

Epidemiological findings on Hepatitis C infection in a tertiary level hospital in mid-northern Anatolia in Turkey: A four-year analysis

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Received 6 March 2019; received in revised form 16 September 2019; accepted 18 September 2019

Abstract. The hepatitis C virus (HCV) is a blood-borne pathogen that causes acute or chronic infection of the liver, sometimes leading to serious liver damage and fatality. The objective of this study was to evaluate HCV prevalence in patients attending the Regional Training and Research Hospital for Medical Examination and Surgery in Samsun Province of Turkey between 2014 and 2017. Blood specimens taken from 152 596 patients were screened for HCV infection by using the anti-HCV assay. Seropositive samples were subjected to polymerase chain reaction (PCR) testing in order to determine whether the HCV infection was active. Genotyping was then performed. Overall, HCV seropositivity and active HCV infection were 2.76% and 2.05%, respectively. Foreign nationals accounted for 5.61% of the seropositive samples and 1.37% of active HCV infective samples. We further report that 2017 was the year with the highest seroprevalence which was 3.64%. HCV genotype 1 was the most common genotype detected in residents of Samsun Province at 89.86%, followed by Genotype 3 at 4.54%. This study provides important information on the levels of HCV infection in the Samsun region of Turkey. The data indicate that there was a rising trend of HCV infection between 2014 and 2017.

INTRODUCTION

Hepatitis C virus (HCV) is a small, enveloped, single-stranded, positive-sense RNA virus of the genus *Hepacivirus* in the family *Flaviviridae*. HCV causes a persistent infection, which is the most important risk factor in the etiology of fibrosis, chronic hepatitis, cirrhosis and hepatocellular carcinoma (Kwon *et al.*, 2014). More than 185 million people are estimated to be infected with HCV worldwide (Mohd-

Hannifah *et al.*, 2013; Kwon *et al.*, 2014; Messina *et al.*, 2015; Niu *et al.*, 2016). There are many possible routes of transmission of HCV. However, blood transfusion and intravenous drug use are the most common, followed by orodental intervention, body piercing, tattooing, shared shaving equipment and sexual activity during the perinatal period (Villena 2006; Altindis *et al.*, 2016). Seven genotypes of HCV have been reported, comprising 67 confirmed and 20 provisional subtypes identified on the basis of whole

genome sequencing (Messina *et al.*, 2015; Nyan *et al.*, 2016). The different HCV genotypes have distinct geographical distributions worldwide (Chen *et al.*, 2017). Genotypes 1, 2 and 3, which are described as epidemic strains, have a wide distribution across the globe, whereas genotypes 4, 5 and 6, which are described as endemic strains, are only normally found in certain areas (Gower *et al.*, 2014; Messina *et al.*, 2015; Chen *et al.*, 2017). In Turkey, six genotypes have been reported in previous studies, among which genotype 1 was the most prevalent.

The aim of this study was to investigate the HCV prevalence in a tertiary level hospital in Samsun, Turkey from 2012 to 2017.

MATERIALS AND METHODS

Approval for this study was received from the Clinical Research Ethics Board of Samsun Training and Research Hospital [reference number EAH/ KAEK / KS-143-2017/20 of October, 2017].

This study was conducted at the Samsun Training and Research Hospital, a tertiary level hospital in Samsun which is the biggest city on the northern coast of Turkey with a population over one million, providing health care services to approximately 750,000–800,000 people every year. The HCV-related laboratory data of 152,596 patients who came to the various clinics of the hospital for medical examination and surgery between 2014 and 2017 was collated. Patients were categorized in six age groups. Patients up to 18 years of age were included in the ‘children’ group, which was subdivided into the 0–14 and the 15–18 age ranges. Patients over 19 years of age were included in the adults group that was subdivided into four age categories, namely, 19–35, 36–54, 55–70 and > 70 years. Only the first specimen of patients who had provided multiple specimens was evaluated.

In order to detect antibodies against HCV, serum samples were tested using a fully automated electrochemiluminescence immunoassay (Elecsys Anti-HCV immunoassay, Roche Diagnostics, Germany) on a Modular Analytics E170 analyzer, according to the manufacturer’s instructions. The results

were interpreted by assessment of the cut-off index COI (signal sample/signal cutoff). A COI <0.90 was considered non-reactive, a COI between 0.90 and 1.0 was interpreted as indeterminate, and a COI ≥ 1.0 was interpreted as reactive.

To determine whether HCV patients were viremic, the quantity of HCV-RNA in seropositive serum samples was investigated by using the real-time PCR based COBAS ampliprep/COBAS Taqman HCV-RNA assay (Roche Diagnostics, Germany). A value of <15 UI/ml was accepted as the lower limit of quantitation for HCV-RNA positivity. HCV-RNA positive samples were sent to the Duzen Laboratories (Ankara, Turkey, www.duzen.com.tr) for genotyping.

The data was categorized by year, gender and age group. Due to the presence of discrete variables in the dataset, non-parametric analytical methods were used. For the evaluation of some categories with an unbalanced number of subjects or that had less than 5 subjects, statistical calculations and the estimation of asymptotic standard error was carried out using the modelling technique described by Ogasawara (2002). The comparisons by year, gender and age, the distribution of anti-HCV antibodies, and HCV-RNA and RNA sub/genotypic frequencies, were analysed with a Bayesian approach (Alkema *et al.*, 2007). Accordingly, confidence intervals were calculated with asymptotic standard errors in structural equation modelling (Gardner & Altman 1989). All analyses and calculations were performed with version 9.8.3 of the SAS software (2009).

RESULTS

In this study, the data of 152,596 patients with a mean age of 48.48 years \pm 0.05 were evaluated. Both demographic data of this study and the results of the tested patients had been distributed in Table 1, according to gender, years, age groups and nationality variables. The overall anti-HCV seropositivity was 2.76%, whereas it was also found to be 2.37% and 3.25% for males and females, respectively. The anti-HCV prevalence in

Table 1. The distribution of anti-HCV and HCV-RNA status of tested patients with according to patient characteristics

Variables	No of tested	% of tested	HCV status					
			Anti-HCV			HCV-RNA		
			positive	%	<i>P</i>	positive	%	<i>P</i>
Genders*								
Female	67 144	44.01	2 182	3.25	<0.0001	1 634	2.43	<0.001
Male	85 452	55.99	2 024	2.37		1 492	1.75	
Years								
2014	45 032	29.51	1 144	2.54	<0.0001	656	1.46	<0.001
2015	48 711	31.92	1 145	2.35		912	1.87	
2016	28 714	18.81	820	2.86		647	2.25	
2017	30 139	19.75	1 097	3.64		911	3.02	
Age Groups								
0-14	2 887	1.89	27	0.94	<0.0001	14	0.48	<0.001
15-18	4 417	2.89	60	1.36		48	1.09	
19-35	36 534	23.94	725	1.98		725	2.28	
36-54	46 873	30.72	1 070	2.28		838	1.79	
55-70	37 794	24.77	1 422	3.76		1 103	2.92	
>70	24 091	15.79	902	3.74		584	2.42	
Nationality								
Turkish	152 032	99.63	3 970	2.60		3 083	2.01	
Foreign	564	0.37	236	0.16		43	0.04	
Total	152 596	100.00	4 206	2.76		3 126	2.05	

* mean age of t 48.48 years ± 0.05.

females was significantly higher than in males ($P<0.0001$). The years 2015 and 2017 had the lowest and highest anti-HCV prevalences at 2.35% and 3.64%, respectively. There was a highly significant difference for anti-HCV prevalence across the individual years of the 4-year study ($P<0.0001$).

As detailed in Table 2, we report a significant difference in the prevalence of HCV antibodies in the different years and genders ($P<0.0001$). The anti-HCV prevalence across the analyzed period from 2014 to 2017 increased significantly for both genders from 1.98% to 3.08% for males and 2.83% to 4.32% for females ($P<0.0001$). The highest prevalence rates for gender for both males and females were in 2017, while the lowest prevalence rates for both genders were in 2015. Furthermore, there were highly significant differences between the genders within years ($P<0.001$). As seen in Table 3, there were statistically significant differences in the overall rates of HCV

antibody prevalence by age group and year, with the highest seroprevalences in the 55–70 and >70 year age groups at 3.76% and 3.74%, respectively ($P<0.001$). There were significant increases in anti-HCV antibody prevalence in the 55–70 age group from 3.18% to 5.17% and the >70 age group from 2.88% to 6.25% between 2014 and 2017. In contrast, there were significant decreases in the anti-HCV prevalence in the 15–18 age group from 2.45% to 1.05% ($P=0.002$), and the 19–35 age group from 2.07% to 1.83% ($P=0.041$) in the same period. No anti-HCV prevalence could be determined in the 0–14 age group in 2016 and 2017.

78.38% (3,297/4,206) of patients who were anti-HCV positive were screened for HCV-RNA using real-time RT-PCR. 21.62% (909/4,206) of patients could not be screened for HCV-RNA because they did not return to the hospital. The results for the HCV viremic patients were detailed in Tables 1, 4 and 5. The overall HCV-RNA positivity was 2.05%.

Table 2. The distribution of anti-HCV positive patients according to the gender and years

Gender	Years				<i>P</i>
	2014	2015	2016	2017	
Female (%)	2.98	2.83	3.20	4.32	<0.0001
n/N	572/19 175	596/21 024	430/13 439	584/13 506	
Male (%)	2.21	1.98	2.55	3.08	
n/N	572/25 857	549/27 687	390/15 275	513/16 633	

N: the total number of patients tested; n: the number of anti-HCV positives patients.

Table 3. The distribution of Anti-HCV seropositivity according to age groups and years

Age Groups	Anti-HCV (+)	Years				<i>P</i>
		2014	2015	2016	2017	
0–14 (%)	0.94	2.27	0.97	–	–	<0.001
n/N	27/2 887	18/792	9/930	**/578	**/587	
15–18 (%)	1.36	2.45	0.72	1.53	1.05	=0.002
n/N	60/4 417	26/1 061	11/1525	12/782	11/1 049	
19–35 (%)	1.98	2.07	1.80	2.37	2.82	=0.041
n/N	725/36 534	233/11 253	219/12 179	145/6 106	128/6996	
36–54 (%)	2.28	2.29	2.02	2.18	2.82	<0.001
n/N	1070/46 873	327/14 267	305/15 068	191/8 784	247/8 754	
55–70 (%)	3.76	3.18	3.34	3.76	5.17	<0.001
n/N	1422/37 794	337/10 614	386/11 561	289/7 684	410/7 936	
>70 (%)	3.74	2.88	2.89	3.83	6.25	<0.001
n/N	902/24 091	203/745	215/7 448	183/4 780	301/4 817	

** No positive could be detected; n: positives; N: the total number of patients tested.

Table 4. Distribution of HCV-RNA positive patients according to genders and years. (n=3126)

Gender	HCV-RNA (+)	Years				<i>P</i>
		2014	2015	2016	2017	
Female (%)	2.43	1.78	2.32	2.50	3.47	<0.001
n/N	1634/67 144	341/19 175	487/21 024	336/13 439	470/13 506	
Male (%)	1.75	1.22	1.54	2.04	2.65	
n/N	1492/85 452	315/25 857	425/27 687	311/15 275	441/16 633	

N: the total number of patients tested; n: positives.

The percentages of HCV-RNA prevalence were 2.43% for females ($P < 0.001$) and 1.75% for males ($P < 0.001$) (Table 4). The HCV-RNA prevalence in females was significantly

higher than in males. In addition, we found a statistically significant difference among the years; with the highest percentage of viremic patients being in 2017 (3.02%) and

Table 5. Distribution of viremic HCV patients according to age groups and years (n=3126)

Age Groups (%)	HCV-RNA (+)	Years				P
		2014	2015	2016	2017	
0–14 n/N	0.48 14/2 887	0.63 5/792	0.97 9/930	– **/578	– **/587	<0.001
15–18 n/N	1.09 48/4 417	1.51 16/1 061	0.66 10/1 525	1.41 11/782	1.05 11/1 049	<0.001
19–35 n/N	1.48 539/36 534	0.95 107/11 253	1.56 190/12 179	2.15 131/6 106	1.59 111/6 996	=0.041
36–54 n/N	1.79 838/46 873	1.43 204/14 267	1.71 258/15 068	1.90 167/8 784	2.39 209/8 754	<0.001
55–70 n/N	2.92 1103/37 794	2.06 219/10 614	2.72 314/11 561	2.95 227/7 684	4.32 343/7 936	<0.001
>70 n/N	2.42 584/24 091	1.49 105/745	1.76 131/7 448	2.32 111/4 780	4.92 237/4 817	<0.001

** No positive could be detected; n: positives; N: the total number of patients tested.

the lowest (1.46%) in 2014 ($P<0.001$, Table 1). Furthermore the HCV-RNA prevalence was higher in the 55–70 and >70 years age groups than in the other age groups in 2017 ($P<0.001$, Table 5).

All results related to genotyping are presented in Table 4. We performed genotype analysis of 858 samples of the 3,126 HCV-RNA positive samples, of which 410 (47.78%) were from males and 448 (52.22%) from females; 97.1% of the 858 samples were from Turkish citizens and 2.9% were from foreign citizens. Genotype 1, including subtypes 1b (79.72%) and 1a (10.14%) were the most common at 89.86%, followed by genotype 3, including subtype 3a, at 4.54%, and with genotypes 2 and 4 both at 2.80%. Subtype 1b was the most common between 2014 and 2017 at 79.72% compared to subtypes 1a and 3a, which were the second and the third most prevalent at 10.14% and 1.17%, respectively. Furthermore, there were significant differences in genotype frequency for years ($P<0.001$). However, there were no differences in the frequency of genotypes between 2014 and 2016 ($P>0.05$). Although the increment in the prevalence of genotype 1a was more than for the other genotypes ($P<0.001$), there were remarkable increases in the prevalence of all genotypes. Genotype 3a was not detected in Samsun in 2014 or

2015 but it was detected in 2016 and 2017 at 0.12% and 1.05%, respectively. In addition, there was an incidence of 0.35% of genotype 4 in 2014. However, it was not detected in 2015 and 2016 but the incidence increased sharply to 2.45% in 2017. There were increases in the incidences of genotypes 2 and 4 in 2017 compared to 2014, although the differences were not significant ($P>0.05$). Details of HCV genotyping for genders and year are also detailed in Table 5. The prevalences of genotypes 3 and 4 were higher in males at 1.86% and 1.51%, respectively, than in females at 1.51% and 1.29%, respectively. Conversely, the prevalences of subtypes 1a, 1b and 3a were slightly higher in females than in males. Separately, genotype 2 was found in equal proportions in females and males at 1.40%.

As can be seen in Table 6, the data for genotype distribution and the age groups 0–14 and 15–18 was not assessed statistically due to insufficient data. However, all of the identified HCV genotypes, with the exception of genotype 1, were detected in the age groups 19–35, 36–54, 55–70 and >70 years. Genotype 1b was identified in all age groups; the highest values were for the 55–70 and >70 year age groups at 30.07% and 18.53%, respectively ($P<0.001$).

The results for foreigners are in Table 7. Of the 152 596 patients, 564 (0.37%) were foreign nationals, of whom the vast majority (67.55%) are from Syria, followed by Iraq (19.86%). The rest (12.59%) came from Asian and European countries. Of the foreign nationals, 41.84% (236/564) were anti-HCV positive. In addition, the proportion of seropositive foreign nationals of all seropositive cases was 5.61% (236/4206). The percentage of anti-HCV positivity was

higher for foreign nationals than for Turkish citizens ($P < 0.001$, Table 6). Of the anti-HCV positive foreign nationals, only 18.22% (43/236) were checked for HCV-RNA because 193 of them did not return to the clinics.

Genotyping was conducted in 25 of 43 HCV-RNA positive foreign citizens, whereas 18 were not be tested due to insufficient RNA amounts. Although they had been called back in order to do resampling, but the return also did not materialize. In the

Table 6. Distribution of viremic patients who were performed genotyping according to gender, age groups years and HCV genotypes (n=858)

Variables	Genotypes						Total	P
	1a	1b	2	3	3a	4		
Sex n/ (%)								
Female	52/6.06	354/41.25	12/1.40	13/1.51	6/0.70	11/1.28	448/52.21	=0.027
Male	35/4.07	330/38.46	12/1.39	16/1.86	4/0.47	13/1.51	410/47.79	
Ages n/ (%)								
0-14	-	2/0.23	-	-	-	-	2/0.23	NA
15-18	1/0.16	6/0.70	-	-	1/0.16	-	8/0.93	=0.043
19-35	9/1.10	105/12.23	1/0.16	9/1.10	1/0.16	4/0.46	129/15.03	<0.001
36-54	171/9.81	154/17.94	9/1.10	11/1.28	2/0.23	4/0.46	197/22.96	<0.001
55-70	24/7.97	258/30.07	7/0.81	2/0.23	3/0.35	11/1.28	315/36.71	<0.001
>70	26/3.03	159/18.53	7/0.81	7/0.81	3/0.35	5/0.58	207/29.95	<0.001
Years n/ (%)								
2014	8/0.93	120/13.98	1/0.16	2/0.23	-	3/0.35	134/15.61	<0.001
2015	3/0.35	209/24.35	3/0.35	-	-	-	215/25.05	<0.001
2016	2/0.23	103/12.00	-	2/0.23	1/0.16	-	108/12.59	<0.001
2017	74/8.62	252/29.37	20/2.33	25/29.13	9/1.10	21/2.44	401/46.75	<0.001
Total n/ (%)	87/10.30	684/79.72	24/2.78	29/3.37	10/1.16	24/2.78	858/100.0	<0.001

Table 7. The nationality distribution of foreign nationals and the results of anti-HCV and HCV-RNA prevalences with the distribution of genotypes (n=564)

Nationality	Total n/%	Anti-HCV Positivity n/%	HCV-RNA Positivity (%)	Genotypes					
				1a	1b	2	3	3a	4
Azerbaijan	5/0.88	2/0.05	2/0.06					1	
Georgia	6/1.06	1/0.02	1/0.03		1				
Iran	1/0.18	1/0.02	1/0.03					1	
Pakistan	2/0.35	2/0.02	2/0.06		2				
Syria	381/67.55	21/45.09	2/70.86	2	9		1		2
Iraq	112/19.85	4/0.09	4/0.12		2				1
Russia	8/1.41	6/0.14	5/0.16		1			2	
Others	49/8.68	6/0.14	1/0.03						
Total n/%	564/0.37	23/65.61	43/1.38	2/0.23	15/1.75		1/1.16	4/0.46	3/0.34

genotype distribution among foreign citizens, 1b was the most prevalent at 1.75%, followed by 3a at 0.47%, and 4 at 0.35%. The proportions for genotype 1a and 3 were lower at 0.23% and 0.12%, respectively, and genotype 2 was not detected.

DISCUSSION

Viral hepatitis is one of the leading causes of death worldwide. As of 2015, approximately 325 million people were living with chronic viral hepatitis infection, with a resulting death toll of 1.35 million (WHO 2017). An estimated 71 million people worldwide are also reported to have chronic hepatitis stemming from HCV, including approximately 1.75 million newly infected people at the end of 2015 (Polaris Observatory 2015). HCV-related diseases are of growing global concern due to the burdens they place on the health of individuals and the resulting personal and socioeconomic costs (Razavi *et al.*, 2013).

The worldwide anti-HCV prevalence was reported at 1.6%, corresponding to 115 million people in 2015. In the European Union (EU) countries, the HCV seroprevalence ranged between 0.1% and 5.9% (Polaris Observatory 2015). HCV seroprevalence was also reported to be greater than 5% in some African and Asian countries (Manns *et al.*, 2017). According to previous studies, the HCV seroprevalence in Turkey ranged between 0.6% and 2.1% (Yildirim *et al.*, 2009; Gultepe *et al.*, 2013; Tozun *et al.*, 2015). In the current study in Samsun, Turkey, the anti-HCV prevalence was 2.76%, revealing a higher rate than the overall HCV prevalence rate in Turkey.

Furthermore, HCV seroprevalence considerably increased from 2.54% to 3.64% between 2014 and 2017. This can be attributed to a number of risk factors such as surgical and orodental interventions, mother-to-child transmission, unsafe sexual practices and close contact with HCV-carriers (Aygen *et al.*, 2017). Being over 50 years of age was also reported to be a major risk factor for HCV seropositivity in Turkey (Tozun *et al.*, 2015). In our study, the gender-

related HCV seropositivities were higher than reported in previous studies (Yildirim *et al.*, 2009; Gultepe *et al.*, 2013), and more frequently observed in females. Furthermore, there was a substantial increase in the prevalence in the 55–70 and >70 age groups. Before 1989, patients who were being subjected to surgical intervention, orodental intervention and transfusions of blood or its products were likely to be at risk of HCV infection. In particular, female patients who are now ≥ 50 years of age could have also been infected through gynecological interventions when they were between 20 and 30 years old.

In the present study, a total of 564 patients of foreign nationality, whom most of them were from Syria, were checked for anti-HCV antibodies, and the overall seropositivity was 5.61%, which may be interpreted as a risk factor for local residents.

The global estimated prevalence of viremic HCV was reported to be 1.0%, corresponding to 71.1 million viremic infections (Ambachew *et al.*, 2019). There are differences in the distribution of HCV prevalence among regions. It has reported that the prevalence of HCV viremic individuals is 0.5%–0.7% in the Asia-Pacific region, 1.9%–6.4% in Central Asia, 0.2–2.1% in East Asia, 0.5%–3.8% in South Asia, 0.3%–2.5% in Central Europe, 1.1%–3.3% in Eastern Europe, 0.1%–1.2% in Western Europe, 0.3%–0.9% in Central and South America, 0.6%–1.0% in North America, and 0.2%–6.3% in North Africa and the Middle East (Polaris Observatory 2015). In Turkey, the prevalence of viremic HCV infections was 0.8%, which is considered to be a low value (Polaris Observatory 2015). However, the mean viremic HCV prevalence in Samsun was 2.05% in the current study, with an alarming increase from 1.46% to 3.02% between 2014 and 2017. In the current study, many factors may have paved the way for the rise in the prevalence of viremic HCV in Samsun. Among them, the non-awareness of individuals of their positive HCV infection status; low economic status of many patients; low education levels; body piercing, tattooing and acupuncture practices; orodental and surgical interventions; unsafe sexual

practices; and close contact with HCV positive patients, may be contributing to the increase of HCV prevalence.

The current study also revealed that the prevalence of viremic HCV infections in Samsun was higher in females than in most other studies (Umumararungu *et al.*, 2017; Nazir *et al.*, 2017). The higher infection rate of females may be related to sexual contact with their spouses who are not aware that they are HCV carriers, possibly as a consequence of having unprotected sex with an infected person, as well as the above-mentioned factors.

In our study, the genotype 1 was the most common HCV genotype detected in Samsun among both local residents and foreign nationals living there. In previous studies carried out in Turkey, genotype 1b, with a prevalence rate of over 60%, was reported to be the most common among the HCV genotypes (Sağlık *et al.*, 2014; Altindis *et al.*, 2016). Moreover, it was also reported at 97.4% in the north-western part of the Black Sea region of Turkey. In current study, the prevalence of 1b at 79.72% was higher than the average percentage in Turkey, whereas it was lower than reported in the north-western area of the Black Sea region (Aktas *et al.*, 2010). Furthermore, our results were consistent with the rates in Europe, including Romania, Latvia, Estonia, Lithuania, Italy and Portugal. Additionally, genotype 1b was the most commonly detected type in foreign nationals from the Middle East, in contrast to a previous report indicating the dominance of genotype 3a among foreigners from the Middle East (Sağlık *et al.*, 2014). The dominance of genotype 1b among foreign nationals reported here is interesting given that the vast majority of them came from Syria and Iraq where genotype 4 was earlier reported to be most common genotype (Polaris Observatory 2015). Separately, the current study demonstrated an approximately 9-fold increase in the percentage of genotype 1a in 2017 in comparison to 2014. Significant increase in the prevalences of genotypes 3 and 4 were also demonstrated in 2017 in the current study, although the incidences were still lower than the overall percentages that were reported for both

genotypes 3 and 4 at 6.7% and 7.3%, respectively, in an earlier study (Altindis *et al.*, 2016). The refugee movement from Syria and Iraq may have played a small role in these increments due the fact that both genotypes have been reported as more prevalent in the Middle East and North Africa; the prevalences of genotypes 3 and 4 were reported to be 1.8% and 59.0% for Syria, respectively, and 17.1% and 52% for Iraq, respectively (Kwon *et al.*, 2014).

In our study, the prevalence of active HCV infection increased in patients over 55 years of age. This data is consistent with previous studies reported from Turkey (Altindis *et al.*, 2016) and other countries, including the USA (Ditah *et al.*, 2014), Rwanda (Umumararungu *et al.*, 2017), Pakistan (Nazir *et al.*, 2017) and Uganda (Abdel-Azez *et al.*, 2000). In Italy, Petruzzello *et al.* (2013) reported a higher prevalence of genotype 1b in patients between 51 and 60 years of age. Likewise, Altindis *et al.* reported that genotype 1b was the most prevalent in patients over 55 in Turkey, which is also in agreement with our results.

One of the main limitations of the present study was the number of seropositive patients who did not return to the hospital for HCV-RNA testing, i.e., 21.62% and 81.77% for Turkish citizens and foreign nationals, respectively. Interestingly, the percentage of seropositivity among foreign nationals who did not return for HCV-RNA testing was remarkably higher than for those who did return for HCV-RNA testing. This was the case not only for foreign nationals but also for Turkish citizens; these people who were diagnosed as HCV positive but are not receiving treatment pose a substantial risk to public health.

CONCLUSIONS

HCV is an acknowledged global health problem and WHO has a strategic plan to eradicate it worldwide by 2030. In this context, surveillance and epidemiological studies are critical to the achievement of the eradication goal. There is a need to develop and implement large and exhaustive

studies to reveal the epidemiological situation regarding HCV right across Turkey. Our study showed a remarkable increase in HCV infection in Samsun during the short period analysed, namely 2014 to 2017. In light of these results, we recommend urgent planning for further studies and the implementation of health policies and practices that increase the level of detection of HCV and its treatment, as well as control strategies, e.g. the counselling of affected individuals and the implementation of community awareness and education campaigns at the local, regional and national levels that can contribute to the eradication of this disease across Turkey.

Conflicts of Interest

All authors declare that they have no conflict of interests.

Acknowledgements. The authors thank Gregory T. Sullivan for helpful comments and the proof reading of a nearlier version of the manuscript.

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