Brief Report

Molecular Epidemiology of Hepatitis C Virus Infection— Status Quo and outlook

Muhammad Imran Khan[1] , **Hafiz M.N. Iqbal[2], Muhammad Bilal[3*]**

[1]School of Life Sciences and Medicine, University of Science and Technology of China, Hefei 230036, Anhui, P.R. China
[2]Tecnologico de Monterrey, School of Engineering and Sciences, Monterrey, 64849, Mexico
[3]School of Life Science and Food Engineering, Huaiyin Institute of Technology, Huaian 223003, P.R. China

Abstract
Hepatitis C virus (HCV) infection has been a global health problem and, according to the recent report, more than 71 million people (which equals to almost 1% of population) have HCV infection. Onset of HCV infection is often acute and asymptomatic. In majority of cases, especially in underdeveloped countries, HCV infection remains undiagnosed for a long time. HCV has eight different genotypes, named from one to eight, which differ from each other at 31%-33% of nucleotides. Each genotype is further classified into several subtypes. Collectively, 86 subtypes have been recognized which differ from each other at < 15% nucleotide sequence. Determination of genotype of pathogen has been proven an effective means from the aspect of epidemiology. It is an important stage in the processes of decision-making and selecting appropriate therapeutic regimen. Studies have indicated that certain genotypes are found in countries or regions where direct acting antivirals are available against HCV infections. Developing awareness programs via extended approaches can prove useful in controlling the prevalence of HCV as well as other infectious diseases.
Keywords: Molecular epidemiology, Hepatitis C virus, Genotype determination, Nucleotides, Awareness programs

Introduction

Hepatitis C virus (HCV) infection is a global health issue and, according to the recent report, more than 71 million people (which equals to almost 1% of population) suffer from HCV infection (1). Significant literature advocates that HCV infection is transmitted through direct or indirect contact with blood, blood products, or blood contaminated materials (1). Infected patients develop a chronic carrier state, which is estimated to be around 70%-80% and is spreading globally due to no available vaccine (1). Chronic HCV infection consequently leads to severe complication like diabetes mellitus, hepatocellular carcinoma, end stage liver disease, liver cirrhosis, etc (2-4). World Health Organization as well as other international and national level organizations have been working very hard to restrict the prevalence of HCV infection. However, it seems a serious challenge to completely eradicate HCV from different countries in the coming years.

Epidemiology of HCV

Onset of HCV infection is often acute and asymptomatic. In majority of cases, especially in underdeveloped countries, HCV infection remains undiagnosed for a long time. It is difficult to accurately configure the accurate epidemiological data of the CHCV infected patients. Population-based data from other countries are less commonly available. A majority of HCV infections are diagnosed suddenly such as upon blood donations, viral screening before surgical interventions at hospital (4), medical fitness examination to travel to foreign country or job requirements.

Diagnosis of HCV infections by these screenings. can give an idea about the prevalence of HCV. But it seems challenging to accurately analyze the epidemiological data. However, the reports have suggested that the prevalence rates vary from country to country, and economic condition of a country may play an important role in controlling it (4). Certain factors (e.g., malpractices in remote areas of various countries, reusing syringes, sharing a shaving razor, etc) are those factors that remain under reported due to, possibly, the differences of culture in various countries as well as the lack of awareness and certain other dominant factors. Although access to modern technology has reduced the influence of such

*Corresponding Author: Muhammad Bilal, Emails: bilaluaf@hotmail.com, bilaluaf@hyit.edu.cn

factors, they still affect the societies severely.

Molecular Epidemiology of HCV

HCV has eight different genotypes, named from one to eight, which differ from each other at 31-33% of nucleotides. Each genotype is further classified into several subtypes. Collectively, 86 subtypes have been recognized which differ from each other at < 15% nucleotide sequence. Genotype 1 accounts for 44%-46% of HCV infections on a global scale and is the most frequent infection worldwide. Genotype 3 is the second most common genotype and makes up 25%-30% of all HCV cases. Third most frequent genotype with 8-15% of HCV cases is genotype 4 (5).

The prevalence of genotypes varies greatly in different regions around the globe (5). For instance, genotype 1 is > 80% in South America and Central Europe, but it is rare in Central sub-Saharan Africa and is said to be 2%. Similarly, genotype 3 is 71% in Central Asians, while genotype 4 is 98% in Central sub-Saharan Africa and Middle. Likewise, genotypes 2 and 6 are most commonly found in Eastern Asia. The given information indicates regional predominance of various viral genotypes possibly due to environmental factors or barriers in transmissions of certain types of genotypes of HCV. However, there is a mix of genotypes in western Europe, possibly be due to continuous migratory flows. Furthermore, studies have shown that specific genotype is associated with specific type of mode of transmission. For examples, genotype 1a is transmitted by transfusion, while genotype 1a and genotype 3 are transmitted through intravenous drug users (6).

Determination of genotype of pathogen has been proven an effective means from the aspect of epidemiology. It is an important stage in the processes of decision-making and selecting appropriate therapeutic regimen. Studies have demonstrated that certain genotypes are found in countries or regions where direct acting antivirals are available against HCV infections (7).

Conclusion

Desiderius Erasmus was quoted as saying "Prevention is better than cure". Although different therapies are available to cure, to restrict the prevalence is the top priority. In this regard, various strategies are being considered to control the prevalence of HCV infection. But due to limited access to sources of spread of HCV infection, it prevalence is uncontrolled in various parts of the world and no standard treatment. Developing awareness programs via extended approaches was proven useful in controlling the prevalence of HCV and other infectious diseases. It was found that the remote and rural areas were likely more important sources for the spread of infections than other areas; therefore, it was recommended that special awareness campaigns should be arranged in the remote and rural areas. It was also suggested that the regional and local governmental as well as non-governmental organizations may have played an important role in raising the awareness on a public scale.

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