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Unraveling the contact patterns and network structure of pig shipments in the United States and its association with porcine reproductive and respiratory syndrome virus (PRRSV) outbreaks

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ABSTRACT

The analysis of the pork value chain is becoming key to understanding the risk of infectious disease dissemination in the swine industry. In this study, we used social network analysis to characterize the swine shipment network structure and properties in a typical multisite swine production system in the US. We also aimed to evaluate the association between network properties and porcine respiratory and reproductive syndrome virus (PRRSV) transmission between production sites. We analyzed the 109,868 swine shipments transporting over 93 million swine between more than 500 production sites from 2012 to 2014. A total of 248 PRRSV positive occurrences were reported from 79 production sites during those 3 years. The temporal dynamics of swine shipments was evaluated by computing network properties in one-month and three-month networks. The association of PRRS occurrence in sow farms with centrality properties from one-month and three-month networks was assessed by using the multilevel logistic regression. All monthly networks showed a scale-free network topology with positive degree assortativity. The regression model revealed that out-degree centrality had a negative association with PRRS occurrence in sow farms in both one-month and three-month networks [OR = 0.79 (95% CI, 0.63–0.99) in one-month network and 0.56 (95% CI, 0.36, 0.88) in three-month network] and in-closeness centrality model was positively associated with PRRS occurrence in sow farms in the three-month network [OR = 2.45 (95% CI, 1.14–5.26)]. We also describe how the occurrence of porcine epidemic diarrheac (PED) outbreaks severely affected the network structure as well as the PRRS occurrence reports and its association with centrality measures in sow farms. The structure of the swine shipment network and the connectivity between production sites influenced on the PRRSV transmission. The use of network topology and characteristics combining with spatial analysis based on fine scale geographical location of production sites will be useful to inform the design of more cost-efficient, risk-based surveillance and control measures for PRRSV as well as other diseases in the US swine industry.

1. Introduction

A better understanding of the structure of the pork value chain allows the assessment of the risk of infectious disease dissemination in the swine industry (Bigras-Poulin et al., 2007; Thakur et al., 2014; Relun et al., 2016). The modern commercial pork industry is based on a multi-site production system in which each production site has a highly specialized role to improve productivity (Key and McBride, 2007). Consequently, the shipment of live swine between production sites has become a need more than a choice. However, the increased complexity of swine shipment networks as well as the number of swine shipments between production sites have direct implications in the risk of introduction and spread of infectious diseases. A better understanding of the swine shipment network structure may facilitate the establishment of cost-effective surveillance, preventive and control strategies to mitigate infectious disease transmission between production sites.

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Social network analysis (SNA) is becoming the methodology of choice to describe complex network structures (Wasserman and Faust, 1994). In the field of epidemiology, SNA can be used to identify potential super-spreaders or super-receivers of diseases that may affect swine as well as other livestock species (Dubé et al., 2009; Martínez-López et al., 2009; Martin et al., 2011; Yatabe et al., 2015). It has also been used in combination with cluster analysis to identify the area, time periods and production sites that could be considered at high risk of disease introduction and spread (Martinez-Lopez et al., 2009b). Another study of the swine trade network in France evaluated the structural vulnerability of the network to the spread of infectious diseases (Rautureau et al., 2012). In northern Germany, SNA was used to explore the network topology of the pork supply chain in order to identify potential disease transmission patterns within the network (Büttner et al., 2013). Similarly, a study of swine shipments in Ontario, Canada, applied SNA to evaluate the heterogeneous contacts among production sites and provide more realistic parameters to simulate disease transmission (Dorjee et al., 2013). A recent study of the swine industry in four European countries revealed that the swine trade network structure and properties were substantially different among swine industries based on their production systems (Relun et al., 2016) which has important implications for disease transmission. To the best of author's knowledge, no studies have characterized the swine movement networks in the US, which limits the implementation of science-based policies for better prevention and control of diseases transmitted through swine trade.

In this context, we were interested not only in characterizing the US swine shipment network in a typical multi-site swine production system but also in evaluating the impact of network structure, properties and temporal dynamics on the spread of infectious diseases. For such purpose, we used porcine respiratory and reproductive syndrome (PRRS) for which highly detailed information was available and is considered to be the disease with the highest economic impact in the US swine industry (Holtkamp et al., 2013). PRRS virus (PRRSV) is considered to be transmitted between sites through both direct contacts between infected and naïve swine herds (i.e. swine shipments) (Mortensen et al., 2002) and indirect contacts (i.e. airborne spread) (Brockmeier and Lager, 2002). While there are several studies to evaluate the impact of airborne transmission (Cho et al., 2007; Pitkin et al., 2009; Dee et al., 2010), the role of swine shipments in PRRSV transmission has been scarcely documented (Thakur et al., 2014).

The main objective of this study was to characterize the network structure and dynamics of swine shipments in a typical multi-site swine production system in the US. Secondly, we aimed to evaluate the role that network structure and characteristics may have in PRRSV transmission between production sites. The result of this study will provide a better understanding of the network structure of the US swine industry as well as valuable parameters to inform infectious disease transmission models. Methods and results are planned to be integrated into the Disease BioPortal platform (http://bioportal.ucdavis.edu) to support the implementation of risk-based surveillance and target interventions to better prevent and control PRRS and other swine diseases in the US.

2. Material and methods

2.1. Data

2.1.1. Swine demographics and shipment data

Swine demographics and swine shipment records for this study were provided by a pork production company managing more than 500 production sites located in one state in the US. The state, name and exact number of production sites are omitted here to preserve confidentiality. Swine shipments from January 2012 to December 2014 were included in the study. Production site information was comprised of the production site ID, production site type and, latitude and longitude of the centroid location of production site. Production sites were categorized into eight different types based on pork value chain: sow farm, gilt development unit (GDU), nursery, finishing farm, wean-to-finish farm (WF), boar stud, packer and cull station. Shipment records involved production site ID of origin and of destination, date of a shipment and number of swine in a shipment. Swine shipments to cull stations and packers were excluded from the analysis because they were considered as dead-end points and were external to the production system, thus were out of the scope of this study. The total number of shipments considered in the present study was 109,868.

2.1.2. PRRSV sample collection and classification

PRRSV ORF5 sequences were obtained from the veterinary diagnostic laboratory at Iowa State University originating from submitted samples between January 2012 to December 2014. Samples were submitted to the laboratory when clinical signs of suggested PRRS. In total, 248 PRRS confirmed diagnostic cases from 79 production sites during 3 years were considered in this study.

2.2. Data analysis

2.2.1. Network analysis

Swine production sites and swine shipments were defined as nodes and directed edges respectively. The three-year network from January 2012 to December 2014 was established and separated into 36 static one-month sub-networks and 12 three-month sub-networks to evaluate dynamics of the network structure at different time scales. Networks with shorter time scales than one month (i.e., daily and weekly) were also explored but not used for the analysis as they had an insufficient number of nodes. Simple digraphs were used for the estimation of general network properties for the complete network and temporal sub-networks. Specifically, the number of nodes and edges, density, average path length, diameter, clustering coefficient, size and numbers of giant weak components and giant strong components were measured. Despite of the intrinsic bias of the aggregation of repeated edges into a single edge, we used simple digraphs due to the complexity and discernable incompatibility of analysis of weighted networks in large networks (Barrat et al., 2004 and Opsahl et al., 2010). The definitions used for general network properties are summarized in Table 1. Small-world topology was determined by comparing the estimated average path length and clustering coefficient with same estimates in equivalent size random networks based on the Erdos-Renyi model (Erdos and Rényi, 1960). A network was assumed to have small-world topology if it has similar or smaller average path length and six times greater clustering coefficient than estimates of the equivalent random network (Watts and Strogatz, 1998). These properties were used to evaluate the general characteristics of the network structure and to compare the US network with swine shipment networks described in three other important swine production countries (i.e., France, Germany and Canada).

Centrality measures referred to as in-degree, out-degree, in-closeness, out-closeness, betweenness and eigenvector centrality were computed for both simple (i.e., un-weighted) and weighted digraphs. The definitions used for the centrality properties are presented in Table 1. Degree assortativity was calculated based on unweighted in-degree and out-degree centrality measures in each production site of one-month networks. The assessment of scale-free topology in the one-month networks was performed by fitting a power-law distribution defined as $p(x) \sim x\hat{(}-\alpha)$ (x: centrality degrees, α: constant) into probability distributions for the unweighted in-degree and out-degree centrality measures.