Hepatocellular carcinoma (HCC) is a leading cause of cancer-related death worldwide. Risk factors for the development of HCC in patients with chronic hepatitis B virus (HBV) infection are being elucidated. Thirty-one HBV/HCC patients were enrolled for this study. A fragment of 1,306 bp (S/POL) was amplified, sequenced and genotyped by phylogenetical analysis using reference sequences. Among HCC patients, 96.7% were cirrhotic patients, 64.5% were Caucasians, 80.6% men and mean age was 56.5 years (range 39-85 years). The mean values of clinical variables were: AFP: 2505.8ng/mL; ALP: 134U/L; AST: 58.9U/L ALT: 44.4U/L; GGT: 134U/L and Platelets: 137.3mil/mm3. HCC tumors were identified by: Screening program–22.6%, Causal Finding–16.1% and Symptoms–61.3%. From 7 cases included within screening program, 28.5% presented an early stage HCC (single nodule<2cm). The majority of patients were BCLC early stage (BCLC-A–54.8%) and applicability of TACE and resection treatments was more frequently: 38.7% and 22.5%, respectively. Furthermore, tumors in BCLC-B and BCLC-C stages were detected in patients with symptoms. The frequency of HBV genotypes among HCC patients was A1 (41.6%), C2 (16.6%), D3 (16.6%), A2 (8.3%), F2a (8.3%) and D1 (8.3%). HBV/A1 and male sex were more prevalent in these patients. HBV/C2, commonly found in Asia, was the second most prevalent genotype. These results agreed with the distribution of HBV genotypes circulating in Brazil, where HBV/A1 is the most prevalent, being predominant in the Northern and Northeastern states. Data demonstrate that the majority of HCC patients are diagnoses within symptoms stage that limits the chance for precocious diagnosis and effective therapy. However, the screening program showed a positive result for detection of very early tumors in HBV patients. According to this result, we concluded that is necessary to invest in the adherence of patients to the screening program. FAPESP 2011/50562-0, FFM and HCFMUSP.

**HV684 - DETECTION OF A NOVEL NOROVIRUS RECOMBINANT STRAIN IN AN AFRICAN-DESCENDANT COMMUNITY FROM THE AMAZON REGION, BRAZIL, 2008**


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Norovirus, a major cause of acute gastroenteritis outbreaks worldwide, are constantly evolving. This ability is reflected in the speed and efficiency with which these viruses spread and remain in human population. The present study reports the detection of a novel recombination event among norovirus genotypes in Brazil in the year of 2008. Initially the fecal sample (QUI 38F1) was tested for the presence of NoV antigen using the RIDASCREEN® Norovirus 3rd Generation enzyme immunoassay kit. To confirm the immunoassay positive result two RT-PCR methodologies were
used. Region B (ORF1) and region D (ORF2) of NoV genome were amplified by using specific primers and PCR reaction conditions. The sample QUI 38F1 yielded positive results with the three methodologies used. Amplicons obtained were purified and directly sequenced in both directions using the Big Dye Terminator Reaction Kit® (v. 3.1) and an ABI Prism 3130xl DNA sequencer. Assignment of the strain to specific NoV genotypes was made according to the Genotyping Tool available on line (Noronet) and the phylogenetic analysis was performed using MEGA version 5.05. In order to investigate the possibility of a recombination event in the sample studied, ORF1/2 junction region was amplified with primers Mon 431/432 and G2SKR. Phylogenetic analysis carried out with partial polymerase and capsid sequences resulted in QUI 38F1 clustering within two different genotypes, GII.7 (ORF1) and GII.20 (ORF2), confirming the results obtained with the genotyping tool. Plot analysis revealed potential recombination of QUI 38F1 within two parental strains [GII.7 (Gwynedd) and GII.20 (Leverkusen)] and identified the breakpoint located at 60 nt upstream the ORF1/2 overlap. The present study revealed a novel NoV intergenotype recombinant strain detected in a relatively isolated, African-descendant community living in Northern Brazil. To our knowledge, this is the first description of NoV intergenotype GII.7/GII.20 recombinant strain. The study was funded by the Foundaion for Research Support of the State of Pará (Fundação de Amparo à Pesquisa do Estado do Pará - Secretaria de Estado de Desenvolvimento, Ciência e Tecnologia) grant code MS/CNPQ/SECTAM – 001/2006, agreement 032/2007, and by Evandro Chagas Institute, Secretary of Health Surveillance (IEC/SVS), Ministry of Health, Brazil.

HV689 - DETECTION OF HUMAN PAPILLOMAVIRUS TYPE 16 IN CERVICAL ADENOCARCINOMA: CASE REPORT

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Background: Human Papillomavirus (HPV) infection is a necessary cause of cervical cancer, and is etiologically associated with a subset of cancers of the anus, oropharynx, penis, vagina, and vulva. Several studies have proposed an association between HPV infection and oesophageal, laryngeal, oropharyngeal, lung, urothelial, breast, cervix and colon cancers. Objective: To investigate the presence of Human Papillomavirus (HPV) DNA in cases of cervical adenocarcinoma. Material and Methods: Four samples were obtained from cases of cervical adenocarcinoma diagnosed and treated at the Hospital Guilherme Álvaro in Santos-São Paulo, Brazil. DNA was extracted from formalin fixed and paraffin-embedded tumor tissues using QIAamp DNA Mini Kit (Qiagen). The quality of DNA extracted was verified by amplifying the human CCR-5 gene. Detection of HPV DNA was performed by PCR using primers GP5 and GP6. HPV positive and negative controls were performed. The presence of DNA was verified by agarose gel electrophoresis. The