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A study on genomic diversity of norovirus using deep sequencing approach

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A study on genomic diversity of norovirus using deep sequencing approach: Norovirus (NoVs) are the leading cause of epidemic and sporadic gastroenteritis outbreaks worldwide affecting across all age groups, responsible for approximately 90% of all outbreak of viral gastroenteritis. Each year, mortality due to NoV is estimated at 570-800 in the United States, with approximately $777 million in health-care costs. NoV, a genus within the *Caliciviridae* family, is small non-enveloped virus with a positive single-stranded RNA genome of 7.5-7.7 kb organized into three open reading frames (ORFs). ORF1 encodes six non-structural proteins, including RNA dependent RNA polymerase (RdRP). ORF2, ORF3 encode VP1 and VP2 capsid proteins. Generally, the genome of RNA virus has been known to change constantly from mutational event and revealed novel variant. In the previous reports, the NoV GII.4 strains had been known to evolve at a rate of 4.3-9.0X10-4 mutations per site per year and to share a most recent common ancestor in the early 1980s. The goal of this study was to analyze NoV complete sequence and detect variants using next generation sequencing (NGS) method. Sequence reads of NoV were constructed to GII.4 whole genome sequence and were assembled with reference genome. In phylogenetic analysis, the sequence was clustered with 2006b variants. Moreover, VP1 (i.e. capsid protein) were revealed that the amino acid sequence altered three sites in hyper variable domains, and it led to changes in protein structure. Continued molecular studies of NoV by NGS, including approaching of complete genome, is important for monitoring emerging strains in our strategy to prevent of NoV outbreaks in Korea.

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