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Surveillance of porcine reproductive and respiratory syndrome virus in the United States using risk mapping and species distribution modeling

Moh A. Alkhamis^{a,b,*}, Andreia G. Arruda^c, Carles Vilalta^a, Robert B. Morrison^a, Andres M. Perez^a

^a Department of Veterinary Population Medicine, College of Veterinary Medicine, University of Minnesota, St. Paul, USA

^b Faculty of Public Health, Health Sciences Center, Kuwait University, Kuwait

^c Department of Veterinary Preventive Medicine, College of Veterinary Medicine, The Ohio State University, Columbus, USA

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ABSTRACT

Porcine reproductive and respiratory syndrome virus (PRRSv) outbreaks cause significant financial losses to the U.S. swine industry, where the pathogen is endemic. Seasonal increases in the number of outbreaks are typically observed using PRRSv epidemic curves. However, the nature and extent to which demographic and environmental factors influence the risk for PRRSv outbreaks in the country remains unclear. The objective of this study was to develop risk maps for PRRSv outbreaks across the United States (U.S.) and compare ecological dynamics of the disease in five of the most important swine production regions of the country. This study integrates spatial information regarding PRRSv surveillance with relevant demographic and environmental factors collected between 2009 and 2016. We used presence-only Maximum Entropy (Maxent), a species distribution modeling approach, to model the spatial risk of PRRSv in swine populations. Data fitted the selected model relatively well when the modeling approach was conducted by region (training and testing AUCs < 0.75). All of the Maxent models selected identified high-risk areas, with probabilities greater than 0.5. The relative contribution of pig density to PRRSv risk was highest in pig-densely populated areas (Minnesota, Iowa and North Carolina), whereas climate and land cover were important in areas with relatively low pig densities (Illinois, Indiana, South Dakota, Nebraska, Kansas, Oklahoma, Colorado, and Texas). Although many previous studies associated the risk of PRRSv with high pig density and climatic factors, the study here quantifies, for the first time in the peer-reviewed literature, the spatial variation and relative contribution of these factors across different swine production regions in the U.S. The results will help in the design and implement of early detection, prevention, and control strategies for one of the most devastating diseases affecting the swine industry in the U.S.

1. Introduction

Infection with the porcine reproductive and respiratory syndrome virus (PRRSv) causes significant financial losses to the swine industry of North America, where the pathogen is endemic (Neumann et al., 2005; Holtkamp et al., 2013). The disease is characterized by reproductive and respiratory disorders in sows and growing pigs, respectively (Quaife, 1989; Elazhary et al., 1991). PRRSv strains are classified into two types referred to as type I, or European strain, and type II, or North American strain, with the latter causing most of the outbreaks in the United States (U.S.) (Ropp et al., 2004; Murtaugh, 2009). PRRSv-infected pigs may transmit the virus through all secretions (Rossow, 1998). Movement of infected pigs and contaminated fomites, as well as air, have been shown to maintain PRRSv circulation and facilitate disease spread across the U.S. (Cutler et al., 2011; Perez et al., 2015).

PRRSv maintains an endemic state in North America, with annual seasonal increases in the number of outbreaks. However, the disease also causes occasional seasonal epidemics through new emerging viral strains (Arruda et al., 2015). These epidemics cause heavy losses to industry as they result in far-reaching direct losses and require prompt allocation of diagnostic, control, and prevention resources. Many studies have identified associations between season and both number of outbreaks and emergence of new PRRSv strains (Holtkamp et al., 2010; Tousignant et al., 2015). Similarly, other studies were able to establish associations between herd size and frequency of PRRSv outbreaks (Holtkamp et al., 2012; Kwong et al., 2013; Truong and Gummow, 2014). Therefore, it is generally accepted that both demographic and climatic factors contribute to the risk of the introduction, maintenance, and spread of PRRSv in the U.S.

Surveillance has a key role in providing information for the

* Corresponding author at: Department of Veterinary Population Medicine, College of Veterinary Medicine, University of Minnesota, 225 Veterinary Medical Center, 1365 Gortner Avenue St. Paul, MN 55108, USA.

E-mail address: malkahmi@umn.edu (M.A. Alkhamis).

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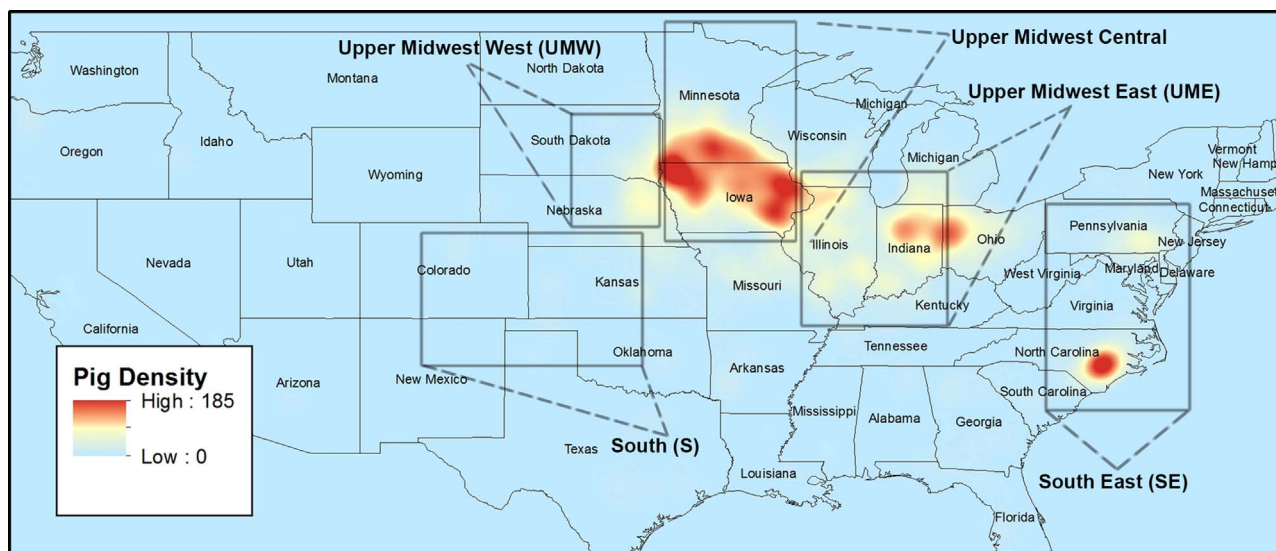


Fig. 1. Pig density (pig farms per square kilometre), spatially smoothed by a kernel density function, according to the U.S. Department of Agriculture (USDA) Census of Agriculture. The map has been divided into five swine production areas.

development of intervention activities for PRRSv control. In the U.S., surveillance activities are under constant implementation; however, because PRRSv reporting is not mandatory, these vary substantially between regions and production systems. On-going monitoring of selected growing pig sites and passive surveillance triggered by clinical signs are common examples of such activities (Perez et al., 2015). However, all surveillance activities have not been sufficient to prevent the emergence of PRRSv strains. Furthermore, aspects related to the transmission dynamics of PRRSv within and among production systems and/or regions in North America are not completely understood (Alvarez et al., 2016). Past studies demonstrated the role of environmental conditions in the transmission dynamics of PRRSv (Kwong et al., 2013; Nathues et al., 2014; Truong and Gummow, 2014). However, there is no available peer-reviewed information on the quantification of the combined effect of factors such as season and herd size on the spatial range of high-risk areas for PRRSv outbreaks. Identification of high-risk areas with suitable environmental and demographic conditions and times at which PRRSv outbreaks are likely to occur are integral components of risk-based surveillance, with the ultimate objective of allowing for timely decisions in regards to allocation of intervention resources.

Species distribution models (SDM) have recently become a popular tool for risk mapping of human and animal infectious diseases, with the ultimate goal of guiding risk-based surveillance activities (Scholte et al., 2012; Slater and Michael, 2012; Herrick et al., 2013; Nogareda et al., 2013; Prosser et al., 2013; Quintana et al., 2013). SDMs have a unique ability to extract associations between hypothesized risk factors (e.g. herd size and climate) and disease occurrence (or presence), using these associations to characterize the environmental and demographical prerequisites of a pathogen. Subsequently, these associations are projected to predict the spatially explicit distribution of PRRSv in non-sampled or underreporting regions or swine production systems (Elith et al., 2011).

Here the relative contribution of selected factors to the risk of PRRSv occurrence in the most important swine production regions of the U.S. was estimated. The null hypothesis was that the contribution of selected factors to spatial PRRSv risk was homogenous through out swine producing regions in the U.S. Furthermore, we assessed whether the extent at which hypothesized factors influenced PRRSv risk was similar for different regions after accounting for demographic variables. Our study integrated spatial information regarding PRRSv surveillance with relevant demographic and environmental factors, providing useful

insights into the spatial epidemiology of PRRSv. Results may be used to guide risk-based surveillance activities including early detection, control, and prevention of one of the most devastating diseases affecting the U.S. swine industry.

2. Materials and methods

2.1. Data source

We used a confidential dataset obtained from a voluntary PRRSv reporting program referred to as the Morrison Swine Health Monitoring Project, MSHMP (MSHMP, 2016), which includes data from approximately 40% of the total number of sows in the country. Data were collected from July 29th 2009 to September 28th 2016 from breeding farms across the U.S. The dataset contained information including geographical location (latitude and longitude) and affiliated production system as well as weekly PRRSv status, including date at which outbreaks were reported, for each sow farm that reported to the MSHMP. PRRSv farm status was determined following criteria described elsewhere (Holtkamp et al., 2011; Tousignant et al., 2015). Briefly, sow farms are classified into categories: i) status 1 indicates actively infected herds in which pigs are shedding the virus; ii) status 2 denotes stable herds, where no shedding can be detected in weaned pigs for at least 90 days and the herd is undergoing a PRRSv elimination procedure, with status 2fvi and 2vx designating stable herds using live virus exposure or vaccination as a control measure, respectively; iii) status 3 refers to herds that are provisionally negative, with new gilts testing ELISA negative for at least 60 days; and iv) status 4 is reserved for ELISA-negative herds, which have either never been infected, or have previously been infected but all infected sows have been removed and replaced, or herds that had been in category 3 for a year.

We used a smoothed kernel density function with a spatial resolution of 5 km² to represent the geographical density of PRRSv outbreaks in the swine production regions across the U.S. to protect data confidentiality. The resolution of 5 km² was chosen to match the resolution at which predictors were recorded. We defined five regions across the U.S. (Fig. 1) to include infected farms located in: a) Pennsylvania down to North Carolina (South East; SE); b) Illinois and Indiana (Upper Midwest East; UME); c) Minnesota and Iowa (Upper Midwest Central; UMC); d) South Dakota and Nebraska (Upper Midwest West; UMW); e) Kansas and Oklahoma, with parts from Colorado, Texas and New Mexico (South; S). These regions are characterized by high (SE, UME,

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