

A stochastic spatial-explicit agent-based modeling framework to better understand transmission dynamics of swine diseases in the US: the example of porcine reproductive and respiratory syndrome (PRRS).

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Background:

A better understanding of the spread patterns and high-risk areas for disease transmission under different epidemiological scenarios is extremely valuable to better support decision making and more cost-effective resource allocation. In the case of endemic diseases, we can use a combination of mechanistic and data-driven models to better understand transmission dynamics and, at the same time, being able to test the validity and reliability of our models using real-life collected data. Once validated those models can be readily used to inform decision making and mitigate the disease impacts in endemic settings as well as easily adapted to simulate other diseases and epidemiological scenarios. Porcine reproductive and respiratory syndrome (PRRS) is a viral disease that affects all production stages of pigs. The disease is characterized by late-term abortions, mummified or still-born fetuses, increased piglet mortality, and weak piglets in breeding populations. These piglets often have poor growth performance due to respiratory morbidity from the virus and co-infections. PRRS is endemic to the United States and causes significant economic losses to the swine industry. Some modeling attempts to evaluate PRRS within and between herd transmission have been previously published (e.g. Canada, Arruda et al., 2016, 2017; Thakur et al., 2015a,b; Jeong et al., 2014; Valdes-Donoso et al., 2018). But there are very few, if any, of these studies that have used fine-scale agent-based approach, with detailed real trade contact information as well as PRRS virus molecular data (i.e. viral sequences) to inform, parameterize and validate the model. Thus, the objective of this study was to develop a stochastic agent-based model utilizing fine scale data about the site demographics, contact structure and estimated transport routes to simulate within and between-farm transmission of PRRS in the US swine industry.

Methods:

An agent-based model was created using the GAMA software to simulate movement of PRRS within and between farms. The model was parameterized and validated using real data collected from midwestern production systems. Briefly, the daily PRRS spread within and between a particular farm is modelled using a spatial stochastic agent-based model in which pigs are assumed to be in one of five possible states: “Susceptible”, “Infected”, “Infectious”, “Clinical signs” or “Vaccinated”. The daily transition from “Susceptible” to “Infected” state is modelled by considering direct contacts (i.e. the movement of infected pigs between animals and farms) or indirect contacts (i.e. local spread, fomites, movement of vehicles transporting pigs or products or movement of people). The transition from “Susceptible” to “Infected” state differs depending on the age of the pig, the production stage or type of farm. The transition from “Infected” to “Infectious” and from “Infectious” to “Clinical Signs” states have been modelled by using the latent and incubation period of PRRS as well as considering the biosecurity and management practices on farm. The transition from “Susceptible” to “Vaccinated” have been modeling using standard vaccination protocols in different production sites. Data and parameters related with pig demographics; movements of pigs within and between production systems; PRRS viral sequences, among other information, was obtained from swine industry collaborators. Thousands of scenarios (i.e., 10.000) were run to evaluate the magnitude, duration and spatial spread of diverse PRRS subtypes under different epidemiological conditions (i.e. different farm type or farm size of index farms; high vs low density areas; involvement of farms with low vs high biosecurity practices, etc.). An extensive sensitivity analysis was also been performed to evaluate robustness of the model and to identify more influential input parameters.

Results:

Model results for diverse epidemiological scenarios are summarized using: the median and 95% probability intervals; graphs and maps with the number of infected, quarantined and culled farms and animals; the duration (in days) of the epidemic; the proportion of farms infected by direct contacts (i.e. animal movements), by local spread, by movements of people and of vehicles; the risk of a farm to become infected, defined as the number of times that a farm becomes infected considering all simulations; the effective reproduction ratio, R , defined as the amount of secondary infections caused by one infected farm in a not naïve population. We also generated risk maps and estimates of the direct impact of different PRRS molecular subtypes under different epidemiological scenarios. Most (>80%) of the sites identified to be at high risk for PRRS occurrence by the model reported real PRRS outbreaks, which proves that the model is valid and reliable.

Conclusion and Relevance:

Due to the economic burden of PRRS on the US swine industry, and still the limited understanding of the patterns of the virus propagation, we believe that our modeling framework allows better understanding and hypothesis testing about transmission dynamics and supports the implementation of risk-based, more cost-effective interventions. This study provides new outlooks on agent-based models for this disease by utilizing genomic information for different strains of the virus and by validation with real data from swine production systems. Future studies will focus on the evaluation of the cost-effectiveness of the implementation of different control strategies (e.g. diverse biosecurity measures, vaccination programs, etc.) as well as to adapt the model to other swine diseases such as African Swine fever.

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