

## PUBLIC HEALTHWORKER SAFETY

**Title:** Noroviruses in finisher swine: prevalence and relatedness to human noroviruses - NPB #08-183

**Investigator:** Linda J. Saif

**Institution:** The Ohio State University Research Foundation

**Co-Investigator:** Wondwossen Gebreyes

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### Scientific Abstract.

Noroviruses (NoVs) are the leading cause of foodborne illness. A potential exists for interspecies transmission of NoVs or the emergence of new epidemic human strains by genetic recombination of human and porcine NoVs. However, an extensive sequence database is lacking for porcine NoVs. Without knowing the diversity of swine NoVs and their relatedness to human strains, it is impossible to pinpoint the possible origin (swine or human) of NoV contaminants reported in pork. The objectives of this study are: 1) to study the prevalence of porcine NoVs in finisher swine barns; 2) to identify newly emerged porcine NoVs and determine the genetic relatedness between porcine and human NoVs. We tested 313 pooled samples from 1436 individual finisher pig fecal samples collected from 33 barns belonging to 9 farms and 3 production systems (BC1-3) in North Carolina. A reverse transcription (RT)-PCR coupled hybridization assay was used to screen for known porcine NoVs. Two more RT-PCR assays were performed to detect genetically diverse NoVs and other caliciviruses. Sequence analyses of representative strains did not identify human NoVs or new porcine NoVs, but revealed a new porcine enteric calicivirus, St-Valerien-like virus (WGP93C strain). We further characterized the first US St-Valerien-like virus WGP93C strain to expand the porcine enteric calicivirus sequence database. Finally, a real time RT-PCR for the detection of St-Valerien-like viruses was developed and used to perform the first prevalence study of these new viruses.

The prevalence of porcine NoVs was 18.5% (range of 5.0-51.7% among farms). It was significant higher in BC2 (32.3%) than BC1 (15.1%) and BC3 (9.2%) production systems. The St-Valerien-like viruses were also endemic in NC farms with a prevalence of 21.1% (range of 2.6-80.0% among farms). Pigs of production system BC1 shed St-Valerien-like viruses in significantly higher frequencies (34.5%) than in the other two production systems (7.3% and 18.4%, respectively). Overall there was no significant difference in NoV or St-Valerien-like virus prevalence among the treatments (three biocides Biosentry, Synergize, Virkon-S and hot water control). The complete genome of WGP93C strain was sequenced and our data supports that the St-Valerien-like viruses represent a new genus within *Caliciviridae*.

The differences among the three production systems are mainly the “origin” of the pigs. Each of the production systems is fully independent and they have their own genetics/breeding units, farrowing sites where the sampled pigs originated, etc. Our finding suggests that breed differences or infection incidence in earlier production stages might affect incidence at the sampled finisher stage. Genetic differences in human blood

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For more information contact:

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

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types are known to affect susceptibility to human NoVs. Whether genetic factors affect pig susceptibility to porcine NoVs requires further investigation. There is no report that porcine NoVs cause clinical signs in finisher pigs. However, like most RNA viruses, NoVs undergo constant genetic mutation during viral replication and new variants emerge constantly that may have altered host and tissue tropism and/or disease patterns. Nevertheless, because some porcine and human NoV strains are genetically and antigenically related and frequent recombination results in new variants, a potential may exist for the zoonotic emergence of new endemic human NoV strains from porcine NoVs. Therefore, continuously monitoring the prevalence and diversity of NoVs in pigs will provide important information to identify or refute swine or pork products as sources for possible human NoV transmission and infection. Finally, the biocides did not affect the prevalence of porcine NoVs or St-Valerien-like viruses. These results are consistent with the fact that NoVs are extremely stable in the environment and resistant to many disinfectants. Whether the St-Valerien-like viruses cause disease in pigs, including younger pigs or occur in other species, including humans, requires further investigation.