

Genotypes pattern of Hepatitis C virus infection in Kermanshah city

Kirmanşah şehrinde Hepatit C virüsü enfeksiyonun genotip paternleri

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Dear Sir,

One of the most common causes of chronic liver disease is Hepatitis C all over the world. Furthermore, WHO estimated that the prevalence of HCV is almost 2-3%,^{1,2} nonetheless, many studies reported the considerable differences on geographical point of view. Blood Transfusion Organization, reported HCV prevalence is 0.5% to 5% in Iran; Sistan-and-Baluchistan province as the most prevalent region.³

Many developing countries, Iran with no exception, the most prominent cause for liver cirrhosis, hepatocellular carcinoma and liver transplantation is chronic hepatitis C. HCV has an important role on public health with over 170 million infected individuals; which lead to increase in health care costs.⁴ Almost 80% of HCV infections may lead to chronic infection and nearly 10-20% of which may result to fibrosis and cirrhosis, and finally up to 5% may lead to hepatocellular carcinoma.⁵ It is worth to note that the rate of HCV infection increased in cases with multiple risk factors.

Although, Sayad et al.⁶ reported 967196 people live in Kermanshah, of which 8400 individuals may have HCV infection which will lead to be a heavy burden on the health care system and finally lost of expenses. Here we have attempted to establish a catalogue of HCV infection in Kermanshah by carrying out genotypes distribution among 50 HCV individuals from Kermanshah City.

For this descriptive study, family members of patients with hepatitis C in Kermanshah city, Iran were enrolled. A total of 50 serum samples from

participants suspected of hepatitis C were collected and processed for Nested PCR as per manufacturer's instructions. The final PCR product obtained was subjected to electrophoresis in 2% agarose gel containing ethidium bromide along with ladder. The banding pattern, to determine genotype specific bands, was photographed in Gel Doc System.

Out of the total 50 serum samples, 7 were found to be positive for HCV-RNA. The genotype 3a was the most predominant genotype, followed by 4 non genotypes. Prevalence of HCV genotypes has been reported from different areas of Iran. For example, Hajia et al.⁷ Reported Type 3a was the most frequent type (46.6%), followed by type 1 which is in consistent with our study. However another study reported the highest frequency was noted for subtype 1a (44.9%) followed by subtype 3a (39.6%), and 1b (11.3%).⁸

In comparison with neighbours of Iran, Turkey and Pakistan the pattern of our genotypes was different, where genotype 1b and 1a has been found to be the most prevalent subtype.⁹⁻¹⁰

In conclusion, although this study having relatively less participants, however, for public health policy makers we recommend a surveillance system which may lead to decrease the spread of HCV infection. Moreover, detection of HCV genotypes in different regions can be used for the purpose of molecular epidemiology.

It can be also concluded that HCV genotype 3a is the most predominant genotype in Kermanshah. The state of the preventive and therapeutic strate-

gies should be implemented to control the spread of HCV infections and it is necessary in order to decrease the health care system cost.

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REFERENCES

1. Shepard CW, Finelli L, Alter M. Global epidemiology of hepatitis C virus infection. *Lancet Infect Dis* 2005;5:558-567.
2. Brown RS Jr, Gaglio PJ. Scope of worldwide hepatitis C problem. *Liver Transpl* 2003;9: S10-13.
3. Zaborowski P, Cianciara J. Viral hepatitis: problems of management. *Terapia* 2000; 5:4-10.
4. Suliman QA, Muhammad NZ, Muhammad ZS, Zeenat HN, Muhammad YT. Prevalence of HCV genotypes in district Mardan. *Virology* 2013;10:902-904.
5. Saravanan S, Velu V, Nandakumar S, et al. The prevalence of hepatitis B virus and hepatitis C virus infection among patients with chronic liver disease in South India. *Int J Infect Dis*. 2008;12:513-518.
6. Saeed FS, Keyvani H, Rezaii M; Asadi T. Seroepidemiology of Hepatitis C in Kermanshah (West of Iran, 2006). *Hepatitis Monthly* 2008;8:141-146.
7. Hajia M, Amirzargar A, Khedmat H, et al. Genotyping Pattern among Iranian HCV Positive Patients. *Iranian J Publ Health*, 2010;39:39-44.
8. Ziyaeyan M, Alborzi A, Jamalidoust M, et al. Prevalence of hepatitis C virus genotypes in chronic infected patients, southern Iran. *Jundishapur J Microbiol* 2011;4:141-146.
9. Altindis M, Yilmaz S, Dikengil T, et al. Seroprevalence and genotyping of hepatitis B, hepatitis C and HIV among healthy population and Turkish soldiers in Northern Cyprus. *World J Gastroenterol* 2006;12:6792-6796.
10. Chakravarti A, Dogra G, Verma V, Srivastava AP. Distribution pattern of HCV genotypes & its association with viral load. *Indian J Med Res* 2011;133:326-331.