Validation of the Effects of a SNP on SSC4 Associated with Viral Load and Weight Gain in Piglets Experimentally Infected with a 2006 PRRS Virus Isolate

A.S. Leaflet R2924

Andrew Hess, Ph.D. Student, Department of Animal Science;
Nicholas Boddicker, Geneticist, Genesus, Inc.;
Bob Rowland, Professor, Kansas State University;
Joan Lunney, Research Scientist, USDA, ARS, BARC;
Graham Plastow, Professor, University of Alberta;
Jack C.M. Dekkers, Professor, Department of Animal Science

Summary and Implications

Host genetic differences in viral load (VL) and weight gain (WG) during challenge were assessed for five trials of ~200 commercial crossbred piglets each, all from different commercial suppliers. Piglets were experimentally infected with porcine reproductive and respiratory syndrome virus (PRRSV) isolate KS-2006-72109 in order to validate the effects of a SNP previously identified on SSC4 (WUR10000125), whereby AB individuals had increased WG and reduced VL when experimentally infected with PRRSV isolate NVSL-97-7895. VL was defined as the area under the curve of logged viremia from 0-21 dpi. WG was defined as the weight gained from 0-42 dpi. The SNP effects on VL and WG were assessed. AB individuals had higher WG and lower VL than AA individuals, suggesting this marker may be useful for genetic selection of pigs for increased resistance or reduced susceptibility to PRRSV isolates that differ genetically and possibly pathogenically.

Introduction

Porcine reproductive and respiratory syndrome (PRRS) is the most costly disease to the North American pork industry, and vaccines, biosecurity measures, and proposed methods for eradication have had limited success. The aim of the PRRS Host Genetics Consortium (PHGC) is to identify genomic markers and pathways, associated with host response to PRRSV, which could potentially be used for genetic selection of pigs for increased resistance or reduced susceptibility to virus infection. Such pigs may potentially improve the success of some of the other strategies.

Boddicker et al. (2012) identified a SNP on SSC4 (WUR10000125) for which the favorable allele (B) was associated with reduced viral load (VL) and increased weight gain (WG) under infection with the NVSL-97-7895 PRRSV isolate. The objective of this study was to test the effects of this SNP when infecting pigs with a different, more recent isolate of PRRSV (KS-2006-72109), in order to assess the usefulness of this marker for genetic selection of pigs with increased resistance or reduced susceptibility to PRRSV that is not dependent on virus isolate. The KS-2006-72109 isolate has 89% amino acid sequence identity with NVSL-97-7895 in the GP5 viral gene.

Materials and Methods

Following the same experimental design as described by Boddicker et al. (2012), ~200 commercial crossbred piglets per trial, each from different genetic backgrounds, for a total of 5 trials, were experimentally infected intramuscularly and intranasally with 10^5 tissue culture infectious $dose_{50}$ of PRRSV isolate KS-2006-72109 at 28-35 days of age. Blood samples were collected at -6, 0, 4, 7, 11, 14, 21, 28, 35, and 42 days post infection (dpi). Body weight was collected weekly from infection to 42 dpi. Viremia was measured using a qPCR assay for PRRSV RNA, and VL was defined as the area under the curve of Log viremia from 0-21 dpi. WG was defined as weight gain from infection to the end of the trial. Pigs were genotyped using the 60K SNP chip, which includes the SSC4 WUR10000125 SNP. Analyses were carried out using PROC MIXED in SAS (v9.2). Trial nested with parity and the number of B alleles for the SSC4 SNP were fitted as fixed effects, weight and age at infection as covariates, and litter and trial nested with pen as random effects.

Results and Discussion

Consistent with previous findings, individuals that were heterozygous for the SSC4 SNP had greater WG (0.95±0.32 kg, $p=0.0031$, $n_{AA}=682$, $n_{AB}=167$) and lower VL (-3.89±0.78 units, $p<0.0001$, $n_{AA}=431$, $n_{AB}=86$) compared to their AA counterparts. The number of BB individuals was too small to get accurate estimates. The size of the effect for the SSC4 SNP was approximately half the reported value for the NVSL-97-7895 isolate for WG (0.95±0.32 vs 2.0±0.4 kg) but comparable for VL (-3.89±0.78 vs -4.1±0.6 units). These results suggest the SSC4 SNP may be useful for genetic selection of pigs for increased resistance or reduced susceptibility to PRRSV isolates that differ genetically and possibly in pathogenicity. Future work will involve estimating the genetic parameters for VL and WG under infection with KS-2006-72109, comparing these to those reported by Boddicker et al. (2012), and performing a complete genome-wide association study to identify other genomic regions associated with VL and WG that may be in common or different between these two PRRSV isolates, in

order to assess how different PRRSV isolates affect host response to PRRSV infection.

Acknowledgements

This work was supported by Genome Canada, USDA ARS, and breeding companies of the PHGC and PigGen Canada.