Prevalence of active HCV Infection and identification of its common Genotypes in District Mardan, Pakistan

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Abstract

The present study demonstrate the prevalence of active Hepatitis C viral infection and identification of its common genotypes circulating in district Mardan. A total of 582 patients were enrolled in this study in which 267 were male and 315 were female. Out of 582 samples, 329 were found HCV RNA positive through real-time PCR. The rates of active HCV infection were 59.9% in male while 53.6% in female. Age group above 60 were found with high rate of HCV infection, that is 80%. Out of 329 samples. Further a sum of 220 PCR based HCV RNA positive samples were screened for identification of HCV genotypes. Out of 220 positive samples Genotype 3a was found in 68.1%, 1a in 11.3%, 1b in 4.5%, Mixed-genotype in 4% and 3b in 2.7% while Untypable genotype in 9.5%. It was concluded from the present study that occurrence of active HCV infection rate were high in District Mardan and 3a was the most common genotype present in District Mardan.

Key words: GCMDBR, Mardan, Khyber Pakhtunkhwa.

Introduction

Hepatitis C infection is one of the major causes of liver diseases all over the world. HCV is the main cause of Hepatitis C infection and the majority of patients with chronic hepatitis is live untreated, which may cause hepatocellular carcinoma (HCC) and finally liver cirrhosis¹. Hepatitis C virus belongs to the family Flaviviridae and is an RNA virus². Hepatitis C virus is the principal source of chronic liver disease³ with estimated 170-200 million infected persons globally⁴ counting about 17 million in Pakistan⁵.

The main cause of HCV transmission in Pakistan is multiple use of syringes, minor and major surgery, dental procedures, blood and blood product transfusion, using of razors for multiple shaving or shaving in the shops of barbers, sharp instruments, nail cutters, tooth brushes and sexual transmission⁶. Hepatitis C virus has major six genotypes and each genotype has several subtypes⁷. The distributions of these genotypes are different globally and this difference is about one third of the variation in the genetic material from country to country. Genotypes 1, 2 and 3 are circulated worldwide. In Europe, Japan and USA, 1a and 1b are the most prevalent genotypes¹¹. HCV subtype 3a is the major genotype present in India¹³. Nepal¹⁵ and Pakistan⁶. The genotype 4 of Hepatitis C Virus is more prevalent in North Africa and Middle East¹⁶, genotype 5 in South Africa and the genotype 6 appears to be most common in Hong Kong¹⁷. In Pakistan, the most prevalent HCV genotype is 3a, followed by 3b and 1a, with a strong association linking to chronic Hepatitis C viral infection and Hepato cellular carcinoma in Pakistan associated with genotype 3a¹⁸. The present study evaluated prevalence rate of active HCV infection and identification of its common genotypes present in general population of District Mardan.

Material and Methods

Study Design: This was lab based observational and descriptive cross-sectional study carried out from January 2011 to March 2011 at District Mardan.

Study Area and Studied population: The present study was carried out in district Mardan, Khyber Pakhtunkhwa. For the current study general population of district Mardan were selected. Patients from various areas of district Mardan were attended D.H.Q hospital and Mardan Medical Complex and was screened for HCV RNA through Enzyme linked immune Sorbent assay (ELISA) and ICT strip methods. A sum of 582 patients were found positive by ELISA and ICT strip method. Out of these 582 ELISA and ICT strip positive patients, 315
were female and 276 were male. Serological and biochemical
data of these patients were recorded. For further confirmation of
HCV RNA blood samples were taken from these patient, sera
was separated and send to Genome Center for Molecular Based
Diagnosis and Research Lahore (GCMBDR). GCMBDR is a
state of the art molecular based diagnostic laboratory with
responsive, precise and consistent detection tests on cost-to-cost
basis utilizing PCR and real-time PCR procedures.

Data collection: Data was collected from Genome Center for
Molecular Based Diagnostics and Research.

Statistical Analysis: All results were presented in percentage
form and were analyzed through Statistix 9 version software.
Chi square test were used for significance relationship amongst
the categorical parameters. P-value <0.005 are considered as
significant.

Results and Discussion

Gender wise and Age wise prevalence of HCV infection in
District Mardan: In the current study a total of 582 patients
were enrolled in which the rate of active HCV infection was
56.5% (n=329). Of these 582 samples 267 were male and 315
were female in which the rate of Hepatitis C virus infection
59.9% and 53.6% respectively which are shown in table 1. Active Hepatitis C viral infections in various age group were
shown in figure 1. All the patients were categorized into three
groups from 0-30 years, 31-60 years and above 60 years (table
1, figure 1).

Distribution of HCV Genotype in Both Gender of District
Mardan: The table 2 show the rate of HCV genotypes and
Subtypes in district Mardan. Out of 329 positive samples 220
were further studied for HCV genotypes and subtypes. Out of
these 220 positive samples genotype 3a was found in 68.1%
(n=149), 1a in 11.3% (n=25), 1b in 4.5% (n=10), Mixed 4%
(n=9) and 3b in 2.7% (n=6) patients while 9.5% (n=21) were
found with Untypable genotype. The rate of Hepatitis C virus
Genotypes and Subtypes between male and female patients were
shown in table 3 (table 2, table 3).

Discussion: HCV has come to the top regarding virus-induced
liver diseases in several parts of the globe and have acquired
demic proportions in our population, but there is no national
data variety system for evaluation of genotypes regarding HCV
infection. The results on the geographic supply of genotypes
regarding HCV are amongst the largest of their kind from
Pakistan.

<table>
<thead>
<tr>
<th>Gender</th>
<th>Total HCV Elisa and ICT strip Positive samples</th>
<th>HCV RNA Detected</th>
<th>Percentage</th>
<th>P Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Male</td>
<td>267</td>
<td>160</td>
<td>59.9%</td>
<td>0.0006  significant</td>
</tr>
<tr>
<td>Female</td>
<td>315</td>
<td>169</td>
<td>53.6%</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>582</td>
<td>329</td>
<td>56.5%</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>HCV Genotypes</th>
<th>Subtypes</th>
<th>No. of isolates</th>
<th>Percentage</th>
<th>P-Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1a</td>
<td>25</td>
<td>11.3%</td>
<td>0.9998  Non-significant</td>
</tr>
<tr>
<td></td>
<td>1b</td>
<td>10</td>
<td>4.5%</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>3a</td>
<td>149</td>
<td>68.1%</td>
<td></td>
</tr>
<tr>
<td></td>
<td>3b</td>
<td>06</td>
<td>2.7%</td>
<td></td>
</tr>
<tr>
<td>Untypable</td>
<td></td>
<td>21</td>
<td>9.5%</td>
<td></td>
</tr>
<tr>
<td>Mixed</td>
<td></td>
<td>09</td>
<td>4%</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td></td>
<td>220</td>
<td>100%</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>HCV Genotypes</th>
<th>Subtypes</th>
<th>Male</th>
<th>Female</th>
<th>Total</th>
<th>P-Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1a</td>
<td>15(6.8%)</td>
<td>10(4.5%)</td>
<td>25(11.3%)</td>
<td>0.8722  Non-significant</td>
</tr>
<tr>
<td></td>
<td>1b</td>
<td>8(3.6%)</td>
<td>2(0.9%)</td>
<td>10(4.5%)</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>3a</td>
<td>63(28.6%)</td>
<td>86(39.5%)</td>
<td>149(68.1%)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>3b</td>
<td>01(0.4%)</td>
<td>05(2.2%)</td>
<td>06(2.7%)</td>
<td></td>
</tr>
<tr>
<td>Untypable</td>
<td></td>
<td>10(4.5%)</td>
<td>11(5%)</td>
<td>21(9.5%)</td>
<td></td>
</tr>
<tr>
<td>Mixed</td>
<td></td>
<td>05(2.2%)</td>
<td>04(1.8%)</td>
<td>09(4%)</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td></td>
<td>102(46.3%)</td>
<td>118(33.6%)</td>
<td>220</td>
<td></td>
</tr>
</tbody>
</table>
According to Attaullah et al., and Sher Zaman Safi et al., that genotype 3a, 3b, 1a, 1b and 2a were the common genotypes in Khyber Pakhtunkhwa while Genotype 4, 5, and 6 were absent and were rare in Pakistan.

The first finding of our research is to find out the rate of active Hepatitis C viral infection in male and female patients of District Mardan. Out of 582 samples 329 (56.45%) were found HCV RNA positive, in which the rate of HCV infection in male was 59.9% (n=160) and in female were 53.6% (n=169). There is no large difference of the rate of HCV infection between both genders. The HCV infection is more in male as compared to female. The increases of HCV in male were due to more interaction with population and surrounding environment. Our research with the agreement of the studies of Masroor et al., and Ali et al., in which the rate of HCV in male was 58.2% and female was 42.8%. While in a study conducted in Provence Punjab every one of the genotypes were distributed in the same frequency in male and females which may be the geographical differences or differences in the mode of living in both of the provinces.

The second objective of research to finds out HCV in different age groups. Out 582 samples the rate of Hepatitis C viral infection in age range 0-30 years were 50% (n=146), 57.69% (n=146) were from age range 31-60 years and 80% (n=20) were from above 60 years. The results show that the HCV infections were high in all age groups but infection rate is significantly higher in the age group above 60 years. This may be due to the low immunity to resist to Hepatitis C viral infection. According to the study of Inamullah et al., highest prevalence of HCV was recorded in age group 20-30 and this may due to the geographical difference. While by another study, the HCV occurrence was higher in young individuals compared to older persons and seemed to be indicative connected with reduced success rate beyond 40 years. Furthermore, the age group between 31-40 years showed that males of the group are at danger of having an HCV disease while females’ old group between 41-50 years displayed high HCV disease rate than males with not clear of the factors involving in this gender. In Provence, Punjab the prevalence in different age groups was different which was shown by as a study conducted in Provence Punjab which essentially the most impacted age range regarding affected individuals has been 21-40 decades when compared having adolescent in addition to more mature age groups.

The third finding of our research to demonstrate the distribution of HCV genotypes in subtypes in the population of District Mardan. Out 220 positive samples the rate of 3a was 68.1% (n=149), 1a were 11.3% (n=25), Untypable were 9.5% (21), 1b were 4.5% (n=10), Mixed were 4% (n=9) and 3b were 2.7% (n=6). This study shows that the 3a are the most common in the HCV infected population of Mardan. Other studies also show that the 3a were more common in the population of Pakistan such as Inamullah et al., Ali et al., and Idrees and Riazuddin. The present study was also correlated to another study which was conducted in district Mardan, according to which the genotype 3a was probably the most predominant genotype involving HCV RNA constructive samples that has a prevalence involving 90.3%. The current study also compared with other study conducted in Punjab; another Provence of Pakistan, in which the most prevalent genotype was also 3a (71%) was about similar to our study.

**Conclusion**

It is concluded from the present study that active Hepatitis C virus infection are high in District Mardan. Patients with age group above 60 are found with high rate of HCV infection.
Genotype 3a was found most common genotype in district Mardan. In females the Subgenotypes 3a were more common as compared to male. It is recommended to take further study, need of awareness and interferon therapy programs and HCV genotyping.

References


