

22nd NAPRRS/NC229 International Conference of Swine Viral Diseases

NAPRRS/NC229 ICSVD provides a forum for bringing together the members of swine disease community from all over the world. The latest meeting was held in Chicago, Illinois, in January 2026. Two selected abstracts from the proceedings are included below.

The full proceedings can be found at: <https://vetmed.illinois.edu/about-the-college/pathobiology/north-american-prrs-symposium/>

Investigation of porcine reproductive and respiratory syndrome outbreaks across Ohio during early 2025

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Porcine reproductive and respiratory syndrome (PRRS) is one of the most economically significant swine diseases worldwide and disease outbreaks remain a persistent challenge across the industry. While biosecurity serves as a primary defense, even the most biosecure operations continue to experience PRRS outbreaks each year. The aim of this project was to identify gaps in biosecurity and determine potential risk factors associated with PRRSV outbreak occurrence. A cross-sectional survey of swine farms was conducted during in-person farm visits between March and April 2025 to investigate PRRS L1C.5.32 outbreaks identified from January to April of the same year in Ohio, USA. A structured questionnaire, filled during site visit interviews, captured information on six key topics: vaccination status, demographics, biosecurity, feed and water management, animal movement and disposal management, and outbreak details. Of approximately 12 sites reporting an outbreak during this period, 5 were visited and surveyed. These were mainly growing pig sites (75%), with an average herd size of 2,125 pigs. The two farthest sites were located approximately 150 miles away from each other, showing little evidence for “local” transmission. Two of the five sites visited reported vaccinating their animals against PRRS. The surveyed farms reported use of barn specific boots and coveralls (100%), Danish entry (60%), and showering in (60%) for farm staff and visitors. All sites reported the use of a visitor log, though only one farm reported having visitors to the barn within the two weeks prior to the outbreak date. Four of five farms (80%) shared full-time workers across farms within the same production system. All sites composted dead pigs. Qualitative observations during the farm visits highlighted potential risks associated with swine density and movements in the surveyed site regions, including the use of local transfer stations and local multi-species markets, and potential sharing of manure pumping services. Furthermore, biosecurity measures including the use of showers and visitor logs appeared inconsistently implemented upon the visit, with a lack of verification procedures in place noted. **Acknowledgements:** We would like to acknowledge Ohio Pork Council for their collaboration and funding.

Recombination events of porcine reproductive and respiratory syndrome virus (PRRSV)

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Porcine reproductive and respiratory syndrome (PRRS) is the most devastating disease in the US swine industry with PRRS virus (PRRSV) Type 2 (North America) being the most predominant strain in the United States. Recombination is an important evolutionary mechanism in RNA viruses, and this study is an attempt to understand those evolutionary patterns in PRRSV and identify eventual recombination events between the vaccine strains and field isolates of PRRSV 2. Forty-seven field isolates of PRRSV collected at different times during the period 2007-2021 were sequenced along with three vaccines (Fostera PRRS, Ingelvac PRRS MLV, Ingelvac PRRS ATP). The library preparation was performed using Nextera XT kit and 150 bp paired-end sequencing was performed on an Illumina MiSeq instrument. On average, 2.5 million reads per sample were generated. Sequences from six vaccine strains (Ingelvac PRRS MLV, Ingelvac PRRS ATP, Fostera PRRS, Prime Pac PRRS RR, Prevacent PRRS and PRRSGard), including three that have been sequenced in this study were retrieved from NCBI and other laboratories. Bioinformatics analysis was primarily conducted using CLC Genomics Workbench 15.0.1. Following the removal of adapters, short reads, and low-quality sequences, reads were mapped to PRRSV 1 and PRRSV 2 reference genomes. The optimal reference genomes, identified via BLAST, were then used for mapping, and consensus sequences were extracted at 30X coverage. The majority of field isolates were found to be PRRSV 2, with distinct clades within PRRSV 2 correlating with sample collection times. Leveraging insights from the phylogenetic tree, samples were assessed for recombination using Simplot++ v1.3, with confirmation via GARD from Datamonkey v2.0. Although no recombination was detected between vaccines and field strains in our samples, some recombination events were identified between vaccines and previously sequenced field isolates found in NCBI, as well as among field isolates in our own samples. Notable novel recombinants included S45 (S26 x OK274266; USA), S6 (S11 x S42; USA), and PQ316100 (OP866751 x Fostera Vaccine; China). A comprehensive understanding of viral evolution and the identification of recombinants are crucial for developing effective disease management strategies, and enhanced genomic surveillance will significantly aid the swine industry in combating this devastating disease.

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