

A Survey Determining the Different Genotypes of Hepatitis C Amongst Subjects Reporting to a Tertiary Care Centre in Punjab

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ABSTRACT

Background: HCV poses a challenge to the improvement in the development of vaccines and pan-genotypic treatments, which require the consideration of global trends in HCV genotype prevalence. Therefore, the development of national treatment strategies using DAA therapies requires a detailed understanding of relative HCV genotype prevalence and subtypes. The aim of the present study is to determine different Genotypes of Hepatitis C Amongst Subjects Reporting to a Tertiary Care Centre in Punjab.

Materials and Methods: The present study included 437 subjects with hepatitis C reporting to the Medicine department, GMC Patiala. The genotypes obtained were matched with the chart obtained by the manufacturer. All the results obtained were arranged in the tabulated form and analysed using SPSS software.

Results: Out of total 292 non cirrhotic patients Genotype 3 was found to be most prevalent in 125 patients (42.8%), followed by genotype 1 in 107 patients (36.6%) and genotype 4 in 58 patients (19.8%). There were 73 males and 52 females amongst genotype 3, and 71 males and 36 females with genotype 1. There was 1 male with genotype 2. There was 1

male with genotype 5. Out of total 145 cirrhotic patients; 40 (27.6%) patients had genotype 1, and 84 (57.9%) had genotype 3, 20 (13.8%) had genotype 4, and 1 (0.68%) genotype 5.

Conclusion: In the above study genotype 3 was most prevalent amongst patients with hepatitis C. Genotype 1 was the second most common type.

Keywords: Hepatitis, Genotype, Viral.


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INTRODUCTION

Hepatitis C virus (HCV) exhibits high genetic diversity, characterized by regional variations in genotype prevalence. This poses a challenge to the development of vaccines and pan-genotypic treatments, which require the consideration of global trends in HCV genotype prevalence. Hepatitis C virus (HCV) is a globally prevalent pathogen and a leading cause of death and morbidity.¹ The most recent estimates of disease burden show an increase in sero prevalence over the last 15 years to 2.8%, equating to >185 million infections worldwide.² Persistent HCV infection is associated with the development of liver cirrhosis, hepatocellular cancer, liver failure, and death³, and HCV is now the most common cause of death in HIV-positive patients on highly active antiretroviral therapy.⁴ While the incidence rate of HCV infection is apparently decreasing in the developed world, deaths from liver disease secondary to HCV infection will continue to increase over the next 20 years.⁵ HCV exhibits an extraordinarily high degree of genetic diversity—substantially

greater than that of the HIV-1 pandemic—creating a major challenge for the development of both HCV vaccines and pan-genotypic drug therapies. At present, the duration of treatment, cure rates, and the need for adjuvant interferon and ribavirin with the new DAA therapies remain dependent in part on HCV genotype and subtype. Therefore, the development of national treatment strategies using DAA therapies requires a detailed understanding of relative HCV genotype prevalence and subtypes. The aim of the present study is to determine different Genotypes of Hepatitis C Amongst Subjects Reporting to a Tertiary Care Centre in Punjab.

MATERIALS AND METHODS

The present study included 437 subjects with hepatitis C reporting to the Medicine department, GMC Patiala for treatment. Study was carried out in Hepatitis C patients coming to GMC Patiala over one year from January 1, 2017 to 31st December 2017.

Samples of serum were obtained from the subjects for the extraction of viral RNA. The genotypes obtained were matched with the chart obtained by the manufacturer. All the results obtained were arranged in the tabulated form and analysed using SPSS software. The results were expressed as percentage.

RESULTS

The study involved 437 subjects with the mean age of 41.76 +/- 10.32 years. Table 1 shows the genotype of 292 subjects without cirrhosis. There were 71 males and 36 females with genotype 1 (36.6%). There was 1 male with genotype 2 (0.2%). There were 73 males and 52 females with genotype 3 (42.8%). There were 36 males and 22 females with genotype 4 (19.8%). There was 1 male with genotype 5 (0.2%). There were 67 subjects between 20-30 years of age. There were 89 subjects between 31-40 years of age. There were 74 subjects between 41-50 years of age. There were 42 subjects between 51-60 years of age. There were 20 subjects more than 60 years of age.

Table 2 shows the genotypes of 134 subjects with compensated cirrhosis. There were 37 (27.6%) subjects with genotype 1 out of which 26 were males and 11 were females. There were 78 (58.2%) subjects with genotype 3 out of which 47 were males and 31 females.

There were 18 (13.4%) subjects with genotype 4 out of which 11 were males and 7 females. There was 1 male (0.7%) with genotype 5. There were 4 subjects between 20-30 years of age. There were 21 subjects between 31-40 years of age. There were 43 subjects between 41-50 years of age. There were 40 subjects between 51-60 years of age. There were 26 subjects more than 60 years of age.

Table 3 shows the genotypes of 11 subjects with decompensated cirrhosis. There were 3 (27.3%) subjects with genotype 1 out of which, 2 were males and 1 females. There were 6 (54.5%) subjects with genotype 3 out of which, 4 were males and 2 females. There were 2 (18.2%) subjects with genotype 4 out of which, 1 was male and 1 female.

Table 1: Genotype of non-cirrhosis subjects

Genotype	1		2		3		4		5		Total
	M	F	M	F	M	F	M	F	M	F	
20-30	19	6	-	-	19	13	4	6	-	-	67
31-40	20	12	-	-	23	16	11	6	1	-	89
41-50	21	10	-	-	15	13	09	06	-	-	74
51-60	07	05	01	-	11	08	06	04	-	-	42
>60	04	03	-	-	05	02	06	-	-	-	20
Total	71	36	01	-	73	52	36	22	01	-	292

Table 2: Genotypes of subjects with compensated cirrhosis

Genotype	1		2		3		4		5		Total
	M	F	M	F	M	F	M	F	M	F	
20-30	-	-	-	-	03	-	01	-	-	-	04
31-40	06	02	-	-	05	05	02	01	-	-	21
41-50	07	02	-	-	19	09	05	01	-	-	43
51-60	10	03	-	-	12	09	03	02	01	-	40
>60	03	04	-	-	08	08	-	03	-	-	26
Total	26	11	-	-	47	31	11	07	01	-	134

Table 3: Genotypes of subjects with decompensated cirrhosis.

Genotype	1		2		3		4		5		Total
	M	F	M	F	M	F	M	F	M	F	
41-50	01	01	-	-	03	-	01	01	-	-	07
51-60	01	-	-	-	-	01	-	-	-	-	02
>60	-	-	-	-	01	01	-	-	-	-	02
Total	02	01	-	-	04	02	01	01	-	-	11

DISCUSSION

HCV exhibits an extraordinarily high degree of genetic diversity—substantially greater than that of the HIV-1 pandemic—creating a major challenge for the development of both HCV vaccines and pan-genotypic drug therapies. With the introduction and advent of hepatitis C virus by scientist Choo et al⁶, a large variety of patients

non-A, non-B hepatitis were etiologically defined and classified. Complementary DNA cloning technique and RNA sequencing was used for the identification of virus. At different geographical regions of the world various heterogeneous types of genotypes of HCV have been identified. There are six major genotypes with several different subtypes have been identified.⁷ There are few

studies⁹⁻¹² demonstrating the presence of different HCV genotypes in India. HCV types namely 1a, 1b, 2a, 3a, 3b, and 3g have been found in the past studies from northwestern India^{8,13} and genotype 1 has shown predominance over genotype 3 in case of southern India.⁹ In recent study, genotype 3 has shown prevalence in various parts of India.¹³ In the present study, there were 292 non-cirrhotic patients. There were 107 subjects with genotype 1, out of which 71 were males and 36 females. There was 1 male with genotype 2. There were 73 males and 52 females, out of total 125 subjects with genotype 3. There were 36 males and 22 females, out of total 58 subjects with genotype 4. There was 1 male with genotype 5. Amongst 134 compensated cirrhotic patients, there were 26 males and 11 females out of total 37 subjects with genotype 1. There were 47 males and 31 females with genotype 3. There were 11 males and 7 females with genotype 4. There was 1 male with genotype 5. Amongst 11 decompensated cirrhotic patients, there were 2 males and 1 female out of total 3 subjects with genotype 1. There were 4 males and 2 females out of 6 patients with genotype 3. There was 1 male and 1 female with genotype 4. In south East Asian countries genotype 3 is more prevalent, and in US and Western Europe genotype 1 is more prevalent.¹⁴ Different genotypes in different regions help in prediction of the origin of HCV virus. A study by Amarapurkar D et al in 2001 found that hepatitis C genotype 3 is common in India, Genotype 1 runs a more severe course, faster progression and non-responders to interferon as compared with genotype 2 and 3.2. The disease severity, progression, and response to treatment varies according to the genotype.^{15,16}

CONCLUSION

In the above study genotype 3 was most prevalent amongst patients with hepatitis C. Genotype 1 was the second most common type. Persistent HCV infection is associated with the development of liver cirrhosis, hepatocellular carcinoma, liver failure, and death. Detection of genotype is very important for the genotype specific management of hepatitis C, so as to obtain the maximum sustained viral response.

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