Acute gastroenteritis (AGE) is a major cause of childhood morbidity and mortality worldwide. Among the viruses that cause AGE the sapoviruses (SaVs), members of the Caliciviridae family, seems to be very important since they are associated with sporadic cases and outbreaks of AGE occurring in schools, day care centers and cruise ships. The most frequently observed symptoms on a SaV infection are diarrhea, vomiting and abdominal pain. The virus transmission occurs by the fecal-oral route, primarily through contact person-to-person, intake of contaminated water and/or food, and aerosolized particles generated during episodes of vomiting. The study aimed to detect and genotype SaVs in fecal samples from hospitalized children with and without gastroenteritis in São Luís, MA, during the period of June 1997 to June 1999. Nucleic acids were extracted from SaVs by the silica method and were subsequently tested by RT-PCR using the primers pair P289 and P290. Specimens were considered positive when showing amplicons of 331 bp. The positivity rate was 8.1% (11/136), with 15.2% (7/46) in the diarrheal specimens and 4.4% (4/90) in non-diarrheal ones (p <0.04). One sample was sequenced and classified as GII.1. Of the positive cases, 27.3% were associated with fever, vomiting and anorexia, and 18.2% with fever, anorexia and abdominal pain. The presence of asymptomatic cases reinforces the suggestion that even in the absence of clinical symptoms the virus continues to spread. SaVs detection in samples of children under two years corroborates published data that this age group is the most affected, as well as the highest percentage of positive cases are in the group with clinical manifestation. The genotype found (GII.I) in this study was also detected in Belém, in samples of diarrheic children collected in different years (1998-2000 and 2003) and in Parauapebas in 2006, both in Pará state. Therefore, the results of this research are relevant as they demonstrate the circulation of SaVs in São Luís and reinforce that further studies should be developed, as there is still lack of information regarding the epidemiology of this virus. Financial Support: PIBIC/CNPq Keywords: sapovirus, gastroenteritis, children, São Luís

HV284 - CIRCULATION OF NOROVIRUS PANDEMIC VARIANT GII.4 SYDNEY 2012 AND NEW ORLEANS 2009 IN CHILDREN FROM MANAUS, AMAZONAS, BRAZIL


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Norovirus (NoV) is a enteric pathogen known to cause pandemics of acute gastroenteritis worldwide. In developing countries, its estimated cause 200,000 deaths in children under 5 years old. In the EUA, some authors related that after the increased use of rotavirus vaccine, NoV become the primary cause acute gastroenteritis. Due NoV suffer a dynamic process of mutation and recombination, providing a great genetic diversity and this is the basis for its adaptability. These events have led to the emergence of variant strains, mainly of linage GII.4, which has caused epidemics globally. In 2012, fecal specimens were collected from children until five years old from the city of Manaus, Amazonas, Northern Brazil. The samples were tested for NoV initially by EIE and the positive samples by reverse transcription-polymerase chain reaction (RT-PCR) using a pair of primers with target the polymerase gene. The positive samples identified as GII.4 NoV were tested by PCR and sequenced using the primers EVP2F and EVP2R. These primers were designed to amplify the antigenic region of the viral capsid (VP1 protein), subdomain P2, allowing identification of variants. Samples were sequenced in
Vesiculovirus is a genus in the family Rhabdoviridae. In the Americas, Indiana and New Jersey serotypes of vesiculovirus, are both endemic and responsible for vesicular stomatitis, a disease of cattle, horses and pigs, responsible for important economic losses. In Brazil, it have been reported other vesiculovirus, such as Piry, Carajas, Cocal, Alagoas and Maraba. Curiously, serologic surveys in human populations of different regions of Brazil, have shown approximately 10% of seropositivity to Piry virus. However, the disease produced by Piry virus has not been reported, except for one accidental case in the laboratory. There is a poor knowledge on the human infection and the disease by vesiculovirus as well as a limitation on the diagnosis which is based in serologic tests and performed in few laboratories. Ten years ago, our group reported a conventional RT-PCR to vesiculovirus. As we show in this on going study, the conventional RT-PCR evolved into a SYBR green I-based real-time RT-PCR that amplifies 221 bp of the G gene of Brazilian vesiculovirus. Our preliminary results show that it was able to amplify genomes of 4 Brazilian Vesiculovirus (Piry, Carajas, Alagoas and Indiana) with a higher sensitivity than the conventional RT-PCR. The melting curve of the real time RT-PCR, 81.41 ± 0.50 °C, has shown that it is specific for Brazilian vesiculovirus and do not generate primer-dimers or non-specific products. The sera of 165 patients with acute febrile illness, from Sinop city, in Mato Grosso State, were collected during the dengue outbreak of 2011 - 2012 and tested by the real time RT-PCR and no positive samples were found. This real time RT-PCR is reproducible, specific, and could become a useful tool for the diagnosis of infections. It could also be used in a surveillance program to better evaluate the importance of Brazilian vesiculovirus in human disease. FINANCIAL SUPPORT: FAPESP - Fundação de Amparo à Pesquisa do Estado de São Paulo Nº. 13/14929-1, Fellowship Nº. 13/02256-2, 12/02836-6, 12/24150-9.

HV288 - INFLEUNZA A H1N1 PD09: LABORATORY SURVEILLANCE OF SUSPICIOUS DEATHS OF SEVERE ACUTE RESPIRATORY SYNDROME IN THE STATE OF SAO PAULO, BRAZIL - 2013


IAL - Instituto Adolfo Lutz, Av. Dr. Arnaldo, 355 - Cerqueira César, São Paulo - SP, 01246-000

In April 2009 a new influenza A virus called H1N1pd09 virus was identified in humans resulting in the first influenza pandemic of the 21st century with 5,700 deaths. After this time the pandemic activity is declining, however, the transmission of the virus remains. The disease presents clinical and transmission characteristics similar to those of seasonal influenza.