

The frequency of hepatitis C virus genotypes with chronic hepatitis C referred to Nikopour clinic in Yazd

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ABSTRACT

The aim of this study was to investigate the frequency of hepatitis C virus genotypes with chronic hepatitis C referred to Nikopour clinic of Yazd during 2010-2020. In this cross-sectional study RT-PCR was used to determine the genotype of hepatitis C virus. The patient information was recorded in a questionnaire and finally the data were analyzed by SPSS software. During this study, 104 patients with hepatitis C were evaluated with a mean age of 42.9 years. The most common hepatitis C virus genotypes were 3a, 1a and 3, respectively. The HCV genotype was significantly associated with risk factor and history of blood transfusion in patients. Considering that the predominant genotype is 3a and about 35.6 %, seems that genotype determination would be a candidate for treatment.

Keywords: Genotype, hepatitis C, frequency, Yazd

INTRODUCTION

Hepatitis C is a worldwide virus that affects more than 170 million populations. The majority of these Hepatitis C Virus (HCV) cases are asymptomatic carriers, but chronic

contamination develops in the majority (85 %) of infected people [1-4].

HCV has a significantly higher level of genetic variation than the HIV-1 pandemic, posing a significant challenge for the production of both HCV- related vaccines

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types and prescribed pan-genotypic medications [5-7].

Several subtypes, notably 1a, 1b, 2a, and 3a, have already been identified as being widely spread around the world and accounting for a significant proportion of HCV infections in regions with the high prevalence. Infected bloods, blood products types, inoculating drug use, and other ways are believed to have transmitted these supposed "epidemic subtypes types" quickly in the decades before HCV was discovered [8-10].

The aim of this study was to consider the frequency of hepatitis C virus genotypes in patients with long-lasting hepatitis C in Yazd, Iran.

MATERIALS AND METHODS

This cross-sectional descriptive-analytical study was performed on patients with chronic hepatitis C in Nikopour clinic in Yazd after the approval of the university ethics committee. Sampling was done by census of patients with chronic hepatitis C.

All patients with chronic hepatitis C who referred to Nikopour Clinic between 2010 and 2020 and whose case was available were eligible for the study. Patients whose records and information were not available or whose hepatitis C virus genotype was not identified were excluded.

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RT-PCR (Reverse Transcription polymerase chain reaction) and Universal primer HCV were used to determine the genotype.

Other required information includes: age, sex, duration of illness, history of injecting drug use, history of blood transfusions, history of suspected sexual intercourse, marital status, occupation, risk factors (history of dialysis, hemophilia, thalassemia and tattooing) and co-infection with HBV and HIV was recorded in a pre-prepared questionnaire. After determining the test results, HCV genotype was recorded in the questionnaire.

After collecting the information, finally the information obtained by SPSS software version 21 was statistically analyzed (with appropriate statistical methods including descriptive statistics methods (frequency indices and relative percentage) and Chi-square test). In all cases, a significance level of less than 0.05 was considered.

RESULTS

In this study, 104 patients with hepatitis C were evaluated with a mean age of 42.9 ± 10.66 years with a range of 22 to 65 years. Among patients, 97 (93.3 %) were male and 7 (6.7 %) were female. 67 patients (64.4 %) were married, 24 patients (23.1 %) were

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single and 13 patients (12.5 %) had died their life partners.

The age group distribution in the present study showed that the majority of patients were in the age group of 30 to 40 years (29.8 %). 15.4 % of patients were less than 30 years old.

In terms of education, the majority of patients had a diploma (43.3 %) and after that the highest frequency was related to the cycle degree (31.7 %). Also, occupationally, 45.2 % of patients were self-employed.

69 patients (66.3 %) had a history of injecting drug addiction, 12 patients (11.5 %) had a history of blood transfusion and 35 patients (33.7 %) had a history of high-risk sexual behaviors. The results of the present study also showed that in terms of risk factors such as tattooing, cupping, hemophilia, thalassemia and dialysis, 36 (34.6 %) had tattoos, 13 (12.5 %) had cupping and 1 (1 %) had hemophilia and other patients or 54 patients (51.9 %) had no risk factor. Only one patient had a history of co-infection with hepatitis B. The mean duration of the disease in patients with hepatitis C was 2.1 ± 2.76 years. The results of the present study showed that the most common hepatitis C virus genotypes were 3a, 1a and 3 with a frequency of 35.6 %, 14.4 % and 11.5 %, respectively. Also, mixed type (simultaneous

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infection with several genotypes) had a frequency of 11.5%. The most common genotype in men and women was genotype 3a and mixed. Genotypes 1, 1a and 4 were also present in females. No other genotypes were observed in females.

The most common genotype in all age groups was genotype 3a. After genotype 3a, in age group less than 30 years, genotype 1a and 3, in age group 30-40 years, genotype 3, in age group 40-50 years, 1a and 1ab and in age group over 50 years, genotype 2ac had the highest frequency. Frequency distribution of HCV genotype was not significantly related to patients' age ($p = 0.11$).

Genotype 3a was more common in most occupations. Also, frequency distribution of HCV genotype in patients with hepatitis C had no significant relationship with patients' occupation ($p = 0.23$). Also, was no significant relationship between HCV genotype distribution and patients' marital status ($p = 0.76$). The distribution of HCV genotype had no significant relationship with the history of high-risk sex in patients ($p = 0.38$). The most common genotype in people with a history of high-risk sexual behavior was genotype 3a, 3 and 1a.

There was a significant relationship between the frequency distribution of HCV genotype

and the presence of risk factor in patients (p = 0.001) (Table 1). Also, the frequency distribution of HCV genotype showed a significant relationship with the history of

blood transfusion in patients (p = 0.009) (Table 2).

Table 1. Frequency distribution of HCV genotypes in patients with chronic hepatitis C according to the presence or absence of risk factor

Genotype	No risk factor		Tattooing		Cupping		Hemophilia		Total	
	N	P	N	P	N	P	N	P	N	P
1	2	3.7	2	5.6	0	0	0	0	4	3.8
1a	7	13	8	22.2	0	0	0	0	15	14.4
1ab	5	9.3	3	8.3	0	0	0	0	8	7.7
1b	2	3.7	0	0	1	7.7	0	0	3	2.9
2ac	4	7.4	1	2.8	2	15.4	0	0	7	6.7
2b	1	1.9	0	0	0	0	1	100	2	1.9
3	7	13	2	5.6	3	23.1	0	0	12	11.5
3a	17	31.5	13	36.1	7	53.8	0	0	37	35.6
4	3	5.6	1	2.8	0	0	0	0	4	3.8
Mixed	6	11.1	6	16.7	0	0	0	0	12	11.5
Total	54	100	36	100	13	100	1	100	104	100

N= Number; P= Percent % ; P-value= 0.001

Table 2. Relationship between frequency distribution of HCV genotype and the history of blood transfusion

Genotype	Yes		No		Total	
	N	P	N	P	N	P
1	1	8.3	3	3.3	4	3.8
1a	0	0	15	16.3	15	14.4
1ab	1	8.3	7	7.6	8	7.7
1b	1	8.3	2	2.2	3	2.9
2ac	1	8.3	6	6.5	7	6.7
2b	2	16.7	0	0	2	1.9
3	0	0	12	13	12	11.5
3a	4	33.3	33	35.9	37	35.6
4	1	8.3	3	3.3	4	3.8
Mix	1	8.3	11	12	12	11.5
Total	12	100	92	100	104	100

N= Number; P= Percent % ; P-value= 0.009

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Finally, there was no significant relationship between the history of injecting drug use in patients, the duration of the disease and the education of patients with the frequency distribution of HCV genotype with $p= 0.48$, $p= 0.11$, $p= 0.35$, respectively.

DISCUSSION

In current study, the majority of patients had a diploma degree. 66.3 % had a history of drug addiction. Tattooing was most risk factor. Only one patient had a history of co-infection with hepatitis B. The most usual hepatitis C virus genotype was 3a. Frequency of mixed genotypes was 11.5 %. Frequency dissemination of HCV genotype was not significantly related to patients' age, occupation, marital status and the high-risk sex history. But, there was a significant association between the frequency distribution of HCV genotype and the presence of risk factor in patients and also history of blood transfusion in patients.

A study in Tehran, Iran showed that the maximum frequency was related to genotype 1a. Mixed genotypes types were also observed in 1.6 % cases [11].

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In another study in Balochistan, Pakistan a total of serum samples (3351 samples) were assayed by type-particular genotyping investigation. From all of HCV RNA positive cases, 2039 were men and 1312 were women. The most genotype in Pakistan was type 3a [12] and was similar to current research.

A study has assayed the spreading HCV genotypes in an Iranian great community of HCV infected cases. The main frequency was related to subtype 1a followed by 3a type. Mixed genotypes types were also observed in 2.5% of the total cases [13]. Another study in Iran showed that 1a was also the common subtype in Iran [14].

In the United States a study recognized HCV RNA titers and genotypes types related to infected patients in the country people. In that study 1a had the most frequency among subtypes types of virus [15].

In another study in Yazd, a central province in Iran, HCV genotype 3 was the main genotype in the investigated community and followed by two subtypes 1a and 1b [16].

CONCLUSION

Since the predominant genotype in this study was 3a, it appears that genotype

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identification for each patient should be considered as a main factor for treatment.

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