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Abstract (poster session)

A novel study on rapid molecular characterisation of group A rotavirus in Turkey using PCR-reverse line blot hybridisation

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Objectives: Group A rotavirus related acute gastroenteritis in infants and young children has evolved a significant impact on morbidity and mortality not only in developing but also in developed countries. The study was done to determine the diversity of co-circulating rotavirus strains in Turkey, and to provide a baseline for future assessment of possible effects of vaccine implementation in selecting novel versus common rotavirus strains. Detection and genotyping of rotavirus strains from stool samples in children with gastroenteritis in Turkey were examined using polymerase chain reaction-reverse line blot hybridization (PCR-RLB). Compared to conventional RT-PCR, PCR-RLB has known to be more robust, cheap, time saving and suitable to be implemented in developing country. **Methods:** Stool samples were collected from 495 paediatric patients with acute gastroenteritis and screened for rotavirus infection from several hospitals in Turkey. The samples were provided by different paediatric clinics in Anatolian regions of Turkey such as Afyon, Bursa, Istanbul, and Ankara from May 2010 through May 2011. **Results:** Of 495 stool samples, 238 samples were rotavirus ELISA positive and subsequently characterized by PCR RLB. Most of strains (97%) belonged to genotypes G1–G4, and G9, associated with either P[8] or P[4], commonly found in humans worldwide. We found that the percentage of G1P[8] is a predominant strain of Rotavirus (43,3) and followed by G4P[8] (26,5), G9P[8] (19,3), G2P[4] (13), G2P[8] (1,7), G1P[4] (1,3), G12P[8] (1,3), G12P[4] (1,3), G9P[4] (0,8) and G4P[6] (0,4). In 22,1 % of cases, viruses exhibited either a G or P type typical of animal viral strains (G9 and G12), suggesting gene reassortment events between rotaviruses of different origin. Novelty, this study has characterized G12 as a newly emerging genotype in Turkey. In addition, we detected 17 patients with mixed infection in RLB hybridization membrane. However, there were untypable G genotype in 30 patients and P genotype in 6 patients. **Conclusion:** The numbers and genotypes of likely natural reassortants of common genotype rotaviruses were found to be correlated with the observed numbers and genotypes of mixed infections. Large variation in the relative frequency of different rotavirus genotypes was observed between different seasons and/or areas of Turkey, suggesting independent evolution or differential introduction of viral strains with respect to both time and space.