779. Genotyping dead animals improves post-weaning survival of pigs in breeding programs

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Abstract

A premise was tested that genotyping both surviving and dead pigs will realise more genetic gain in post-weaning survival (PWS) than genotyping only surviving animals. Stochastic simulation was used to estimate the rate of true genetic gain in different genotyping scenarios that differed in varying proportions of genotyping dead animals. Selection was for only PWS that had heritability of 0.02. Mortality was assumed 10%. The trait was controlled by 7,702 biallelic quantitative trait loci distributed across a 30 Morgan genome. We used 54,218 biallelic single nucleotide polymorphisms (SNPs) that were used in genomic prediction. Genotyping both surviving and dead animals realised 12 to 24% more genetic gain than genotyping only surviving animals. The power of detecting SNP effects increased when animals of extreme phenotypes are genotyped. Therefore, genotyping both surviving and dead pigs realised more genetic gain than genotyping only surviving animals.

Introduction

Post-weaning survival (PWS) is an economically important trait for growing pigs (Knol *et al.*, 2016; Hermesch *et al.*, 2014). The trait is easy to record but is lowly heritable (h^2=0.02-0.06) with low prediction accuracy (Leite *et al.*, 2021; Harper *et al.*, 2019). It can particularly benefit from genomic selection as shown by an increase in the prediction accuracy of genomically estimated breeding value (GEBV) for PWS from 20 to 50% when prediction included genomic information (Leite *et al.*, 2021; Knol *et al.*, 2016). However, one of the challenges when applying genomic selection to survival is that, for practical reasons, only surviving animals may be genotyped. This has the potential to introduce prediction bias and reduce accuracy (Leite *et al.*, 2021). In general, genotyping phenotypically contrasting animals can increase the genetic gain, accuracy of GEBV and decrease the bias of GEBV for continuous trait in comparison to genotyping only top animals because information on phenotypically extreme values results in more accurate estimates of SNP effects (Gowane *et al.*, 2019, Chu *et al.*, 2020). For the case of PWS, genotyping phenotypically contrasting animals refers to the scenario of genotyping both surviving and dead animals. This indicates that genotyping both surviving and dead animals is expected to realise more genetic gain than genotyping only surviving animals. Based on this reasoning, it was tested if genotyping all animals in the birth cohort realises more genetic gain (ΔG) for PWS than genotyping only surviving selection candidates.

Methods

Procedure. Stochastic simulation was used to estimate the ΔG_{true} realised for PWS. All surviving animals and 0, 20, 40, 60, 80, and 100% of randomly selected dead animals were genotyped. Genomic breeding values (GEBVs) were used in optimum contribution selection (OCS), and pedigree information was used to constrain inbreeding to 0.01 per generation. Post-weaning survival had an initial value of 90% and heritability of 0.02 on the observed scale (Harper *et al.*, 2019). It was controlled by 7,702 biallelic QTL distributed across a 30M genome. The genome contained 54,218 biallelic genetic markers that were used to calculate GEBV. Simulation of genomes in a founder population was detailed in the study by Henryon

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et al. (2019). Breeding schemes were run for 10 discrete generations and replicated 30 times. Each replicate was initiated by sampling a unique base population from the founder population. Animals in the base populations were randomly selected in generation $t = 1$. In generations $t = 2 \ldots 10$, selection candidates were allocated matings by OCS.

Breeding scheme. Population consisted of 20 sires and 300 dams that were selected in every generation. Each sire was randomly mated with 15 dams. Each dam produced six progeny with a sex ratio of progeny of one to one.

Simulating phenotype. The true breeding value (TBV) was calculated as the sum of additive genetic effects at the 7,702 QTLs. Its residual value e_i was sampled from $e_i \sim N(0, \sigma_e^2 = 0.79$ on the underlying scale). The target observed-scaled heritability (h_o^2=0.02) was transformed to heritability on underlying scale (h_l^2 =0.06) according to the following formula (Dempster and Lerner, 1050):

$$h_l^2 = \frac{h_o^2 K(1-K)}{z^2} \quad (1)$$

Where K is the proportion of survivability incidence which was assumed 90% in this study, z is the height of normal distribution curve at threshold.

The liability of animal i was calculated as $l_i = a_i = e_i$, where a_i is the animal's TBV and e_i is the residual value. Phenotype of individual animal i, y_i was assigned as $y_i = 1$ when liability exceeded the threshold value for survivability of 90% and otherwise $y_i = 0$.

Genomic prediction. A liability threshold (probit) model was used to estimate the breeding value for the post-weaning survival trait.

$$l = Xb + Z_1 a + Z_2 c + e \quad (2)$$

where b is the fixed generation effect, a and c are vectors of random additive genetic effect and random common environmental effect respectively, e is the vector of random residual error. The co(variance) structure of the random effects was:

$$\begin{pmatrix} \boldsymbol{a} \\ \boldsymbol{c} \\ \boldsymbol{e} \end{pmatrix} \sim N\left(\begin{bmatrix} 0 \\ 0 \\ 0 \end{bmatrix}, \begin{bmatrix} \boldsymbol{A}\sigma_a^2 & 0 & 0 \\ 0 & \boldsymbol{I}\sigma_c^2 & 0 \\ 0 & 0 & \boldsymbol{I}\sigma_e^2 \end{bmatrix} \right)$$

Where I is an identity matrix, σ_a^2=0.06 is the additive genetic variance on the underlying scale, σ_c^2=0.15 is the common litter variance and σ_e^2=0.79 residual variance on the underlying scale that was used to sample phenotype. Single-step genomic breeding value (ssGBLUP) was estimated using H matrix instead of A.

Comparisons. Rate of true genetic gain (ΔG_{true}) was calculated in each replicate as a linear regression of average true breeding values of animals born in generations $t = 5$ to 10 (G_t) on time t. Accuracy of GEBV was calculated in each generation as the correlation between true breeding values (TBVs) and GEBV of surviving animals. Generation averages were averaged across the 30 replicates. Bias of GEBV in each replicate was calculated as the regression of TBV on GEBV of surviving animals. All results are presented as the mean of 30 replicates.

The ADAM software (Pedersen *et al.*, 2009) was used for simulating a breeding program. The DMU package (Madsen *et al.*, 2006) was used for predicting GEBV and OCS was carried out by the EVA software (Berg *et al.*, 2009).

Results

Compared to traditional pedigree selection, the addition of genotype information on all surviving animals resulted in 70% more true genetic gain. Genotyping both surviving and dead pigs realised a higher ΔG_{true} compared with genotyping only surviving pigs (Table 1). Genotyping all surviving pigs and 20-100% of the dead pigs realized 12-23% more genetic gain than genotyping only surviving animals. Compared to only genotyping surviving animals, the greatest realised gains were made when 20% of dead animals were also genotyped (a 12% increase). Thereafter, increasing genotyping dead animals by 20% only resulted in a realised 4-6% increase.

Genotyping both surviving and dead animals increased accuracy of GEBVs. Genotyping all surviving pigs and 20-100% of the dead pigs generated GEBVs that were 12.5 to 18% more accurate respectively, than genotyping only surviving animals (Table 1). Meanwhile, bias was reduced by 7% when also genotyping all dead pigs.

Discussion

In this simulation study, the benefits of genotyping both surviving and dead pigs were assessed based on changes in genetic gain, prediction accuracy and bias of GEBV for PWS in surviving animals as compared to the genotyping only surviving pigs and pedigree selection. Since single-step method was used in this simulation, relationship information about ungenotyped dead pigs was available from the genotyped surviving pigs. As a result, genotyping only surviving pigs provided additional genetic gain and increased prediction accuracy compared to the pedigree selection. However, genotyping both surviving and dead pigs refers to the genotyping phenotypically contrasting animals and that realised more genetic gain and increased prediction accuracy in comparison to genotyping only surviving animals. The finding in this study is in agreement with other studies using continuous trait (Gowane *et al.*, 2019; Chu *et al.*, 2020). When animals of extreme phenotypes are genotyped, the power of detecting SNP effect increased because most of the genetic information is captured in animals of extreme phenotypes (Huang and Lin, 2007). This resulted in higher genetic gain in PWS when both surviving and dead animals were genotyped in this simulation study. One might argue that additional genetic gain in PWS due to genotyping dead pigs might be because of genotyping additional animals not because of dead animals specifically. To explore

Table 1. Rate of true genetic gain (ΔG_{true}, expressed on underlying scale), prediction accuracy and bias of estimated breeding value for post-weaning survival in different proportion of genotyping dead animals. Standard error is shown in parenthesis.[1]

Genotyping strategy	ΔG_{true}	Accuracy	Bias
Pedigree selection only	0.051 (0.002)	0.199 (0.007)	1.20 (0.05)
Genotype all surviving animals	0.087 (0.003)	0.264 (0.008)	1.22 (0.04)
Geno surviving + 20% dead	0.097 (0.004)	0.297 (0.007)	1.24 (0.03)
Geno surviving + 40% dead	0.101 (0.003)	0.317 (0.006)	1.29 (0.03)
Geno surviving + 60% dead	0.105 (0.002)	0.318 (0.006)	1.19 (0.03)
Geno surviving + 80% dead	0.107 (0.003)	0.322 (0.006)	1.23 (0.02)
Geno surviving + 100% dead	0.104 (0.003)	0.312 (0.006)	1.13 (0.02)

[1] Geno surviving = all surviving animals were genotyped. Results were the mean of 30 replicates.

this hypothesis, additional scenarios were simulated where equal number of live or dead animals were genotyped in addition to genotyping fixed numbers of live animals. Findings of additional simulations (results not shown) clearly indicated that additional genetic gain was achieved from genotyping both live and dead animals. Therefore, the hypothesis turned out to be true that genotyping both surviving and dead animals realised more genetic gain as compared to genotyping only surviving animals.

This study assumed PWS to be 90% so that the benefit of genotyping different proportions of dead animals could be shown. In reality, PWS is greater than 90% because of high biosecurity in nucleus populations. Variation of a binary trait depends on proportion of incidence. If the mortality rate ranges from 3 to 5% in the nucleus population, data will lack enough variation for breeding value estimation. The low incidence of PWS in nucleus populations could be circumvented by adding mortality information from commercial herds. Genotyping commercial dead pigs could be used to add crossbred pigs in the reference population, since relationships between animals can be efficiently estimated with genomic data instead of keeping pedigree. If the commercial dead pigs are genotyped and added in the reference population for selection in nucleus, prediction accuracy of GEBV for post-weaning survival may increase. However, the benefit of genotyping commercial population depends on the correlation between purebred and crossbred populations (Van Grevenhof and Van der Werf, 2015). Therefore, it is worth investigating the benefit of genotyping commercial dead pigs to increase the accuracy of GEBV for PWS in the nucleus.

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