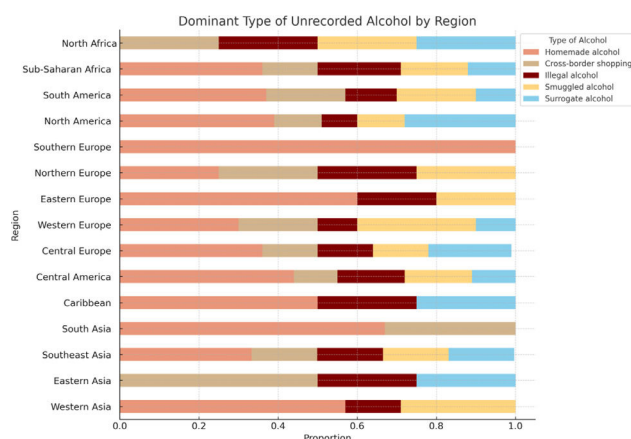


Results: We collected 116 survey responses from 44 countries. Homemade alcohol was the predominant form of unrecorded alcohol consumed, representing the largest share in most regions. Consumers were predominantly male and of working age. Rural consumption of homemade alcohol exceeded that of urban areas, whereas smuggled and cross-border alcohol were mainly consumed in urban areas. Among at-risk groups unrecorded alcohol consumption was highest in drug users and lowest in pregnant women and prisoners. Binge drinking was the most pattern for homemade, illegal, and smuggled alcohol; heavy drinking predominated for surrogate alcohol; and moderate drinking was most common for cross-border purchases. Sub-Saharan Africa had the highest prevalence of heavy drinking across all unrecorded alcohol categories, whereas North America had the highest prevalence of heavy drinking in the surrogate alcohol category. Only 21% of physicians reported "always" asking patients about unrecorded alcohol use, whereas 4.6% reported "never" doing so. A combined 52% indicated they "usually" or "Rarely" ask about unrecorded alcohol use.

Conclusions: Unrecorded alcohol use is widespread, driven by homemade sources, with higher prevalence in rural areas and among people who consume drugs, while physician screening remains limited.

Conflict of interest: None

Dominant type of unrecorded alcohol by region



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#162

IDENTIFICATION OF NOVEL INTESTINAL MICROBIOTA-BASED MARKERS ASSOCIATED WITH DYSBIOSIS, SEPSIS AND SHORT-TERM MORTALITY IN ALCOHOL-RELATED DECOMPENSATED CIRRHOSIS AND ACUTE-ON-CHRONIC LIVER FAILURE

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Introduction and Objectives: Decompensated cirrhosis (DC) and acute-on-chronic liver failure (ACLF) related to alcohol present high morbidity and mortality and complications such as sepsis and multi-organ failure. The intestinal microbiota (IM) suffers from marked

dysbiosis, altering SCFA biosynthesis and affecting the gut-liver axis. The microbial pathways involved, poorly understood in these pathologies, could represent useful prognostic markers.

To evaluate the relative quantification of bacterial SCFA genes in the IM of patients with DC and ACLF, and their association with different clinical outcomes and alpha-diversity.

Materials and Methods: Retrospective analytical study. Fecal samples from 19 ACLF patients, 16 DC, and 16 healthy controls (HC) were included. The butCoA, buk, ackA, and mmdA genes were quantified by qPCR. ROC curves and Kaplan-Meier analyses were performed using GraphPad. Approval number: CI-01023. No conflicts of interest are reported.

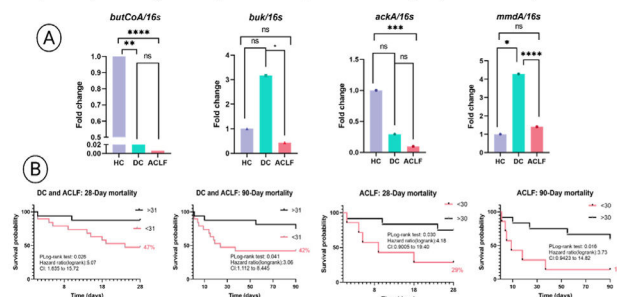
Results: Relative abundances of butCoA and ackA genes were significantly decreased in DC and ACLF patients ($p < 0.05$), whereas mmdA increased in DC. buk increased in patients who died at 28 days ($p < 0.01$) and showed a negative correlation with alpha-diversity, being associated with dysbiosis. Furthermore, buk and but-CoA discriminated 28-day mortality in DC and ACLF (AUROC 0.75 and 0.85, respectively). In Kaplan-Meier analyses, increased buk was associated with 28-day mortality of 53% in DC and 71% in ACLF.

Conclusions: Intestinal microbiota of DC/ACLF showed reduction of butCoA, ackA, and mmdA, correlating with functional loss. Increased buk was associated with 28-day mortality, loss of alpha-diversity and sepsis. These findings propose novel microbial biomarkers in the Mexican population which will have to be validated later.

Conflict of interest: None

(A) Relative quantification of bacterial genes encoding SCFA biosynthesis-related genes in feces of the three study groups and (B) Kaplan-Meier mortality analysis on 28- and 90-day mortality in DC and ACLF patients, according to the Cq value cut-off point for the buk gene, established by ROC curves.

ACLF patients, according to the Cq value cut-off point for the buk gene, established by ROC curves.



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#164

EFFECTS OF MELATONIN AND PHYSICAL EXERCISE ON SECONDARY BILIARY CIRRHOSIS

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Introduction and Objectives: Cirrhosis is characterized by the formation of septa and fibrotic nodules in the liver parenchyma, and it is a relevant public health problem. Bile duct ligation (BDL) is an effective experimental model for inducing secondary biliary cirrhosis.

Melatonin (MLT) has antioxidant, antifibrotic, and cytoprotective properties. Physical exercise (EX) has shown beneficial effects in different diseases.

To investigate the effects of MLT and EX on BDL-induced biliary cirrhosis in rats.

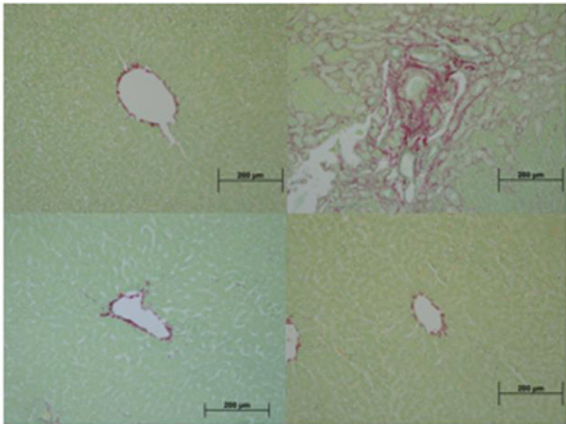
Materials and Methods: The study, was approved by CEUA/HCPA (2021-0642). We used 26 male Wistar rats (60 days, $\pm 350\text{g}$), distributed into four groups: CO, BDL, BDL+MLT, and BDL+EX. BDL was performed on day 1 in the experimental groups. From the 15th day onwards, MLT (20 mg/kg/day) was administered and the swimming protocol was started. On the 29th day, blood (for analysis of AST, ALT and FA) and liver were collected. Data were analyzed by One-Way ANOVA with Student-Newman-Keuls post-test (mean $\pm$ SE; $p < 0.05$).

Results: AST, ALT and FA were increased significantly in the LDB group vs. CO ($p < 0.05$), with reduction in the LDB+MLT and LDB+EX groups ($p < 0.05$). The Picrosirius staining indicated intense fibrosis in the LDB group, this effect was attenuated by treatments. GPx activity was reduced in the LDB group ($p < 0.01$), but increased with MLT and EX. CAT increased in the LDB group and decreased with treatments ($p < 0.05$). Nitric oxide levels increased in the LDB group and decreased with MLT.

Conclusions: MLT and EX promoted protective effects in the liver of rats with biliary cirrhosis, attenuating biochemical, oxidative and fibrotic changes.

Conflict of interest: None

Histological analysis of the liver (Picrosirius)



Picrosirius staining. Magnification 200X. CO: control, BDL: bile duct ligation group, BDL+MLT: BDL plus melatonin group and BDL+EX: BDL plus exercise group. BDL group presented portal fibrosis widening and ductular reaction. BDL+MLT and BDL+EX groups presented significant decrease in fibrosis.

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#168

ARTIFICIAL INTELLIGENCE FOR SURVIVAL PREDICTION IN HEPATOCELLULAR CARCINOMA: DEVELOPMENT AND VALIDATION OF A CLINICAL DATA-DRIVEN MODEL IN A COHORT OF 129 PATIENTS

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Introduction and Objectives: To develop and validate a predictive survival model for patients with hepatocellular carcinoma (HCC) associated with metabolic dysfunction–associated steatotic liver disease (MASLD), using artificial intelligence applied to widely available clinical and laboratory data. Additionally, to compare the model’s performance with traditional prognostic scores commonly used in HCC risk stratification.

Materials and Methods: This retrospective study included 129 patients with confirmed HCC and underlying MASLD. Clinical, laboratory, and tumor-related variables were analyzed, including metabolic comorbidities, liver function markers, tumor burden, cirrhosis-related complications, and established prognostic scores (Child-Pugh, FIB-4, and ALBI). The predictive model was built using Cox proportional hazards regression with L2 regularization to manage high-dimensional data and minimize overfitting. The XGBoost (Extreme Gradient Boosting) algorithm was implemented, with random allocation of the dataset into a training cohort (80%) and an internal validation cohort (20%). DeepSurv, a deep learning–based survival model, was also explored as a complementary strategy.

Results: The regularized Cox model demonstrated robust predictive performance, achieving a concordance index (C-index) of 0.774 in the validation cohort. The variables most strongly associated with reduced survival included tumor thrombosis (HR 8.27), hepatic encephalopathy (HR 4.66), and spontaneous bacterial peritonitis (HR 6.51), all statistically significant. The proposed model outperformed widely used prognostic scores such as BCLC, CLIP, and ALBI, showing superior discriminative ability for survival prediction in patients with HCC-MASLD.

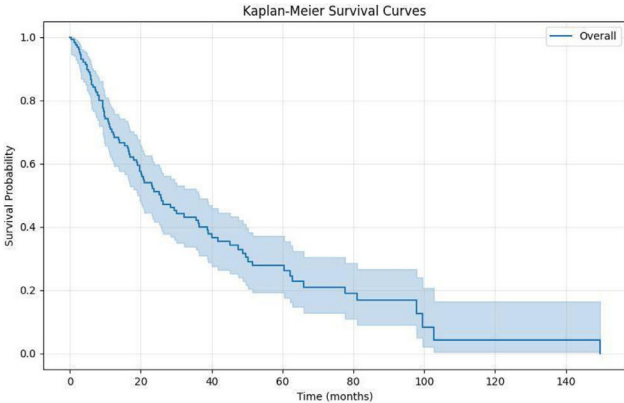
Conclusions: The AI-based model, built using easily accessible clinical and laboratory data, demonstrated superior performance in predicting survival in patients with HCC-MASLD. This approach enables more precise and scalable risk stratification, with direct applicability in real-world clinical practice.

Conflict of interest: None

Comparative Predictive Performance: Our Model Versus Traditional Prognostic Scores (C-index)

Model	Approach	C-index
Our Model	AI + Cox regression with L2 regularization	0.774
BCLC	Clinical staging	~0.60-0.68
CLIP	Clinical score	~0.62-0.70
ALBI	Objective liver function score	~0.65-0.70
HCC Risk	Continuous clinical variables	~0.72-0.74

Survival Curves in MASLD-Related HCC Based on AI-Identified Prognostic Variables



<https://doi.org/10.1016/j.aohep.2025.101974>