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Epidemiological Study of Hepatitis C Virus Infections and Their Genotypes in the Iraqi Population During 2022

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Abstract:

Background: The Hepatitis C virus (HCV) is thought to infect 170 million people globally, making it a viral pandemic. Most people with HCV infection progress to chronic illness, and infection with the virus is now the primary cause of liver transplantation. **Objective:** This paper assesses HCV infection prevalence and genotype distribution across fourteen provinces in Iraq, investigates the main reasons for virus transmission, and determines the correlation between viral load and infection with different genotypes/subtypes among the Iraqi population in 2022. **Methods:** In this epidemiological study, 738 specimens were analyzed using Enzyme-linked immunosorbent assay (ELISA), chemiluminescent immunoassay, real-time polymerase chain reaction (RT-PCR), and Western blot procedures to detect HCV infections. **Results:** Most specimens, 94.2%, tested positive for HCV, and various genotypes/subtypes were identified. The study found the highest frequency of HCV infections in June and a geographical prevalence with the most significant number of cases in Baghdad. Viral load analysis showed significant stratification across age groups, sex, and the presence of different viral genotypes/subtypes. It also showed that HCV infections were significantly associated with detection sources such as surgical procedures, renal failure, and thalassemia tests. **Conclusion:** This study underscores the importance of blood-borne transmission of HCV in Iraq and calls for enhanced preventive measures. The findings stress the need for effective therapies and potential vaccine development, given the global impact of HCV. The research is supported by references discussing hepatitis C spread and management, highlighting the challenges faced in different regions and patient demographics. Future research based on the findings presented in the referenced research paper should prioritize in-depth studies into the behavioral, medical, and socioeconomic factors contributing to the high prevalence of HCV in the Iraqi population. These could include longitudinal studies to monitor the long-term efficacy of preventive measures and treatment protocols in various demographic groups. Moreover, genetic studies would be beneficial in understanding the relationships between HCV genotypes/subtypes and disease progression or therapeutic outcomes better.

Keywords: HCV, genotypes, Iraqi provinces, RT-PCR, ELISA.

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الكشف عن اصابات فيروس التهاب الكبد الوبائي نوع سي وأنماطها الوراثية في المجتمع العراقي خلال عام 2022

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الخلاصة:

يُعتقد أن فيروس التهاب الكبد الوبائي نوع سي يصيب 170 مليون شخص على مستوى العالم، مما يجعله وباءً فيروسيًا. يتطور معظم الأشخاص المصابين بعدوى فيروس التهاب الكبد إلى مرض مزمن، وتعد الإصابة بالفيروس الآن السبب الرئيسي لزراعة الكبد. تهدف هذه الدراسة الى تقييم مدى انتشار وتوزيع النمط الوراثي لعدوى فيروس التهاب الكبد الوبائي نوع (سي) عبر أربعة عشر محافظة في العراق، وتبحث في الأسباب الرئيسية لانتقال الفيروس، وتحدد العلاقة بين الحمل الفيروسي والعدوى بالأنماط الوراثية وأنواعها الفرعية المختلفة بين السكان العراقيين في عام 2022. طرق العمل: في هذه الدراسة الوبائية، تم تحليل 738 عينة باستخدام اربعة انواع من الاختبارات تتضمن: *ELISA*، والمقايسة المناعية الكيميائية، و*RT–PCR*، Western blot للكشف عن عدوى فيروس التهاب الكبد *C*. النتائج: كانت نتيجة اختبار غالبية العينات، 94.2%، إيجابية لفيروس التهاب الكبد الوبائي (سي)، وتم تحديد بالأنماط الوراثية وأنواعها الفرعية المختلفة. ووجدت الدراسة أن أعلى معدل لتكرار الإصابة بفيروس التهاب الكبد الوبائي سي في شهر حزيران/يونيو، وانتشار جغرافي مع أكبر عدد من الحالات في بغداد. أظهر تحليل الحمل الفيروسي *viral load* وجود اصابات كثيرة عبر الفئات العمرية والجنس ووجود أنماط وراثية وأنواع فرعية فيروسية مختلفة. كما أظهر أيضًا أن عدوى فيروس التهاب الكبد الوبائي (سي) ارتبطت بشكل كبير بمصادر الكشف مثل العمليات الجراحية والفشل الكلوي واختبارات الثلاسيميا. الاستنتاج: تؤكد هذه الدراسة على أهمية انتقال فيروس التهاب الكبد الوبائي (سي) عن طريق الدم في العراق وتدعو إلى تعزيز التدابير الوقائية. وتؤكد النتائج على الحاجة إلى علاجات فعالة وتطوير لقاحات محتملة، نظرا للتأثير العالمي لفيروس التهاب الكبد الوبائي. يتم دعم البحث بمراجع تناقش انتشار التهاب الكبد *C* وإدارته، مع تسليط الضوء على التحديات التي تواجهها المناطق المختلفة والتركيبة السكانية للمرضى. يجب أن تعطي الأبحاث المستقبلية المستندة إلى النتائج المقدمة في هذا البحث الأولوية للدراسات المتعمقة حول العوامل السلوكية والطبية والاجتماعية والاقتصادية التي تساهم في ارتفاع معدل انتشار فيروس التهاب الكبد الوبائي (سي) بين السكان العراقيين. ويمكن أن تشمل هذه الدراسات رصد فعالية التدابير الوقائية وبروتوكولات العلاج على المدى الطويل في مختلف المجموعات السكانية. علاوة على ذلك، فإن الدراسات الجينية لفهم العلاقات بين الأنماط الجينية و الانواع الفرعية لفيروس التهاب الكبد *C* وتطور المرض و نتائجها العلاجية ستكون مفيدة بشكل أفضل.

1. Introduction

The hepatitis C virus (HCV) is thought to infect 170 million people globally, making it a viral pandemic. Most people with HCV infection progress to chronic illness, and infection with the virus is now the primary cause of liver transplantation [1]. The most closely related human viruses are dengue virus, yellow fever virus, and hepatitis G virus. HCV is a ribonucleic acid virus (RNA) virus that is a member of the flavivirus family, which primarily attacks hepatocytes and potentially B lymphocytes [2]. The RNA-dependent RNA polymerase used by viruses to replicate is incredibly robust and does not have a "proofreading" function. This allows viruses to evolve into distinct but related quasispecies within infected individuals quickly and poses a significant obstacle to immune-mediated control of HCV. Membrane-associated viral replication takes place in the cytoplasm, and

assembly and release through secretory pathways are coupled to lipoprotein biogenesis [3]. Based on molecular relatedness, numerous subtypes and six unique but related HCV genotypes have been discovered. The most prevalent genotypes in the United States (US) and Western Europe are 1a and 1b, followed by 2 and 3. Although prevalent in other regions- such as Egypt for genotype 4, South Africa for genotype 5, and Southeast Asia for genotype 6- the other genotypes are almost nonexistent in these nations. Meanwhile, 1a genotype/subtype, 1b genotype, 4 genotype, 4a genotype, 4c/d genotype, 4h genotype, and finally, 6 t genotype are detected by this study to be present in Iraq. Understanding one's genotype is crucial since it can be used to predict how an antiviral treatment will work; genotypes 2 and 3 are linked to stronger responses than genotypes 1 [4,5,6]. The majority of people who contract HCV have persistent viremia along with varying degrees of fibrosis and inflammation in their livers. While more estimates indicate that at least 50% of hepatocytes harbor the virus [7]. Only a tiny portion of hepatocytes may become infected, according to earlier research on persistent HCV infection. It has been suggested that the existence of lymphocytes in the hepatic parenchyma is proof of immune-mediated injury. The establishment and maintenance of potent, virus-specific responses by helper T cells and cytotoxic T lymphocytes is linked to viral clearance [8]. Helper T cell responses seem crucial since viremia's resurgence has been associated with the depletion of these cells. Individuals with chronic HCV infection appear to have a relatively weak response from cytotoxic T cells, which is sufficient to inflict collateral damage through the development of inflammatory cytokines in the liver but not enough to contain viremia and genetic evolution of the virus [9]. The incidence of superinfection with different genotypes and, in animal models, reinfection upon re-challenge with closely related strains are additional indications that individuals with chronic HCV infection may not have good immunity. The investigation of HCV infections in the Iraqi population was prompted by the fact that HCV infections are five times more common than HIV-1 infections and that nosocomial transmission of the infection from patient to patient via colonoscopy, dialysis, and surgery was the primary cause of infection. This study aimed to detect different genotypes in Iraq to support the database for their presence in the country and their mode of detection to limit virus transmission.

2- Materials and Methods

2.1 Data source

A total of 738 suspected blood specimens were collected from January to December 2022 in 14 Iraqi provinces. Serum or plasma was extracted from specimens for initial screening of HCV and transporting of samples in cooled boxes with ice packs to the Referral Laboratory /Central Public Health Laboratory (CPHL) in Baghdad for diagnosis. The collected samples were 728 Iraqi and 10 foreign individuals. Collected specimens were from patients whose ages ranged from 3 years to 76 years old (36.2±16.8) and were 406 males and 332 females.

2.2 Diagnosis of HCV infection

2.2.1 Serological analysis by using the ELISA technique

Antibodies for hepatitis C virus (HCV) ELISA test kit (Fortress U.K) was used to determine levels of HCV antibodies in the serum or plasma of suspected patients. This kit is a solid-phase enzyme-linked immunosorbent assay based on the principle of indirect ELISA for detecting of various antibodies against HCV in human serum or plasma. Purified HCV antigen is pre-coated on the microplate, and the enzyme-labeled anti-HCV complex will combine with HCV antibody in human serum or plasma. Add 100 µl diluent, then 10µl of controls and suspected serum or plasma was added to a solid micro well pre-coated with recombinant HCV antigens, and wells were covered with a sealer and incubated at 37°c for 30

minutes. After a washing step, 100 µl of conjugate was added to each well and incubated at 37° c for 30 minutes. After the washing step, 50 µl of TMB substrate A and 50 µl of TMB substrate B were added into each well and incubated at 37° c for 15 minutes. The reaction was stopped by adding 50 µl of stop solution. The wavelength was red at 450-630 nm within 10 minutes. Specimens with OD ratio ≥ 1.00 were initially considered positive and were re-tested in duplicate before a final interpretation was made.

2.2.2 Real-time PCR

HCV Real-TM Quant Dx kit (Sacace, Italy) was used to detect HCV in the plasma of suspected humans qualitatively. HCV Real-TM Quant Dx Kit is a Real-Time test for the quantitative detection of the HCV in human plasma or serum. After HCV RNA was extracted, a real-time PCR technique was used for amplification and delectation of HCV or HCV IC utilizing probes specific with fluorescent reporter dye. During the amplification, in each thermal cycle the PCR products at high temperatures separated into single strands, following primer annealing and extension when the temperature is lowered. A billion-fold or considerable amount of target sequences was exponentially amplified during repeated cycling PCR. Fluorescent reporter dye allows monitoring the detection and quantification of the target sequences without needing to open the reaction tube or using a gel after the amplification. For each individually processed specimen, the Internal Control (IC) serves as an extraction and an amplification control to identify possible inhibition. IC is detected in another channel rather than the HCV RNA. HCVIC-L is a lyophilized Internal Control and represents recombinant RNA-containing-structure which carried through all steps of analysis, from nucleic acid extraction to PCR amplification-detection. The inclusion of HCV Rec IC facilitates the monitoring of the extraction process, assessment of potential PCR inhibition, and verification of RNA loss during extraction, hence allowing for accurate calculation of HCV viral load. The assay has been verified against the 4th WHO International Standard for HCV for Nucleic Acid Amplification Techniques (NIBSC code: 06/102 15), with results expressed in International Units/mL (IU/mL). The target sequence for the HCV Real-TM Quant Dx assay is in the 5′utr region of the HCV genome, which is a highly conserved specific region for HCV. SaMag Viral Nucleic Acids Extraction Kit (Sacace REF SM003) automated nucleic acid purification system was used for HCV-RNA extraction. 50 µl of eluted suspected serum or plasma samples were obtained from the RNA purification step, and tubes were closed and placed in a Real-time PCR instrument to run as follows: hold step at 50 ºC for 15 minutes, hold step at 95 ºC for 15 minutes. After that, the first cycling step at 95 ºC for 5 seconds, 60 ºC for 20 seconds, and 72 ºC for 15 seconds. A second cycling step at 95 ºC for 5 seconds, 60 ºC for 30 seconds, and 72 ºC for 15 seconds.

2.2.3 Western blot detection

The MP diagnostic HCV BLOT 3.0 kit (western blot assay, Germany) was used to detect antibodies specific to HCV manually. 2 ml of diluted wash buffer was added and incubated at room temperature for 2 minutes, then 2 ml of blotting buffer was added. After that, 20 µl of samples was added and incubated for 1 hour at room temperature; then washed three times with 2 ml of diluted buffer, then 2 ml of working conjugate solution was added and covered for 1 hour. After that, 2 ml of substrate solution was added to each well. After 15 minutes, the strips were aspirated and rinsed with grade water to stop the reaction. The strips were mounted on the worksheet, and the bands were observed to grade the results.

2.2.4 Chemiluminescent

LIASON®XL murex HCV Ab/AG HT kit (DiaSorin Industries, Italy) was used for chemiluminescent immunoassay (CLIA) technology for the combined qualitative

determination of HCV antibodies in human serum or plasma. The technique for qualitative assessment of specific IgG to hepatitis C virus (HCV) is an indirect chemiluminescence immunoassay (CLIA). Two specific recombinant antigens for HCV (core and NS4) are utilized for coating magnetic particles (solid phase), a third ready-to-use aqueous HCV antigen (biotinylated NS3) is also included. The biotinylated antigen is captured during the first incubation by streptavidin-coated magnetic particles, and if HCV antibodies are present in the calibrator, samples, or controls, they will bind to the solid phase through the recombinant HCV antigens. During the second incubation, a mouse monoclonal antibody to human IgG, linked to an isoluminol derivative (isoluminol-antibody conjugate), reacts with IgG to HCV already bound to the solid phase. The unbound material is removed with a wash cycle after each incubation. Afterwards, the initial reagents are added, and a flash chemiluminescence reaction is induced. The light signal, and consequently the quantity of luminol-antibody conjugate, is measured by a photomultiplier as relative light units (RLU) and is indicative of IgG to HCV presence in the calibrator, samples, or controls. The detection of HCV antibodies in the specimens is established by comparing the chemiluminescence reaction signal to the assay calibration cut-off value. The analyzer automatically calculates the signal-to-cutoff (S/CO) ratios and then grades the results. The cut-off discriminating between the presence and absence of HCV Ab has a S/CO value of 1.0. Patient results should be interpreted as follows: Samples with a S/CO value of less than 0.80 are considered non-reactive for HCV antibodies. In contrast, samples with a S/CO value equal to or greater than 1.00 are considered reactive for HCV antibodies. Samples with S/CO values greater than or equal to 0.80 and less than 1.00 are considered equivocal. Samples with S/CO values greater than or equal to 0.80 and less than 1.00 are considered equivocal. Equivocal samples should be retested in duplicate to confirm the initial result. Samples having at least 2 out of the 3 results equal to or above the S/CO value of 1.0 are considered reactive. Samples with a minimum 2 out of the 3 results less than the S/CO value of 1.0 are classified as non-reactive.

2.3 Genotypes detection

AC004/24 GEN-CB2.0 version 5 kit (NUCLEAR LASER MEDICINE S.r.i / Italy) was used for the detection of genotypes. The kit allows the genotyping of the most common genotypes and subtypes of Hepatitis Virus C (HCV). The kit is compatible with the amplified products obtained with reference AA896/24.

Genotypes: 1, 2, 3, 4, 5, 6 and 7

Subtypes: 1a, 1b, 2a/2c, 2b, 3a, 3b, 3c, 3k, 4a, 4b, 4c/4d, 4e, 4f, 4h, 5a, 6a/6b, 6g, 6m, 6t e 7a depending on the bands formed on the strands of the kit.

2.4. Statistic evaluation

GraphPad Prism 8.0.0 and IBM SPSS (statistical analysis in social science) Statistics 25.0 (IBM Corp., Armonk, NY) statistical software programs were utilized to manage and carry out these analyses of frequencies, percentages, and graphs. When data for continuous variables are not normally distributed, the normality test is used to characterize the median with an interquartile range, and the Kruskal-Wallis test is used to compare continuous variables. The two-tailed Fisher exact test was used for categorical variables, and the two-way ANOVA test was used for continuous variables. The Pearson Chi-square test is used to compare categorical variables, which are reported as numbers and percentages. A probability *(p)* value of 0.05 was used to define statistical significance.

3- Results:

3.1 Baseline characters of HCV patients

A total of 738 suspected blood samples were taken throughout 2022. Results obtained from the four ways of detecting viral infection revealed that 695 patients (94.2%) were positive, while 43 (5.8%) were negative. The collected samples were divided into four age groups: firstly, ≤ 20 years were 131 (18.9%) of about (13.1 ±7.1) interquartile range, secondly 21-40 years were 289 (30.8 ± 6.5), thirdly 41-60 years were 249 (51.1 ± 6.2) and finally elders ≥ 60 years were 26(70 ± 8.5) were positive with high significant relationship between infection with the virus and the four age groups (*p <0.001)*. Results categorized in Table 1 revealed that there was a non-significant correlation of (*p <0.753)* between final result detection and sex of patients; about 381 (54.8%) of positively infected patients were men, while 314 (45.2%) were women. Table 1 also shows that about 689 (99.1%) of individuals incorporated in this study were Iraqi, and 6 (0.9%) were foreign individuals, which means a high significant correlation of (*p <0.002)*. This may lead us to the possibility of increasing infections during 2022.

Table 1: Baseline characters of Human Hepatitis C virus patients

Character		Final result detection†				*p*-value
		Positive		Negative		
		No.	%	No.	%	
Sex	Male	381	54.8	25	58.2	0.753
	Female	314	45.2	18	41.8	
Nationality	Iraqi	689	99.1	39	90.7	**0.002**
	Foreign	6	0.9	4	9.3	
		No. (%)		**Mean ±Std**		
*Age groups (year)	≤20	131 (18.9)		13.1 ± 7.1		**<0.001**
	21-40	289 (41.6)		30.8 ± 6.5		
	41-60	249 (35.8)		51.1 ± 6.2		
	> 60	26 (3.8)		70 ± 8.5		
Statistical analysis		Pearson X^2 =245.19; df=3; ***p*<0.001**				

†: detection by at least two assays (ELISA for Antibody detection, 4th generation ELISA for antibody and antigen, Chemiluminescence and Western blot assay);*for positive results only; D.F.: Degree of freedom; *p*: Probability of Two-tailed Fisher exact, Person test for categories variable and ANOVA test for continuous variable (significant *p*-value is indicated in bold).

3.2 Distribution of Human Hepatitis C virus load stratified to age groups, sex, and viral genotypes/subtypes

Results in Table 2 revealed a highly significant relationship between viral load and infection with different genotypes of HCV (*p <0.002)* as follows: 24 (4.86 IQR: 0.95-14.15) of positive cases were infected with 1a genotype/subtype, 5(5.12 IQR: 1.51-60.03) were infected with 1b genotype, 7 (36.38 IQR: 16.45-56.77) were infected with 4 genotypes, 5 (6.24 IQR: 0.91-16.78) were infected with 4a genotype, 4 (18.81 IQR: 3.11-21.11) were infected with 4c/d genotype, 2(81.71) were infected with 4h genotype and finally 7 (0.4 IQR: 0.05-7.44) were infected with 6 t genotype, respectively.

Table 2: Distribution of Human Hepatitis C virus load stratified to age groups, sex, and viral genotypes/subtypes.

Patient group		Viral load copies/ml for positive detection†		*p*-value
		N= 53	Median (IQR)×10^5	
*Age groups (year)	≤20	10	4.29 (0.38-14.23)	0.067
	21-40	21	5.48 (1.7-20.42)	
	41-60	18	13.12 (1.20-43.73)	
	> 60	4	79.25 (0.05-81.10)	
Sex	Male	36	9.71 (0.66-43.75)	0.404
	Female	17	4.62 (1.46-16.45)	
HCV Genotypes / Subtypes	1a	24	4.86 (0.95-14.15)	**0.02**
	1b	5	5.12 (1.51-60.03)	
	4	7	36.38 (16.45-56.77)	
	4a	5	6.24 (0.91-16.78)	
	4c/d	4	18.81 (3.11-21.11)	
	4h	2	81.71	
	6t	7	0.4 (0.05-7.44)	

†: Estimation 53 cases for viral load detection after treatment by at least two assays (ELISA for Antibody detection and quantity reverse transcriptase RT-PCR assay); IQR: inter quarter range; p: Probability for Kruskal-Wallis, Mann-Whitney Test.

3.3 Appearance of HCV infections in the Iraqi population during the months of 2022

Figure 1 explains the appearance of HCV infections in the Iraqi population during the months of 2022. The highest frequency of HCV infections appeared in June, followed by September and then April. Infection frequency decreased during October and August, then March, July, January, December, February, November, and finally May.

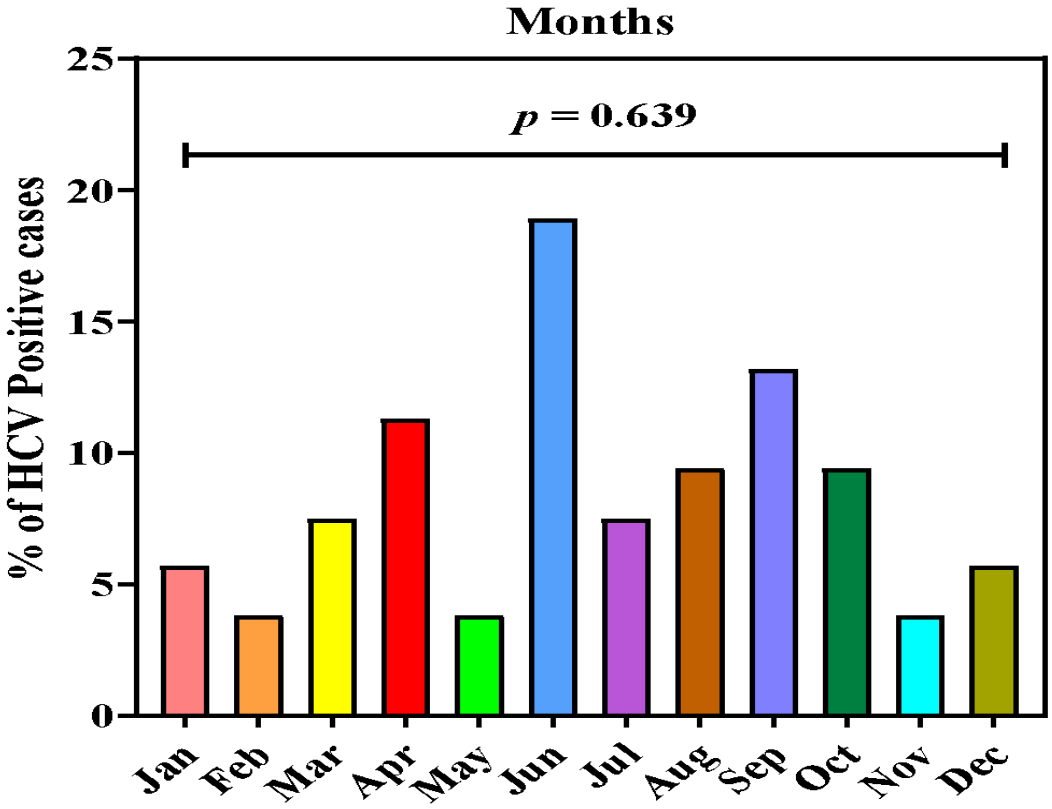

Figure 1: Appearance of human hepatitis C virus infections in the Iraqi population during 2022. *p*: probability of Pearson Chi-square test (to compare categorical variables).

3.4 Distribution of hepatitis c virus infections stratified to 14 Iraqi provinces

Figure 2 explains the distribution of HCV infections through 14 Iraqi provinces. Baghdad province had the highest number of infected individuals, followed by Kirkuk, then Thiqar, Wasit, Diyala, Diwania, Saladin, and Babil. Meanwhile, Najaf Karbala, Muthana, Basra, and Ninawa had a lower infection percentage of 2.3 %. Erbil province had only 0.4% infections.

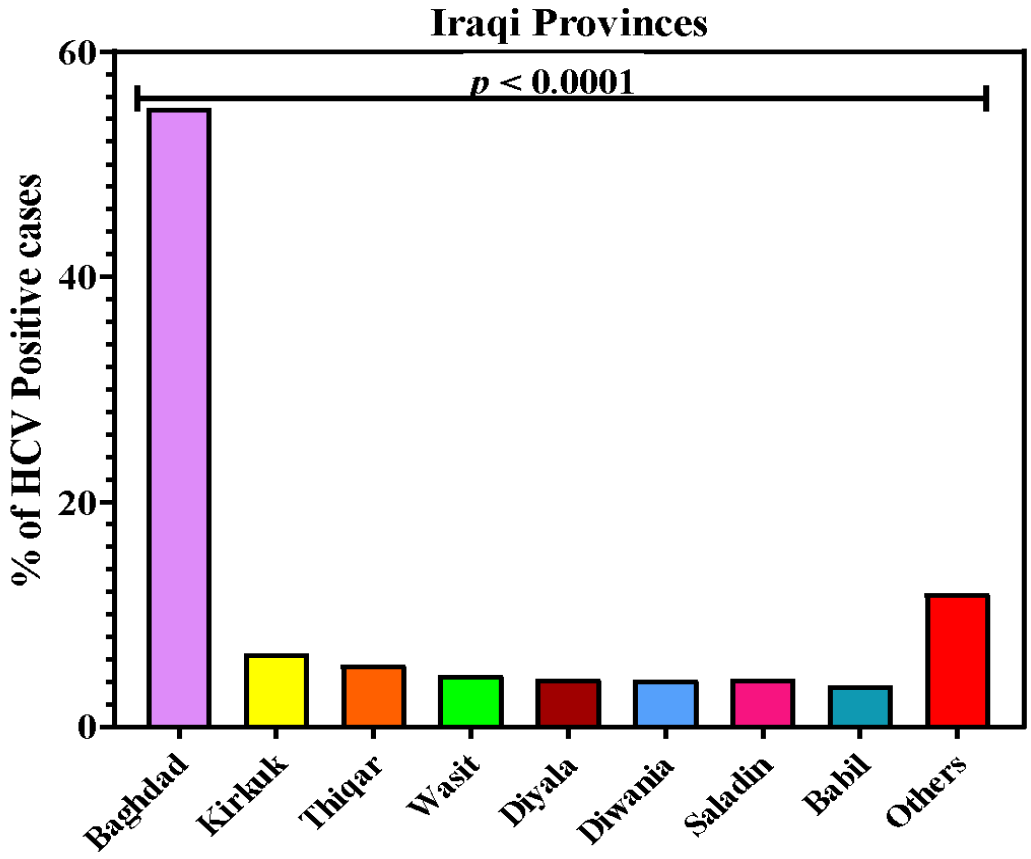

Figure 2: Distribution of Human Hepatitis C virus infections among Iraqi provinces during 2022; others included 2.3% of infection in Najaf, Karbala, Muthanna, Basra, and Ninawa, and 0.4% in Erbil provinces. *p*: probability of Pearson Chi-square test (to compare categorical variables).

3.5. Distribution of the HCV patients stratified to age groups and sex

Figure 3 shows the distribution of the HCV patients stratified according to age groups and sex. The figure shows that there was a non-significant relationship between many positive HCV infections and the four age groups (p=0.246) when the highest percentage of infections appeared in the adult group (21-40) years with a higher percentage of infected males than females, 41-60 years old comes in the second place followed by ≤ 20 years then <60 years.

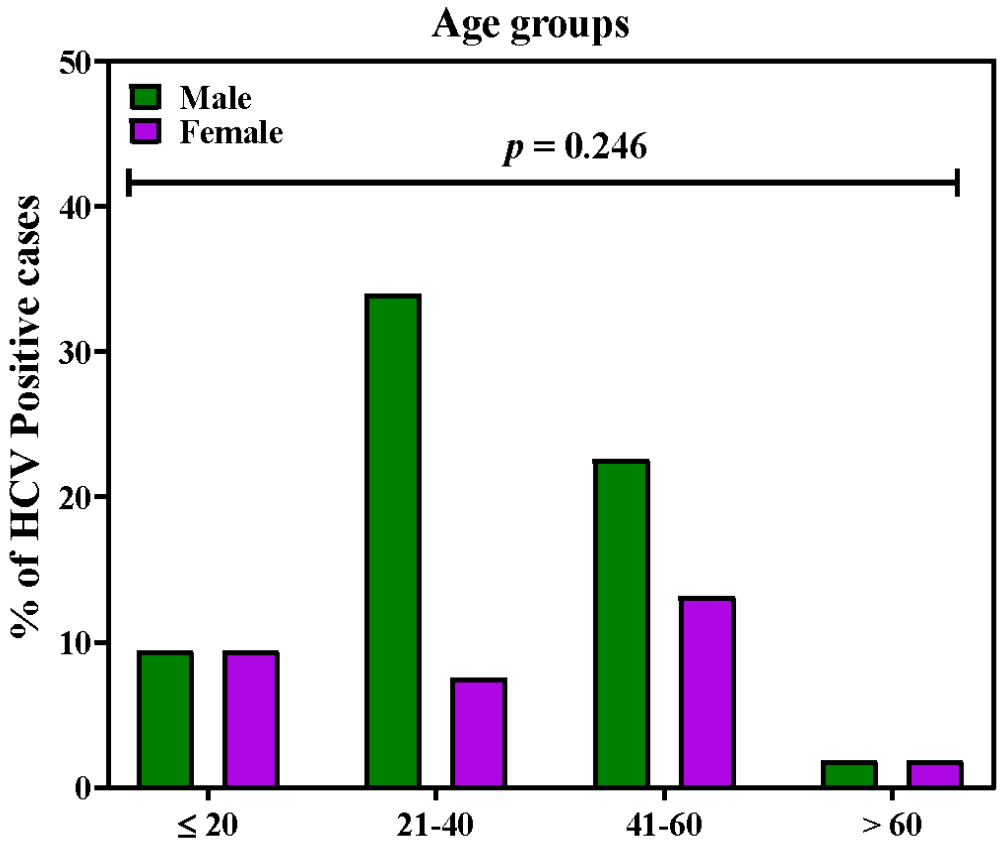

Figure 3: Distribution of the HCV patients stratified to age groups and sex. *p*: probability of Two-way ANOVA test to compare categorical variables.

3.6 Detection source of HCV infections during 2022

Figure 4 explains the detection source of HCV infections included in this study during 2022. There was a highly significant relationship between several positive HCV cases and probable source of detection ($p<0.0001$). The figure also revealed that about 19.4% of infections with the virus were detected via surgery, 26% were detected by renal failure test, 37.3% were detected during thalassemia test, 1% in expatriates, 1.4% percentage was detected during marriage check, 3% were detected by densities and diabetes, 3.7% detected during hemophilia test and 4.8% was detected during routine medical staff check and finally 2.2% were detected by other means including contact with contaminated body fluids, midwives, barbers, test tube babies, and prisoner patients.

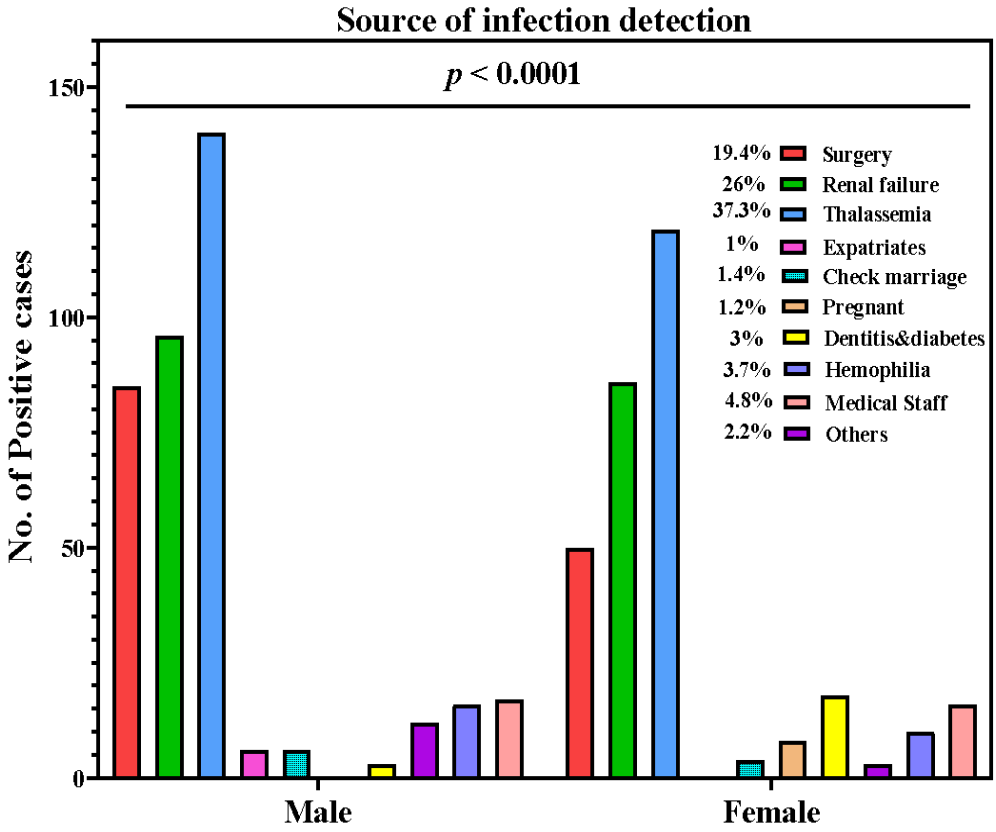

Figure 4: Detection source of Hepatitis C virus infections in this study during 2022. *p*: probability of two-way ANOVA test (to compare sex and source); others included contact, midwife, barber, test tube baby, and prisoner patients.

4. Discussion

Hepatitis C virus is a major cause of serious liver disease and hepatocellular carcinoma (HCC), and it is currently the most common reason for liver transplantation. Hepatitis C virus (HCV) poses a significant worldwide health challenge as a result of increasing infection rates, the limited efficacy of available treatments, and the absence of a vaccine to mitigate its effects. The main factor contributing to the acquisition of the virus is the use of drugs by intravenous injection, and individuals who engage in this practice, known as intravenous drug users (IDUs), are the most heavily impacted group by HCV infection in industrialized countries. The introduction of both antibody and nucleic acid testing for blood screening has greatly reduced the incidence of new cases of post-transfusion HCV in the United Kingdom (UK) [10]. While not enforced globally, there is still rigorous screening of blood donors, and there are occurrences of HCV infections after transfusions in places with poor resources. The unintentional spread of HCV during large-scale efforts, such as the one focused on providing injectable treatment for schistosomiasis in Egypt, has also contributed to a prevalence of up to 15% in specific nations.

Contrary to the hepatitis B virus, the transmission of HCV through sexual contact is rare. An extensive and prolonged investigation, encompassing 895 monogamous heterosexual partners of patients with chronic HCV infection and covering a duration of over 8000 person-years, demonstrated an extremely low or insignificant probability of sexual transmission. In contrast, there is an increasing prevalence of acute hepatitis C among men who engage in sexual activity with other men (MSM) and are also HIV-positive. The incidence of instances

within the MSM community in the United States and Europe is progressively rising. Transmission among this group primarily occurs via mucous membranes rather than the skin [11]. It is linked to the frequency of sexual partners, the sharing of drugs through the nose or anus, and engaging in high-risk sexual practices. Most specialists recommend that individuals infected with HCV utilize barrier methods of contraception. However, they do not advocate for the continued use of these precautions in stable, monogamous partnerships.

The transmission of HCV from mother to infant has been recorded, with the risk found in most investigations being less than 5%. Women co-infected with both HCV and HIV have a greater than twofold higher probability of transmitting HCV to their offspring compared to those who are just infected with HCV [12]. According to current studies, the European Paediatric HCV Network affirms that there is no advantage in preventing the transfer of HCV from mother to child through either an elective Caesarean section or abstaining from nursing. Mothers who are infected with both HCV and HIV should follow the current HIV guidelines, which give priority to the mother's choice but recommend considering a Caesarian section at 38 weeks. The thorough analysis of the natural development and results of persistent HCV infection has been thoroughly recorded in various comprehensive studies. The Hepatitis C virus (HCV) is responsible for causing cirrhosis, a condition that can result in the life-threatening progression of end-stage liver disease or HCC in around 20–30% of infected individuals during their lifetimes. Contributing factors to the advancement of the illness include advanced age at the time of infection, male gender, and excessive alcohol consumption [13]. The empirical basis for the progression of disease has informed the creation of rigorous models that portray the course of infection. These models have been used to predict the future impact of the illness [14].

The projected prevalence of patients in the UK with compensated cirrhosis caused by HCV infection is expected to rise from 3705 in 2005 to 7550 by 2015. By 2015, it is anticipated that the number of instances of decompensated cirrhosis or HCC will increase to 2540, and there is a significant projected increase beyond that [15]. Cohort studies indicate that people with substantial liver fibrosis resulting from hepatitis C may have a more unfavorable outcome in comparison to those with fibrosis caused by other reasons. A prior study suggested a potential link between hepatitis virus infection and lymphoid and myeloid malignancies [16]. According to a 2019 analysis, there was a greater occurrence of the phenomenon among individuals aged 40 to 50. This could be attributed to a greater prevalence of renal disorders in older age groups. Furthermore, the prevalence of hepatitis C was previously observed to be higher among patients who underwent hemodialysis for a duration exceeding 5 years compared to those who received treatment for a shorter timeframe [17]. To encourage the patient's first compliance with ART therapy, it may be advisable to delay the administration of antibiotics to a newly diagnosed individual with a significantly impaired psychological condition [18]. Moreover, it is essential to adhere to established protocols and perform thorough research to understand the origins of the sickness, evaluate the probability of complications, and, most importantly, choose an efficient therapy. To enhance the probability of identifying new infections, the objective can be achieved by leveraging contemporary technology and instruments that offer a more comprehensive comprehension of diseases, along with bolstering the capacities of the national laboratories in every province of Iraq [19]. The cost of eliminating HCV must be taken into account. However, it should be remembered that investment in drug treatments must be considered the long-term overall reduction in the costs of the hepatic and extrahepatic complications of HCV infection and the direct and indirect costs of management. The study's limitations were that

the kits tested here performed adequately, but future quantitative assays will aim to improve both the sensitivity and the linear range of HCV RNA detection.

5. Conclusion

The prevalence of the HCV epidemic continues to increase in significance. While the occurrence of HCV is decreasing in certain regions, the overall impact of the disease caused by this group of long-lasting infections is still increasing. By 2030, it is projected that HCV will result in significantly greater illness and death rates in developed nations compared to HIV. Assessing the natural history of HCV infection has proven challenging due to the typically asymptomatic beginning of the acute phase and the lack of symptoms in the early stages of chronic infection. Due to the possibility of a time-lapse of over 30 years between infection and the onset of cirrhosis, only a limited number of prospective studies have been conducted. However, the data obtained from both retrospective and prospective research enables us to draw some definitive conclusions. The majority of individuals who experience an acute infection will develop a chronic infection, and it is uncommon for viremia to spontaneously clear once a chronic infection has been established. The majority of persistent infections will result in hepatitis and varying levels of fibrosis, sometimes accompanied by non-specific symptoms such as weariness. Severe problems and mortality typically arise exclusively in individuals with cirrhosis, a condition that is expected to manifest in 15 to 20 percent of the affected population. Based on current patterns, HCV infection is expected to persistently affect world health in the foreseeable future.

6. Recommendations

The recommendations expand on previous recommendations for preventing HCV infection focused on screening and follow-up of blood, plasma, organ, and tissue donors. These recommendations in this report provide broader guidelines for preventing transmission of HCV, identifying, counseling, and testing persons at risk for HCV infection, and providing an appropriate medical evaluation and management of HCV-infected persons. Based on currently available knowledge, these recommendations were developed by CDC staff members after consultation with experts. This report is intended to serve as a resource for healthcare professionals, public health officials, and organizations involved in developing, delivering, and evaluating prevention and clinical.

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Ethical responsibilities of authors

The College of Science Research Ethics Committee approved the study protocol (University of Baghdad) (Reference: CSEC/1931/0045).

Disclosure and conflict of interest

Conflict of Interest: The authors declare that they have no conflicts of interest.

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