



Complete Genome Sequence of a Novel Recombinant GII.P16-GII.1 Norovirus Associated with a Gastroenteritis Outbreak in Shandong Province, China, in 2017

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ABSTRACT We report here the complete genome sequence of a novel recombinant GII.P16-GII.1 norovirus identified from eight fecal samples collected during an acute gastroenteritis outbreak in Jinan, Shandong Province, China, in 2017. The virus had nucleotide identities of 99% and 91% in the ORF1 and ORF2 genes of related strains, respectively.

Noroviruses are a leading cause of acute viral gastroenteritis worldwide (1). Based on viral capsid protein (VP1) sequences, noroviruses are divided into 7 genogroups (GI to GVII), which are subdivided into more than 30 genotypes (2). With the frequent emergence of recombinant noroviruses, the U.S. Centers for Disease Control and Prevention recently developed new genotyping methods for VP1 and RNA-dependent RNA polymerase (RdRp) that increase the ability to conduct worldwide surveillance of noroviruses (3).

Eight fecal samples from patients treated during an acute gastroenteritis outbreak in Jinan, Shandong Province, China, in 2017 were diluted into a 10% (1:10 [wt/vol] ratio) viral suspension with phosphate-buffered saline. Total RNA was extracted from the supernatant using a QIAamp viral RNA minikit (Qiagen). The norovirus was detected by targeting the spanning ORF1 and ORF2 genes as previously described (3). A novel recombinant norovirus was identified and designated GII.P16-GII.1. One strain named SDJN170450 was selected for full-length genome sequencing, as previously reported (3).

The complete genome of SDJN170450 was 7,518 nucleotides (nt), excluding the poly(A) tail. Its genome contained 3 open reading frames (ORFs), as follows: ORF1 encoded a nonstructural polyprotein with a length of 1699 amino acids (aa), and ORF2 and ORF3 encoded VP1 and VP2 with lengths of 535 and 259 aa, respectively. Interestingly, the ORF1 sequence of SDJN170450 had the highest nucleotide identity (99%) with the emerging GII.P16 gene of the GII.P16-GII.2 norovirus that predominated in the winter of 2016 to 2017, while the VP1 sequence had the best BLAST search results of 91% and 98% nt and aa identities, respectively, with those of the GII.1 strain Hu/GII.1/Ascension208/2010/USA (GenBank accession number AFA55174). Therefore, we postulate that this GII.1 virus originated from a recombination event between a newly emerged GII.P16-GII.2 virus and a GII.1 virus. Furthermore, SDJN170450 contained 15 aa mutations in VP1, with 5 aa near histo-blood group antigen binding site II compared to that of the GII.1 prototype strain Hawaii/1971/US (AAB97768). The functional importance of these mutations needs further investigation.

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This is the first detection and report of the complete genome sequence of a novel GII.P16-GII.1 norovirus involving a gastroenteritis outbreak. In the last 3 years, rare genotypes have replaced the previously predominant GII.4 genotype (4) as the epidemic viruses causing norovirus outbreaks. These include the novel GII.17 variant in the 2014–2015 season (5) and the GII.P16-GII.2 virus in the 2016–2017 winter season (3), both emergent through the acquisition of a novel RdRp gene (6, 7). Since its first identification in the GII.P16-GII.4_Sydney 2012 norovirus in 2015, the emerging GII.P16 gene has been detected in diverse VP1 genotype viruses (3, 8–10). The GII.P16 protein of the reemerging GII.P16-GII.2 and GII.P16-GII.4_Sydney 2012 viruses contains polymerase mutations near a position known to influence protein function and viral transmission (7, 10). These mutations are also shown in the novel GII.P16-GII.1 norovirus. Therefore, we postulate that the advantageous polymerase and amino acid mutations in the capsid protein have produced a highly transmissible GII.1 virus. Close surveillance of its national and global spread is necessary.

Accession number(s). The complete genome sequence of the GII.P16-GII.1 norovirus SDJN170450 has been deposited in GenBank under the accession number [MG572182](https://www.ncbi.nlm.nih.gov/nuccore/MG572182).

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