

## Environmental contamination assessment in farms undergoing an outbreak with PRRS 1-4-4 Lineage 1C

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### Key Points

- There is little understanding of contributing factors aiding the 1-4-4 L1C PRRSV rapid transmission and biosecurity breaches
- Environmental detection in recently infected farms was possible although detection was low
- Most positive samples originated from exhausting fans, showing the virus may exit a positive barn via that route

### Background:

During the fall of 2020 a new variant of the porcine reproductive and respiratory syndrome virus (PRRSV) emerged. The new variant was classified as a 1-4-4 Lineage 1C virus, and rapidly spread throughout Minnesota. It is not understood what factors aided this virus to transmit rapidly and break through current biosecurity practices.

### Objective:

The overarching goal of this project was to determine whether PRRS 1-4-4 L1C RNA can be detected in outside areas of farms undergoing an outbreak.

### Materials and Methods:

A convenient sample of breeding and growing pig farms undergoing a PRRS 1-4-4 L1C outbreak were included in this study. Farms were visited 3-4 times after the virus had been detected. One farm located in the epicenter of where this new virus emerged was chosen as a negative control. At each farm, a set of environmental (i.e. surface) samples were collected by wiping a 1ft x 1ft area with a regular, moistened Swiffer dry sweeping cloth. Between twenty-three and twenty-six samples were collected from different surfaces including employee vehicles, barn and D&D doorknobs, anteroom and D&D room floors, exhaust/pit fan housings and loading chutes. An exterior particle deposition sample was collected by placing aluminum foil between 50-100 ft away from the barn, in 4 locations around the farm (i.e N, S, W and E). Environmental samples were collected and shipped to the University of Minnesota Veterinary Diagnostic Laboratory for individual PRRS RT-PCR testing.

### Results:

Out of 95 environmental samples collected at 4 pig farms undergoing a PRRS 1-4-4 L1C outbreak, 8 (8.4%) yielded a positive RT-PCR result (Table 1). Six out of the eight positive samples originated from fan housing samples (i.e. tunnel or pit). The farm that was used as our negative control and that is in the epicenter of the outbreak tested negative. Today this farm remains free of the virus.

**Table 1.** Summary of PRRS RT-PCR results from environmental samples collected on farms undergoing a 1-4-4 L1C outbreak in the Midwest.

Farm ID	Farm Type	Number of Samples Collected	Number of RT-PCR positive samples	Location of Positive Samples (Ct Values)
1*	Breeding	26	0	
2	Breeding	26	2	Two exhaust fan housings (30.29, 37.01)
3	Growing	23	1	Exhaust fan housing (35.85)
4	Breeding	23	0	
5	Growing	23	5	Three exhaust fan housings (33.96, 34.36, 35.98), ante-room floor (35.38), mortality doorknob (36.35)

\*Farm #1 was the negative control.

### Conclusions and Implications:

Overall, detection of environmental contamination with PRRSV in recently infected farms is possible. Although detection was low, the concentration of viral RNA in the sample can be significant. Most of the positive samples originated from exhaust fan housings, suggesting that virus was becoming airborne and exiting the barn, as expected. Based on the results of this study, a more comprehensive sampling approach should be designed to further understand the probability of the virus being carried out of a barn housing positive pigs.

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