

RNA Electrophoretic Patterns and Phylogenetic Analysis of Rotavirus Genotypes [Ptype] (VP4) in Children with Acute Gastroenteritis in Tehran-Iran

Eskandarian S, Modarres Gilani SH, Rahbarimanesh AA, Nategh R, Edalat R, Sohrabi A, Motamedi Rad M, Sayari AA*

* samiraeskandarian@yahoo.com

ABSTRACT

Background and objective: Acute gastroenteritis has been established as the major public health problem in worldwide children. Rotavirus is the most important etiological agent of gastroenteritis among children, It is also major cause of children malnutrition. Rotavirus, which is a member of the reoviridae family, has a genome 11 dsRNA segment that are enclosed in a triple-layered capsid. Rotaviruses are classified into G-type and P-type. Therefore, determining the prevalent and types of rotaviruses within region is essential to prepare for introducing a vaccine. The genotype diversity of group A human Rotavirus and phylogenetic analysis of P-type detected by RT-PCR and DNA-Sequencing.

Material and method: A total of 285 stool specimens were collected from children with diarrhea admitted to two pediatric hospitals in Tehran-Iran. Stool samples positive in RNA-PAGE were genotyped by Multiplex RT-PCR method. P-genotypes of rotavirus isolated were sequenced between 2008 and 2010.

Result: We found relatively high prevalence rate of rotavirus gastroenteritis in children. 29.1% stool specimens were positive. P [8] (81.92%) was the dominant of genotype, followed by P [4] (8.4%), P [6] (7.2%) and mix type (2.4%). The peak of incidence was in the winter. A few sequence of P-genotypes strains isolated showed high level of similarity to strains from other Asian countries.

Conclusion: we reported the VP4 genotype of rotaviruses –associated childhood diarrhea with high prevalence of P [8] genotype. Rotavirus strain surveillance programs are important for future vaccine formulation in Iran.

Keywords: Human Rotavirus; VP4; Gastroenteritis; Genotype