CHAPTER 7

Summary

The present study, we reported the prevalence and genotypic distribution of NoV and SaV during 2015-2016 in children hospitalized with acute gastroenteritis in Chiang Mai, Thailand. Of 812 stool samples, 164 (20.2%) and 15 (1.8%) were identified as NoV and SaV, respectively. Of these, NoV GII.4 (58.9%) was the most predominant genotype, followed by GII.2, GII.3, GII.17, GII.6, GII.7, GII.13, GII.14, GII.15, GII.21, GI.6, and GI.5. Among the NoV GII.4 variants, the Sydney 2012 was the most predominant variant during 2015-2016, while the other variants detected in this study were Asia 2003 and New Orleans 2009. In addition, mixed infection of 2 viruses in the same samples were found and observed as co-infection between NoV GII and NoV GI, and between NoV GII and SaV. The seasonality of NoV and SaV infection were observed in the dry and cold seasons (December, 2015-March, 2016). Interestingly, increasing of NoV GII.2 detection was observed in 2016. Characterization of partial RdRp and VP1 nucleotide sequences of GII.2 strains revealed that half of GII.2 strains circulating in 2016 were the GII.P16/GII.2 recombinant strains. For SaV, majority of the strains belonged to GI.1 (52.9%). The GI.2 and GII.5 were found at 35.3% and 11.8%, respectively. Altogether, the information from this study demonstrated the diversity of NoV and SaV with the high prevalence of NoV GII.P16/GII.2 recombinant strains in 2016 in Chiang Mai, Thailand.

In addition, we identified and characterized NoV GII recombinant strains circulating in Chiang Mai area during the 2005-2015. Among 298 NoV positive samples, the recombinant strains were characterized by analysis of the partial sequence of ORF1 (RdRp)/ORF2 (capsid VP1) junction. Phylogenetic analyses of partial RdRp and capsid VP1 regions resulted in the identification of 21 (6.98%) recombinant strains. Among these recombinant strains, 9 recombination patterns were detected; including GII.Pe/GII.4, GII.Pg/GII.1, GII.Pg/GII.12, GII.P7/GII.6, GII.P7/GII.14, GII.P12/GII.4, GII.P16/GII.2, GII.P16/GII.13, and GII.P21/GII.3. Circulating of variety patterns of NoV

recombinant strains may result in the increasing of the viruses to escape from human immunity and may be the cause of NoV outbreaks in communities.