

# Distribution of HCV Genotype among the Patients Treated for Chronic Hepatitis C in Albania

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**Abstract:** ***Background:** Distribution of Hepatitis C Virus [HCV] genotypes may be changed over time. Epidemiological studies on distribution models of HCV genotypes in Albanian population might assist for better treatment options and preventive strategies. **Aims:** This study was conducted to determine distribution HCV genotypes in Albania by gender and age among the patients treated for HCV. **Methodology:** In this cross-sectional study, between April 2006 and December 2015, 265 patients identified with hepatitis C and under treatment were included. Frequency of different genotypes among patients was assessed according to gender, age at the time of sampling. **Results:** HCV genotype 1b was the predominant genotype [56 %] followed by genotype 2a/2c [17 %] among the Albanian patients with chronic HCV. A higher prevalence of 1b genotype of HCV was observed among male patients and those younger. **Conclusion:** Genotype 1b is the most prevalent genotype of HCV among the Albanian patients with chronic HCV. The sex and age affect the distribution of the genotype of HCV.*

**Keywords:** genotype, HCV, Albania

## 1. Introduction

Hepatitis C virus [HCV] is considered the most common cause of chronic liver diseases. It has been estimated that approximately 170-200 million individuals are infected with HCV all over the world [1]. Due to advance to cirrhosis and hepatocellular carcinoma, HCV infection causes a high morbidity and mortality rates and globally approximately 350000 people die every year due to HCV infection [2].

HCV belongs to the genus hepacivirus in the Flaviviridae family classified into six major genotypes and multiple subtypes. HCV genome is a 9.6 Kb single stranded RNA sequence flanked at both ends by untranslated regions [5' UTR and 3' UTR] [3].

HCV genotypes have their own unique pattern of disease development and response to antiviral therapy [4]. Several epidemiologic studies on the distribution of HCV genotypes have been conducted all over the world as they help to clarify the clinical status of HCV infection. Furthermore, they also facilitate the treatment options and preventive strategies [5].

The distribution patterns of Hepatitis C virus genotypes vary significantly in different countries. Genotypes 1, 2, and 3 are the most frequently encountered genotypes worldwide [6] [7]. However, some significant differences are noticed when subtype distribution is investigated. Genotype 1a and 1b are the predominant genotypes in the United States and Europe, respectively [8 9].

In North America and Northern Europe, subtype 1a is the most common and followed by 1b, 2a and 2b. The most common subtype in Southern and Eastern Europe is 1b, followed by genotypes 2 and 3 [10 11]. HCV genotype 2 is particularly prevalent in countries of West Africa [4].

Genotype 3a is more frequently found in Australia and South Asia [12] whereas genotype 4 is the predominant genotype in countries of Northern and Central Africa particularly Egypt. Moreover, genotypes 5 and 6 are frequently found in South Africa and Asia, respectively [3].

All these HCV genotypes show 31-34% heterogeneity in their nucleotide sequences and approximately 30% heterogeneity in their amino acid sequences [13].

As the distribution of HCV genotypes can be changed over time, the epidemiological studies may reveal distribution patterns of HCV genotypes among population to facilitate treatment options and preventive strategies. Thus our study aims to shed light on distribution HCV genotypes in Albania by gender and age among the patients treated for HCV.

## 2. Methodology

The study was designed as perspective one for a period of time from 2006 to 2015. In this study, we included patients identified with hepatitis C and under treatment with HCV. The infection primarily diagnosed with HCV infection by the third generation Enzyme Linked Immunosorbent Assay (ELISA) and then referred by physicians to the virology laboratory for determination of HCV genotypes prior to antiviral therapy.

From each patient was obtained the consent of participation in the study at collection points.

The demographic information including gender, age was retrieved from patients' medical records. The age was divided in the group age by ten.

**HCV genotyping**

HCV genotyping was performed a line probe assay, LiPA (Line Probe Assay-LiPA, Bayer), a reverse hybridization test that can associate the 5' NCR genome in products of a post PCR amplification of DNA amplicons. This assay allows differentiation of 6-major HCV genotypes (1-6) and 15 subtypes (1a, 1b, 2a/2c, 2b, 3a, 3b, 3c, 4a, 4b, 4c4d, 4e, 4f, 4h, 5a, 6a) [14 15]

**Analyzing**

Pearson's chi square test was used to assess the distribution of genotype of HCV according to the age groups and sex. The SPSS was used to analyze the data

**3. Results**

This perspective study shed light on the distribution of HCV genotype among the patients with chronic HCV and under treatment.

**Table 1:** The demographic characteristic of the sample

Demographic characteristics	Frequency (%)
<b>Age ( in groups in years)</b>	
≤20	4.5
21-30	18.5
31-40	20.0
41-50	26.4
51-60	20.0
61-70	10.2
≥71	0.4
Total	100
<b>Sex</b>	
Male	52.8
Female	47.2
Total	100

In the table one is presented the distribution of the sample by demographic characteristics [sex and age in the moment of sampling. In total, 265 patients have been included in the study for a period of 10 years.

One in four patients belonged to the age groups 41-50 years old. The vast majority of the participants belonged to the age group of 31-60 years old [66.4%] and most of the patients are male (53 vs 47%).

**Table 4:** Distribution of HCV genotypes by age groups

age group	genotype								Total [ number]
	1b	1a	2	2a/2c	3	4a	2b	4e/4c	
In years	% Within the group age	% Within the group age	% Within the group age	% Within the group age	% Within the group age	% Within the group age	% Within the group age	% Within the group age	
<20	75	0	0	17	8	0	0	0	12
21-30	72	6	4	8	4	2	0	4	49
31-40	60	0	17	9.5	8	6	0	0	53
41-50	69	6	7	14	3	0	1	0	70
51-60	38	0	19	30	6	2	4	2	53
61-70	22	0	33	33	0	4	4	4	27
>71	0	0	0	100	0	0	0	0	1

The 2a/2c and 2b is more prevalent at older age more than 50 years old. The genotype 1b prevalence is decreasing and 2a/2c is increasing over the age of the patients

In the table 2 is presented the distribution of sample by the HCV genotype.

**Table 2:** Distribution of the sample by the genotype of HCV

Genotypes of HCV	%
1b	56.6
1a	2.6
2	13.2
2a/2c	17.7
3	4.5
4a	2.3
2b	1.5
4e/4c	1.5
Total	100

The most prevalent genotype is genotype 1b (55.6 % of cases) followed by genotype 2a/2c and 2.(with 17.7 and 12 %, respectively) The less prevalent genotype is genotype 2b and 4e/4c with only 1.5 % of the cases. The distribution of HCV genotypes by sex was also observed in this study.

**Table 3:** Distribution of HCV genotypes by sex

Genotype HCV	Male	Female
1b	58.57	54.40
1a	4.29	0.80
2	12.14	14.40
2a/2c	12.14	24.00
3	7.86	0.80
4a	0.71	4.00
2b	2.14	0.80
4e/4c	2.14	0.80

The distribution of HCV genotypes is found variable among male and female patients [see table 3]. Interestingly, in both female and male, 1b genotype is prevalent. But among female patients, the genotype 2a/2c and 2 is more prevalent than male patients; 1a and 3 genotype are most prevalent among male patients rather than female patients. The difference in the distribution of the genotype HCV by sex is significant when is analyzed at chi square technique [p=0.01]. Distribution of HCV genotypes was found variable among age groups ( see table 4 ) Genotype 1b is more prevalent among the younger (until 50 years old). In particular, among patients less than 20 year old the genotype 1b is encounter for 75 % of the cases.

The distribution of genotypes of HCV by age groups is significant where it is analyzed in chi square technique (p=0.048)

#### 4. Discussion

Performing investigations on distribution patterns of HCV genotypes in our country is essential for better understanding of HCV infection as well as implementation of preventive and therapeutic strategies. To our knowledge this is the first study that provides data on a large sampling (265 patients).

The most prevalent genotypes of HCV among patients with chronic hepatitis c under treatment are 1b and less prevalent 1a, 2b, 4a/4c.

The finding of our study is consistent and comparable with a previous studies on HCV genotypes distribution in Albania, which have concluded that the 1b genotype is the most prevalent [16], [17] and with the finding of the studies among the countries of eastern Europe in which HCV 1b has been reported prevalent in other south eastern European countries, including Greece, Serbia, Montenegro, Slovenia, Croatia, and Bosnia and Herzegovina[18]-[22]

Interestingly, in both female and male, 1b genotype is prevalent. The model of distribution of HCV genotype among female and male patients is different with the genotypes 2a/2c and 2 more prevalent among females and 1a and 3 more prevalent among males

In contrast to our finding, no sex variation was reported in HCV genotypes distribution in Algeria [23]. However, in Libya, genotype 4 was frequently found in females, whereas HCV genotype 1 was frequently found in males [24].

In addition, 1b genotype was higher among younger patients [< 50 years old] compared to older ones [> 50 years] in where the genotype 2a/2c is most prevalent.

However, in Italy the genotype 1b is most prevalent among the elder which is inconsistent with our findings [25,26]

Our study included a larger sample of patients and broad range of years compared with the previous study and consequently the finding of our study should be considered as reliable.

In conclusion, we observed that the HCV genotype 1b is the predominant genotype in Albania followed by 2a. The incidence of genotype 1b was observed to be higher among younger in our country Further studies are needed to identify the possible risk factors in transmission of HCV for effective implementation of preventive strategies to reduce young people exposure to this infection.

Periodically investigations of HCV genotypes are needed to monitor distribution patterns of genotypes to facilitate treatment options and preventive strategies in our country Albania

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