

JOINT EVENT

10<sup>th</sup> International Virology Summit  
&  
4<sup>th</sup> International Conference on Influenza & Zoonotic Diseases  
July 02-04, 2018 | Vienna, Austria

### Full-genome sequence analysis of an uncommon norovirus from South Korea

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Noroviruses (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 (strain JW) 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. Strain JW showed maximum identity with strain YO284; however, comparison of the amino acid sequence of ORF2, which functions as an antigen, showed substitutions in several amino acids. 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 Lee has completed his Master's from Jun-Nam University, South Korea. He is pursuing his PhD from Catholic-University, South Korea. His major is Molecular-biology and Virology.

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