Genomic Differences between Preweaning Survival and Mortality of Piglets Following PEDV Outbreaks

A.S. Leaflet R3109

Francesca Bertolini, Postdoctoral Research Associate, ISU;
John C. S. Harding, Professor, University of Saskatchewan, Canada;
Benny Mote, Assistant Professor, University of Nebraska-Lincoln;
Graham S. Plastow, Professor, University of Alberta, Canada;
Max Rothschild, Distinguished Professor, ISU

Summary and Implications

Porcine Epidemic Diarrhea (PED) is a serious and potentially devastating disease in the US and Canadian pig industries. To investigate if there is genetic resistance to PEDV a total of 156 dead and 106 surviving neonatal piglets infected with PEDV were genotyped with over 60,000 genetic markers to investigate genetic differences between the two groups. This allows for the identification of genomic regions that could be linked to susceptibility/resistance to virus infection and in cellular components that are involved in the PED virus infection cycle, providing new insights on the genetic resistance to this disease

Introduction

PED is a disease that affects pigs at all ages caused by a virus (PEDV), which belongs to Coronavirus family. Once the infection has started, the disease spreads rapidly within a herd, generally affecting entire barn. While death rates are very low in adult animals, mortality in pre-weaning piglets could be close to 100% prior to the development of passive immunity. This disease has been relatively common in Asia and Europe since the 1970s, while in the US and Canada, cases of PED were first diagnosed beginning in April 2013. Although the mortality rate in naïve suckling pigs is very high, field reports indicate it is not 100%. No studies have been undertaken to investigate potential genetic differences between dead and surviving neonatal piglets in a PEDV outbreak prior to the development of passive immunity.

Materials and Methods

In this research, 156 dead and 106 surviving neonatal piglets from five PED outbreak farms located in USA, Canada and Germany were considered. Sampling occurred within 3 weeks of the initial onset of PED, prior to the development of maternal immunity. Surviving piglets experienced PED diarrhea but did not succumb to the disease during lactation. Piglets were genotyped with the 80K SNP chip. A total of 60,969 autosomal SNPs were used in an Fst genetic analysis comparing dead and surviving samples using non- overlapping 1Mb windows and the results were normalized across the analysis. The most divergent regions (±200kb) were investigated and the annotated (identified) genes included in those regions were analyzed with "GOrilla" and "EnriChr" software.

Results and Discussion

A total of 7 regions across the pig genome were considered as most different between dead and survived pigs. These regions are located in chromosomes 2, 4 and 15 (Figure 1). These regions contained 162 identified genes. The analysis with "GOrilla" revealed enrichment for genes that belong to the Golgi apparatus and membrane, together with genes involved in ion transporter, metabolism, and ATPase activity. Analysis with "EnriChr" showed that several genes were under or over expressed in several coronavirus infections in humans. Considering that the PED virus is a coronavirus and that it is known that assembly of the PED virus occurs by budding through intra cytoplasmic membranes, such as the endoplasmic reticulum and Golgi apparatus, these results have strong biological meaning, providing a preliminary but important direction for the comprehension of the genetic resistance to this disease. These results may provide opportunities to further identify mutations which confer resilience.
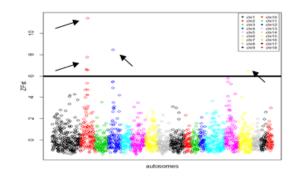
Acknowledgments

Figure 1: Plot of the normalized Fst (ZFst) values, represented by dots. Each autosome has a different color, as indicated in the legend. The black horizontal line represents the threshold above which a dot is significantly divergent