Laboratory and Epidemiology Communications

Epidemiology and Molecular Characterization of Sapovirus and Astroviruses in Japan, 2008–2009

Wisoot Chan-it, Aksara Thongprachum, Shoko Okitsu, Masashi Mizuguchi, and Hiroshi Ushijima

Department of Developmental Medical Sciences, Institute of International Health, Graduate School of Medicine, The University of Tokyo, Tokyo 113-0033; and Aino Health Science Center, Aino University, Tokyo 150-0002, Japan

Communicated by Takaji Wakita

(Accepted June 3, 2010)

Sapovirus (SaV) and human astrovirus (HAstV) are known to cause acute gastroenteritis in infants and young children (1,2). As a member of the family Caliciviridae, SaVs have a single-stranded positive sense RNA genome and are divided into five genogroups (GI–GV). At least 13 genotypes can be distinguished within GI and GII (3). HAstVs belonging to the family Astroviridae have been classified into eight serotypes HAstV-1–HAstV-8. In general, HAstV-1 is the most prevalent whereas type 3, 4, 7, and 8 are rare (4,5).

A total of 662 fecal specimens were collected from non-hospitalized children with acute gastroenteritis in pediatric clinics in six localities in Japan (Tokyo, Sapporo, Saga, Osaka, Shizuoka, and Maizuru) during July 2008–June 2009. RNA was extracted and purified using the QIAamp Viral RNA Mini kit (Qiagen, Hilden, Germany). Multiplex RT-PCR with specific primers resulted in the identification of SaV and HAstV (6). Nucleotide sequences of SaV- and HAstV-positive PCR products were determined using Big-Dye terminator cycle sequencing kit and ABI Prism 310 Genetic Analyzer (Applied Biosystems, Foster City, Calif., USA). Phylogenetic trees were generated using the MEGA version 4 (7). The sequences of strains detected in the study had been submitted to GenBank under accession nos. HM030920–HM030923 and HM106431–HM106446 for SaVs and HM212532–HM212542 for HAstVs.

Out of 662 fecal specimens tested, SaV and HAstV were detected in 20 (3%) and 11 (1.7%) cases, respectively. Most of SaV (n = 18, 90%) and HAstV (n = 10, 91%) infections occurred in infants and children <3 years of age. SaV prevalence increased slightly during the cold months from December to February (n = 12), while HAstV exhibited a peak in April (n = 6), corresponding with spring. In a phylogenetic tree, the majority of SaV sequences belonged to GI/1 genotype (n = 15, 75%), followed by GII/1 (n = 4, 20%), and GII/3 (n = 1, 5%) (Fig. 1). HAstV-1 (n = 10, 91%) was the most prevalent followed by HAstV-3 (n = 1, 9%). This phylogenetic tree clearly showed that HAstVs-1 could be classified into four lineages (1a–1d), in which our nine strains clustered into lineage 1d and the other strain into lineage 1a (Fig. 2).

According to the past 6 years of SaV surveillance, SaV GI/1 was the most prevalent genotype during 2003–2004, and thereafter genotype GI/6 dominated over the GI/1 in 2004–2005 (6). Then, the GI/6 was replaced by GI/1 from 2005 until 2007 (8,9). Surprisingly, GI/1 emerged as a predominant strain in 2007–2008 (10). Surprisingly, GI/1 emerged and became the prevailing genotype in the present study, while GIV suddenly disappeared. This sudden disappearance of GIV might indicate that the virus appeared at the time that the pediatric popula-
tion lacked antibodies against this strain, and the virus disappeared as the population began to acquire viral immunity. It is also possible that such a virus could not find the environmental conditions that contribute to its ability to cause acute gastroenteritis.

HAvst-1 has been the most commonly identified genotype worldwide (1,4,11). However, some studies have reported the predominance or co-circulation of other genotypes of HAvstV, such as 2, 3, and 4 (5,12–14). We found a predominance of HAvstV-1 circulation among the studied population, although genotype 3 has also been found. Interestingly, the study confirmed that maximum HAvstV prevalence can occur during the warmer months, which is in agreement with a previous report (12).

The data obtained in this study shows that SaVs and HAvstVs are important enteric viruses co-circulating in Japanese infants and children. The epidemiology and genetic diversity of HAvstV is only beginning to be addressed in Japan. Further epidemiological studies should be continued in order to identify the trend of these viruses in the coming year.

Acknowledgments This study was supported by Grants-in-Aid from the Ministry of Education, Culture, Sports, Science and Technology and the Ministry of Health, Labour and Welfare, Japan.

The authors gratefully acknowledge the cooperation extended by Drs Shuichi Nishimura, Hideaki Kikut, Tsuneyoshi Baba, Atsuko Yamamoto, Kumiko Sugita, Masaaki Kobayashi, Shintaro Hashira, and Takeshi Tajima for fecal specimen collection.

Conflict of interest None to declare.

REFERENCES