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7th International Conference on

Proteomics & Bioinformatics

October 24-26, 2016   Rome, Italy

An analysis of norovirus genome using next-generation sequencing

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To overcome the technological constraints of the Sanger sequencing, next generation sequencing (NGS) technologies were developed. It has become very rapidly a standard tool in pathogen discovery. In recent years, NGS techniques are increasingly being used for outbreak monitoring, metagenomic studies and virus detection. Incorporating deep sequencing techniques into virus diagnostics on clinical samples and foods samples that can be detected and at the same time provides additional information on the characterization of the detected viruses. The objective of this study was development of detection method for NoV GII.4 using NGS. Alignment of the norovirus sequences from underground water samples was performed with CLC Workbench software packgea and DNAstar softare. Similarity, and capsid epitope analyses detected GII.4 Sydney strains by NGS data. An amino acid sequence of the epitopes of the capsid P2 domain was same amino acid in Sydney 2012 strains. NGS technologies will provide an information for epidemiologic studies of NoV.

Biography

Jeong-Su Lee has completed his PhD from Chung-Buk University, Republic of Korea. He is currently working as a Scientific Researcher for the Division of Microbiology, Ministry of Food and Drug Safety. His main research include the study for prevention of infectious diseases and control any public health related issues in Korea.

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J Proteomics Bioinform 2016
ISSN: 0974-276X JPB, an open access journal

Proteomics & Bioinformatics 2016
October 24-26, 2016

Volume 9, Issue 11(Suppl)

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