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Researchers create algorithm to predict PEDV outbreaks

NORTH CAROLINA STATE UNIVERSITY

Researchers from North Carolina State University have developed an algorithm that could give pig farms advance notice of porcine epidemic diarrhea virus (PEDV) outbreaks. The proof-of-concept algorithm has potential for use in real-time prediction of other disease outbreaks in food animals.

PEDV is a virus that causes high mortality rates in preweaned piglets. The virus emerged in the U.S. in 2013 and by 2014 had infected approximately 50 percent of breeding herds. PEDV is transmitted by contact with contaminated fecal matter.

Gustavo Machado, assistant professor of population health and pathobiology at NC State and corresponding author of a paper describing the work, developed a pipeline utilizing machine-learning techniques to create an algorithm capable of predicting PEDV outbreaks in space and time.

Machado, with colleagues from the University of Minnesota and Brazil's Universidade Federal do Rio Grande do Sul, used weekly farm-level incidence data from sow farms to create the model. The data included all pig movement types, hog density, and environmental and weather factors such as vegetation, wind speed, temperature and precipitation.

The researchers looked at "neighborhoods" that were defined as a 10-kilometer radius around sow farms. They fed the model information about outbreaks, animal movements into each neighborhood and the environmental characteristics inside each neighborhood. Ultimately, their model was able to predict PEDV outbreaks with approximately 80 percent accuracy.

The most important risk factor for predicting PEDV spread was pig movement into and through the 10 km neighborhood, although neighborhood environment - including slope and vegetation - also influenced risk.

"This proof-of-concept model identified the PEDV spread bottleneck in North Carolina and allowed us to rank infection risk factors in order of importance," Machado says. "As we get more data from other farm sites across the U.S., we expect the model's accuracy to increase. Our end goal is to have near real-time risk predictions so that farmers and veterinarians can provide preventative care to high-risk areas and make decisions based on data."

Next steps for the researchers include improving the model to predict a wider range

of diseases and expanding it to include other industries, such as poultry.

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The work appears in Scientific Reports, and is supported by the National Pork Board and the Swine Health Information Center.

Note to editors: An abstract of the paper follows.

"Identifying outbreaks of Porcine Epidemic Diarrhea virus through animal movements and spatial neighborhoods"

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Abstract:

The spread of pathogens in swine populations is in part determined by movements of animals between farms. However, understanding additional characteristics that predict disease outbreaks and uncovering landscape factors related to between-farm spread are crucial steps toward risk mitigation. This study integrates animal movements with environmental risk factors to predict the occurrence of porcine epidemic diarrhea virus (PEDV) outbreaks. Using weekly farm-level incidence data from 980 farms, we applied machine learning algorithms to quantify associations between risk factors and PEDV outbreaks with the ultimate goal of predicting the occurrence of disease at the farm level. Our best algorithm predicted outbreaks during one-week periods with >80% accuracy. The most important predictors included pig movements into neighboring farms (within 10 km). Other important neighborhood attributes included hog density, environmental and weather factors such as vegetation, wind speed, temperature, and precipitation, and topographical features such as slope. Our neighborhood-based approach allowed us to simultaneously capture disease risks associated with long-distance animal movement as well as local spatial dynamics. The model presented here forms the foundation for near real-time disease mapping and will advance disease surveillance and control for endemic swine pathogens in the United States.

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