



Molecular Surveillance and Characterization of Enterovirus Infection in Patients with Acute Gastroenteritis in Thailand: 2019-2022

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Abstract

Enteroviruses (EVs) have been recognized as potential causative agents of acute gastroenteritis (AGE) in children in several countries worldwide. This study aimed to investigate the epidemiology and molecular characteristics of EV infection in children admitted to hospitals with AGE in Chiang Mai, Thailand, from 2019 to 2022. A total of 1148 fecal samples collected from patients with AGE were screened for the presence of EV using reverse transcription–polymerase chain reaction (RT-PCR). The prevalence, co-infection with common diarrheal viruses, and seasonal pattern of EV infection were examined. The genotypes of EV were identified based on the VP1 sequence and phylogenetic analysis. The overall prevalence of EV in AGE patients was 8.8% (101/1148). After the COVID-19 outbreak in 2019, a significant decrease in the EV infection rate was observed ($p < 0.05$). Co-infection of EV with other enteric viruses was 31.7% (32/101), while EV single infection was observed in 68.7% (69/101) of cases. The seasonal pattern of EV infection showed a high prevalence during the rainy season. EV species A was the most prevalent (37.5%), followed by species B (32.3%), species C (29.2%), and species D (1.0%). Twenty-five genotypes of EV were identified, with coxsackievirus A2 (CV-A2) (13.5%), CV-B2 (7.3%), and CV-A24 (5.2%) being the most predominant genotypes. In summary, this study revealed the molecular epidemiology and diversity of EV in Chiang Mai, Thailand, during 2019-2022, with a high incidence of CV-A2. The data provide useful information for further investigation into the potential association between specific EV genotypes and AGE in future studies.

Keywords: Acute gastroenteritis, Coxsackievirus, Enterovirus, Pediatric patients, Thailand