A novel recombinant norovirus was detected in the diarrheal feces of nine patients in an outbreak in Kawasaki City, Japan, in 2016. The viral genome showed nucleotide sequence identities of 95.1% and 97.2% to the closest strains in the regions of 5′-terminus to ORF1 and ORF2 to 3′-terminus, respectively.

Norovirus is a major causative pathogen of acute gastroenteritis in humans of all age groups (1). The virus is classified into genogroups I to VII (GI to GVII) (2). Patients with gastroenteritis are typically infected by noroviruses GI and GII, which have 9 and 22 genotypes, respectively. Although the emergence of recombinant strains, norovirus experts recommend that genotyping for worldwide surveillance use two proteins: the RNA-dependent RNA polymerase (RdRp) gene in open reading frame 1 (ORF1) and the capsid viral protein 1 (VP1) gene in ORF2 (3).

To our knowledge, this is the first report of a complete genome sequence of norovirus GI.P16-GII.4_Sydney2012. Norovirus infection is caused mostly by the GII.4 genotype, followed by GII.2, GII.3, GII.6, and GII.17 (8–11). The most prevalent GII.4 contained GI.P4 and GI.Pe RdRp sequences, and GI.P16 strains with various VP1 genotypes have been detected in some countries (12–20). The amino acid identity was 95 to 100% among GI.P16 RdRp sequences, and these diverged phylogenetically into two clusters. GI.P16 showed an amino acid identity of 88 to 93% to GI.P4 and GI.Pe in the RdRp sequences. Some proteins within ORF1 are associated with the pathogenesis of norovirus (21, 22). Additionally, recent reports have shown that an interaction between the human norovirus GI RdRp and GI VP1 proteins, but not the murine norovirus VP1, enhanced host RIG-I-dependent interferon signaling activity via replicative RNA in a human cell line, whereas the GI VP2 downregulated the innate immune signaling (23, 24). Norovirus GI exhibits genetic diversity among the genotypes in the capsid sequence, which is crucial for host entry and the production of blocking antibodies, and also in the nonstructural polyprotein-coding sequence (25–28). Therefore, appropriate combinations of ORF1 and ORF2-ORF3 sequences may be associated with the enhancement of norovirus pathogenesis and infectivity, which leads to the prevalence of restricted genotypes.

Accession number(s). The GenBank accession number for the norovirus Hu/GII/IP/2016/GI.P16-GII.4_Sydney2012/Kawasaki194 genome sequence is LC175468.

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