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Risk factors for Hepatitis C virus (HCV) transmission and efficiency of antiviral therapy in chronically infected patients

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Background: This study monitored the prevalence and genotype distribution of HCV in patients suspected for infection as well as risk factors for infection and transmission of HCV in northeast Croatia.

Methods: From January 2009 to December 2011, 405 plasma specimens of patients suspected for HCV infection were tested by the COBAS TaqMan HCV test v2.0 (Roche Diagnostics); 77 HCV-positive samples were genotyped using the Linear Array HCV Genotyping test (Roche); 33 HCV-positive patients with unfavorable liver tests were further treated with anti-viral therapy and monitored at weeks 28 and 53. Risk factors for HCV infection and transmission were analyzed from patient-filled questionnaires (age, sex, risk behavior etc.) and their clinical data (age at initial HCV infection, degree of liver inflammation and fibrosis).

Results: Out of 405 tested patients, 198 (48.8%) were HCV-positive and the highest prevalence of infection was found in men and women between 30 and 40 years of age. HCV genotype distribution in northeast Croatia was similar to other European regions: G1 was the most common (66.6%), followed by G3 (22.1%), G4 (10.4%), and G2 (1.3%); genotypes G5 and G6 were not detected. Viral therapy evaluated at week 53 demonstrated that 58% of patients were virus-free, 12% had lower viral load while 12% showed no change in viral load. Moreover, HCV G1-infected patients showed a delayed response to antiviral therapy when compared to G3 and G4-infected patients: 31% G1-, 40% G3- and 50% G4-infected patients were virus-free at week 28; 58% G1-, 60% G3- and 50% G4-infected patients were virus-free at week 53. Significant risk factors for HCV infection and transmission in northeast Croatia include history of blood transfusion, surgery before the year 1993, and body piercing in 31-40 year-old men ($p<0.05$).

Conclusion: Our results strengthen the importance of early testing for HCV infection in men showing the symptoms of chronic hepatitis (muscle pain, appetite loss, history of jaundice) since they are statistically more often intravenous drug, piercing, and tattoo users then women in our region.

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Variation of interleukin-28B at rs12979860 in injection drug users with HCV infection in a Chinese population

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Background: Hepatitis C virus (HCV) infection is a leading cause of liver disease globally. Recently, several genome-wide association studies have reported the strong association between single nucleotide polymorphisms (SNPs) near the interleukin-28B (IL28B) gene and the treatment outcome for chronic HCV infection. In Hong Kong, needle-sharing in injection drug users (IDU) continues to be a major route of HCV transmission. We conducted a follow-up study on HCV RNA-positive IDU to determine the genotype frequency of a SNP upstream of IL28B and their association with HCV genotype.

Methods: A total of 273 IDU positive for anti-HCV and HCV RNA were included. Genomic DNA was extracted from whole blood samples, and the most strongly associated SNP near the IL28 gene, rs12979860, was determined by real-time PCR using a custom TaqMan genotyping kit.

Results: The rs12979860 genotype distribution was CC in 237 IDU (86.8%), CT in 35 IDU (12.8%), and one case (0.4%) with TT genotype. The distribution of rs12979860 genotypes in the IDU population was in Hardy-Weinberg equilibrium ($P = 0.810$). Variation in the IL28B genotypes was not observed as compared with 300 healthy blood donors (CC: 87.0%, CT: 11.7%, and TT: 1.3%; $P = 0.430$). With regard to HCV genotype, HCV 1b and HCV 6a were the two commonest genotypes circulating in our local IDU population. Of the 105 IDU infected with HCV genotype 1 and 145 IDU with genotype 6, the frequency of the rs12979860 CC genotype was 81.9% and 88.3%, respectively, which were not different significantly ($P = 0.509$).

Conclusion: In conclusion, the favorable rs12979860 CC genotype frequently observed in our Chinese population supports a potential role of incorporating IL28B SNP genotyping for the clinical workup of patients infected with HCV genotypes 1 and 6. Integrating the assessment of host and viral factors (age, gender, and HCV genotype) in combination with pre-treatment screening of IL28B rs12979860 polymorphism may provide useful prognostic information prior to interferon-based combination therapy for chronic HCV infection. This combined assessment may facilitate the development of new therapeutic approaches for the non-responders to conventional HCV therapies.

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