

## Porcine Deltacoronavirus Incidence in the U.S.

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### Key Points

- PDCoV was detected in 186 sites from 22 production systems located in 16 U.S. states
- For sites that experienced more than one PDCoV outbreak, the interval between outbreaks had a median of 2.11 years
- The yearly cumulative incidence (Figure 1) ranged from 0.44% in 2017 to 4.28% in 2023

### Introduction

PDCoV, an enveloped RNA virus, causes atrophic enteritis in neonatal piglets, leading to diarrhea, malabsorption, dehydration, and death. In February 2014, PDCoV emerged in the United States (US) as the country was still managing the recent emergence of another coronavirus (i.e., Porcine Epidemic Diarrhea virus—PEDv). At this stage, reported laboratory testing reported that PDCoV was detected in 25–30% of the clinical samples, with cases being detected in over 10 states (1,2,3). To this date, PDCoV occurrence in the U.S. has been mostly described as the percentage of positive submissions. However, laboratory submissions will more frequently represent clinically relevant cases in which the probability of testing positive is higher than in the general population. Thus, we described the yearly cumulative incidence of PDCoV amongst MSHMP participating breeding herds.

### Methods

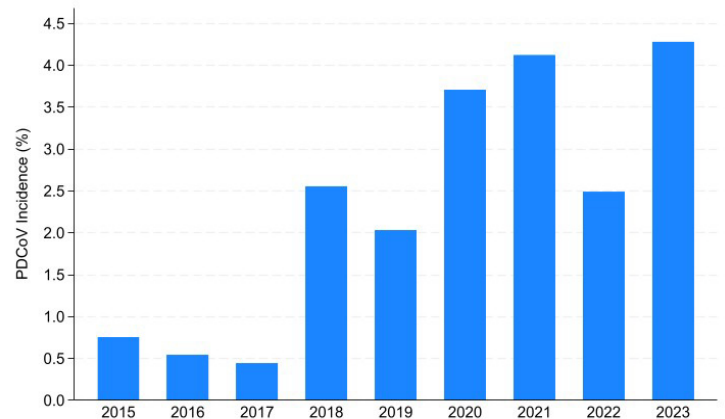
MSHMP participants are encouraged to report any detected outbreaks to the MSHMP. Yearly cumulative incidence was calculated using the number of breeding herds reporting either PRRS, PEDv, or PDCoV statuses (i.e., sites that were sharing information for at least one of the main diseases monitored by MSHMP) as the denominator and reported cases as the numerator. Case locations were described according to U.S. Census regions.

### Results

Since January 2015, a total of 244 PDCoV outbreaks have been reported to MSHMP and these originated from 186 sites belonging to 22 production systems located in 16 U.S. states. During the entire period, one hundred and forty herds reported one PDCoV outbreak, thirty-six herds reported PDCoV twice, eight reported it three times, and two herds reported PDCoV outbreaks four times. For sites that experienced more than one PDCoV outbreak during the study period, the interval between outbreaks had a median of 2.11 years (interquartile range—IQR: 1.7–2.80, ranging from two months to almost 5 years). Although all cases occurred in the Midwest in 2015 and 2016, cases from 2017 originated only from the South and have been occurring in both regions since, with the majority of cases occurring in the South. The yearly cumulative incidence (Figure 1) ranged from 0.44% in 2017 to 4.28% in 2023.

### Discussion

In 2017, a shift in the spatial distribution of cases from the Midwest to the South was observed. Our voluntary monitoring project allowed us to estimate the PDCoV incidence in U.S. breeding herds as participating production systems and veterinary clinics reported the detection of the virus per their routine monitoring and standard care. However, no standardized classification of PDCoV status has been proposed that would allow us to estimate disease prevalence fluctuations through time. Moreover, the absence of universally adopted standardized criteria for declaring a herd negative post-outbreak hampers our ability to have a comprehensive understanding of an outbreak's duration. Efforts to standardize monitoring and classifying a herd as negative after an outbreak should be made if the goal is to better understand the disease dynamics. The findings underscore the importance of continued monitoring and strengthened control measures to mitigate the impact of PDCoV in U.S. breeding herds.



**Figure 1.** PDCoV yearly cumulative incidence in U.S. breeding herds between 2015 and 2023.

The full paper can be found at <https://www.mdpi.com/1999-4915/16/3/445>



### References

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