HV360 - DETECTION OF ARBOVIRUS IN ADULT MOSQUITOES TRAPPED IN RIO DE JANEIRO, BRAZIL: IMPROVEMENTS OF THE SURVEILLANCE SYSTEM

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Arthropod-borne viruses (arboviruses) may cause human disease, ranging from mild febrile illness to encephalitis and death. Most of the characterized human pathogenic arbovirus species belong mainly to 3 families: Togaviridae, Flaviviridae, and Bunyaviridae. During the last decade several countries worldwide have been facing the burden of introduction and re-introduction of arboviruses such as dengue virus (DENV), chikungunya virus, Japanese encephalitis virus, and West Nile virus in urban areas. Arboviruses are a very diverse group. In Brazil, DENV is the most important arbovirus causing hundreds of deaths annually. The city of Rio de Janeiro is an important tourist destination. Thus, it has been playing an important role on arbovirus introduction into Brazil. The last DENV epidemic in the state of Rio de Janeiro was caused by co-circulation of DENV serotypes 4 and 1 and the number of cases reached 213,058. Many questions remain unanswered regarding the factors that influence the DENV outbreaks. The ecology of vectors, seasonal variation, abundance of infected mosquito females and the movement of vectors between human modified environment and urban forest may influence the course of DENV epidemics. The present work represent an observational ecologic study of the circulating arboviruses in vectors. Six areas were chosen in the city of Rio de Janeiro and Nova Iguaçu, as trapping sites of adult mosquitoes using BG Sentinel® traps and aspirators. After morphological species identification on chilled tables mosquitoes were pooled according to species and homogenized. Extracted RNA from homogenized mosquito pools was screened by RT-PCR for flaviviruses, alphaviruses, phleboviruses and orthobunyaviruses. After 12 months of continuous trapping 22,202 and 52,000 mosquitoes were collected in the cities of Rio de Janeiro and Nova Iguaçu, respectively. Flavivirus RNA was detected in 01 pool from Rio and 13 pools from Nova Iguaçu, respectively. Sanger sequencing of the amplicons demonstrated the presence of different genotypes of DENV serotype 4 and DENV serotype 2 respectively. Our findings may provide a solid base to determine the underlying causes of the seasonal fluctuations of DENV activity and the relative abundance of the mosquito vector species. This information can be used as a basis for vector control programs and might provide an early warning of the presence of DENV in the state of Rio de Janeiro. Financial Support: FAPERJ, BNI (Germany).

HV361 - ANALYSIS OF VP4, VP6 AND VP7 GENES OF G1P[8] ROTAVIRUS STRAINS CIRCULATING IN AMAZON REGION, AFTER ROTAVIRUS VACCINE INTRODUCTION


Worldwide, it was recently estimated that group A rotaviruses (RVA) account for about 197,000 deaths of children aged 0-5 years, with the major disease burden occurring in low-income countries. The monovalent, oral rotavirus vaccine Rotarix® (GlaxoSmithKline Biologicals, Wavre, Belgium) contains a human-derived G1P[8] rotavirus strain and was introduced into the Brazilian National Immunization Program in 2006. G1P[8] genotype appear dominant in several settings, accounting for approximately 50% of cases of rotavirus-related gastroenteritis during childhood. Several studies have shown the broad antigenic and genetic diversity of RVA strains, hence the importance of monitoring changes at the molecular level - of outer capsid proteins (VP4 and VP7) as well as of the middle capsid protein VP6. Serotype/genotype specificities are defined by outer shell VP7 and VP4 proteins, whereas VP6 relates to group- and subgroup specificities. Objective: To assess the genetic variability of the structural VP4, VP6 and VP7 genes from G1P[8] strains; obtained from stool samples from children hospitalized for acute diarrhea in Belém, Pará, Brazil, from 2009 to 2011. Methodology:
RNA extracts from 8 G1P[8]-positive fecal samples were analyzed. All samples were subjected to polymerase chain reaction preceded by reverse transcription (RT-PCR) and the cDNA was further subjected to sequencing using the Big Dye Terminator® Kit (Applied Biosystems) method, as described by the manufacturer. Results: Sequencing analyses of structural genes VP4, VP6 and VP7 from the 8 G1P[8] strains showed 97.9%, 98.1% and 98.1% nucleotide similarity rates, respectively. When analyzing deduced amino acid sequences of VP6, VP4 and VP7 proteins of G1P[8] samples, similarity rates of 96.2, 94.5%, and 93.1% were observed, respectively. Regarding the lineage of the samples the VP4 gene belonged to lineage 3, the VP6 gene belonged to genotype I1 and regarding VP7 gene all samples belonged to lineage 1. Conclusion: Overall the 8 G1P[8] RVA strains clustered into the same clade, although not grouping into the same lineages for VP4 and VP7 genes of the vaccine samples showing a divergence between the G1P[8] strains circulating in our region and vaccine samples. This study highlights the need for continuous monitoring of rotavirus G1P[8] strains with regards to genetic variability, since the vaccine used in Brazil possesses homologous genotype composition. Key words: Rotavirus, G1P[8] genotype, genes VP4, VP6 and VP7, vaccine

HV372 - HERPESVIRUS DETECTION AND GENOTYPING IN MENINGOENCEPHALITIS IN NORTHERN BRAZILIAN
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Herpesviruses infect more than 90% of the world’s population and persist indefinitely in a latent form. These viruses are large double-stranded DNA and show ability to establish a lifelong latency in sensory ganglia and to invade and replicate in the central nervous system (CNS). Both primary infection and reactivation can cause neurological disease, including meningitis and encephalitis. Herpes meningoencephalitis is a severe neurological condition. It’s the most common cause of sporadic viral encephalitis which is potentially fatal. Usually herpes encephalitis cases are associated with infection by Herpes simplex (HSV-1 and HSV-2). In untreated cases the mortality rate is approximately 70%. This study aims to detect and genotype herpesviruses in cerebrospinal fluid (CSF) of patients with meningoencephalitis from the Northern Brazilian Region, whose samples were sent to the Enterovirus Laboratory of the Evandro Chagas Institute for viral infection research. The study population was predominantly composed of adults (58.5%). Mean age of patients studied was 34 years, and the minimum age 2 months and the maximum 83 years. All CSF samples were subjected to DNA extraction, followed by two PCR reactions - one using consensus primers Herp1/Herp2 for detection of CMV, HSV-1, HSV-2 and EBV that amplify 518bp, and the other for detection of VZV using VP22 and VM20 primers that amplifies 275bp. Herpesvirus genotyping was performed through the automatic sequencing of nucleotide bases. From January to July 2015 were received 65 CSF samples in the Laboratory of Enterovirus. The overall prevalence of herpesviruses was 32.3% (21/65) and EBV was the most prevalent (38.1%), followed by the HSV-1 (33.3%) and VZV (14.3%). We could not identify the genotype in 3 samples (14.3%). The age group was not significantly associated with infection by herpesviruses. The high prevalence of EBV observed in this study may be due to the fact that more than 90% the general population has latent EBV infection. Our data highlight the major role of Herpesvirus as a cause of meningoencephalitis in our region and warrant the conduct of further and broader study on this subject. Keywords: cerebrospinal fluid, Herpes viruses and meningoencephalitis.

HV377 - MOLECULAR PROFILE OF GROUP A ROTAVIRUS IN THE WESTERN AMAZON, BRAZIL
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INSTITUTO EVANDRO CHAGAS

Group A rotaviruses (RVA) are the main etiological viral agents of acute gastroenteritis in children less than five years of age worldwide, resulting in more than 197,000 deaths annually. In 2005, it was recorded the largest outbreak of acute diarrheal disease associated with the RVA in Brazil, with most cases in the city of Rio Branco, Acre state. Objective (s): This study aimed to describe the genotypic variability of RVA in children under five years of age in the city of Rio Branco, Acre, Brazil. Materials and Methods: From January to December 2012, 488