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Genotyping of Rotaviruses in Pediatric Patients with Gastroenteritis by Using Real-Time Reverse Transcription Polymerase Chain Reaction

Authors : Recep Kesli, Cengiz Demir, Riza Durmaz, Zekiye Bakkaloglu, Aysegul Bukulmez

Abstract : Objective: Acute diarrhea disease in children is a major cause of morbidity worldwide and is a leading cause of mortality, and it is the most common agent responsible for acute gastroenteritis in developing countries. With hospitalized children suffering from acute enteric disease up to 50% of the analyzed specimen were positive for rotavirus. Further molecular surveillance could provide a sound basis for improving the response to epidemic gastroenteritis and could provide data needed for the introduction of vaccination programmes in the country. The aim of this study was to investigate the prevalence of viral etiology of the gastroenteritis in children aged 0-6 years with acute gastroenteritis and to determine predominant genotypes of rotaviruses in the province of Afyonkarahisar, Turkey. Methods: An epidemiological study on rotavirus was carried out during 2016. Fecal samples obtained from the 144 rotavirus positive children with 0-6 years of ages and applied to the Pediatric Diseases Outpatient of ANS Research and Practice Hospital, Afyon Kocatepe University with the complaint of diarrhea. Bacterial agents causing gastroenteritis were excluded by using bacteriological culture methods and finally, no growth observed. Rotavirus antigen was examined by both the immunochromatographic (One Step Rotavirus and Adenovirus Combo Test, China) and ELISA (Premier Rotaclone, USA) methods in stool samples. Rotavirus RNA was detected by using one step real-time reverse transcription-polymerase chain reaction (RT-PCR). G and P genotypes were determined using RT-PCR with consensus primers of VP7 and VP4 genes, followed by semi nested type-specific multiplex PCR. Results: Of the total 144 rotavirus antigen-positive samples with RT-PCR, 4 (2,8%) were rejected, 95 (66%) were examined, and 45 (31,2%) have not been examined for PCR yet. Ninety-one (95,8%) of the 95 examined samples were found to be rotavirus positive with RT-PCR. Rotavirus subgenotyping distributions in G, P and G/P genotype groups were determined as; G1:45%, G2:27%, G3:13%, G9:13%, G4:1% and G12:1% for G genotype, and P[4]:33%, P[8]:66%, P[10]:1% for P genotype, and G1P[8]:%37, G2P[4]:%21, G3P[8]:%10, G4P[8]:%1, G9P[8]:%8, G2P[8]:%3 for G/P genotype . Not common genotype combination were %20 in G/P genotype. Conclusions: This study subscribes to the global agreement of the molecular epidemiology of rotavirus which will be useful in guiding the alternative and application of rotavirus vaccines or effective control and interception. Determining the diversity and rates of rotavirus genotypes will definitely provide guidelines for developing the most suitable vaccine.

Keywords : gastroenteritis, genotyping, rotavirus, RT-PCR
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