

Prevalence of HCV virus genotypes in Albania

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ABSTRACT

The epidemic of Hepatitis C virus infection is continuously evolving in Albania such as in Europe. Until now the intravenous drug use has become the main risk factor for the HCV transmission, prevalent infections have increased and genotype distribution has changed and diversified. Meanwhile in Eastern European countries epidemiological data are limited such as in Albania. Through this study, we furnish more information about the prevalence of HCV virus genotypes in Albania. Methods: In this study we enrolled 174 subjects HCV RNA positive during the period 2007-2015 with an median age of 38.7 years old, from the Public Health Institute and National Blood Transfusion Centre, Albania. Results: The HCV virus genotype 1b is the most frequent with 35.6% (62/174). It's important to mention that genotype 3 and 3a is more frequent among IDU (Intravenous drug users). Conclusions: Even though limited data, we noticed that HCV virus genotype 1b is the most frequent in Albania such as in other countries of Central-South Europe. Parenteral route of transmission of different subtypes of this virus in Albania is very evident, but further epidemiological studies are required.

Keywords - HCV, Genotypes, IDU, Albania

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I. INTRODUCTION

Hepatitis C is a blood born virus that remains a large health care burden to the world. It exhibits high genetic diversity, characterized by regional variations in genotype prevalence. This poses a challenge to the improved development of vaccines and pan-genotypic treatments, which require the consideration of global trends in HCV genotype prevalence. The World Health Organization (WHO) estimates that 3%, of the world's population is infected by HCV [1]. Chronic Hepatitis C infection is associated with the development of liver cirrhosis, hepatocellular cancer, liver failure, and death [2]. HCV strains are classified into seven major genotypes and multiple subtypes, on the basis of phylogenetic and sequence analyses of whole viral genomes [3]. Even though the global HCV epidemic was widespread by 1980, it was not until 1989 that the virus was identified as the leading cause of non-A non-B hepatitis [4]. HCV genotypes have their own unique pattern of disease development and response to antiviral therapy. The contemporary global geographic distribution of HCV genotypes is complex. It has already been established that a few subtypes—specifically 1a, 1b, 2a, and 3a—are widely distributed across the globe and account for a large proportion of HCV infections in high-income countries [5,6,7]. Subtype 1a is the most common in North America and Central Europe, followed by genotypes 1b, 2a and 2b. Meanwhile, the most common subtype in Southern and Eastern Europe is 1b, followed by genotypes 2 and 3 [8,9]. HCV genotypes 1 and 2 are primarily in West Africa, genotype 3 in South Asia, genotype 4 in Central Africa, genotype 5 in Southern Africa and genotype 6 in South East Asia (3,5,6). Only one genotype 7 infection has been reported once it was isolated in Canada from a Central African immigrant (10). The epidemiology of HCV infection in Europe is evolving. It results 1.7% and accounting over 13 million of estimated cases. The lowest prevalence is 0.9%, reported from Western Europe and the highest is 3.1% , reported from Central Europe. Genotype distribution does not show high variability among the three areas studied. The predominant genotype is G1, followed by G3, G2, G4, G5 and G6 (11). Because epidemiological data are the basis for the development of preventive strategies so to eradicate HCV infection, to facilitate treatment options and as the distribution of HCV genotypes can be changed over time, it's important to realize studies to evaluate the patterns of HCV genotypes among the population. For this reasons we realize this study, to evaluate the distribution of HCV genotypes in Albania among the persons that resulted HCV-RNA positive.

II. METHODS

In this study we enrolled the data of 174 subjects that resulted HCV- RNA positive, during the period 2007-2015, from Public Health Institute and the National Blood Transfusion Centre of Albania. From the data resulted to be six groups of population like: hospitalized, thalassaemic, hemodialised, IDU, transfusional centre and general population.

The test used to diagnosed HCV virus was Enzyme Linked Immunosorbent Assay (ELISA), third generation (ABBOTT) and Polymerase Chain Reaction (PCR). Statistical analyses were done with Chi square, performed by using Excel 2007. The value of $p < 0.01$ were considered statistically significant for the test.

III. RESULTS

This study highlights on the distribution of HCV genotypes among the subjects that resulted HCV RNA positive. The most frequent HCV virus genotype is 1b with 35.6% (62/174), while genotype 1 is found in 22.4% (39/174). Other genotypes noticed are 2c with 8.6% (15/174) and genotypes 3a with 7.5% (13/174) and 2a/c with 6.9% (12/174). (Table 1, Figure 1)

| GENOTYPES | No. | Freq. % |
|-----------|-----|---------|
| 1 | 39 | 22.4% |
| 1a | 6 | 3.4% |
| 1b | 62 | 35.6% |
| 2 | 9 | 5.2% |
| 2a | 1 | 0.6% |
| 2a/c | 12 | 6.9% |
| 2c | 15 | 8.6% |
| 3 | 7 | 4.0% |
| 3a | 13 | 7.5% |
| 4 | 7 | 4.0% |
| 4a | 1 | 0.6% |
| 4c | 1 | 0.6% |
| 4d | 1 | 0.6% |

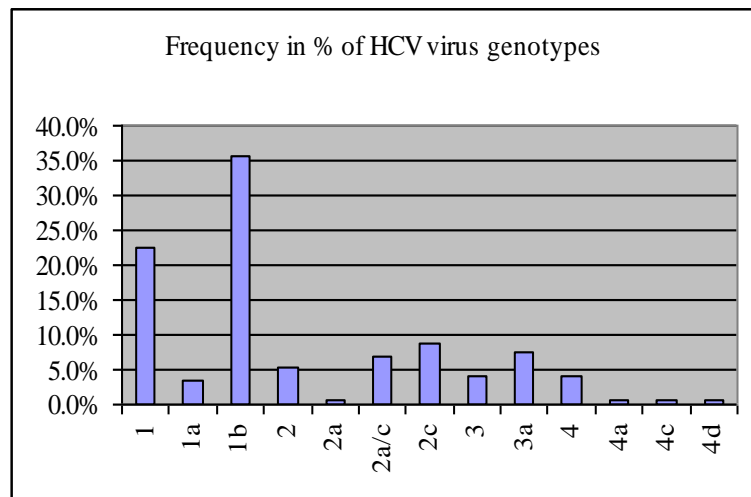


Table 1. HCV Genotypes frequency

Figure 1. Frequency in % of HCV virus genotypes

Meanwhile the demographic characteristics (Gender, Group-Age) of the sample resulted that 62.64% of the subjects are females and 37.36% are males (Figure 2). 13.79% of them belonged to the group-age < 25 years old, 64.37% belonged to the group age 25-50 years old and 21.84% belonged to the group-age > 50 years old (Figure 3)

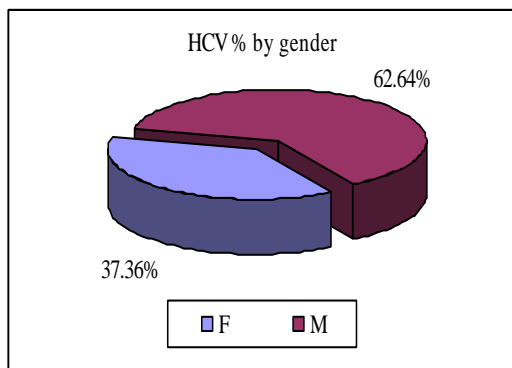


Figure 2. HCV % by gender

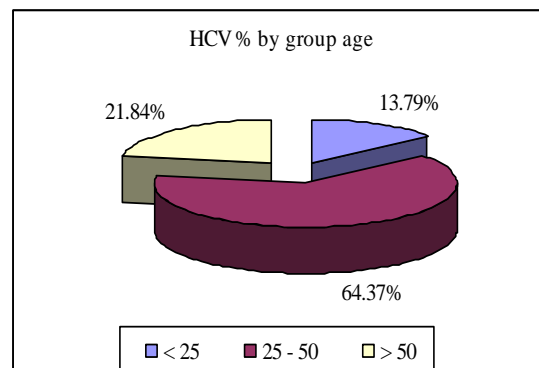


Figure 3. HCV % by group age

For both females and males the most frequent genotypes are 1 and 1b (Figure 4).

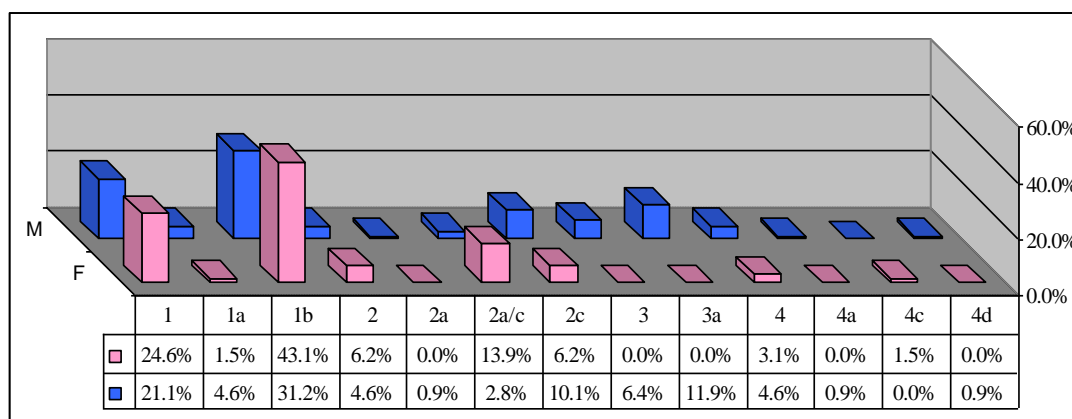


Figure 4. Distribution of HCV genotypes by gender

In Figure 5 is presented the distribution of HCV genotypes by group-age and the most frequent genotype among subjects < 25 years old is G1, among subjects 25-50 years old is G1b and among subjects > 50 years old is G1. The value of $p < 0.01$ were considered statistically significant for the test.

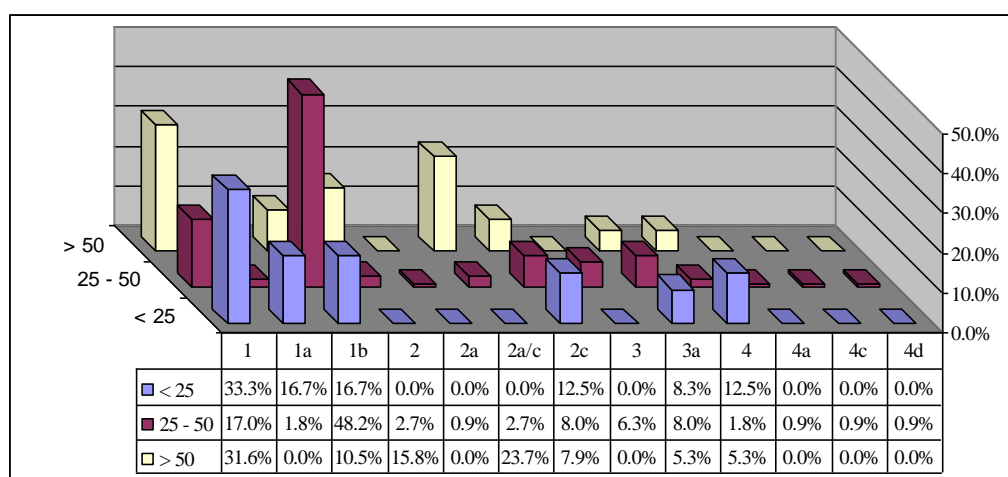


Figure 5. Distribution of HCV Genotypes by Group Age

From this study resulted that 48.55% of the subjects belong to the group of hospitalized patients (gastro-pathology department and department of infectious diseases), 31.79% are general population, 10.98% IDU, 5.2% are patients under hemodialysis treatment, 2.89% Transfusion Center. (Figure 6)

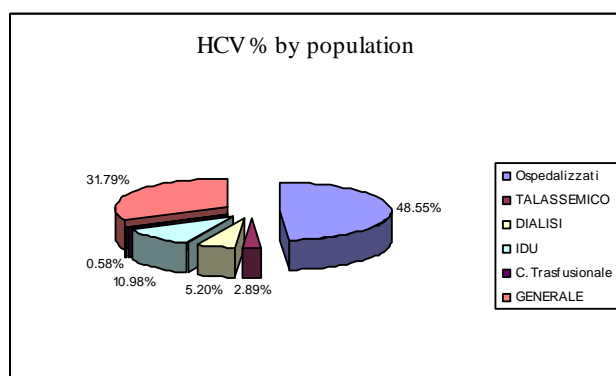


Figure 6. HCV % by population

In Table 2 is shown the distribution of HCV genotypes among Hospitalized, Thalassaemic patients, Hemodialised, IDU, Transfusional Centre and General population. At the group of patients hospitalized the most prevalent genotype is 1 and 1b. Among the IDU the most prevalent genotype resulted to be 3 and 3a genotypes and among the general population genotype 1b is the most prevalent. Meanwhile among the patients under hemodialysis treatment have more frequent the genotypes 1 and 4 and about the group of thalassaemic patients they have more frequent the genotypes 1 and 1b. The value of $p < 0.01$ were considered statistically significant for the test.

| Population | Genotype [%] | | | | | | | | | | | | |
|--------------------|--------------|------|------|------|-----|------|------|------|------|------|-----|-----|-----|
| | 1 | 1a | 1b | 2 | 2a | 2a/c | 2c | 3 | 3a | 4 | 4a | 4c | 4d |
| Hospitalized | 33.3 | - | 31.0 | 9.5 | - | 14.3 | 1.2 | 2.4 | 3.6 | 3.6 | - | 1.2 | - |
| Thalassaemic | 60.0 | - | 40.0 | - | - | - | - | - | - | - | - | - | - |
| Hemodialised | 66.7 | - | 11.1 | 11.1 | - | - | - | - | - | 22.2 | - | - | - |
| IDU | 5.3 | 21.1 | - | - | - | - | - | 26.3 | 42.1 | - | 5.3 | - | - |
| Trasfusional Cntr. | 100.0 | - | - | - | - | - | - | - | - | - | - | - | - |
| General | - | 3.6 | 60.0 | - | 1.8 | - | 25.5 | - | 3.6 | 3.6 | - | - | 1.8 |

Table 2. Distribution of HCV genotypes among different groups of population.

IV. CONCLUSION

Even though limited data, we noticed that HCV virus genotype 1b is the most frequent in Albania such as in other countries of Central-South Europe [12-15]. Parenteral route of transmission of different subtypes of this virus in Albania is very evident, but further epidemiological studies are required.

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Biography

Dr. Pranvera Dragusha, graduated in 2010 in the Faculty of Medicine and Surgery at the Catholic University “Our Lady of Good Counsel”, by presenting a thesis on “The Prevalence and Characteristics of Metabolic Syndrome among Apparently Healthy Adults in Albania”.

In 2011 she started her specialization at the University Hospital Centre “Mother Teresa”, in Albania and became an Internal Medicine specialist in 2015.

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