

– 48.0, $p=0.031$ and OR 2.51; 95% CI 1.06 – 5.97, $p=0.036$, respectively). A comparative table of different subgroups is attached.

Conclusions: The use of amikacin was associated with renal function deterioration in patients with liver cirrhosis and sepsis, mainly in Child-Pugh C cirrhosis and with initial serum creatinine > 2.0 mg/dl.

Table 1. Evaluation of the development of renal function deterioration in different groups of patients depending on the use or not of Amikacin

		Renal function deterioration	Without Renal function deterioration	Valor p
According to initial creatinine level				
Creatinine <1.5 (N = 166)	Amikacin	13 (36)	35 (27)	0.282
	Without Amikacin	23 (64)	95 (73)	
Creatinine 1.5 - 1.99 (N = 33)	Amikacin	4 (33)	4 (19)	0.357
	Without Amikacin	8 (67)	17 (81)	
Creatinine ≥ 2.0 (N = 28)	Amikacin	7 (78)	6 (32)	0.029
	Without Amikacin	2 (22)	13 (68)	
Initial suspicion of infection by Gram (-) bacteria according to infectious focus				
Suspected Gram (-) infection (N = 171)	Amikacin	21 (48)	41 (32)	0.066
	Without Amikacin	23 (52)	86 (68)	
Without suspicion of Gram (-) infection (N = 57)	Amikacin	4 (28)	4 (9)	0.071
	Without Amikacin	10 (71)	39 (91)	
According to the development of septic shock				
With septic shock (N = 74)	Amikacin	16 (57)	22 (48)	0.437
	Without Amikacin	12 (43)	24 (52)	
Without septic shock (N = 154)	Amikacin	9 (30)	23 (19)	0.165
	Without Amikacin	21 (70)	101 (81)	
According to Child-Pugh Score				
Child-Pugh A – B (N = 104)	Amikacin	10 (34)	18 (24)	0.280
	Without Amikacin	19 (66)	57 (76)	
Child-Pugh C (N = 123)	Amikacin	14 (50)	27 (28)	0.033
	Without Amikacin	14 (50)	68 (72)	
According to MELD-Na Score				
MELD-Na < 20 (N = 77)	Amikacin	3 (25)	14 (21)	0.524
	Without Amikacin	9 (75)	51 (78)	
MELD-Na ≥ 20 (N = 150)	Amikacin	21 (47)	31 (30)	0.034
	Without Amikacin	24 (53)	74 (70)	

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P-18 ANTI-HBC POSITIVITY IS AN INDEPENDENT PREDICTIVE FACTOR FOR HCC DEVELOPMENT AND SHOULD BE INCORPORATED TO THE HCC RISK SCORE PREDICTION MODEL IN ADVANCED FIBROSIS

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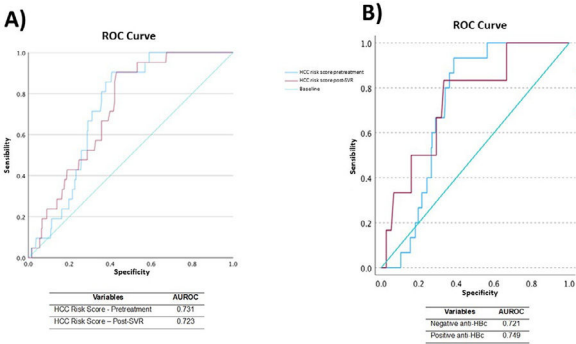
Conflict of interest: No
Introduction and Objectives: After hepatitis C virus (HCV) treatment with direct-acting antivirals (DAAs), the sustained viral response increased to 95%, although it may be lower in advanced fibrosis. Continuous follow-up of HCV cured individuals is essential. In that context, identifying higher risk populations to intensify its surveillance is important to allow early hepatocellular carcinoma

(HCC) detection and optimize costs. Our group previously demonstrated a risk association between anti-HBc and HCC, since the presence of hepatitis B virus infection has oncogenic properties. Our objective is to evaluate the HCC risk score prediction model accuracy in our population and investigate the inclusion of anti-HBc positivity in the model.

Patients / Materials and Methods: This is a retrospective, observational, descriptive and analytic study in a series of cases in which 365 HCV patients were evaluated. Demographic, clinical and laboratory data were obtained through electronic medical records. The HCC risk score was applied before and after SVR.

Results and Discussion: A total of 21 patients had HCC diagnosis after RVS (5.75%). The variables associated with higher HCC occurrence were: genotype 3 ($p=0.025$), AST pretreatment ($p=0.026$), elastography > 10kPa ($p=0.003$) and advanced fibrosis ($p=0.016$). Among advanced fibrosis patients, positive Anti-HBc ($p=0.047$) was an independent predictor factor associated with HCC. After univariate analysis, genotype 3 and positive anti-HBc were predictive factors of HCC occurrence in advanced fibrosis. When applying the HCC risk score before treatment, the area under the receiver operating characteristic curve (AUROC) was 0.731, while after SVR had a slightly lower value (0.723) – Figure 1A. After incorporating anti-HBc to all other variables used in HCC risk score, the accuracy was 0.744 – Figure 1B.

Conclusions: The HCC risk score is a validated prediction model of HCC occurrence before and after SVR. Anti-HBc positivity might be a good candidate to be incorporated to the model.



HCC risk score ROC curves. A) Pretreatment x Post-SVR. B) After anti-HBc incorporation

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P-19 ASSOCIATION OF TM6SF2 GENE POLYMORPHISMS WITH CARDIOVASCULAR RISK IN PATIENTS WITH METABOLIC DYSFUNCTION –ASSOCIATED STEATOTIC LIVER DISEASE (MASLD) IN A HISPANIC ADULT POPULATION

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Conflict of interest: No
Introduction and Objectives: Genes that influence lipids have led to the discovery of a non-synonymous variant (rs58542926) located in the TM6SF2 gene (transmembrane 6 member of

superfamily 2) that is associated not only with the serum lipid levels, including serum total cholesterol, low-density cholesterol (LDL-C), and triglycerides, but also the risk of cardiovascular disease. The Dallas Heart Study reported that rs58542926 is associated with hepatic fatty infiltration. *Objective:* To establish the frequency of the C> T polymorphism in the TM6SF2 gene (rs58542926).

Patients / Materials and Methods: A multistage random sample was drawn from an inpatient population between 40 and 70 years of age.

We analyzed the DNA of thirty-five (35) patients. Genomic DNA was extracted from peripheral blood leukocytes. For genotyping of SNP rs58542926, the following pair of primers was used: forward = 5'- GGT CTT GGC ACA AAT CCG GT-3' and reverse = 5'- AAG AGA AAT TGG CAG CTG GA-3'.

Results and Discussion: The frequency of the minor allele T (KK) was 0.000 and the frequency of the ancestral allele C (EE) was 1.0000; These frequencies were similar to those observed in a frequency report from the 1000 genomes project (<http://browser.1000genomes.org/>). The association with fatty liver infiltration may be due to the founder effect, genetic drift, or possibly population inbreeding. In addition, it could be a selective disadvantage compared to other pathologies such as fatty liver.

Conclusions: The results for the C/C and C/T genotypes studied are like those of other previous studies. The presence of the ancestral C allele (EE) in 100% of the patients suggests a probable genetic deviation or founder effect, probably increasing the frequency of this allele over the other existing alleles.

SAMPLE	1622	1623	1624	1525	1626	GenotYPE
TM6SF2 rs58542926	G	G	C	T	C	C/C
1	G	G	C	T	C	C/C
2	G	G	C	T	C	C/C
3	G	G	C	T	C	C/C
4	G	G	C	T	C	C/C
5	G	G	C	T	C	C/C
6	G	G	C	T	C	C/C
7	G	G	C	T	C	C/C
8	G	G	C	T	C	C/C
9	G	G	C	T	C	C/C
10	G	G	C	T	C	C/C
11	G	G	C	T	C	C/C
12	G	G	C	T	C	C/C
13	G	G	C	T	C	C/C
14	G	G	C	T	C	C/C
15	G	G	C	T	C	C/C
16	G	G	C	T	C	C/C
17	G	G	C	T	C	C/C
18	G	G	C	T	C	C/C
19	G	G	C	T	C	C/C
20	G	G	C	T	C	C/C
21	G	G	C	T	C	C/C
22	G	G	C	T	C	C/C
23	G	G	C	T	C	C/C
24	G	G	C	T	C	C/C
25	G	G	C	T	C	C/C
26	G	G	C	T	C	C/C
27	G	G	C	T	C	C/C
28	G	G	C	T	C	C/C
29	G	G	C	T	C	C/C
30	G	G	C	T	C	C/C
31	G	G	C	T	C	C/C
32	G	G	C	T	C	C/C
33	G	G	C	T	C	C/C
34	G	G	C	T	C	C/C
35	G	G	C	T	C	C/C

Results: TMG polymorphisms

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P-20 HIGH PREVALENCE OF CHRONIC HEPATITIS B IN ACHE COMMUNITIES IN THE DEPARTMENT OF CANINDEYU-PARAGUAY

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Conflict of interest: No

Introduction and Objectives: Hepatitis B is a disease that can lead to cirrhosis, acute liver failure, hepatocellular carcinoma, or death. Paraguay is considered a country with a low incidence of hepatitis B. The discovery of two cases of hepatocellular carcinoma associated with hepatitis B, in a community of the Aché indigenous group in the Department of Canindeyú, motivated an initial investigation that aroused the suspicion of a high rate of hepatitis B in those communities. *Objectives:* Determine the prevalence of hepatitis B in the Aché communities of the department of Canindeyú-Paraguay in order to program therapeutic and preventive measures in said population.

Patients / Materials and Methods: A joint working group was organized between the Ministry of Health and a Medical University. The population studied were the inhabitants of the “Kué Tuvý” and “Chupa Pou” communities, of the Aché ethnic group in the department of Canindeyú, Paraguay. In November 2022 and March 2023, a total of 399 natives attended the call made by community leaders and were subjected to capillary blood detection tests for HBsAg. In patients with a positive test, the following were performed: clinical history, physical examination, anthropometry, and abdominal ultrasound.

Results and Discussion: In the first community of 226 people tested, 17 were positive. In the second community, 173 samples were taken and 19 were positive. Globally it represents a prevalence of 9.02% (36/399). The positive cases for HBsAg were distributed by sex: 53% men and 47% women, with an age range of 21 to 56 years with a median of 38 years.

Conclusions: The prevalence of hepatitis B in Aché communities in Paraguay is much higher than in the general population, so it is necessary to carry out a microelimination and prevention plan.

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P-21 THE ROLE SP-INDUCED MAST CELL ACTIVATION IN LIVER FIBROSIS

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