List of Publications
Publications

Publications on Ph D research work


5. Vaishali S Tatte and Shobha D Chitambar. Multiple gene characterization of rotavirus strains: Evidence of discordance in genetic linkage among the VP7, VP4, VP6 and NSP4 encoding genes. (Communicated).

Other Publications


Tatte VS, Gentsch JR, Chitambar SD.
Rotavirus Group, National Institute of Virology, Pune, India.

Abstract
A total of 1,591 fecal specimens were collected in 1993-1996 and 2004-2007 from adolescents and adults with acute gastroenteritis in Pune, India for detection and characterization of rotavirus. At the two time points, group A rotavirus was detected in 8.6% and 16.2% of the adolescents and 5.2% and 17.2% of the adults, respectively. Reverse transcription-PCR with consensus primers followed by multiplex genotyping PCR detected common strains G1P[8], G2P[4], G3P[8], and G4P[8] in a total of 53.1% of the samples from 1993 to 1996, while the only prevalent strain identified in 2004-2007 was G2P[4] (23.5% of total). Uncommon rotavirus strains (G1P[4], G2P[8], G9P[6]P[4]) increased from 7.8% (1993-1996) to 41.2% (2004-2007), while the prevalence of mixed rotavirus infections was high (39%/35%) at both time points. Mixed infections detected by multiplex PCR were confirmed by sequencing two or more individual genotype-specific PCR products of the VP7 and VP4 genes from the same sample. Phylogenetic analysis of the sequences showed circulation of a heterogeneous rotavirus strain population comprising genotypes G1 (lineages I and Iib), G2 (lineages I and Iib), G4 (lineage Ia), P[4] (lineages P[4]-5 and P[4]-1), P[8] (lineages P[8]-II and P[8]-III), and P[6] (M37-like lineage). The VP6 gene sequences of the nontypeable strains were most homologous to animal strains. This study documents the molecular epidemiology of rotavirus strains in adolescents and adults in India, and suggests that it may be important to monitor these strains over time for the potential impact on rotavirus vaccines under development for use in the Indian population. J. Med. Virol. 82:519-527, 2010. (c) 2010 Wiley-Liss, Inc.

PMID: 20087938 [PubMed - indexed for MEDLINE]

Sequence and phylogenetic analysis of the VP6 and NSP4 genes of human rotavirus strains: evidence of discordance in their genetic linkage.

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Abstract

NSP4 and VP6 genes of a total of 118 rotavirus strains detected in adolescent and adult cases of acute gastroenteritis (AGE) in 1993-1996 and 2004-2007 were characterized to determine their diversity and genetic linkage. Eighty-two percent and 89% of the strains showed amplification of NSP4 and VP6 genes respectively in RT-PCR. Sequencing and phylogenetic analysis of the VP6 genes showed distribution of genogroups in the lineages 1-1 (1.4%), 1-2 (50.7%) and 11-4 (47.9%) in the 1990s and 1-2 (73.5%) and 11-4 (26.5%) in 2000s, indicating diversity in genogroups at both time points. Amino acid divergence within the genogroup II strains from 1990s and genogroup I strains from the 2000s was noteworthy (4.7-6.7%). Sequencing and phylogenetic analysis of the NSP4 genes showed almost equal distribution (45.0-55.0%) of genotypes A and B however, higher amino acid divergence within the genotype B strains (up to 9.3%) than in genotype A strains (up to 2.9%) at the two-time points. Nearly 70% of the strains showed NSP4-A-VP6-I or NSP4-B-VP6-II genetic linkage. The discordance in the linkage noted in 29.7% of the strains was predominated by NSP4-B and VP6-I combination and appeared strikingly high in the infections caused by unusual and mixed rotavirus strains. This is the first report to describe the phylogenetic analysis of rotavirus NSP4 and VP6 genes and their discordance in adolescent and adult cases with AGE from India. The extensive diversity within the rotavirus genes and their relationship revealed by this study emphasizes the need for evaluation of the rotavirus vaccines being used currently. Copyright 2010 Elsevier B.V. All rights reserved. PMID: 20542145 [PubMed - in process]

Tatte VS. and Chitambar SD.

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Abstract:

Genetic variability of rotaviruses circulating in Pune, India at the two time points was determined by characterizing VP4 genes in 131 rotavirus strains detected in adolescent and adult cases of acute gastroenteritis. The multiplex RT-PCR classified the VP4 genes in 73 P[4] (43.2%), 69P[8] (40.8%) and 27 P[6] (16.0%) genotypes. Sequencing and phylogenetic analysis revealed increase in the prevalence of P[4]-5 and P[8]-2 and decline of P[8]-3 lineages in 2000s as compared to those identified in 1990s (92.8% Vs 100%, 4.2% Vs 33.3%, and 93.7% Vs 66.7% respectively). Low level circulation of the P[4]-1 (7.1%) and P[8]-4 (2.1%) and presence of only P[6]-1 lineages was also detected at both time points. The strains with different VP4 genotype specificities displayed 0.2-2.3% amino acid divergence and a significant difference (P<0.01) in their association with common and nontypeable G strains between the two time points studied.

This is the first report to describe the intragenotypic diversity in the rotavirus VP4 genes from adolescent and adult patients of acute gastroenteritis from India. VP4 being one of the major protective antigens, monitoring the mutations in this protein would be crucial to understand the evolutionary changes in rotaviruses and devise more effective vaccine strategies in developing countries.

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Diversity in the VP7 encoding genes of rotavirus strains recovered from adolescent and adult cases of acute gastroenteritis

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Abstract:

A study was conducted to examine the diversity in the VP7 genes of rotavirus strains circulating in adolescent and adult cases of acute gastroenteritis during two different time periods, 1993-1996 and 2004-2007. The multiplex RT-PCR carried out on 131 rotavirus positive fecal specimens detected 65 (49.6%) single and 48 (36.6%) mixed infections of VP7 genotypes that included 43G1 (38.1%), 37G2 (32.7%), 8G3 (7.1%), 15G4(13.3%) and 10G9(8.8%) specificities. Sequencing and phylogenetic analysis of the VP7 gene amplicons revealed the presence of G1-IA (4.7%), G1-IB (69.8%) and G1-IC (25.5%) lineages within the G1 strains, G2-Iib1 (70.3%) and G2-Iib2 (29.7%) lineages within G2 strains, G3-3S1 (12.5%) and G3- 3S4 (87.5%) lineages within G3 strains, G4-la (6.7%) and G4-lb (93.3%) lineages within G4 strains and G9-III lineage within G9 strains. The variability within VP7 genotypes was evident by 1.4-8.0% and 1.3-3.9% amino acid divergence respectively from the prototype strains and between the groups of strains at the two time points.

This is the first report describing the phylogenetic analysis of VP7 genes of rotaviruses from adolescent and adult cases of acute gastroenteritis in India. As adults infected with rotavirus could act as a source of infection and affect the epidemiology of rotaviruses in children, genetic analysis of the rotavirus strains circulating in adults is required. The intragenotypic diversity within VP7 genes demonstrated by the present study highlights the need for constant surveillance of rotavirus infections to understand better the evolution and transmission of group A rotaviruses in the community.