Abstract

In the present study, molecular surveillance of rotavirus strains prevalent in Haryana was carried out. Rotavirus constitutes the largest proportion of diarrhea associated morbidity and mortality in children below five years of age. India accounts for one fifth of global rotavirus diarrhea associated mortality. The Indian Government has accepted the recommendation of WHO to include rotavirus immunization in the national vaccination schedule. A very robust pre-vaccination surveillance of Rotavirus strains prevalent in various Indian states is a prerequisite for a successful rotavirus vaccination program. Percent positivity of 21.95% in the 410 diarrheic stool samples collected during a two year span indicated the significant Rotavirus disease burden in Haryana.

Long electropherotypes were most commonly detected (86.66%) in this part of the country with the exception of one case where the exact clustering pattern of genomic RNA segments could not be interpreted. Rotavirus incidence was highest in the age group of 6 to 23 months, which constitute more than 65% of disease burden. A clear association of seasonality (colder months) with increased rotavirus infection was established in this study. A total of 74.4% of positive samples could be G- genotyped using published typing primers whereas 71.1% could be P- genotyped with the published primer set by seminested RT-PCR. VP4 and VP7 gene of these untypeable samples were cloned and sequenced. Further genotyping on the basis of nucleotide sequence was done by RotaC tool.


Haryana G1P[8] strains exhibited more amino acid variations with 116E as compared to Rotarix and RotaTeq. Mutation at position 96 observed in Haryana G2, is capable of escaping Rotarix induced immune response. Haryana G9 strains displayed maximum similarity with 116E vaccine. Haryana G12 strain displayed very less similarity with all the existing vaccines and high amino acid difference at important antigenic epitopes.

Local circulating P[8] & P[4] exhibited very low similarity with Indian vaccine 116E whereas P[6] exhibited high amino acid difference with all the existing vaccine. Interestingly, Haryana rotavirus VP6 gene displayed high similarity with bovine rotavirus strains as compared to human strain, indicating the occurrence of reassortment. Haryana strains NSP4 gene displayed high amino acid difference with the RotaTeq NSP4 gene as compared to 116E & Rotarix. qRT-PCR standardized in study detected G1P[8], G2P[4], G9P[8] & G12P[6] strains but could not detect G9P[11]. The assay was found 2 log more sensitive than reverse transcription PCR and 6 log more sensitive than ELISA & PAGE. The present study reports high rotavirus positivity in diarrhea cases and some of Haryana strain exhibited mutations capable of escaping vaccine induced immune response. This underscores the need of continuous molecular surveillance of rotavirus in this region.