Genomic prediction including imprinting effects for average daily gain, backfat thickness, and intramuscular fat content in Japanese Duroc pigs

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Summary

This study evaluated the performance of two models including imprinting effects based on genomic data by estimating variance components and assessing prediction accuracy for average daily gain (DG), backfat thickness (BF), and intramuscular fat (IMF) content in Japanese Duroc pigs. These two models including imprinting effects were (1) model ADI based on genotypic values and (2) model DPM based on gametic values. The models were compared to model A, which included only additive genetic effects. A total of 836 animals were genotyped using the Illumina PorcineSNP60 BeadChip. The reference population comprised 444 animals for DG and BF, and 166 animals for IMF. The test population comprised 136 animals for all traits. Prediction accuracy was evaluated by calculating Pearson correlation coefficients between the predicted phenotypic values and observed phenotypic values. For all traits, compared to model A, estimates of total genetic and residual variances were larger in model ADI and smaller in model DPM. Broad-sense heritabilities of DG, BF, and IMF estimated from model A exceeded those from model ADI by 13%, 10%, and 9%, and exceeded those from model DPM by 12%, 8%, and 7%, respectively. Models ADI and DPM did not improve prediction accuracy in the test population and even yielded lower prediction accuracies for DG and IMF. In contrast, for all traits, the prediction accuracies in the reference population obtained from models ADI and DPM were higher than those from model A. These results might be due to overfitting in models ADI and DPM or the number of animals in the reference population.

Keywords: imprinting effect, genomic best linear unbiased prediction, Duroc pig

Introduction

Genomic imprinting is an epigenetic process involving DNA methylation and histone modifications that distinguishes the expressions of maternal and paternal alleles. An imprinted gene shows lower expression than the copy from the other parent. The imprinting effect contributes to the variation of quantitative traits such as carcass composition and growth traits in models based on pedigree information (Neugebauer et al., 2010; Tier & Meyer, 2012). Nishio & Satoh (2015) recently developed models incorporating the imprinting effect using genome-wide single nucleotide polymorphisms (SNPs). However, there is little information on the performance of these models using real livestock data. Therefore, this
study evaluated the genetic variance components and prediction accuracy determined by two models using phenotypes and SNP markers in Japanese Duroc pigs.

**Material and methods**

**Data**

Genotypes, phenotypes, and pedigree information have been reported previously by Sato et al. (2016). A total of 836 purebred Duroc pigs from the National Livestock Breeding Center in Japan were used. Pigs in the first and second generations were regarded as the base population, and closed breeding was subsequently performed from the third to the seventh generation. The pigs were selected on the basis of average daily gain (DG) from 30 to 105 kg, backfat thickness (BF) at 105 kg weight, ultrasonically measured loin eye muscle, and intramuscular fat (IMF) content. This study focused on DG, BF, and IMF because these traits are reported to exhibit an imprinting effect (Guo et al., 2016; Neugebauer et al., 2010). DG and BF were measured in all pigs, and IMF was measured in slaughtered sib-tested pigs. The descriptive statistics for three traits are shown in Table 1.

All pigs were genotyped using an Illumina PorcineSNP60 BeadChip. A total of 38,114 SNPs across 18 chromosomes met the following requirements: each SNP had a minor allele frequency greater than 0.01, a call rate score greater than 0.95, and a Hardy–Weinberg equilibrium test with a \( P \)-value <0.001.

**Table 1. Descriptive statistics for all traits and numbers of animals with records**

<table>
<thead>
<tr>
<th>Trait</th>
<th>Number</th>
<th>Mean</th>
<th>SD</th>
<th>Maximum</th>
<th>Minimum</th>
</tr>
</thead>
<tbody>
<tr>
<td>DG (kg)</td>
<td>776</td>
<td>1094.0</td>
<td>112.8</td>
<td>1440.1</td>
<td>750.6</td>
</tr>
<tr>
<td>BF (cm)</td>
<td>776</td>
<td>3.2</td>
<td>0.6</td>
<td>4.9</td>
<td>1.8</td>
</tr>
<tr>
<td>IMF (%)</td>
<td>302</td>
<td>5.0</td>
<td>1.6</td>
<td>9.8</td>
<td>1.5</td>
</tr>
</tbody>
</table>

\(^1\)DG: daily gain, BF: backfat thickness, IMF: intramuscular fat content.

**Analyses**

The data were analyzed using model A, which included only additive genetic effects, and two models that included an imprinting effect. The two models proposed by Nishio & Satoh (2015) were based on genotypic values (model ADI) and gametic values (model DPM) as follows:

\[
\begin{align*}
\mathbf{y} &= \mathbf{X} \boldsymbol{\beta} + \mathbf{Z} \boldsymbol{a} + \mathbf{G} \boldsymbol{d} + \mathbf{e} \\
\mathbf{a} &= \mathbf{A} \boldsymbol{a} + \mathbf{G} \boldsymbol{d} \\
\mathbf{d} &= \mathbf{D} \boldsymbol{d}
\end{align*}
\]

where \( \mathbf{y} \) is a vector of observation; \( \mathbf{X} \) is a vector of fixed effects including the sex of animals (three levels; boar, barrow, and gilt) and generation (seven levels); in model A is vector of additive genetic effects; \( \mathbf{Z} \), \( \mathbf{G} \), \( \mathbf{A} \), and \( \mathbf{D} \) in model ADI are vectors of genetic effects but have no biological meaning ( and are additive and dominance effect when there is no imprinting); and \( \mathbf{e} \) are the vectors of paternal and maternal gametic effects, respectively; \( \mathbf{e} \) is a vector of random residual effects; and \( \mathbf{G} \) are known incidence matrices.

All models were trained with an implementation of MCMC using the R package BGLR (Pérez & de los Campos, 2014). For each analysis, a single Markov chain was run for
100,000 iterations; the first 50,000 iterations discarded as burn-in, and the rest were thinned by a factor of 10.

**Heritability estimation and prediction accuracy**

Variance components were estimated by using the phenotypes of all animals with records. Broad-sense heritability ($H^2$) was defined as the proportion of total genetic variance relative to phenotypic variance. The dataset was divided into the reference population with genotypes and phenotypes, and the test population with only genotypes. All animals from the first to fifth generation were used as the reference population. Meanwhile, the test population comprised sib-tested animals from the sixth to seventh generation. The reference population comprised 444 animals for DG and BF, and 166 animals for IMF (Table 2). In the analysis of IMF, there were few animals in the reference population, because IMF was only measured in sib-tested animals. The test population comprised 136 animals for all traits. For DG and BF, there were 332 animals from the sixth to seventh generation. However, only 136 sib-tested animals were selected from among 332 animals to evaluate the prediction accuracy of the same animals for DG, BF, and IMF. Prediction accuracy in the reference population () and test population () was evaluated by calculating Pearson correlation coefficients between the predicted phenotypic values () and .

**Table 2. Characteristics of the reference and test populations for all traits**

<table>
<thead>
<tr>
<th>Generation</th>
<th>Animal group</th>
<th>Number of animals</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>DG</td>
</tr>
<tr>
<td>1–5</td>
<td>Reference population</td>
<td>166</td>
</tr>
<tr>
<td></td>
<td>Sib-tested</td>
<td>278</td>
</tr>
<tr>
<td></td>
<td>Non-sib-tested</td>
<td>136</td>
</tr>
<tr>
<td>6–7</td>
<td>Test population</td>
<td>196</td>
</tr>
<tr>
<td></td>
<td>Sib-tested</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Non-sib-tested</td>
<td></td>
</tr>
<tr>
<td>All</td>
<td></td>
<td>776</td>
</tr>
</tbody>
</table>

DG: daily gain, BF: backfat thickness IMF: intramuscular fat content.

**Results and discussion**

For all traits, compared to model A, estimates of total genetic and residual variance were larger in model ADI and smaller in model DPM (Table 3). This resulted in high broad-sense heritabilities in models ADI and DPM. Broad-sense heritabilities for DG, BF, and IMF from model A exceeded those from model ADI by 13%, 10%, and 9% as well as those from model DPM by 12%, 8%, and 7%, respectively. In model DPM, maternal gametic variance for DG was larger than paternal gametic variance, whereas there were no differences between the variances of maternal and paternal gametic effects for BF or IMF.

For all traits, the prediction accuracies in the reference population obtained from models ADI and DPM were higher than those from model A. In the test population, for DG and IMF, model A provided the highest accuracies in the test population, followed by models ADI and DPM. Meanwhile, for BF, there were no differences in prediction accuracies in the test population among the three models. These results might be due to overfitting in models ADI and DPM. Guo et al. (2016) estimated the genetic parameters of additive, dominance, and imprinting effects, and used model ADI to assess their impacts on the prediction accuracies for DG and BF in Danish Duroc pigs. They report that imprinting variance accounts for approximately 1.4% of the phenotypic variance for DG and 1.3% for BF. However, model
ADI did not improve prediction accuracy. Hence, the present results are consistent with those of Guo et al. (2016). The lack of superiority of models ADI or DPM compared to model A could also be due to the number of animals in the reference population. The prediction accuracy of models ADI and DPM was low for IMF, because the reference population comprised only 166 animals. Thus, the advantage of including imprinting effects is expected to be larger when a larger dataset is available.

In conclusion, imprinting effects contribute to the genetic variation of DG, BF, and IMF in Japanese Duroc pigs. However, genomic prediction considering imprinting effects did not improve prediction accuracy because of an overfitting problem and the small number of animals in reference population.

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List of References


