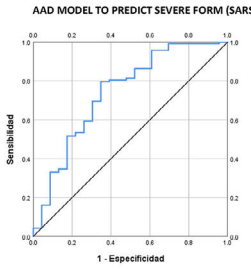
Model		Non-standarized Coeficients		StandarizedCoeficients	P	95% Confidence Interval for B		Colinearity statistics	
		B	Error Desv.	Beta		Inferior limit	Superior limit	Tolerance	VIF
1	C	2.721	.131		.000	2.462	2.980		
	AST	-.229	.033	-.512	.000	-.293	-.164	1.000	1.000
2	C	3.161	.198		.000	2.770	3.551		
	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.



https://doi.org/10.1016/j.aohep.2021.100513

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

Hugo Fainboim[1], Nicolas Dibenedeto[2], Paz Silvia[1], Mendizabal Manuel[3], Soledad Campuzano[1], Micaela Martinez[4], Luciana Tadey[5], Gabriel Deluchi[5], Bouzas Belen[5], Mammana Lilia[5], Diego Flichman[4]

[1] *Unidad de Hepatopatías Infecciosas, Hospital de Infecciosas F.J Muñiz, Buenos Aires, Argentina*
[2] *Hospital Arrecifes, Buenos Aires, Argentina*
[3] *Hospital Universitario Austral, Buenos Aires, Argentina*
[4] *Instituto de Investigaciones Biomédicas en Retrovirus y Sida, Buenos Aires, Argentina*
[5] *Unidad de VirologÍa, Hospital de Infecciosas "Francisco J. Muñiz", Buenos Aires, Argentina*

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.

https://doi.org/10.1016/j.aohep.2021.100514

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

Fernando Bessone[1], Nelia Hernandez[2], Raymundo Parana[3], Manuel Mendizabal[4], Adriana Sanchez[2], Vinicius Nunes[3], Ezequiel Ridruejo[5], Daniela Schiodi[2], Genario Santos[3], Eduardo Fassio[6], Schinoni Maria I.[3], Hugo Tanno[1], Martin Tagle[7], Pedro Montes[8], Marco Arrese[9], Nahum Mendez-Sanchez[10], Javier Brahm[11], Marcos Girala[12], Isabel Lizarzábal M.[13], Edgardo Mengual[13], Enrique Carrera[14], Fernando Contreras[15], Inmaculada Medina-Caliz[16], Mercedes Robles-Díaz[16], Aida Ortega-Alonso[16], Miren García-Cortes[16], Ismael Alvarez-Alvarez[16], Hao Niu[16], Elvira Bonilla[16], Isabel Lucena M.[16], Andrade Raul J.[16]

[1] *Hospital Provincial del Centenario, University of Rosario School of Medicine, Rosario, Argentina*
[2] *Clínica de Gastroenterología, Hospital de Clínicas, Universidad de la República, Montevideo, Uruguay*
[3] *Hospital Universitário Prof. Edgard Santos-UFBA, Salvador, Brazil*
[4] *Hospital Universitario Austral, Buenos Aires, Argentina*
[5] *Centro de Educación Médica e Investigaciones Clínicas, Buenos Aires, Argentina*
[6] *Hospital Alejandro Posadas, Buenos Aires, Argentina*
[7] *Clínica Anglo Americana, Lima, Perú*
[8] *Hospital Nacional Daniel Alcides Carrion, Callao, Perú*
[9] *Departamento de Gastroenterología. Facultad de Medicina Pontificia Universidad Católica de Chile, Chile*
[10] *Fundación Clínica Médica Sur, Mexico City, Mexico*
[11] *Hospital Clínico Universitario de Chile, Chile*
[12] *Hospital de Clínicas, Asunción del Paraguay, Paraguay*
[13] *Hospital Universitario de Maracaibo, Maracaibo, Venezuela*
[14] *Hospital de Especialidades Eugenio Espejo, Quito, Ecuador*
[15] *Universidad Nacional Pedro Henriquez, Santo Domingo, República Dominicana*
[16] *Servicios de Aparato Digestivo y Farmacología Clínica, Hospital Universitario Virgen de la Victoria,*