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ORIGINAL ARTICLE

Changes in the epidemiology and distribution of the hepatitis C virus genotypes in North-Eastern Spain over the last 35 years

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Abstract

Background: Genotypic distribution and epidemiology of HCV infection in Western Europe countries has changed over the last decades.

Aim: To establish the local genotypic profile and characterize the associated demographic variables.

Material and method: All the genotyping from 1988 to 2015 were considered. Associated demographic variables were included in logistic regression models. Genotyping was carried out with updated commercial kits.

Results: Genotype 1b was the most prevalent (42.4%) followed by 1a (22.5%), 3 (18.6%), 4 (10.6%) and 2 (4.6%). The prevalence of 1a was higher in males, in patients younger than 45 and in intravenous drug users (IDU). 1b was more frequent in older than 45, with transfusion-associated and parenteral/nosocomial infections and in immigrants from Eastern Europe. Genotype 2 was highly prevalent in the postransfusional route (54.9%). Genotype 3 prevalence was high in males, in patients younger than 45, in IDU (69.3%) and in Asian and Eastern European immigrants. Genotype 4 was high in males, in patients younger than 45, and in IDU (63.5%). 1a, 3, 4 were the most prevalent genotypes in HIV-coinfected patients. There was a significant decline in genotype 1b and an increase in genotypes 3 and 4 over time.

Conclusions: There has been a decline of genotype 1b, associated with transfusion or parenteral/nosocomial infections, and increases in the prevalence of genotypes 1a, 3 and 4 associated with male gender and IDU, now the most prevalent infection route. Immigration

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contributed with genotype 2 infections from Africa and genotype 1b and 3 infections from Eastern Europe and Asia.

PALABRAS CLAVE
VHC;
Genotipos;
Virus de la hepatitis C;
Hepatitis C crónica;
Epidemiología

Cambios en la epidemiología y distribución de los genotipos del virus de la hepatitis C en el nordeste de España durante los últimos 35 años

Resumen

Antecedentes: La distribución genotípica y la epidemiología de la infección por el VHC en los países de Europa Occidental ha variado en las últimas décadas.

Objetivo: Establecer el perfil genotípico local y distinguir las variables demográficas asociadas.

Material y método: Se han tenido en cuenta todas las genotipificaciones desde 1988 a 2015. Las variables demográficas asociadas se incluyeron en modelos de regresión logística. La genotipificación se realizó con kits comerciales actualizados.

Resultados: El genotipo 1b fue el más prevalente (42,4%), seguido por 1a (22,5%), 3 (18,6%), 4 (10,6%) y 2 (4,6%). La prevalencia de 1a fue mayor en varones, en pacientes menores de 45 años y en consumidores de drogas por vía intravenosa (CDVI). El genotipo 1b fue más frecuente en pacientes mayores de 45 años, con infecciones relacionadas con la transfusión y de tipo parenteral/nosocomial, y en inmigrantes de Europa Oriental. El genotipo 2 fue muy prevalente en la vía postransfusional (54,9%). La prevalencia del genotipo 3 fue elevada en varones, en pacientes menores de 45 años, en CDVI (69,3%) y en inmigrantes asiáticos y de Europa Oriental. El genotipo 4 fue elevado en varones, en pacientes menores de 45 años y en CDVI (63,5%). Los genotipos 1a, 3 y 4 fueron los más prevalentes en pacientes coinfectados con el VIH. Hubo una disminución considerable del genotipo 1b y un aumento en los genotipos 3 y 4 en el tiempo.

Conclusiones: Se ha producido una disminución del genotipo 1b, relacionado con transfusiones o infecciones parenterales/nosocomiales, y un aumento en la prevalencia de los genotipos 1a, 3 y 4, relacionados con el sexo masculino y los CDVI, que actualmente son la vía de infección más prevalente. La inmigración contribuyó con infecciones del genotipo 2 de África e infecciones de los genotipos 1b y 3 de Europa Oriental y Asia.

Background

Hepatitis C virus (HCV) infection constitutes a severe public health problem with approximately 80 (64–103) million viremic patients worldwide,[1] and a natural history leading to liver cirrhosis which entails a risk of hepatocellular carcinoma between 1 and 5% per year.[2,3] HCV shows a great genetic variability due to its high replication rate and the reduced capacity of the viral polymerase to correct the errors of the genome that appear during replication. This variability has resulted, in addition to quasi species in every infected subject, in seven viral genotypes (denoted 1 to 7) and more than 67 subtypes (denoted alphabetically a, b, c, etc.).[4] The majority of infections are caused by genotypes 1a, 1b, 2, 3 (almost exclusively 3a) and 4, while infections with genotypes 5, 6 and 7 are less frequent or limited to specific geographic areas.[1,5]

The viral genotype has been determinant in the therapeutic guidelines of chronic HCV infection with pegylated-interferon plus ribavirin[6] and with first-generation protease inhibitors.[7,8] Although its usefulness has been greatly reduced by the introduction of new pangenotypic oral treatments,[9–11] genotype determination remains crucial due to the marked geographical differences in the genotypic profiles which may be affected by migration trends and by changes in the routes of infection.[1,5,12–16]

At the end of World War II there was an explosive spread of genotype 1b infections associated with the mass implementation of blood transfusions and unsafe health practices in Western countries.[15] Almost simultaneously there were a significant spread of genotype 1a linked to unsafe health practices and the rapid expansion of intravenous drug use (IDU).[15] These changes paralleled with a marked increase in genotype 3a infection from the Asian continent associated with the heroin trade and IDU[16] and migratory movements of certain populations.[17] The spread of genotype 4, endemic in the Middle East, Egypt and Central Africa, to Europe has had different epidemiological settings. While in Egypt genotype 4a spread was propagated by mass parenteral treatment campaigns for the control of schistosomiasis during the twentieth century,[18] the spread of other subtypes of genotype 4 in the developed world, especially in Europe, is much more recent and is linked to demographic movements and, above all, to IDU.[19,20]

The aim of this study was to establish the genotypic profile of HCV infection in the study area of Girona, Catalonia,