

POSTER 55

THE MOLECULAR EPIDEMIOLOGY AND ANTIBODY PRODUCTION FOR NOROVIRUS

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Norovirus (NoV) is one of the most important nonbacterial agent causing acute gastroenteritis in humans. To characterize the molecular epidemiology of human NoVs from various districts of South Korea, stool specimens were collected from children under 5 years of age suffering from diarrheal disease from 8 domestic hospitals in South Korea from November 2005 to November 2006. 114 of the 762 (15.0%) stool specimens were identified as NoVs. 12 of the 114 (10.5%) specimens were determined to belong to GI strains and 102 (89.5%) of the 114 specimens belonged to the GII strains. Whereas 12 GI NoVs among the total 114 NoVs were classified further into only one genotype, GI-6 accounting for 10.5%, 102 GII NoVs were classified further into GII-2, GII-3, GII-4, GII-5, GII-6, GII-8 as well as a C1-120 genotype accounting for 0.9%, 7.9%, 71.9%, 5.3%, 1.8%, 0.9%, and 0.9%, respectively. Phylogenetic analyses of identified NoVs were conducted with the nucleotide sequencing data from RT-PCR about GI (314 bp) and GII (305 bp) capsid regions.

Another trial had been made to prepare novel polyclonal antibodies for development of the rapid diagnosis kit based on the ELISA system. As antigens, both ORF2 and ORF3 regions (nucleotide positions 5745 to 6560 and 6704 to 7450) inserted into the pET-SUMO protein expression vector. The expressed and purified proteins were injected into the mice and rabbits for the production of antibodies.

Our study is the first large-scale epidemiological study in South Korea showing diverse NoVs genogroups and a potential novel strain from a large number of samples from eight hospitals located in a variety of provinces. Continuous epidemiological studies and fast detection system of NoV infections in South Korea are necessary to address effectively and efficiently and solve public health problems in South Korean communities.