variability of HBoV is low and phylogenetic studies indicate that there are two strains circulating alongside around the world. However, as it is still a relatively new virus, more detailed studies of its variants should be carried out. In our study, 955 samples of nasopharyngeal aspirate from children under 2 years old with acute respiratory disease, patients at Santa Casa de Misericordia Hospital, São Paulo, were analyzed from February 2008 to February 2010 in order to determine the prevalence and genetic variability of HBoV stock. Using the PCR method, we obtained 47 (4.8%) positive samples for HBoV from which 27 showed coinfection with other respiratory viruses; 45 samples from a fragment of 658 nt were sequenced in the VP1/VP2 region. The phylogenetic analysis, when compared with GenBank sequences representing several countries, showed the presence in our samples of species 1 of HBoV similar to those circulating in Japan and Taiwan. Genetic variation in our samples were below 2%, both among themselves and when compared with samples from the GenBank of the same genotype. Financial support: FAPESP e CNPq

Palavras-chaves: Human Bocavirus, Molecular Biology, Genetic Variability, Respiratory.

MOLECULAR CHARACTERIZATION OF G AND P GENOTYPES OF ROTAVIRUS AMONG CHILDREN LESS FIVE YEARS IN THE AMAZON REGION

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Área: 05 - Virologia Humana e Saúde Pública

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Group A rotaviruses (RVs-A) are the most common etiological agents of severe diarrhea in children less five years, causing an estimated 611,000 deaths annually worldwide. Rotavirus genus belongs to the Reoviridae family and its genome has been divided into 11 segments of double-stranded RNA (dsRNA). Proteins VP4 and VP7 define P and G genotypes, respectively. This study aims to characterize G and P genotypes of rotavirus circulating in the Amazon region during August 2009 to June 2010. Fecal suspensions were prepared, dsRNA was extracted and subjected to PAGE. RNAs were transcribed with reverse transcriptase and amplified by the polymerase chain reaction (PCR) using primers 4con2/4con3 (VP4) and end9/beg9 (VP7), followed by Nested-PCR. The RT-PCR products were purified, quantified and subjected to automated sequencing. Phylogenetic analysis was performed using the programs BLAST and MEGA 3. From August 2009 to June 2010, 96 samples were received of IEC from LACENS for detection of RVs-A, all being subjected to PAGE and RT-PCR. Of the 45 samples analyzed by Nested-PCR were identified G2 genotypes in 27.7%, G9 in 12.8% and G12 in 5.5%. The genotypes P [4], P [6] and P [8] were found in 31.2%, 6.2%, 46.8%, respectively. Twenty nine percent (13/45) of the RT-PCR products were subjected to sequencing. The samples of G9 genotype grouped into lineage III, G2 genotype into lineage II and G12 genotype into lineage III. P [4] genotype samples grouped into lineage 5, P [8] genotype into lineage III and P [6] genotype into lineage I of the dendrogram. The several possibilities of binary combinates between the P and G genotypes can lead to the emergence of new genotypes. Therefore, our findings provide evidence of great diversity concerning circulation of usual and unusual genotypes of rotavirus in the Amazon region by hence improving our knowledge on the molecular epidemiology of RVs-A infection in our region. Financial support: IEC/SVS/MS

Palavras-chaves: children, diarrhea, genotypes, rotavirus.

MOLECULAR ANALYSIS OF VP1 AND VP3 GENES OF ROTAVIRUSES CIRCULATING IN BELÉM, PARÁ, BRAZIL

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Rotavirus are the major etiological agents of viral acute gastroenteritis in infants and young children and constitute an important cause of infantile mortality in developing countries. Currently, 4 and 6 genotypes are described for VP1 and VP3 rotavirus genes, respectively. This study aimed to characterize rotavirus genes that encode VP1 and VP3 structural proteins of G1, G2, G3, G4 and G9 rotavirus genotypes circulating in Belém, Pará, before and after universal vaccine introduction in Brazil (Rotarix®). A total of 19 fecal samples were collected between 1997 and 2008 from children
hospitalized due to acute diarrhea. Fecal suspensions were prepared and viral genome was extracted. Subsequently, dsRNA was reverse transcribed and amplified by polymerase chain reaction for partial VP1 and VP3 genes using consensus primers. PCR products were purified and sequenced automatically. The sequences obtained were compared and made available to GenBank database. The phylogenetic analysis was performed using MEGA3 software. Twelve samples were selected in pre vaccine period and 7 samples in post vaccine period. VP1 and VP3 genes were amplified in all specimens. With respect to VP1 gene, samples denoted a R1 pattern in 79% (15/19) and R2 in 21% (4/19) of cases. Two samples were more similar to porcine prototypes of strains when VP1 genes were compared. With regards VP3 gene, were identified M1 (79%,15/19) and M2 (21%,4/19) types circulating. It was observed that samples bearing R1 type-specificity were related with M1 genotype and those R2 type with M2 specificity. Sample RV101099 (G3P[8]) showed a high homology for VP1 and VP3 genes with bovine prototypes and was classified as R1M1. The current work is the first report about VP1 and VP3 molecular characterization of rotavirus in Northern of Brazil. These results help to improve the knowledge on the genomic diversity of such viral agents, and may have potential importance in the interspecies transmission events. Financial support: CNPq.

**Palavras-chaves:** diarrhea, rotavirus, structural proteins.

**Fragile temporal trends among HIV-1 BF1 recombinant samples in Rio de Janeiro**

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HIV-1 molecular epidemiology studies carried out in Rio de Janeiro (RJ), Brazil, have identified the occurrence of subtypes B, F1, B’ and BF1 recombinants. This study tries to trace the temporal dynamics of the HIV-1 BF1 recombinant forms from 1990-2010 in RJ, Brazil. The HIV-1 proviral DNA of ninety six males from three distinct time periods, 1990-1992; 1998-2002 and 2006-2010, of the RJ Aids epidemic was extracted and genetically characterized based on protease/reverse transcriptase (PR/RT) and C2-V3/env regions. The PCR products were sequenced, and aligned according to reference sequences of the distinct HIV-1 subtypes. Phylogenetic analysis was performed to determine their recombination profiles (Bootscan analysis-Simplot) and to infer the phylogenetical relationship among them and with those CRF_BFs already described. Phylogenetic analysis of the C2-V3/env and PR/RT regions was carried out for the three time periods. From the 36 HIV-1 samples collected from 1990-1992, 40,5% samples were characterized as subtype B, 40,5% as B’, 5,4% as F1 and 13,6% as BF1 recombinants. From the 20 samples collected from 1998-2002, 55% were subtyped as B, 15% as B’, 10% as F1 and 20% as BF1 recombinants. From the 38 samples collected from 2006-2010, 56% were classified as B, 26% as B’, 5% as F1, 10,5% as BF1 and 2,5% as F1C recombinants. The phylogenetic relationship among BF1 recombinant samples and those CRFs_BF previously described was investigated, and most of the study samples was characterized as URFs, one sample were classified as CRF40_BF1-like and two samples was CRF12_BF1- related. Our findings indicate that CRF40_BF has been circulating since the begging of AIDS epidemic in Rio de Janeiro. A fragile temporal trend among the HIV-1 BF1 recombinant samples were verified, probably, as a consequence of a reduced phylogenetic relationship among them.

**Palavras-chaves:** HIV-1, Subtypes, recombinant, Rio de Janeiro.

**HEAVY CHAIN ANTIBODIES: AN ALTERNATIVE TOOL TO TREAT YELLOW FEVER**

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**Área:** 01 - Imunobiológicos

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Yellow fever (YF) is a viral hemorrhagic febrile disease caused by a Flavivirus and transmitted by insects of the Culicidae family. Despite prophylactic treatment through vaccination, about 200000 cases per year of sylvatic and urban YF are reported worldwide. The problem of how to treat patients with YF or with vaccine-associated adverse effects represents a significant gap in disease management. In addition to conventional antibodies, camelids produce immunoglobulins G composed exclusively of heavy chains, in which the antigen binding site is formed only by the single domain, called VHH. The VHHs have several advantages when compared to murine or human antibodies; besides their small size