

Original Article

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Determining Hepatitis C Virus Genotype Distribution of Amasya Area in Turkey

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Background: Hepatitis C virus (HCV) is one of the most common reasons for liver carcinoma, cirrhosis and chronic liver deficiency worldwide. Knowing the genotype of HCV with many genotypes before the treatment would be clinically useful in organizing the treatment and follow up. Retrospective investigation of HCV genotypes in chronic hepatitis C patients applying to our hospital was aimed in the current study.

Methods: Results of 82 chronic hepatitis C patients sent to Amasya University Sabuncuoğlu Şerefeddin Education and Research Hospital Microbiology Laboratory between 2010-2014 with positive anti-HCV and HCV-RNA were included in the study. Viral genotyping was made by Qiagen one step RT-PCR (Qiagen, hilden, Germany) and ABI PRISM 3730 (Perkin Elmer, USA) systems using real-time polymerase chain reaction method.

Result: 79 (96.34%) of the patients were genotype 1, 2 (2.42%) were genotype 2 and 1 was (1.21%) genotype 3. The most common sub-types were found genotype 1b (69.51%) and genotype 1a (20.73%) in order.

Conclusion: HCV genotype 1 (96.34%) is seen in high ratios in our area and the most common sub type is genotype 1b (69.51%).

Key words: Hepatitis C virus, Chronic Hepatitis, HCV genotype

Introduction

Hepatitis C virus which is a shelled and single fibered RNA virus from Flaviviridae family is one of the most important reasons of hepatitis, cirrhosis and hepatocellular carcinoma. With number of people infected by HCV virus reaching 200 million and chronic acute infections reaching 80% constitute a serious threat (1,2). In the studies made, the prevalence of this infection worldwide is 1-5% and this ratio is reported as 1-2,4% in our country, Turkey (3,4).

Assessing the genotype of HCV which is known to have 6 major genotypes at least and over 80 sub-types is very important for organizing the treatment and follow-up (5,6). While genotypes 1, 2 and 3 are common in the world, genotype 4 is common in Middle East and Egypt, genotype 5 is common in South Africa and

genotype 6 is common in Far East. Genotype 1b with high resistance to the treatments is common in our country (7, 8). Retrospective evaluation of HCV genotype results in HCV-RNA positive blood samples of patients with HCV infections was aimed in our study.

Study Design

Genotype distribution of 82 patients which was sent to Microbiology Lab of Amasya University Education and Research Hospital between 2010-2014 with positive HCV-RNA were examined in our study. Viral genotyping was made using Qiagen one step RT-PCR (Qiagen, hilden, Germany) and ABI PRISM 3730 (Perkin Elmer, USA) systems in order using real-time polymerase chain reaction (Rt-PCR) method.

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Results

Eighty two chronic hepatitis c patients consisting of 33 (40.24%) male and 49 (59.76%) female patients with positive anti-HCV and HCV rna were included in our study. Genotype information and epidemiological data of patients whose ages were between 23-77 and average age was 57.9 were evaluated retrospectively using hospital automation system and patient file information.

Table-1:Distribution of HCV genotypes and subtypes

Genotypes	Genotype 1			
	1	1a	1b	1a/1b
N	4	17	57	1
%	4.87	20.73	69.51	1.22
Total	79 (%96.34)			

Genotype 2		Genotype 3	Total
2a	2b	3	
1	1	1	82
1.22	1.22	1.22	%100
2(%2.44)		1(%1.22)	82 (%100)

As the HCV genotype distributions of these patients were examined, 79 (96.34%) were genotype 1 (57 genotype 1b, 17 genotype 1a, 4 genotype1 and 1 genotype 1a/1b), 2 (2.44%) were genotype 2 (1 genotype 2a, 1 genotype 2b) and 1 (1.22%) was genotype 3. The types were not determined in 4 samples of genotype1. The most common sub types in the patients were found as 1b (69.51%) and 1a (20.73%) in order. The genotype distribution we obtained is shown in *Table-1*.

Discussion

There are many factors affecting the chronicalization of the infection in HCV infected people and prognosis of this chronicalized infection. The main among these factors are use of alcohol, gender of the patient, old age, genotype of the virus, co-infection with another hepatitis virus and viral load amount. The main factor which determines the medicine dose containing peg-interferon and ribavirin combination to be used during the treatment and treatment application period is genotype of HCV (9-12). Although the treatment duration in infections caused by HCV genotype 1 and 4 is longer than infections caused by genotype 2 and 3, the medicine dose is also higher. The positive response to the treatment is higher in infections caused by genotype 2 and 3. (11)We were concerned about the fact that HCV genotype 1 (96.34) which is more resistant to the treatment was in higher ratios in the study in our area than similar studies in our country. Isolation prevalence of genotype 1 in hcv infected patients in

studies in different areas was found 93.3% in İzmir area(13), 92.8% in Trabzon area (14), 83.4% in Antalya area (15) and 62.4% in Kayseri area (16).

In recent studies in our country, it was observed that the dominant HCV genotype was 1b. Isolation prevalence of 1b genotype isolated from HCV infected patients was found 57.6% in Kayseri area (16), 63.3% in Antalya area (15) %63.3, 80.2% in İzmir area (13) and 84.7% in Mersin area (17). The result of our study was 69.51% which was in line with previous similar recent studies in our country. The most common sub type after genotype 1b was genotype 1a (20.73%). Although genotype 1a was the second in prevalence in Antalya (15) (14.7%), Trabzon (14) (5.3%) and İzmir (13) (12.9%) areas similar to our study, genotype 4 was isolated as the second in Kayseri area (16) (32%).

Genotype 2 (1.22%) and genotype 3 (1.22%) which are seen different from genotype 1 (96.34) which is common in our area were observed rarely. It was stated that the spreading of HCV genotypes between different areas may be caused by migration or travelling.(18) It was considered that the genotype variety other than genotype 1 which is the prevalent type in our area and low rates of other genotypes can be related to the fact that our area does not take immigrants.

Conclusion

As a result the most commonly isolated genotype in patients infected with hcv in our study which reflects the hcv genotype distribution in our area was genotype 1b (69.51%) and the fact that genotype 1, the infections of which show a worse prognosis, has a higher prevalence in our area (96.34%) made us worry. Also the fact that nearly all of the genotypes isolated were genotype 1 made us question the cost-efficiency situation. As using different molecular methods and the low number of patients in our study prevented objective results, covering many areas and using standard methods would be more useful.

Conflict of Interest

The authors declare that no conflict of interest exists in publishing this article.

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