HV340 - CIRCULATION PROFILE OF RESPIRATORY VIRUSES IN GOIANIA, GOIÁS

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Acute respiratory infection (ARI) remain a major cause of morbidity and mortality in children worldwide, particularly among developing countries. Evaluation of incidence, etiology and seasonal profile of respiratory infections can help to identify risk groups and design health control measures. Although some studies have tried to observe seasonal patterns for respiratory viral infections in Brazil, no data is available for Mid-West region so far. The surveillance for Acute Severe Respiratory Syndrome (SRAG) headed by Brazilian Ministry of Health for Mid-West region have just been established and few results were observed, due to the low number of samples collected. Given that, our study aimed the molecular investigation of viral respiratory pathogens in children from Goiânia – Goiás during one year. Between August 2012 and 2013, 225 children with four to 14 years old were recruited in five healthcare centers. We designed a Multiplex Nested-PCR protocol for detection of 16 common respiratory viruses, divided in three different reactions. Respiratory viral pathogens were detected throughout the entire study period. Viral detection rate showed positive correlation with relative air humidity and rainfall, with positive cases occurring mainly during the rainy season, period of the year comprising months with high relative air humidity (RH) and high amount of rainfall. RSVA and B peaked between January and March 2013, trimester marked by high RH and rainfall. Influenza viruses were detected predominantly between April and June 2013, during the RH fall after a long rainy season. HBoV positive samples peaked at April 2013, and Rhinovirus, which was the most frequent virus detected, showed no clear detection pattern. These findings provide the first data contributing to delineate the circulation profile of respiratory viruses in Goiânia, using molecular techniques and enrich the knowledge about these pathogens in Brazil, especially Mid-West region. Financial Support: Fundação de Amparo a Pesquisa de Goiás - FAPEG.

HV342 - MOLECULAR CHARACTERIZATION OF NOROVIRUS STRAINS DETECTED IN HOSPITALIZED CHILDREN DURING A THREE-YEAR STUDY IN BELÉM, PARÁ, BRAZIL
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Acute gastroenteritis (AGE) remains an important public health problem all around the world, accounting for billions of cases and millions of deaths every year, mainly in developing countries. In the last years, Norovirus (NoV) has emerged as an important cause of AGE, affecting people of all age groups, especially children under five years and the elderly. Norovirus presents a broad genetic diversity, which might potentially favors its escape from the host immune system leading to successive infections by different strains. The aim of this study was the detection and genotyping of NoV strains from stool samples of children hospitalized for AGE in Belém, Pará, Northern Brazil. From March/2012 to March/2015 434 stool samples were screened for NoV by Enzyme Immunoassay (EIA). The positive samples were subjected to RT-PCR using primers Mon 431/432 and G2SKR, which target the polymerase-capsid junction region of NoV genome and generates amplicon of 550 bp. A semi-nested PCR was followed in samples from which amplification could not be yielded in the first step. The primers used in this step were COG2F and G2SKR, which target the C region of viral capsid, resulting in an amplicon of 390 bp. These amplicons were further purified and subjected to direct sequencing. Results were analyzed using the software Bioedit (v.7.2.5) and sequences were compared to other sequences deposited in the GenBank. Phylogenetic trees were constructed using MEGA (v. 6.0). A positivity rate of 21.4% (93/434) was yielded by EIA and sequences were obtained from 71 (76.3%) NoV positive samples. Genotyping showed the predominance of GII.4 (88.7%-63/71) strains, corresponding to New Orleans and Sydney variants. In addition, the following genotypes were also found: GII.2 (1.4%-1/71), GII.6 (1.4%-1/71), GII.7 (2.8%-2/71) and GII.17 (2.8%-2/71) strains. Noticeably, a recombination between GII.7/GII.6 was identified in two samples. This study showed a significant prevalence of NoV among children admitted for AGE in Belém; furthermore, a broad genetic
diversity of strains circulating in this period (2012-2015). Our findings highlight the need for continuous genotyping of circulating NoV strains, allowing for a better understanding of viral evolution, particularly with regards to the emergence of new strains with pandemic potential. In addition, NoV genotyping seems critical since a truly successful NoV vaccine will need to confer protection against various epidemiologically important types. Financial Support: Fapespa; CNPq; Instituto Evandro Chagas/SVS/MS.

HV344 - SURVEILLANCE OF INFLUENZA A AND B VIRUSES, HUMAN RESPIRATORY SyncTICIAL VIRUS AND HUMAN METAPNEUMOVIRUS IN THE NORTH AND NORTHEAST REGIONS OF BRAZIL


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Acute Respiratory Infections (ARI) are typically characterized by sudden onset and course with variable severity; they occur at high frequency and prevention can be difficult to achieve. ARIs are the leading cause of seeking for medical care and abstention activity around the world. ARIs account for about 2.2 million deaths annually; it is estimated that 90-95% of cases are caused by viruses including: the Influenza A virus (FluA) and Influenza B viruses (FluB), Human respiratory syncytial virus (HRSV) and Human metapneumovirus (HMPV). This study aims to determine the prevalence of ARIs caused by these viruses in community setting in Northern and Northeastern of Brazil. From July 2014 and June 2015, 1,987 clinical specimens (nasopharyngeal aspirates or swabs) were collected from patients with symptoms of ARI in the states of Pará, Amazonas, Acre, Maranhão, Amapá, Roraima, Parába, Pernambuco e Rio Grande do Norte and sent to the Respiratory Virus Laboratory of the Evandro Chagas Institute, for viral diagnosis research. Viral nucleic acid was extracted from the clinical specimens using a commercial kit. The detection of viral genome was performed by real-time Polymerase Chain Reaction preceded of Reverse Transcriptase (qRT-PCR), using specific primers and probes to Flu A (H3N2 and H1N1pdm), Flu B, RSV and HMPV. Of 1,987 patients analyzed, 342 (17.2%) were positive for any of the investigated viruses, 116 (33.9%) were positive for the Influenza A (H3N2), 45 (13.3%) for Influenza B, 150 (43.8%) for HRSV and 31 (9%) for HMPV. No positive sample was detected for Influenza A (H1N1pdm). Our data showed that the viral ARIs were more frequent in children and young adults, especially during July and August 2014 and from March to May 2015. HRSV was predominant accounting for 43.8% of the positive samples. Continuous monitoring of the viral etiology in ARIs is of particular importance in regard to implementation of the prevention and control measures including the introduction of effective, strain specific composition of vaccines. Financial Support: IEC/SVS/MS.

HV345 - HUMAN RHINOVIRUS DETECTION AMONG PATIENTS WITH ACUTE RESPIRATORY INFECTION IN GUARAPUAVA-PR

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Acute respiratory infections (ARI) are the most common cause of morbidity around the world, resulting in a huge impact in the health and economy of populations. Respiratory viruses are the leading pathogens causing ARI, and human rhinovirus (HRV) is the most common identified virus in these cases. To investigate the frequency of HRV detection among ARI cases of Guarapuava-PR city, nasal swab samples were collected from symptomatic patients in a local health center from June to August 2014. The collected samples were processed and tested for molecular detection of HRV by polymerase chain reaction preceded by reverse transcription step (RT-PCR), with primers targeting a region of the virus genome that comprise part of the 5’ noncoding region, the entire VP4, and the 5’ terminus region of the VP2 gene. In the period of the study 74 samples were collected: 16 in June, 19 in July, and 39 in August. The median age of patients was 39 years old, ranging from 1 to 79. The recorded frequency for each symptom presented by patients was: coryza 96%, cough 72%, headache 61%, myalgia 57%, sore throat 54%, chills 42%, and fever in 32%. Thirteen samples yielded a positive result for the presence of HRV by RT-PCR, representing 18% of total. Four of the HRV positive samples was from patients under 10 years old, three from patients between 11 and 20 years old, one between