Original Article

Frequency of Different HCV Genotypes in Faisalabad

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ABSTRACT

Introduction: Hepatitis C Virus (HCV) is thought to be one of the major causative agent of viral hepatitis. A large number of HCV infected patients develop chronic hepatitis which often results in liver cirrhosis and even progress to hepatoma

The HCV genotype is the strongest predictive parameter for sustained virological response (SVR). Patients with different HCV genotypes respond differently to antiviral therapy. Firm evidence has been established that patients with genotypes 2 and 3 are more likely to achieve SVR to combination therapy than Genotype 1 patients.

Methods: A total of 93 patients from Faisalabad, who were HCV RNA positive were tested for genotyping.

Results: Out of the 93 tested serum samples 84 were typable and 9 were found to be untypable. In the typable samples most prevalent genotype was found to be type 3a and common cause of untypable genotypes was a low viral load.

Conclusions: The most common type of HCV infection in Faisalabad is due to genotype 3a and the common cause of untypable genotype is probably low viral load.

INTRODUCTION

Hepatitis C Virus is thought to be one of the major causative agent of viral hepatitis after hepatitis A and hepatitis B infection. A large number of HCV infected patients develop chronic hepatitis which often results in liver cirrhosis and sometimes even progresses to hepatoma[1].

The world Health Organization estimates that approximately 3% of the world population is infected with HCV. There are about 170 million patients with HCV infection in the world and 3-4 million individuals are diagnosed as new cases every year out of these 170 million, 10 million, are in Pakistan[2,3].

HCV is a member of the Flavivirus family. It is an RNA virus. The genome comprises of a untranslated region (5′ UTR) of 341 bases followed by a single continuous open reading frame (ORF). The ORF comprised of 3 structural genes (C, E1, E2) and 4 non-structural genes (NS2, NS3, NS4 and NS5). The 5′UTR is the most highly conserved region of the genome and thus has been used is most laboratories to develop sensitive detection assays for HCV, RNA [4,5]. The envelope region (E1, E2/ NS1) demonstrates the highest mutation rates. Following the cloning of the HCV genome, several, HCV isolates from different parts of the world were obtained and sequenced [6,7]. Comparisons of the sequences have led to the identification of several distinct genotypes that differ from each other as much as 33% over the whole viral genome [8]. A nomenclature was proposed to identify and assign genotypes of HCV [9]. According to it HCV can be classified into six major genotypes and several subtypes.

The prevalence of HCV genotypes differs considerably among geographical regions [6,10]. In this study, HCV genotyping was performed for patients who were confirmed HCV, RNA PCR positive to determine the variations and identify the predominant HCV genotypes in Faisalabad.

The HCV genotype is the strongest predictive parameter for sustained virological response (SVR) [11]. Patients with different HCV genotypes respond differently to alpha interferon [12]. Firm evidence has been established that patients with genotypes 2 and 3 are more likely to achieve SVR to combination therapy then Genotypes 1 patients. SVR is achievable in 65% of patients infected with Genotype 2 & 3 and only 30% of patients infected with genotype 1 [13,14]. Therefore the patient genotype should be taken into consideration when prescribing interferon Ribavirin combination therapy.

METHODS

A total of 93 patients from different regions of Faisalabad, who were HCV RNA positive were tested by type specific genotyping in two different laboratories i.e. Centre for applied molecular biology and Agha Khan university laboratory. The results were analysed for the frequency of different genotypes of hepatitis C in Faisalabad. In those patients who were found to be untypable for any genotype quantitative analysis of HCV RNA was done.

RESULTS

Out of the 93 tested serum samples 84(90.32%) were typable with the current available techniques and 9 (9.67%) were found to be untypable speed. In the typable samples most prevalent genotype was found to be type 3a in a total of 81(87.09%) patients. 1(1.07%) patient had genotype 1a. Mixed infection by two different genotypes was observed in 2 patients. One (1.07%) was infected by both type 3a and 1a and the other (1.07%) was infected with genotype 3a and 1b. Out of untypable genotypes 7(77.78%) patients were found to have a low viral load.

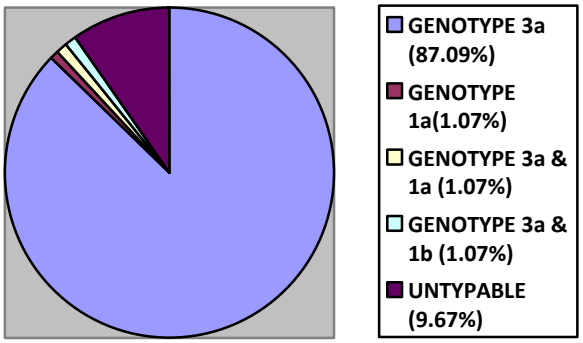

Chart-1: Frequency of various genotypes in Faisalabad

Table-1
Prevalence of Various Genotypes In Faisalabad

	Typable HCV Genotypes				Unty-pable	Total
	3a	1a	3a and 1a	3a and 1b		
pts	81	1	1	1	9	93

CONCLUSIONS

The most common type of HCV infection in Faisalabad is due to genotype 3a and the common cause of untypable genotype is probably low viral load.

DISCUSSION

Studies have been conducted in different parts of the world to see the prevalence of different genotypes. These studies have helped not only in solving epidemiological problems but they are also helpful in making therapeutic decisions while treating these patients. It has been demonstrated that the severity of disease, response to therapy and prognosis depends on several factors out of which genotype is an important factor [15,16].

Substantial regional difference appears to exist in the distribution of HCV genotype. Thus knowledge on the distribution of various genotypes in our locality is essential for therapeutic & prognostic reasons. In the present study the frequency of various genotypes of HCV present in Faisalabad were studied. Out of 93 patients who were positive for HCV RNA, on genotyping 81 patients had genotype 3a, 1 patient had genotype 1, 1 patient had genotype 3a & Ia, 1 patient hag genotype 3a & Ib, and 9 patients were untypable. Other local studies showed that the most prevalent genotype in the province of Punjab, NWFP & Sindh was 3a followed by 3b. But a clear difference was observed in the province of Balochistan where the predominant genotype was 1a. Balochistan shares a long border with Iran, in the west where predominant genotype is1. It is quite possible that genotype 1 may have entered into Pakistan from Iran through local persons who cross borders for job & trade [17].

A large local study tested 3351 serum sample for genotype. 1664 (49.05%) were genotype 3a; 592 (17.66%) genotype 3b; 280 (8.35%) genotype 1a; 252 (7.52%) genotype 2a; 101 (3.01%) genotype 1b; 50 (1.49%). So the most common genotype was found to be 3a [15].

In an Indian study out of 170 patients. 80 were genotype 3a, 27 were genotype 3b, 21 were genotype 1b, 16 were genotype 1a, 6 were genotype 4 and 3 were genotype 2a. So the most prevalent genotype was 3 followed by 1. 17 samples were untypable in this study [18].These untypable samples had low level of viraemia. In our study 9 sample were untypable. Out of 9 seven sample had a low viral load. It is believed that a low viral load can reduce the efficiency of PCR genotyping of the sequence within the 5´UTR regions.

Studies from other South East Asian countries suggest the prevalence of genotype 1 and 3. Variants genotyping (1a, 1b, 2a, 2b, 3a, 3b, 3c, 3d, 3e & 3f) have been reposted from Nepal [19]. In Japan subtype 1b is responsible for up to 73% of cases of HCV infection [20]. Genotype 1a, 1b, 2a, 2b and 3a have been isolated in Russia, with predominance of genotype 1b [21] High prevalence of genotype 1b has also been reported from China [22]. Variants of type 1 & 3 along with the existence of type 2 have been reported from Singapore, Thailand, Indonesia, Philippines & South Korea [23]. With reference to this worldwide information our study correlates with the genotyping pattern of South, East, Asian population suggesting a high prevalence of variants of genotype 3 followed by genotype 1. Furthermore, genotype 3a has been found to be the most common HCV genotype in the Indian subcontinent which was also the commonest genotype in our study.

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