The Genetic Basis of Natural Antibody Titers and Relationships with Disease Resilience in Pigs

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Summary and Implications

In typical pig nucleus breeding programs, it is difficult to select pigs for disease resilience because the breeding animals are raised under high-health conditions. Thus, indicator traits that can be measured on young healthy pigs and that are genetically correlated with disease resilience in commercial environments are needed in order to be able select for disease resilience.

The objective of this study was to investigate the levels of natural antibodies (NAb) in blood from young healthy pigs as potential predictors of disease resilience. NAb and total IgG levels in blood were genetically correlated with their subsequent resilience after a polymicrobial challenge. Although further research is needed, these results suggest that NAb and IgG levels in blood measured on young healthy pigs can be used as indicator traits to select for improved disease resilience in pigs.

Introduction

The swine industry suffers major economic losses due to diseases. Hence, selecting pigs for disease resilience can be an effective way to improve productivity of the swine industry. However, selection for disease resilience is difficult because nucleus breeding populations are typically raised in a high-health biosecure environment. Therefore, the development of indicators of disease resilience that can be measured in young healthy pigs may be a practical method to select for disease resilience. Natural antibodies (NAb) are part of the innate immune system and play essential roles in the first line of defense to pathogens. Based on previous studies, the level of NAb in blood is associated with health status and disease in dairy cattle and chicken. This is the first research to study the possibility of using NAb titers in blood as potential indicators of general disease resilience in pigs. Results presented here are an update of a 2018 Animal Industry report and includes more data, as well as results on total IgG.

Materials and Methods

The data used in this study were from a natural disease challenge project at CDPQ in Québec Canada. The model consists of three phases: (1) a healthy quarantine nursery for ~21 days after weaning; (2) a challenge nursery (the first time that the piglets are exposed to disease) for around 30 days duration; (3) a challenge finisher for around 18 weeks duration prior to slaughter. The natural challenge was established by introducing naturally infected pigs in the challenge rooms and is maintained through contact with new batches of 60 to 75 healthy pigs from the quarantine nursery with pigs from previous batches in a continuous flow system. A total of 28 batches and 1,799 Large White by Landrace barrows were used for this research.

Blood samples were collected around 35 days of age, prior to entry into the challenge nursery. Levels of IgG and IgM NAb titers that bind four common antigens: (lipopolysaccharide (LPS), lipoteichoic acid (LTA), peptidoglycan (PDG), and keyhole limpet hemocyanin (KLH)), as well as total IgG, were measured by indirect ELISA. Disease resilience data were collected until the pigs reached market age.

A 650k Affymetrix Axiom Porcine Genotyping Array was used to genotype all pigs for 658,692 genetic markers across the genome. After quality control, 498,717 markers and 1695 pigs remained and were used to create a genomic relationship matrix for analysis.

The ASReml 4 software was used to estimate genetic parameters, using a model with batch and entry age as fixed effects and litter and animal as random effects. Both single-marker regression (GenABEL) and Bayesian variable selection (GenSel) were used for genome-wide association studies (GWAS).

Results and Discussion

Similar results were obtained in terms of heritability of NAb titers as in a previous report . The heritability of IgG NAb tended to be lower (12 to 22%), while the heritability of IgM NAb was moderate to high (33 to 53%). Opposite trends were obtained for the maternal or litter effects, with IgG NAb showing large maternal effects (44 to 52% of phenotypic variance) and IgM NAb having relatively low maternal effects (0 to 10%). The heritability of total IgG in plasma was also relatively low (16%), while the maternal effect of total IgG was moderately high (23%).

For phenotypic correlations, IgG NAb titers were positively correlated with total IgG levels in blood (0.21 to 0.51), while phenotypic correlations of IgM NAb levels with total IgG tended to be low (0.04 to 0.21).

For genetic correlations, IgG NAb titers were highly positively correlated with total IgG level (0.45 to 0.81),

while IgM NAb levels were negatively correlated with total IgG levels in plasma (-0.07 to 0.06), except for NAb to LTA (0.45).

Compared to a previous report, estimates of genetic correlations of NAb with subsequent disease resilience traits tended to be larger but still had large standard errors: higher antibody levels in plasma of young healthy pigs tended to be genetically correlated with lower mortality and fewer medical treatments, except for NAb IgG to KLH and NAb IgM to LTA with mortality and treatments in the challenge nursery. Although most genetic correlations of antibody levels with resilience traits were in the expected direction (higher Ab higher resilience), some correlations were in the opposite direction and require further research.

Conclusion

These results demonstrate that NAb titers and total IgG levels in blood measured at a young healthy stage are potential genetic predictors of disease resilience and mortality of pigs under disease challenge.

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