

## Prevalence of Different Genotypes of Hepatitis C amongst Subjects Reporting to the Hospital

Kanhaiya Lal Khanna

Assistant Professor, Department of Pathology,  
Career Institute of Medical Sciences and Hospital, Ghaila, Lucknow, Uttar Pradesh, India.

### ABSTRACT

**Background:** Hepatitis C virus exhibits a varied genetic diversity that shows regional variations in the genotypic prevalence. Hepatitis C virus is a globally prevalent pathogen that is a major cause of death and morbidity. The most recent studies determining the disease burden showed an elevation in sero prevalence over the last 15 years to 2.8%, similar to >185 million infections around the world. The present study was conducted with the aim to determine different Genotypic variation of Hepatitis C Amongst Subjects Reporting to the hospital.

**Materials and Methods:** The present study included 438 subjects with hepatitis that reported to the reporting to the Department of General Pathology, Career Institute of Medical Sciences and Hospital, Ghaila, Lucknow, Uttar Pradesh, India. The serum obtained was mixed with guanidinium thiocyanate, betamercaptoethanol and sarcosyl. Phenol and chloroform were used for extracting RNA followed by precipitation with isopropanol. The genotypes thus obtained were made to match with the chart obtained by the manufacturer. All the results obtained were arranged in the tabulated form and analysed using SPSS software.

**Results:** There were 73 males and 34 females with genotype 1. There was 1 male with genotype 2. There were 72 males

and 55 females with genotype 3. There were 38 males and 20 females with genotype 4. There were 26 males and 12 females with genotype 1. There were 49 males and 29 females with genotype 3.

**Conclusion:** From the above study it can be concluded that genotype 3 is most prevalent amongst subjects with hepatitis C.


**Keywords:** Hepatitis, Genotype, Viral.

### \*Correspondence to:

**Dr. Kanhaiya Lal Khanna**  
Assistant Professor,  
Department of Pathology,  
Career Institute of Medical Sciences and Hospital,  
Ghaila, Lucknow, Uttar Pradesh, India.

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### INTRODUCTION

Hepatitis C virus exhibits a varied genetic diversity that shows regional variations in the genotypic prevalence. This poses a great challenge for the development of vaccines and pan-genotypic management that requires the reflection of global trends in the prevalence of hepatitis C genotype. Hepatitis C virus is a globally prevalent pathogen that is a major cause of death and morbidity.<sup>1</sup> The most recent studies determining the disease burden showed an elevation in sero prevalence over the last 15 years to 2.8%, similar to >185 million infections around the world.<sup>2</sup> Persistent hepatitis C viral infection is related to the development of cirrhosis, hepatocellular carcinoma, liver failure, and ultimately death,<sup>3</sup> and hepatitis C virus is now the leading reason of death amongst the HIV-positive subjects, those are on highly active antiretroviral therapy.<sup>4</sup> With advancements in development the incidence rate of hepatitis C infections are apparently decreasing in the developed nations, deaths from liver disorder after hepatitis C infection will continue to surge over the

next 20 years.<sup>5</sup> Hepatitis C virus exhibits an extremely high degree of genetic variation—substantially more than of HIV-1 pandemic—forming a major challenge for the formation of vaccines and pan-genotypic drug therapies. Therefore, the formation of national treatment goals using DAA therapies requires a detailed understanding of relative prevalence and subtypes of genotype of HCV. The present study was conducted with the aim to determine different genotypic variation of Hepatitis C Amongst Subjects Reporting to the hospital.

### MATERIALS AND METHODS

The present study included 438 subjects with hepatitis that reported to the Department of General Pathology, Career Institute of Medical Sciences and Hospital, Ghaila, Lucknow, Uttar Pradesh, India. The study was approved by the institute's ethical board and all the subjects were informed about the study and a written consent was obtained from them in their vernacular

language. All the subjects were made to give their blood samples and samples of serum were obtained from them, that was used for extracting viral RNA. Reverse transcriptase chain reaction using line probe assay was used for estimating viral RNA. The serum obtained was mixed with guanidinium thiocyanate, betamercaptoethanol and sarcosyl. Phenol and chloroform were used for extracting RNA followed by precipitation with isopropanol.

From this complementary DNA was obtained. Polymerase chain reaction was used for Amplification of cDNA. Reverse hybridization using line probe assay was done. The genotypes thus obtained were made to match 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.

**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	18	7	-	-	18	14	5	5	-	-	67
31-40	21	11	-	-	22	17	12	5	-	-	88
41-50	22	9	-	-	16	12	08	07	01	-	75
51-60	08	04	-	-	12	09	07	03	-	-	41
>60	04	03	01	-	04	03	06	-	-	-	21
<b>TOTAL</b>	<b>73</b>	<b>34</b>	<b>1</b>	<b>-</b>	<b>72</b>	<b>55</b>	<b>38</b>	<b>20</b>	<b>1</b>	<b>-</b>	<b>294</b>

**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	05	03	-	-	06	04	01	02	-	-	21
41-50	07	02	-	-	19	09	05	01	-	-	43
51-60	12	02	-	-	12	09	02	03	01	-	41
>60	02	05	-	-	09	07	-	03	-	-	26
<b>TOTAL</b>	<b>26</b>	<b>12</b>	<b>-</b>	<b>-</b>	<b>49</b>	<b>29</b>	<b>09</b>	<b>09</b>	<b>01</b>	<b>-</b>	<b>135</b>

**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	-	-	02	01	01	01	-	-	7
51-60	-	01	-	-	-	01	-	-	-	-	2
>60	-	-	-	-	01	01	-	-	-	-	2
<b>TOTAL</b>	<b>1</b>	<b>2</b>	<b>-</b>	<b>-</b>	<b>3</b>	<b>3</b>	<b>01</b>	<b>01</b>	<b>-</b>	<b>-</b>	<b>11</b>

**RESULTS**

The study involved 438 subjects with the mean age of 42.74 +/- 10.22 years. Table 1 shows the genotype of subjects without cirrhosis. There were 73 males and 34 females with genotype 1. There was 1 male with genotype 2. There were 72 males and 55 females with genotype 3. There were 38 males and 20 females with genotype 4. There was 1 male with genotype 5. There were 67 subjects between 20-30 years of age. There were 88 subjects between 31-40 years of age. There were 75 subjects between 41-50 years of age. There were 41 subjects between 51-60 years of age. There were 21 subjects more than 60 years of age. Table 2 shows the genotypes of subjects with compensated cirrhosis. There were 26 males and 12 females with genotype 1. There were 49 males and 29 females with genotype 3. There were 9 males and 9 females with genotype 4. There was 1 male 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 41 subjects between 51-60 years of age. There were 26 subjects more than 60 years of age.

Table 3 shows the genotypes of subjects with decompensated cirrhosis. There was 1 male and 1 female with genotype 1 between 41-50 years of age. There was 1 male with genotype 1 between 52-60 years of age. There were 2 males with genotype 3 between 41-50 years of age. There was 1 female between 51-60 years of age with genotype 3. There was 1 male and 1 female between 41-50 years of age with genotype 4.

**DISCUSSION**

Hepatitis C virus exhibits a very high degree of genetic variation—considerably greater than that of the HIV-1 genotypes—thus making a major challenge for the formation of both vaccines and pan-genotypic drug treatment modalities. With the advent of hepatitis C virus by a physician Choo et al<sup>6</sup>, a large majority of subjects with non- A, non-B hepatitis were etiologically classified as hepatitis C infections. The technique used for identification of virus was complementary DNA cloning technique with RNA sequencing. At different geographical locations of the nations different heterogeneous varieties of genotypes of hepatitis C virus have been found. There are six major genotypes with several

subtypes have been seen.<sup>7</sup> There are few studies<sup>8-12</sup> that showed that the presence of different Hepatitis C genotypes in India. The major types are namely 1a, 1b, 2a, 3a, 3b, and 3g have been identified from the past studies conducted in northwestern India<sup>8,13</sup> and genotype 1 is predominant over genotype 3 in areas of southern India.<sup>9</sup> In recent studies, genotype 3 was more relevant in various parts of India.<sup>13</sup> In the present study, there were 71 males and 36 females with genotype 1. There was 1 male with genotype 2. There were 73 males and 34 females with genotype 1. There was 1 male with genotype 2. There were 72 males and 55 females with genotype 3. There were 38 males and 20 females with genotype 4. There was 1 male with genotype 5. There were 67 subjects between 20-30 years of age. There were 88 subjects between 31-40 years of age. There were 75 subjects between 41-50 years of age. There were 41 subjects between 51-60 years of age. There were 21 subjects more than 60 years of age. There was 1 male and 1 female with genotype 1 between 41-50 years of age. There was 1 male with genotype 1 between 52-60 years of age. There were 2 males with genotype 3 between 41-50 years of age. There was 1 female between 51-60 years of age with genotype 3. There was 1 male and 1 female between 41-50 years of age with genotype 4. In the south east asian areas there is predominance of genotype 3 and the in United states and western Europe there is prevalence of genotype 1.<sup>14</sup> Different genotypes in different areas help in predicting the origin of Hepatitis C virus. According to a study by Amarapurkar D et al conducted in the year 2001 showed that hepatitis C genotype 3 is more prevalent in India, Genotype 1 has a more severe course, quicker progression and non-responders to interferon as compared with genotype 2 and 3.<sup>2</sup> The severity of disease, progression and response to the management strategies varies according to the genotype.<sup>15,16</sup>

## CONCLUSION

From the above study it can be concluded that genotype 3 is most prevalent amongst subjects with hepatitis C. Genotype 1 was the second most commonly found genotype. Hepatitis C is a very frequent form of hepatitis that is seen amongst 80% of the subjects. It is progressive in nature and can also advance to carcinoma and cirrhosis.

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