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## Full-Genome sequence analysis and molecular characterization of an uncommon *Norovirus* from South Korea

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**N**oroviruses (NoVs) are major causal agents of acute gastroenteritis in humans. NoV GII.4 is the predominant genotype globally. However, uncommon and minor types of NoVs are consistently detected and some have been shown to dominate over GII.4. Therefore, the prevalence of dominant and uncommon NoVs makes the identification of these viruses important for the prediction and prevention of pandemics. In this study, the full-genome sequence of a NoV detected in Korea was extensively characterized. The full-length genome was 7510 nucleotides long, and phylogenetic analysis based on the whole-genome sequences, including open reading frame (ORF)1, ORF2, and ORF3, indicated that it belonged to the GII.21 genotype. GII.21 is not a prevalent epidemiological agent of acute gastroenteritis in humans, but it is consistently found in gastroenteritis patients from several countries. The present study provides the first full-genome sequence analysis of NoV GII.21 isolated from a patient in Korea. Our findings provide not only valuable genome information but also data for epidemiology studies, epidemic prevention, and vaccine development strategies.

### Biography

Jae Woong has completed his Master at the age of 33 years from Jun-Nam University in Korea. He is working at Catholic-University in Korea at PhD course. His major is Molecular-biology and Virology.

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