

## CHAPTER VII

### SUMMARY

The present study investigated the epidemiology and characterization of gastroenteritis viruses isolated from children hospitalized with acute gastroenteritis in Chiang Mai, Thailand in 2007. Of 160 fecal specimens tested, 48.8% (78 of 160) were found to be positive for gastroenteritis viruses, including rotaviruses (RVs), noroviruses (NoVs), sapoviruses (SaVs), astroviruses (AstVs), and adenoviruses (AdVs). Of these, group A rotavirus was the most predominant virus with the prevalent rate of 27.5%, followed by norovirus genogroup II (NoV GII) (13.8%), sapoviruses (3.1%), adenoviruses (1.3%), astroviruses (0.6%) and NoV GI (0.6%). Mixed infection of two viruses in the same fecal sample was found at 1.9%. Molecular characterizations of G- and P-genotypes, VP6 genogroup and NSP4 genetic group of rotaviruses revealed that the majority of G-P genotype combinations were G1P[8] (70.2%), followed by G2P[4] (19.2%), G3P[8] (8.5%) and G1P[4] (2.1%). In addition, analysis of VP6 genogroup revealed that 80.9% of rotaviruses belonged to VP6 genogroup II (GII) and 19.1% belonged to VP6 GI. Most of rotaviruses belonged to NSP4 genetic group Wa (B) at 80.9% and the rest 19.1% belonged to NSP4 genetic group KUN (A). For noroviruses, based on nucleotide sequence and phylogenetic analyses, a wide variety of norovirus subtypes were detected, including GI/14, GII/2, GII/3, GII/4, GII/6, GII/7, GII/13, GII/16 and GII/new. In contrast, only one subtype of sapoviruses, SaV GI/1, was detected in this study. Furthermore, astroviruses, AstV1d and AstV2, and adenoviruses, Ad1, Ad3, and Ad41 were also detected in this surveillance.