

PEDV in the Literature

Novel Porcine Epidemic Diarrhea Virus Variant with Large Genomic Deletion, South Korea

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Abstract

Since 1992, porcine epidemic diarrhea virus (PEDV) has been one of the most common porcine diarrhea-associated viruses in South Korea. We conducted a large-scale investigation of the incidence of PEDV in pigs with diarrhea in South Korea and consequently identified and characterized a novel PEDV variant with a large genomic deletion.

This study is a cross-sectional for PEDV discovered in fecal and intestinal samples collected from diarrheic pigs from South Korea throughout 2008. Out of the 2,634,205 samples were PEDV positive by S gene RT-PCR, and a PEDV S gene variant was discovered in 3 samples taken from suckling piglets from a single farm. This variant (MF3809) had a large 204 amino acid (aa) deletion in the S gene (Both S1 and S2 regions, position 713-916) and had a 93.3-98.5% nucleotide (nt) and 92.0-98.0% aa similarity to the other PEDV strains in GenBank. Also, 2 small aa insertions at 59-62 and 140 as well as a smaller deletion at 163-164 were detected.

Another PEDV variant characterized by Wang et al. in 2014 known as S-INDEL variant or OH851 has 3 amino acid deletions in the spike protein compared to other PEDV strains. The spike genes of these two variants (MF3809 and OH851) do not show similar variations to common PEDV strains and should not be confused with one another. The MF3809 sequence has a significant amino acid deletion which sets it apart from known field strains. Whereas it's unclear how this large deletion may have changed the virus, or if the pathogenicity and tissue tropism would be affected given the spike protein's role in host interactions.

While unlike the US S-INDEL variant, the MF3809 strain has a parallel comparison to typical PEDV strains as Porcine Respiratory Coronavirus (PRCV) has to Transmissible Gastroenteritis Virus (TGEV). The MF3809 strain has a 204 aa deletion (713-916 in the C-terminus of S1 and the N-terminus of S2) in the S protein while PRCV has a 224 aa deletion in a different location of the S protein (N-terminal region of S protein). The PEDV strain MF3809 may have a similar clinical comparison to PRCV and TGEV with reduced pathogenicity due to the large spike deletion. Supporting this notion, another paper evaluating PEDV variants (Oka et al., 2014) describes a variant with a 197 aa deletion in the N-terminal region of the S protein and "produce[s] diffuse and faint (without a clear edge) plaques compared to other PEDV strains" which occurred during isolation. Aside from pathogenicity, a large deletion in PEDV could also be similarly beneficial to the Korean hog population if it offers cross-protective immunity as PRCV does with TGEV.

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Oka, Tomoichiro, et al. "Cell culture isolation and sequence analysis of genetically diverse US porcine epidemic diarrhea virus strains including a novel strain with a large deletion in the spike gene." *Veterinary microbiology* 173.3-4 (2014):258-69. http://tc.liblink.umn.edu/sfx_local?sid=Entrez%3APubMed&id=pmid%3A25217400&issn=0378-1135