

The Correlation between Different Risk Factors of Hepatitis C and Different Genotypes

Abstract

Background: Hepatitis C infection is one of the health problems in the world. Several known risk factors are responsible in transmission of this infection. We are going to study the prevalence of these risk factors for different genotypes of hepatitis C and if possible, specify probable relations between each risk factor and transmission of each genotype. **Materials and Methods:** This is a cross-sectional study done on 270 people who had positive anti-hepatitis C virus (HCV) antibody and HCV RNA. Demographic specificity and possible risk factors were collected using a questionnaire, and statistical analysis was done by SPSS software (version 20). Chi-square test used to estimate the prevalence and relation between each qualitative risk factor and HCV genotype transmitted. Analysis of variance was used for studying the prevalence and relation between quantitative risk factors and HCV genotypes. **Results:** The sample size was 270 persons. Of these, 217 (80.4%) were men and 185 (68.5%) were infected with genotype Type III. Most people were in age range of 31–40 years old 92 (34%). Single people were 126 (46.7%) and 169 (62.6%) were high school and university graduated. Tattooing as a risk factor had a meaningful relation with hepatitis C genotype ($P < 0.001$). **Conclusions:** According to the findings, most people in central provinces of Iran with hepatitis C are carrying genotype III, with most prevalent risk factors such as intravenous drug use and unsafe sexual activity. Besides, tattooing had a significant association with hepatitis C genotype, so that in these groups of people, genotype I was more frequent isolated virus.

Keywords: Genotype, hepatitis C, risk factor

Introduction

Hepatitis C infection is one of the significant health problems in the world because of its high tendency of converting to chronic liver disease, hepatic failure, and hepatocellular carcinoma. Known risk factors for transmission of hepatitis C are blood transfusion, intravenous (IV) drug use, unsafe sex, unsterile medical procedures, and needle stick. Also, tattooing, phlebotomy and acupuncture may have role, as potential ways, in transmission of hepatitis C. The most prevalent hepatitis C virus (HCV) genotype in the world is Type I and the others are in the next levels.^[1,2] The prevalence of HCV genotypes are different in several parts of the world, and some of the risk factors are responsible in transmission of especial HCV genotype. So, determining different risk factors and significance of each in relation to different genotypes of hepatitis C can be a way for prevention and treatment of hepatitis C. Most of the studies and medical literature

up to now, have been focused on total prevalence of each risk factors, but their association with HCV genotype is ignored. The studies about HCV genotype and risk factors are limited in Iran, so, we are going to conduct this study on the prevalence of these risk factors one by one for different genotypes of hepatitis C. Could be determine, if there is an especial risk factor for each genotype of HCV to transmit or not? This study can be an effort to clarify the role of different risk factors considering genotypes, to prevent, treat and reduce the prevalence of HCV.

Materials and Methods

This is a cross-sectional study done between February 2013 and July 2013 in referral laboratory. This study doesn't have a special direction. The target group, are the samples in hepatology and infectious referral laboratory, which are from the central part of Iran including Isfahan, Kohgiluyeh and buyerahmad, Chahar Mahal and Bakhtiari, some parts of Fars, Arak and

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Lorestan. These samples were tested by polymerase chain reaction (PCR) and result of antibody (Ab) assay were registered in the patients' files. The inclusion criteria were the people who had positive anti-HCV Ab and confirmed by HCV RNA and genotyping. Patients with positive anti-HCV Ab but negative HCV RNA were excluded from the study. The sample size was 270 patients calculated by formula with accuracy rate of 0.06 and confidence interval of 95%. This research is confirmed by moral committee of Isfahan University of Medical Sciences. We chose randomly all anti-HCV Ab and HCV RNA positive patients from central parts of Iran who were referred to referral laboratory by specialists for PCR and genotyping. Demographic informations like age, sex, education level, marital status and HCV risk factors like IV drug use, blood transfusion, being incarcerated with IV drug users (IVDUs), unsafe sexual activity, history of unsanitary dental manipulation, surgery, accident and blood transfusion, suturing and other medical procedures with unsterile instruments, needle stick, tattooing, acupuncture and phlebotomy were extracted and registered by the researcher in files of laboratory for each patient. Kiagen kit for extraction of viral RNA and genotype detection used. Synthesis of C-DNA was done by Italian Sacace kit on extracted RNA (with Moloney Murine Leukemia Virus enzyme for 30 min in 37°C). The HCV genotype is extracted with sacace kit, which is PCR-based. This extraction was done on the 342 5' untranslated region part of HCV genome. Finally, different viral genotype makes different PCR product which are as below:

- HCV genotype Ia → 338 bp
- HCV genotype Ib → 395 bp
- HCV genotype II → 286 bp
- HCV genotype IIIa → 227 bp.

Different PCR products were electrophoreses on agarose 4% made by etedium bromide gel in the tris borate EDTA 0.5 × buffer and is detected with ultraviolet technology.

Statistical analysis was done by SPSS software (version 20) (statistical package for social science) (IBM, Armonk, NY, United states of America). Chi-square test was used to estimate the prevalence and relation between each qualitative risk factors and HCV genotype transmitted. Analysis of variance (ANOVA) was used for studying the prevalence and relation between quantitative risk factors (such as episodes of blood transfusion) and HCV genotypes.

Results

The sample size was 270 persons. Of these, 217 (80.4%) were males, and the rest were females. The youngest patient in this study was 14 and the eldest was 67 years old. The average age for each genotype was as following:

- Genotype I → 36.1 ± 10.3 years old
- Genotype II → 33.7 ± 9.5 years old
- Genotype III → 34.9 ± 10.3 years old.

A total of 62 (23%) persons were infected with genotype Type I, 23 (8.5%) genotype Type II and 185 (68.5%) genotype Type III [Table 1]. We checked education level and marital status that can be seen in Table 2. Totally, 9 persons didn't mention their marital status, which were named as missed samples. The frequency of each risk factors for different genotypes can be seen in Table 3, and the frequency of quantitative risk factor (episodes of blood transfusion) is seen in Table 4. 12 (19.4%) people with genotype 1,3 (13%) people with genotype 2 and 31 (16.8%) people with genotype 3 knew that they were affected with hepatitis C [Table 5].

Discussion

We studied HCV genotypes considering association of different risk factors. The most prevalent HCV genotype in this study was genotype Type III. In recent studies done in Iran, the most prevalent genotype, was Type III^[3,4] and studies in other countries including, Saudi Arabia revealed

Table 1: The frequency of different HCV genotypes

| Type of genotype | Frequency (%) |
|------------------|---------------|
| I | 62 (23) |
| II | 23 (8.5) |
| III | 185 (68.5) |
| Total | 270 (100) |

HCV: Hepatitis C virus

Table 2: Frequency of sample's demographic informations

| Variable | Frequency (%) |
|---------------------------|---------------|
| Age | |
| <20 years old | 19 (7) |
| 21-30 years old | 78 (28.9) |
| 31-40 years old | 92 (34) |
| 41-50 years old | 57 (21.1) |
| >50 years old | 24 (9) |
| Sexuality | |
| Male | 217 (80.4) |
| Female | 53 (19.6) |
| Education level | |
| Illiterate | 53 (19.6) |
| Elementary school diploma | 6 (2.2) |
| Middle school diploma | 42 (15.6) |
| High school diploma | 132 (48.9) |
| Bachelor | 30 (11.1) |
| Master and higher degrees | 7 (2.6) |
| History of marital status | |
| Single | 126 (46.6) |
| Married | 115 (42.5) |
| Divorcee | 20 (7.4) |
| Missed | 9 (3.3) |
| Total | 270 (100) |

Table 3: Frequency of different HCV genotypes for each risk factors

| Variable | Frequency (%) | | | P |
|---------------------------|---------------|-------------|--------------|--------|
| | Genotype I | Genotype II | Genotype III | |
| IVDU | 8 (12.9) | 5 (21.7) | 38 (20.5) | 0.387 |
| Being in prison with IVDU | 7 (11.3) | 6 (26.1) | 25 (13.5) | 0.203 |
| High-risk sexual activity | 20 (32.3) | 9 (39.1) | 76 (41.1) | 0.467 |
| Surgical procedures | 8 (12.9) | 5 (21.7) | 25 (13.5) | 0.539 |
| Dental procedures | 17 (27.4) | 2 (8.7) | 41 (22.2) | 0.182 |
| History of suture | 7 (11.3) | 3 (13) | 27 (14.6) | 0.803 |
| Other medical procedures | 1 (1.6) | 2 (8.7) | 9 (4.9) | 0.304 |
| History of needle stick | 0 | 2 (8.7) | 6 (3.2) | 0.06 |
| Tattooing | 13 (21) | 0 | 8 (4.3) | >0.001 |
| Acupuncture | 2 (3.2) | 2 (8.7) | 8 (4.3) | 0.601 |
| History of phlebotomy | 3 (4.8) | 2 (8.7) | 18 (9.7) | 0.49 |

IVDU: Intravenous drug use, HCV: Hepatitis C virus

Table 4: Frequency of blood transfusion for different HCV genotypes

| Episodes of blood transfusion | Genotype I | Genotype II | Genotype III |
|-------------------------------|------------|-------------|--------------|
| Never | 56 | 22 | 162 |
| 1 time | 4 | 1 | 16 |
| 2 times | 2 | 0 | 6 |
| 3 times | 0 | 0 | 1 |
| Total | 62 | 23 | 185 |

HCV: Hepatitis C virus

Table 5: Frequency of people who know the way they affected HCV

| Type of genotype | Frequency | Knowing how they affected Frequency (%) |
|------------------|-----------|---|
| Genotype I | 62 | 12 (19.4) |
| Genotype II | 23 | 3 (13) |
| Genotype III | 185 | 31 (16.8) |
| Total | 270 | 46 (17) |

HCV: Hepatitis C virus

genotype IV as the most prevalent,^[5-7] genotype Type II in Chinese and Brazilian prisoners,^[8,9] Type II in Greek IVDUs^[10] and Type I in other Countries.^[1,11,12]

One-way ANOVA did not find a meaningful relation between the average age with different genotypes ($P = 0.58$), in other studies, the age of 40 and older, explained as one of the risk factors.^[13]

Also, the average age for female prisoners in the province of Isfahan was 34.54 ± 11.2 years old.^[14]

Of 270 HCV positive patients, most patients (80.45%) were male which was compatible with recent researches of hepatitis C that males were dominant^[3,11,13,15-17] except for a Yemanian study which majority were female.^[18,19]

We can say that the most patients in this study were high school and university graduated. In other countries, the prevalence of HCV was more in those people with education level under diploma and university degrees.^[18] The most patients in one study in Isfahan had elementary school degrees^[14] and in yemen, most patients had the lowest education level.^[18] We studied the prevalence of the HCV risk factors one by one for different genotypes of HCV and their relations. The most frequent risk factors between them were unsafe sexual activity and IVDU but no meaningful relation to HCV genotypes found ($P < 0.05$) in other studies done on the prevalence of HCV risk factors, the most prevalent were, IVDU, multiple sexual partner, being in prison some time in their lifetime, and blood transfusion especially in hematologic diseases such as hemophilia but there wasn't any study to investigate the relation of the risk factors with different HCV genotype in these patients.^[20-23] Tattooing as a risk factor had a meaningful relation with hepatitis C genotype ($P < 0.001$) but in other studies, this relation has not been studied and tattooing is mentioned just as a risk factor.^[24]

Totally, 46 patients knew how they had been sick with hepatitis C, but we could not find a similar result in other studies. Hepatitis C is a worldwide problem and 85% of cases have affinity to become chronic hepatitis, cirrhosis and finally hepatocellular carcinoma, so, defining the prevalence of hepatitis C risk factors and genotypes, and their relations help us to prevent HCV transmission and treat it.

Conclusion

The most prevalent genotype in central parts of Iran is genotype Type III, which is relevant with other studies. Most patients were male with high school diploma and higher education level, most of them were single (46.7%) that was matched with recent studies in Iran. The most prevalent risk factors were IVDU and high-risk sexual activity. Tattooing had a meaningful relation with hepatitis C genotype and in these patients, genotype I was the most prevalent.

This study is limited to central part of Iran (Isfahan), so we suggest more studies in other parts of Iran for studying the prevalence of HCV risk factors and genotypes and their relations, so we can draw a protocol to prevent and treat HCV.

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Nil.

Conflicts of interest

Isfahan University of Medical Sciences.

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