pathogenic CoV were isolated from humans, CoV SARS (Severe Acute Respiratory Syndrome) and the CoV MERS (Middle East Respiratory Syndrome) with a mortality rate of 10 and 42%, respectively. Subsequent studies have identified CoV in bats all over the world including CoV with great genetic similarity and capable to use the same cell receptor of SARS and MERS CoV. Despite the great diversity of CoV in bats, the large number of bat species in Brazil and the classification of Atlantic Forest Biome (AFB) as a hotspot region for emergence of new infectious disease, studies about the occurrence and diversity of CoV in bats in Brazil are scarce. The present study aims to evaluate the diversity of coronavirus in bats from Urban and Forest Fragments of São Paulo State located inside the Atlantic Forest biome. Intestine samples from bats received by the Center of Zoonosis Control of São Paulo Municipality (N=132) and Oral/Rectal Swabs Samples collected from bats from Forest Fragments, inside or close to São Paulo Metropolitan area, were screened for CoV RNA (N=119). Shortly, total nucleic acid were obtained from 30mg of intestine tissue extracted in NucliSENS® easyMAG® automatic extractor (BioMerieux). cDNA was prepared using random primers and subjected to a modified pancoronavirus Nested PCR. We screened a total of 251 individuals of 31 distinct species including members of Phyllostomidae, Molossidae and Vespertilionidae bat family. Alphacoronavirus RNA was detected in one intestine sample obtained from CCZ SP (Phyllostomus discolor) and 7 swabs samples from bats of Forest Fragments of SP state (Artibeus lituratus, Glossophaga soricina and Sturnira lilium) presenting a general prevalence of 0.7 and 5.9% respectively. CoV sequences obtained from bats of same genus presented high nucleotide sequence with sequences detected in other studies from bats of geographically distant regions. Similar results were previously reported for a variety of bat CoVs and are taken as evidence of coevolution of CoV genotypes and specific host genera. Our results demonstrate the need for expanded and continuing surveillance of CoVs in bat fauna, including those in the AFB regions of Brazil.

**BV202 - MOLECULAR ANALYSIS OF NOROVIRUS SPECIMENS FROM CHILDREN ENROLLED IN A 1982-1986 COLLECTION SAMPLES IN BELÉM, BRAZIL: A COMMUNITYBASED LONGITUDINAL STUDY**

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Several molecular studies have shown a high degree of norovirus (NoV) genetic diversity, and although numerous genotypes are known to infect humans, genogroup II strains have remained dominant in most outbreaks of gastroenteritis (GE) and cases of GE at both hospital and community levels. Specimens were collected during a longitudinal, community-based study carried out in the city of Belém, North Brazil, over 3 years (October 1982 to March 1986), where 20 children were followed up from birth to 3 years of age. A total of 229 samples were screened for NoV by Real Time PCR targeting polymerase gene (RdRp) and the positives were characterized by the regions B (RdRp) and C or D (VP1 gene). In case of a disagreement between the two regions genotyped, the junction region between ORFs 1/2 was considered to suggest a recombination event. Samples classified as GII.P4/GII.4 were analysed by P2 region to determine the current variants. Nucleotide sequences analyses were made by maximum likelihood method with 1000 bootstrap replicates. An overall positivity of 16.1% (37/229) was observed, including GI (16.2% 6/37) and GII (83.8%31/37) genogroups. Cases of NoV reinfection in at least two month intervals were observed and 12 children developed at least one case of asymptomatic NoV infection. 48.6% (18/37) NoV positive samples were subjected to nucleotide sequencing analysis targeting at RdRp gene: GI.P3 (n=1), GII.Pa (n=1), GII.Pc (n=1), GII.P4 (n=5), GII.P6 (n=5), GII.P7 (n=3), GII.P12 (n=1) and GII.P22 (n=1). The VP1 gene allowed the characterization of 14 (77.8%) samples of the 18 previously genotyped: GI.3 (n=1), GII.4 (n=4), GII.6 (n=4), GII.7 (n=1), GII.12 (n=1), GII.14 (n=1), GII.22 (n=1). In three cases were suggested recombination events (GII.P12/GII.2, GII.P7/GII.14, GII.Pa/GII.12) and four samples genotyped as GII.P4/GII.4 were analysed to identify variants, but any one showed contemporary counterparts. Three children developed consecutive NoV infections by different genotypes. The present report documents the importance of NoV as a
cause of childhood infection during a longitudinal study conducted more than 30 years ago, demonstrating prolonged shedding; high prevalence in controls; possible resistance to infections; and relationship between breastfeeding and susceptibility to infections at community level, besides a broad genetic diversity likewise it can be currently observed.

**BV203 - NATURAL HISTORY OF NOROVIRUS INFECTIONS IN CHILDREN FROM BELÉM, PARÁ: A COMMUNITYBASED LONGITUDINAL STUDY**

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Norovirus (NoV) are the most important pathogen when considered outbreaks of AGE in human populations. The genotype GII.4 is the most prevalent worldwide and is responsible by the majority of the global epidemics (pandemics) of viral aetiology. The objective of this study was to detect and characterize the infections by NoV that occurred in children followed up in the community from birth until the three years old, residents in neighbourhoods of low socioeconomic status from Belém, between 1982 and 1986. Fecal specimens were obtained during a community-based longitudinal study whose total of 2,013 samples were collected. It was tested a subset of 216 fecal samples belonging to three children residents in the districts of Barreiro (n=69), Marco (n=77) and Terra Firme (n=70) of which were collected feces fortnightly or when they have diarrhea. Samples were tested by quantitative PCR (qPCR) using the kit Superscript III OneStep RT PCR Systems with Platinum Taq (Invitrogen) for the detection of GI and GII genogroups. Positive samples by qPCR were submitted to Seminested RT PCR reaction using primers JV13I/JV12Y (first step) and JV13I/G1 or JV12Y/NoroIIIR (second step) for GI and GII, respectively. The positive ones were sequenced aiming the partial characterization of region A of the viral polymerase gene. The phylogenetic construction was performed using the method of NeighborJoining Kimura 2 parameters, with bootstrap of 1,000 replicates. The positivity of 14.3% (31/216) was observed, being 13% (28/216) for GI and 1.8% (4/216) for GII. One sample was positive for both GI and GII. It was possible to classify 60.7% (17/28) of GII and 100% (4/4) of GI, being observed the genotypes GII.P4 (58.8%), GII.P6 (11.8%), GILPa (5.8%), GIIinconclusive (11.8%) and GII.Pnew (11.8%). For genogroup I it was observed the genotypes: GLP5 (25%), GL.P7 (25%), GL.Pd (25%) and GL.P (25%). The highest frequency of infection was detected in the age range of 6 to 12 months (p = 0.0024) and it was not determined no seasonality for NoV in the period of study, showing peaks in November 1983, August 1984 and September 1985. These results demonstrated the diversity of NoV in children in the community circulating in the 1980s, causing mainly asymptomatic cases. In addition, it was observed that the GI.4 was the most prevalent genotype since that time. This study contributed to a better understanding of this pathogen in gastrointestinal infections.

**BV222 - EVALUATION OF MYRCIARIA FLORIBUNDA IN VITRO ACTIVITY AGAINST ZIKA VIRUS**


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Zika virus (ZIKV) had an increase in the number of cases reported in the past few years. Diseases like microcephaly and Guillain-Barre syndrome are commonly associated with the ZIKV infection. Due to its upsurge severity studies in the development of medicines to inhibit virus replication have become essential. In this sense, Myrciaria floribunda is a widely spread tree, especially in the north of Brazil, whose essential oil properties have been documented for antimicrobial, anti-inflammatory and antitumor activities. The stem and leaf of M. floribunda were extracted with dichloromethane, ethyl acetate and hexane. To evaluate the antiviral activity of the extracts, VERO cells, growing in 24 wells plates with 1 x 105 cells/well density, were infected with ZIKV (1 x 104 PFU) using 0,1 MOI for one hour at 37°C in 5% CO2 atmosphere. Afterwards, the cells were treated with the extracts in two concentrations, 10 and 30µg/mL, in 5% FBS medium. The cells were lysed by three freezing and thawing cycles, the supernatant was titrated by plaque essay. The plaque remained in an incubator for five days, subsequently the supernatant was removed and crystal violet was added. The inhibition percentage of M. floribunda hexane, dichloromethane and acetate leaf extracts at 30µg/mL was above 85%. On the other