

CHAPTER 7

Summary

The present study investigated the prevalence of human and porcine rotaviruses at the same period of time and performed molecular characterization of rotavirus genotypes circulating in Chiang Mai and Lamphun provinces. Human group A rotaviruses were detected in 137 out of 401 (34.2%) fecal specimens collected during January 2013 through February 2014 from children hospitalized with diarrhea. In addition, 113 out of 491 (23.0%) stool specimens collected from diarrheic piglets during January 2011 to March 2014 were positive for group A rotaviruses. Among these, 9 different G-P combinations of human rotaviruses were detected with the G3P[8] was the most predominant genotype at the prevalence of 49.6%, followed by G1P[8] (23.4%), G2P[4] (13.9%), while G1P[4], G8P[8], G2P[8], G9P[8], and mixed-infection of G3 in combination with P[8] and P[4] were detected at lower prevalence of 4.4%, 2.9%, 2.2%, 2.2%, and 0.7%, respectively. Interestingly, the uncommon strain of human rotavirus G9P[19] was detected in this study at 0.7%. For the G-P combinations of porcine rotaviruses, 16 different G-P combinations were detected with the G4P[13] was the most prevalent genotype (29.2%), followed by G4P[23] (14.1%), G5P[23] (11.5%), G4P[6] (9.7%), G3P[23] (7.0%), G5P[13] (6.1%), G3P[13] (4.4%), G3P[6] and G5P[6] each of 2.7%. In addition, other G-P combinations were detected at lower prevalence of 2.0% in each of the following G-P combinations, including G3P[19], G4P[7], G9P[19], G9P[23], G9P[7], G4P[19], and G11P[13] strains. However, G4 and G11 in combination with P nontypeable strains were also detected at each of 0.9%. It should be noted that porcine rotavirus G9P[19] genotype carry VP7, VP4, VP6, NSP4, and NSP5 nucleotide sequences closely related to those of human rotavirus G9P[19] detected in the same study.

In addition, the phylogenetic analysis of human rotavirus strain G9P[19] indicated that VP4, VP7, VP6, NSPA4, and NSP5 genes were found to be more closely related to those of porcine rotavirus reference strains than to human rotavirus reference strains. The genotype constellation of the human and porcine rotavirus G9P[19] strains were assigned as the G9-P[19]-I5-E1-H1 genotype for the VP7-VP4-VP6-NSP4-NSP5 genes. The finding implies that interspecies transmission and reassortment events between human and porcine rotaviruses circulating in Chiang Mai and Lamphun provinces have been occurred in nature.



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