**Materials and Methods:** Cost/patient/year was calculated for patients treated with LTA+SMT and compared to those treated with SMT only. Incidence of clinical complications and healthcare resource utilization (HCRU) were gathered from the ANSWER trial. Pharmacological costs (spironolactone, furosemide, human albumin) were gathered from the "Health Care Price Bank" and CMED. Costs of clinical complications (spontaneous bacterial peritonitis, other bacterial infections, hepatic encephalopathy, renal dysfunction, hepatorenal syndrome, refractory ascites) and other HCRU (LTA administration visit, large volume paracentesis, hospitalizations) were gathered from the literature and ANS. All costs were transformed to 2021 Brazilian Reals (R$). A univariate sensitivity analysis was performed by applying a 20% increase/decrease to all variables.

Results: The overall cost for patients treated with LTA+SMT was R$118,759 and R$189,675 lower than that for patients treated with SMT only for SUS and ANS, respectively. The additional cost of LTA (R$30,767 and R$59,897, respectively) was compensated by a reduction in complications and HCRU (R$149,526 and R$249,572, respectively).

Conclusions: Our study suggests that should the clinical outcomes of the ANSWER trial translate to real-world effectiveness, LTA administration to patients with cirrhosis and uncomplicated ascites may lead to cost savings for the SUS and ANS in Brazil.
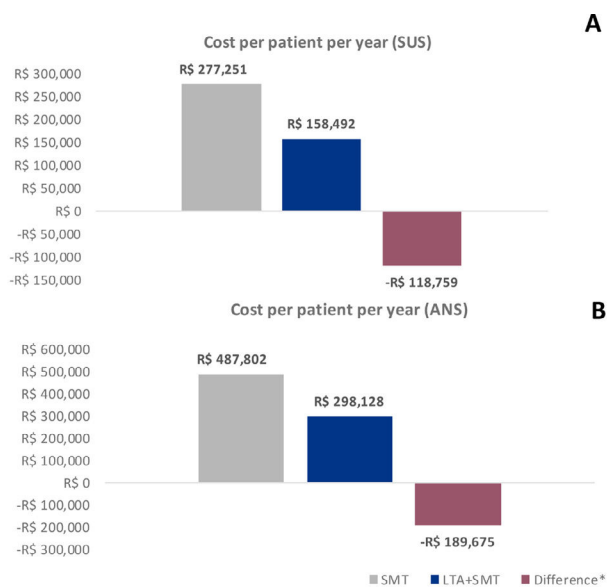
A: cost per patient per year treated with SMT and SMT + LTA and incremental difference from the public healthcare system perspective (SUS). **B**: cost per patient per year treated with SMT and SMT + LTA and incremental difference from the private healthcare system perspective (ANS).
LTA: Long-term albumin; SMT: Standard Medical Treatment
*SMT+LTA vs SMT: negative values indicate savings

O-2 CHARACTERIZATION OF SERUM LEVELS OF BILE ACIDS, EXTRACELLULAR VESICLES AND ITS CARGO IN ALCOHOL-ASSOCIATED LIVER DISEASE

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Introduction and Objectives: Alcohol consumption is among the five main factors responsible for the burden of disease and mortality. It is associated with changes in serum bile acids, and in recent years, extracellular vesicles (EVs) and their Cargo have shown special interest in various lines of research due to their role in intercellular communication. This study aimed to characterize the serum levels of bile acids, changes in their composition, extracellular vesicles and their cargo in alcohol-associated liver disease (ALD).

Materials and Methods: Prospective cohort, years 2019-2021. They were divided into four groups; control group, alcohol-associated hepatitis (AH), alcohol-related cirrhosis, and alcohol use disorder (AUD). Measurement of serum bile acids and C4 was performed through Liquid Chromatography /Tandem Mass Spectrometry, serum measurement of FGF19 and the serum concentration of extracellular vesicles through NTA (nanoparticle tracking analysis) and their cargo of bile acids.

Results: A greater concentration of total bile acids was measured in the AUD group (1366.28 ng/ml) compared to the control group (552.42 ng/ml) (p = 0.003). The concentration of chenodeoxycholic acid is higher in the group of patients with AH (734.23 ng/ml) (p=0.04). The EVs concentration is higher in the HA groups (1.292 $E^{11} \pm 6.4E^{10}$ particles/ml) and in AUD (9.9E^10+ 4.9E^ particles/ml) (p=0.005). It was possible to analyze the Cargo of BA in exosomes with proportional differences between the groups.

Conclusions: Serum bile acids, both in concentration and composition, are modified in patients with AUD and HA, respectively; both present a higher concentration of exosomes, which could be a hepato-specific, dynamic and potentially prognostic biomarker in subjects with ALD.

Figure 1.
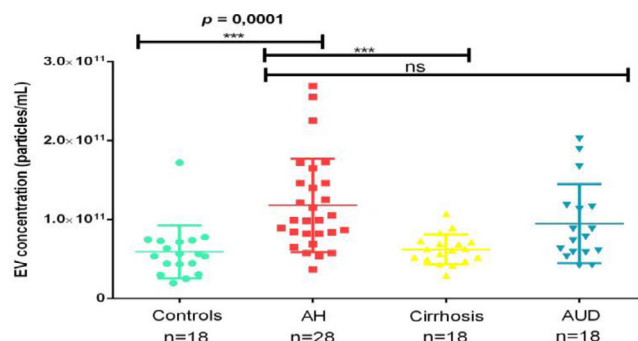
O-4 CLINICAL, HISTOLOGICAL AND SEROLOGICAL FEATURES OF AUTOIMMUNE-LIKE ACUTE LIVER INJURY AFTER SARS-COV-2 VACCINATION

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Introduction and Objectives: Acute autoimmune-like liver injury has been increasingly reported after vaccination against SARS-CoV-2. Pathogenesis, steroid requirement and long-term prognosis are unknown. This study aimed to evaluate clinical, serological and histological features, response to treatment and prognosis in patients with post-vaccination acute hepatitis.

Materials and Methods: We included patients without known pre-existing liver diseases with transaminase levels $\geq$ 2.5 upper limits of normal within 90 days after the SARS-CoV-2 vaccine with an available liver biopsy. Clinical data and outcomes after a six months follow-up were collected.

Results: 17 patients were included,12 females, median age 60 (51,5/66) exposed to vectorial (Sputnik V n=7, AstraZeneca n=6), inactivated (Sinopharm n=3) or ARNm Vaccines (Moderna=1). In 8 patients, liver injury developed after the first dose and in 7 after the second dose and in 2 after the third dose. The median time to the development of injury was 33(23,50/53,50) days. Eight patients had a history of extrahepatic autoimmune disease and five patients had metabolic syndrome and used statins. Immune serology showed anti-antinuclear antibody in 10 (58,8%), anti-smooth muscle antibody in 5(29,4%). 14/17 patients presented with elevated IgG levels. Liver histology showed lobular hepatitis in 13/17, portal hepatitis in 17/17 with plasmocytic lymphocytic infiltrate and 4/17 had eosinophils, 6/17 with severe interface hepatitis, and one patient had fibrosis Ishak stage $\geq$3. 12/17 (70,5%) were treated with steroids. Transaminases improved in 17 cases and normalized in 6/12 by month 6. Only 1/17 developed liver function deterioration, yet no patient required liver transplantation. Most patients tolerated the tapering of steroids and in 6 azathioprine was started before month 3.

Conclusions: Long-term follow-up might help to differentiate between induced classical autoimmune hepatitis, autoinflammatory self-limited events, or drug-induced liver injury in these patients.

O-5 INTEGRATED ANALYSIS OF ARCHAEAL, FUNGAL AND PROTOZOAN GUT TRANSCRIPTOME IN METABOLIC ASSOCIATED FATTY LIVER DISEASE (MAFLD) IN ARGENTINA

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Introduction and Objectives: Fungi, archaea and protozoa are the least known members of the gut microbiome, but they could represent a niche for biomarkers discovery to risk-stratify MAFLD patients. This study aimed to identify gut metatranscriptomic signatures in MAFLD patients from Argentina.

Materials and Methods: Stool samples, diet, demographic and clinical data were obtained from 33 biopsy-proven MAFLD patients (12 simple steatosis (SS) / 21 steatohepatitis (SH)) and 19 healthy volunteers (HV). PNPLA3 rs738409 SNP was genotyped. RNA-seq was performed in NovaSeq6000®. Data were analyzed with Maaslin2-v1.2.0, bioBakery-v1.8 and DESeq2-v4.1.

Results: BMI was higher among MAFLD patients than in HV (q=4.49 $\times$ 10^{-6}). The risk GG genotype of PNPLA3-SNP was more prevalent among SH (q=0.0198). In MAFLD patients and in subjects with the GG genotype, differentially expressed genes (DEGs) of fungi, such as *Fusarium proliferatum* and *Candida sorbophila*, were up-regulated (q<0.01). After comparing transcript abundance, *Saccharomucetaceae* was the most active family among MAFLD patients, whereas *Aspergillaceae* family prevailed in HV. DEGs of methanogenic archaea and protozoa, such as *Fonticula alba* and *Blastocystis spp.*, were highly expressed in MAFLD and SH after comparing them to HV and SS groups, respectively. The analysis of the functionally active protozoan families revealed that the *Blastocystidae* and *Fonticulidae* families were more functionally abundant in MAFLD and SH groups after comparing to HV and SS, respectively (Figure exhibits the statistically significant differences between groups). In subjects with the GG genotype, DEGs of *Fonticula alba* were up-regulated and those of *Blastocystis spp.* were less expressed after comparing to those with CC/CG genotypes. In SH, functional profiling of archaeal and fungal DEGs revealed an over-representation of viral capsid assembly and phage shock processes, whereas copper metabolism, peptidoglycan turnover and non-autophagic vacuolization were enriched by protozoan DEGs.

Conclusions: The switch in microbiome signatures characteristic of MAFLD onset and progression is achieved through the activity of several community members.