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Accuracy of Genomic Prediction for PRRS Antibody Response

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Cover Page Footnote
The work presented here was supported by grants from Genome Canada, the Canadian Swine Health Board, and PigGen Canada.

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Summary and Implications

The accuracy of genomic prediction for antibody response to Porcine Reproductive and Respiratory Syndrome (PRRS), measured as S/P ratio, was evaluated using two independent datasets of Landrace x Large White females. Results demonstrate that antibody response during a PRRS outbreak can be predicted with high accuracy using genetic markers in two regions on chromosome 7. One of these regions includes the Major Histocompatibility Complex. The high accuracy for this region indicates that marker effects are consistent across Landrace x Large White populations.

Introduction

Porcine Reproductive and Respiratory Syndrome (PRRS) causes increased abortions, stillbirths and mummies in reproductive sows. Previous genetic analyses of PRRS antibody (Ab) response, measured as PRRS ELISA Sample-to-Positive (S/P) ratio, showed this trait to be positively genetically correlated with favorable sow reproductive performance during a PRRS outbreak, being mainly controlled by two Quantitative Trait Loci (QTL) on *Sus scrofa* chromosome (SSC) 7. One of these QTL encompassed the Major Histocompatibility Complex (MHC) region and the other was at ~130 Mb on SSC7. The objective of this work was to evaluate the use of high-density Single Nucleotide Polymorphism (SNP) genotypes to predict PRRS Ab response of sows during an outbreak.

Materials and Methods

Antibody response was measured as S/P ratio using a commercial ELISA test in two independent datasets. The training dataset included data on 1,648 F1 (Landrace x Large White) replacement gilts that were sourced from 17 multiplier herds with high-health status from 6 genetic sources and introduced into 22 commercial farms with historical cases of natural disease challenges. Blood samples were collected 40.1±14 days after entry, while animals followed standard acclimation procedures. The validation dataset included 580 sows from a commercial multiplier herd that had undergone a PRRS outbreak. Blood samples were collected 46 days after the estimated day of the outbreak.

All pigs were genotyped, using different versions of the Porcine SNP Chip (60K v1, 60K v2, and 80K). After quality control, 38,678 SNPs that were common to all versions were used for analyses. The training dataset was used to estimate the effects of SNPs on S/P ratio, using the Bayes-B method, in five scenarios: using all SNPs across the genome (ALL_SNP), only SNPs in the two QTL (SSC7_SNP), only SNPs in the MHC QTL (MHC_SNP), only SNPs in the 130 Mb QTL (130Mb_SNP), and all SNPs outside the two QTL (Not7_SNP). SNP estimates were used to predict S/P in the validation dataset. Accuracy of genomic prediction was calculated as the correlation between predicted and S/P ratio pre-adjusted for fixed effects, divided by square root of heritability.

Results and Discussion

Genomic prediction accuracies for S/P ratio across the five scenarios evaluated are presented in Figure 1. Moderate to high accuracies were observed for all scenarios, except Not7_SNP (0.15), indicating that the rest of the genome has little predictive ability for S/P ratio. The highest accuracy was for the SSC7_SNP scenario (0.63). Slightly greater accuracy was obtained with MHC_SNP (0.55) compared to using all SNPs (0.49). Lastly, 130Mb_SNP had a moderate accuracy of 0.30.

Acknowledgments

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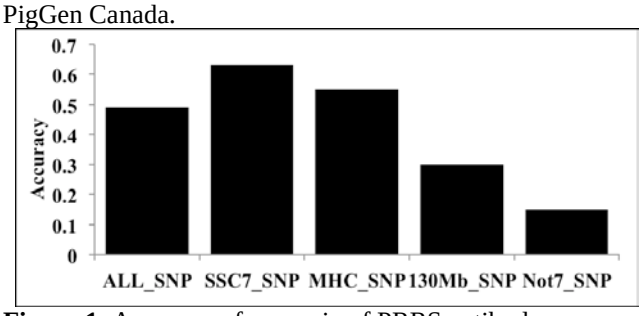

Figure 1. Accuracy of genomic of PRRS antibody response (S/P ratio) across the 5 training scenarios