RESEARCHABSTRACT

pork checkoff

SWINE HEALTH

Title: Understanding the effect of concurrent PCV2a or PCV2b infection on the evolution of the PRRSV during serial passage in pigs – **NPB #09-200**

Investigator: Tanja Opriessnig

Institution: Iowa State University

Date Submitted: April 1, 2012

Scientific Abstract

PRRSV is recognized as possessing a high degree of genetic and antigenic variability. Viral diversity has led to questions regarding the association of virus mutation and persistent infection in the host and has raised concerns on protective immunity, the ability of diagnostic assays to detect novel variants, and the possible emergence of virulent strains. The purpose of this study was to determine if PCV2 increases the ability of PRRSV to change over time during serial passage in pigs and to determine if there is a difference in the PRRSV mutation rate between pigs concurrently infected with PCV2a or PCV2b. After 8 consecutive passages of PRRSV alone (group 1) or PRRSV with PCV2a (group 2) or PCV2b (group 3) in pigs, the sequences of the complete genes encoding the structural proteins of envelope (ORF 5), matrix (ORF6), nucleocapsid (ORF7) and partial ORF4 were obtained and analyzed. Thirteen, four, and two different nucleotide mutations were detected in group 1 (PRRSV only), group 2 (PRRSV-PCV2a), and group 3 (PRRSV-PCV2b) during the consecutive passages, respectively. 5 and 2 of the mutations resulted into amino acid alterations in group 1 and group 2, respectively. One of the amino acid substitutions present in group 1 had changed their polarity, that is, the hydrophilic 16Ser in ORF4 mutated into hydrophobic 16Tyr. The results from this study indicated that, besides ORF5, structural genes of ORF4 and ORF6 were shown to mutate and these results further confirm that PRRSV evolves continuously in *in vivo*.

For more information contact:

National Pork Board • PO Box 9114 • Des Moines, IA 50306 USA • 800-456-7675 • Fax: 515-223-2646 • pork.org