

# Complete Genome Sequence of a Novel Recombinant GII.Pe\_GII.17 Norovirus Strain from Hong Kong in 2015

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**The complete genome sequence of a novel recombinant GII.Pe\_GII.17 norovirus strain, tentatively named GII.17 Hong Kong 2015, was determined. RNA-dependent RNA polymerase has 95.6% and 98.4% and viral protein 1 has 90.6% and 95.9% identity at the nucleotide and amino acid levels, respectively, to the closest sequences in GenBank.**

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Norovirus is a leading cause of acute gastroenteritis in all age groups worldwide (1). Genetically, norovirus is classified into at least 6 genogroups which are further subdivided into over 40 genotypes (2). In the winter of 2014–2015, a novel variant of norovirus genogroup II genotype 17 (GII.17), called Kawasaki 2014, emerged and became predominant in Asia (3–6) and was sporadically detected in the United States (7) and Europe (8). Genetic recombination has been proposed as one mechanism behind the emergence of novel norovirus variants (9). Here, we report the complete genome sequence of a novel recombinant norovirus strain with the RNA-dependent RNA polymerase (RdRp) closely related to GII.Pe of the current pandemic variant GII.4 Sydney 2012 and the viral protein 1 (VP1) belonging to the GII.17 genotype but distantly related to all known GII.17 variants. The norovirus GII.17 genotype is undergoing rapid evolution and intergenotypic recombination.

This recombinant norovirus strain (GII/Hu/HKG/2015/GII.Pe\_GII.17/CUHK-NS-682) was retrieved from a stool specimen of a 63-year-old man on 30 June 2015 in our ongoing, hospital-based norovirus surveillance in Hong Kong (10, 11). Viral RNA was extracted from 10% stool suspension using a Mag-MAX viral RNA isolation kit (Thermo Scientific). Conversion of viral RNA to cDNA was performed using SuperScript III reverse transcriptase (Thermo Scientific) with a tagged oligo dT primer. Seven overlapping PCR fragments covering the whole genome were amplified using high fidelity Phusion DNA polymerase (Thermo Scientific), followed by Sanger sequencing. DNA chromatograms were manually curated, and contigs were generated using ChromasPro software version 1.7.6 for Windows (Technelysium). Primers used were available upon request.

Norovirus genotyping was performed using NoroNet's norovirus genotyping tool (<http://www.rivm.nl/mpf/norovirus/typingtool>). Preliminary analysis of our norovirus strain indicated that the genotypes of RdRp and VP1 belonged to GII.Pe and GII.17, respectively, suggesting an intergenotypic recombinant. BLAST analysis was performed on RdRp and VP1 separately. The recombinant's RdRp GII.Pe had the highest nucleotide (95.6%) and amino acid (98.4%) identity to Hu/GII/BG1C0391/2012/

BGD (GenBank accession no. KJ685406), which was a GII.4 Sydney 2012 strain. Interestingly, the recombinant's GII.17 VP1 was distantly related to the recently emerged Kawasaki 2014 variant (Hu/GII/JP/2015/GII.P17\_GII.17/Kawasaki308; GenBank accession no. LC037415) with only 77.0% and 86.7% identity at the nucleotide and amino acid levels, respectively. Instead, the recombinant's GII.17 VP1 had the highest nucleotide (90.6%) and amino acid (95.9%) identity to a GII.17 strain dating back to nearly 40 years ago (Hu/GII.17/C142/GF/1978; GenBank accession no. JN699043). Notably, the observed VP1 amino acid difference of ~4% with the closest GII.17 VP1 warrants the assignment of our recombinant norovirus strain as a new GII.17 variant, tentatively named GII.17 Hong Kong 2015. Overall, the complete genome of the recombinant norovirus shared the highest nucleotide identity of 90.3% to Hu/GII.17/C142/GF/1978.

This is the first complete genome sequence of a novel recombinant GII.Pe\_GII.17 norovirus. Our data indicate that norovirus GII.17 is undergoing rapid evolution and intergenotypic recombination, providing important insights into GII.17 evolution. Acquisition of the RdRp gene from the current pandemic GII.4 Sydney 2012 variant highlights the epidemic or even pandemic potential of norovirus GII.17.

**Nucleotide sequence accession number.** The complete genome sequence of the recombinant norovirus strain GII/Hu/HKG/2015/GII.Pe\_GII.17/CUHK-NS-682 has been deposited in GenBank under the accession number [KT589391](https://www.ncbi.nlm.nih.gov/nuccore/KT589391).

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M.C.W.C. and P.K.S.C. conceived the study. M.C.W.C. designed and supervised the study. T.-N.H. and K.K. performed experiments. M.C.W.C. analyzed data and drafted the manuscript. All authors critically reviewed the manuscript and approved the final revision. M.C.W.C. has access to all data and is responsible for the scientific integrity of this work.

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