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GENOME SEQUENCES

Near-Complete Genome Sequence of a Human Norovirus GII.P7-GII.6 Strain Detected in a Maryland Patient in 2018

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ABSTRACT Genomic recombination is a crucial mechanism used to generate genetic variation in human noroviruses. Recombinant variants have been increasingly identified and have contributed to sporadic cases and epidemic outbreaks of acute gastroenteritis globally. We report the near-complete genome of a novel recombinant norovirus GII.P7-GII.6 strain detected in an adult with norovirus gastroenteritis in the United States in 2018.

Human noroviruses, members of the *Norovirus* genus of the family *Caliciviridae*, are the leading cause of acute viral gastroenteritis worldwide (1). Currently, noroviruses can be classified into at least 7 known genogroups (GI to GVII) and further subdivided into at least 32 genotypes among the human-associated groups (GI, GII, and GIV) (2). The high genetic diversity of noroviruses has been attributed to rapid evolution and intragenotype genomic recombination driven by selection pressures or high mutation rates (3). Although the most common norovirus genotypes reported were GII.4 (4), more and more recombinant variants have emerged and contributed to sporadic cases and epidemic acute gastroenteritis outbreaks. In the 2017–2018 season, several recombinant strains were identified and found to be responsible for more than 60% of the 655 norovirus outbreaks reported to CaliciNet (https://www.cdc.gov/norovirus/reporting/calicinet/data.html). Among them, GII.P7-GII.6 accounted for 4% of the reported genotypes. Here, we report the first near-complete genome sequence of a norovirus GII.P7-GII.6 strain, associated with a sporadic case of acute gastroenteritis in Maryland in 2018.

Viral RNA was extracted from the supernatant of a 10% (wt/vol) norovirus-positive stool sample in phosphate-buffered saline using a QIAamp viral RNA minikit (Qiagen). The library was generated using a TruSeq stranded mRNA prep kit (Illumina), pooled with six other samples, and sequenced on the MiSeq platform (Illumina). Raw data imported into CLC Genomics Workbench (CLC Bio) were first trimmed with a quality score limit of 0.05 and a maximum number of ambiguities of 2 and then assembled *de novo* with a minimum contig length of 200 bp, a minimum length fraction of 0.8, and a minimum similarity fraction of 0.8. One contig covering the norovirus genome sequence, with an average coverage of 195×, was assembled from 15,105 of the total 6,350,046 paired-end reads (100 bp) generated from this sample. The genome sequence of GII.P7-GII.6/Maryland/2018/USA, annotated with both CLC Genomics Workbench and Sequin, was 7,534 nucleotides (nt) long with an average GC content of about 52%. Determined with the module "find open reading frame" within the CLC Genomics Workbench, this genome was found to contain (i) three open reading frames (ORFs), ORF1 (5,088 nt), ORF2 (1,644 nt), and ORF3 (780 nt), and (ii) a 3′ untranslated region (UTR) 43 nt long. Four nucleotides of the 5′ UTR and the first six nucleotides of ORF1 were missing when aligned to known complete sequence reference strains. Virus typing using the Norovirus Genotyping Tool version 1.0 (5) demonstrated that this sequence

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was a recombinant strain composed of GII.7 ORF1 and GII.6 ORF2 (bootstrap value, 100). The CaliciNet lab-based human calicivirus typing tool also typed this sequence as a recombination of GII.P7 for the polymerase region and GII.6 for the capsid region. A full-length genomic sequence BLAST search revealed 90% nucleotide identity with a GII.P7-GII.6 variant from the same area in Maryland in 2014 (GenBank accession number KX268709), although both GII.P7-GII.6 variants (GenBank accession numbers KX268709 and MK301293) show that the recombination point occurs within the junction of ORF1 and ORF2. These results indicate that a GII.P7-GII.6 strain was circulating in the United States in 2018. This sequence provides an additional reference sequence for phylogenetic analysis and epidemiological studies regarding circulation of this strain in the United States. The difference between the two GII.P7-GII.6 variants from the same area in Maryland in 2014 and in 2018 further demonstrates the genetic diversity of noroviruses.

Data availability. The genome sequence of the GII.P7-GII.6/Maryland/2018/USA strain has been deposited in GenBank under the accession number MK301293. The raw sequence data have been deposited in the SRA under the accession number SAMN10611964.

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We have no conflict of interest.

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