67.022
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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67.023
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: A total of 96 samples yielded adequate PCR product for sequencing and genotyping (86%). Twenty subjects 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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67.024
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
HBeAg expression at a transcriptional level. The envelope genes were characterised in a total of 18 HCC patients, the pre-S gene was mutated in 72% of the patients. Deletions across pre-S1/pre-S2, pre-S2 initiation codon mutations with internal deletions and S gene nonsense mutations were prevalent. The HBV mutations described in this study have been associated with increased risk for HCC.

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67.025
Seroprevalence of Human Immunodeficiency Virus, Hepatitis B and C Viruses Among Blood Donors in Chabahar Iran

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Background: Transfusions can be a quick and easy route for the transmission of infectious agents such as HIV, HBV and HCV. Evaluation of the prevalence among blood donors (BDs) is a common and easy method to obtain the epidemiology of these infections in a community. We performed this study to determine HIV, HBV and HCV seroprevalence among BDs in one of the main commercial ports in Iran.

Methods: The sample included 5409 consecutive donors (17—65 years) who donated blood from 2002 to 2003. HBsAg, anti-HCV and anti-HIV were investigated by ELISA in blood samples. If the results of ELISA samples were reported to be positive in the HIV and HCV cases, the confirmation was done with RIBA/Western blot.

Results: Most of BDs were motivated ones with 42%; who donate at regular intervals, 38% were first-time voluntary and 20% were voluntary donors with the history of at least one donation. Among BDs, 95.7% were male. The seroprevalence of HBsAg, HCV-Ab and HIV-Ab among BDs was 2.4%, 3.7% and 1.3% respectively in the first evaluation while 78.1% prevalence of HBsAg and viral load affect treatment response. HCV genome is conserved among genotypes but the variability of the virus variants allows tracing infections by sequence analysis. In order to evaluate the nosocomial transmission of HCV infection in a urology clinic, a phylogenetic analysis of HCV strains was performed in the core genomic region.

Conclusion: Using COBAS CORE II ELISA technique for detecting anti-HCV antibodies we tested ten sera prelevated from a urology clinic. We performed COBAS AMPLICOR HCV MONITOR test in the positive sera for the viral load. We found a significant viral load in seven cases, which were submitted to Neighbor-Joining phylogenetic analysis and interpreted with MEGA 3 Program. The phylogenetic analysis, based on the HCV core region, was realized by comparing the amplified sequences from the four sera with other Romanian sequences from genotype 1b strains and with other different geographic genotypes’ sequences, selected from data bases.

Results: We found a strong recent epidemiological link for three genotype 1b strains, which form a group, the genetic distance between them being very short (0.004—0.007). The other HCV strains served as controls and manifested different lineage degrees between themselves or compared with other analyzed strains.

Conclusion: This study confirmed the strong relationship between three HCV strains and the nosocomial transmission of the infection. Phylogenetic analysis in the core region represents a useful tool for tracing infections and routes of viral transmission.

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67.027
Molecular Epidemiology of HCV Genotypes in Injecting Drug Users in Hong Kong

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Background: Previous studies have shown that both genotypes 1b and 6a HCV were common among injecting drug users (IDU) in Hong Kong, but absence of subjects characteristics make further understanding of the molecular epidemiology difficult. We earlier reported a high prevalence of 85% of HCV in local IDUs. The present analysis was subsequently conducted to characterize the HCV genotypes.