



Short communication

Emerging G9 rotavirus strains in the northwest of China

Mustafizur Rahman^{a,c,*}, Xue-lei Yang^b, He Sun^b, Khandaker Mahzebin^d,
Natasha Willemina Verstappen^a, Luís Novo^a, Jelle Matthijnsens^a, Marc Van Ranst^a

^a Laboratory of Clinical and Epidemiological Virology, Rega Institute, University of Leuven, B-3000, Leuven, Belgium

^b Xinjiang Pediatric Institute, People's Hospital of Xinjiang, 91 Tianchi Road, Urumqi, People's Republic of China

^c International Centre for Diarrhoeal Disease Research, Bangladesh (ICDDR,B), Mohakhali, Dhaka-1212, Bangladesh

^d Stamford University Bangladesh, 51, Siddeswari Road, Dhaka-1217, Bangladesh

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ABSTRACT

Although G9 rotaviruses have become one of the important rotavirus genotypes worldwide, they have been uncommon in China. Recently, we reported G9 rotaviruses as a highly prevalent genotype in Xinjiang, the northwest part of China [Yang, X., Matthijnsens, J., Sun, H., Muhamaiti, J., Zhang, B., Nahar, S., Van Ranst, M., Rahman, M., 2008. Temporal changes of rotavirus strain distribution in a northwest city of China, 1996–2005. *Int. J. Infect. Dis.*, June (Epub ahead of print)]. Here we report the genetic variations of the Xinjiang-G9 rotaviruses isolated between 1999 and 2005. Sequence analysis of the VP7 genes of Xinjiang-G9 strains indicated that they were more closely related to the contemporary global G9 strains than to the prototype Chinese G9 strains. However, their VP4 genes were most similar to those from the locally circulating G1P[8], G2P[4], G3P[6] and G3P[8] strains. This indicates that reassortment rather than antigenic drift might be the preferred evolutionary mechanism for the emergence of the G9 rotaviruses in Xinjiang. These findings will be of major significance for understanding the emergence of newly introduced rotavirus strains.

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Rotaviruses remain one of the most common diarrhea causing agents in children. Among the 19 G and 27 P genotypes, G1P[8], G2P[4], G3P[8] and G4P[8], were the most common in humans before 1995 (Estes and Kapikian, 2007; Matthijnsens et al., 2008a). However, genotype G9 and G12 have emerged respectively from the mid-1990s and 2000s (Matthijnsens et al., 2008; Rahman et al., 2005, 2007a,b). In addition, several rotavirus genotypes (G5 and G8) have shown their ability as potential candidates for the next emerging rotavirus strains (Duan et al., 2007; Esona et al., 2004; Gentsch et al., 2005; Hong et al., 2007; Matthijnsens et al., 2006; Santos and Hoshino, 2005). Although G9 rotaviruses have become one of the important rotavirus genotypes in many countries (Bresee et al., 2005; Santos et al., 2005), surprisingly, they have not been reported as a common strain in China. The first G9 strain was detected in China in 1994 and was isolated sporadically in the following years (Fang et al., 2002; Qian et al., 1994; Zhang et al., 2006). Studies conducted during 2000–2006 in different cities of China indicated that G9 strain was an uncommon strain (Fang et al., 2005; Wang et al., 2007; Yang et al., 2007; Zhang et al., 2006). Nevertheless, consistent detection of G9 strains was reported outside mainland

China, such as in Taiwan and Hong Kong (Chen et al., 2005; Lai et al., 2005; Lin et al., 2006; Lo et al., 2005). We recently reported considerably high numbers of G9 rotavirus strains from Xinjiang, China (Yang et al., 2008). In the present study, we analyzed the VP7 and VP4 gene segments of the Xinjiang-G9 strains to reveal their origin and their evolutionary relationships with other rotavirus strains. A total of 29 G9 rotaviruses were identified during 1999–2005 in Xinjiang, China. In addition, several P[4], P[6], and P[8] strains from Xinjiang were also analyzed to establish their genomic relationships with the G9 strains. The stool specimens were transported from Xinjiang to the Laboratory of Clinical and Epidemiological Virology, Rega Institute, University of Leuven in Belgium for further molecular characterization.

Rotavirus RNA extraction, reverse transcription (RT)-PCR and nucleotide sequencing were carried out as was described by Yang et al. (2008). The chromatogram sequencing files were inspected using Chromas 2.23 (Technelysium, Queensland, Australia), and consensus sequences were prepared using SeqMan II (DNASTAR, Madison, WI). Nucleotide and amino acid sequence similarity searches were performed using the National Centre for Biotechnology Information (NCBI, National Institutes of Health, Bethesda, MD) BLAST (Basic Local Alignment Search Tool) server on GenBank database, release 161.0 (Altschul et al., 1990). Multiple sequence alignments were calculated using CLUSTALX 1.81 (Thompson et al.,

* Corresponding author. Tel.: +32 16 332184; fax: +32 16 332131.

E-mail address: Rahman.mustafizur1@gmail.com (M. Rahman).

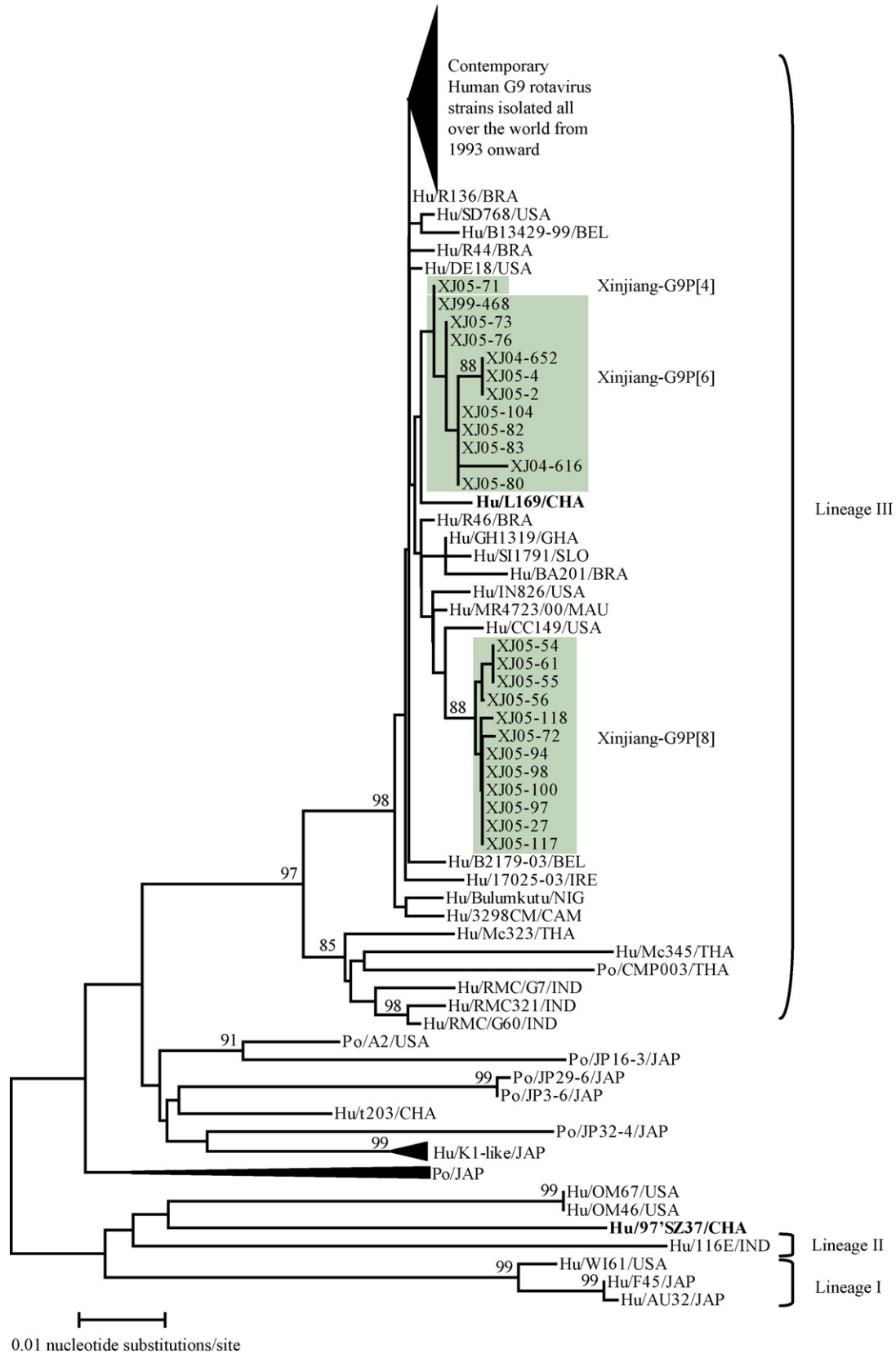


Fig. 1. Phylogenetic dendrogram based on partial VP7 nucleotide sequences (nt 49–761) of the G9 rotavirus strains. Xinjiang-G9 strains are shaded; other Chinese G9 strains are in bold. The numbers adjacent to the nodes represent the percentage of bootstrap support (of 1000 replicates) for the clusters to the right of the node. Bootstrap values lower than 75% are not shown. Hu, human; Po, porcine. Accession numbers are available upon request. BEL, Belgium; BRA, Brazil; CAM, Cameroon; CHA, China; GHA, Ghana; IND, India; IRE, Ireland; JAP, Japan; MAU, Mauritius; NIG, Nigeria; SLO, Slovenia; THA, Thailand; USA, the United States.

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