Results: A total of 6,991 patients from all 66 dialysis facilities in RS State were enrolled. Most patients (93.3%) were on hemodialysis. All patients completed HCV screening and 454 (6.5%) were anti-HCV positive. So far, nine units have completed the proposed model, with 89 anti-HCV positive patients that resulted in 49 (55.5%) with detectable HCV RNA by PCR. All viremic patients started HCV therapy. Interim analysis showed SVR in 21 (95.5%) of 22 patients.

Conclusions: A collaborative care model increased the rates of diagnosis and treatment for HCV in dialysis facilities to levels near those established by the World Health Organization towards HCV elimination up to 2030.

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O-20 MOLECULAR AND BIOLOGICAL CHARACTERIZATION OF HEPATITIS B VIRUS SUBGENOTYPE F1b CLUSTERS: UNRAVELING ITS ROLE IN HEPATOCARCINOGENESIS

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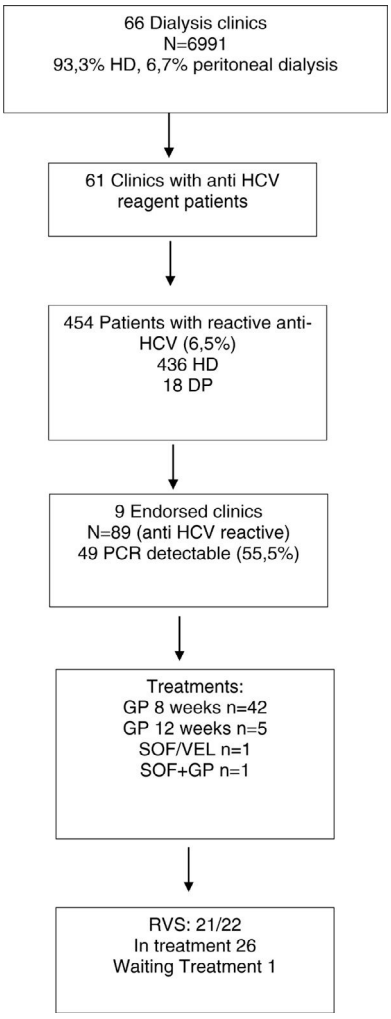
Introduction and Objectives: Hepatitis B virus subgenotype F1b infection has been associated with the early occurrence of hepatocellular carcinoma in chronically infected patients from Alaska and Peru. In Argentina, however, despite the high prevalence of subgenotype F1b infection, this relationship has not been described. This study aimed to unravel the observed differences in the progression of the infection, and an in-depth molecular and biological characterization of the subgenotype F1b was performed.

Materials and Methods: 99 subgenotype F1b full-length sequences were obtained, and phylogeny was addressed by the maximum likelihood method. The replicative capacity of the subgenotype F1b clones was assessed by qPCR, Southern and Northern blot analysis. Antigen expression was detected by electrochemiluminescence and Western blot. The analysis of signaling pathways associated with hepatocarcinogenesis was assessed by RT-qPCR.

Results: Phylogenetic analysis of subgenotype F1b genomes revealed the existence of two highly supported clusters. One of the clusters, designated as gtF1b Basal included sequences mostly from Alaska, Peru, and Chile, while the other, called gtF1b Cosmopolitan, contained samples mainly from Argentina and Chile. The clusters were characterized by a differential signature pattern of eight nucleotides distributed throughout the genome. *In vitro* characterization of representative clones from each cluster revealed major differences in viral RNA levels, virion secretion, and antigen expression levels. Interestingly, differential regulation in the expression of genes associated with tumorigenesis was also identified.

Conclusions: This study provides new insights into the molecular and biological characteristics of the subgenotype F1b clusters and contributes to unraveling the different clinical outcomes of subgenotype F1b chronic infections.



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O-21 EVIDENCE OF SUBOPTIMAL PUBLIC HEALTH POLICIES ON HEPATOCELLULAR CARCINOMA IN THE AMERICAS: A HUGE DEBT OF OUR REGION

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