



Molecular Epidemiology and Genetic Diversity of Circulating Rotavirus Strains Following Vaccine Implementation in Thailand

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Abstract

Rotavirus A is one of the world's leading causes of acute gastroenteritis among children under the age of five. Two live-attenuated oral rotavirus vaccines, Rotarix and RotaTeq, have been introduced into the routine immunization programs in many countries and proven to be highly effective in reducing the burden of rotavirus-associated morbidity and mortality. In Thailand, these two vaccines have been included in the national childhood immunization program since 2020. The objectives of this research were to conduct a molecular epidemiological study and characterize rotavirus genotypes circulating in pediatric patients diagnosed with acute diarrhea in Chiang Mai, Thailand from 2020-2023 after the implementation of rotavirus vaccines by using real-time polymerase chain reaction (real-time PCR) and nucleotide sequencing. Out of 1,192 stool specimens, 60 (5.0%) were positive for rotavirus A. G3P[8] was detected as the most predominant genotype (55.0%), followed by G8P[8] (15.0%), G1P[8] (13.2%), G9P[8] (3.3%), G2P[4] (3.3%), G1P[6] (1.7%), G9P[4] (1.7%), and G8P[X] (1.7%). In addition, uncommon rotavirus strains G3P[9] (1.7%), G3P[23] (1.7%), and G5P[23] (1.7%), were also detected in this study. The G3P[9] strain displayed a genetic background similar to feline rotavirus, while G3P[23] and G5P[23] strains demonstrated a genetic background similar to porcine rotavirus, as previously detected in Thailand. In conclusion, there was a dramatic change in the prevalence of rotavirus A infection and the diversity of rotavirus A genotypes among pediatric patients in Chiang Mai, Northern Thailand during the rotavirus post-vaccination period. The finding obtained from this research contribute to a better understanding of rotavirus epidemiology in the post-vaccination era.

Keywords: *Gastroenteritis, Epidemiology, Rotavirus, Thailand*