Differential distribution of hepatitis C virus genotypes in different patient’s cohorts

Minassian ML (1); Vladimisky SN (1); Soto SS (1); Altabert NR (1); Otegui LO (1); Brajerman LS (1); Sentinel Units for Viral Hepatitis (2); González JE (1).

BACKGROUND
Genotyping of Hepatitis C virus (HCV) continues to be epidemiologically relevant. In Argentina sub genotype (sGt) 1b is the most prevalent followed by 1a. The circulation of sGt 2c, 3a and 4a was also reported although at a lower frequency.

The aim of the present study was to analyze and compare the HCV Gt distribution, in particular the relation sGt 1b/1a, studying two cohorts of patients.

RESULTS

The different distribution of Gt2 in both cohorts reflects its prevalence previously reported in Córdoba province. The different proportion of sGt 1a and 1b in both cohorts reflects a different prevalence in risk factors, demographic characteristics and in the origin of the populations studied. Differences by region of origin should be studied in greater depth, but could be due, among other causes, to differences in risk factors not analyzed in this study, such as intravenous drug addiction, which is not reported in the referral of samples to the NRLHV.

CONCLUSIONS

In the multivariate analysis (OR; CI 95%) the proportion sGt1b/1a evidenced an association with: Gender (1.65; 1.13-2.43); Age (from 41 years: 2.9; 1.83-4.63); HIV (0.31; 0.18-0.54); and Geographic region (reference: FPU); Cuyo (11.05; 3.1-39.44), Northwest (4.93; 1.30-18.77), Pampeana (4.94; 1.43-17.08) and Patagonia (2.22; 0.64-7.71); showing a greater proportion of sGt1a in the regions Metropolitana, Northeast, Patagonia and FPU.The variable Cohort was significant only in the univariate analysis (0.35; 0.25-0.50).

Conflicts of Interest: None

Contact Information
NAME: Jorge E. Gonzalez
TEL NO: +54 911 6330304
EMAIL: jegonzalez@anlis.gov.ar

Methods
Cohort 1 (C1): 294 patients studied between June 2011-August 2016 at the National Reference Laboratory for viral Hepatitis (NRLHV). Mean age 46 years, 68% male. 49% HIV co-infected. The majority of patients (37%) came from public hospitals from the Metropolitana region (Buenos Aires City and surroundings), 12% of patients were prisoners at Federal Prison Units (FPUs).

Cohort 2 (C2): 528 patients studied between January 2007-July 2015 at the Sentinel Unit Network (SU)-27 public Hospitals located in 18 out of the 24 provinces of the country-which are implicated in intensive surveillance for viral hepatitis. Mean age 49 years, 51% male, 8% HIV co-infected. The majority of patients (55%) came from Pampeana region (Center); Córdoba, Mar del Plata, Rosario and Santa Fe cities.

The distribution of Gt was analyzed according to the following variables: age (up to 40 years, from 41 years), gender, HIV co-infection, Cohort and origin categorized by geographic region and FPU. Statistical analysis was performed using unvariable and multivariable logistic regression; p<0.05 was considered statistically significant.

In C1 the genotypes were determined by LIPA; in C2 by LIPA (60%) and RFLP (37%) (no data 3%).

Bivariant Distribution of hepatitis C virus genotypes in different patient’s cohorts

<table>
<thead>
<tr>
<th>VARIABLES</th>
<th>C1 NRLHV</th>
<th>C2 SU</th>
</tr>
</thead>
<tbody>
<tr>
<td>HIV Co-infection</td>
<td>52.0%</td>
<td>48.0%</td>
</tr>
<tr>
<td>Gender</td>
<td>Female 31.3%</td>
<td>Male 68.7%</td>
</tr>
<tr>
<td>Age</td>
<td>No data 6.8%</td>
<td>Up to 40 years 18.7%</td>
</tr>
<tr>
<td>Geographic Region</td>
<td>Cuyo 15.0%</td>
<td>Metropolitana 36.7%</td>
</tr>
</tbody>
</table>

Conclusions
The different distribution of Gt2 in both cohorts reflects its prevalence previously reported in Córdoba province. The different proportion of sGt 1a and 1b in both cohorts reflects a different prevalence in risk factors, demographic characteristics and in the origin of the populations studied. Differences by region of origin should be studied in greater depth, but could be due, among other causes, to differences in risk factors not analyzed in this study, such as intravenous drug addiction, which is not reported in the referral of samples to the NRLHV.