Research Article

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Genotype Distribution of HCV in Patients with Chronic Hepatitis C in a University Hospital

Bir Üniversite Hastanesinde Kronik Hepatit C Hastalarındaki HCV Genotip Dağılımı

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ABSTRACT

Objectives: Hepatitis C virus (HCV) infection is a public health issue of great importance. HCV genotyping helps in monitoring prognosis, selecting appropriate antiviral drugs, monitoring side effects, and deciding on treatment duration. The aim of this study was to determine the HCV genotypes in our hospital to reveal their distribution over time and to contribute to epidemiological data by evaluating the relationship between HCV genotypes and viral load.

Materials and Methods: Serum samples from 144 patients diagnosed with chronic hepatitis C between January 01, 2019 and December 31, 2023 were included in this study. HCV-RNA loads were determined using a Bosphore quantification kit (Anatolia, Turkey) via a Montania 4896 thermal cycler (Anatolia, Turkey). HCV genotypes were detected using the Bio-Rad CFX96 system with the Diagnotech HCV genotyping quantitative polymerase chain reaction kit targeting the 5'NS5B region.

Results: The most frequently detected genotypes in our hospital were genotypes 1b (34.7%, genotype 3 with 32.6% and genotype 1 with 15.3%). The lower mean age of genotype 3 patients was statistically significant compared with the ages of patients with genotypes 4 and genotype 1b ($p<0.001$). It was found to be statistically significant that the median viral load of patients with genotype 1 was lower than that of patients with genotype 1b and genotype 3 ($p=0.046$). The higher frequency of genotype 4 among foreign nationals was statistically significant ($p=0.034$).

Conclusion: HCV genotypes vary between regions based on geographical location, migration, socioeconomic level, and drug

ÖZ

Amaç: Hepatit C virüsü (HCV) enfeksiyonu önemli bir halk sağlığı sorunudur. HCV genotiplendirilmesi hastalık prognozunun izlenmesinde, uygun antiviral ilaçların seçilmesinde, yan etkilerin takip edilmesinde ve tedavi süresine karar verilmesinde yardımcı olmaktadır. Bu çalışmanın amacı, hastanemizdeki HCV genotip dağılımını ortaya koymak ve HCV genotipleri ile viral yük arasındaki ilişkiyi değerlendirerek epidemiyolojik verilere katkı sağlamaktır.

Gereç ve Yöntemler: Bu çalışmaya 1 Ocak 2019-31 Aralık 2023 tarihleri arasında kronik hepatit C tanılı 144 hastanın serumları dahil edilmiştir. Hastaların HCV-RNA viral yükleri, Montania 4896 ısı döngü cihazı (Anatolia, Türkiye) aracılığıyla Bosphore (Anatolia, Türkiye) kantitifikasyon kiti kullanılarak tespit edilmiştir. HCV genotipleri, 5'NS5B bölgesini hedefleyen Diagnotech HCV genotipleme kantitatif polimeraz zincir reaksiyonu kiti ile Bio-Rad CFX96 cihazı kullanılarak tespit edilmiştir.

Bulgular: Hastanemizde en sık tespit edilen genotipler; genotip 1b (%34,7, genotip 3 %32,6 ve genotip 1 %15,3) olmuştur. Genotip 3 hastalarının yaş ortalamasının genotip 4 ve genotip 1b hastalarının yaş ortalamasından daha düşük olması istatistiksel olarak anlamlı bulunmuştur ($p<0,001$). Genotip 1'e sahip hastaların ortalama viral yükünün genotip 1b ve genotip 3'e sahip hastalardan daha düşük olması istatistiksel olarak anlamlı bulunmuştur ($p=0,046$). Yabancı uyruklular arasında genotip 4 sıklığının daha yüksek olması istatistiksel olarak anlamlı bulunmuştur ($p=0,034$).

Sonuç: HCV genotipleri coğrafi konum, göç, sosyoekonomik düzey ve ilaç kullanımına bağlı olarak bölgeler arasında farklılık

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use. Therefore, molecular studies on this issue are important for appropriate antiviral drug treatment and duration.
Keywords: Chronic viral hepatitis C, genotype, epidemiology

göstermektedir. Bu nedenle, bu konudaki moleküler çalışmalar uygun antiviral ilaç tedavisi ve süresi için önemlidir.
Anahtar Kelimeler: Kronik viral hepatit C, genotip, epidemiyoloji

Introduction

Hepatitis C virus (HCV) infection may cause acute and chronic HCV infections and lead to complications, such as liver failure, cirrhosis, and hepatocellular carcinoma, with high mortality and morbidity (1). HCV infection is a major health problem worldwide, and approximately 85% of acute HCV infections progress to chronic HCV infection. The World Health Organization reports that approximately 58 million people worldwide are affected by chronic HCV infection, and approximately 1,5 million people become infected with HCV each year (2,3). In Turkey, approximately 1 million people are infected with HCV.

HCV is usually transmitted through sexual intercourse, intravenous drug use, blood transfusion, and surgical and dental procedures (4). The most important characteristic of HCV infection is that it can cause chronic HCV infection and become resistant to antiviral drugs as a result of mutations in host cells (5). Different HCV genotypes exist due to differences in nucleotide sequences among regions of the HCV genome (6). The nucleotide sequences of HCV genotypes differ by 30-35%, and there is at least a 15% difference between the nucleotide sequences of the subgroups of HCV genotypes (5,7). The main factors affecting HCV genotype distribution are socioeconomic level, geographical location, migration, and intravenous drug use.

The most common HCV genotype worldwide is genotype 1 with a rate of 46-49%, followed by genotype 3 at 22% (8,9). When the distribution in the world is analyzed; genotype 1 is more common in North and South America, genotype 2 in East Asia, genotype 3 in Asia and Europe, genotype 4 in the Middle East and North Africa, genotype 5 in South Africa, and genotype 6 in Southeast Asia (10). HCV genotyping helps in monitoring prognosis, selecting appropriate antiviral drugs, monitoring side effects, and deciding on the treatment duration (11).

The aim of this study was to determine the HCV genotypes in our hospital, monitor their distribution over the years, and contribute to the epidemiological data by revealing the relationship between HCV genotypes and viral load.

Materials and Methods

Serum samples taken from 144 patients diagnosed with chronic HCV infection between January 01, 2019 and December 31, 2023 were included in this study. HCV-RNA levels were determined using a Bosphore quantification kit (Anatolia, Turkey) via a Montania 4896 thermal cycler (Anatolia, Turkey). Results are expressed as International units per milliliter (IU/mL). HCV genotypes were detected on a Bio-Rad CFX96 PCR thermal cycler (California, USA) using a Diagnotech HCV genotyping qPCR kit (Diagnotech, Turkey) targeting the 5'NS5B region.

This retrospective study was approved by the Ethics Committee on Non-Medicine and Non-Medical Device Research of Necmettin Erbakan University (decision number: 2024/4963, date: 17.05.2024).

Statistical Analysis

The data obtained were analyzed using Statistical Package for Social Sciences 21.0 package program. In descriptive analyses, frequency data were presented as number (n) and percentage (%), whereas numerical data were presented as median (minimum-maximum). The conformity of numerical data to the normal distribution was analyzed by visual (histogram) and analytical methods (Kolmogorov-Smirnov test). For numerical variables that were found not to conform to normal distribution, the Kruskal-Wallis test was used to compare more than two independent groups. Post-hoc Mann-Whitney U test and Bonferroni correction were performed for pairwise comparisons between groups with statistically significant differences. The chi-square (χ^2) test and Fisher's exact test were used to compare categorical variables (statistical significance $p<0.05$).

Results

Of the patients whose results were included in the study, 66.7% were male and 95.8% were Turkish nationals. Of the samples, 34.7% were obtained in 2019, 20.1% in 2021, 18.1% in 2022, 16% in 2020, and 11.1% in 2023. The most frequently detected genotypes were type 1b (34.7%), type 3 (32.6%) and type 1 (15.3%) (Table 1).

The median age of the patients included in the study was determined as 40.00 (29.00-71.00). The median viral load of the patients was determined as 190000 (12500-1519366.50) (Table 2).

When the median ages of the patients were compared according to the detected HCV genotypes, a statistically significant difference was observed ($p<0.001$). In the post-hoc analyses, the difference was attributed to the median age of patients infected with type 3 being lower than that of patients infected with type 4 and type 1b (Table 3).

A statistically significant difference was observed when comparing the median viral loads of patients according to the HCV genotypes detected in patients ($p=0.046$).

In the post-hoc analyses, the difference was attributed to the median viral loads of patients with type 1 being lower than those of patients with type 1b and type 3 (Table 4).

There was a statistically significant difference between the years in which the disease was detected according to HCV genotypes ($p<0.001$). In post-hoc analyses, a lesser number of cases were found in individuals with type 1 genotype in 2019, whereas a greater number of cases were found in 2022 and 2023.

Table 1. Distribution of gender, year, nationality, and genotype

	n	%
Gender		
Male	96	66.7
Female	48	33.3
Year		
2019	50	34.7
2020	23	16.0
2021	29	20.1
2022	26	18.1
2023	16	11.1
Nationality		
Turkish	138	95.8
Foreign	6	4.2
Genotype		
Type 1	22	15.3
Type 1a	7	4.9
Type 1b	50	34.7
Type 2	7	4.9
Type 3	47	32.6
Type 4	5	3.5
Type 1 + Type 1b	2	1.4
Type 1b + Type 3	1	0.7
Type 2 + Type 3	2	1.4
Type 4 + Type 3	1	0.7

Table 2. Age and viral load

	Median (Q1-Q3)	Minimum-maximum
Age	40.00 (29.00-71.00)	18.00-94.00
Viral load	190.000 (12.500-1.519.366,50)	10,00-48.100.000,00

Table 3. Comparison of patient age according to genotype

	n	Median (Q1-Q3)	p-value
Genotype			
Type 1	22	30.50 (24.75-64.25)	<0.001
Type 1a	7	41.00 (32.00-71.00)	
Type 1b	50	67.50 (58.00-79.00)	
Type 2	7	40.00 (31.00-77.00)	
Type 3	47	30.00 (27.00-36.00)	
Type 4	5	57.00 (47.00-77.50)	
Mixed infection	6	59.00 (31.25-73.00)	

In post-hoc analyses, the number of individuals infected with the type 1 genotype was lower in 2019 but was higher in 2022 and 2023. A statistically significant difference was found between the nationalities of the patients based on the HCV genotypes, a statistically significant difference was found (p=0.034). In post-hoc analyses, the rate of infection with genotype 4 was lower in Turkish patients, whereas the rate was higher in foreign patients (Table 5).

Discussion

Hepatitis C infection is a significant public health issue due to its high rate of chronicity, potential for severe liver diseases, various modes of transmission, and the absence of effective vaccines (12). Diagnosis of HCV infection is based on the detection of HCV-specific antibodies using enzyme-linked immunosorbent assay (ELISA). If the ELISA result is positive; HCV viral core antigen or viral genomic RNA (HCV-RNA) must be tested to confirm the diagnosis. In 80-90% of patients, anti-HCV antibodies become positive six to twelve weeks after exposure (13). The identification of HCV genotypes is important for adjusting the dosage of antiviral agents, determining the duration of treatment, monitoring treatment response, and predicting patient prognosis (7,14). Various studies were conducted to investigate the frequency of HCV genotypes in our region and country (Table 6). It has been reported that the majority of HCV infection in Turkey is caused by genotype 1, and its prevalence varies between 57.1% and 97.1% 15). The most common subtype in Turkey is genotype 1b, with a prevalence of 52.7%-97.4% (16,17).

Table 4. Comparison of viral loads according to genotypes

	n	Median (Q1-Q3)	p-value
Genotype			
Type 1	22	22.000,00 (535,00-255.000,00)	0.046
Type 1a	7	390.000,00 (11.085,00-1.800.000,00)	
Type 1b	50	426.204,00 (17.440,00-2.281.547,00)	
Type 2	7	480.000,00 (100.000,00-2.700.000,00)	
Type 3	47	200.000 (21.000,00-1.882.634,00)	
Type 4	5	120.000,00 (7.725,00-7.733.381,50)	
Mixed infection	6	55.000,00 (5.325,00-1.565.894,50)	

In our study, as in previous data, the most frequent genotype was genotype 1 at a rate of 54.9%, and the most common subtype was genotype 1b at a rate of 34.7%. When the relationship between age and genotype was analyzed, the lower age of genotype 3 patients compared with genotype 1b patients was statistically significant. According to the data in the literature, the ages of patients infected with genotype 1 were statistically significantly higher compared with those infected with other genotypes. (18,19). In various studies conducted in Turkey, no statistically significant relationship was found between HCV-RNA load and genotype (15,20).

In our study, the low viral loads of patients infected with genotype 1 were statistically significant compared with those infected with genotypes 1b and 3. We believe that the coronavirus disease 2019 pandemic may lead to variations in the viral loads of infections caused by different HCV genotypes, and the increase in strains that cannot be subtypes may also be related to the pandemic. Different results have been reported in studies investigating genotype distribution and gender association. While some studies have found that genotype 1b is more commonly observed in women and genotype 3 in men, other studies have established that there is no statistical significance between genotype and gender (4,21,22). In a study examining the HCV genotype distribution in Syria between 2004 and 2006, the most frequently detected genotype was 4, with a rate of 59% (23). In various studies conducted in Turkey, the frequency of genotype 4 has been reported as 0-11%. In these studies, it was stated

Table 5. Comparison of gender, year, and nationality according to genotype

	Type 1	Type 1a	Type 1b	Type 2	Type 3	Type 4	Mixed	p-value
Gender								
Male	17 (77.3%)	5 (71.4%)	25 (50.0%)	5 (71.4%)	37 (78.7%)	4 (80.0%)	3 (50.0%)	0.059
Female	5 (22.7%)	2 (28.6%)	25 (50.0%)	2 (21.3%)	10 (21.3%)	1 (20.0%)	3 (50.0%)	
Year								
2019	0 (0.0%)	1 (14.3%)	25 (50.0%)	2 (28.6%)	17 (36.2%)	3 (60.0%)	2 (33.3%)	<0.001
2020	0 (0.0%)	1 (14.3%)	9 (18.0%)	1 (14.3%)	10 (21.3%)	1 (20.0%)	1 (16.7%)	
2021	2 (9.1%)	0 (0.0%)	9 (18.0%)	1 (14.3%)	15 (31.9%)	1 (20.0%)	1 (16.7%)	
2022	10 (45.5%)	3 (6.0%)	3 (6.0%)	3 (42.9%)	5 (10.6%)	0 (0.0%)	2 (33.3%)	
2023	10 (45.5%)	2 (28.6%)	4 (8.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	
Nationality								
Turkish	21 (95.5%)	7 (100.0%)	50 (100.0%)	7 (100.0%)	44 (93.6%)	3 (60.0%)	6 (100.0%)	0.034
Foreign	1 (4.5%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	3 (6.4%)	2 (40.0%)	0 (0.0%)	

that the frequency of genotype 4 was rapidly increasing in our country because of migration as a result of the war in Syria and that its surveillance was important because genotype 4 was more resistant to treatment (23,24). In our study, we detected genotype 4 at a rate of 3.5%, similar to the literature data.

Treatment may fail in patients infected with mixed genotypes. In various studies conducted in our country, the prevalence of mixed genotype has been reported as 0-8.6% (7,25,26).

In our study, the mixed genotype rate was 4.2%, which was in line with the literature. In a study conducted in our hospital in 2019, the most common genotype was genotype 1b at a rate of 58.9%, and it was observed that there was no change in the most dominant genotype in our hospital (18).

Study Limitations

The retrospective nature of our study is one of the limitations due to the inability to identify risk factors and modes of transmission.

Conclusion

In conclusion, the detection of HCV genotypes is important in determining appropriate antiviral therapy, its duration, and monitoring prognosis. Because the genotype distribution in Turkey varies by region, more molecular epidemiological studies on HCV genotypes are required.

Table 6. Percentage of genotype distribution (%) in some studies conducted in Turkey within the last five years

Study	Year	Genotype 1	Genotype 1a	Genotype 1b	Genotype 2	Genotype 3	Genotype 4	Genotype 5	Genotype 6	Mixed
Kuru et al. (23)	2020	-	4.2	85.8	0.6	3	11	-	-	-
Sarı et al. (26)	2020	12.3	12.5	53.7	5.3	11.8	3.6	0.4	-	-
Ağca et al. (27)	2021	5.8	6.1	72.8	2	9.2	2.5	0.1	-	1.5
Özkaya et al. (28)	2021	3.4	3.7	82.8	1.8	6.7	0.9	-	-	0.6
Alacam et al. (29)	2022	2.6	13.2	56.2	6.7	14	8.8	1.3	0.2	8.6
Arıcı et al. (30)	2022	7.5	10.6	59.3	2.6	15.3	2.1	-	-	2.6
Bozlak et al. (11)	2023	-	8.5	71	12	12 (3a)	6	-	-	-
Cırıt et al. (31)	2023	51.5	-	-	1.3	21.4	20	4.6	-	1.23
Our Study	2024	15.3	4.9	34.7	4.9	32.6	3.5	-	-	4.2

Ethics

Ethics Committee Approval: This retrospective study was approved by the Ethics Committee on Non-Medicine and Non-Medical Device Research of Necmettin Erbakan University (decision number: 2024/4963, date: 17.05.2024).

Informed Consent: Retrospective study.

Footnotes

Authorship Contributions

Concept: E.K., A.C., M.Ö., Design: E.K., A.C., M.Ö., Data Collection or Processing: B.E., Analysis or Interpretation: B.E., E.K., A.C., M.Ö., Literature Search: B.E., E.K., A.C., M.Ö., Writing: B.E., M.Ö.

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References

1. Dilbaz N, Kuloğlu M, Evren EC, Paltun SC, Bilici R, Noyan CO, Kulaksizoglu B, Karabulut V, Umut G, Unubol B, Ucbilek E. HCV genotype distribution among people who inject drug in Turkey: findings from multicenter and cross-sectional study. Subst Abuse. 2023;17:11782218231157340.
2. Guntipalli P, Pakala R, Kumari Gara S, Ahmed F, Bhatnagar A, Endaya Coronel MK, Razzack AA, Solimando AG, Thompson A, Andrews K, Enebong Nya G, Ahmad S, Ranaldo R, Cozzolongo R, Shahini E. Worldwide prevalence, genotype distribution and management of hepatitis C. Acta Gastroenterol Belg. 2021;84:637-656.
3. World Health Orfanization. Global hepatitis report 2024. Action for access in low- and middle-income countries. 2024;1:17-19. Available from: https://www.who.int/publications/i/item/9789240091672
4. Tiryaki Y, Çetin Duran A, Özçolpan OO. Distribution of hepatitis C virus genotypes in Aydın province. Viral Hepat J. 2018;24:70-74.
5. Ergünay K, Abacıoğlu H. Clinical impact of hepatitis C virus genomic variations. Mikrobiyol Bul. 2015;49:625-635.(Turkısh).
6. Sanlidağ T, Akçali S, Ozbakkaloğlu B, Ertekin D, Akduman E. Manisa bölgesinde hepatit C virus genotiplerinin dağilimi [Distribution of hepatitis C virus genotypes in Manisa region, Turkey]. Mikrobiyol Bul. 2009;43:613-618. (Turkısh).
7. Selek MB, Baylan O, Karagöz E, Özyurt M. Changes in hepatitis C virus genotype distribution in chronic hepatitis C infection patients. Indian J Med Microbiol. 2018;36:416-421.
8. Robaeys G, Bielen R, Azar DG, Razavi H, Nevens F. Global genotype distribution of hepatitis C viral infection among people who inject drugs. J Hepatol. 2016;65:1094-1103.
9. Petruzziello A, Marigliano S, Loquercio G, Cozzolino A, Cacciapuoti C. Global epidemiology of hepatitis C virus infection: An up-date of the distribution and circulation of hepatitis C virus genotypes. World J Gastroenterol. 2016;22:7824-7840.
10. Gower E, Estes C, Blach S, Razavi-Shearer K, Razavi H. Global epidemiology and genotype distribution of the hepatitis C virus infection. J Hepatol. 2014;61(1 Suppl):S45-57.
11. Balkan Bozlak ÇEB, Gümüs A, Yılmaz A. Hepatitis C genotype assay and sequence analysis at a university hospital in Eastern Türkiye. Kafkas J Med Sci. 2023;13:279-286.
12. Çekin Y, Gür N, Çekin AH, Altuğlu İ, Yazan Sertöz R. Antalya Eğitim ve Araştırma Hastanesinde kronik hepatit C hastalarının genotip dağılımının araştırılması [Investigation of hepatitis C virus genotype distribution in patients with chronic hepatitis C infections in Antalya Training and Research Hospital, Turkey]. Mikrobiyol Bul. 2014;48:484-490.
13. Li HC, Lo SY. Hepatitis C virus: virology, diagnosis and treatment. World J Hepatol. 2015;7:1377-89.
14. Wilson EM, Rosenthal ES, Kattakuzhy S, Tang L, Kottilil S. Clinical laboratory testing in the era of directly acting antiviral therapies for hepatitis C. Clin Microbiol Rev. 2017;30:23-42.
15. Caliskan A, Kirisci O, Ozkaya E, Ozden S, Tumer S, Caglar S, Guler SA, Senol H. Distribution and predominance of genotype 3 in hepatitis C virus carriers in the province of kahramanmaras, Turkey. Hepat Mon. 2015;15:e25142.
16. Gökahmetoğlu S, Atalay MA, Kılınç A. Determination of the hepatitis C virus genotypes with "pyrosequencing" method. Erciyes Medical Journal. 2011;33:99-102.
17. Aktaş E, Ogedey ED, Külah C, Beğendik Cömert F. Zonguldak bölgesinde hepatit C virüsü genotipleri [Hepatitis C virus genotypes in a province of western Black-Sea region, Turkey]. Mikrobiyol Bul. 2010;44:647-650.
18. Gülseren YD, Esenkaya Taşbent F, Özdemir M, Feyzioğlu B. Hepatitis C genotypes in patients with chronic hepatitis C ınfection: a three-year evaluation. FLORA. 2020;25:347-353.(Turkısh).
19. Tüzüner U, Saran Gülcen B, Özdemir M, Feyzioğlu B, Baykan M. Seven-year genotype distribution among hepatitis C patients in a city in the central Anatolia region of Turkey. Viral Hepat J. 2018;24:12-17.
20. Sağlik İ, Mutlu D, Öngut G, İnan D, Öğünç D, Can Sarinoğlu R, Özhak Baysan B, Gültekin M, Çolak D. Akdeniz Üniversitesi Hastanesinde kronik hepatit C enfeksiyonu olan hastalarda hepatit C virüs genotipleri: Beş yıllık sonuçların değerlendirilmesi [Distribution of hepatitis C virus genotypes among patients with chronic hepatitis C infection in Akdeniz University Hospital, Antalya, Turkey: a five-year evaluation]. Mikrobiyol Bul. 2014;48:429-437.
21. Öz S, Köroğlu M, Özbek A, Demiray T, Karabay O, Trak G, Altındiş M. Hepatitis C virus genotype distribution in Sakarya province; three-year retrospective study. OTSBD. Aralık 2019;4:444-453.(Turkısh).
22. Bulut ME, Topalca US, Murat A, Teke L, Canalp HZ, Ocal M, Bayraktar B. HCV genotype distribution of patients with chronic hepatitis C in Istanbul. Sisli Etfal Hastan Tip Bul. 2021;55:86-92.
23. Kuru C, Hamidi AA. Genotype distribution of the hepatitis C virus and demographic features of patients in the province of Karabük. Viral Hepat J. 2020;26:163-166.
24. Altindis M, Dal T, Akyar I, Karatuna O, Gökahmetoğlu S, Tezcan Ulger S, Kulah C, Uzun B, Sener AG, Özdemir M, Aydoğan S, Kuskucu MA, Midilli K, Otlu B, Celen MK, Buruk Kurtulus, Guducuoğlu. Six-year distribution pattern of hepatitis C virus in Turkey: a multicentre study. Biotechnol Biotec Eq. 2015;30:335-340.
25. Kulah C, Altindis M, Akyar I, Gokahmetoglu S, Sayiner A, Kaleli I, Fidan I, Altuglu I, Aydin F, Topkaya A, Us T, Findik D, Ozdemir M, Oztürk E, Ulger ST, Karsligil T, Cekin Y, Aksaray S, Uzunoglu E, Aktas O, Uslu H, Cetinkol Y, Gureser AS, Ece G, Toptan H, Koroglu M, Comert F. The prevalence of mixed genotype infections in turkish patients with hepatitis C: a multicentered assessment. Clin Lab. 2019;65.
26. Sarı ND, Karatas A, İnci A, Yörük G. Evaluation of hepatitis C virus genotype distribution in domestic and foreign patients. Türkiye Klinikleri J Med Sci. 2020;40:148-153.
27. Ağca H, Ener B, Sağlık İ, Yılmaz E, Kazak E. Retrospective evaluation of hepatitis C Virus genotypes. Turk Mikrobiyol Cem Derg. 2021;51:303-308.(Turkısh).
28. Özkaya E, Buruk CK, Aydın F, Kaklıkkaya N, Baran I, Tosun İ. Distribution of hepatitis C virus genotypes: 18 years of experience in an academic center. Viral Hepat J. 2021;27:118-123.
29. Alacam S, Bakir A, Karatas A. Hepatitis C virus genotypes and viremia in a tertiary hospital in Istanbul, Turkey. J Infect Dev Ctries. 2022;16:668-674.
30. Arıcı N, Kansak N, Adaleti R, Aksaray S, Ankaralı H. Distribution of HCV genotypes in local and ınternational chronic hepatitis C patients: a six-year evaluation. ANKEM Derg. 2022;36:101-107.(Turkısh).
31. Cırıt OS, Demir Y, Yıldırım MS, Alpaslan B, Avcıoglu F, Doğan Y, Astam P. Genotype distribution of hepatitis C virus in the province of Gaziantep, a 10-year evaluation. Acta Microbiol Immunol Hung. 2023;70:348-352.