viruses and bacteria detected in adenoid and middle ear secretion, and in only 5 (13%) there was agreement between middle ear and nasopharyngeal secretions. The data strongly indicate that SOM is not directly caused by any of the viruses or bacteria tested, but their presence is likely due to stasis of secretions and biofilm consequent to the mechanical obstruction of the Eustachian tube by hypertrophic adenoids. Financial support: FAPESP, CAPES and CNPq.

**HV416 - GENOTYPIC CHARACTERIZATION OF ROTAVIRUS STRAINS IN CHILDREN HOSPITALISED FOR ACUTE DIARRHEA IN BELÉM, PARÁ, BRAZIL IN POST-VACCINE INTRODUCTION PERIOD**


Gastroenteritis is the second leading cause of death, being rotavirus (RV) is the most common enteropathogen, accounting for an estimated 453,000 deaths in children <5 years in 2008. The RV is devoid of envelope with genome composed of 11 segments of double-stranded RNA (dsRNA) that codes for 12 proteins. The VP4 and VP7 proteins make-up the outer layer shell of the RV particle and define 37 P and 27 G genotypes, respectively. The public health impact of RV disease, its genotypic diversity and the need for assessing vaccine effectiveness are among current priorities. In addition, the monitoring of circulating strains rotavirus vaccine introduction is strongly recommended, since new or emerging strains may pose a threat to vaccination strategies. Objective (s): Genotypic characterization of previously untyped rotavirus strains obtained from children hospitalized for diarrhea after countrywide introduction of rotavirus vaccine. Material and Methods: Stool specimens were obtained during a case-control study to assess vaccine effectiveness in Belém, Pará, Brazil, from May 2008 to May 2011. A total of 122 previously G and/or P untyped, were selected. Of these we could examine 76 in this study, 44 of which only were not G-typed, 16 only were not P-typed and 16 were not typed for G and P. The viral dsRNA of samples were extracted from fecal suspensions and submitted to RT-PCR and seminested PCR, using primers to G and P genotypes not usually detected. PCR products were subsequently purified and sequenced. Results: For G, 56 samples were possible typed by subjected to either seminested-PCR or sequencing reaction we identified: G1 types (5.4%, n=3), G2 (3.6%, n=2), G3 (1.8%, n=1) and G12 (89.3%, n=50). P genotype was characterized in 27 samples by sequencing reaction, with the following specificities: P[4] (29.6%, n=8), P[6] (11.1%, n=3), P[8] (44.5%, n=12) and P[9] (14.8%, n=4). The dual characterization was determined for 67 samples (88.2%), among which the unusual combinations G12P[6] (68.7%, n=46), G12P[9] (3%, n=2) and G3P[9] (1.5%, n=1) were identified. Conclusion: The identification of unusual genotypes among samples not previously typed underscores the importance of continuous monitoring and characterization of circulating RV strains, particularly in the current scenario of post-vaccine introduction in Brazil. Possible circulation of new or unusual genotypes may represent a challenge to current vaccination strategies. FINANCIAL SUPPORT: FAPESP, IEC

**HV420 - LOSS OF DISEASE CONTROL AFTER SUPERINFECTION OF A LONG TERM NON PROGRESSOR HIV-1 POSITIVE INDIVIDUAL FROM RIO DE JANEIRO, BRAZIL**

Caetano, D.G.; Côrtes, F.H.; Vorsatz, C.; Grinsztejn, B.; Veloso, V.G.; Bello, G.; Morgado, M.G.

1. Laboratório de Aids e Imunologia Molecular IOC/FIOCRUZ - Instituto Oswaldo Cruz da Fundação Oswaldo Cruz, Av. Brasil, 4365, Manguinhos, Rio de Janeiro - RJ, 21040-360

2. Instituto de Pesquisa Clínica Evandro Chagas - Fiocruz, Av. Brasil, 4365, Rio de Janeiro, RJ, 21040-360

Long Term Non Progressor (LTNP) patients are a rare segment of the HIV-1+ population that maintain high levels of T-CD4+ cells for more than 8 years after infection in the absence of antiretroviral therapy. Some studies identified infected LTNP with more than one viral lineage with divergent effects in pathogenesis, characterized by maintenance or loss of progression control. Here we report the case of a LTNP diagnosed in year 2000 and that has been shown control of the T-CD4+ cell levels (median of 1093 cells/mm3; IQR