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Role of animal movement and indirect contact among farms in transmission of porcine epidemic diarrhea virus

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ABSTRACT

Epidemiological models of the spread of pathogens in livestock populations primarily focus on direct contact between farms based on animal movement data, and in some cases, local spatial spread based on proximity between premises. The roles of other types of indirect contact among farms is rarely accounted for. In addition, data on animal movements is seldom available in the United States. However, the spread of porcine epidemic diarrhea virus (PEDv) in U.S. swine represents one of the best documented emergences of a highly infectious pathogen in the U.S. livestock industry, providing an opportunity to parameterize models of pathogen spread via direct and indirect transmission mechanisms in swine. Using observed data on pig movements during the initial phase of the PEDv epidemic, we developed a network-based and spatially explicit epidemiological model that simulates the spread of PEDv via both indirect and direct movement-related contact in order to answer unresolved questions concerning factors facilitating between-farm transmission. By modifying the likelihood of each transmission mechanism and fitting this model to observed epidemiological dynamics, our results suggest that between-farm transmission was primarily driven by direct mechanisms related to animal movement and indirect mechanisms related to local spatial spread based on geographic proximity. However, other forms of indirect transmission among farms, including contact via contaminated vehicles and feed, were responsible for high consequence transmission events resulting in the introduction of the virus into new geographic areas. This research is among the first reports of farm-level animal movements in the U.S. swine industry and, to our knowledge, represents the first epidemiological model of commercial U.S. swine using actual data on farm-level animal movement.

1. Introduction

Mathematical and computational modeling of infectious diseases is a common approach to simulating the spread of disease in a population, exploring key epidemiological parameters that drive transmission, and evaluating alternative control strategies (Brooks-Pollock et al., 2015; Craft, 2015; VanderWaal et al., 2017). In livestock populations, network-based models based on data on animal movements between farms have been a key area of research (Bajardi et al., 2012; Craft, 2015; Green et al., 2006; Kao, 2002; Kao et al., 2007; Rossi et al., 2015). However, animal movement data is rarely available for livestock industries in the United States due to the lack of a comprehensive national livestock traceability program. This limits capabilities to predict the dynamics of infectious diseases at the landscape, regional, and national levels and hinders development of risk-based surveillance and control measures based on movement data. Animal movement data may be particularly important for the swine industry, where production is highly vertically integrated in that pigs are moved between multiple premises between birth and slaughter, with each premise potentially located in different states (Valdes-Donoso et al., 2017). Such frequent and long distance movement makes the U.S. swine industry vulnerable to infectious disease epidemics.

In addition to direct contact among farms via animal movements, indirect contact may occur between farms due to windborne propagation of aerosols and dissemination of fomites by personnel, contaminated vehicles, and feed (Alonso et al., 2014; Alvarez et al., 2016; Beam et al., 2015; Dee et al., 2014; Kim et al., 2017; Lowe et al., 2014; O'Dea et al., 2015; Pasick et al., 2014). Although the potential importance of such mechanisms in creating transmission opportunities between swine premises has been shown in experimental studies and outbreak investigations (Alonso et al., 2014; Bowman et al., 2015; Lowe et al., 2014; Pasick et al., 2014), indirect contact is less often accounted for in epidemiological models (Arruda et al., 2016; Martinez-Lopez et al., 2011; Thakur et al., 2015; Yadav et al., 2016). Models of pathogen spread in livestock populations focus primarily on animal movement and, in some cases, local spatial spread based on proximity

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between premises (Brooks-Pollock et al., 2015). Attempts to account for indirect contact are hindered due to lack of data on which farms are connected via indirect contact. However, the structured nature of U.S. swine companies provides an ideal opportunity to infer patterns of indirect contact among farms and explore the joint impact of direct and indirect transmission on the spread of pathogens.

In May 2013, a new pathogen emerged and rapidly spread in the United States swine industry, resulting in major production impacts due to a mortality rate in neo-natal piglets of up to 100% (Saif et al., 2012). The disease was caused by porcine epidemic diarrhea virus (PEDv), an RNA coronavirus in the family *Alphacoronaviridae* that previously was circulating in Asia (Huang et al., 2013; Stevenson et al., 2013). As the name suggests, clinical signs of PEDv include watery diarrhea and vomiting. By the end of June 2014, PEDv had spread to 30 states and impacted approximately 50% of breeding herds (Goede and Morrison, 2016). PEDv may have resulted in the deaths of at least 7 million piglets, and it may take up to 12 weeks for infected sow farms, where breeding and farrowing occur, to recover their pre-infection piglet production levels (Goede and Morrison, 2016). Furthermore, surviving piglets exhibit poor growth during the growing period (Alvarez et al., 2015).

Despite the rapid between-farm spread of PEDv within the U.S. swine industry, there are a number of competing hypotheses concerning the main mechanisms of between-farm transmission, with no clear resolution on the relative importance of each of these mechanisms. For example, while contaminated feed may have contributed to the rapid emergence of PEDv (Dee et al., 2014; Pasick et al., 2014), there is also substantial evidence that movement of infectious pigs contributes to spread within a single flow of animals (i.e., movement of pigs from farrowing/sow farms to nurseries, and subsequently to finishing farms where fattening occurs) (Bowman et al., 2015). On a larger spatial scale, states between which there were high rates of pig movement exhibited more synchronous PEDv epidemics in terms of weekly case incidence, suggesting that pig movements created epidemiological linkages among states (O'Dea et al., 2015).

Unrelated to animal movements, there is evidence that local spatial spread between farms also occurs as infected farms are more clustered geographically than expected by chance (Alvarez et al., 2016). PEDv virus can also be recovered from air samples collected up to 16 km from infected farms (Alonso et al., 2014). Taken together, these studies suggest that windborne aerosols could contribute to between-farm transmission, especially at distances less than 4.8 km (Alonso et al., 2014; Alvarez et al., 2016). In addition, fomites may also contribute to between-farm spread. For example, market trucks that move pigs to slaughter facilities may function as mechanical vectors for fomites if they become contaminated at the slaughter facility and subsequently transmit the disease to naïve farms (Lowe et al., 2014).

The spread of PEDv in U.S. swine represents one of the best documented emergences of a highly infectious pathogen in the United States livestock industry, providing a unique opportunity to parameterize models of pathogen spread in U.S. swine. The objective of this research is to apply epidemiological modeling approaches to simulate the spread of PEDv at the regional scale in order to answer unresolved questions concerning factors facilitating between-farm transmission. Using real-world data on observed pig movements during the initial phase of the PEDv epidemic, we develop a network-based and spatially explicit epidemiological model that simulates the spread of PEDv via both indirect and direct movement-related contact. By fitting this model to the observed epidemiological dynamics in a geographically isolated production company of nearly 400 farms, we (i) evaluate the relative contribution of each of six direct and indirect mechanisms of between-farm transmission, and (ii) determine the most likely transmission mechanisms responsible for long-distance jumps, and (iii) discuss how these methods can be used to help producers mitigate future outbreaks. This research is among the first reports of farm-level animal movements in the U.S. swine industry (Lee et al., 2017; Valdes-Donoso et al., 2017) and, to our knowledge, represents the first epidemiological model of commercial U.S. swine using actual data on farm-level animal movement.

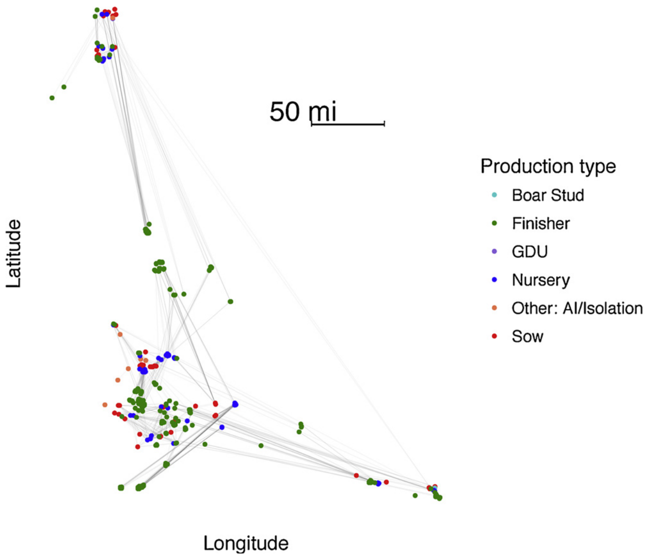

Fig. 1. Map of farm locations (colored nodes) and between-farm pig movements (gray lines) occurring between May through September 2013.

2. Materials and methods

2.1. Data source

Data on farm attributes, management, and between-farm pig movements were available for a single production company, or “system,” located in the Great Plains states of the west-central United States (Fig. 1). Swine production systems in the U.S. are “vertically integrated” in that different stages of production (from birth of piglets through slaughter) occur at different premises specializing in that particular stage. Primary production types included sow farms (housing sows during gestation and farrowing [birthing] periods and pre-weaning piglets), nursery farms (housing weaned piglets for approximately six to eight weeks), and finishers (where pigs are moved after the nursery period to fatten them for slaughter). Replacement gilts (young females) are usually brought into sow farms from gilt development units (GDUs), which are located either on the sow farm or at a separate farm. High biosecurity production types involved in maintenance of genetic stock included boar studs (premises housing boars used as studs for artificial insemination) and AI/Isolation units. A summary of farms in the study by production type is provided in Supplementary Table S1. Farm attribute data included the geographic location as UTM (Universal Transverse Mercator) coordinates, herd size, and production type for each of 376 company-managed farms.

Farm management data were available for each farm regarding the feed mill from which feed was sourced and the organizational “flow” to which the farm belonged. Flows were defined as groups of farms that were managed as a unit and shared support services, personnel, and truck washes. This production system was geographically isolated from other swine farms; however, the locations of 84 neighboring swine farms from seven neighboring systems were also available, as these farms may play a role in local disease transmission.

The first PEDv case in this system occurred on May 9, 2013 in a sow farm. Therefore, pig movement data spanned a timeframe from May 4, 2013 to October 1, 2013, as it was assumed that the farm may have been infectious prior to detection of clinical signs. Movement data included the date of each movement, total number of animals of moved, and the premise ID of the source and destination farms. During this five-