

Diversity of Enterovirus Genotypes Circulating in Pediatric Patients with Acute Gastroenteritis in Thailand from 2019 to 2022

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Abstract : Acute gastroenteritis (AGE) is a common cause of morbidity and mortality in infants and young children worldwide, especially in developing countries. Enterovirus(EVs) have been identified in patients with AGE in many countries around the world, and some studies have revealed that EV infection is associated with gastrointestinal symptoms and plays a role in AGE. As a potential causative pathogen of AGE in humans, continuous detection and identification of EVs in pediatric patients with AGE is needed. In this study, we aimed to investigate the prevalence, seasonal distribution, and molecular characteristics of EVs circulating in pediatric patients with AGE in Thailand from 2019 to 2022. A total of 1422 stool specimens were collected for this study. RT-PCR amplification of the 5'UTR was used to screen for EV positive samples. EV genotyping was determined based on nucleotide sequence and phylogenetic analysis of the VP1 sequences. EV prevalence in pediatric AGE patients was 8.3% (118 out of 1,422). Among these, 35.6% of EV infection cases were caused by species A, followed by species C and B (33.1% and 30.5%, respectively). A total of 26 EV genotypes were identified in this study. Poliovirus 3 and coxsackievirus A2 were the predominant genotypes detected(14% and 13%, respectively). EV was detected all year round with higher prevalence between July and December. In summary, this study reports EV's prevalence and genotype diversity in pediatric patients with AGE in Thailand during 2019-2022.

Keywords : enterovirus, epidemiology, acute gastroenteritis, genotype

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