

## 2025 Research Highlights from MSHMP – Part 2

The MSHMP Team

Our research group continues to drive innovation in swine health by focusing on critical challenges faced by the industry. Through collaborative efforts, our recent publications explore diverse aspects of swine disease detection, management, and epidemiology, contributing to the broader understanding of swine health and welfare. Below are three of our latest research contributions:

### 1. Economic impact of productivity losses attributable to porcine reproductive and respiratory syndrome virus in United States pork production, 2016-2020

This study quantified the economic burden of Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) on U.S. pork production from 2016 to 2020, updating previous industry cost estimates. Using production and health data from breeding and growing pig herds, researchers estimated annual productivity losses exceeding \$1 Billion. The study identified regional and temporal variations in PRRSV impact, emphasizing the ongoing need for coordinated disease prevention strategies. Findings serve as a benchmark for evaluating the cost-effectiveness of emerging control measures, including vaccines and biosecurity interventions.

Osemeke O, Silva GS, Corzo CA, Kikuti M, Vadnais S, Yue X, Linhares D, et al. Economic impact of productivity losses attributable to porcine reproductive and respiratory syndrome virus in United States pork production, 2016 to 2020. *Prev Vet Med.* 2025;118:106627. doi:10.1016/j.prevetmed.2025.106627. doi:10.3390/pathogens14090940.



### 2. Complete Genome and Recombination Analysis of a Novel Porcine Reproductive and Respiratory Syndrome Virus 2 (Variant 1H.18) Identified in the Midwestern USA

Genomic surveillance remains vital for tracking PRRSV evolution and emergence. This research characterized a newly identified PRRSV-2 variant, lineage 1H.18, detected in the Midwestern United States. Whole-genome sequencing and recombination analysis revealed complex genetic exchange events between existing PRRSV lineages, highlighting the virus's ongoing evolution and adaptability. The study underscores the importance of continuous molecular monitoring to detect novel variants early and assess their potential implications for vaccine performance and diagnostic sensitivity.

Herrera da Silva JP, Rossow S, Paploski IAD, Kikuti M, Corzo CA, et al. Complete genome and recombination analysis of a novel porcine reproductive and respiratory syndrome virus 2 (variant 1H.18) identified in the Midwestern USA. *Viruses.* 2025;17(6):863. doi:10.3390/v17060863. doi:10.3390/ani15162434.



### 3. Senecavirus A Incidence in U.S. Breeding Herds: A Decade of Surveillance Data

Drawing from ten years of Morrison Swine Health Monitoring Project data, this study examined temporal and spatial patterns of Senecavirus A (SVA) in U.S. breeding herds. Results showed fluctuating incidence rates with distinct seasonal peaks and regional clustering. The longitudinal dataset provided valuable insight into SVA's endemic dynamics and demonstrated the effectiveness of ongoing monitoring in early detection and outbreak response. These findings reinforce the role of national surveillance programs in mitigating the impact of emerging and reemerging swine diseases.

Kikuti M, Yue X, Melini CM, Vadnais S, Corzo CA. Senecavirus A incidence in U.S. breeding herds: A decade of surveillance data. *Animals.* 2025;15(11):1650. doi:10.3390/ani15111650.



Through these publications, our group continues to advance the field of swine health, driving progress in disease detection, variant monitoring, and epidemiological mapping. We are excited to share these findings with the scientific community and industry stakeholders to foster innovation in animal health management. A full list of MSHMP-related publications is available on our website: <https://mshmp.umn.edu/>