

DETECTION AND GENETIC CHARACTERIZATION OF NOROVIRUS IN ENVIRONMENTAL WATER SAMPLES IN THAILAND

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Abstract. The aim of this study was to detect and characterize noroviruses (NoVs) in environmental water samples. One hundred and fourteen water samples were collected from a river and irrigation canals in central Thailand during 2006-2007. NoVs were detected by RT-nested PCR in 13% of the samples. The river samples (22%) contained NoVs at a higher frequency than the irrigation canal samples (4%). Among the 15 NoV-positive samples, 9 harbored genogroup (G) I, 2 samples with GII, and 4 samples with mixed GI and GII. DNA sequencing of PCR amplicons and phylogenetic analysis of partial capsid gene revealed that 5 samples were of genotype GI-2, 1 sample was GI-6, and 1 sample was a mix of GI-2 and GII-unclassified genotypes. NoVs in water samples quantified using quantitative RT-PCR were in the range of 4.91×10^2 - 1.26×10^3 copies/ml for NoV GI and 3.51×10^3 copies/ml for NoV GII. This is the first study demonstrating the presence of NoV variants in water samples collected from a river and the adjacent canals of Thailand.

Keywords: norovirus, genotype, water, RT-nested PCR

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