Association Studies of Genetic Susceptibility to Hepatitis B and C in U.S. Population

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Background

Hepatitis B and C are two major global public health problems. Of 2 billion people who have been infected with the hepatitis B virus (HBV), more than 350 million have chronic (lifelong) infections. There are about 170 million people worldwide who are infected with hepatitis C virus (HCV). Persistent carriage rates, which confer an increased risk of liver complications, liver failure, or end-stage carcinoma, are ~5-10% in hepatitis B, compared with ~75-85% of hepatitis C infection. Understanding why some individuals acquire and progress to chronic HBV and HCV infection and others do not is a priority in the prevention of these diseases.

Methods

Using DNA collected from 7,159 participants aged 12 and older enrolled in phase 2 (1991-1994) of the Third National Health and Nutrition Examination Survey (NHANES III), we analyzed the associations between 77 genetic variants in 34 candidate genes and risk for acquisition, persistence and progression of HBV and HCV.

Results

Genetic variants in the promoter of C-reactive protein *(CRP)* showed increased susceptibility to HBV infection (rs3093066, $p < 0.0001$, OR 2.10, 95%CI 1.47-3.00), but protection against HCV infection (rs1800947, $p = 0.0002$, RR 0.07, 95%CI 0.02-0.30).

Three polymorphisms in other genes also appeared to be strongly protective against HCV infections: CAT (rs769214, $p = 0.0003$, RR 0.53, 95%CI 0.34-0.75), CYP1A1 (rs2606345, $p < 0.0001$, RR 0.44, 95%CI 0.30-0.66) and TNF (rs361525, $p = 0.0007$, RR 0.23, 95%CI 0.10-0.56).

Conclusion

These findings emphasize the importance of studying human genetic variations as a guide to combating infectious diseases.