Evaluation of Serum Viremia of Pigs with Alternate Genotypes for a Major Gene after Natural PRRSV Infection on a Commercial Farm

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Summary and Implications

The objective of this study was to investigate alternative measures to evaluate serum viremia after natural Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) infection of pigs on a commercial farm. Viremia measurements (area under the curve at 21 days from the start of the trial, maximum viremia, time to maximum viremia, and ratio of maximum viremia over time to maximum viremia) were estimated using a LOESS function for each animal. Genetic marker WUR10000125 (WUR) on chromosome 4 was typed for 199 barrows and its association with viremia traits was tested. The analysis revealed that maximum viremia was significantly ($P<0.01$) lower for pigs with the AB genotype. Maximum viremia can be used as the indicator trait of the severity of the infection in commercial farms where animals differ in the time of the initial infection.

Introduction

Porcine reproductive and respiratory syndrome virus (PRRSV) causes severe reproductive and economic losses, respiratory disease, increased mortality, and reduced growth rates in pigs. A vaccine that provides full protection to PRRSV is not available, but management strategies can alleviate production losses. One measure of the level of infection of PRRSV consists of measuring the concentration of the virus in blood serum. The pattern of the concentration of the virus in serum after infection follows a curve as depicted in **Figure 1**. The peak of the curve represents the highest or maximum level of the concentration of the virus in blood, which then declines with the possibility of another peak due to re-infection or rebound. In an experimental setting, drawing blood several times from initiation to 60 or 120 days after infection allows for estimation of the level of infection over time.

The use of biomarkers, such as genetic markers, can aid to reduce the severity of the infection. However, testing biomarkers in a commercial setting also requires measures of the level of viremia over time in situations in which animals are at different stages of infection. An example of such a biomarker is the Single Nucleotide Polymorphism (SNP) WUR10000125 (WUR) on chromosome 4, for which allele B has been associated with a reduction of the viremia levels in blood and with an increased growth in infected herds. The objective of this study was to investigate alternative measures of the viral load of PRRSV after infection in a commercial swine farm and evaluating the effect of genotype at the WUR SNP.

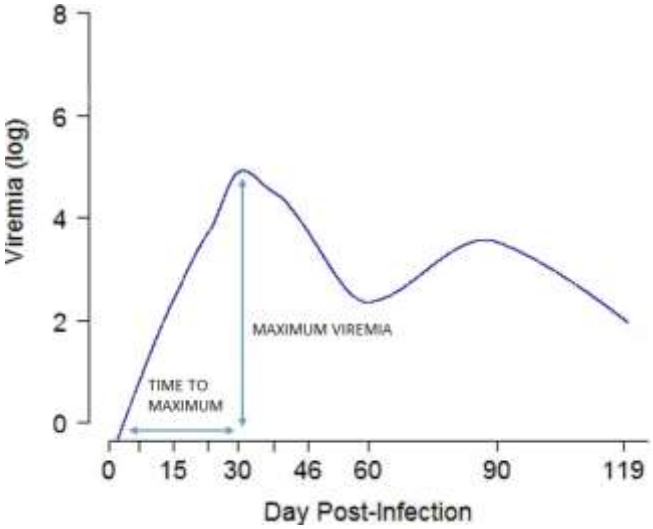

Figure 1. Level of serum viremia over time for one pig after infection, showing maximum viremia and time to maximum viremia

Materials and Methods

Animals: A total of 199 barrows from 15 Landrace sires and 40 Large White dams were used to investigate alternative measures of the level of infection to PRRSV. Right after weaning, animals were moved to a farm with a history of PRRSV infection. Genotypes for the WUR SNP were determined for each piglet.

Serum Viremia over Time: Drawing blood was carried out weekly and curves of the concentration of viremia over time were constructed using a LOESS function, a procedure that originated as LOWESS (LOcally WEighted Scatter-plot Smoother). The LOESS function sets a low-degree polynomial at each point using weighted least squares, and gives more weight to points near the point whose response is being estimated and less weight to points further away. This fitting is necessary to account for the natural variation

in the concentration of viremia due to sampling and the methodology to measure viremia in serum. The following viremia measurements were estimated from the LOESS function for each animal: 1) area under the curve at 21 days from the start of the trial, 2) maximum viremia, 3) time to maximum viremia, and 4) ratio of maximum viremia and time to maximum viremia. In addition, the slope of the linear regression for each individual was used as a measure of growth rate.

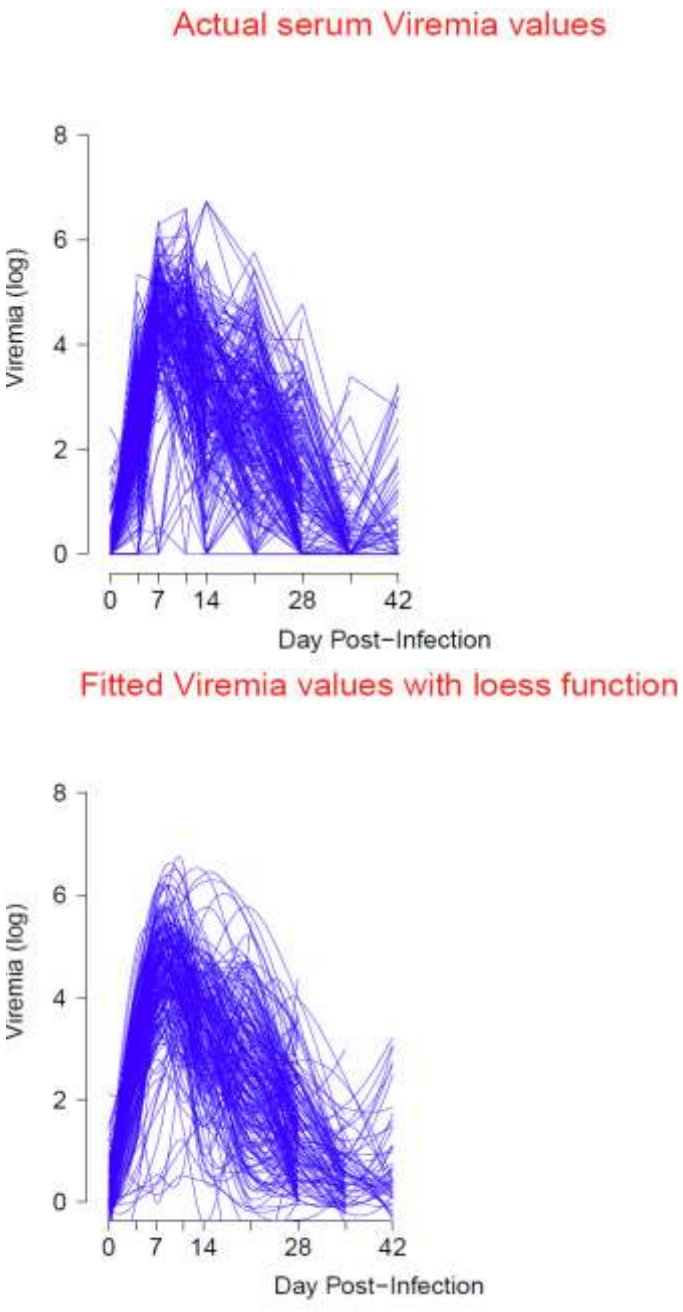

Figure 2. Plots of the actual and LOESS fitted viremia curves for the 199 barrows of the trial.

Data Analysis: Data were analyzed using ASReml software (Gilmour et al., 2009 release 3.0). The model included the fixed effects of the mean, pen, and the random effect of sire and dam. Heritability was estimated as 4 times the sire component divided by the phenotypic variance.

Results and Discussion

The trends over time of the viremia concentration before and after fitting a LOESS function are given in **Figure 2**. This figure illustrates how fitting the LOESS function smoothens the viremia curves. Area under the curve at 21 days was higher in AA than in AB pigs, with the difference being near significance (P=0.057). Maximum viremia was significantly (P<0.01) higher in AA pigs, whereas the other traits were not significantly different between AA and AB pigs. The average LOESS function for animals with AA and AB genotypes is in **Figure 3**. Animals with the AB genotype had a lower and earlier peak (maximum viremia) and showed a similar response across individuals. In contrast, animals with the AA genotype had a much broader and higher peak, suggesting that these animals had large variation in the time when they reach their maximum viremia, which was also much higher. Heritability estimates were very low for all viremia traits except for the area under the curve at 21 days, which was heritable at 20%. These results support previous findings associating allele B to lower viremia levels.

The estimate of heritability for growth rate was 0.24. Numerically, pigs with the AA genotype had slightly lower growth rate, but this difference was not significant (P=0.58).

Repeated blood sampling followed by analysis of the level of viremia allows identification of the peak at which animals have the largest level of viremia in the blood. This trait is appropriate for evaluating biomarkers in commercial situations in which animals naturally differ in the time and/or initial level of infection.

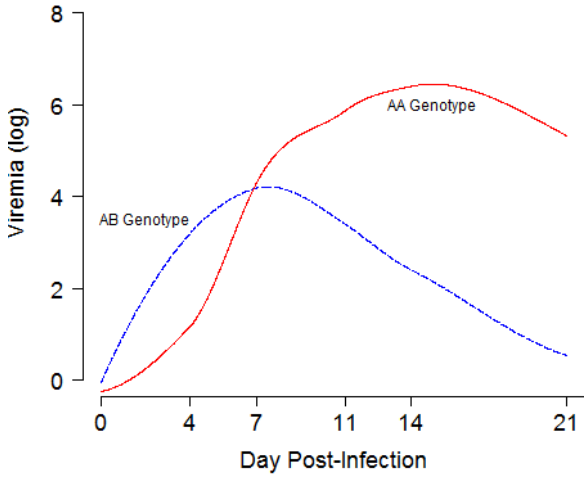

Figure 3. Plots of the average predictors of the LOESS function for serum viremia levels in animals with WUR AA and AB genotypes.

Conclusions

Our results suggest that maximum viremia is a good indicator of the severity of PRRSV infection and confirm that carriers of allele B at the WUR SNP on chromosome 4 have lower viremia in blood following PRRSV infection.

Acknowledgements

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