Human Virology: HV
in the coding region of the MBL2 gene have been investigated and showed a great importance in susceptibility to various types of viral infections. In our study, we analyzed exon 1 MBL2 single nucleotide polymorphisms (SNPs) in a group of 35 patients with HPV and cervical lesions of low/high degree in order to evaluate their influence on the onset of infection and the cancer development. As a control group, we studied 44 healthy individuals not presenting HPV infection. The biological material was obtained from peripheral blood and cytobrush. The detection of HPV was performed by PCR with primers MY09/11. The SNPs located in exon 1 of the MBL2 gene were genotyped by real-time PCR and grouped according to the variant A/O, using High Resolution Melt. All populations analyzed were found in Hardy-Weinberg equilibrium ($X^2 = 0.50, p = 0.48$). In relation to the allele frequencies no evidence of any association of MBL2 SNPs between patients with HPV/cervical lesion and the control group was found ($OR = 1.008, 95\%CI = 0.47 - 2.14, p = 1$). For the genotypic frequencies, as observed before, no differences were identified between the groups ($OR = 1.09, 95\%CI = 0.39 - 3.01, p = 1$), observing similar frequencies to AA (50%), AO (43%) and OO (7%). Although MBL is an important molecule in the innate immune system, controlling the early stages of infection, our results did not show any direct association between the SNPs presence in the MBL2 gene and an increased susceptibility to cancer development when associated with HPV.

Financial support: FACEPE

HV153 - CO-INFECTION AND CLINICAL ASPECTS INVOLVING HUMAN RHINOVIRUS IN ACUTE RESPIRATORY DISEASES IN YOUNG CHILDREN

Costa, L.E.1, Oliveira, T.F.M.S.1, Freitas, G.R.O.1, Tolardo, A.L.1, Paula, N.T.1, Dias, E.H.1, Chávez, J.H.1, Ueira, C.2, Queiroz, D.A.O.1, Silveira, H.L.1, Yokosawa, J.1.

1. Instituto de Ciências Biomédicas; ICBiM; Av. Amazonas, 1720, bloco 4C, Campus Umuarama. CEP. 38400-782. Uberlândia, MG
2. Instituto de Genética e Bioquímica; INGB; Av. Amazonas, 1720, bloco 4C, Campus Umuarama. CEP. 38400-782. Uberlândia, MG
3. Hospital de Clínicas; HC; Av. Amazonas, 1720, bloco 4C, Campus Umuarama. CEP. 38400-782. Uberlândia, MG

Human rhinovirus (HRV) has been frequently implicated as a major agent in respiratory infections of the upper respiratory tract (URT) in children. In order to investigate the presence of a second respiratory virus and the role of co-infection in disease severity, we have collected and tested, by RT-PCR and immunofluorescence assay, 469 nasopharyngeal aspirates from children ≤5 years old presenting acute respiratory disease. HRV was detected in 46.1% (216/469) samples, with no age group predominance; dual infections involving HRV were further investigated in 184 samples: HRV as the sole agent was detected in 58.7% (108/184) samples and a second virus was detected in 41.3% (76/184) cases: 43.4% (33/76) with respiratory syncytial virus (RSV), followed by 18.4% (14/76) human metapneumovirus (hMPV), 18.4% (14/76) parainfluenza virus (PV) (4 for PV1, 5 for PV2 and 5 for PV3), 11.8% (9/76) adenovirus (AdV), and 6.6% (5/76) influenza virus A. In the cases whose symptoms were available, those involving lower respiratory tract (LRT), represented by bronchiolitis and pneumonia, and those of URT were, respectively: 58.7% (44/75) and 41.3% (31/75) in dual infection cases; and 42.1% (45/107) and 57.9% (62/107) in HRV solo infection cases. These results suggested that co-infections lead to a more severe respiratory disease in young children, as indicated by the higher percentage of cases with LRT infection ($p=0.0362$). However, RSV is known to be a major cause of infections of LRT. By eliminating RSV cases from the co-infection group, the rates of LRT in both groups were very similar. Nevertheless, and in contrast to other reports, our results showed that HRV was implicated in a high number of severe respiratory diseases, even in solo infections. Further analysis, involving the identification of HRV species and risk factors presented in each case might provide further epidemiological and molecular data that may associate HRV infections and disease severity.

Financial support: CAPES, CNPq, FAPEMIG, Programa de Pós Graduação em Imunologia e Parasitologia Aplicadas e Instituto de Ciências Biomédicas / Universidade Federal de Uberlândia

HV154 - SOCIOECONOMIC AND IMMUNOLOGICAL ASPECTS OF CITOMEGALOVIRUS INFECTIONS IN PATIENT WITH CANCER UNDER TREATMENT AT THE HOSPITAL OPHIR LOYOLA, BELEM-PA.


Instituto Evandro Chagas; IEC; Rodovia BR-316 km 7 s/n - Leivliandi - 67030-000 - Ananindeua / Pará / Brasil

Cytomegalovirus (CMV) is an opportunistic agent prevalent worldwide that causes acute infections, becoming latent and prone to recurrences, when causes high morbidity and mortality in immunocompromised patient. Few studies on this subject have been conducted in the Amazon. Considering that cancer is the second cause of death in our country, this study was conducted to assess the socioeconomic aspects and immune response to CMV in 251 individuals with cancer of both genders and in different age groups, under intensive chemotherapy at the Hospital Ophir Loyola, Belém-Pa. Serology was done for IgG and IgM anti-CMV antibodies by ELISA, and epidemiological data were obtained by a questionnaire. It was observed that 86% of the individuals had monthly income equivalent to ≤2 minimum wages, and 40% (n=101) of them received governmental financial support ("bolsa família"). As for the
occupations, 27% were students, 14% were housewives, 16% did not provide occupational information, and 43% had miscellaneous occupations. Regarding laboratorial results, 96.8% of the individuals had IgG and 1.6% had IgM antibodies. The highest frequency of IgG antibodies was in the 1-9-year-old age group (23.1%), whereas the lowest was in the 20-29-year-old group (6.8%). The most frequent serological profile was IgG(+) / IgM(+) (95.5%) and less frequent was IgG(+) / IgM(-) (0.9%). Acute infection occurred in a child with acute myeloid leukemia, two patients with uterine cancer, and one with Hodgkin’s lymphoma, all of them after one year of treatment. Immunosuppression caused by chemotherapy might have contributed to the opportunistic infection in these patients. The serological profile IgG(+)/ IgM(-) is compatible with the high endemicity of CMV in low socioeconomic groups, as observed in this study.

Financial Support: IEC/SVS/MS

HV155 - EPIDEMIOLOGICAL FEATURES OF HUMAN PAPILOMAVIRUS (HPV) IN BRAZILIAN POPULATION IN THE PERIOD FROM 2008 TO 2011

Nonaka, C.K.V.; Resende, F.A.; Almeida, V.C.O.

Departamento de Genética Molecular, Instituto Hermes Pardini; HP; Belo Horizonte, Minas Gerais, Brazil

The hybrid capture test has shown greater sensitivity/specificity in the analysis of viral DNA in the group of HPV low and high-risk. The determination of HPV types (PCR-RFLP) also helps in conducting an appropriate treatment for patients affected by this viral infection. Our objective was to measure the epidemiological features of HPV infection (low and high oncogenic risk) by hybrid capture and investigate the seroprevalence of HPV by PCR-RFLP. For the study were used quantitative and descriptive data of 42,531 patients affected by this viral infection. Our objective was to measure the epidemiological features of HPV infection (low and high oncogenic risk) by hybrid capture and investigate the seroprevalence of HPV by PCR-RFLP. For the study were used quantitative and descriptive data of 42,531 patients, from 2008 to 2011, the Division of Molecular Genetics of the Instituto Hermes Pardini, who had medical referral for suspected infection HPV. The methodology was based on the Digene Hybrid Capture System HPV, a hybridization solution able to detect 18 HPV types: low-risk (6/11/42/43/44) and high-risk (16/18/31/33/35/39/45/51/52/55) by hybrid capture and investigate the seroprevalence of HPV by PCR-RFLP. For the study were used quantitative and descriptive data of 42,531 patients, from 2008 to 2011, the Division of Molecular Genetics of the Instituto Hermes Pardini, who had medical referral for suspected infection HPV. The methodology was based on the Digene Hybrid Capture System HPV, a hybridization solution able to detect 18 HPV types: low-risk (6/11/42/43/44) and high-risk (16/18/31/33/35/39/45/51/52/55/56/58/59/68). Of the samples analyzed, 23,814 (56%) were negative and 18,717 (44%) positive (14,778 women, 3,939 men). In women, the prevalence of positive found was: 55.1% high-risk, low-risk 13.2% and positive for both 31.7%. In males, the prevalence of positive was: 37.7% high-risk, 33.3% low-risk and 29% for both. In relation to age, the highest incidence for HPV high-risk in both sexes was between 16-30 years (9,676 positive women and 2,244 men) and 31-45 years (3,829 positive women and 1,226 men). 298 samples were analyzed by PCR-RFLP for typing of HPV in 2011 (49.3% negative, 37% positive and 13.7% undetermined). In women, 52.3% were positive for high-risk, 30.7% positive for low-risk and 17% for both. The prevalence found was: 14.8% HPV-16 and 12.5% for HPV-6. In men, 76.2% were positive for low-risk, 19% positive for high-risk and 4.8% for both. The prevalence was: 47.6% for HPV-6 and 23.8% for HPV-11. The incidence of HPV infection was higher in women for both low and high-risk. The potential seriousness of HPV infections is suggested by the apparent increase in the number of HPV infections being diagnosed.

HV156 - DETECTION AND QUANTIFICATION OF ARARAQUARA HANTAVIRUS GENOMIC RNA BY REAL TIME qRT-PCR

Machado, A.M.; Souza, W.M.; Machado, A.R.S.R.; Figueiredo, L.T.M.

Centro de Pesquisa em Virologia - FMRF - USP; CPV - FMRF - USP; Av. Bandeirantes 3900 - Monte Alegre - Ribeirão Preto, SP, 14049-900.

Hantaviruses are rodent-borne Bunyaviridae that produce human disease. Human infection commonly occurs by inhalation of aerosolized infected rodent excreta. In the Americas, since 1993, Hantavirus Pulmonary Syndrome (HPS) has been recognized as an important public health problem. In Brazil, more than 1300 HPS cases have been reported. The aim of this study was to standardize a real time RT-PCR to detect and quantify the genomic RNA of Araraquara hantavirus (ARAV) from biological samples: serum, urine, saliva, tissue or cell culture supernatant infected. Culture supernatant of infected cells were subjected to conventional RT-PCR for amplification of ARAV RNA using primers described above where? The amplicon obtained (256 nucleotides) was purified and cloned into pCR 2.1 TOPO vector (Invitrogen, USA). This vector was linearized using BamHI (Fermentas - BRA), purified and subjected to reverse transcription using T7 RNA polymerase (Invitrogen - USA). RNA obtained was purified using QIAamp viral RNA kit (Qiagen - USA) and quantified using Nanodrop (Thermo Scientific - USA). A serial dilution was carried out by obtaining samples containing between 103 to 1011 copies / ml. All dilutions were subjected to real time RT-PCR using SuperScript ® III Platinum ® SYBR ® Green One-Step qRT-PCR and primers described above where? with the purpose of developing a concentration curve. RNA samples extracted from urine, saliva, serum of infected rodents were also subjected to real time RT-PCR described above to obtain the number of copies of viral RNA in the samples. The standard curve showed reliability of detection between 103 to 1011 copies / ml, with regression coefficient (R2) of 0.882 and amplification efficiency (EFP%) of 92.5%. Viral RNA extracted of biological samples of infected rodents showed detection and quantification between 104 to 106 copies/ml. This technology will allow rapid detection and quantification of viral copies in biological samples, allowing future studies: viral load in tissues of infected rodents, the relationship between viral load and pathogenesis, among others.