

## SWINE HEALTH

**Title:** Sequencing and characterization of genes encoding capsid proteins VP4, VP6 and VP7 from field porcine rotavirus strains, **NPB #12-099**

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### Scientific Abstract

The Veterinary Diagnostic Laboratory (VDL) at Kansas State University in Manhattan, KS, received over 200 swine fecal samples of suspected rotavirus infections between 2012 and 2014. The single-primer amplification technique was employed to create cDNA of the double-stranded RNA genome segments. This sequence-independent method enabled us to amplify any rotavirus segments present in the fecal samples in an unbiased manner. This, coupled with next-generation sequencing technology, is a clear advantage over traditional sequencing because of its ability to generate full-length sequences of all eleven genome segments, even in samples that have mixed rotavirus infections. One hundred and fifty-four samples were successfully sequenced, and 97% of those yielded full or partial sequences for all eleven rotavirus gene segments, enabling the full genome constellations to be recorded. Twenty samples yielded sequences from two rotavirus groups (A&B, B&C, or A&C), and one sample produced sequences from all three common rotavirus groups (A, B, and C). The prevalence of porcine group A rotavirus has shifted, as nearly 60% of all the sequenced samples contained group C rotavirus, with group A at 37% and group B at 18%. The VP7, VP4, VP6, and NSP1 gene segments displayed the greatest diversity, based on the number of putative and/or confirmed genotypes identified in our sample set. The prevalence of particular porcine sero- or genotypes has also shifted during the period of time that researchers have been tracking them, and a total of 30 new putative group B and C rotavirus genotypes were identified.

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