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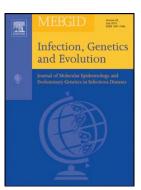
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Full-length genome analysis of two genetically distinct variants of porcine epidemic diarrhea virus in Thailand

Thaniwan Cheun-Arom^a, Gun Temeeyasen^a, Thitima Tripipat^a, Pavita Kaewprommal^b, Jittima Piriyapongsa^b, Suchada Sukrong^c, Wanchai Chongcharoen^d, Angkana Tantituvanont^d, Dachrit Nilubol^{a,*}

^aDepartment of Veterinary Microbiology, Faculty of Veterinary Science, Bangkok, Thailand ^bGenome Technology Research Unit, National Center for Genetic Engineering and Biotechnology, National Science and Technology Development Agency, Pathumthani, Thailand

^cDepartment of Pharmacognosy and Pharmaceutical Botany, Faculty of Pharmaceutical Sciences, Chulalongkorn University, Bangkok, Thailand ^dDepartment of Pharmaceutics and Industrial Pharmacy, Faculty of Pharmaceutical Sciences, Chulalongkorn University, Bangkok 10330, Thailand

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 Download English Version:

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