

CHAPTER VII

SUMMARY

The present study investigated the epidemiology and molecular characterization of diarrheal viruses in adults with diarrhea in Chiang Mai, Thailand. A total of 332 fecal specimens were collected from patients admitted to Maharaj Nakorn Chiang Mai Hospital with diarrhea in 2008. Of these, diarrheal viruses were detected in 14 of 332 (4.2%) specimens. Five Types of viral pathogens were identified, including adenovirus (AdV), Aichi virus (AiV), enterovirus (EV), human parechovirus (HPeV), and norovirus (NoV GII). It was found that AdV and EV were detected as the most predominant virus with the prevalent rate of 1.2% each (4 of 332), followed by AiV (0.9%, 3 out of 332) and NoV GII (0.6%, 2 out of 332). In addition, mixed infection of 2 viruses between NoV GII and HPeV was also detected in one fecal specimen (0.3%).

Nucleotide sequence and phylogenetic analyses of 4 AdV strains demonstrated that AdV found in this study belonged to 3 distinct genotypes, AdV24 (CMHA158/08), AdV25 (CMHA9/08), and AdV40 (CMHA263/08 and CMHA599/08). For EV, various EV genotypes were identified, including each strain of echovirus 30 (CMHA59/08), poliovirus 3 (CMHA42/08), enterovirus 99 (CMHA414/08), and coxsackievirus A20 (CMHA136/08).

In addition, analysis of nucleotide sequences of 3 NoV GII strains (CMHA10/08, CMHA49/08, and CMHA552/08) revealed that all of NoV GII

detected in the present study belonged to NoV GII/4. It is interesting to note that NoV GII/4 strains are divided into 2 distinct variants, NoV GII/4 variants 2006a (CMHA10/08) and variant 2006b (CMHA49/08 and CMHA552/08).

All 3 AiV strains found in this study were classified into 2 distinct genotypes. One strain (CMHA135/08) of AiV was identified as genotype A, while another two strains (CMHA32/08 and CMHA317/08) belonged to genotype B. It is interesting to note that this is the first report of AiV genotype B detected in Thailand.

Moreover, based on nucleotide sequence and phylogenetic analyses of HPeV, only 1 strain was identified in this study and it belonged to HPeV1.

In conclusion, this study reported for the first time of viral pathogens that cause diarrhea in adults in Chiang Mai, Thailand. These preliminary data highlight molecular epidemiology of diarrheal viruses in adult patients in Chiang Mai, Thailand.