

Molecular epidemiology of rotavirus G2 infection over a 16-year period (1992-2008) in the Amazon Region of Brazil*

Epidemiologia molecular de rotavirus genótipo G2 na Amazônia Brasileira ao longo de 16 anos (1992-2008)

Epidemiología molecular del rotavirus genotipo G2 en la Amazonía Brasileña durante 16 años (1992-2008)

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Introduction: In Brazil, it is estimated that rotavirus (RV-A) annually causes 3,352,053 episodes of diarrhea, 655,853 visits to emergency rooms, 92,453 hospitalizations and 850 deaths involving children under 5 years of age. Rotavirus belongs to the family *Reoviridae*, genus *Rotavirus*. The viral particle consists of three concentric layers of protein and the viral genome of 11 segments of double-stranded RNA. As based on molecular approaches, there are currently 23 G genotypes and 31 P genotypes, of which strains bearing G1P[8], G2P[4], G3P[8], G4P[8] and G9[P8] dual type-specificities are of importance as a cause of human disease. Among the G genotypes detected so far, G2 represents one of the most important, and it is usually associated with the P4 genotype. The re-emergence of genotype G2 of RV has been observed on a continental scale early after introduction of rotavirus vaccines in several Latin American countries.

Objective: This study was aimed at the molecular characterization of samples of G2 strains obtained from children participating in several studies on RV-A gastroenteritis in the Amazon Region of Brazil, from 1992 to 2008. **Materials and**

Methods: We selected 53 rotavirus G2 samples that were sequenced for VP7 and 38 samples for VP4. These samples were genotyped by RT-PCR, and all products were purified, quantified and sequenced. Samples were also subjected to electrophoresis of RNA segments. The obtained sequences of VP4 and VP7 genes were aligned and edited using the program Bioedit (v.6.05), and compared with other sequences registered in the RVA GenBank using the BLAST program. A phylogenetic tree was made using the program Mega 2.1. **Results and Discussion:** Of the 53 total samples sequenced for the VP7 gene, phylogenetic analysis revealed two lineages (II and III) and three sublineages (IIa, IIc, IIe), which circulated in the population during different periods. Samples of sub-lineages IIa and IIc showed a mutation at aminoacidic position 96 (Asp/Asn). This modification may result in a conformational change of epitopes recognized by anti-RV neutralizing antibodies. The G2 strains circulating in Belém, Pará State, Brazil were identical to those circulating in other states of the Amazon Region that were included in the study. The VP4 gene was sequenced in the region of VP8*, yielding 36 isolates that belonged to genotype P[4] and three that belonged to genotype P[6]. We could identify two strains: P[4]-4 occurred from 1998-2000; P[4]-5 occurred during the 1993-1994 and 2006-2008 time periods. Our findings sustain recent reports indicating a worldwide reemergence of G2 genotypes of variant IIc, which were established in the population in combination with genotype P[4]-5. **Conclusion:** The high homology among the G2 strains circulating in the various states covered in this study suggests that detected mutations have surpassed geographical and temporal barriers. Our analysis was targeted at VP7 and VP4 genes only and this may not fully reflect the potential variability of circulating G2 strains; further studies are therefore needed to assess full genomic characterization.

Keywords: Rotavirus Infections; Diarrhea, Infantile; Molecular Epidemiology; Genotype; Reverse Transcriptase Polymerase Chain Reaction.

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