

Negligence of Hepatitis C Virus Genotyping in Pakistan: Reason for the Increasing Non- Responsiveness to Interferon Therapies

Zeeshan Nasim, Iqbal Munir*, Aqib Iqbal and Mian Afaq Ahmad

Institute of Biotechnology and Genetic Engineering, Peshawar, Pakistan

Hepatitis C is a widespread contagious liver disease caused by Hepatitis C virus (HCV). HCV is a single stranded RNA virus of the family Flaviviridae. It is estimated that almost 180 million people are affected worldwide and more than 350,000 people die every year from Hepatitis C-related liver diseases. The prevalence of Hepatitis C in developing countries is quite high. In Pakistan, approximately 10 million people are infected chronically with HCV [1] with overall prevalence of 6% in general population of Pakistan, with high morbidity and mortality [2].

Being an RNA virus, HCV exploits all known mechanisms of genetic variation to ensure its survival [3]. The adaptability and high rate of mutation is the main cause of extensive genetic heterogeneity which results in the production of new types, subtypes and quasispecies. There are six major genotypes of HCV (numbered from 1 to 6) although some experts believe that there may be as many as 11 genotypes. Genotypes 1, 2, 3 are found worldwide, HCV genotype 4 is prevalent in the Middle East, Egypt and Africa, 5 in South Africa while genotype 6 is predominant in Southeast Asia [1]. In Pakistan; 1, 2 and 3 are the most prevalent HCV genotypes [2].

Genotyping of HCV is crucial prior to commencing interferon therapy as the severity of disease, type and duration of anti-viral therapy and clearance of HCV from the body, all depend upon HCV type or subtype [4]. On the basis of these differences, "specialized therapies" have been formulated for the efficient cure of hepatitis C caused by different genotypes. But unfortunately in Pakistan, no importance has been given to viral typing before starting the therapy as a result all patients receive a "generalized therapy" (INF α -2b; 3 million units three times/week and ribavirin as Rebetol; given according to weight i.e. 75 kg or below were given 1000 mg whereas patients weighing above 75 kg were given 1200 mg per day for 24 weeks), not capable of eradicating viral infection by different genotypes. Increased cases of non-responders to interferon therapies are the consequences. Non-responders, after the completion of unsuccessful therapy, then go through "specialized therapy" (normally once-weekly injections of 180 μ g of peginterferon alfa-2a as Pegasys along with daily ribavirin as Rebetol for 24 weeks) resulting in the loss of patient's health, wealth, and time.

In this study; we randomly selected a total of 88 patients who completed a generalized antiviral therapy (normally recommended for infections with HCV genotype 3a) without prior genotyping, for response to the therapy. For determination of active HCV infection, blood samples were collected from the randomly selected patients, centrifuged to separate serum, from which RNA was extracted. The extracted RNA was reverse transcribed into cDNA and subsequently amplified in PCR reactions, following the procedure of Idrees et al. [5]. Results indicated that only 57.95% (51/88) have achieved Sustained Virological Response (SVR) while 42.05% (37/88) patients were non-responders i.e. had active HCV infection, pointing towards the failure of antiviral therapy. The non-response (42.05%) was high as compared to the reported studies with as low as 18.4% non-response cases. HCV genotype 1b was the pervasive genotype among the non-responders followed by 1b, 3b, 3a and 2b (Table 1).

HCV genotype	Non-responders					Total
	1a	1b	2b	3a	3b	
Number	8	19	1	3	6	37
Percent	21.62%	51.35%	2.70%	8.10%	16.22%	

Table 1: HCV genotypes 1a and 1b were predominant in non-responders to combination INF therapy.

This high incidence of non-response (42.05%) could have been significantly reduced by characterizing the HCV into genotypes and subtypes and then treating the patients accordingly with a "Specialized therapy". Therefore, genotyping of HCV should be practiced in Pakistan before starting antiviral therapy for best results.

References

1. Safi AZ, Waheed Y, Sadat J, Solat-UI-Islam, Salahuddin S, et al. (2012) Molecular study of HCV detection, genotypes and their routes of transmission in North West Frontier Province, Pakistan. *Asian Pac J Trop Biomed* 2: 532-536.
2. Idrees M, Riazuddin S (2008) Frequency distribution of hepatitis C virus genotypes in different geographical regions of Pakistan and their possible routes of transmission. *BMC Infect Dis* 8: 69-78.
3. Domingo E, Holland JJ (1997) RNA virus mutations and fitness for survival. *Annu Rev Microbiol* 51: 151-178.
4. EASL International Consensus Conference on hepatitis C (1999) *J Hepatol* 30: 956-961.
5. Idrees M, Lal A, Naseem M, Khalid M (2008) High prevalence of hepatitis C virus infection in the largest province of Pakistan. *J Dig Dis* 9: 95-103.

*Corresponding author: Iqbal Munir, Professor, Institute of Biotechnology and Genetic Engineering, The University of Agriculture Peshawar, Pakistan, Tel: +923459721966; E-mail: iqmunir@aup.edu.pk

Received November 11, 2014; Accepted November 27, 2014; Published November 29, 2014

Citation: Nasim Z, Munir I, Iqbal A, Ahmad MA (2015) Negligence of Hepatitis C Virus Genotyping in Pakistan: Reason for the Increasing Non- Responsiveness to Interferon Therapies. *J Antivir Antiretrovir* 7: 001-001. doi:10.4172/jaa.1000112

Copyright: © 2015 Nasim Z, et al. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.