

Review Article

Prevalence of HCV Genotypes in Various Geographical Regions

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ABSTRACT

Hepatitis C Virus (HCV) belongs to the Flaviviridae family. It's a positive -sense single- stranded RNA virus. The RNA contains about 3000 amino acids. It was first found in the year 1989. HCV is an important emerging viral infection affecting most parts of the world. HCV has several genotypic variations and is crucial for clinical, epidemiological studies and treatment. Genotypes play a vital role in SVR. It contains 7 genotypes (1-7) and various subtypes. The types are identified by gene order of the HCV RNA 5'-C-E1-E2-p7-NS2-NS3-NS4A-NS4B-NS5A-NS5B-3. This paper summarizes the prevalence of genotypes in various geographical regions and the methods to identify different genotypes.

1. INTRODUCTION

HCV belongs to the Flaviviridae family. It's a positive -sense single- stranded RNA virus. The RNA contains about 3000 amino acids. It was first found in the year 1989. Hepatitis C Virus is one of the major causative agents of viral hepatitis (Hepatitis C). Approximately 71 million people are affected by chronic HCV. In the year 2016-3,99,000 died of Hepatitis C mostly by cirrhosis and hepatocellular carcinoma. The major transmission of HCV is due to unscreened blood transfusion, non-sterile syringes, mass immigration, Sexual contact, poverty and poor education. [1]

The HCV RNA has a molecular weight of about 9.6kb. This virus is a major cause of acute hepatitis. The determination of HCV genotypes is essential for the appropriate antiviral treatment. The most common method for detecting the genotypes is Quantitative analysis by PCR. In the middle of 2015 and 2016 sudden outbreaks were observed, wherein the sources were obtained from hospital practices of reusable needles to the patients. Human immunodeficiency virus (HIV), leprosy, hemophilia, and hemodialysis. Screening for HCV is not recommended rapidly although the medical committee can take implements prior to screening blood before commencing the treatment to the

patient. The genotype of a patient should be taken into consideration before prescribing antiviral drugs. [2]

2. METHODS

The types are identified by gene order of the HCV RNA 5'-C-E1-E2-p7-NS2-NS3-NS4A-NS4B-NS5A-NS5B-3. This precursor is cleaved into 10 different proteins, Structural proteins = E1, E2, p7 Non-structural proteins = NS3, NS2, NS5A, NS5B, NS4A, NS4B. The highest mutation rate was observed in the E1, E2, and S1. 5'UTR is the highest conserved region and hence it is mostly used in laboratories for sensitive detection assays of the HCV RNA. [3]

3. TECHNIQUES FOR DETECTION

3.1. PCR

In polymerase chain reaction, a specific portion of the HCV sequence 5'UTR was extracted and processed with restriction fragment length polymerization following the line probe reverse hybridization and finally, they were identified using TaqMan PCR.[4] Other sequences used for identification are Core - E1, NS5B, p7. [5]

3.2. SANGER METHOD

The above - mentioned sequence were terminated from nucleotides along with the suitable primer and other enzymes, Gel electrophoresis was performed and the results were computerized and used for confirming the genomic sequences of HCV.

3.3. ENZYME IMMUNOASSAY (EIA)

EIA usually determines the presence or absence of certain metabolite or antimicrobial secretion against the specific enzyme identified with the color change.

3.4. BLOOD SCREENINGS

Before transplant, transfusion screening of HCV is implemented to control the exploitation.

3.5. OTHER METHODS

In ELISA screening technique Hepatitis C Virus RNA was observed. HCV Quantification was performed with COBAS AmpliPrep through the TaqMan kit.

4. PREVALENCE IN VARIOUS GEOGRAPHICAL REGIONS

4.1. CHINA

In Mainland China, regional differences of HCV genotypes have been noted. China is an important area for drug smuggling. Intravenous drug abuse has become a major risk factor for HCV. [2] In northern China subtype, 2a is prevalent, subtype 3b is prevalent in Yunnan, and genotype 6 is common in the southern part of Mainland China.

4.1.1. PREVALENCE OF HCV GENOTYPES IN MAINLAND, CHINA

According to figure 1 and 2 it's shown that subtype 1b is highly predominant between both the sexes, whereas subtype 2a is more predominant in women race than the male while subtype 3b is more common in male than female and subtype 6a is again more common in males than females and subtype 3a is more common in women than men [3]. According to figure 3, it can be said that subtype 1b and 2a are prevalent in Mainland China.

4.2. UNITED STATES

In the US, the death of the Human immunodeficiency (HIV) patients is lesser than the death of the patients due to liver cirrhosis caused by hepatitis c virus. 70% of HCV patients will remain

infected if they are not treated early. After 30 years of infection the primary mild infection will lead to the several conditions like liver failure, death in 41% of the patients. This geographical study shows among 50 states with major division like: Northeast, Midwest, West north central, South, West and so on. [5]

4.3. PAKISTAN

In Pakistan, HCV is prevalent due to mass immigration, illegal drug supply from Afghanistan, non sterilized syringes, unscreened blood transfusion, contaminated razors, poverty, and poor education. [6] In Pakistan, the most affected area was Balochistan the second most affected area was Punjab. [7] Genotype 3 is more prevalent in Punjab with 68.94%, Sindh with 76.88% and Balochistan with 60.71% and KPK with 58% [8].

4.4. INDIA

In India, Blood transfusion and unsafe injections are the main reasons for the prevalence of HCV in India. HIV and HCV co-infection have been prevalent in India. [9] Arunachal Pradesh has about 7.89% of HCV infections followed by Andhra Pradesh with 2.02%, West Bengal with 0.71% and Maharashtra with 0.09%. According to figure 5 Genotype 3 is highly predominant in India followed by genotype 1 and genotype 2.

4.5. CENTRAL AFRICA

In Central Africa, a new genotype was found with subtype 7a. This is based on less than or equal to 30% between the nucleotide level, while other subtypes would differ about 15% - 23%. [13] In this, the newly isolated sequence was found to be "QC69" and previously QC272 was known to be positive for Anti-HCV. This genotype of HCV was found only in Africa.

4.6. JAPAN

In Japan, HCV predominance was observed since the 1900s by the drug designed for schistosomiasis with unsterilized needle, illegal methamphetamine usage, and unscreened blood transfusion. This gave rise to more HCV carriers and comparatively less anti-HCV producers. The incidence of HCV with 70% of carriers with acute hepatitis and 30% of past infection. The prevalence was detected using ELISA, Polymerase chain reaction for HCV-RNA. The genotype of 1 with subtypes with a and b were observed more in Japan.

4.7. SOUTH KOREA

In South Korea, the emergence of HCV was positive since 1991 through blood and it was noted very less in 1992. But the transmission was noted by unauthorized drug ingestion, aging, and tattoo. The occurrence of HCV causing acute hepatitis, hepatocellular carcinoma. This HCV presence in patients gives rise to the development of anti-HCV among different factors like - age group, sex, and geographical distribution. Where male with 0.75% and female with 0.83% according to the increase in age is represented in the below graph. The geographical distribution of HCV in various parts is listed below from the area of Gyeonggi, Seoul, Daegu, Gwangju, Jeonbuk, Jeju, and Ulsan.

4.8. EGYPT

In Egypt, the predominance of HCV is different from other countries which include several factors such as late and poor diagnosis, lack of data, economically less to support the current advancements and treatment. Since 2007 their only aim is to control and eliminate the HCV spread. Thus, the scenario is different the distribution can only read through the economic level of the society. The below table shows represent the data based on the patient's socio-economy. The genotype 4 is more in Egypt with 92.5%, genotype 1 with 3.6%, mixed genome infection with 3.2% and less than 1% of other genotypes. The Democratic health survey (DHS) depicts the viral genome rise with 7% and sero-prevalance with 10% in 2015 shows the viral condition has been reduced to 30% from 2008.

5. MIXED INFECTIONS

Mixed infection isn't a global threat but is prevalent in few areas with rare combination of subtypes. For example, In China the following subtypes combination was seen "1b-2a, 2a-6a, 1b-3b, 1b-6a, 3a-3b, 1b-3a". In Pakistan, the frequently noticed mixed infections subtypes "1a-3a, 1b-3a, 2b-3a, 2a-3a, and 1a-3b".

6. CONCLUSION

Hepatitis C is a globally potent viral infection causing most of the Liver associated clinical conditions. The researchers have found out that the response produced by α -interferon was different for each genotype. Based on the patient's genotype, the combination of interferon and Ribavirin treatment can be carried out. Public awareness should be

spread about the implications of this chronic infection. HCV has resulted in significant mortality rates over the years. To minimize the spread, risk factors should be eliminated or reduced.

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Table 1: HCV contains about 7 genotypes and various sub-types seen in Table -1¹⁰

Geographical distribution	Types & subtypes based on predominance of infection
China – Mainland	1b, 2a, 3b, 6a, 3a
India	North – 3 South – 1
Pakistan – Faisalabad	3a
Central Africa	7a
Japan	1b
UN	1a, 1b
South Korea	1b, 2a
Taiwan, Hong Kong	1b
Australia	1a
Egypt	3a,4
Bangladesh	3b

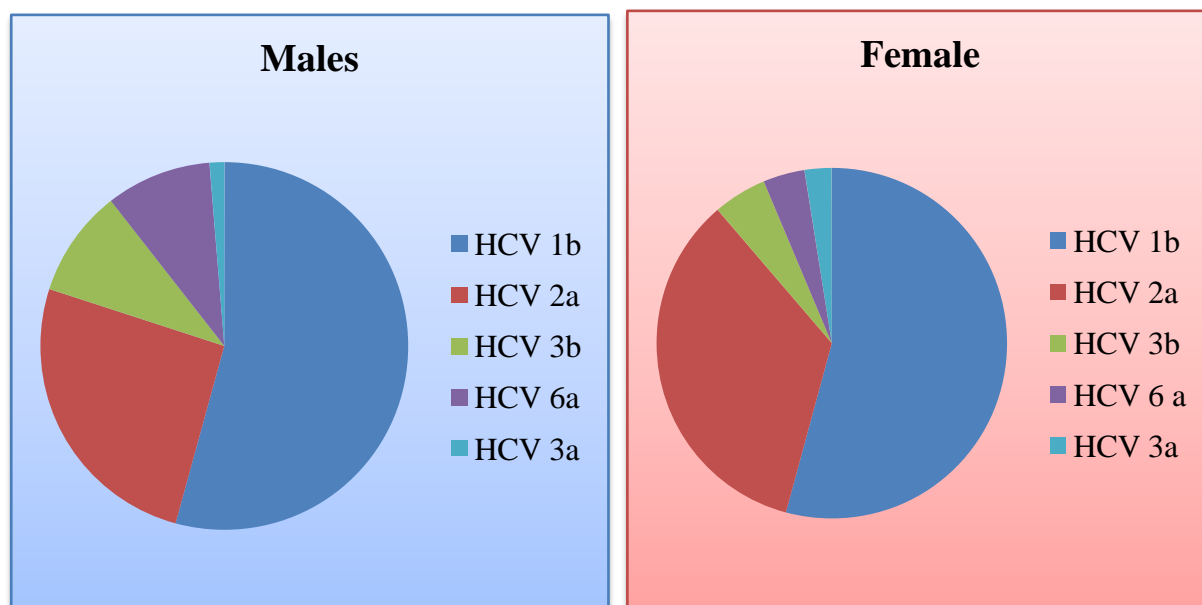


Fig.1. Prevalence HCV genotypes in mainland, China in Males and Females

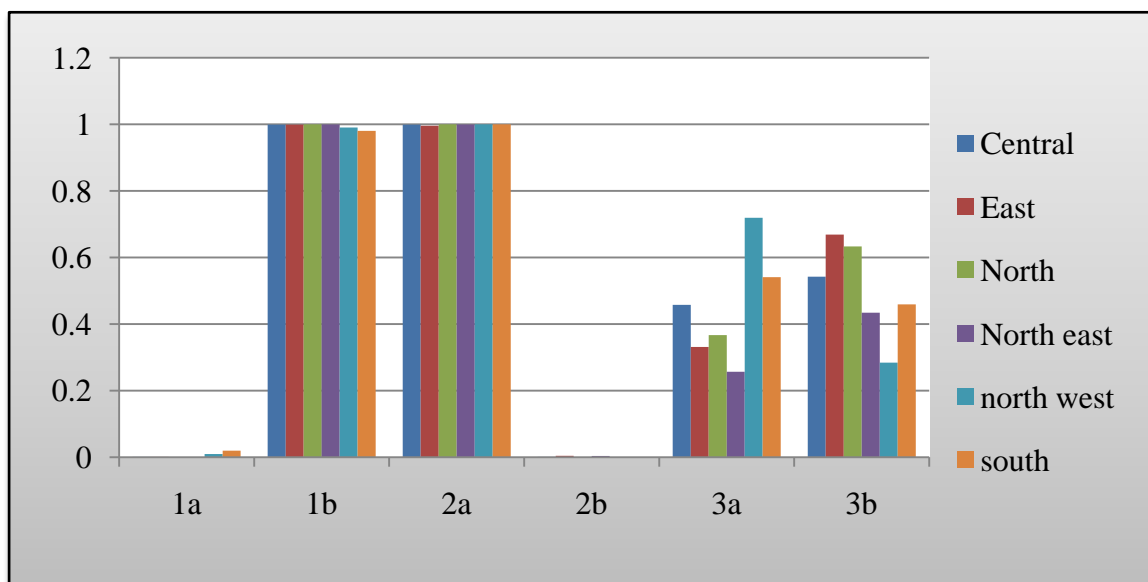


Fig.2. Prevalence of HCV genotypes in different countries.

Table 2: Geographical distribution of HCV

Geographical distribution	Percentage
NORTH EAST	1.43
New England	1.40
Maine	1.06
Rhode Island	2.12
Vermont	1.45
New Jersey	1.35
MIDWEST	1.14
Ohio	1.35
Wisconsin	0.71
SOUTH	1.80
South Atlantic	1.55
Delaware	1.97
DISTRICT OF COLUMBIA	3.27
Florida	1.66
Georgia	1.17
Maryland	1.86
Mississippi	1.59
WEST	2.14
Colorado	1.74
New Mexico	2.76
Montana	1.94
Alaska	2.19
Hawaii	1.48
Washington	2.30

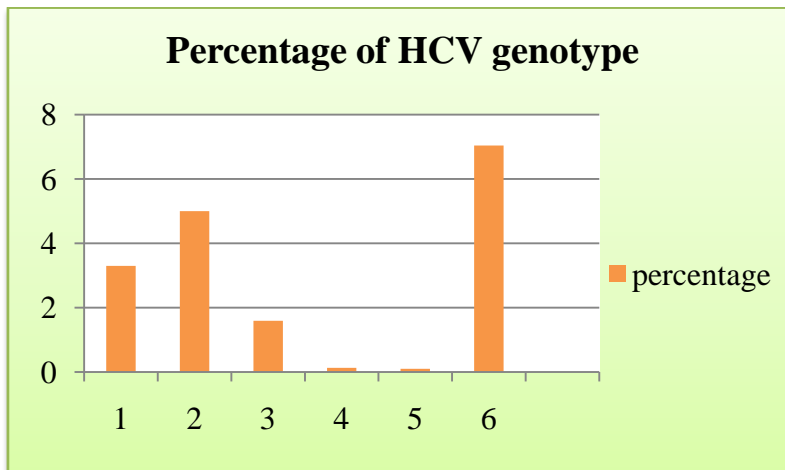


Fig.3. Percentages of HCV genotypes

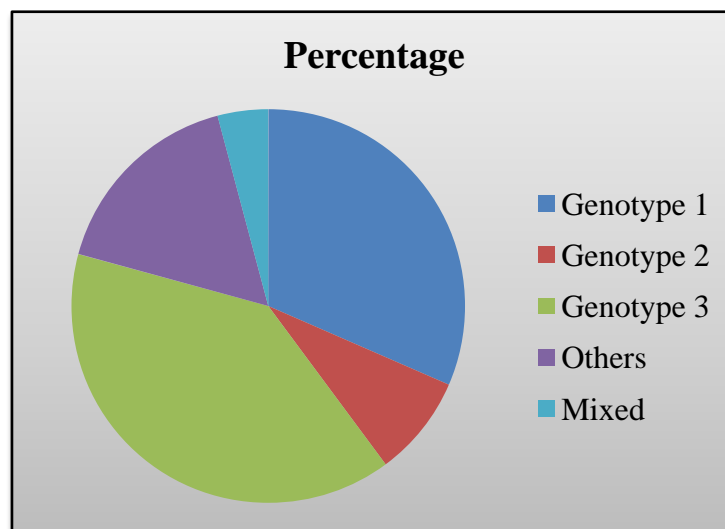


Fig.4. Percentages of different genotypes

Table 3: Percentage was reported by the ELISA technique.

State	Percentage of HCV
Punjab	1.09%
Delhi	1.57%
Gujarat	55.3%
Maharashtra	0.7%
Rajasthan	0.75%
Tamil Nadu	1.4%

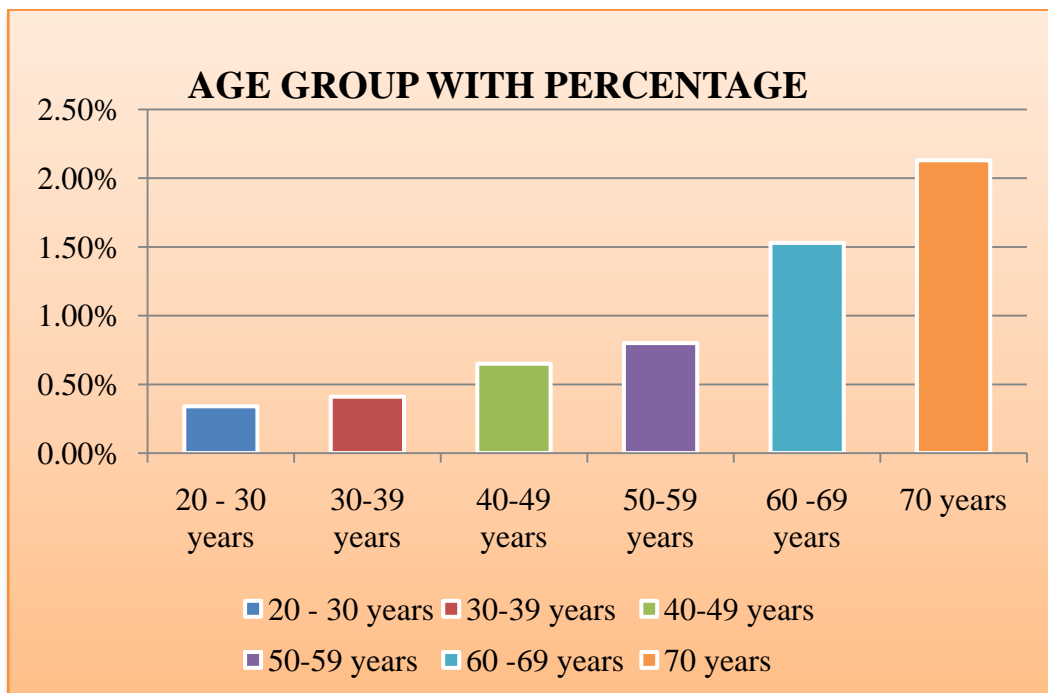


Fig.5. Age wise distribution of HCV

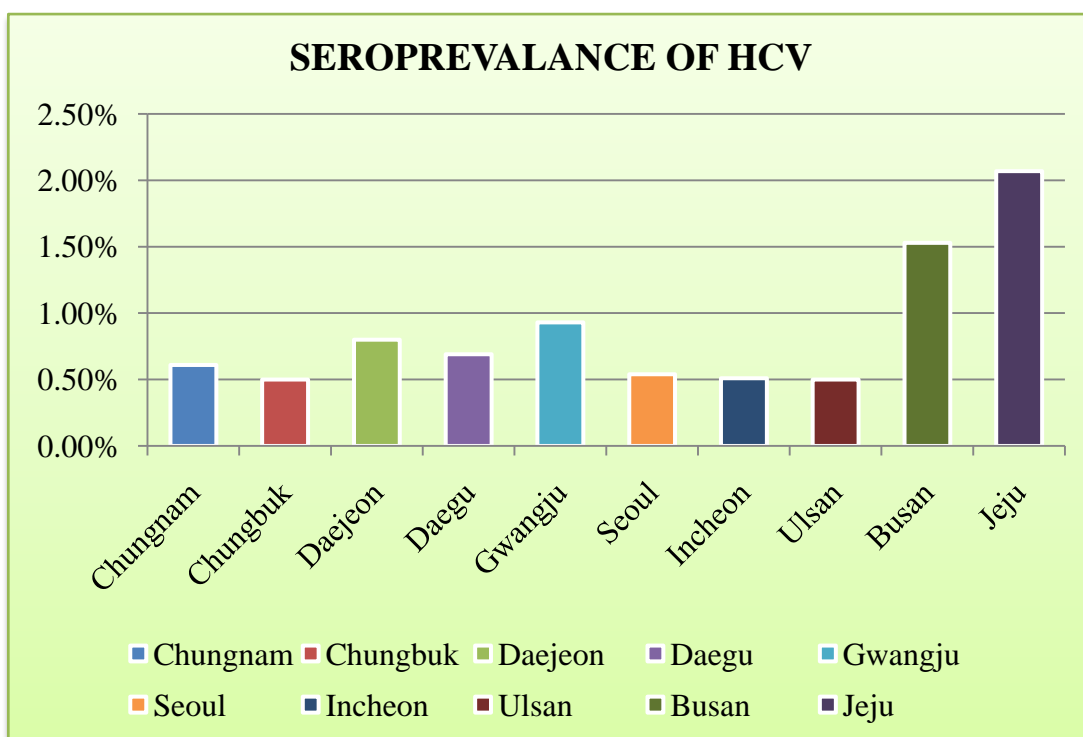


Fig.6. Seroprevalence of HCV

Table 4: Area wise distribution of HCV

Geographical area related with wealth	Prevalence of HCV (in percentage)
Rural areas	12
Urban areas	7

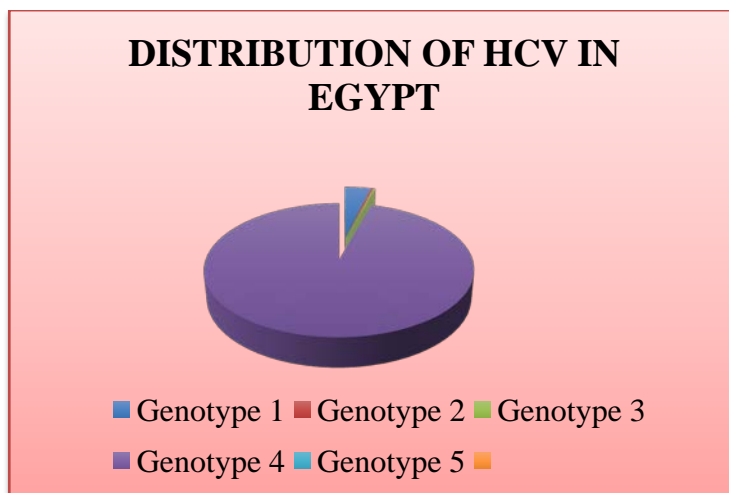


Fig.7. Distribution of HCV in Egypt

Table 5: Distribution of HCV genome

Distribution of HCV genome	Percentage
Genome type 1	3.60%
Genome type 2	0.40%
Genome type 3	0.20%
Genome type 4	92.50%
Genome type 5	0.10%

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