 101–113.

Akanno E.C., Schenkel F.S., Sargolzaei M., Friendship R.M., Robinson J.A.B. (2014): Persistency of accuracy of genomic breeding values for different simulated pig breeding programs in developing countries. Journal of Animal Breeding and Genetics, 131, 367–378.

Boichard D., Ducrocq V., Croiseau P., Fritz S. (2016): Genomic selection in domestic animals: Principles, applications and perspectives. Comptes Rendus Biologies, 339, 274–277.

Cabling M.M., Kang H.S., Lopez B.M., Jang M., Kim H.S., Nam K.C., Choi J.G., Seo K.S. (2015): Estimation of genetic associations between production and meat quality traits in Duroc pigs. Asian-Australasian Journal of Animal Sciences, 28, 1061–1065.

Chang H.L., Lai Y.Y., Wu M.C., Sasaki O. (2017) Genetic correlations between male reproductive traits and growth traits in growth performance tested Duroc, Landrace and Yorkshire breed boars. Animal Science Journal, 88, 1258–1268.

Chen P., Baas T.J., Mabry J.W., Dekkers J.C.M., Koehler K.J. (2002): Genetic parameters and trends for lean growth rate and its components in U.S. Yorkshire, Duroc, Hampshire, and Landrace pigs. Journal of Animal Science, 80, 2062–2070.

Choi J.G., Cho C.I., Choi I.S., Lee S.S., Choi T.J., Cho K.H., Park B.H., Choy Y.H. (2013): Genetic parameter estimation in seedstock swine population for growth performances. Asian-Australasian Journal of Animal Sciences, 26, 470–475.

Choy Y.H., Mahboob A., Cho C.I., Choi J.G., Choi I.S., Choi T.J., Cho K.H., Park B.H. (2015): Genetic parameters of pre-adjusted body weight growth and ultrasound measures of body tissue development in three seedstock pig breed populations in Korea. Asian-Australasian Journal of Animal Sciences, 28, 1696–1702.

Christensen O.F., Madsen P., Nielsen B., Ostersen T., Su G. (2012) Single-step methods for genomic evaluation in pigs. Animal, 6, 1565–1571.

Do D.N., Strathe A.B., Jensen J., Mark T., Kadarmideen H.N. (2013): Genetic parameters for different measures of feed efficiency and related traits in boars of three pig breeds. Journal of Animal Science, 91, 4069–4079.

Dube B., Mulugeta S.D., Dzama K. (2014): Investigating maternal effects on production traits in Duroc pigs using animal and sire models. Journal of Animal Breeding and Genetics, 131, 279–293.

https://doi.org/10.17221/150/2018-CJAS

Gianola D., de los Campos G., Hill W.G., Manfredi E., Fernando R. (2009): Additive genetic variability and the Bayesian alphabet. Genetics, 183, 347–363.

Guo X., Christensen O.F., Ostersen T., Wang Y., Lund M.S., Su G. (2016): Genomic prediction using models with dominance and imprinting effects for backfat thickness and average daily gain in Danish Duroc pigs. Genetics Selection Evolution, 48, 67.

Habier D., Fernando R., Dekkers J. (2007): The impact of genetic relationship information on genome-assisted breeding values. Genetics, 177, 2389.

Hoque M.A., Kadowaki H., Shibata T., Oikawa T., Suzuki K. (2009): Genetic parameters for measures of residual feed intake and growth traits in seven generations of Duroc pigs. Livestock Science, 121, 45–49.

Imboonta N., Rydhmer L., Tumwasorn S. (2007): Genetic parameters and trends for production and reproduction traits in Thai Landrace sows. Livestock Science, 111, 70–79.

Jiao S., Maltecca C., Gray K.A., Cassady J.P. (2014): Feed intake, average daily gain, feed efficiency, and real-time ultrasound traits in Duroc pigs: II. Genomewide association. Journal of Animal Science, 92, 2846–2860.

Kapell D.N., Ashworth C.J., Walling G.A., Lawrence A.B., Edwards S.A., Roehe R. (2009): Estimation of genetic associations between reproduction and production traits based on a sire and dam line with common ancestry. Animal, 3, 1354–1362.

Kim J.I., Sohn Y.G., Jung J.H., Park Y.I. (2004): Genetic parameter estimates for backfat thickness at three different sites and growth rate in swine. Asian-Australasian Journal of Animal Sciences, 17, 305–308.

Legarra A., Robert-Granie C., Manfredi E., Elsen J.-M. (2008): Performance of genomic selection in mice. Genetics, 180, 611–618.

Lourenco D.A.L., Tsuruta S., Fragomeni B.O., Chen C.Y., Herring W.O., Misztal I. (2016): Crossbreed evaluations in single-step genomic best linear unbiased predictor using adjusted realized relationship matrices. Journal of Animal Science, 94, 909–919.

Misztal I., Tsuruta S., Lourenco D., Aguilar I., Legarra A., Vitezica Z. (2014): Manual for BLUPF90 Family of Programs. University of Georgia, Athens, USA.

Rothschild M.F., Ruvinsky A. (2011) The Genetics of the Pig. CABI, Wallingford, UK.

Samore A.B., Fontanesi L. (2016): Genomic selection in pigs: State of the art and perspectives. Italian Journal of Animal Science, 15, 211–232.

Simianer H. (2009): The potential of genomic selection to improve litter size in pig breeding programmes. In: Proc. 60th Annu. Mtg., European Association for Animal Production (EAAP), Barcelona, Spain, 210.

Su G., Christensen O.F., Ostersen T., Henryon M., Lund M.S. (2012): Estimating additive and non-additive genetic variances and predicting genetic merits using genome-wide dense single nucleotide polymorphism markers. PLoS ONE, 7, e45293.

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