**Tracking between-farm PRRSV-2 transmission and its potential routes through the virus genetic relationship and farm-based data**

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**Key Points:**

- Within a single swine-dense region of the U.S., three distinct PRRSV-2 variants (belonging to the L1A lineage that includes 1-7-4 viruses) had different geographic distributions.
- Analysis of genetic data showed that most farms were responsible for limited onward transmission, but 28% of the total farms acted as super-spreaders.
- Animal movement was strongly associated with between-farm PRRSV-2 transmission.
- Based on the genetic data, local spread of PRRSV-2 (within a radius of <10 km) did not appear to be a major mode of between-farm transmission.

## Introduction

In the pig farming industry, porcine reproductive and respiratory syndrome (PRRS) is a big problem globally, causing various health issues in pigs which leads to serious economic losses for farmers. In the U.S., PRRS is mainly caused by a virus called PRRSV-2, which spreads easily between pigs on different farms. The virus can move through direct contact between pigs or indirectly through contaminated objects, equipment, or even through the air. Despite efforts to control it, the disease persists, making it essential to understand how it spreads between farms.

## Methods

We studied the genetic relationship of PRRSV-2 ORF5 gene from 206 outbreak samples obtained from 144 farms between 2014 – 2017 in an intensive swine production region in the U.S. We combined this genetic data with detailed records of live animal movements between these farms. Analyzing the virus's genetic profile enabled us to trace potential infection pathways between pigs, while the movement data provided insights into how PRRSV-2 could likely spread between farms based on these infection patterns. By employing network analysis, we connected these farm-to-farm transmission pathways with farm-specific information such as herd size, type, and geographic location, shedding light on the primary routes through which PRRSV-2 might propagate among farms.

## Results & Discussion

The three largest PRRSV-2 variants, grouped by their ORF5 genetic profile, caused outbreaks in different geographic areas (Figure 1), highlighting distinct clusters where the virus spread. The estimated between-farm transmission network indicates that the study area experienced PRRS endemicity, with over 70% of farms capable of transmitting the virus to at most one other farm within a year (farm-level reproduction number (R) <= 1). However, 28% of farms acted as super spreaders, transmitting the virus to more than a single farm (R > 1). Network analysis revealed that live animal movement significantly contributed to between-farm transmission. Conversely, local area spread within a 10 km radius, such as airborne transmission, appeared unlikely to be a major route. Interestingly, over 80% of transmission events could not be linked to animal movement, suggesting other potential transmission routes through unrecorded long-distance connections between farms. Findings of this study emphasize the critical role of consistent PRRS monitoring and effective risk communication within and between production systems for preventing PRRS outbreaks.

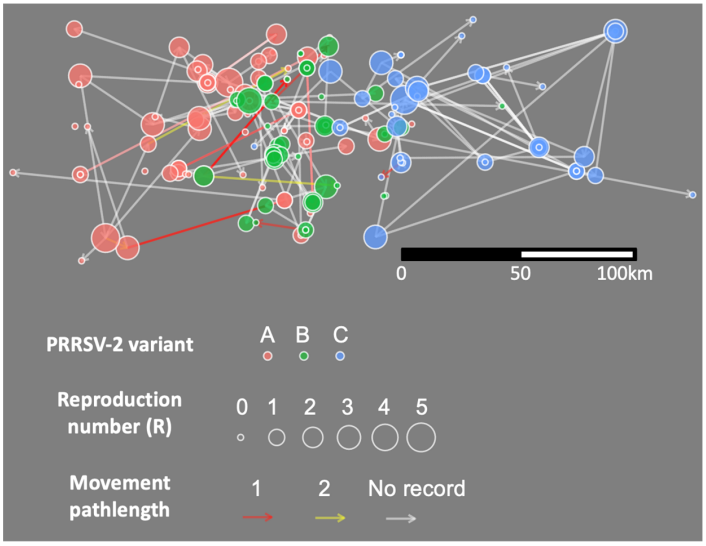


Figure 1. Estimated spatial network of farm-to-farm PRRSV-2 transmission, based on genetic inference.

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