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A Gastroenteritis Outbreak Attributed to Sapovirus Genogroup V in Yokohama, Japan

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Sapovirus (SaV) is single-stranded positive-sense RNA virus in the family Caliciviridae. Acute gastroenteritis caused by Sapoviruses predominantly occurs in infants and young children. The SaV genome is 7.3–7.5 kb long and encodes 2 or 3 open reading frames. SaV strains can be divided into 5 genogroups, GI–GV, on the basis of the capsid gene. GI, GII, GIV, and GV infect humans, whereas GIII infects porcine species. According to a genotyping study in Japan conducted between 1998 and 2005, the GI and GII genogroups accounted for 95% of SaV strains (1). SaV GIV became dominant in 2007 and was replaced by GII.3 in 2008 (2). Information about SaV GV is limited.

Here we describe an outbreak of gastroenteritis associated with the SaV GV strain among primary school students and characterize the strain on the basis of the nucleotide sequence in the capsid region. To our knowledge, this is the first report of an outbreak attributable to the SaV GV strain in Japan.

An outbreak of gastroenteritis occurred at a primary school in Yokohama, Japan, on June 7, 2010, when 36 of 830 students developed symptoms of gastroenteritis. Of these 36 children, 12 were students in one of three 2nd grade classes. In total, 46 of 830 students displayed symptoms of gastroenteritis up to June 11, as shown in Fig. 1. We collected stool samples from 2 students (aged 7–8 years) and tested them for diarrheal viruses. Although Norovirus was suspected to be the pathogen, no norovirus genome was detected in the 2 samples. Therefore, the samples were tested for the presence of SaV using real-time reverse transcription-polymerase chain reaction (RT-PCR). SaVs were detected in both the samples.

A partial sequence from the polymerase gene to the end of the SaV genome (3,160 nucleotides) was amplified for further molecular analysis. RT-PCR was performed using the sapp36 G5 (5'-AGCAGTACGRTTG CAGAGTGGC-3') and SV-G5-R primers to amplify the partial polymerase gene. Nested RT-PCR was performed using the SV-F14 and TX30SXN primers for the first PCR and the primers SV-F14, SV-R13, SV-R14, SV-G5-F522 (5'-TGTCGGYGCCGTGGAYTACC-3'), SV-G5-R1510 (5'-CAGCCATCATGTTTTCAGGGGA-3'), SV-G5-F1331 (5'-CAACATGGACGGTTGCAATTACAC-3'), and TX30SXN for the second PCR (1,3).

The PCR products were directly sequenced using the BigDye Terminator Cycle Sequencing Kit and Genetic Analyzer 3130 (Applied Biosystems, Inc., Foster City, CA, USA). Phylogenetic analysis was conducted using MEGA 4 software (http://www.megasoftware.net/). Multiple sequence alignment was performed using Clustal W, and a dendrogram based on nucleic acid sequences was constructed using the neighbor-joining method based on Kimura’s two-parameter distance matrix, with 1,000 bootstrap replicates. The sequence reported in this manuscript has been deposited in the DDBJ/GenBank/EMBL databases under the accession number AB924385.

The sequences of the 2 samples were 100% identical and were classified in genogroup V by phylogenetic analysis when their full capsid-encoding regions were compared (Fig. 2). The nucleotide sequence homology between our strain and SaV GV NongKhai-24/Thailand (AY646856) was 98% in the capsid region of the viral genome. The NongKhai-24 strain was isolated from a hospitalized infant in NongKhai, Thailand, between November 2002 and April 2003 (4). In the Japanese outbreak analyzed here, no patient was hospitalized and the symptoms were mild. Analysis of the sequence of the capsid gene (1,710 nucleotides) from our strain and that from NongKhai-24 revealed an amino acid difference from G to N at nucleotides 75–77 of the VP1 gene.

In conclusion, this study demonstrates that the SaV GV strain caused the outbreak of gastroenteritis in Japan in June 2010. To our knowledge, this is the first...
Fig. 2. Phylogenetic tree based on the capsid nucleotide sequences of SaV strains. The SaV strain identified in this study is indicated in bold letters. The percentage bootstrap support is indicated at each node (values <80% are omitted). The scale represents nucleotide substitutions per site.

documented gastroenteritis outbreak attributable to the SaV GV strain in Japan.

Conflict of interest None to declare.

REFERENCES