

EV1098

ePoster Viewing

Virology non-HIV/non-hepatitis

Genetic evolution of human enteroviruses circulating in Thailand during 2006 to 2014

K. Sangsiriwut¹, P. Noisamdaeng¹, J. Prasertsopon¹, C. Klinmalai¹, D. Changsom¹, R. Buathong², S. Iamsirithaworn², A. Mungaomklang³, K. Chokephaibulkit⁴, P. Puthavathana¹

¹Department of Preventive and Social Medicine Faculty of Medicine Siriraj Hospital Mahidol University, Bangkok, Thailand

²Department of Disease Control Ministry of Public Health, Nonthaburi, Thailand

³Debaratana Nakhon Ratchasima Hospital Ministry of Public Health, Nakhon Ratchasima, Thailand

⁴Department of Pediatrics Faculty of Medicine Siriraj Hospital Mahidol University, Bangkok, Thailand

Objective: Based on full genome sequencing, this study aimed to investigate the genotypes and genetic evolution of 28 enterovirus (EV) strains circulating in Thailand during 2006 to 2014. These strains were isolated from pediatric patients mostly ill from hand foot and mouth disease (HFMD).

Methods: Viruses were isolated from pediatric patients mostly ill from hand foot and mouth disease (HFMD) using Vero cells and RD cells as the host system. Genomic viral RNA was sequenced directly; and the nucleotide sequences obtained were edited using Bioedit software. The complete genome sequences were aligned and phylogenetic tree was constructed using MEGA4 software. Homologous recombination was analyzed using Simplot software.

Results: Phylogenetic analysis of VP1 gene regions of these 28 EV isolates showed that 21 belonged to EV71 (comprising 17 subgenotype B5, 1 C4a and 2 C4b and 1 C2), 6 Coxsackie A16 (CA16) and 1 CA6. All of the 6 CA16 strains belonged to genotype B2a. Similarity plots and bootscan analyses were employed using the old EV71 strains and CA16 strain G-10 as the reference strains. Based on complete genome sequences, recombination between EV71 and 3D polymerase region of CA16 were detected in all 3 EV71 genotype C4. These recombinant strains were isolated in 2006, 2008 and 2014. Nevertheless, genotype B5 which first emerged in 2011 becomes the major circulating strain causing outbreaks in Thailand annually.

Conclusion: HFMD is an important epidemic disease in Childhood in Asia and Pacific region. According to the information available, the major strains causing large outbreaks in China for longer than 6 years belongs to genotype C4; and so do in Hong Kong and Korea; while genotype C2 and C4 are prevalent in Japan, genotypes B4 and B5 are prevalent in Malaysia and Singapore, and genotype C5 is prevalent in Vietnam. During 2006 to 2014, many genotypes were occasionally detected in Thailand and neighboring countries, but genotype B5 is the major circulating strain. We found genetic recombination between EV71 genotype B and 3D polymerase region of CA16. Nevertheless, these recombinants were the minority; and cannot replace or overcome the B5 genotype circulating in Thailand.