

Molecular Epidemiology of Rotavirus in Post-Vaccination Era in Pediatric Patients with Acute Gastroenteritis in Thailand

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Abstract : Rotavirus A is one of the leading causes of acute gastroenteritis in children younger than five years of age, especially in low-income countries in Africa and South Asia. Two live-attenuated oral rotavirus vaccines, Rotarix and RotaTeq, have been introduced into routine immunization programs in many countries and have proven highly effective in reducing the burden of rotavirus-associated morbidity and mortality. In Thailand, Rotarix and RotaTeq vaccines have been included in the national childhood immunization program since 2020. The objectives of this research are to conduct a molecular epidemiological study and to characterize rotavirus genotypes circulating in pediatric patients with acute diarrhea in Chiang Mai, Thailand, from 2020-2022 after the implementation of rotavirus vaccines. Out of 858 stool specimens, 26 (3.0%) were positive for rotavirus A. G3P[8] (23.0%) was detected as the most predominant genotype, followed by G1P[8] (19.2%), G8P[8] (19.2%), G9P[8] (15.3%), G2P[4] (7.7%), G1P[6] (3.9%), G9P[4] (3.9%), and G8P[X] (3.9%). In addition, the uncommon rotavirus strain G3P[23] (3.9%) was also detected in this study, and this G3P[23] strain displayed a genetic background similar to the porcine rotavirus. In conclusion, there was a dramatic change in the prevalence of rotavirus A infection and the diversity of rotavirus A genotypes in pediatric patients in Chiang Mai, Northern Thailand, in the rotavirus post-vaccination period. The finding obtained from this research contributes to a better understanding of rotavirus epidemiology after rotavirus vaccine introduction. Furthermore, the identification of unusual G and P genotype combination strains provides significant evidence for the potential interspecies transmission between human and animal rotaviruses.

Keywords : rotavirus, infectious disease, gastroenteritis, Thailand

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