## ORT.25 - Human Pegivirus Challenge: Detection and Molecular Characterization in HCV/HIV Coinfected Individuals.

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**Introduction:** Human pegivirus (HPgV), formerly known as GB virus C, is a member of the Flaviviridae family of single-stranded, positive-sense RNA viruses and has genomic similarity to hepatitis C virus (HCV). However, unlike HCV, HPgV is lymphotropic (non-hepatotropic), establishes a subclinical infection and is not related to hepatitis or any other disease. Epidemiological data indicate that HPgV is highly prevalent in populations worldwide. The viremia in general populations varies, being lower (1–5%) in developed countries and higher (up to 20%) in developing ones. Due to the shared transmission route, co-infection in individuals with underlying conditions as HIV, HCV, patients receiving haemodialysis and people who inject drugs is common and HPgV viremia up to 45% has been reported. Several studies reported that HPgV infection is associated with delayed HIV disease progression as indicated by higher CD4 cell counts, lower HIV RNA levels and longer disease-free survival. Conversely, in HCV-infected individuals, studies have indicated that HPgV infection is likely to be associated with slower HCV clearance, leading to a higher likelihood of persistent infection. To better understand the impact of HPgV in co-infections, it is needed to know epidemiological characteristics of this virus. In Brazil, most HPgV studies were performed in São Paulo and in HIV co-infection. Data about HPgV on triple co-infection (HPgV-HCV-HIV) and its influence on the natural history of HCV-HIV is rare.

**Objective:** The aim of this study was to determine the prevalence and genotypic distribution of HPgV in patients attended at a hospital in Rio de Janeiro.

**Methodology**: A RT-PCR assay for specific amplification of 5´UTR region of HPgV genome was performed in 174 serum samples collected from patients under health treatment at a hospital in Rio de Janeiro. The samples were classified into three groups: 56 samples form HCV/HIV coinfected individuals; 58 from HCV mono-infected and 60 from HIV mono-infected individuals. All positive samples were submitted to direct sequencing for genotyping and molecular characterization.

**Results:** The overall prevalence of HPgV-1 was 17.2% (30/174). Among HCV/HIV coinfected patients, HPgV prevalence was 14.3% (8/56), and all of them were successfully sequenced. Phylogenetic analysis revealed the presence of genotypes 2a (12.5%), 2b (62.5%) and 3 (25%). HPgV was also found in coinfection with HCV (8.6%; 5/58) and HIV (28.3%; 17/60).

**Conclusion**: Our findings demonstrate the high frequency of HPgV among HCV/HIV coinfected, HCV and HIV monoinfected individuals attending a public hospital in Rio de Janeiro. Circulating HPgV genotypes described here have already been reported in past Brazilian studies, but this is the first data about HCV/HIV patients in Rio de Janeiro city. This study intends to contribute with insights about epidemiological characteristics and impact (if there is any) of HPgV in the natural course of HCV and/ or HIV infection.

**Keywords:** Human Pegivirus; Epidemiology; HIV/HCV Coinfection