Sequence-based genotyping of hepatitis B virus in general population

Ali Karimi¹, Ma’soumeh Moezzi², Reza Imani³

Received: 3 August 2014  Accepted: 4 October 2014  Published: 27 January 2015

Abstract
Background: Hepatitis B Virus (HBV) causes acute and chronic liver disease worldwide. HBV has eight genotypes (A to H) which is the reflection of its genome with their characteristic geographical distribution. Each genotype could have different pathogenic and therapeutic characteristics. There have been few records on HBV genotyping in general population from our region. This study aimed to determine hepatitis B genotypes using sequencing in the general population of Shahrekord, a Southwestern region of Iran.

Methods: A total of 3000 serum samples (cluster sampling method) were enrolled from general population tested for HBsAg using ELISA. Using appropriate extraction kit, HBV DNA was extracted from HBsAg positive samples and each was subjected to nested PCR for detection of HBV DNA. Finally, using sequencing, the samples were used for HBV genotyping. Data were analyzed by SPSS 19 using descriptive statistics, chi square, and Fisher’s exact test. P-value < 0.05 was considered as the level of significance.

Results: Out of 3000 serum samples, 40 (1.3%) were positive for HBsAg. HBV DNA was detected in 10 out of 40 (25%) of the samples studied. Genotype D was the predominant HBV type found in all of these 10 HBV positive samples.

Conclusion: Genotype D is probably the predominant HBV type in our region.

Keywords: Chronic hepatitis B, nested polymerase chain reaction, genotyping.


Introduction
One of the most important health problems worldwide is hepatitis B virus (HBV) infection. There are about 400 million persons who are chronically infected by this virus. Chronic carriers are exposed to the development of complications arising from hepatitis B infection, resulting in cirrhosis, hepatocellular carcinoma, liver failure or death (1, 2). HBV genotype is one of the most important factors that influence the outcome of infection (2, 3). Based on sequence divergence in the entire genome, HBV has been classified into at least 8 genotypes (A–H) that differ >8% from each other at the nucleotide level (2). Recently, an additional provisional genotype (I) isolated from Southeast Asians (4) and a variant were also candidate as the tenth genotype J (5). Most genotypes can be split into subgenotypes that differ >4% from each other, such as HBV-A1 and HBV-A2 (6, 7).

As specific clinical associations with each genotype become increasingly apparent, HBV genotyping is becoming more and more important (6). It has been shown that HBV origin, course of infection, the severity of the disease (6-8), prognosis and response to antiviral treatment (7, 9), patterns of serological reactivity and replication of the virus (7) are mainly genotype

1. Associate Professor, Medicinal Research Center, Shahrekord University of Medical Sciences, Shahrekord, Iran. alikarimi72@skums.ac.ir
2. (Corresponding author) Assistant Professor, Department of Community Medicine, Shahrekord University of Medical Sciences, Shahrekord, Iran. lmoezzi@yahoo.com
3. Associate Professor, Department of Infectious Diseases, Shahrekord University of Medical Sciences, Shahrekord, Iran. rastabi966@gmail.com
Genotyping of hepatitis B virus

HBV genotypes regarding regional host population and endemicity have been widely consid-
ered. Accordingly, HBV/B and HBV/C are predominant in most parts of Asia, including
China and Japan (11). Genotypes A, D and F are prevalent among the five geo-
graphic regions of Brazil. Genotype A was most prevalent in the United States (12) while
the most common HBV genotype in Canada was B (13). Genotypes E and F are
confined to Africa and the Americas (14).

HBV/G has a global distribution, and
HBV/H was first revealed in Central Amer-
ica (15). HBV genotypes I and J have been
sporadically reported from Asia and Japan,
respectively (4, 5). Genotype D is also pre-
dominant in the Middle East, including
Iran (16).

Iran located in an intermediate endemic
region for chronic HBV infection with
prevalence rate of 2-8% (17). But, studies
show improvement and prevalence tran-
sition from moderate to low (0.1-2%), due to
vaccination in recent years (18,19). Geno-
type D has been reported as the predomi-
nant genotype in different regions of Iran
(20-27). In our region, although there are
some reports regarding HBV infection
among chronically infected patients (27-
29), there has been no report of HBV geno-
types in general population. Therefore, this
population-based study was aimed to de-
termine HBV genotypes in general popula-
tion of Chaharmahal va Bakhtiari, south-
western Iran.

Methods
Serum samples

This is a descriptive, cross-sectional and
population-based study. The sample popu-
lation consists of rural and urban adults
over 15 years in Chaharmahal va Bakhtiari
province. The sample size was decided to
include 3000 individuals based on statisti-
cal advice, national prevalence of hepatitis
dependent. Thus, understanding genotype
distribution is important for epidemiologic
characterization of HBV transmission and
to control infection (10).

Geographic distribution of HBV geno-
types is influenced by the geographical
region, climate, occupation, etc. HBV geno-
type A is more prevalent in eastern Asia
and tropical regions of Brazil. Geno-
types E and F are confined to Africa and
the Americas (14).

HBV/G has a global distribution, and
HBV/H was first revealed in Central Amer-
ica (15). HBV genotypes I and J have been
sporadically reported from Asia and Japan,
respectively (4, 5). Genotype D is also pre-
dominant in the Middle East, including
Iran (16).

PCR amplification and detection of HBV
dNA

HBV DNA was extracted from the
HBsAg positive serum samples using an
extraction kit (QIAamp MinElute Virus
Kits, Qiagen, Germany) and subjected to
nested PCR according to the manufactu-
er's instructions using appropriate primers
and positive control provided by kit (Plas-
ma-Serum HBV PCR Detection Kit, Norgen-
Canada). Strict measures were adopted
to prevent any contamination. An aliquot
of water was used as negative control.
Samples were considered positive if they
yielded at least two positive results in two
different reactions and were considered
negative when there were two negative re-
results in two different reactions. To detect
PCR product, the PCR products were ana-
yzed by electrophoresis through a poly-
acrylamide gel, stained with silver nitrate
and photographed.

HBV sequencing and phylogenetic analy-
sis

Detection of HBV genotypes was per-
formed using sequencing. For sequencing,
the PCR products were purified by Exo
SAP-IT kit (USB Corporation, Ohio, USA)
according to the manufacturer’s instruc-
tion. Sequencing reactions were performed
using 1-5μl purified PCR products, 1μl
BigDye reaction mix (Life Technologies,
Applied Biosystems, Darmstadt, Germany)

http://mjiri.iums.ac.ir
and 0.5μM of the HBV primers, with the same primers as those used for PCR amplification of pre-S region. The sequences obtained were compared with published sequences from the same genomic region of 8 HBV genotypes available in National Center for Biotechnology Information (NCBI) GenBank. Alignment was performed using CLUSTAL W in MEGA 5 software. The phylogenetic tree reconstruction was carried out using Maximum Composite Likelihood method and MEGA 5 software (Ibis therapeutics Carlsbad, Carlsbad, CA, USA). This method is a new genotyping strategy established by Ma et al in Shenyang, China (30). Data were analyzed by SPSS 19 using descriptive statistics, chi square, and Fisher’s exact test. P<0.05 was considered as the level of significance.

**Results**

Out of 3000 serum samples obtained from healthy individuals, 40 (1.3%) were positive for HBsAg using ELISA (data not shown). Ten out of 40 (25%) were positive for HBV DNA using nested PCR (Figure 1). Demographic characteristics are shown in Table 1. Chi square and Fisher’s exact tests revealed no significant difference between these cases and HBV PCR negative individuals. The results of sequencing method showed that genotypes D was the predominant HBV type found in all of these 10 HBV positive samples (Figs. 2 and 3).

**Discussion**

This is the first study aimed to evaluate the distribution of HBV genotypes in the general population of a Southwestern province of Iran, Charmahal va Bakhtiari. Based on a sequence divergence of 8% or greater of the entire genome sequences or a sequence divergence of 4.2% of the S genome sequences, HBV includes at least eight genotypes (A-H) (2) with two additional genotypes recently named I and J.

![Fig. 1. Polyacrylamide gel electrophoresis of the reaction, products of nested PCR and a 50 KB DNA markers. The second round of amplification products (1-8), the positive (PC), the negative controls (NC), and molecular weight marker (M) are shown.](http://mjiri.iums.ac.ir)
Genotyping of hepatitis B virus

There have been a number of reports indicating that most HBV genotypes are restricted to geographical regions and associated with a host population around the world, while others tend to have a worldwide distribution, or still remain unknown (3,4). Just as with the genotypes, the distribution of HBV subgenotypes is also distinctly geographic (8,9). It has been suggested that polymorphism, transmission, mutation and the evolutionary history of HBV have led to the above outcomes.

Different biological and epidemiologic behaviors have been attributed to HBV genotypes (6). Accordingly, they are closely associated with outcome of chronic liver disease, antiviral response, severity of the diseases, and disease time course. Therefore, detection and monitoring of HBV genotypes are very important to clarify the pathogenesis, route of infection and virulence of the virus and also in epidemiologic setting (7-9).

Studies of the distribution of HBV geno-
types have largely been conducted among patients with chronic hepatitis B (CHB) from Iran (26). However, limited studies carried out to determine genotypes of this virus in Iranian general population (24). Accordingly, this is the first study aimed to understand the overall distribution of HBV genotypes in general population from a Southwestern province of Iran. Our results identified genotype D as the predominant genotype in this region. These findings are concordant with those of the previous studies conducted in the different regions of the country where only genotype D was detected in CHB patients (26). Although in this study, HBV genotype D was detected in apparently healthy individuals in the general population, all these results, together, from different regions, confirm that genotype D may be the only genotype circulating in this country both in CHB patients and most probably in the general population. This result is also consistent with other published reports from other countries of the Middle East (16,25) indicating predomiance of this genotype in this region of the world.

It has been suggested that HBV genotypes have a characteristic geographic distribution and are closely related to the process of human evolution and migration (16,25). It was found that genotype D is the predominant HBV genotype in South Asia and the Middle East including India, Afghanistan and Iran (16) and is dominant in most parts of Europe (25). Historically, Aryans who firstly colonized to the North of the Caspian Sea migrated to Iran, India, and Europe. Therefore, there is a possibility that the population of this colony has been infected with genotype D before their migration and then transmitted the virus to the following generations after their migration. Thus, this may be the best explanation for the prevalence of genotype D in India, Iran and most parts of the Europe. In countries with high levels of immigration in the Europe and North America a variety of genotypes are being reported (24) which may depict the impact of immigration on HBV genotype distribution. Also, the dominance of this genotype in Iran and the neighboring countries (25) may indicate immigration among these countries which results in circulation of this genotype among these populations.

The clinical outcomes of the individuals infected with HBV of genotype D are still controversial. It has been suggested that it causes severe chronic liver diseases more frequently than other genotypes (1,3,16); it causes high risk of provoking fulminant hepatitis as well. However, there are some reports indicating HBV genotype D is related to acute self-limited hepatitis (9). Furthermore, HBV genotype D has been found in the majority of asymptomatic carriers (84.2%) and has not been found in patients with liver cirrhosis; hepatocellular carcinoma is lower in genotype D (17). No association between HBV of genotype D and distinct clinical phenotypes has been found in the Turkish population infected with HBV (16). Based on our findings, apparently no clinical symptoms were seen in the infected healthy individuals. From these results, together, it may be concluded that the infection caused by genotype D mainly is mild and/or asymptomatic.

Conclusion

The results of this study may provide useful regional epidemiologic information. However, as these results cannot be generalized for all Iranian population, a large scale, nationwide study should be done to determine HBV genotypes in general population of Iran.

Acknowledgments

This paper was obtained from a research project, funded by Deputy of Research and Technology of Shahrekord University of Medical Sciences (grant number: 1446). Hereby, we gratefully thank Shahrekord University of Medical Sciences for funding this work.

References

1. Günther S. Genetic variation in HBV infec-
Genotyping of hepatitis B virus


