# Frequency of Hepatitis C Virus Genotypes in Chronic Hepatitis C Patients at Peshawar Institute of Medical Sciences, Peshawar

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## ABSTRACT

**Background:** Hepatitis C infection is highly prevalent in Pakistan. Six genotypes have been identified up till now. The most prevalent is genotype 3 in Pakistan. However, literature has shown variations among different regions in the prevalence of different genotypes.

**Objective**: The Purpose of this study was to determine what is the prevalence of most common genotype of hepatitis C in the Peshawar district of KPK, Pakistan.

**Material and Methods:** This cross-sectional study was conducted from July 2017 to July 2020 at Peshawar Institute of Medical Sciences, Peshawar in collaboration with Department of Biochemistry, Khyber Medical College, Peshawar, Khyber Pakhtunkhwa, Pakistan. Those patients whose blood sample turned out positive for Anti-HCV antibodies then underwent to PCR for HCV RNA. By using ROTOR Gene TM technique Genotype was found out. Data was analyzed by using SPSS version 18.

**Results:** A total of 776 patients meeting the inclusion criteria, aged between 12 to 65 years, were included in this study, out of which 413 (53.22%) and 363 (46.78%) were males and females respectively. Regarding HCV genotyping; 388 (50.0%) were type 3a, 28 (3.60%) 3b, 117 (15.07%) type 2a, 22 (2.83%) types 2b, 18(2.31%) type 1a and14 (1.80%) 1b. 17 (2.19%) patients mixed types 2a and 3b, 16 (2.10%) were combined3a and 3b and 156(20.1%) were un-type able.

**Conclusion:** The most common genotype in population residing in Peshawar district is genotype 3a and the second most common genotype is genotype 2a.

**Key Words:** HCV genotype, HCV-RNA, PIMC, PCR, ELSA, ROTOR Gene

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## INTRODUCTION

Across the world viral hepatitis is quite common. Hepatitis C virus (HCV) is transmitted by blood and products blood-borne pathogen and has been a major health care concern worldwide.[1] Chronic hepatitis C is a major cause of morbidity across the world and approximately 71 million people are infected chronically.[2] Approximately 75% of the people infected with hepatitis C progress to chronic infection which causes chronic liver disease out of which 20% of people progress to cirrhosis liver in less than 20 years from onset of the disease.[3] In Pakistan the prevalence of chronic hepatitis C is around 47%. There are eleven different genotypes of hepatitis C and six genotypes have been found to be significant mostly.[4] In Pakistan most prevalent genotype is genotype 3 (69.10%) and the second most prevalent is genotype 2 (4.20%) followed by genotype 4 (2.20%).[5] The main advantage of finding out genotype is to streamline the treatment against specific hepatitis C genotype. Determination of genotype is necessary in choosing the right treatment for hepatitis C virus infection. Direct acting antiviral (DAA) drug is very effective in treating hepatitis C virus infection across the world.[6]

We decided to conduct this study in Peshawar district to find out most common genotype in already diagnosed hepatitis patients for appropriate treatment planning. After reviewing load of literature we came to know that in fact very few facilities are available for genotype testing and most of the treatments are started blindly without knowing genotype which could be used to decide best treatment and duration. By analyzing our data we will help our health care worker to choose best treatment based on the most probable genotype.

## MATERIAL AND METHODS

The present descriptive cross-sectional study was performed over three years between July 2017 to July 2020 at Pak International Medical College (PIMC) and Allied Hospitals and Department of Biochemistry, Khyber Medical College, Peshawar, Khyber Pakhtunkhwa, Pakistan. Convenience sampling was adopted as method of sampling.

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Patients were chosen from either gender between 12 to 65 years of age with chronic HCV infections and were included on the basis of predetermined selection criteria. Each patient was informed and a written consent was taken from all the patients. Our study included patients that were previously on treatment or untreated at all. All patients were chosen from district Peshawar having a valid National Identity Card. Patients with already hepatitis B virus (HBV), hepatitis D virus (HDV) and HIV infections were not included in the present study. After confirming on 3rd generation ELISA and further confirmed by Rotor Gene TM, real time quantitative PCR were analyzed for HCV genotypes. Tables were used for recording of data and analysis was done by employing SPSS version 18. We used paired two samples t-test for means to check the difference among different groups of genotypes and hence for significant difference if any.

## RESULTS

There are six main hepatitis C virus genotypes throughout the world. A total of 776 patients meeting the inclusion criteria, aged between 16 to 65 years of either gender, were included in this study in which 413 (53.22%) were males and 363 (46.78%) were females respectively (Figure 1). In our study regarding HCV genotyping it was found that 388 (50.0%) were type 3a, 28 (3.60%) 3b, 117 (15.07%) type 2a, 22 (2.83%) types 2b, 18 (2.31%) type 1a and 14 (1.80%) 1b, 17 (2.19%) patients mixed types 2a and 3b, 16 (2.09%) type 3a plus 3b and Un-type-able were 156 (20.14%) as depicted in table1.

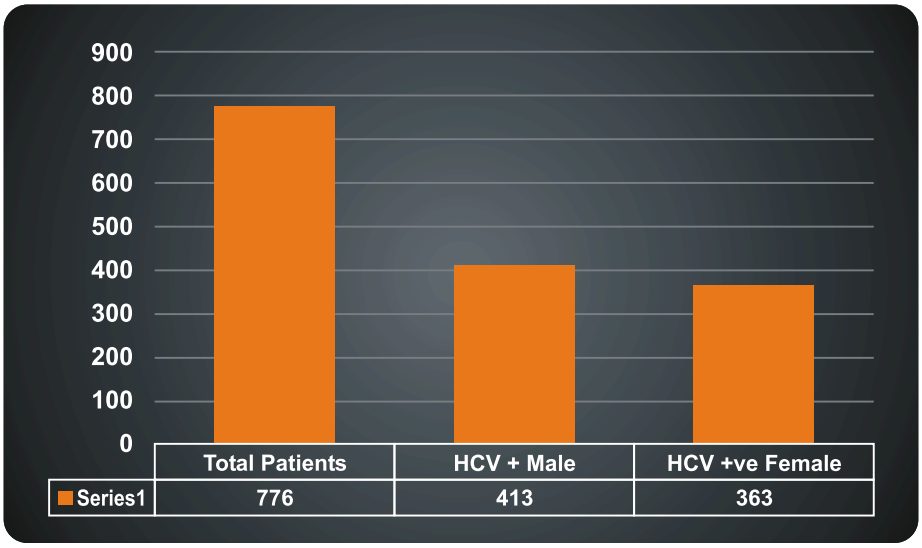



**Figure 1: Gender Wise Distribution of HCV Positive Subjects (n=776).**

**Table 1. Numbers of Different Genotypes and their Percentage in the Sample (n=776)**

| S. No. | Genotypes Variant | Percentage | No of Patients |
|---|---|---|---|
| 1 | 3a | 50.0 | 388 |
| 2 | 3b | 3.60 | 28 |
| 3 | 2a | 15.07 | 117 |
| 4 | 2b | 2.83 | 22 |
| 5 | 1a | 2.31 | 18 |
| 6 | 1b | 1.80 | 14 |
| 7 | 2a+3b (mixed) | 2.19 | 17 |
| 8 | 3a+3b (combined) | 2.06 | 16 |
| 9 | Un-type able | 20.14 | 156 |

## DISCUSSION

Hepatitis C is one of the most common cause of virus-related chronic liver disease which can lead to cirrhosis of the liver and hepatocellular carcinoma, and hence causes significant morbidity and mortality.[8]Hepatitis C is a disease that have affected around 10 million people in Pakistan. With such a high incidence of HCV, Pakistan is world's second most HCVinfected country, after Egypt.[9] Being a serious health issue, it is critical to establish effective prevention and treatment initiatives. Because treatment regimen and duration is genotype specific, information about genotype has become increasingly important in securing this strategies.[10] Therefore, the data reported here represent a comprehensive struggle to detect various HCV subtypes in the Peshawar region the capital of Khyber Pakhtunkhwa province.

With a 50% prevalence rate, our data clearly showed that genotype 3a is most abundant strain in our region. In a study undertaken by Sajid and Ayaz Ahmad *et al*., (2014) in district Mardan, similar results were obtained, where subtype 3a was predominant.[11] Another research project carried out in various geographical regions of Punjab, by Hafsa Aziz and Abida Raza *et al*., (2013) was consistent with our study reporting 88% prevalence of genotype 3a strain.[10] In all previous studies genotype 3a is dominant strain.[12,13]

A meta-anlysis from 117 countries, analyzing data of 1217 different studies Jane P. Messina and Isa Humphreys *et al.,* (2014) identified genotype 3a as the dominant strain in India and Pakistan which was parallel to our data.14 Furthermore comparable results were reported from other Asian countries like Thailand and India.[15,16]

However genotype 1 is the predominant strain in USA and Western Europe, which is in contrast to present study.[17] Genotype 1b was shown to be the most common subtype of HCV in Azerbaijan patients coming to Iran, seeking medical care.[18] Another intriguing finding in our study is that subtype 2a is the second most frequently circulating genotype which concurs with the study carried out by Umar and Mazhar (2016)[19] but in contrast to the study of Sajid and Ayaz, where 3b was the second frequent subtype of HCV.[11]While another study by Amina Gul (2016) reported higher frequencies of mixed genotype in the province of Khyber Pakhtunkhwa after subtype 3a[20] and genotype 1 was described as second most common subtype in Pakistan by Hafsa Aziz (2013)[10]. Arshad *et al*., (2020) found genotype 2a to be the second most common strain of HCV in KPK population when researching the epidemiological pattern of HCV genotype in the population.[21] The findings of this study are consistent with those of recent study drug addicts, which identified genotype 2a as the second prevalent strain after 3a.[22] As a result it has been found that genotype 2a is becoming more prevalent in Khyber Pakhtunkhwa. Similar substitution of a frequent genotype by an uncommon one has been seen during the last two decades in Venezuela.[23]

## CONCLUSION

In conclusion, we have observed that genotype 3a is the most common genotype in Peshawar followed by 2a. In our province prevalence of 2a is rising. The prevalence of genotype 2 is less as compare to genotype 3a or 2a. As genotype 2 and 3 are most prevalent in Peshawar we can offer short duration of treatment in type 2 and 3 with better results.

## RECOMMENDATION

More research on larger scales should be undertaken on regular basis to acquire a full understanding of genotype distribution and evolution trends in order to adopt proper treatment and prevention methods.

## CONFLICT OF INTEREST

None

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**DATA SHARING STATEMENT:** The data that support the findings of this study are available on request from the corresponding author. The data are not publicly available due to privacy or ethical restrictions.

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**AUTHOR'S CONTRIBUTION**

The following authors full fill authorship criteria as per ICMJE guidelines;

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|---|---|
| **Bilal M, Shaheen G:** | Idea conception, drafting the work, final approval, agreed to be accountable for all the work. |
| **Khan A, Khan TM:** | Design of the work, data acquisition, critical rivision, final approval, agreed to be accountable for all the work. |
| **Nazir M, Ahmad MT:** | Data analysis, drafting of the work, final approval, agreed to be accountable for all the work. |
| **Ahmed MH, Ahmed Z:** | Data interpretation, critical revision, final approval, agreed to be accountable for all the work. |