



Molecular characterization of G and P rotavirus genotypes, G9 strain, from children with acute gastroenteritis in the Metropolitan Region of Belém, Pará State, from 1999 to 2007

Caracterização molecular dos genótipos G e P de rotavírus, cepa G9, de crianças com gastroenterite aguda na Região Metropolitana de Belém, Estado do Pará, de 1999 a 2007

Caracterización molecular de los genotipos G y P de rotavirus cepa G9, de niños con gastroenteritis aguda en la Región Metropolitana de Belém, Estado de Pará, de 1999 a 2007

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Abstract

Rotavirus (RV) is the major viral agent associated with gastroenteritis and is responsible for 39% of all diarrheal cases requiring hospitalization, as well as approximately 520 thousand deaths among children under five years of age. Rotavirus belongs to the *Reoviridae* family, genus *Rotavirus* and its genome consists of 11 segments of double-stranded RNA which encode six structural viral proteins (VPs) and six non-structural viral proteins (NSPs). VP4 and VP7 proteins make up the outer layer of the RV particle and define the two genotypes, P and G, respectively. To date, at least 23 G genotypes and 31 P genotypes have been identified. G9-type RV strains, which are associated with a more severe disease in humans, have emerged globally. Dual type-specificities have been reported, and G9 strains most often belong to the P[8] genotype. While G9 genotype includes six distinct lineages, four distinct lineages are currently recognized as belonging to the P[8] genotype. The aim of this study was to characterize the VP4 and VP7 genes of the RV G9 genotypes that circulated in the Metropolitan Region of Belém, Pará, in northern Brazil from 1999 to 2007. The viral dsRNA of 38 samples was extracted from fecal suspensions and analyzed using polyacrylamide gel electrophoresis to determine electropherotypes, followed by sequencing reactions. Overall, 32 selected G9P[8] samples were analyzed, all of which possessed long electropherotype. Phylogenetic analysis of the VP7 gene showed that all G9 strains belonged to lineage 3 with a high degree of similarity between them; only eight nucleotide changes have been detected in this lineage. However, only three of these amino acid substitutions were observed in our study, occurring at positions 43 (I→V), 66 (A→V) and 73 (Q→R). Of interest, the substitutions at positions 43 and 73 were only found in samples from 2007. Phylogenetic analysis of the VP4 gene revealed that all of the P[8] strains belonged to lineage 3, with 15 nucleotide changes corresponding to four amino acid substitutions at positions 108 (V→I), 172 (R→K), 173 (I→V) and 275 (K→R). The amino acid substitutions at positions 172 and 275 were observed only in RV isolates from 1999 to 2002. Overall, the RV G9 samples showed high homology throughout the entire study period. Interestingly, strains isolated in 2007 were the most divergent with respect to both VP4 and VP7 genes. Our data underscore the need for continuous surveillance of circulating RV strains in our region to detect the emergence of new genetic variants that would pose a challenge to current RV immunization strategies. This should include close monitoring of the genetic diversity of emerging G9 strains.

Keywords: Genetic Variation; Genotype; Gastroenteritis.

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