

MCP4 (p = 0.032), CCL19(p = 0.024), EN.RAGE(p = 0.014), SCF(p = 0.01) and IL 18(p = 0.054) showed a positive correlation with the fibrosis stage. A combined score including CCL19 and MCP.4 revealed a sensitivity of 81% and an Odds Ratio of 2.202 for advanced fibrosis.

Conclusions: Standard non-invasive fibrosis scores showed poor performance in HDV G3 infection. We here suggest that the determination of CCL19 and MCP.4 may be used to identify patients with advanced fibrosis. Moreover, this study gives novel insights into the immunopathogenesis of HDV G3 infection.

<https://doi.org/10.1016/j.aohep.2023.101027>

O-18 ETHNIC DISPARITIES IN HISPANIC POPULATION WITH ALCOHOL ASSOCIATED LIVER DISEASE AND TRANSPLANT ENLISTED PATIENTS: A RETROSPECTIVE STUDY OF TWO LARGE DATABASES IN THE UNITED STATES FROM 2011-2018

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Introduction and Objectives: there are different variables in patients with alcohol associated liver disease (ALD) and enlisted patients for liver transplant (LT), such as ethnicity, that determine health disparities in access, morbidity and mortality. This study aimed to assess and measure the impact of ethnicity in ALD and patients enlisted for LT.

Materials and Methods: we conducted a retrospective study using U.S databases, the National Health and Nutrition Examination Survey (NHANES) and the United Network for Organ Sharing (UNOS) from 2011 to 2018. We created a multivariate model analyzing the clinical characteristics of the interviewed patients for NHANES. Alcohol consumption and ethnicity were self-reported. We also created a competing risks model for time to LT in enlisted patients.

Results: of the 39,156 interviewed patients, 17.1% identified as Hispanic. In this group, the prevalence of ALD was 9.0% and the average consumption of pure alcohol was 2.3 L/year. The multivariate-adjusted model showed that Hispanics were

independently associated with a higher risk of ALD (OR 1.30; 95%CI: 1.05-1.60, p=0.018). Of the enlisted patients, 13.6% were Hispanic. White ethnicity, lower age, male sex, higher MELD score, renal failure, lower BMI, higher education and private insurance were associated with a higher rate of LT. Hispanics were independently associated with a lower LT (HR 0.80; 95%CI: 0.74-0.87, p<0.001).

Conclusions: ethnicity is an important factor in healthcare outcomes. This is a growing area of interest, and research should be carried out to better our understanding of the impact that these disparities have on patients. Studying ethnic minority groups is needed to enable researchers to face the challenges of reducing and ultimately eliminating health disparities.

Table 1. Competitive Risk Model for Patients Enlisted for Liver Transplant

Variable	Univariate Model hazard ratio (IC 95%)	P Value	Adjusted Multivariate Model	P Value
Whites (ref)	ref	ref	ref	ref
vs Blacks	1.18 (1.07-1.31)	0.002	1.03 (0.87-1.23)	0.726
vs Hispanics	0.90 (0.85-0.95)	<0.001	0.80 (0.74-0.87)	<0.001
vs Asian	0.85 (0.72-1.00)	0.046	0.98 (0.82-1.19)	0.867
vs Other	0.83 (0.71-0.98)	0.026	0.82 (0.64-1.04)	0.100
Men	1.13 (1.08-1.18)	<0.001	1.01 (0.94-1.07)	0.875
Age at Enlistment	0.98 (0.98-0.99)	<0.001	0.99 (0.98-0.99)	<0.001
MELD (Model for End-Stage Liver disease)	1.26 (1.24-1.26)	<0.001	1.04 (1.03-1.05)	<0.001
Diabetes Mellitus	0.97 (0.92-1.02)	0.187	-	-
Hepatocellular carcinoma	1.02 (0.92-1.14)	0.66	-	-
Obesity	0.99 (0.98-0.99)	0.010	0.99 (0.98-0.99)	0.16
Renal Failure	1.60 (1.54-1.67)	<0.001	1.40 (1.32-1.47)	<0.001
Education <"High school"	ref	ref	ref	ref
Education "Some College"	1.03 (0.98-1.08)	0.195	0.99 (0.93-1.06)	0.860
Education "College-Bachelor"	1.07 (1.02-1.12)	0.006	1.04 (0.97-1.11)	0.263
Medicare	ref	ref	ref	ref
Medicaid	1.01 (0.93-1.11)	0.721	0.98 (0.89-1.09)	0.760
Private Insurance	1.18 (1.10-1.27)	<0.001	1.01 (0.93-1.10)	0.784

<https://doi.org/10.1016/j.aohep.2023.101028>

O-19 COLLABORATIVE CARE TOWARDS MICROELIMINATION OF HEPATITIS C VIRUS IN A DIALYSIS POPULATION IN SOUTHERN BRAZIL

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Introduction and Objectives: Hepatitis C virus (HCV) eradication from dialysis facilities in a community using direct acting antivirals (DAAs) may be achieved more effectively under a collaborative care model, including a network of hepatologists, nephrologists and specialized dialysis staff. This study aimed to evaluate the prevalence of HCV infection in patients undergoing renal replacement therapy in all registered dialysis units operating in Rio Grande do Sul State (RS), in Southern Brazil. Furthermore, to implement a strategy to treat HCV infection locally at these units.

Materials and Methods: All dialysis units in RS State were contacted between January 2020 and January 2022 to provide results of anti-HCV screening in dialysis patients. Those with positive results were discussed via telemedicine with a team of two hepatologists and one nephrologist located in Clinics Hospital of Porto Alegre, a tertiary health care facility. Dialysis staff was instructed to test HCV RNA with polymerase chain reaction (PCR) and calculate FIB-4 and APRI scores. Viremic patients were selected for therapy and those with FIB-4 >3.25 and/or APRI >1.5 were required to undergo ultrasonography and/or elastography. DAA therapy was started locally by the dialysis unit staff under the supervision of the hepatologists.

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.

<https://doi.org/10.1016/j.aohep.2023.101029>

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

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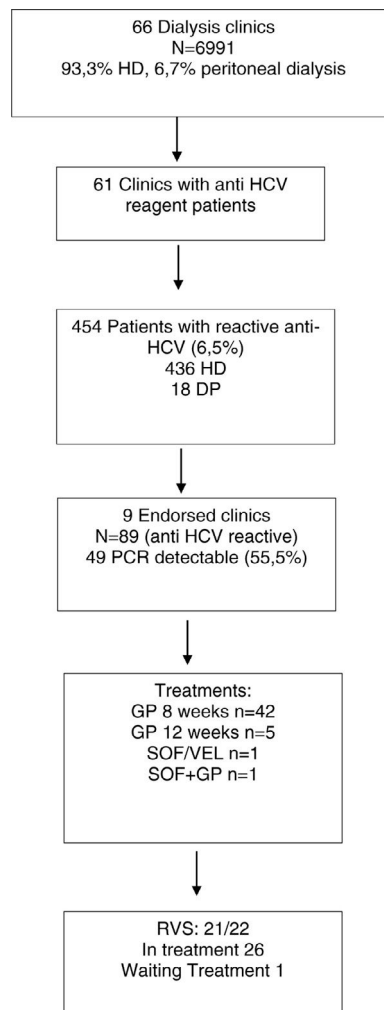
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Introduction and Objectives: Hepatitis B virus subgenotype F1b infection has been associated with the early occurrence of hepatocellular carcinoma in chronically infected patients from Alaska and Peru. In Argentina, however, despite the high prevalence 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.



<https://doi.org/10.1016/j.aohep.2023.101030>

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

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