ANALYSIS OF NOROVIRUS GII GENETIC DIVERSITY IN OYSTER DURING 2015 WINTER SEASON IN OYSTER
CULTIVATION AREA OF NORTHERN EASTERN JAPAN
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ABSTRACT

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Norovirus is one of the recent leading causative agents for acute gastroenteritis around the world these decades. Among norovirus genotypes, GII is the most prevalent genogroup worldwide. Norovirus is mostly transmitted through contaminated sewage water which flows to the shellfish harvesting site. Oyster was suggested to be one of the pathways of norovirus transmission through their filter feeding mechanism. Six oyster samples were collected from Japanese oyster cultivation area, in January and February, 2015. Digestive tissues were excised from oysters and nucleic acid extraction was carried out followed by amplification and purification. Finally, the GS Junior system was applied to perform pyrosequencing on the norovirus amplicons. Norovirus GII.3, 4 and 17 were detected in each sample. The norovirus GII.4 Sydney 2012 was dominant variant for five samples, while Den Haag 2006b was found as high as 96% in one sample. By applying pyrosequencing to oyster samples, genomic information of norovirus could be obtained. This research provided a better understanding of the genetic diversity of norovirus in study area.

KEYWORDS

Norovirus, Gastroenteritis, Oyster, Pyrosequencing