

#111 - ALTERATION OF GUT MICROBIOTA COMPOSITION IN THE PROGRESSION OF LIVER DAMAGE IN CHILEAN PATIENTS WITH METABOLIC DYSFUNCTION-ASSOCIATED STEATOTIC LIVER DISEASE

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ZAZUETA A¹, Valenzuela L¹, Ortiz N¹, Pinto A¹, Torres V¹, Guinez D², Aliaga N², Merino P², Sandoval A², Covarrubias N², Cattaneo M², Madrid A², Roblero J², Ponichik J², Gotteland M¹, Magne F¹, Beltran C¹

¹UNIVERSIDAD DE CHILE, Santiago, Chile

Introduction: Metabolic dysfunction-associated steatotic liver disease (MASLD), is a diverse and complex liver disorder associated with metabolic syndrome. The global prevalence of MASLD has increased over the past decades, from 21.9% in 1991 to 37.3% in 2019, becoming a global public health problem. Interestingly, South America has experienced the most rapid change in MASLD prevalence (2.7% per year) and severity. The pathogenesis of MASLD involves multiple factors, including excessive lipid accumulation, genetic and epigenetic influences, insulin resistance, and gut microbiota alterations. The composition of gut microbiota is associated with geographical location and may contribute to the development and severity of MASLD.

Objectives: The aim of this study was to identify microbial signatures in Chilean MASLD patients and in the progression of MASLD.

Methods: This study included a total of 40 subjects among them 7 healthy controls (HC), 6 NO MASLD, 14 MASLD without fibrosis, and 13 MASLD with fibrosis. DNA was extracted from fecal samples and the v3-v4 region of the 16S rRNA gene was sequenced. Statistical analyses were performed using R software.

Results: No significant differences were observed in alpha diversity or beta diversity. Nevertheless, the Canonical correspondence analysis (CCA) clusters the gut microbiota samples in 3 groups, suggesting a possible association between MASLD and the gut microbiota. Revealing significant alterations in MASLD patients compared to HC and NO MASLD. MASLD patients had higher proportions of Veillonellaceae family and Bilophila genus, but lower abundance of Defluviitaleaceae family, Erysipelotrichaceae genus, Senegalimassilia genus, Defluviitaleaceae UGG-011 genus, and Lachnospiraceae ND 3007 genus compared to HC.

Conclusions: These differences in microbial composition may play a role in the development and progression of MASLD. Moreover, specific microbial taxa were associated with different stages of liver fibrosis, indicating potential links between gut microbiota and MASLD severity.