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Letters to the Editor

Viral genotypes and human rs12979860 polymorphism of the IFNL3 gene in hepatitis C infected patients in Southern Brazil

Dear Editor,

Hepatitis C virus (HCV) infection is a global health problem and approximately 80% of the patients develop chronic hepatitis C, which can progress to liver cirrhosis and hepatocellular carcinoma. HCV genotype is a classical predictor of the success of the standard treatment (interferon-α in combination with ribavirin). HCV genotype 1 carriers have usually a lower rate of response than patients infected with HCV genotypes 2 and 3.[1] Human single nucleotide polymorphisms near the gene for interferon-λ3 (IFNL3; formerly known as *IL28B*) were also recently associated with spontaneous HCV clearance and sustained response to interferon-based therapy.[2] The present study aimed to determine the frequency of the HCV and *IFNL3* genotypes in hepatitis C patients from the North region of Rio Grande do Sul state, Southern Brazil.

Adult individuals with chronic hepatitis C attended in referral services for patient care in Passo Fundo (a medium-sized urban center in the North region of Rio Grande do Sul state) were selected from August 2010 to July 2011. Socio-demographic data were obtained from a structured questionnaire and patient medical records were reviewed to obtain clinical and virological information. *IFNL3*-molecular analysis was performed as previously described.[2] The study was approved by the Research Ethics Committee of the Universidade Luterana do Brasil (ULBRA).

A total of 191 HCV-infected patients were included in the study. Patients were predominantly female (52.9%) and had a mean age of 51.6 ± 11.4 years. Approximately half of the participants ($n = 92$, 48.2%) received blood transfusions and 75 patients (39.3%) reported that this condition was the possible HCV transmission route. Use of sharp objects (26.7%) and needle sharing (17.8%) were also cited as possible transmission factors. HCV genotype 1 was found in 76 (39.8%), genotype 2 in 46 (24.1%) and genotype 3 in 69 patients (36.1%). HCV genotype 1 was significantly more often in users of illicit drugs, while genotype 2 was more frequently found in women and old people. Sixty patients (31.4%) showed the CC, 97 (50.8%) CT and 34 (17.8%) TT *IFNL3* genotypes (Table 1).

Some HCV genotypes have a restricted geographical distribution (genotypes 4-6), while others (genotypes 1-3) are more broadly disseminated. HCV genotype 1 is the most prevalent in the world.[1] In the present study, genotype 1 was also demonstrated in the highest frequency, followed by genotypes 3 and 2, respectively. Other studies in Brazil have also shown the occurrence of these three genotypes, but genotype 1 with frequencies over 60%, while genotype 2 lower than 10%.[3,4] This unusual high frequency of HCV genotype 2 confirms the results observed in a previous study.[5] In the present report it was further demonstrated the high proportion of old women infected with this genotype. *IFNL3* CC genotype, a good human prognostic factor of treatment outcome, was also found in a percentage similar to other Brazilian study.[2]

In conclusion, the data obtained in the present study have shown a high frequency of HCV genotype 2 in an urban center in Southern Brazil and suggest the HCV genotypes could have different transmission routes.

Table 1 – Distribution of socio-demographic and epidemiological characteristics in patients stratified according to HCV genotypes.

Variable	Total (*n* = 191)	HCV genotypes			
		1 (*n* = 76)	2 (*n* = 46)	3 (*n* = 69)	*p*
Male gender	90 (47.1)	42 (55.3)	15 (32.6)	33 (47.8)	0.052
Age (years)	51.6 ± 11.4	50.0 ± 10.0	55.6 ± 13.8	50.7 ± 10.6	0.024
Skin color					0.204
White	126 (66.0)	44 (57.9)	37 (80.4)	45 (65.2)	
Mixed/mulatto	54 (28.2)	27 (35.5)	7 (15.2)	20 (28.9)	
Black	11 (5.8)	5 (6.6)	2 (4.3)	4 (5.8)	
Educational level					0.156
Complete primary education or less	97 (50.8)	33 (43.4)	23 (50.0)	41 (59.4)	
Secondary or higher education	94 (49.2)	42 (56.6)	23 (50.0)	28 (40.6)	
Possible forms of HCV infection[a]					0.577
Sex	19 (9.9)	8 (10.6)	1 (2.2)	10 (14.5)	
Blood transfusion	75 (39.3)	26 (34.2)	23 (47.8)	27 (39.1)	
Infected material	51 (26.7)	19 (25.0)	15 (32.6)	17 (24.6)	
Hemodialysis	2 (1.0)	–	1 (2.2)	1 (1.4)	
Sharing needles	34 (17.8)	19 (25.0)	5(10.9)	10 (14.5)	
Occupational exposure	7 (3.7)	2 (2.6)	1 (2.2)	4 (5.8)	
Smoking drug use	37 (19.4)	25 (32.9)	1 (2.2)	11 (15.9)	<0.001
Snorting drug use	28 (14.7)	19 (25.0)	1 (2.2)	8 (11.6)	0.001
Injecting drug use	21 (11.0)	13 (17.1)	1 (2.2)	7 (10.1)	0.026
Blood transfusion	92 (48.2)	33 (43.4)	25 (54.3)	34 (49.3)	0.491
Hemodialysis	4 (2.1)	1 (1.3)	1 (2.2)	2 (2.9)	0.831
Tattoo	343(17.3)	18 (23.7)	6 (13.0)	9 (13.0)	0.163
Piercing	4 (2.1)	–	1 (2.2)	3 (4.3)	0.129
IFNL3 – CC genotype	60 (31.4)	21 (27.6)	17 (37.0)	22 (31.9)	0.339

Variables expressed as number (percentage) or mean ± standard deviation.

[a] Totals do not coincide due to lack of data from certain participants in the study.

Conflicts of interest

The authors declare no conflicts of interest.

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