

Prevalence and Transmission of Hepatitis C in the Latino Community

by Jose Azocar, MD, DSc

The epidemiology of hepatitis C (HCV) has been most extensively characterized in Caucasians. Therefore, little is known about prevalence and transmission rates of HCV infection within non-Caucasian ethnic groups.

A seroprevalence study in a sample of 500 randomly selected Latino patients living in Western Massachusetts showed a prevalence of 8% with anti-HCV antibodies was found (95% CI 5.8% -10.7%), significantly higher than the 1.8% described in the general population in the U.S. In parallel, a case-control study for evaluating risk factors for HCV infection in Latinos was undertaken. Our sample was largely unemployed, with unstable marital status, living in high population density, and suffered high rates of intra-familial incarceration. Our data suggest that this low socioeconomic status and accompanying low level of education were not independently associated with HCV infection. This data contrast with previous reports that poverty and absence of high school diploma were independently associated with HCV infection in a Latino population. Our results show that **risk factors associated with blood-borne disease such as intravenous drug (IVD) use, tattooing, high-risk sexual behavior, and history of incarceration are the main risk factors for HCV infection** in this population.

In our HCV-infected population the most common HCV genotype was genotype 1 (73.2%); with the remaining corresponding to infection by the HCV genotypes 2, 4 and 3 (15.2%, 7.8% and 1.5%), similar to the one described in other ethnic groups in the U.S. Among our Latino subjects who had been exposed to HCV infection, 22.5% had no detectable HCV-RNA in plasma and were considered to have undergone spontaneous virus clearance (SC), while 77.5% developed chronic viremia (CV) as determined by the presence of both HCV-RNA in plasma and anti-HCV antibodies. We found no relationship between the viral outcome (SC vs. CV) and age, gender, or coinfection with HIV-1 and or HBV. Most of our population was male and reflect the epidemiology of HCV in our population. As expected, the population with CV had a significantly higher number of subjects with abnormal ALT values, a hallmark of HCV-associated chronic liver disease.

Previous studies on genetic determinants of the viral outcome indicate that polymorphism of MHC genes (major histocompatibility complex) may be important determinants of an effective immune response leading to SC. In Caucasians, the class II alleles DRB1*0110 and DQB1*0301 are associated with SC, while in other ethnic groups, different class II alleles are associated with the same outcome. In our Latino population we found that class II alleles DRB1*11 and DQB1*0501 are associated with CV. The conflicting associations reported between class II alleles and the HCV-viral outcome according to ethnicity may suggest that class II MHC alleles, although associated with the viral outcome are not primarily responsible for determining the characteristics of the anti-HCV immune response and viral outcome. Rather, we believe that this association may reflect a linkage disequilibrium situation between class II and other genes within the MHC.

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