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VIRUSES

Complete Coding Genome Sequences of Uncommon GII.8 Sapovirus Strains Identified in Diarrhea Samples Collected from Peruvian Children

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ABSTRACT We report here two complete coding genome sequences of novel genotype GII.8 sapovirus strains identified in diarrhea samples collected from two Peruvian children. The complete coding genome sequences of both GII.8 variants were determined using the Sanger sequencing method.

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After the successful deployment of the rotavirus vaccine, sapovirus (SaV) has emerged as one of the major viral pathogens causing acute gastroenteritis in children under 5 years of age (1–4). Saposviruses are classified into five genogroups (GI to GV) (5), and at least 21 genotypes have so far been identified. However, novel genogroups and genotypes continue to be reported in Asia, Europe, and America (5, 6). Here, we provide whole-genome coding sequences of two novel SaV GII.8 strains—Hu/GII.8/Peru143/PNV021589/2009 (Peru-143) and Hu/GII.8/Peru330/PNV010961/2008 (Peru-330)—which complement our previous report of the partial capsid sequence (7). These genomic data will contribute to a better understanding of the transmission, pathogenicity, and evolutionary process of SaV.

Peru-143 and Peru-330 were characterized through Sanger sequencing, using two different diarrheal stool samples from children 18 and 21 months old, respectively (8). Briefly, viral RNA was extracted from 20% stool suspension using the QIAamp MinElute virus spin kit and stored at −80°C until analyzed. cDNA synthesis was done using SuperScript III reverse transcriptase (Thermo-Fisher Scientific, Waltham, MA, USA) and oligo(dT) primer. The complete coding sequences and the 3′ untranslated regions (UTRs) were obtained from four overlapping PCR fragments, which were purified by Illustra-ExoProStar (GE Healthcare, Buckinghamshire, United Kingdom) and sequenced using the primer-walking method. Sanger sequencing utilized BigDye Terminator version 3.1 cycle-sequencing chemistry and a Thermo-Fisher 3730 genetic analyzer (Thermo-Fisher Scientific). The resulting sequences were mapped using strain Hu/GII.8/Miaoli/05-099-515478/2014/TW (GenBank accession number KX894315.1) as a reference, manually assembled, curated using MEGA7 (9), and annotated using Unipro UGENE version 1.26 (10). Eventual recombination patterns were analyzed using the RDP4 package (11).

The nearly complete genomes (without the 5′ UTRs) of SaV Peru-143 and Peru-330 consist of 7,451 and 7,452 nucleotides (nt), respectively. The sequenced genomes were both predicted to contain two major open reading frames (ORF) from nt position 1 to 6837 (ORF1, encoding 2,278 amino acids [aa]) and from 6837 to 7337 (ORF2, encoding

166 aa). The predicted 3′ UTR lengths are 113 nt for Peru-143 and 114 nt for Peru-330. The multiple-sequence alignment matrix in Unipro UGENE showed that both Peruvian strains had 99% nt sequence similarity. Furthermore, 2,433 of 2,444 aa (>99.5%) were similar between both Peruvian sequences, while 2,408 of 2,444 aa (98.5%) were similar between the Taiwanese sequences (GenBank accession numbers KX894314 and KX894315) and Peru-143. Maximum likelihood phylogenetic trees based on the complete coding sequences grouped the Peruvian and Taiwanese strains in the same GII.8 branch in related but distinct clusters. Based on RDP4 outputs and on the structure of phylogenetic trees, there was not enough evidence to consider Peru-330 and Peru-143 recombinant strains. The detection of GII.8 SaVs in Taiwan and Peru suggests a possible ubiquitous circulation of GII.8 SaVs in different regions.

Accession number(s). The genome sequences reported here have been deposited in GenBank under the accession numbers MF462287 (Peru-143) and MF462288 (Peru-330).

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