HV138 - SEASONAL TRENDS OF VIRAL RESPIRATORY TRACT INFECTION BY HMPV IN A SUBTROPICAL REGION

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Human Metapneumovirus (hMPV) is a member of the Metapneumovirus genus within the Paramyxoviridae family. Though hMPV was only discovered in 2001, a large body of work has already shown that it is the aetiologic agent of a substantial proportion of upper and lower acute respiratory tract infections throughout the world. To evaluate the seasonal trends of hMPV infections in a subtropical environment, we analyzed climatic, spatial, and temporal data for children presenting to Santa Casa de Misericórdia’s Hospital in São Paulo, Brazil with respiratory symptoms. During the study period (feb/08 to apr/11), 1389 children presented and 53 hMPV cases (3.8%) were identified by PCR. In terms of annual seasonality, hMPV predominated in winter months between July-November over 2008 and 2009, with few cases in apr/10 and mar/11. The results indicated that low peak and high peak outbreak seasons have different population dynamics, which would probably lead to a lag between stimulus and event for low peak outbreak seasons. The hMPV trends were associated with onset of drought and falling temperatures, with mild environmental temperatures monthly (mean cases 16°C, minimum monthly average 10°C, maximum monthly average 23°C) and medians total precipitation (mean cases 140mm/month, minimum monthly average 0mm, maximum monthly average 468mm). It is important to note that when these variables start to decline, are usually associated with a severe increase in levels of air pollutants that have been consistently correlated with respiratory health issues. Identification of additional factors that affect hMPV seasonality may help develop a model to predict the onset of epidemics. Financial support: FAPESP/CNPq.

HV139 - MOLECULAR ANALYSIS OF VP1, VP2 AND VP3 GENES OF ROTAVIRUSES SPECIES A (RVA) CIRCULATING IN BELEM, PARÁ, BRAZIL

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Rotaviruses are the major etiological agents of viral acute gastroenteritis in infants and young children and constitute an important cause of infantile mortality in developing countries. The previous knowledge of epidemiologic aspects of the infection, antigenic and molecular characteristics of RVA constitutes indispensable information for success of behaviours of control and prophylaxis of this disease. Recently, a new classification system was proposed based on whole-genome sequence analysis. For the VP1, VP2 and VP3 genes of RVA there are 4, 5, and 6 genotypes described. This study aimed to characterize RVA genes that encode VP1, VP2 and VP3 structural proteins from G1, G2, G3, G4 and G9 RVA genotypes circulating in Belém, Pará, Brazil, before and after Rotarix® vaccine introduction in Brazil. A total of 19 fecal specimens were selected between 1997 and 2008 from children hospitalized due to acute diarrhea, being twelve samples from pre vaccine period and 7 samples in post vaccine period. Fecal suspensions were prepared and viral genome was extracted. Subsequently, dsRNA was reverse transcribed (RT) and amplified by polymerase chain reaction (PCR) for partial VP1, VP2 and VP3 genes using consensus primers. PCR products were purified and sequenced automatically. The sequences obtained were compared and made available to GenBank database. The phylogenetic analysis was performed using MEGA3 software. This study has been approved by the Committee in Ethics and Research from the IEC. VP1, VP2 and VP3 genes were amplified in all specimens. Fifteen samples (79%-15/19), presented R1-C1-M1 genotypes with regards VP1, VP2 and VP3 genes, respectively and 21% (4/19) were classified as R2-C2-M2. Three samples stood out in analyses of VP1 and VP2 genes because they were more similar to porcine prototypes. Sample RV101099 (G3-P[8]-R2-C2-M2) showed a high homology to all genes analyzed with bovine prototypes. Among the samples analyzed, had predominance of R1-C1-M1 genotypes. The current work is the first report about VP1, VP2 and VP3 molecular characterization of RVA in Belém, Pará. These results help the knowledge on the genomic diversity of rotavirus, and may have potential importance in the interspecies transmission events. Financial support: CNPq, IEC/SVS/MS.

HV140 - EPSTEIN-BARR VIRUS AND KAPOSI’S SARCOMA HERPESVIRUS INFECTION IN PATIENTS LIVING WITH HUMAN IMMUNODEFICIENCY VIRUS IN BRAZIL


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Epstein-Barr virus (EBV) and Kaposi’s sarcoma associated herpesvirus (KSHV) are two gammaherpesviruses consistently associated with the development of human immunodeficiency virus (HIV) infection. The aim of this study was to determine the prevalence of KSHV and EBV infections in HIV-infected patients in Brazil. A total of 150 HIV-positive patients were included in the study. KSHV and EBV DNA were detected by polymerase chain reaction (PCR) using primers designed for the KSHV ORF74 and EBV EBNA-1 genes. The prevalence of KSHV infection was 9.3%, while the prevalence of EBV infection was 14.7%. The prevalence of KSHV and EBV infections in HIV-positive patients in Brazil was lower than that reported in previous studies in other regions of the world. Further studies are needed to determine the factors associated with the low prevalence of KSHV and EBV infections in HIV-infected patients in Brazil.