Genomic Prediction for Reproductive Traits of Commercial Sows in Health Challenged Herds

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Cassie Scanlan, Graduate Student, Department of Animal Science, Iowa State University;
PigGen Canada, PigGen Canada;
Benny Mote, Assistant Professor, Department of Animal Science, University of Nebraska-Lincoln;
Philip Willson, Research Scientist, Canadian Centre for Health and Safety in Agriculture, University of Saskatchewan;
John Harding, Associate Professor, Department of Large Animal Clinical Sciences, University of Saskatchewan;
Graham Plastow, Professor, Department of Agricultural, Food and Nutritional Science, University of Alberta;
Jack Dekkers, Distinguished Professor, Department of Animal Science, Iowa State University;
Nick Serão, Assistant Professor, Department of Animal Science, Iowa State University.

Summary and Implications

The present study performed genomic prediction for reproductive performance of sows in commercial farms with a history of health problems. Accuracies of genomic predictions for lifetime performance were low to moderate, ranging from 0.11 (TNB) to 0.45 (NBD). Accuracies of genomic prediction for later parity performance using parity 1 performance were low, ranging from -0.07 (NSB in parity 3) to 0.19 (NBD in parity 2), with average accuracies by trait ranging from 0.04 (NSB) to 0.16 (NBD). Although most accuracies were low, the moderately high accuracies for some lifetime performance traits shows that genomic prediction can be used to improve reproductive performance in commercial sows.

Introduction

Sow reproduction is a key component of profitability in the swine industry. High producing sows that stay in the herd through productive parities enhance profitability. Reproductive traits, such as number of piglets born alive (NBA) are slower to change using genetic selection due to low heritability (~10%), expression after normal selection age, and sex-limited expression (i.e. only females show the phenotype). Selection for performance under lower heath status further increases this difficulty because disease traits are not expressed in the nucleus because of its high health status. However, genomic information can be used to connect information back to the nucleus, which can then be used to improve the accuracy of selection. In order to use this genomic information across many populations, it is also important to verify that the marker effects found in one population are predictive of those in another. The objective of this study was to perform genomic predictions for reproductive performance of sows in commercial herds with a history of health problems.

Materials and Methods

Reproductive performance (1 to 4 parities) data and genotypes (~40K SNPs) were available for 2,604 crossbred (Landrace x Large White) sows, for a total of 7,635 farrowing records. Animals from 17 high-health multipliers from 7 breeding companies (PigGen Canada) were shipped to 23 commercial farms with recent history of common infectious diseases. Gilts entered farms with an average of 53 animals per contemporary group (CG). Traits included total number of piglets: born (TNB), born alive (NBA), stillborn (NSB), mummified (MUM), born dead (NBD), and weaned (NW). Genomic predictions were performed using Bayes-B (pi=0.995) with seven-fold cross-validation using each company in turn for validation and the others for training. The model included the effects of CG (fixed) and SNP (random), and the net number of fosters (covariate) for NW. Genomic predictions were done for animal lifetime performance (sum performance across parities) for each trait and using first parity performance as the training set to predict subsequent parity performance. Accuracy was calculated as the weighted average correlation between the genomic estimated breeding value (GEBV) and adjusted phenotype across validation sets divided by the square root of heritability of the trait.

Results and Discussions

Results can be seen in Table 1. Accuracies for lifetime performance were low to moderate, with the TNB having the lowest accuracy (0.11) and NBD having the highest accuracy (0.45). Accuracies using parity 1 as a prediction of subsequent reproductive performance were low overall. The accuracy of using parity 1 to predict parity 2 ranged from -0.03 (NBA) to 0.19 (NBD), to predict parity 3 from parity 1 ranged from -0.07 (NSB) to 0.17 (TNB), and to predict parity 4 from parity 1 ranged from 0.02 (NW) to 0.18 (NBA).

Although most accuracies were low, the moderately high accuracies for some lifetime performance traits, like the born dead traits (NSB, MUM, and NBD) shows that genomic prediction can be used to improve performance under natural health challenge in sows.

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Tables

Table 1. Genomic prediction accuracies (SD)[1] for lifetime performance and parity 1 performance as a predictor of performance in parities 2, 3, and 4.

Trait[2]	LT[3]	P1-2[4]	P1-3[5]	P1-4[6]
TNB	0.11 (0.04)	-0.02 (0.01)	0.17 (0.01)	0.13 (0.01)
NBA	0.17 (0.02)	-0.03 (0.01)	0.11 (0.01)	0.18 (0.01)
NSB	0.32 (0.01)	0.09 (0.01)	-0.07 (0.01)	0.09 (0.01)
MUM	0.39 (0.02)	0.05 (0.01)	NE[7]	0.10 (0.02)
NBD	0.45 (0.02)	0.19 (0.01)	0.12 (0.02)	0.17 (0.02)
NW	0.13 (0.04)	0.001 (0.01)	0.15 (0.01)	0.02 (0.01)

[1.] SD, weighted standard deviation of accuracies
[2.] TNB, Total number of piglets born; NBA, Number of piglets born alive, NSB, Number of stillborn piglets; MUM, Number of mummified piglets; NBD, Number of piglets born dead; NW, Number of piglets weaned.
[3.] LT, Lifetime performance (sum total of parity performance)
[4.] P1-2, Parity 1 performance used as a predictor of parity 2 performance
[5.] P1-3, Parity 1 performance used as a predictor of parity 3 performance
[6.] P1-4, Parity 1 performance used as a predictor of parity 4 performance
[7.] NE, not estimable due to heritability of 0 for MUM in parity 3.