Evaluation of Prevalence of RT-PCR Based HCV Infection in Thalassemia and Hemodialysis Patients in Kerman Province (Iran)

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Keywords: Hepatitis C; Thalassemia; Hemodialysis patients

Background: Patients suffer from thalassemia and chronic renal failure on maintenance hemodialysis; have been exposed to blood-born infections, especially hepatitis C due to long-term transfusion. Recently, hepatitis C is one of the main health concerns in these patients. The aim of this study was to determine the prevalence of hepatitis C and related risk factors in thalassemic and hemodialysis patients in Kerman province of Iran.

Methods: in this cross-sectional we have totally examined 384 patients (203 hemodialysis cases and 181 thalassemia cases) by RT-PCR in Kerman. The information was obtained by question are then followed by blood sampled obtaining and RT-PCR. Statistical analysis were done using t-test and Chi-square methods

Results: We found that 130 cases out of 384 were infected by HCV. Our finding also showed that 16 cases were female (17%) while we found 114 (83%) cases of infected male patients

Conclusions: The prevalence of hepatitis C infection is very high in thalassemia and hemodialysis patients and based on other studies our results showed that the prevalence of HCV infection in Kerman is more than other provinces of Iran. Hepatitis C in these patients, is more higher in Kerman province than other provinces of Iran.

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Molecular Epidemiology of Hepatitis C Virus in Southern China

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Hepatitis C virus (HCV) infection has become a significant public health problem in Southern China. Guangxi is one of the provinces hardest hit by the virus. Molecular epidemiology of HCV infection in injection drug users (IDUs) in Guangxi Province would be important for understanding the epidemiology and be beneficial for improving prevention and control.

Methods: IDUs were recruited from Liuzhou methadone clinic, Guangxi, Southern China. Blood samples were collected. HIV and HCV serology was determined. HCV RNA was extracted and NS5B region was amplified using RT-PCR. HCV genotype was determined by phylogenetic analysis (MEGA 3.0).

Results: Of 260 IDUs, 184 were HIV/HCV coinfected, and 76 were HCV monoinfected. Overall, subtype 6a (46%) was predominant, followed by 3a (20%) and 3b (16%). There was no significant difference in HCV genotype distribution between HIV/HCV coinfection group and HCV monoinfection group ($p > 0.05$). The genetic distance of genotype 6 between individuals is shorter than that of other genotypes.

Conclusion: Genotype 6a is the predominant of HCV in IDUs in Southern China. It represents a relatively recent introduction of the genotype to the region. Because of the needle-sharing in IDUs in South-eastern Asia and the higher rate of viral mutation, more subtypes may be identified. Phylogenetic analysis shows the even distribution of HCV sequences in coinfection group and monoinfection group. This may indicate that HIV and HCV have spread during a relatively short period.

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Characterisation of Complete Hepatitis B Virus Genomes Isolated from Black Southern Africans with HBV-associated Hepatocellular Carcinoma

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Hepatitis B virus (HBV) infection is endemic in Africa. As many as 98% of black Africans are infected during their lives and about 10% (65 million) have chronic HBV infection, which is the cause of 70—80% of all hepatocellular carcinoma (HCC) cases. Despite this high prevalence of HBV and the high incidence of HCC in Africa, relatively few complete HBV genomes from African HCC cases have been deposited in international data bases. In order to gain a clearer understanding of the role of genetic variants and mutants in the development of HCC, the complete genomes of HBV isolated from southern African HCC patients were amplified and molecularly characterized. HBV DNA was extracted from forty HBsAg-positive HCC patients. Twenty six complete genomes were successfully amplified, cloned and sequenced from nine HCC patients. Phylogenetic analyses of the complete genomes and the individual open reading frames of HBV isolates from the HCC patients, led to the classification of all the isolates within subgenotype A1. No isolates belonging to subgenotype A2 and genotype D were identified even though these genotypes/subgenotypes have been shown to circulate in South Africa. Seventy-eight percent of the patients carried HBV strains with the double basic core promoter (BCP) mutation (1762T/1764A), previously shown to reduce HBeAg expression. All five HBV genomes isolated from one patient contained novel complex BCP rearrangements, which introduced 2 HNF1 and 1 putative HNF3 transcription factor binding sites. These mutations can enhance viral replication and simultaneously abolish