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ABSTRACT

Porcine epidemic diarrhea virus (PEDV) has continued to cause sporadic outbreaks in Thailand since 2007 and a pandemic variant containing an insertion and deletion in the spike gene was responsible for outbreaks. In 2014, there were further outbreaks of the disease occurring within four months of each other. In this study, the full-length genome sequences of two genetically distinct PEDV isolates from the outbreaks were characterized. The two PEDV isolates, CBR1/2014 and EAS1/2014, were 28,039 and 28,033 nucleotides in length and showed 96.2% and 93.6% similarities at nucleotide and amino acid levels respectively. In

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