Pigs Can Be Selected for Increased Natural Resistance to PRRS Without Affecting Overall Economic Value in the Absence of PRRS

A.S. Leaflet R3192

Jenelle Dunkelberger, Graduate Research Assistant, Iowa State University; Pramod K. Mathur, Senior Geneticist, Topigs Norsvin; Marcos S. Lopes, Research Geneticist, Topigs Norsvin; Egbert F. Knol, Director of Research, Topigs Norsvin; Jack C. M. Dekkers, Distinguished Professor, Animal Science, Iowa State University

Summary and Implications

Results from previous studies have shown that guanylate binding protein 5 (*GBP5)* is a major gene for host response to porcine reproductive and respiratory syndrome (PRRS). The effect of WUR10000125 (WUR), a genetic marker for *GBP5*, on host response to infection has been validated across breeds, populations, and following infection with multiple isolates of PRRS virus (PRRSV). For this marker, pigs with the B allele have lower viremia and higher growth rate under PRRS challenge. However, there is limited knowledge regarding the effect of WUR under non-challenged conditions. Therefore, the objective of this study was to estimate the effect of WUR on performance in commercial lines under normal, non-challenged conditions. Results indicate that WUR marker genotype was associated with some traits for the sire lines, but that the effect of WUR differed by trait and by line. In addition, WUR had no significant effect on the overall selection index value for any of the lines. Based on these findings, selecting for the B allele is expected to result in progeny with improved performance under PRRS challenge without adversely affecting overall performance under normal, non-challenged conditions.

Introduction

Porcine reproductive and respiratory syndrome (PRRS) is an extremely devastating disease that can affect pigs during all stages of production. The disease has plagued the industry for nearly 30 years without a single, effective disease control strategy. The difficulty of controlling PRRS is primarily driven by the high mutation rate of the virus, thereby complicating the development of an efficacious, cross-protective vaccine. In the absence of effective control measures, recent effort has been invested to identify genes or genetic markers that are associated with resistance or susceptibility to PRRS virus (PRRSV) infection.

Analysis of data from PRRS Host Genetics Consortium experimental infection trials has shown that the gene guanylate binding protein 5 (*GBP5*), located on chromosome 4, harbors a natural mutation associated with resistance/susceptibility to PRRS. SNP WUR10000125 (WUR), present on commercial genotyping arrays, can be used as a genetic marker for this gene. To date, the effect of WUR has been validated across breeds, genetic sources, following infection with different isolates of PRRSV, and most recently, co-infection with PRRSV and porcine circovirus type 2b. However, the favorable (B) allele under PRRSV infection has a low frequency in most commercial populations, suggesting that the B allele may be negatively associated with an important reproduction or finishing trait under non-challenged conditions and thus, has been selected against in high-health nucleus herds. Therefore, the objective of this study was to estimate the effect of WUR on economically important traits in commercial lines under normal, non-challenged conditions.

Materials and Methods

Data were from purebred dam lines A (n=9,264) and B (n=18,458), corresponding to a Landrace and Large White line, respectively, and purebred sire lines C (n=7,228) and D (n=8,868), corresponding to a synthetic and Pietrain line, respectively. Deregressed estimated breeding values (dEBVs), which represent the genetic value of an individual as a parent, were analyzed for each trait for each line. DEBVs, rather than trait phenotypes, were used for analyses since dEBVs can be used to estimate the effect of WUR on reproduction traits for both males and females. Reproduction traits analyzed included total number born, number stillborn, litter mortality, farrowing survival, and lactation survival. Finishing traits included backfat, daily feed intake, lifetime daily gain, and daily gain during test. DEBVs for each trait were analyzed using an animal model in ASReml 4.0 with WUR, PRRS_Vacc (whether/not a pig was vaccinated with a PRRS modified live virus vaccine) and WUR*PRRS_Vacc fitted as fixed effects. Residuals were weighted by corresponding reliability of dEBV. Total merit selection index value was analyzed using the same model, but without weighting the residuals.

Results and Discussion

No significant effect of WUR was detected on any of the reproduction or finishing traits for the dam lines ($P \geq 0.14$). Some significant effects of WUR were detected for analyses of the sire lines, but the magnitude and direction of these effects differed by trait and by line.

For the D sire line, a significant effect of WUR ($P<0.001$) on litter mortality was detected, where BB pigs (n=266) had significantly greater litter mortality than AB

(n=1,684) or AA (n=4,056) pigs. The quality of litter mortality data for sire lines is, however, typically low, because individual records are not available to calculate dEBVs and cross-fostered piglets are included in recording the trait. For the C sire line, the B allele was associated with significantly lower feed intake (P=0.004) and, consequently, significantly lower lifetime daily gain (P=0.001) and daily gain during test (P=0.002). However, the opposite direction of effect was detected for the D sire line, where the B allele was associated with significantly higher feed intake (P<0.001) and a tendency for higher daily gain during test (P=0.09). The effect of WUR on overall selection index value was not significant for any of the lines (P≥0.15).

In conclusion, WUR marker genotype was associated with some traits for the sire lines, but the effect of WUR differed by trait and by line. However, regardless of the effect on individual traits, no effect of WUR on overall selection index value was detected for any line. Therefore, selecting for the B allele is expected to result in progeny with improved performance under PRRS challenge without adversely affecting the overall performance under normal, non-challenged conditions.

Acknowledgements

This work was supported by the USDA ARS NIFA grants 2012-38420-19286 and 2013-68004-20362 and by Topigs Norsvin.