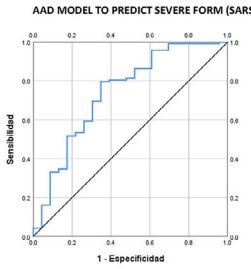
Model		Non-standarized Coeficients		StandarizedCoeficients	P	95% Confidence Interval for B		Colinearity statistics	
		B	Error Desv.	Beta		Inferior limit	Superior limit	Tolerance	VIF
1	C	2.721	.131		.000	2.462	2.980		
	AST	-.229	.033	-.512	.000	-.293	-.164	1.000	1.000
2	C	3.161	.198		.000	2.770	3.551		
	AST	-.194	.034	-.435	.000	-.261	-.127	.878	1.139
	DD	-.081	.028	-.221	.004	-.135	-.026	.878	1.139
3	C	3.896	.414		.000	3.077	4.714		
	AST	-.185	.034	-.413	.000	-.252	-.118	.860	1.163
	DD	-.070	.028	-.190	.014	-.125	-.014	.844	1.185
	Age	-.218	.108	-.148	.046	-.433	-.004	.915	1.093

AST, aspartate aminotransferase; C, constant; DD, D dimer; VIF, variance inflation factors.

Resume of the model:

1. R=0.512, r^2=0.262, r^2 adjusted=0.256, standard error=0.331.
2. R=0.552, r^2=0.305, r^2 adjusted=0.294, standard error=0.322.
3. R=0.570, r^2=0.325, r^2 adjusted=0.310, standard error=0.318. Durbin-Watson=1.53.



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O-27 IMPACT OF HBV GENOTYPE F IN THE DIAGNOSIS AND EVOLUTION OF PATIENTS WITH HBEAG-NEGATIVE CHRONIC HBV INFECTION

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Background: The quantitative hepatitis B surface antigen (qHBsAg) threshold of 1,000 IU/ml has been proposed to distinguish HBeAg-negative chronic infections from HBeAg-negative chronic hepatitis, to assess risk of liver disease progression, and to predict HBsAg clearance. There is evidence that qHBsAg vary significantly among genotypes, however, there is scarce data on genotype F, the most prevalent in Latin America.

Aims: To analyze the impact of HBV genotype F on qHBsAg inpatients with HBeAg-negative chronic infection and to describe clinical and virological outcomes.

Methods: HBV-DNA and qHBsAg serum levels of 141 patients with HBeAg-negative chronic infection were correlated with HBV genotype, who were followed for 10.6±7.4 years.

Results: The overall genotype distribution was as follows: F 46.8%, D 26.1%, A 25.2%, and B 0.7% and C 0.7%. While no impact of the HBV genotype on HBV DNA levels was observed, qHBsAg differed significantly among genotypes (p<0.001). The highest HBsAg levels were observed in genotype F (4.0±1.1 Log_{10}IU/ml) followed by genotype A (3.9±0.6 Log_{10}IU/ml) and genotype D (2.4±0.9 Log_{10}IU/ml). In genotype A and F, qHBsAg <3.0 Log_{10}IU/ml were only observed in 10.7% and 11.5% respectively.

Regardless of the HBV genotype, spontaneous clearance of HBsAg was observed in 17 cases. Of these, 12 patients presented qHBsAg <100 IU/ml one year before clearance. Despite, 101 (71.6%) patients showed qHBsAg >3.0 Log_{10}IU/ml, no cases of advanced liver disease or hepatocellular carcinoma were observed at the end of follow-up.

Conclusions: This study provides new insights into the impact of HBV genotypes on serum HBsAg levels, emphasizing the need to implement genotype-specific cut-off to achieve diagnostic certainty in the identification of HBeAg-negative chronic infection and the risk of liver disease progression, particularly on infections with genotypes A and F. Moreover, HBsAg serum levels can became a reliable biomarker to predict HBsAg clearance.

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O-28 DRUG-INDUCED LIVER INJURY IN LATINAMERICA: First ten years' experience of the ongoing LATINDILI Network

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Introduction: In 2011, the Latin-American DILI-Network (LATINDILIN) set up under the guidance of the Spanish DILI Registry a network of hepatologists to prospectively identify and characterize DILI patients.

Aim: To evaluate the drugs more frequently associated with DILI in LA, clinical phenotype and outcome.

Methods: Demographics, clinical and biochemical parameters of all cases included in the LATINDILI Network were analysed according to the type of liver injury (hepatocellular, Hep; cholestatic, Chol and mixed, Mix).

Results: 404 DILI cases were included. Anti-infectives (31%), musculoskeletal system drugs (13%) and herbal products (9.2%) were the main causative therapeutic drug classes. Mean age was 49 years (female sex, 61%). Hep injury predominated (62%) whereas Chol and Mix patterns were 24% and 15% of cases, respectively. Chol patients (mean age 56y) were older than Hep and Mix cases (47 and 50, $p<0.05$). Jaundice was more prevalent in Chol and Mix injury than in Hep cases (65% vs 75% vs 58%, respectively, $p=0.062$), though no differences in hospitalization rates were observed (Hep 43%, Chol and Mix 46%, $p=0.867$). Of note, 12 cases, mostly Hep, had a positive rechallenge. Positive autoantibodies were more common in Hep cases (25% vs Chol 9.1% vs Mix 19%, $p=0.010$), with nitrofurantoin/herbal products as the most common causative agents. Hep cases showed a higher risk of severe/fatal injury (18% vs 6.0% and 1.8% in Chol and Mix cases, respectively, $p<0.001$). The new Hy's law performed as expected, with 14% of ALF/Tx cases. Hep cases more frequently died from liver-related death (3.5%) compared with Chol (1.1%) and Mix (0) cases.

Conclusions: In Latin-American DILI cases with Hep pattern predominated, showing a higher severity and most frequent inadvertent re-exposition. The LATINDILI Network is proving as an important tool for the characterization of DILI singularities in this world region, and improvement of Public Health.

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OP-1 GUT METATRANSCRIPTOMICS AND METABOLOMICS REVEAL ASSOCIATION OF CYSTEINE AND PURINE METABOLISMS WITH METABOLIC ASSOCIATED FATTY LIVER DISEASE (MAFLD)

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Background: The gut microbiome represents a niche for biomarkers discovery to risk-stratify MAFLD patients. However, each population may have unique microbiome signatures and studies are needed in Latin America where MAFLD prevalence and severity are high.

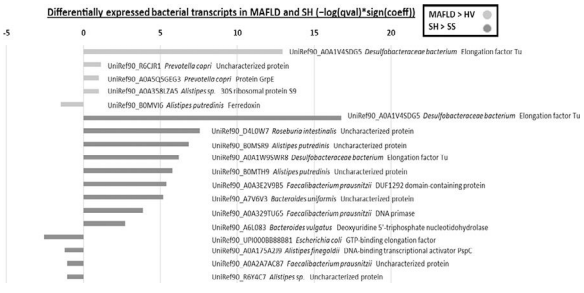
Aims: To identify gut metatranscriptome and metabolome signatures associated with MAFLD and steatohepatitis (SH) in Argentina.

Methods: Stool samples, diet, demographic and clinical data were obtained from 33 biopsy-proven patients (12 simple steatosis -SS- and 21 SH) and 19 healthy volunteers (HV). PNPLA3 rs738409 SNP was genotyped. HPLC, flow injection analysis with MS/MS in tandem and MetaboAnalyst-v4.0 were used for metabolomics. RNA-seq was performed in NovaSeq6000®. bioBakery-v1.8 and Maaslin2-v1.2.0 were used for data analysis.

Results: BMI was higher in MAFLD patients, particularly in SH ($q=4.49e-06$). After adjusting for BMI, 89 and 53 gene family clusters were differentially expressed between HV and MAFLD and between SS and SH, respectively ($q<0.1$). Pathways related to sulfur oxidation, short-chain fatty acid metabolism, purine metabolism and lipopolysaccharide synthesis were enriched in MAFLD patients when compared with HV and in SH when compared with SS, whereas folate synthesis was enriched in SS patients ($q<0.1$). Gene expression associated with Desulfobacteraceae bacteria harbored most of the functional features of MAFLD patients when compared with HV, and of SH patients within the case group (Figure). The PNPLA3 GG genotype was related to decreased hydrolysis of glycerolipids, high expression of *Clostridium cadaveris* and low expression of Desulfobacteraceae bacteria associated genes ($q<0.1$).

Higher concentrations of xanthine, implicated in purine metabolism, and of the sulfur amino acid cysteine were detected in the stool of MAFLD patients when compared with HV, and of SH patients within the case group (BMI-adjusted $q<0.1$).

Conclusion: Cysteine and purine metabolisms are strongly related to MAFLD and SH in Argentinian patients. Cysteine and xanthine could be useful as potential biomarkers.



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* Both Authors Contributed Equally to this Study.