CLINICAL, BIOCHEMICAL AND VIROLOGICAL PROFILE OF PATIENTS WITH CHRONIC HEPATITIS C VIRUS INFECTION-A STUDY FROM UNIVERSITY HOSPITAL IN NEPAL

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Abstract

Introduction: Hepatitis C virus (HCV) infection is a major public health challenge. It is a major cause for cirrhosis and hepatocellular carcinoma worldwide. Both the genotype and viral load of HCV determine the choice of therapy as well as outcome of therapy. The aim of this study was to evaluate clinical, biochemical and virological profile and association of HCV genotypes with viral load and liver biochemical profile.

Material and Methods: This was descriptive observational study of chronic HCV infected patients who attended at the outpatient clinic of Department of Gastroenterology of TUTH, IOM from April 2013 to November 2014. During this study period 38 patients with chronic HCV infection were analyzed. Clinical profile, possible risk factors for transmission of HCV infection and liver biochemical profile were recorded. Virological profile included HCV viral load and HCV genotypes.

Results: Out of 38 patients 34(89.5%) were male and 4(10.5%) were female. Injection drug use (IDU) was the most common mode for acquisition of HCV infection (55.3%). Genotype 3 was found in 21(55.26%) patients and genotype 1 was found in 17(44.74%) patients. There was no significant association between HCV genotypes and serum alanine aminotransferase (ALT) and aspartate aminotransferase (AST) level. And also there was no significant association between HCV viral load and different HCV genotypes.

Conclusions: In our study HCV genotype 3 was the most prevalent genotype in patients with chronic HCV infection. Injection drug use was identified as most common identifiable risk factor for transmission of HCV infection. There was no significant association between different HCV genotypes and serum ALT, AST level and HCV viral load.

Key words: *ALT, AST, genotype, hepatitis C virus, viral load*

Introduction

Hepatitis C virus (HCV) infection is a major public health challenge worldwide. About 170 million people or 3% of world's population are infected with HCV.[1] More than 350,000 deaths annually are attributed to HCV infection, most of which are caused by cirrhosis of liver and hepatocellular carcinoma (HCC).[2] An estimated 27% of cirrhosis and 25% of HCC can be attributed to HCV worldwide.[2] In developed countries, the most important route of HCV transmission is intra-venous drug use, whereas in resource poor countries, invasive procedures or injection-based therapies with contaminated instruments are predominant source of new infections.[3] Different studies from Nepal showed that the sero-prevalence of HCV ranges from 0.35% to 1.73% in blood donors and healthy population with highest prevalence among injection drug users.[4-8] Six different HCV genotypes and

multiple subtypes have been identified on the basis of molecular relatedness.[9] Knowledge of the genotype is helpful for prediction of sustained virological response (SVR) and choice of treatment duration.[10] Chronic HCV infection is associated with a wide variation in serum ALT level, from normal ALT to persistent elevation of ALT. Approximately 25-30% of individuals with chronic HCV infections have persistently normal ALT level.[11]

The aim of this study was to determine clinical, biochemical, HCV genotype distribution and HCV viral load in patients infected with chronic HCV and to assess the relationship between HCV genotype with serum ALT level, serum AST level and HCV viral load.

Material and Methods

This study was a descriptive observational study of chronic HCV infected patients who attended at the outpatient clinic of Department of Gastroenterology of Tribhuvan University, Institute of Medicine (TU, IOM) from April 2013 to November 2014. All the included patients were positive for Anti-HCV by ELISA. All the patients were positive for HCV RNA by Real Time- Polymerase Chain Reaction (PCR). All the patients who were not taking anti-viral treatment for HCV infection were included in this study, but the co-infected patients with hepatitis B virus (HBV) and human immunodeficiency virus (HIV) were excluded. All the information regarding clinical profile, liver biochemical parameters and virological parameters were recorded digitally. Patient's clinical details included age, gender and possible risk factors for HCV transmission. Liver biochemical parameters included serum ALT and AST level. Virological profiles included HCV viral load and HCV genotypes. As HCV genotype and HCV viral load testing facility is not available in Nepal, HCV viral load and genotypes were done in different laboratories in India where RT-PCR for determining HCV viral load and genotypes were available.

The data obtained was entered in Microsoft Excel and exported to further statistical analysis was done using statistical package for social sciences (SPSS) version 20. Standard descriptive statistical analysis was carried out as per demographic, biochemical and HCV viral load. The relationship was analyzed by comparing variables using Student t-test. Results were considered significant if *p*-value was less than 0.05.

Results

During April 2013 to November 2014 there were 38 patients of chronic HCV infection who attended outpatient clinic of Department of Gastroenterology at TUTH, IOM. Among all patients, 34 (89.5%) were male and 4 (10.5%) were female. The mean age of the study population was 38.34 years ± 9.64. The highest numbers of cases i.e. 52.6% were found in the age group between 30 to 40 years. The probable risk factors for transmission of HCV infection was observed to be IDU in 21 (55.3%) patients, combined risk of IDU and tattooing in 8 (21.1%), history of blood transfusion in 2 (5.3%) patients, history of surgery in 1 (2.6%) patient, hemodialysis in 1(2.6%) patient and only tattooing in 1(2.6%) patient. Among 4 (10.5%) patients with chronic HCV infection, risk factor for HCV transmission could not be identified (Table 1).

Table 1. Characteristics of Patients(n=38)

Characteristics	Frequency	Percentage
Gender		
Male	34	89.5
Female	4	10.5
Age (years)		
<30	7	18.4
30-40	20	52.6
>40	11	28.9
Possible risk factors		
IDU	21	55.3
IDU+ Tattooing	8	21.1
History of blood transfusion	2	5.3
History of surgery	1	2.6
Tattooing	1	2.6
Hemodialysis	1	2.6
Unidentified	4	10.5

HCV genotypes		
Genotype 1	17	44.74
Genotype 3	21	55.26
Other Genotypes	0	0

Mean serum ALT and AST level were 86.39 IU/ML ± 46.96 and 76.08 IU/ML ± 69.60 respectively. Mean HCV viral load was 3337815.76 IU/ML ±5087752.64 (Table 2).

Table 2. Biochemical and virological profile of study population (n=38)

Variables	Results [a]
ALT (IU/ML)	86.39±46.96
AST (IU/ML)	76.08±69.60
HCV RNA (IU/ML)	3337815.76±5087752.64

[a] Mean ± SD

HCV genotype 3 was found common in 21 (55.26%) patients and genotype 1 was found in 17(44.74%) patients. HCV genotype 2, 4, 5 and 6 was not found in our study population (Table 1). The statistical analysis showed no significant association between different HCV genotype with mean HCV, viral load as well as mean serum AST and ALT level. (Table 3).

Table 3. Comparisons between HCV genotypes and serum AST, ALT and HCV RNA (n=38)

	Genotype 1 (n=17)	Genotype 3 (n=21)	*p* value
ALT (IU/ML)[a]	78.35±45.29	92.90±48.36	0.349
AST (IU/ML)[a]	71.12±87.72	80.10±52.62	0.698
HCV viral load (IU/ML)[a]	3574804.82 ±5464909.77	3145967.48± 4889692.57	0.800

[a] Mean ± SD

Discussion

This study included 38 patients with chronic HCV infection. Among these patients 89.5% were male and 10.5% were female. Among 38 patients, 34(89.47%) patients had identifiable risk factors for HCV transmission. Injection drug use was most common identifiable risk factor followed by the history of blood transfusion in our study population which was in concordance with the study conducted by Hu KQ from United States.[12] In similar studies from India conducted by R. Abraham and A. Chakravarti also showed the most common identifiable risk factor for HCV acquisition was history of surgery followed by blood transfusion.[13,14] The mode of transmission was not identifiable in 10.5% of patients in this study population. A study from India showed that risk factors were not indentified in 22.53% of patients.[14] There was no published data on the distribution of different HCV genotypes among HCV infected patients found in Nepal. This study showed genotype 3 (55.26%) as the most common genotype followed by genotype 1 (44.74%).

The relationship between serum liver enzyme and degree of liver damage in chronic HCV infection was still not clear in this study but some studies documented.[11,15] However, in some studies, there were no relation between serum ALT level and severity of liver damage histologically found.[13,16] A study done by R. Abraham in India had shown that there was no association between HCV genotype and serum aminotransferases.[13] However, another study done by A Chakravarti in India had shown that serum AST level was significantly higher in genotype 1 as compared to other genotype.[14] A similar study done in Turkey by S. Rota had demonstrated that the serum level of ALT and AST in HCV genotype 4 were significantly higher than those infected with other genotypes.[17] In this study, there was no significant association between HCV genotype and the mean level of serum ALT level and serum AST level was found. In a study from India conducted by R. Abraham found that serum ALT level correlated poorly with HCV genotype[13,14]. There was little information regarding the correlation between the HCV genotype and viral load found. Some studies had shown that there was no relationship between the HCV genotype and HCV viral load.[11,18] A study conducted at Pakistan in 2011 showed a

significant higher HCV viral load in genotype 1 as compared to other genotypes.[19] A similar kind of study done in India also showed that viral load in patients with genotype 1 was significantly higher than other HCV genotypes.[14] In this study, there was no significant association between HCV viral load and HCV genotypes.

Conclusions

In conclusion, this study showed that HCV genotype 3 was the most common genotype followed by genotype 1. Other Genotypes were not found in this study population. This study also revealed that there was no significant relation between the HCV genotypes, serum ALT and serum AST level. Baseline HCV viral load was also not significantly associated with different HCV genotypes.

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