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Molecular characterization of Norovirus isolates from South Korea

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Noroviruses (NoVs) is the dominant etiological agent of acute gastroenteritis in humans and recognized as a major etiologic agent of nonbacterial acute gastroenteritis in all age groups worldwide. Furthermore, variants and recombinant strains of this virus are continuously emerging worldwide. These variants could be related to antigenic variations that alter viral transmission and immune systems in human bodies, thus influencing the patterns of viral activities. Therefore, studies of the genetic diversity and evolution of human NoV could provide important information that may prove useful for controlling human NoV infection. And the full genome sequence analysis of NoVs is important to be able to pursue of sporadic gastroenteritis in the world by NoV. Here, we determined the full-length sequences of a recombinant NoV strain and unique NoV strain isolated from clinical samples in South Korea. Because these strains may result in hazardous NoV outbreaks in Korea, this information should prove to be valuable. The results from this study highlight the many challenges in the identification of new recombination strains and suggest that guidelines be applied for identifying newly emerging recombinant strains of NoV.

Biography

Jae Woong Lee has completed his Master's degree from Jun-Nam University in Korea. He is pursuing his PhD at Catholic University of Korea, South Korea.

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