

PEDV Detection in Manure Pits Confirmed 841 days to 1,949 Days after Disease Outbreaks

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Key points:

- Determining the origin of a PEDV re-infection at a farm is often difficult or inconclusive.
- Manure pits have been shown to harbor virus after a farm has transitioned to a negative status
- PEDV DNA was found in farm manure pits between 46 and 1,949 days post disease outbreak

Introduction

Despite extensive investments in biosecurity measures and protocols, farms still have unexplainable cases caused by porcine epidemic diarrhea virus (PEDV). Many potential sources and vectors of viruses for this disease has been studied in the past. Investigating and finding the source of a PEDV disease re-break is difficult and rarely accomplished. Manure pits have been identified as a risk for harboring PEDV as a source for a disease re-break. Studies have found manure pits to harbor infective PEDV from four¹ to nine months². The purpose of this study is to determine if PEDV can be detected in manure pits for extended periods of time post disease and to determine if an end-point can be reached where manure pits are not considered a risk for a PEDV disease re-break.

Materials and methods

Manure pit samples were collected from swine producers in Eastern Iowa. The exact dates of the most recent PEDV disease outbreak was known and noted at each location before pit sampling. Locations sampled were typical gestation barns, gilt development units, and finishers, each with separate deep manure pits. Samples were collected using Sterile Amies Agar Gel Transport Swabs (JorVet J0867). A piece of twine sufficient in length to reach below the surface of the pit was tied to the handle of the swab. A sinker-style weight was taped to the swab. The swab was lowered between the slats and care was taken to only contact and sample below the top surface of the manure pit. Samples were analyzed by real-time reverse transcription polymerase chain reaction (rRT-PCR) per routine protocols at the Iowa State University Veterinary Diagnostic Lab (ISU VDL).

Results and discussion

Results are reported in Table 1. Positive PEDV PCR results were detected from 46 days to 1,949 days post disease outbreak in this study. PCR test levels ranged from Cycle threshold (Ct) values of 19.9 Ct (55 days post-outbreak) to 29.3 Ct (803 days post-outbreak) to an extremely long time after disease outbreak of 1,949 days (Ct 34.3). The PEDV S1 (first 2.2 kb portion of the spike gene) sequences were determined from the Farm 5 Finisher, Southeast location. The S1 sequence from this case has about 99% nucleotide identity to the U.S. PEDV prototype strains and 94% nucleotide identity to the U.S. PEDV S-INDEL-variant strains.

Sources of PEDV re-breaks continue to frustrate producers and veterinarians. This study indicates that manure pits can continue to be a risk that producers need to evaluate as a source for a PEDV disease outbreak for a much longer time, either through direct exposure to the manure pit's contents, or vectored to susceptible animals by insects such as flies³.

References

1. Steve Tousignant, DVM, Swine Vet Center P.A., St. Peter, MN | Nov 12, 2014, American Association of Swine Veterinarians (AASV)
2. Hein M. Tun, Monitoring Survivability and Infectivity of Porcine Epidemic Diarrhea Virus (PEDV) in the Infected On-Farm Earthen Manure Storages (EMS), *Front Microbiol.* 2016; 7: 265.
3. Allison, G.A. et al, PEDV positive bioassay reveals houseflies (*Musca domestica*) can transmit infectious PEDV to pigs, *Proceedings of the American Association of Swine Veterinarians (AASV)* 2019: 206-208

Farm (outbreak)	Gestation	Date	Ct	Days Post-Infection	
1 (12/28/16)	North	4/26/18	33.5	478	
	South	4/26/18	32.5	478	
	North	4/29/19	32.8	841	
	South	4/29/19	31.1	841	
	South	6/03/19	31.1	875	
	South	7/23/19	31.6	925	
1	Pre – pumping	North	3/21/19	30.7	803
		South	3/21/19	29.3	803
	Post – pumping	North	4/30/19	32.8	842
		South	4/30/19	31.1	842
2 (2/23/18)		6/10/19	34.1	467	
		6/24/19	33.2	481	
3 (3/05/18)	GDU	5/01/18	30.0	46	
4 (3/31/18)	GDU	5/23/18	30.2	53	
	GDU	7/09/18	32.3	99	
	South	7/09/18	31.4	99	
	North	7/09/18	28.7	99	
	GDU	7/08/19	31.0	458	
	GDU	7/15/19	35.8	465	
	GDU	10/28/19	32.0	568	
Finisher					
5 (5/16/19)	North	9/03/19	26.4	107	
5 (7/15/19)	Southeast	9/03/19	26.6	48	
	Southwest	9/03/19	32.7	48	
	Southeast	9/10/19	20.3, 19.9	55*	
6 (2/27/14)	Gestation	8/26/19	34.3	1,979	

*The PEDV S1 (first 2.2 kb portion of the spike gene) sequences were determined. The S1 sequence from this case has about 99% nucleotide identity to the U.S. PEDV prototype strains and 94% nucleotide identity to the U.S. PEDV S-INDEL-variant strains.

Table 1: Farm test results over time in relation to last outbreak date