

Investigation of group A rotavirus G10, G12 genotypes emerging in patients with acute gastroenteritis in a tertiary care hospital

ABSTRACT

Rotaviruses are the most common cause of viral gastroenteritis with the highest mortality and morbidity rates in children aged 0-5 years. The aim of this study was to determine the frequency of rotavirus infection in patients whose stool samples were sent to microbiology laboratory to investigate the etiology of diarrhea, to investigate the rotavirus genotypes that are common in our region and G10, G12 genotypes that have recently become common in the world. Fecal samples of 476 patients aged between 0-92 years who applied between November 2016 and February 2018 were studied via immunochromatographic rapid test and enzyme-linked immunosorbent assay (ELISA) methods. ELISA positive samples were studied by nested reverse transcriptase chain reaction (RT-PCR) and genotyped by agarose gel electrophoresis. Rotavirus was found positive in 18.3% and 17% of stool samples by immunochromatographic test and ELISA, respectively. All ELISA positive samples were also detected as positive by RT-PCR. 18.5% of female patients and 15.7% of male patients were found to be positive and rotavirus positivity was not statistically significant between genders. The frequency of rotavirus in different age groups was 23.5% (6-12 years), 17.3% (13-24 months) and 16% (25-36 months). It was determined that rotavirus cases were most common in the spring. G1, G2, G3, G4, G9, G10, and G12 were detected in 37%, 7.4%, 16.1%, 6.2%, 9.9%, 2.5%, 26% of the samples, respectively. G12 was the most common genotype after G1. The most common G and P genotype combination was G1P[8] (17.2%). This was followed by G12P[8] (11.11%) and G3P[8] (11.11%). P[8] (53%) was found to be the dominant P genotype. In this study, it was observed that rotavirus, which is the cause of childhood diarrhea, can also be encountered in advanced ages and even new genotypes that infect humans worldwide may also be the causative agents. Therefore, we concluded that it is important to investigate new genotypes such as G10 and G12 in molecular epidemiological studies.