The Prevalence of Hepatitis B and Hepatitis C Among Street Children in Tehran, Iran

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Keywords: Hepatitis B; Hepatitis C; Street children

Summary: Nowadays the issue of street children is one of the most important issue facing society, among big, industrial and under developed cities. There are approximately one hundred million children spending their life in the streets. With the last description of the International Organization for street children, many of documental statistics and numbers are less than the actual figures. Many countries are suffering from an individual relation the issue of street children despite possessing common properties, and by controlling this phenomenon each country will get in specific picture.

Materials and methods: The study was taken place on 203 street children that were picked up from different places of Tehran and were shelter at welfare center, which provides shelter for street children. These children were clinical examined by pediatrician then they were requested to answer the questionnaire (gender; age; birth place; educational status; the origin of the family; sleeping place; education, occupation, income and social security of parents; number of siblings; reasons for being in the streets; period of living in the streets; street friends; income; means of earning money; substance use. Smoking was grouped as heavy (10 and more per day), medium (1—9 per day) and rare (a few in a week)). In order to determine the existence of hepatitis B, 3 ml of blood was taken. We used ELISA and PCR method.

Results: Among 203 street children that studied in this research 196 children were boys and 7 children were girls. 6 cases (3%) were HBsAg positive all of the positive cases were boys. There were 3 Iranian and 3 Afghanian kids among positive cases, there were no smokers. They did not have tattoo, all of them had family, one of them lived alone and other 5 cases lived with their family and their average age was and 8 cases were 14 < years.

Conclusion: According to this results, additional laboratory examination for screening acquired infectious disease such as Hepatitis which clinical symptoms may appear few months after exposure to virus but can transmission in this period, are recommended.

doi: 10.1016/j.ijid.2008.05.1105

Assessment of the Selected Cytokines Among Patients Treated for Chronic Hepatitis Type C

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During the last years the possibilities of researching the cytokines coding genes were observed. It was revealed that the relation exists between their polymorphism and susceptibility to autoimmune diseases, inflammatory processes.

The study was made on 41 patients, diagnosed as having Hepatitis C. The patients had the standard treatment with interferon and ribavirin (48 weeks). During the following period of time lasting at least one year, the patients were observed. After this period of time, the tests on detection of RNA virus were performed. Additionally, the lymphoid blood cells were tested for the polymorphism of the cytokines coding genes (TNF alpha, INF gamma, IL-6, IL10) conditioning predisposition towards capability of generation of their different concentration. The results of our study suggest that there is no relation between polymorphism of the tested cytokines coding genes and the response for the HCV infection treated with interferon.

doi: 10.1016/j.ijid.2008.05.1106

Efficacy of Pegylated Interferon Alpha-2a and Ribavirin Treatment in Chronic Hepatitis C Patients Depends on Various Baseline Parameters and Early Viral Kinetics

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Background: to compare efficacy and viral kinetics during treatment in various chronic hepatitis C patients (CHC) and to find some baseline parameters which can predict sustained viral response (SVR).

Methods: 216 CHC pts - 140 men; 142 naive, 37 relapers, and 37 non-responders. 172 genotype 1 (G-1), 4 G-2, 34 G-3, 1 G-4 or G-6, and 4 unknown genotype - were treated with PEG-IFN alpha-2a 180 μg/wk and RBV 1000 or 1200 mg/day. Quantitative detection of HCV RNA was done at baseline (216 pts), 24 hours (83 pts), 14 days (85 pts), 28 days (88 pts), and 84 days (211 pts) after treatment initialization.

Results: 195 pts have completed the treatment period and 179 pts the 24-weeks follow-up period yet. The probability of SVR was significantly higher (P < 0.001) in naive patients (74/114, 64.9%) and relapers (22/30, 73.3%) than in non-responders (9/35, 25.7%); and in G-3 patients (23/28, 82.1%) than G-1 patients (77/143, 53.8%) (P = 0.02). The mean log decline of serum HCV RNA was more considerable in pts with SVR. Undetectable serum HCV RNA at week 12 was more predictive of SVR than early viral response (EVR) - 98/122 (80.3%) versus 104/141 (73.1%) of SVR. The patients with SVR has significantly lower weight (mean 72.8 kg vs. 79.1, P = 0.008), were younger (mean...
36.2, vs. 45.5, \( P < 0.001 \)), and had lower baseline viremia (mean 1.014 × 10^6 IU/mL vs. 2.415 × 10^6 IU/mL, \( P < 0.001 \)). SVR was more frequent in women than in men (43/63, 62.8% vs. 62/116, 53.4%) (\( P = 0.059 \)).

Conclusion: 1) Negative serum HCV RNA at week 12 is more predictive of SVR than EVR. 2) The probability of SVR was significantly higher in patients with lower baseline viremia, body weight and younger adults. 3) Gender was not significant for the efficacy of treatment.

doi:10.1016/j.ijid.2008.05.1107

67.017

Prevalence of Hepatitis C Virus (HCV) Genotype 3a in the Infected Population of Lahore, Pakistan

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Hepatitis C virus (HCV) major public health concerns in Pakistan. A molecular study was conducted to investigate the prevalence of Hepatitis C Genotype 3a in the infected population of Metropolitan. By using primers against the 5′ non coding region of the viral RNA was reverse transcribed into cDNA and for qualitative analysis, the amplification of cDNA was done by first round PCR. Nested PCR was performed with first round PCR product. Amplification of HCV cDNA for genotyping by regular PCR was carried out. For HCV genotyping second round PCR, two different primer mixtures were prepared. Detection of genotype specific band was performed through gel electrophoresis. 232 bp specific band of HCV 3a genotype was determined by comparing with 100 bp DNA size of marker. Our result showed, out of 28 HCV PCR positive samples, fifteen samples have HCV genotype 3a. The prevalence of genotype 3a HCV RNA was found to be 55% in local population of Lahore.

do:10.1016/j.ijid.2008.05.1235

67.019

Hepatitis B Virus in Chronically Infected Patients

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Background: Genomic mutations presented during hepatitis B virus (HBV) reverse transcription could explain its genetic diversity and account for genetically distinct eight genotypes which show distinctive geographically distribution. The main objectives of this study were to determine the prevalence of hepatitis B virus genotypes in patients with chronic hepatitis B, and to look for a relationship between genotypes and risk transmission factors according to HBeAg state.

Patients and methods: A total of 14 serum samples from chronic HBV patients were analysed using INNO-LIPA HBV Genotyping assay (Innogenetics). The presence of mixed genotype infection was verified by sequencing using the BigDye Terminator Cycle Sequencing Kit on an ABI Prism 3130 Genetic Analyzer. Hepatitis B virus HBsAg, anti-HBs, HBeAg and anti-HBe were determined by ADVIA Centaur (Bayer).

Results: Genotype D was the most prevalent (64.3%) followed by genotype A (28.6%). There was a co-infection case (D/E genotypes) that was confirmed by sequencing PCR.