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Abstract

Porcine epidemic diarrhea (PED) has been endemic causing sporadic outbreaks in Thailand since 2007. In 2014-2015, several herds had experienced severe PED outbreaks and the reason of the re-current outbreaks was unknown. Whether or not the introduction of exotic strains or continual evolution of existing PEDV, genetic analyses would provide a more understanding in its evolutionary pattern. In the study, 117 complete spike gene sequences of Thai PED virus (PEDV) collected from 2008-2015 were clustered along with 95 references of PEDV spike sequences, and analyzed with the US sequences dataset (n=99).

The phylogenetic analysis demonstrated that Thai PEDV spike sequences were genetically diverse and had been influenced by multiple introduction of exotic strains. Although Thai PEDV have been evolved into 6 subgroups (TH1-6), Subgroup TH1 strains with the unique 9 nucleotides (CAA GGG AAT) insertion between 688th-689th position of spike (changing amino acid from N to TREY) insertion has become the dominant subgroup since 2014. Thai

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