

CHAPTER 1

Introduction

Acute gastroenteritis is a major cause of morbidity and mortality in infants and young children under 5 years worldwide with the highest incidence in children at the aged range of 6-24 months (Dennehy, 2011). Among the viruses that cause diarrhea rotavirus is the most common cause of severe diarrhea in infants and young children (Cox and Christenson., 2012). Each year, rotavirus causes approximately 2 million hospitalizations and 450,000 deaths in children with the majority of deaths occurring in developing countries in Asia and Africa (Parashar et al., 2003; Tate et al., 2012). The mortality of children under 5 years of age due to rotavirus gastroenteritis in Asia is estimated at a total of 144,679 deaths, with the majority of cases are in Southern and South East Asia. The highest number of deaths located in India (80,981), followed by Pakistan (23,227), Indonesia (14,340), Myanmar (8,681), Bangladesh (5,724) and China (4,716) (Kawai et al., 2012). Rotavirus is transmitted by fecal-oral route and possibly by contaminated surfaces and hands of caregivers. In addition, rotaviruses have been isolated from the environmental water including from irrigation canal water, river water, and oysters in Thailand (Kittigul et al., 2008; 2014a). The clinical manifestations of rotavirus infection range from subclinical to severe gastroenteritis with vomiting and lethal dehydration. In addition, rotaviruses are the major pathogen associated with acute gastroenteritis in variety of animal species. (Estes and Kapikian, 2007; Matthijssens et al., 2011). Among these, porcine rotaviruses are important viral pathogens for pigs as it is a major etiology for diarrheal disease in pig population. Up to date, at least 27 G genotypes and 37 P genotypes of group A rotaviruses have been reported from humans and variety of animal species with various G-P combinations (Matthijssens et al., 2011).

For human rotaviruses, the most common G genotypes are G1, G2, G3, G4, and G9 in combination with P[4] or P[8] genotypes and G1P[8] is the most common genotype detected worldwide (Gentsch et al., 2005; Santos and Hoshino, 2005). In addition, the most common genotypes identified in pigs are G3, G4, G5, and G11, and usually associated with P[6] or P[7] genotypes (Gouvea et al., 1994b). From literature reviews, the G–P combinations of human rotavirus strains circulated in Thailand are G1P[8], G2P[4], G2P[8], G3P[3], G3P[8], G3P[9], G3P[10], G3P[19], G9P[8], G12P[6], and G12P[8], while G2P[27], G3P[6], G3P[13], G3P[19], G3P[23], G4P[6], G4P[13], G4P[19], G4P[23], G5P[6], G5P[13], G9P[7], G9P[13], and G9P[19] have also been identified from pigs in Thailand (Maneekarn and Khamrin, 2014). In Thailand, the uncommon strains are also found in humans and suspected to be cross-infected from animals such as G3P[3] and G3P[9] genotypes, which are closely related to monkey, goat, and cat rotaviruses (Khamrin et al., 2006b; 2007c). Moreover, human rotavirus genotype G9 strains Mc323 and Mc345 have been initially isolated from children hospitalized with diarrhea in Chiang Mai in 1989, and had been shown by RNA-RNA hybridization to be more genetically related to porcine G9 rotaviruses than to human G9 rotaviruses (Urasawa et al., 1992). In 2000, VP7 and VP4 nucleotide and deduced amino acid sequences of Mc323 and Mc345 were analysed and found that both strains belonged to G9P[19] genotype (Okada et al., 2000), with the VP7 sequences closely related to the G9 human rotaviruses reference strains WI61 and F45, while the VP4 sequences showed a close genetic relatedness to that of P[19] porcine rotavirus 4F prototype strain (Bridger et al., 1992). Later, the rotavirus surveillance in pigs in Chiang Mai confirmed that G3P[19] strains was detected frequently in this area (Maneekarn et al., 2006). The VP4 gene (P[19]) of these porcine rotavirus strains were most closely related to P[19] of Mc323 and Mc345, which were isolated previously from children hospitalized with diarrhea in Chiang Mai. It is possible that human G9P[19] strains Mc323 and Mc345 might have arisen by natural reassortment among rotavirus strains of human and porcine origins that circulated in the Chiang Mai area (Maneekarn et al., 2006). Since rotavirus genome contains 11 double-stranded RNA segments, the generation of unusual rotavirus strains may occur through interspecies transmission and reassortment among rotaviruses that infect into the same cell (Dunn et al., 1993; Urasawa et al., 1992; Varghese et al., 2004). Moreover, epidemiological studies of

rotaviruses have been performed extensively worldwide, and novel genotypes, animal-like strains, or animal-human rotavirus reassortants have been increasingly detected (Martella et al., 2010; Matthijnsens et al., 2011). These findings indicate that interspecies transmission of rotaviruses between humans and animals or animals and animals might be taken place in nature (Cook et al., 2004; Gouvea and Brantly, 1995; Nakagomi and Nakagomi T, 1993; Palombo, 2002).

Recently, in Chiang Mai, Thailand, the prevalence of group A rotaviruses causing severe diarrhea in infants and young children was reported at 29.4% (Chaimongkol et al., 2012a) while the prevalence of group A rotaviruses in piglets were detected at 19.8% (Saikruang et al., 2013). Therefore, it is of interest to determine the prevalence of human and porcine rotaviruses consecutively and to perform molecular characterization of rotavirus genotypes circulating in this area. The human rotavirus strains detected were analyzed for their genetic relationship with porcine rotaviruses. In addition, the information from this study might be important for elucidating the evidence of interspecies transmission and genetic reassortment between rotaviruses of porcine and human origins.