

Prevalence of Hepatitis C Genotypes in Jazan Region, Saudi Arabia

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(Received: 28 October 2013; accepted: 05 December 2013)

A molecular study was conducted to investigate the prevalence of Hepatitis C virus genotypes in HCV infected population of Jazan, Saudi Arabia. Samples were collected between February 2010 and March 2013 from all hepatitis C patients referred from peripheral hospitals to King Fahd Hospital. Of the 198 studied participants, 36(18.2%) of them were infected with 1a, 27(13.6%) with 1b, 6(3.0%) with 2 and 9(4.5%) with genotype 3 of hepatitis C. Mixed infection was found in 9 patients [1&4 in 9(4.5%)]. The most prevalent genotype was 3a with rate of 50% followed by genotype 3b and 1a, respectively. Nine samples remained untyped, suggesting the need of further investigation of genotypes in this region. It has been proposed that sequencing of these samples may be helpful to unveil these genotypes and further epidemiology of HCV genotypes. Furthermore, extensive and large scale studies are needed to understand the epidemiology of HCV genotypes, as no such study has been carried in this province. Qualitative analysis of these samples using PCR resulted in 28 positive samples. The PCR positive samples were subjected to genotyping using the method described by Ohno et al (J Clin Microbiol 35:201-202, 1997) with minor modifications. Genotyping of 28 samples revealed three different genotypes including 3a, 3b and 1a. Significance and impact of the study: The present study determined some critical information about the distribution of HCV genotypes in Jazan, Saudi Arabia.

Key words: Hepatitis C Virus, Genotypes, Jazan Region, Saudi Arabia.

Hepatitis is the major health problems globally casting an enormous burden on health care system and major source of patient's misery. Hepatitis C virus (HCV) infection has been recognized as an important occupational hazard for health care workers. Studies have shown that one third of the global population is infected with HBV and 350 million people are lifelong carriers. Different studies ranked Saudi Arabia among the countries with high prevalence of infection Hepatitis B and C. Elliott, 2005 showed that medical students are high risk group for blood born

infections including HBV and HCV, as during the course of clinical work, they are in direct contact with patients, blood, injection and surgical instruments, and the undesirable accidents which happened during the initial period of practical training, and lack of experience and professional skills increases the risk of infection in the course of invasive medical procedures. Many surveys were conducted on students and most of these studies shown that students do not have adequate knowledge about hepatitis C^{5,6}.

Acute hepatitis C is mild and often asymptomatic while chronic hepatitis C is an indolent course but may progress to cirrhosis and HCC¹. It is a slowly progressive infection spread primarily through intravenous drug users, can also spread by sharing of tooth brushes, razors and

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contaminated needles, sexual relations, from mother to child, etc. HCV RNA has not been detected in semen, urine, stool or vaginal secretion and whether it is present in saliva remains controversial². An estimate of 53000 deaths per year caused due to HCV in world. Most HCV infected people remained unidentified until the development of late symptoms, while some remained carrier through their life and do not develop any complication.

HCV genotyping provides valuable epidemiological and therapeutic information. Current therapy, which consists of a combination of pegylated interferon and ribavirin, gives a response rate of between 48% (genotypes 1, 4, 5 and 6) and 88% for genotypes 2 and 3⁵. The duration of therapy is variable as well for different genotypes. These findings indicate the importance of genotype knowledge before therapy. In this connection our studies can be very valuable for the health care providers and clinicians in designing the therapeutic strategies to cope this manic disease in this poorly developed area of Jazan. As such kind of study has not yet been performed in this province³.

Serodiagnosis of hepatitis C virus (HCV) is predominantly based on both enzyme immuno assay (EIA) and confirmation by Western blot assays, which requires extended hours and established laboratory settings with well-trained manpower. HCV rapid test is a step forward towards

the screening at all levels of healthcare settings followed by confirmation using Western blot. It, thus, necessitates the development of a diagnostic tool which could serve both screening and confirmation at all levels of healthcare settings¹¹.

METHODS

Present study was conducted at Molecular Diagnostic and Research Laboratory, King Fahd Central Hospital in Jazan, Saudi Arabia. Samples were collected between February 2010 and March 2013 from Saudi hepatitis C patients referred from peripheral hospitals in Jazan Region to King Fahd Central Hospital. Their ages range between 23 and 55 years. Blood samples were centrifuged, RNA were extracted, and loaded in Real-Time PCR (Abbott) according to the manufacturer's protocol.

RESULTS AND DISCUSSION

It was found most of the patients (111, 56.6%) were infected by genotype 4. 36 (18.18%) were infected by genotype 1a, 27 (13.6) were infected by genotype 1b, 6 patients (3.03%) were infected by genotype 2, and 9 patients (4.54%) were infected by genotype 3. Interestingly, 9 patients (4.54%) were infected by two different genotypes 1 and 4.

Table 1. Prevalence of HCV genotypes in HCV-PCR positive samples

Genotypes						
1a	1b	2	3	4	1&4	Total
36	27	6	9	111	9	198

HCV is known to have marked genetic heterogeneity with nucleotide substitution rate of 1.44×10^{-3} and 1.92×10^{-3} per site per year^{6,7}. Accumulation of nucleotide substitutions in the HCV genome results in diversification and evolution into different genotypes. Presently, HCV can be classified into at least six major and a series of subtypes^{8,9}. There is increasing evidence that patients infected with different genotypes may have different clinical profiles, severity of liver

diseases, and response to alpha interferon therapy¹⁰. Hence, a convenient and reliable HCV genotyping system is essential for large epidemiological and clinical studies. In this context, a genotyping method, based on genotype specific primers for PCR of the core gene, by which HCV isolates can be classified into genotypes was described⁴. Our study indicates that genotype 4 seems to be the most prevalent type in Jazan.

ACKNOWLEDGMENTS

The authors extend their appreciation to the Deanship of Scientific Research at King Saud University.

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