

Video Article

MOLECULAR DETECTION AND GENETIC DIVERSITY OF NOROVIRUS INFECTIONS AMONG CHILDREN IN A PERI-URBAN COMMUNITY IN PERU

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Abstract

Norovirus (NoV) is an important cause of acute gastroenteritis in young children. Norovirus genogroups I and II are the main genogroups that affect humans, each comprising many genotypes. Screening and genotyping of NoV were carried out from stool samples from children living in a peri-urban community in Lima, Peru. Since knowledge on NoV infections in Peru is limited, knowing the frequency and type of NoV infections in a cohort study would allow us to obtain baseline information on this important virus. A total of 1000 stool samples obtained from a community based-epidemiology study were screened for presence of NoV. We used real time RT-PCR with specific GI and GII TaqMan probes that target the open reading frame 1 (ORF1)-ORF2 junction region of NoV genome. Sequences from the N-terminal and shell (N/S) region in the capsid region of NoV genome were amplified by conventional RT-PCR for specific GI and GII genotype analysis by sequencing and further phylogenetic analysis. The screening yielded a total of 14.3% NoV, of which, 1.8% were GI, and 12.5% were GII and 0.4% were co-infections of GI and GII. Genotyping by nucleotide sequencing analysis of the N/S region in the capsid gene revealed three genotypes of genogroup GI (GI.3, GI.5, and an unidentified cluster) and four genotypes of genogroup GII (GII.3, GII.4, GII.6, and an unidentified cluster). The frequency of NoV in the community under study was 14.3% of which 55.7% were of genogroup II. Genotyping revealed that at least six genotypes of each genogroup with unidentified clusters of each genogroup circulated in the community.

Disclosures

No conflicts of interest declared.