

# Genetic Analysis of Reproductive Traits and Antibody Response in PRRS Infected Sows

## A.S. Leaflet R2920

Nick Serão, Postdoctoral Research Associate, Department of Animal Science, Iowa State University; Oswald Matika, Computational Geneticist; Steve Bishop, Professor, The Roslin Institute and R(D)SVS, University of Edinburgh; Bob Kemp, VP of Genetics Program and R&D, Genesus Inc.; John Harding, 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, Professor, Department of Animal Science, Iowa State University

### Summary and Implications

The genetic components of reproductive performance and antibody response of 641 commercial sows were assessed in a commercial herd that faced a PRRS outbreak. Antibody response after the PRRS outbreak was highly heritable and had high genetic correlations with reproductive traits. Many genomic regions were associated with antibody response in this study. These results indicate that there is a significant genomic component associated with PRRS antibody response and its high genetic correlations with reproductive traits during PRRS suggest that this trait could be used as an indicator trait to reduce the impact of PRRS on reproductive performance.

### Introduction

Porcine Reproductive and Respiratory Syndrome (PRRS) causes increased abortions, stillbirths and mummies in reproductive sows. The objective of this work was to study the genetic architecture of reproductive traits and antibody response following a PRRS outbreak in a sow herd.

### Materials and Methods

The dataset available for analysis was obtained from a commercial multiplication herd that experienced a PRRS outbreak during the winter of 2011/12. Farrowing data (number born alive [NBA], number stillborn [NSB] and mummified [NBM], number alive at 24 hours, number weaned, and number fostered) of 5,227 litters from 1,967 purebred Landrace sows, and a pedigree with 2,995 individuals, were used for analysis. The PRRS outbreak date was estimated based on rolling averages of farrowing traits and used to split the data into a Pre- and a Post-PRRS phase. All 641 sows that were in the herd during the outbreak had blood samples collected and were tested for the PRRSV antibodies using ELISA (expressed as sample-to-positive

[SP] ratio) and were genotyped using the PorcineSNP60 BeadChip. Heritability and genetic correlations were estimated separately for the Pre- and Post-PRRS data sets. The genotype data were used to perform genome-wide association studies (GWAS) for SP ratio.

### Results and Discussion

Estimated heritabilities for the reproductive traits ranged from 1% (NBM) to 12% (NSB) in the pre-PRRS phase, and from 6% (NSB) to 12% (number born dead, NBD) for the Post-PRRS phase. SP ratio showed the highest heritability (45%) and had substantial genetic correlations with most traits, ranging from -0.72 (NBM) to 0.73 (NBA). The GWAS detected several genomic regions associated with SP ratio. Two regions on SSC7 separated by 100 Mb accounted for 40% of the genetic variation in SP ratio, including a region encompassing the Major Histocompatibility Complex, which explained 25% of the genetic variance.

### Acknowledgments

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