anti-HCV+, a confirmatory test was performed with PCR HCV-RNA. Neonates of HBsAg+ or HCV+ were follow-up for 3 years.

Results: 2762 births were included during the period under study. Five (0.18%) HBsAg+ pregnant women were identified, median age was 25 years (range 17-36), of which only 1 had anti-HBcIgG+. Given the suspicion of chronic HBV and the delay in obtaining the HBV-DNA results, treatment with tenofovir was started. In successive controls, no chronic HBV infection was diagnosed in neonates. Anti-HCV + was detected in 8 (0.29%) patients, with a median age of 29 years (range 19-38 years), of which only one patient presented detectable HCV-RNA, genotype 4. This patient had a diagnosis of HCV chronic prior to pregnancy and her son presented anti-HCV- at age 3. Finally, one patient with HBsAg+ and another with anti-HCV+, but negative viral loads presented HIV+.

Conclusions: The gestation period is an excellent opportunity to carry out health checks. During the studied period, the seroprevalence of HBsAg+ and anti-HCV+ was very low. These types of interventions are essential to achieve the objectives set by the WHO.

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O-2 EVALUATION OF RISK FACTORS AND PROGNOSIS OF HEPATOCELLULAR CARCINOMA RECURRENCE AFTER LIVER TRANSPLANTATION

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Introduction and Objectives: Liver transplantation (LT) is the preferred treatment for early-stage HCC. Despite restrictive criteria (Milan), recurrence is high and negatively impacts on LT survival. This study aimed to evaluate risk factors and prognosis of HCC recurrence after LT.

Materials and Methods: Retrospective Brazilian university hospital HCC-transplanted cohort (2002 -2021). Patients transplanted for other causes, with a follow-up < 1 year or with incidental HCC at explant were excluded. Primary outcome was recurrence of HCC. Secondary outcomes were survival and time elapsed until HCC diagnosis. Tumor burden was the sum diameter of all nodules at explant. Data extraction was conducted with Excel, and statistical analysis was performed with SPSS.

Results: 186 patients were included (males 123 [66.1%], median age 56 years-old), 153 (82.3%) Milan-in. Locoregional waiting-list therapy was trans arterial chemoembolization (TACE), percutaneous ethanol injection (PEI) or TACE + PEI in 63 (34.2%), 58 (31.5%) and 42 (22.8%) individuals, respectively. Downstaging was achieved in 31 patients (17.8%). Explant analysis with microvascular invasion and Milan-out was detected in 31 (16.9%) and 33 (18%) individuals, respectively. HCC recurrence occurred in 22/183 patients (12%), associated with pre-LT alfa-fetoprotein (AFP) (1.881 [IQR 109-4.510] x 6 [IQR 3-39], p=0.02), Milan-out at explant (59.1% x 11.3%, p<0.0001), microvascular invasion (45.5% x 13.9%, p<0.001), and tumor burden at explant (3.9 cm [IQR 3.2-7] x 3 cm [IQR 2-4], p=0.02). Downstaging had no impact on HCC reappearance. Median recurrence time was 22 months (IQR 10.5-42.5); most frequent sites were lungs (18.2%), liver (13.6%) or multiple (36.4%). Median survival after HCC recurrence was 17 months (IQR 6.5-36).

Conclusions: Tumor burden, Milan-out at explant, microvascular invasion and higher pre-LT AFP levels had a negative impact on HCC recurrence. This can identify patients with higher risk of recurrence by planning screening protocols and making early diagnoses to guide effective treatment.

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O-3 DEVELOPMENT OF LENTIVIRAL VECTORS FOR INHIBITION OF HEPATITIS B VIRUS VIA SMALL INTERFERING RNA

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Introduction and Objectives: It is estimated that chronic hepatitis B virus (HBV) infection accounts for one million deaths/year due to cirrhosis and liver cancer. Currently, several drugs are used in the treatment of HBV; however, a complete cure is still controversial. The major challenge is the persistence of viral covalently closed circular DNA (cccDNA), as well as the ability of HBV to integrate into the host genome, which enables the infection's reactivation. Interfering RNA (RNAi) is a post-transcriptional mechanism of gene silencing and is a promising alternative for the treatment of chronic hepatitis B. We aimed to construct effective RNAi lentiviral vector to silencing HBV proteins (HBsAg, HBcAg, HBeAg) and pre-genomic RNA (pgRNA), via RNAi.

Materials and Methods: The silencing vector candidates targets overlapped Open Reading Frames (ORFs), allowing different viral proteins and the pgRNA to be silenced with a single RNAi. The efficiency of silencing by lentiviral vectors candidates used individually or in combination, have been assessed by quantification of HBV proteins by eletroquimioluminescence and quantification of HBV DNA during the post-transfection period by quantitative PCR.

Results: Three silencing vectors candidates were constructed and tested in silico to prevent off-target effects. Stability and secondary structures have also been tested. Huh7 cells were transfected with 1ug of purified HBV genome circular monomers (genotype A1) and 3 days later, infected with the first lentiviral candidate (siHBV-1), targeting S/Pol genes of HBV (108 TU/mL). From the third day post-infection, HBsAg became undetectable on cells infected by the lentiviral vectors, while untreated controls maintained viral protein expression (p<0.002). HBV DNA were also undetectable by PCR.

Conclusions: siHBV-1was able to silence HBV in vitro. This approach allows long- term, sustained knockdown of HBV replication and gene expression, which can effectively promote HBV clearance in chronic carriers.

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O-4 MBOAT7 RS641738 IS ASSOCIATED WITH PROGRESSION TO CIRRHOSIS IN NON-ALCOHOLIC FATTY LIVER DISEASE IN LATIN AMERICA

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Introduction and Objectives: Latin Americans experience some of the highest global rates of non-alcoholic fatty liver disease (NAFLD) and the prevalence of cirrhosis is increasing in this population. The rs641738 C>T single nucleotide polymorphism (SNP) of MBOAT7 has been associated with NAFLD development and cirrhosis in Europeans with NAFLD. However, the impact of this SNP in Latin Americans is unclear. We aimed to evaluate a cohort of Latin Americans with NAFLD to determine if MBOAT7 effects the risk of cirrhosis in this understudied population.

Materials and Methods: Individuals with NAFLD from 6 South American countries (Argentina, Ecuador, Brazil, Chile, Peru and Colombia) were prospectively recruited via the ESCALON network. Genotyping was performed with the TaqMan-genotyping assay. Genotype frequencies for MBOAT7 were compared using chi-square. Those with hepatocellular carcinoma were excluded.

Results: A total of 278 patients were included, 189 with cirrhosis and 89 without cirrhosis. 55% of the cirrhosis cohort were females compared to 61% of the cohort without cirrhosis (p=0.337). The median ages of those with and without cirrhosis were 64 (IQR 59-70) and 60 years (IQR 52-65), respectively. The MBOAT7 TT genotype was present in 36/189 (19%) of subjects with cirrhosis and 7/89 (8%) of subjects without cirrhosis (OR=2.76, 95% CI: 1.17-6.47, p=0.016). We evaluated the minor allele frequency (MAF) of MBOAT7 in our cirrhosis cohort compared to the Latin American population in the gnomAD database, a genome database with 17,720 sequences belonging to Latin Americans. MAF was elevated in cirrhotics compared to the general Latin American population (43% vs. 33% respectively, OR=1.54, 95% CI: 1.25-1.89, p<0.001).

Conclusions: The rs641738 C>T SNP of MBOAT7 was associated with cirrhosis in a cohort of Latin Americans with NAFLD. Identification of genetic risk factors for liver disease may lead to improved risk stratification and interventional strategies in this population with an increasing burden of liver disease.

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O- 5 HCC RISK SCORE PRE AND POST SUSTAINED VIROLOGICAL RESPONSE IN PATIENTS TREATED FOR CHRONIC HEPATITIS C

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Introduction and Objectives: Introduction: Patients with hepatitis C virus (HCV) with advanced fibrosis (F3/4) still presented a significant risk of developing hepatocellular carcinoma (HCC). There are models for HCC risk prediction, such as the HCC risk score developed by Iannou *et al* 2018. This study aimed to evaluate the prevalence and risk factors for hepatocellular carcinoma development in previously treated chronic HCV patients in an outpatient hepatology clinic at Hospital das Clinicas of University of São Paulo School of Medicine, Brazil.

Materials and Methods: This is a retrospective, observational and descriptive study in a series of 267 HCV patients. Review of patients' medical records, applying HCC risk score immediately before and 6 months after SVR, excluding cases with insufficient data and HCC before treatment of HCV. Data collection is still in progress and final results will be available at presentation.

Results: The total sample of this study consists of 267 patients, of whom, 127 (47.6%) had F4 degree fibrosis. Overall, 17 patients developed HCC after a median follow up period of 3 years (6.4%). The mean of HCC risk score at 3 years calculated in pre treatment was 9.64% and post treatment was 4.32% (p=0.002). An accuracy of this score was slightly better in the pre treatment (AUROC=0.72) versus post treatment (AUROC=0.69) (Figure 1).

Conclusions: HCC risk score post treatment declines more than 50% compared to pre treatment of HCV, as expected in in patients with HCV cure.

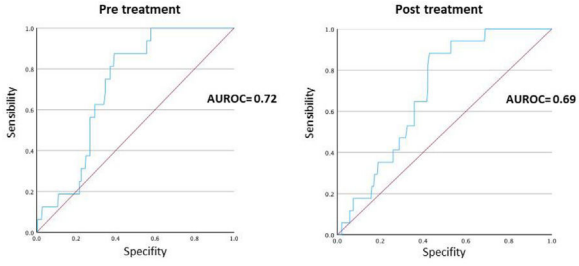

Figure 1. Pre- and post-treatment HCV HCC risk score accuracy

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O-6 EXPLORING THE IMPACT OF INFECTIONS IN PATIENTS WITH ALCOHOL- ASSOCIATED HEPATITIS IN LATIN AMERICA

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