RESEARCH ABSTRACT

SWINE HEALTH

Title: Genetic and antigenic characterization of a recent PRRSV isolate – **NPB #08-260**

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Scientific Abstract

Porcine reproductive and respiratory syndrome virus (PRRSV) is the cause of respiratory disease and reproductive failure in swine. The virus continues to have a significant economic impact on the swine industry in the United States and worldwide. PRRSV is an RNA virus and as such subject to variable rates of mutation and viral recombination. The emergence of novel, virulent strains of PRRSV in herds with prior immunity is not uncommon.

A virulent isolate of PRRSV, responsible for high morbidity and mortality, was isolated from a North Carolina swine farm in 2006. Affected pigs were twelve weeks old and demonstrated clinical signs of lethargy, coughing dyspnea and weight loss with elevated mortality. PRRSV was isolated from affected lung tissue submitted to the Iowa State University Veterinary Diagnostic Laboratory (ISU-VDL). The PRRSV isolate, designated NC16845, was subsequently characterized through genomic sequencing and was evaluated for unique *in vitro* growth characteristics compared to three type 2 PRRSV isolates, which included the prototype VR-2332, MN184 and VR2385 isolated in the mid-90's.

The full length genome of NC16845 was found to be 15,385 nucleotides, which is similar to other type 2 PRRSV isolates that have been previously sequenced; however, restriction fragment length polymorphism (RFLP) analysis demonstrated a unique pattern designated 1-18-2. NC16845 shares an approximate nucleotide homology of 90.5% with atypical PRRSV JA142. Compared to VR-2332, nucleotide differences were identified in the ORF1a region known as non-structural protein 2 (nsp2) region. In addition, this region contained elevated nucleotide degeneracy and a discontinuous nucleotide deletion of 26 bases. Sequence homology with VR-2332 and MN184 was 88.2% and 77.3%, respectively.

NC16845 demonstrated slower replication in cell culture compared to VR-2332, MN184 and VR2385. NC16845 grew to a peak titer of $5.4x10^5$ plaque forming units per milliliter (PFU/ml) at 60 hrs post inoculation which was 4-13-fold lower than the growth of the other viruses. NC16845 was most similar in growth and replication properties to MN-184 PRRSV. Plaque assays resulted in plaques of intermediate size similar to VR2385, but larger than those of MN184 and smaller than the plaques induced by VR-2332. NC16845 plaques were clear and averaged 3.3 mm in diameter. Northern blots revealed NC16845 demonstrated a similar pattern of subgenomic RNA to MN184.

Collectively, these data indicate a slower replication rate and diminished growth properties of virulent PRRSV isolate NC16845 compared to prototype type 2 PRRSV strains. In addition, NC16845 contained fewer subgenomic RNA species similar to previously characterized MN184. The genome contains fewer nucleotide bases than VR-2332 and regions of heterogenous nucleotides with a discontinuous deletion that suggests that PRRSV NC16845 continues to evolve to eliminate dispensable regions of the genome.