Using swine interstate transport records as a predictor of pathogen spread across the USA

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Key Points:
- Accessible transportation records that document interstate swine movement can improve outbreak preparedness.
- We demonstrated that interstate hog transport could predict the spread of PRRSV 1-4-4 L1C Variant (L1C.5).
- High-quality animal movement datasets enable the creation of computational tools that can be used for precision outbreak mitigation.

Why did we do this study?
In the face of a novel outbreak of an economically significant disease in domestic livestock, stopping the spread of the pathogen becomes a national issue. Mitigation efforts must be balanced with maintaining productivity and economic stability to preserve a safe and sustainable food supply. It is difficult to estimate how a pathogen emerging in one location will move across the country and, hence, which areas to target to restrict animal movement to mitigate the spread of disease.

What did we do?
We contacted individual state agencies and collected interstate transport data for hogs through digitizing Certificates of Veterinary Inspection. We used these data to create a national network of interstate swine movement. We evaluated this network as an informative predictor of the spread of a pathogen, using the porcine reproductive and respiratory syndrome virus (PRRSV) L1C 1-4-4 variant as a test case.

How did we do it?
Hog import records from 2020-2022 were aggregated from 28 U.S. states: we prioritized states with the highest hog inventory. For aggregation of the data, we used all movements between states in 2021 (n=23) or substitutes from 2020 (n=2) or 2022 (n=2) when necessary. These data represented approximately 96% of annual interstate swine transport (56 million/58.3 million total head), compared to the gold standard reported by the USDA Meat Animal Production, Disposition, and Income 2021 Summary. Using a statistical approach, we constructed a movement network where each state was linked by the number of pigs that moved between the locations.

We also collected all PRRSV L1C 1-4-4 variant sequences and metadata (n=3,645) from 2020 to August 2023 from a regional diagnostic lab. The sequences were aligned, and a maximum likelihood phylogenetic tree was inferred to describe the evolutionary history of the virus. This dataset was representatively sampled (n=598) and we used a Bayesian phylogeographic analysis to estimate the spatial diffusion of the PRRSV L1C variant at the U.S. state level. The weights from the interstate swine transport network were used as a predictor of spatial diffusion, and their predictive value was tested using a predictor selection algorithm within a generalized linear model.

What did we find?
The interstate transport network was correlated with the spatial dissemination of the PRRSV L1C variant with a posterior inclusion probability of >0.99 and a coefficient of 1.872 (95% HPD interval of [1.3448, 2.4255]), indicating the transport network was highly correlated with the interstate spread of the L1C variant.

What does it mean?
We demonstrated statistical support for interstate swine movement influencing the spread of a PRRSV variant. These results reinforce the value of interstate swine transport and other animal movement datasets in developing tools that increase preparedness for a foreign animal disease outbreak that could spread as animals are moved. These data also suggest that the spread of a pathogen depends on where it enters the U.S. pig population, and in the future, simulation methods could be developed to model spread and how intervention efforts can be directed to minimize disruption to the U.S. swine industry.

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