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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 ≥ 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 ≥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.

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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.

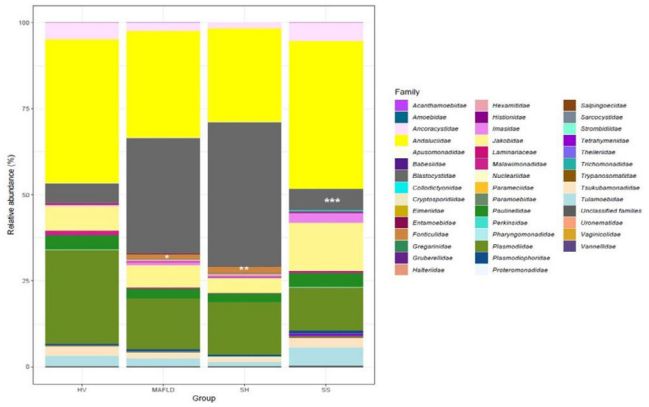

Figure. Relative abundance of the most prevalent functionally active protozoan families. * FDR = 1.26 × 10-7 when compared to HV, ** FDR = 2.9 × 10-18 when compared to SS, and *** FDR = 7.1 × 10-6 when compared to SH.

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O-6 ENHANCED METABOLISM OF AROMATIC AMINO ACIDS AND LOW-DIVERSITY GUT MICROBIOTA: SIGNATURES OF HEPATIC ENCEPHALOPATHY IN DECOMPENSATED CIRRHOTIC PATIENTS FROM WESTERN MEXICO

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Introduction and Objectives: Alterations in the intestinal microbiota in decompensated cirrhosis are recognized as being critical in clinical evolution. The onset of hepatic encephalopathy (HE) worsens the prognosis. Metabolic functions related to intestinal microbiota, such as ammonia production and imbalance of amino acid biosynthesis, are believed to play a key role on the pathophysiology of HE. This study aimed to evaluate the composition and functions of the intestinal microbiota in patients with decompensated cirrhosis and HE.

Materials and Methods: Fecal samples from 31 decompensated cirrhotic patients (20 with HE, 11 without HE) and 18 age-balanced healthy controls (HC) were included. Microbial composition was characterized by 16S rRNA sequencing and analyzed using QIIME2. Metabolic pathways were inferred by PICRUSt2. SCFAs quantification was performed by gas chromatography (GC).

Results: Intestinal microbiota in HE group was characterized by a decreased α-diversity, compared to no-HE group ($p<0.01$) and HC ($p<0.001$); β-diversity was also different between HE vs. no-HE group ($p<0.05$) and HE vs. HC ($p<0.001$). Intestinal microbiota from HE was defined by the presence of taxa such as *Escherichia/Shigella*, Burkholderiales and Lactobacillales. Furthermore, no-HE was characterized by the presence of *Veilonella* and *Bacteroides*. Both groups were depleted of potential beneficial taxa, such as *Ruminococcus* or *Faecalibacterium*, which correlates with diminished levels of fecal SCFAs in these groups. Inferred metabolic pathways showed that HE group was characterized by an enhanced chorismate metabolism, which is a key precursor of aromatic amino acids, along with antibiotic resistance and ammonia-producing pathways. HE and no-HE group showed a significant increase in the metabolism of lipopolysaccharides.

Conclusions: The intestinal microbiota of HE patients exhibit a lower diversity compared with no-HE and HC. It is dominated by *Escherichia/Shigella* and characterized by an enhanced metabolism of aromatic amino acids precursors and ammonia-producing pathways, which suggests its participation in the pathophysiology of HE. These results are described for the first time in western Mexico.

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O-7 LIVER TOXICITY OF TYROSINE KINASE INHIBITORS: A DESCRIPTIVE ANALYSIS FROM SLATINDILI NETWORK

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Introduction and Objectives: Tyrosine kinases (TKs) are a family of proteins with a critical role in controlling cancer phenotypes, and many TK inhibitors (TKI) as anti-cancer agents are available. Mandatory black box warning has been issued for some TKI since 2012, and DILI is the most frequent adverse event quoted. This study aimed to describe the most crucial aspects of DILI linked to TKI in the SLATINDILI registry.

Materials and Methods: We revised data concerning liver injury related to any TKI in the SLATINIDLI registry and consigned epidemiological information, latency, implied drug, biochemical, severity, and evolution.

Results: From thirteen cases identified, imatinib and pazopanib represented four and three cases each. The mean age was 58 years, and eleven were female. Median latency was 64 days, with median ALT and ALP at the onset of 452 U/L (range 233-941) and 199 U/L (range 85-1621), respectively; a hepatocellular pattern was seen in