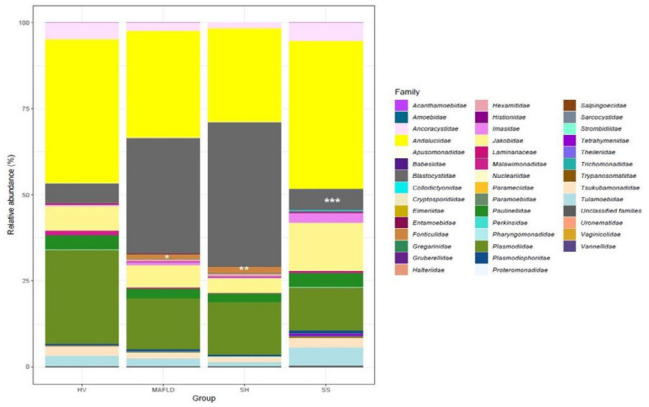

Figure. Relative abundance of the most prevalent functionally active protozoan families. * FDR = 1.26 × 10-7 when compared to HV, ** FDR = 2.9 × 10-18 when compared to SS, and *** FDR = 7.1 × 10-6 when compared to SH.

https://doi.org/10.1016/j.aohep.2023.101015

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.

https://doi.org/10.1016/j.aohep.2023.101016

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