

Original Research Article

Distribution of hepatitis C virus genotypes in patients with chronic hepatitis C infection in Karnataka, South India

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Received: 09 October 2016

Accepted: 13 October 2016

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ABSTRACT

Background: Hepatitis C virus (HCV), an important cause of chronic hepatitis, cirrhosis and hepatocellular carcinoma. HCV is classified into 6 different genotypes. Genotype of the virus helps in predicting response to antiviral therapy and also the type of therapy. Therefore, it is important to know the prevalence of each genotype. Thus the present study was designed to determine the distribution pattern of HCV genotypes in chronic hepatitis patients in Karnataka, south India.

Methods: From October 2012 to September 2016, one hundred and eighty five consecutive patients with chronic hepatitis C infection were included in this retrospective study. Patients were identified from the outpatient registers and data was extracted from liver proforma of medical gastroenterology department, Victoria hospital, attached to Bangalore medical college and research institute, Bangalore. All the patients had anti-HCV antibody-positive test done by ELISA (Tri Dot) test. HCV RNA viral load and genotype was done for all the patients.

Results: Genotype 1 was observed in 145 of 185 (78.38%) patients. Genotype 3 was seen in 35 (18.9%) patients. Five (2.7%) patients showed infection with genotype 4. Seventy two patients (38.91 %) were on haemodialysis for chronic kidney disease (CKD). In CKD patients 67 of 72 (93.1%) were infected with genotype 1 and 5 patients were infected with genotype 3 (6.9%).

Conclusions: The present findings showed that genotype 1 of hepatitis C virus was the most prevalent genotype in patients with chronic hepatitis C in Karnataka, south India.

Keywords: CKD, Genotype, HCV, Prevalence

INTRODUCTION

Hepatitis C is caused by a spherical, enveloped, single stranded RNA virus, which belongs to the family *Flaviviridae* and genus *Flavivirus*. It is a major cause of chronic hepatitis C, throughout the world. WHO estimates that 170 million individuals worldwide are infected with hepatitis C virus (HCV). However, the prevalence of HCV infection varies throughout the world.¹ HCV is classified into 6 genotypes and numerous subtypes. Molecular differences between the genotypes

are relatively large and have a difference of at least 30% at the nucleotide level. The viral genome undergoes mutation and thus the parent strain has different mutants, which coexist as quasispecies in the same individual.²

HCV leads to chronic hepatitis in about 80% of the cases.³ The virus can cause gradual hepatic fibrosis and eventual cirrhosis, end-stage liver disease, and hepatocellular carcinoma.⁴ Without treatment, 33 percent patients have an expected median time to cirrhosis of less than 20 years.⁵

The virus genotype does not influence the presentation of the disease but different strains of HCV may be involved in the disparity in the course of the hepatitis C among infected individuals and difference in the pattern of the disease between countries with different dominant genotypes. Since it is a major predictor of response to antiviral therapy and also determines the type of antiviral drugs, it is important to understand the prevalence of the type of genotype to devise strategies to combat the disease.

Multiple studies have been done on the distribution of various hepatitis C virus genotypes in India.⁶⁻¹³ There is no data from Karnataka on distribution of hepatitis C virus genotypes. We took up this study to find out the prevalence of various genotypes of hepatitis C virus in the patients with chronic hepatitis C infection in Karnataka, South India.

METHODS

From October 2012 to September 2016, one hundred and eighty five consecutive patients diagnosed with chronic hepatitis C infection attending the outpatient department of medical gastroenterology department were included in this retrospective study. Patients were identified from the outpatient registers and data was extracted from liver proforma of medical gastroenterology department, Victoria hospital, attached to Bangalore medical college and research institute.

All the patients had anti-HCV antibody-positive test done by ELISA (Tri Dot) test. HCV RNA viral load and genotype was done for all the patients before starting the combination therapy. HCV RNA quantitative test was done by reverse transcriptase PCR assay on Roche Cobas Ampliprep analyzer (Roche diagnostics GmbH, Mannheim, Germany), ranging from 43 IU/mL to 6.9×10^7 IU/mL. A viral count of <43 IU/mL was considered to be undetectable.

RESULTS

Table 1: Baseline characteristics of study patients.

Characteristics	Median (min-max)
Age	36.8 (21 to 74)
Number of male (%)	147 (79.46%)
CKD patients	72 (38.91%)
Genotype distribution	
1 (%)	145 (78.38%)
3 (%)	35 (18.9%)
4 (%)	05 (2.7%)

Baseline characteristics of study patients are shown in Table 1. Mean age of the patients was 36.8±12.4 years. 147 were male and 38 were females. Genotype 1 was observed in 145 of 185 (78.38%) patients. Genotype 3 was seen 35(18.9%) patients. Five (2.7%) patients

showed infection with genotype 4. Seventy two patients (38.91 %) were on hemodialysis for chronic kidney disease (CKD). In CKD patients 67 of 72 (93.1%) were infected with genotype 1 and 5 patients were infected with genotype 3(6.9%).

DISCUSSION

Hepatitis C infection is the most common cause of chronic liver disease. The severity of hepatitis C, its progression, and response to therapy may vary depending on the genotype.⁵

As regional differences exist in the distribution of HCV genotype, it is important to know the genotype distribution to understand its prognostic implication.¹¹

In our study, genotype 1 was predominant, followed by genotype 3, which is similar to that reported by other workers from southern India.^{7,9} In northern and western India genotype 3 was found to be predominant.^{6,8,10-13} From other parts of the world studies reveal that genotype 3 is prevalent in South East Asia whereas genotype 1 is common in USA and Western Europe.¹⁴ These geographical differences may help in predicting the origin of HCV virus.

In CKD patients on hemodialysis chronic hepatitis C infection is common. Very few studies have reported genotype in these patients.¹⁵⁻¹⁷ In two western studies genotype 1 was commonest.^{15,16} In a study from north India, genotype 3 was the commonest in CKD patients on hemodialysis.¹⁷ In our study genotype 1 was predominant in CKD patients on hemodialysis, which is in trend with geographical prevalence. In CKD patients genotype 1 was seen in 93.1% and genotype 3 in 6.9% of patients.

The severity of disease, its progression, and response to therapy may vary according to the genotype.¹⁸⁻²⁰ A number of studies have reported that severe liver disease occurs in relation to type 1 infection (especially type 1b).^{18,21,22} and that cirrhotic patients infected with HCV type 1b carry a significantly higher risk of developing hepatocellular carcinoma as compared to those infected with other HCV types.²³ But the results of various studies are conflicting.¹⁸⁻²⁰ It is known that genotype 1 is the second most common genotype reported from north India and is the most prevalent genotype in south India, as also seen in the present study. Thus knowledge on the distribution of various genotypes in our country is essential for its prognostic implications in chronic hepatitis C infection.

CONCLUSION

Genotype 1 was found to be the most prevalent genotype in patients with chronic hepatitis C in Karnataka, south India.

Funding: No funding sources

Conflict of interest: None declared

Ethical approval: The study was approved by the institutional ethics committee

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Cite this article as: Kumar JP, Puttamaregowda H. Distribution of hepatitis C virus genotypes in patients with chronic hepatitis C infection in Karnataka, South India. *Int J Adv Med* 2016;3:905-7.