[1] *Laboratório de Gastroenterologia Clínica e Experimental (LIM-07) do Departamento de Gastroenterologia e Hepatologia do Hospital das Clínicas HC-FMUSP da Facultade de Medicina da Universidade de São Paulo, São Paulo, SP, Brazil*
[2] *Departamento de Gastroenterología, Faculdade de Medicina da Universidade de São Paulo, São Paulo, SP, Brazil*
[3] *Laboratório de Carboidratos e Radioimunesaio (LIM-18), Hospital das Clínicas HC-FMUSP da Faculdade de Medicina da Universidade de São Paulo, São Paulo, SP, Brazil*
[4] *Programa de Pós-Graduação em Medicina, Universidade Nove de Julho (UNINOVE), São Paulo, SP, Brazil*

Introduction: Genetic variants in the uncoupling protein 3 (*UCP3*) gene have been associated with obesity, type 2 diabetes and atherogenic lipid profile, with conflicting results.

Objective: Our study evaluated the possible association between *UCP3* single nucleotide polymorphisms (SNPs) with nonalcoholic steatohepatitis (NASH) and metabolic syndrome (MetS) in NAFLD patients.

Methods: *UCP3* SNPs rs1726745, rs3781907 and rs11235972 were genotyped in 158 biopsy-proven NAFLD patients. Patients were evaluated according to the presence of nonalcoholic fatty liver (NAFL) or NASH and, according to the absence or presence of MetS. Statistics were performed with JMP, R and SHEsis software's.

Results: The TT genotype of rs1726745 was protective for MetS (OR=0.18; 95% CI=0.05-0.61; p=0.006) and was associated with lower body mass index (BMI) in the general sample (p=0.01) and in the NASH group (p=0.02). The rs1726745-T was associated with lower values of AST (p=0.001), ALT (p=0.0002), triglycerides (p=0.01) and total cholesterol (p=0.02) in the general sample. There were lower values of aminotransferases strictly in individuals with NASH (AST, p=0.002; ALT, p=0.0007) and with MetS (AST, p=0.002; ALT, p=0.001). The rs3781907-G was associated with lower GGT values (p=0.002) in the general sample and in the NASH group (p=0.004) and with MetS group (p=0.003) and, with protection for advanced fibrosis (OR=0.25; 95% CI=0.08-0.69; p=0.01).The rs11235972-A was associated with lower GGT values (p=0.006) in the general sample and in the NASH group (p=0.01) and with MetS group (p=0.005), with fibrosis absence (OR=0.34; 95% CI=0.14-0.80; p=0.01) and protection for advanced fibrosis (OR=0.17; 95% CI=0.03-0.56; p=0.01). The TAA haplotype was protective for NASH (OR=0.01; 95% CI=0.00-0.12; p=0.002) and TGG haplotype was protective for MetS (OR=0.22; 95% CI=0.07-0.69; p=0.01).

Conclusion: *UCP3* variants were associated with protection against NASH and MetS, in addition to lower values of liver enzymes, lipid profile, BMI and, lesser fibrosis severity in the studied population.

Table 1
Genotype frequencies of *UCP3* polymorphisms according to the presence of metabolic syndrome

UCP3 SNPs 5'->3'	With MetS	Without MetS	OR (CI 95%)	*P value*
rs11235972			-**	0.99
GG	0.706	0.815		
GA	0.254	0.185		
AA	0.040	0.000		
MAF	0.167	0.092		
rs3781907			0.51 (0.05 – 3.88)	0.52
AA	0.609	0.556		
AG	0.313	0.333		
GG	0.078	0.111		
MAF	0.234	0.277		
rs1726745			0.18 (0.05 – 0.61)	0.006*
CC	0.323	0.231		
CT	0.472	0.346		
TT	0.205	0.423		
MAF	0.441	0.596		

OR (odds ratio) for the minor allele in a recessive model obtained in logistic regression analysis adjusted for sex, age, type 2 diabetes mellitus and dyslipidemia. *$P \leq 0.02$.
**OR [2428148 (9.9×1015 – -)]: due the AA genotype absence among Without MetS individuals, it was not possible to calculate precisely the OR.
MAF, minor allele frequency; MetS, metabolic syndrome; SNPs, single nucleotide polymorphisms; *UCP3*, uncoupling protein 3 gene.

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O-21 SOLUBLE CD163 PERFORMANCE AS A NON-INVASIVE BIOMARKER OF DIFFERENT LIVER CONDITIONS

Cairoli Victoria[1], Casciato Paola Cecilia[2], Giadans Cecilia Graciela[1], Ameigeiras Beatriz[3], De Matteo Elena[1], Preciado Maria Victoria[1,#], Valva Pamela[1,#]

[1] *Multidisciplinary Institute for Investigation in Pediatric Pathologies (IMIPP), CONICET-GCBA, Laboratory of Molecular Biology, Pathology Division, Ricardo Gutiérrez Children's Hospital, Gallo 1330, CABA, C1425, Argentina*
[2] *Liver Unit, Italian's Hospital of Buenos Aires, Pres. Tte. Gral. Juan Domingo Perón 4190, CABA, C1199 ABH, Argentina*
[3] *Liver Unit, Ramos Mejía Hospital, Gral. Urquiza 609, CABA, CP1221, Argentina*

Introduction: Development of noninvasive tests to predict liver injury represents a current goal. Soluble CD163 (sCD163) is a specific plasma biomarker of macrophage activation with promising clinical relevance in estimating damage severity and predicting the outcome in different liver conditions.

Aim: To evaluate sCD163 performance as a non-invasive marker of liver damage.

Materials and Methods: sCD163 was quantified by enzyme-linked-immunosorbent assay in plasma from 123 patients (57 HCV, 20 HCV/HIV, 10 HBV, 36 MAFLD) obtained at time of liver biopsy. 20 healthy donors were included as controls. sCD163 values were compared among disease conditions and related to histological parameters of liver damage. Diagnostic performance was assessed by the area under the receiver operating characteristic curves (AUROC).

Results: Patients' sCD163 levels [0.579g/L (0.034 -3.596)] were higher than controls' [0.221g/L (0.116-0.549)] ($p<0.0001$, Mann-Whitney). However, in a detailed analysis according to disease etiology, only viral conditions showed significantly higher sCD163 levels [HCV+ 0.7520g/L (0.168-3.468), $p<0.0001$; HCV+/HIV+ 0.964g/L (0.345-3.596), $p<0.0001$; HBV+ 0.526g/L (0.199-0.802), $p=0.0375$, Dunn's-multiple-comparisons]. MAFLD patients displayed similar sCD163 levels to the control group [0.345g/L (0.0338-1.804)]. HCV mono- and HIV-coinfected patients shared the highest sCD163 levels. In relation to liver injury, HCV+ and HCV+/HIV+ patients specifically displayed a profile with higher sCD163 levels associated with more severe hepatitis. Remarkably, just in HCV+/HIV+ cases these differences were significant ($p=0.0097$ Mann-Whitney) and the AUROC analysis demonstrated a good performance in predicting hepatitis severity [AUROC=0.875; cutoff: 0.672g/L (91.67% sensitivity, 83.33% specificity)]. Concerning fibrosis, only HCV+ and HCV+/HIV+ patients with significant fibrosis displayed a profile with high sCD163 level; however, the AUROC analysis showed good performance just for HCV +/HIV+ patients [AUROC=0.825); cutoff: 0.9640g/L (100% sensitivity, 60% specificity)].

Conclusion: Plasmatic sCD163 is elevated in patients with several liver conditions but it can be particularly used as a marker of liver inflammation and fibrosis in HCV/HIV co-infected patients.

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[#] 'These two authors equally contributed to this work'