



Complete Genome Sequence of a Human Sapovirus GI.2 Variant, Isolated from a Patient in Ireland in 2016

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ABSTRACT We report here the first near-complete genome sequence (7,463 nucleotides) of a human sapovirus GI.2 variant from Dublin, Ireland, detected in an adult with gastroenteritis in 2016.

Human sapoviruses (SaVs), members of the *Sapovirus* genus of the family *Caliciviridae*, are genetically diverse and are causative agents of acute intestinal gastroenteritis (AIG) in humans (1, 2). They are classified phylogenetically into genogroups GI, GII, GIV, and GV, and subdivided into 16 genotypes (GI.1 to GI.7, GII.1 to GII.7, GIV.1, and GV.1) based on the complete sequence for the capsid protein VP1 (1, 3). Studies in Europe have demonstrated that up to 4% of outbreaks of AIG in the Netherlands were associated with human SaV infection, and the predominant strain was determined to be GI.2 (4). Currently, human SaV infection is not notifiable in Ireland, and thus the prevalence of this virus among clinical cases of AIG is not well defined. However, in one study, SaV detected in RNA from stool samples ($n = 562$) represented 10% of all viral pathogens associated with a cohort of patients in Ireland with AIG between 2014 and 2016 (Z. Yandle, G. Tuite, S. Coughlan, J. O’Gorman, F. Cloak, S. Jackson, and C. D. Gascun, presentation at the annual meeting of the European Society Clinical Virology, Lisbon, Portugal, 2016). Here, we report the first complete genome sequence, minus 12 (predicted) nucleotides (nt) from the 5’ end, of a sapovirus GI.2 strain (GenBank accession number MF431582) detected in a 27-year-old symptomatic female in the east of Ireland.

Viral RNA was extracted from the supernatant of a 10% (vol/vol) suspension of sapovirus-positive stool in phosphate-buffered saline using a QIAamp Viral RNA minikit (Qiagen), followed by library construction using a TruSeq mRNA library prep kit (Illumina) and sequencing on the MiSeq platform (Illumina). Data were analyzed using CLC Genomics Workbench (CLC bio). One contig covering the sapovirus genome sequence was assembled from 223,547 reads containing an average coverage of 3,811 \times .

Based on the full-length sequence, a BLAST search showed that sapovirus Hu/GI/BE-HPI01/DE/2012 (GenBank accession number JX993277) and Hu/GI.2/BR-DF01/BRA/2009 (GenBank accession number AB614356) were the nearest neighbors, sharing 98% (7,293/7,458) and 97% (7,249/7,459) nucleotide similarity, respectively, with MF431582. The sequence was typed as a GI *Caliciviridae* sapovirus using the Norovirus Genotyping tool (5). The 7,463-nt genome sequence contained (i) two open reading frames (ORFs), ORF1 and ORF2 of 6,873 and 492 nt in length, respectively, and (ii) predicted 5’ and 3’ untranslated regions of 2 and 101 nt in length, respectively. Independent phylogenetic analysis with either the ORF1 (encoding VP1 and nonstructural proteins) or ORF2 (encoding VP2) sequence revealed that both ORFs cluster with GI.2 sapovirus. Further

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analysis confirmed that the ORF1-encoded polyprotein (2,290 amino acids) shares 99% (2,274/2,290) and 99% (2,266/2,290) homology with the corresponding encoded protein of JX993277 and AB614356, respectively; and the ORF2-encoded protein VP2 (163 amino acids) shares 100% (163/163) and 99% (2,274/2,290) homology with JX993277 and AB614356, respectively. This first full-length genome sequence of human SaV from a patient in Ireland provides an additional reference sequence for establishing a database to facilitate phylogenetic analyses and for conducting epidemiological studies of sapoviruses circulating in Ireland, particularly of their role as causative viral agents of AIG.

Accession number(s). The genome sequence of the sapovirus Hu/GI.2/Dublin/2016/IRL variant has been deposited in GenBank under the accession number [MF431582](https://www.ncbi.nlm.nih.gov/nuclseq/AB614356).

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