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Research Article

Distribution of Genotypes of Viral Hepatitis C in Patients of the Hepatological Center of Almaty

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Abstract

Since the tactics of therapy for chronic viral hepatitis C are determined by the genotype of the virus, accurate determination of the virus genotype by laboratory methods and monitoring the structure of genotypes of viral hepatitis C are essential elements of surveillance of this infection. In this regard, the question of the stability of the picture of genotypic diversity in Almaty 5 years ago is of scientific interest for clinicians and pharmacists. Analysis of the spread of genotypes of viral hepatitis C in Almaty will provide information for further improvement of preventive programs and treatment tactics.

Keywords: Common Bile Duct (CBD); Ultrasound; Supine; Semi-Prone Position

Introduction

Hepatitis C is one of the most common chronic diseases. More than 70% of hepatitis C virus infection end in chronization and the development of serious liver diseases, such as cirrhosis and hepatocellular carcinoma [1,10].

Viral hepatitis remains one of the pressing health problems not only in the world, but also in Kazakhstan. According to official statistics, 30-50 thousand patients with viral hepatitis are registered annually in the Republic of Kazakhstan. (This figure ranges from 13 thousand to 30 thousand by region) [7].

According to the press service and a conference call on the situation with viral hepatitis C, held by the Ministry of Health of the Republic of Kazakhstan on September 12, 2019, it was noted that over the past 20 years the incidence in the Republic of Kazakhstan has decreased by 2.8 times (1999 - 229 cases, 2018 year - 79 cases). Despite the decrease in morbidity, the Republic of Kazakhstan belongs to the region with high endemicity of viral hepatitis [7].

As is known, hepatitis C to be caused by RNA-containing viruses belonging to the flavivirus family. The pathogen is designated as HCV and is divided into several genotypes. Modern medicine knows 11 genotypes of the hepatitis C virus, but the World Health Organization recognizes only 6 of them: genotype 1 (subtypes a, b, c); genotype 2 (subtypes a, b, c); genotype 3 (subtypes a, b); genotype 4 (subtypes a, b, c, d, e, f, h, i, j); genotype 5 (subtype a); genotype 6 (subtype a) [1,2,9].

Genotypes 1, 2 and 3 are most common. One or another subtype of a genotype dominates in different geographical zones: subtype 1a dominates in Northern Europe and North America, while subtype 1b - in Japan, Southern and Eastern Europe, and predominates in Asia. Genotype 2 is significantly less common in these countries compared to genotype 1. At the same time, subtypes 2a and 2b are characteristic of North America, Europe and Japan, and subtype 2c is for Italy. Genotype 3 is most endemic in Southeast Asia, Thailand, India, and Pakistan. Subtype 3a ranks second in terms of detection frequency in most of Europe, USA [1,2,9,10].

Genotypes 4, 5 and 6 have a more local distribution: genotype 4 - in Central and North Africa and the Middle East, genotype 5 is distributed exclusively in South Africa, and genotype 6 is widely represented in Vietnam, Hong Kong and China [1,2,10].

Analysis of the spread of viral hepatitis C genotypes in various population demonstrated the predominance of a particular genotype depending on the route of infection. For example, in European countries, genotype 1a and 3a is associated with infection that occurred during intravenous drug administration, and 1b and 2a - are

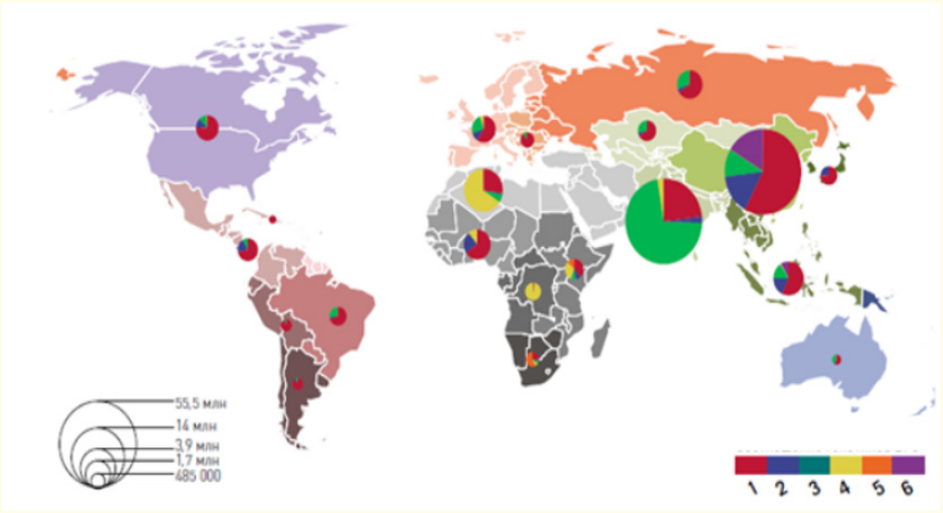

Figure 1: Global distribution of hepatitis C viral genotypes.

associated with transfusion of blood or plasma contaminated with hepatitis C virus [2,4,8]. The spread of genotypes is a dynamic phenomenon and is associated with many factors, primarily with the migration of the population and the predominance of one or another route of infection. In European countries, genotype 3a appeared, previously characteristic of the countries of Central Asia. Its distribution was associated with narcotic traffic from this region, and the main circulation of this genotype was carried out in a subpopulation of intravenous drug addicts. However, later genotype 3a "entered" the general population, and at present, along with genotype 1b, it is dominant in the territory of the Eurasian space [3].

The genotype of the viral hepatitis C is the most important clinically significant factor, since the genotypes of the virus differ in the degree of sensitivity to interferon. Genotype 1 is predominant in frequency and more difficult to treat. Genotype 1 is considered the most common and most dangerous, as it easily adapts to new conditions and treatments. In people infected with such a pathogen, in the vast majority of cases, chronic inflammation develops, while the acute phase is practically not pronounced. In addition, when infected with genotype 1, there is a high probability of relapse [2,8].

Virus genotypes 2 and 3 are less aggressive and easier to treat.

Genotype 2 is less common in the world and is much less likely to cause any complications. In this case, there is a slow progression of the inflammatory process, sometimes the infection resolves on its own, there are practically no relapses. This pathogen responds well to antiviral therapy [4,5].

Genotype 3 is characterized by a high probability of complications, especially severe cirrhosis and hepatocellular cancer, faster pathological changes in the liver. However, the pathogen has a rather high susceptibility to antiviral drugs and is well treatable in the early stages [4,5].

It is confirmed that regardless of the type of therapy (combination therapy with pegylated interferon and ribavirin or interferon monotherapy), patients respond best to treatment if they are infected with genotype 2, somewhat worse if genotype 3, and much worse if infection of genotypes 1 and 4 is present. Therefore, for patients infected with genotypes 2 and 3, the recommended duration of interferon therapy is 24 weeks, and for patients infected with genotype 1 - 48 weeks [4,5].

Genotypes 4, 5 and 6 are the least common in the world and, therefore, are not well studied. Genotypes 4, 5 and 6 are practically not found in Kazakhstan [7].

Since the tactics of therapy for chronic hepatitis C is determined by the genotype of the virus, accurate determination of the genotype of the virus by laboratory methods and monitoring the structure of the genotypes are essential elements of surveillance for this infection. In this regard, the question of the stability of the picture of genotypic diversity of Almaty 5 years ago is of scientific interest for clinicians and pharmacists.

Aim of the Study

To determine the prevalence of genotypes of viral hepatitis C for 2018-2023 in patients observed at the Hepatology Center of the city polyclinic No. 5 of Almaty, Republic of Kazakhstan.

Materials and Methods of Research

The work used a retrospective analysis of the incidence of acute viral hepatitis C and chronic viral hepatitis C in Almaty for 2018-2023 and an analysis of the prevalence of genotypes in patients of the Hepatological Center for 2018-2023. The source of data on morbidity is the official accounting and reporting documentation of the Department of Quality Control and Safety of Goods and Services in Almaty of the Ministry of Health of Kazakhstan. Data on patient genotypes were obtained from the Hepatological Center of the City Polyclinic No. 5 of Almaty.

Genotype of hepatitis C virus was determined by RT-PCR with primers to the core region of the virus genome proposed by T. Ohno and M. Mizokami [6]. For the isolated RNA, reverse transcription (RT) was performed using the Reverta-L kit manufactured by Inter Lab Service of Russia according to the manufacturer's protocol. The cDNA obtained was then amplified in PCR according to the previously described protocol [6]. PCR products were analyzed in agarose gel electrophoresis (2%) in TBE. Amplification product sizes corresponding to different genotypes of viral hepatitis C were as follows: 208 bp for genotype 1a, 234 bp for genotype lb, 190 bp for genotype 2a, 232 bp for genotype 3a.

The obtained indicators of the frequency of detection of different genotypes of viral hepatitis C by years were subjected to statistical processing according to generally accepted methods using variational statistics using the Excel 2003 standard program and the Graph Pad Pism 4 statistical data processing program. Statistical processing of the data included the identification of the reliability of the differences in the values of the indicators in the compared groups using Fisher's test, the differences were assessed as significant at a probability of 95% ($p < 0, 0 5$).

The selection method was divided according to the following criteria: patients at risk for cirrhosis and hepatocellular carcinoma and patients newly registered with a diagnosis of viral hepatitis C.

Results and Discussion

Table 1 presents data on the incidence of acute and chronic viral hepatitis C in Almaty from 2018 to 2023.

Figure 1 shows a graph of the incidence of acute and chronic viral hepatitis, which illustrates that no increase in spontaneous incidence of acute and chronic viral hepatitis was observed. From

Years	Acute viral hepatitis C		Chronic viral hepatitis C	
	Absolute number	Indicator per 100 thousand people.	Absolute number	Indicator per 100 thousand people
2018	14	0,43	257	17,04
2019	8	0,26	252	16,49
2020	11	0,36	233	13,60
2021	10	0,35	204	11,38
2022	6	0,17	210	11,47
2023	7	0,18	199	11,10

Table 1: Incidence of acute and chronic viral hepatitis C in Almaty for 2018-2023.

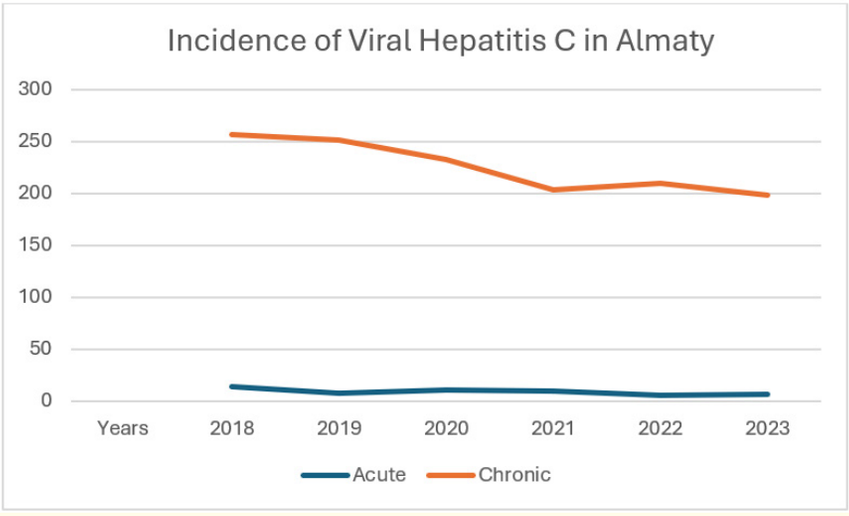

Figure 2: Chart of incidence of acute and chronic viral hepatitis C in Almaty for 2018-2023.

2018 to 2021, there was a gradual decrease in the incidence of chronic hepatitis C, and from 2021 to 2023 there was a stable plateau without a tendency to noticeable increase or decrease.

From the statistical office of the Hepatological Center in Almaty, data on the genotypes of viral hepatitis C was obtained for patients who were registered in the dispensary for 2018-2023 and are presented in Table 2 and Figures 3, 4 and 5.

In 2018, 131 patients were observed, in 2019 – 120, in 2020 – 107, in 2021 – 109, in 2022 – 99, in 2023 – 98.

Years	Genotype of Viral Hepatitis C					
	Genotype 1		Genotype 2		Genotype 3	
	men	women	men	women	men	women
2018	31	38	7	6	28	21
2019	26	27	6	9	33	19
2020	31	42	3	2	20	9
2021	33	35	3	4	20	14
2022	29	34	4	5	18	9
2023	27	31	6	7	19	8
Total	177	207	29	33	138	80

Table 2: Distribution of genotypes of viral hepatitis C among patients of the Hepatological Center in Almaty for 2018-2023.

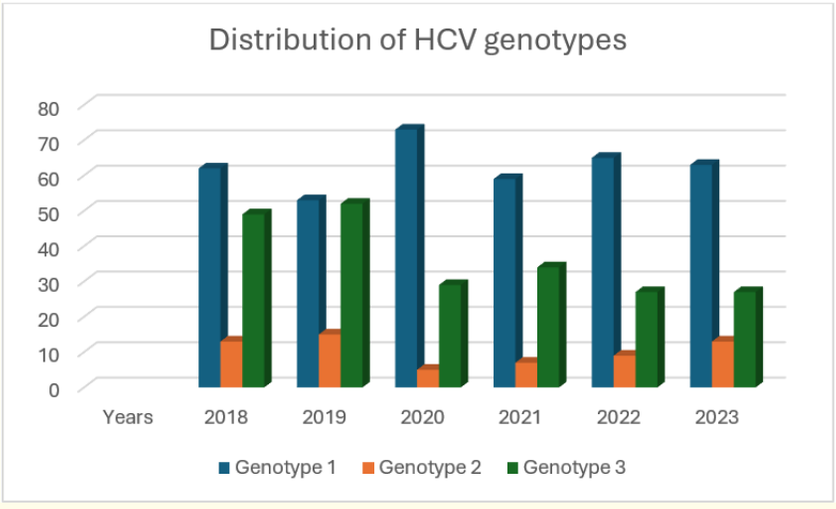

Figure 3: Distribution of genotypes of viral hepatitis C by years.

As can be seen from Figure 3, genotype 1 mainly prevails in patients of the Hepatological Center, which is consistent with world data. The high peak of the genotype 1 frequency occurred in 2020, by 2021 it slightly decreased, in 2022 it slightly increased and remained at this level in 2023. The frequency of occurrence of genotype 3 decreased markedly in 2020, then in 2021 it rose and in 2022 and 2023 the frequency did not change. Genotype 2 represents the smallest amount.

As can be seen from Figure 4, men get viral hepatitis C more often than women.

As can be seen from Figure 5, the frequency of genotypes 1 and 3 is higher in men than in women. The frequency of genotype 2 is almost the same.

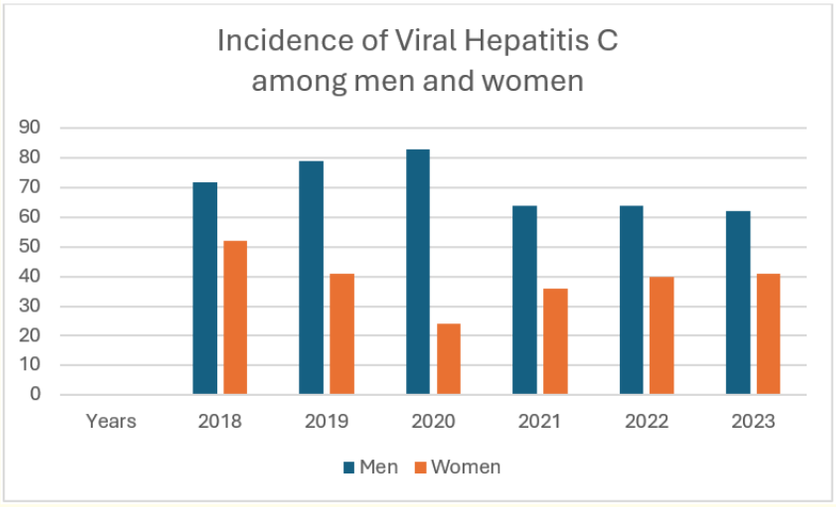

Figure 4: Incidence of Viral Hepatitis C among men and women.

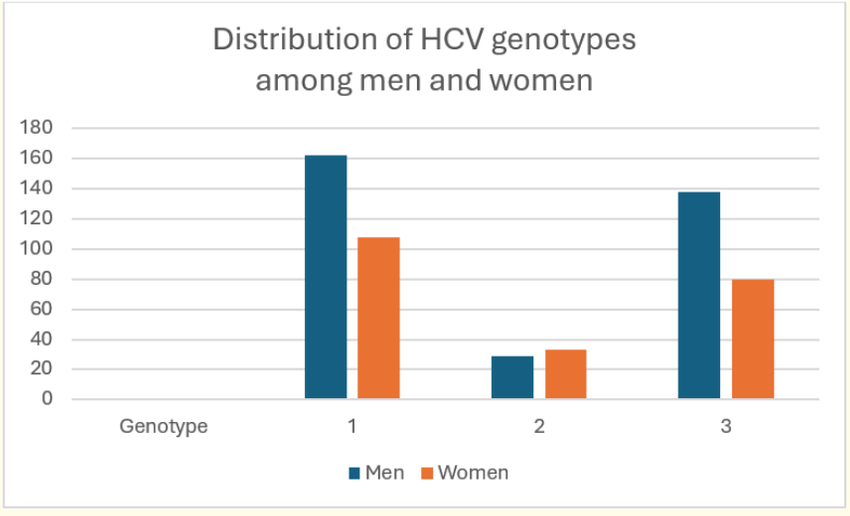

Figure 5: Distribution of HCV genotypes among women and men.

Conclusion

Genotype 1 frequency is predominant and there is no downward trend. This is most likely to the fact that genotype 1 easily adapts to new conditions and treatments. Given that genotype 1 is more difficult to treat, there is a need to develop new therapies to improve efficacy in treatment.

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