ORIGINAL ARTICLE

GENETIC DIVERSITY OF HEPATITIS C AND GENDER PREDISPOSITION: A CROSS-SECTIONAL STUDY

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Background: Hepatitis C is becoming a very common infection in Pakistan. Treatment in the past was partially effective and carried a lot of side effects. Different antiviral regimens are effective in different genotypes. Knowledge of prevalent genotypes is very important not only in treatment, but to design future strategies as well. This study was conducted to see different prevalent genotypes in a semi-controlled group along with their association with gender. **Methods:** This cross-sectional analytical study was carried out at Gastroenterology Department of Combined Military Hospital Lahore from Sep 2016 to Mar 2017. Non-probability consecutive sampling technique was used to recruit 568 patients coming to Gastroenterology OPD with positive Anti HCV and HCV-RNA PCR. Patients having signs of decompensation were excluded. **Results:** There were 297 (52.2%) male and 271 (47.7%) female patients with mean age 48.1±32 years. Genotype 1 was seen in 27 (4.8%), genotype 3 in 524 (92.3%), genotype 3 and 4 in 14 (2.5%), 2 and 3 in 1 (0.2%), and genotype was un-typeable in 2 (0.4%) cases. Genotype 1 and combined 3 and 4 were more frequent in males while genotype 3 was more common in females (p=0.007). **Conclusion:** Genotype 3 is the predominant hepatitis genotype in our population. Genotype 1 is more common in males whereas genotype 3 is more common in females.
Keywords: Genetic diversity, Hepatitis C, Genotype

INTRODUCTION

Hepatitis C was discovered in 1991 and classified in 1994.[1] It belongs to family flavivirus and comprises of 3 structural (C, E1, E2) and 4 non-structural genes (NS 2, NS 3, NS 4, NS 5).[2,3] It has 11 genotypes but there is controversy over genotype 7–11 as some scientists group them in genotype 6.[4] Hepatitis C genotype shows geographic variations with genotype 1 being more prevalent in US, Europe and Japan; genotype 2 in Northern Italy, North America, Europe and Japan; genotype 3 in South East Asia, Europe and US; genotype 4 in North Africa and Middle East; genotype 5 in South Africa; genotype 6 in Hong Kong; genotype 7, 9 in Vietnam; and genotype 10 and 11 in Indonesia.[5] Hepatitis C is prevalent all over the world. Almost 160 million people are suffering from it worldwide.[6] Three million new cases are observed every year. Mortality with Hepatitis C is almost 350,000 persons worldwide every year.[7] Around 3% population is infected in Pakistan.[8] This is in contrast to surrounding countries like India (0.66%), Nepal (1.0%), Myanmar (2.5%), Iran (0.87%), China (1%) and Afghanistan (1.1%).[1,9,10]

Genetic heterogeneity has effect on both diagnosis and treatment. Knowing the prevalent genotype in an area can help in planning future management strategies for eradication and control of disease. We conducted this study to evaluate share of various genotypes in disease burden of Hepatitis C and its distribution in both sexes in a relatively unique population of Pakistan Army.

MATERIAL AND METHODS

This cross-sectional analytical study was conducted at Gastroenterology Department of Combined Military Hospital Lahore from Sep 2016 to Mar 2017 after getting institutional approval. Written informed consent was also obtained from all the participants. Sample size was calculated using WHO sample size calculator as 385, however, we included a total of 568 patients through non-probability consecutive sampling. Patients coming to Gastroenterology OPD with positive Anti HCV and HCV-RNA PCR were included whereas thoese having signs of decompensation like presence of jaundice, ascites, variceal haemorrhage, hepatic encephalopathy were excluded.[11]

These patients underwent HCV Genotype testing by real-time hybridization-fluorescence detection technique on Sa Cycler™ (Sacace Biotechnologies). Data regarding the genotype and gender were collected for each patient involved in the study and entered in SPSS-24 for analysis. Frequency and percentage were calculated for categorical variables like genotype of hepatitis and gender while mean and standard deviation were calculated for numerical variables like age. Association of gender with hepatitis genotype was determined using Chi Square test and $p \leq 0.05$ was considered significant.

RESULTS

The mean age of patients (n=568) was 48.1±32 years ranging from 19 to 80 years. Out of these, 297 (52.2%)

were male and 271 (47.7%) were female; male to female ratio was 1.09:1. Frequency and percentage distribution of different genotypes and combination of genotypes are shown in Table-1 with genotype 3 being most prevalent in our population.

Table-1: Percentage distribution of different genotypes of Hepatitis C virus

Genotype	Frequency	Percentage
1	27	4.8
3	524	92.3
2 and 3	1	0.2
3 and 4	14	2.5
Un-typeable	2	0.4

Table-2 shows the gender distribution of Hepatitis C genotype. Genotype 1, and combined 3 and 4 are more frequent in males compared to females. Genotype 3 is more common in females (p=0.007).

Table-2: Frequency distribution of hepatitis genotype in males and females [n (%)]

Genotype	Male	Female	p
1	17 (5.7)	10 (3.7)	
3	267 (89.9)	257 (94.8)	
2 and 3	–	1 (0.4)	0.007
3 and 4	13 (4.4)	1 (0.4)	
Un-typeable	–	2 (0.7)	
Total	297 (100)	271 (100)	

DISCUSSION

Hepatitis C is a very common infection in our part of the world. It has 6 major genotypes. Knowledge of separate incidence of different genotypes is important for treatment as well as for formulating strategies to control the infection.

In our 568 patients, mean age was 48.1±32 years, maximum number of patients was seen in age group 46–60 years. Male to female ratio was 1.09:1. Amjad Ali et al[12] showed male to female ratio 1.38:1 in their study. This may be because of the demographic peculiarity in that study. No difference in gender was seen by Attaullah et al[5]. In our study genotype 3 alone was seen in 92.3% cases and 2.7% cases had genotype 3 combined with one other genotype. In other local studies as well, genotype 3 was the predominant genotype.[13,14] In study by Amjad Ali et al[12] genotype 1a was found in 6.8%, 1b was found in 4.6%, 2a in 1.3%, 3a in 54.42%, 3b in 8.19% and mixed in 8.19% patients. Survey carried out by Messina JP et al[15] showed prevalence of genotype 1 in 23.2%, genotype 3 in 71.6% and genotype 2 in 2.4% patients in South Asia. Afridi S et al[16] noted genotype 3a in 50% and genotype 3b in 10.72% cases. In a review by Attaullah S et al[5] prevalence of genotype 3 in district Punjab was found to be 68.94%.

Genotype distribution among males and females in our study showed that genotype 1 was more common in males as compared to females. Similar results were seen by Elasifer et al[17] and Shah et al[18] in two different studies. Genotype 3 was found to be more common in females in our study. In a study conducted by Afridi et al[19] in districts of Punjab province similar results were seen (84.7:80.62%). Shah et al[18] found male predominance in Genotype 3 but number of females was quite less in their study (67.8:37.2%). In a study by Inamullah et al[20] genotype prevalence was found to be independent of gender.

Although genotype 3 is the predominant genotype in south Asia as reflected by various studies, the percentage is significantly lower than the one seen in our study. Major difference between other studies and our study is the patient population. Most of our study population belonged to Punjab. Those in service live in a closed community setup separate from the general population. Therefore, we can assume that this figure is the true reflection of various genotypes in this area as the mixing of other genotypes through import from neighbouring countries is less likely. Significant gender variation is seen in genotype 1 and 3 in our study. This may reflect changing patterns in future.

CONCLUSION

Genotype 3 is the predominant genotype in our study population. Genotype 1 is more common in males whereas genotype 3 is more common in females. We should keep these facts in mind while formulating future strategies.

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