The Prevalence and Genotype Distribution of Hepatitis C Virus in Kenya: A Systematic Review and Meta-Analysis

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Abstract

Background Hepatitis C (HCV) is a virus that causes chronic liver disease, end-stage cirrhosis, and liver cancer, yet most infected individuals remain undiagnosed or untreated. Kenya is a country located in Sub-Saharan Africa (SSA) where the prevalence of HCV remains high but with uncertain disease burden due to little population-based evidence of the epidemic. We aimed to highlight the HCV disease burden in Kenya with a summary of the available data.

Methods The study was performed as per the Preferred Reporting Items for Systematic Review and Meta-analysis (PRISMA) guidelines. We searched publications reporting HCV prevalence and genotypes in Kenya between January 2000 to December 2022. The effect size, i.e., the HCV prevalence, was defined as the proportion of samples testing positive for HCV antibody. Study quality was assessed by the Joanna Briggs Institute (JBI) critical appraisal checklist. Due to high study heterogeneity, the studies were categorized into low-, intermediate-, and high-risk for HCV infection. The pooled estimate prevalence per category was determined by the random effects model. This review was registered in the International Prospective Register of Systematic Reviews (PROSPERO) (ID: CRD42023401892).

Results A total of 29 studies with a sample size of 90,668 met our inclusion criteria, a third of which were from the capital city Nairobi (34.5%). Half of the studies included HIV-infected individuals (31%) or injection drug users (20.7%). HCV genotype 1 was the most common, with genotype 4 only slightly less common, and together they accounted for 94% of cases. The pooled prevalence for the low-, intermediate- and high-risk groups were 2.0%, 3.4%, and 15.5%, respectively. Over 80% of the studies had a score of > 6 on the JBI scale, indicating a low risk of bias in terms of study design, conduct and analysis.

Conclusion Our findings demonstrate that there is a higher prevalence of HCV in key populations such as HIV-infected individuals and drug users than in the general population in Kenya. We found that HCV genotypes 1 and 4 were the most common genotypes. More data from the general population is required in order to establish baseline data on the prevalence and genotypes of HCV in Kenya.

Keywords Hepatitis C virus · Kenya · Meta-analysis · Review · Prevalence · Genotypes

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1 Introduction

Hepatitis C virus (HCV) is a great public health concern worldwide. Globally, 71 million people are chronically infected with HCV, with most infections occurring in lower- and middle-income countries (LMIC) where there is limited testing and treatment [1]. Chronic infection can lead to mild illness or can progress to liver cirrhosis, liver failure, and hepatocellular carcinoma (HCC) [2]. The viral hepatitis pandemic takes a heavy toll on lives, communities, and health systems. It is responsible for an estimated 1.4 million deaths per year from acute infection and hepatitis-related liver cancer and cirrhosis– a toll comparable to that of HIV

and tuberculosis. Of those deaths, approximately 47% are attributable to hepatitis B virus (HBV), 48% to HCV, and the remainder to hepatitis A and E viruses [3]. Viral hepatitis is also a growing cause of mortality among people living with HIV. About 2.9 million people living with HIV are co-infected with HCV and 2.6 million with HBV [4].

Despite its high prevalence and highly infectious nature, HCV remains under-diagnosed and underreported in Africa [5]. It has been estimated that such low-income countries have only diagnosed 16% and treated less than 1% of people with HCV [6]. Most of the available data on HCV in Africa are outdated, and because of the paucity of available data, little attention has been given to HCV in Africa. Sub-Saharan Africa (SSA), which includes the country of Kenya, carries a substantial portion of the global burden of chronic HCV infections [7]. In this region, HCV is reported to be the second leading cause of end-stage liver disease and HCC-related mortality [8]. However, a detailed epidemiology and understanding of the disease burden is not available. One major obstacle is the scarcity of reliable data on the prevalence of the disease through population-based studies. Moreover, an estimate of the proportion of the population that has been diagnosed and treated for HCV is also missing. Data from a recent meta-analysis suggested a seroprevalence of 3% for HCV in SSA [9]. However, it is noteworthy that there was substantial regional and national variation in the reported prevalences along with variation in the most likely modes of transmission and risk groups. Using a linear mixed model, the burden of HCV in Africa was later estimated together with a forecast of appropriate interventions by examining at-risk cohorts and weighting based on known populations. Incremental prevalence estimates in southern Africa (0.7%), eastern Africa (3.0%), western Africa (4.1%), and central Africa (7.8%) were calculated [10].

In their systematic review and meta-analysis of the seroprevalence of HCV in Africa, Riou and colleagues provided estimates by region and country, where the pooled estimate of the prevalence of HCV for Kenya stood at 2.8% [10]. However, only six studies were reported, five of them published between 2002 and 2009, and the remaining one published in 2013. Moreover, further details on the data presented were missing, and the review gave an overall estimate of the prevalence only in adults in the general population. Information on specific populations, especially at-risk groups to which interventions should be most directed was not presented. Providing detailed prevalence data is now considered a central policy indicator by which to measure a country's progress towards elimination of a disease [11, 12]. Therefore, the purpose of our review and meta-analysis is to provide an up-to-date and detailed summarization of the data on the prevalence of HCV and its genotypes in the general Kenyan population, as well as in specific populations such as blood donors, drug users, and HIV patients, in particular. We believe that the availability of such epidemiological information will guide future intervention strategies and enhance the repertoire of actions for both preventative and clinical purposes.

2 Methods

2.1 Systematic Review and Meta-Analysis Study Protocol

The study protocol has been prospectively registered within the International Prospective Register of Systematic Reviews (PROSPERO) database [13] with identification ID: CRD42023401892. The main findings were conducted in accordance with the criteria of the Preferred Reporting Items for Systematic Reviews and Meta-Analyzes (PRISMA) [14].

2.2 Search Strategy

To establish that no similar study has been previously registered or published, we searched previous systematic reviews and protocols related to the topic and setting using the PROSPERO database and the Database of Abstracts Review of Effects (DARE). Next, a comprehensive literature search was carried out to retrieve relevant studies published between January 2000 and December 2022. International databases, namely PubMed, Science Direct, and Africa Journals Online (AJOL) were mined independently by two researchers (GNM and HB). To minimize the chance of failing to capture all relevant studies and to find more potentially related studies, the gray literature was consulted via Google Scholar. Furthermore, reference lists within each potentially eligible study were evaluated and hand-searched. A manual search was also conducted for relevant articles as well as references therein. The keywords used were hepatitis C, HCV, prevalence, seroprevalence, Kenya, and Kenyan. The search terms above were used separately and in combination using Boolean operators "OR" and "AND."

2.3 Eligibility Criteria

The following inclusion criteria were adopted: studies that examined and reported the prevalence of HCV in Kenya, including observational studies (non-participatory observations); studies whose full text was available or could be obtained from authors; and studies published in peer-reviewed journals in the English language between January 2000 and December 2022.

The following exclusion criteria were enforced: studies on other forms of viral hepatitis; studies that lacked data on the prevalence of HCV; case reports, reviews, poster presentations, editorials, letters, studies with uncertain methods or that were conducted outside of Kenya; and studies that were published in non-English languages.

2.4 Selection of Studies

The Mendel software was used to assemble and screen the articles, remove duplicates, and streamline the process of study selection. Two reviewers (GNM and HB) independently screened the titles and abstracts. Studies that were repeated in various databases were removed, and a list of all remaining articles was prepared. Qualified articles were selected by evaluating the articles in this list. In the first stage of screening, the titles and abstracts were carefully studied, and unrelated articles were removed according to the inclusion and exclusion criteria. In the second stage, full texts of the selected articles from the screening stage were examined based on the inclusion and exclusion criteria to evaluate their relevance, and unrelated studies were removed. Primary study investigators were contacted for studies for which the full text was not available. To avoid bias, all stages of resource review and data extraction were performed by two researchers independently. In cases where there was a disagreement between the two researchers, a third person reviewed the article.

2.5 Study Quality Assessment

The Joanna Brigg's Institute (JBI) checklist [15] was used to check the methodological quality of the selected studies for determination of any risk of bias. This checklist has 10 questions with the answer to each question being yes, no, unclear or not applicable. A score of 1 was assigned for a 'yes' response and 0 was assigned for 'no' and 'unclear' responses, where a total minimum score of 0 and a maximum score of 9 was assigned. The mean score was computed for each study. Two reviewers (GNM and HB) independently conducted the quality assessment, and disagreements were resolved by consensus.

2.6 Extracting the Data

Information from each of the final papers selected for systematic review and meta-analysis was extracted from a pre-prepared checklist by two reviewers (GNM and HB) working independently, and disagreements were resolved by consensus. The checklist included the title of the article, the name of the first author, the year of publication, place of study, sample size, HCV prevalence, HCV genotype (where

available), study site, HCV tests, study population, and average age.

2.7 Statistical Analysis

The estimated prevalence of HCV was calculated as the number of HCV antibody (HCV-Ab)-positive subjects divided by the total number of subjects screened. The studies were classified into three categories: low-, intermediate-, and high-risk, based on the HCV risk status of the individuals. The overall pooled prevalence estimates for each risk group were computed using a random effects model with the meta package of the statistical software R version 4.0.2 [16]. The test for heterogeneity was evaluated by the X^2 test on Cochrane's Q statistic [17], quantified by I^2 value. The heterogeneities were divided into three categories: less than 25% (low heterogeneity), 25–75% (medium heterogeneity), and more than 75% (high heterogeneity). The random-effects model was selected due to the presence of significant heterogeneity ($I^2 > 50\%$). $P < 0.05$ was considered to indicate a statistically significant difference for all included studies. Sensitivity analysis was performed by removing the study with the smallest or largest sample size. Begg's funnel plot and Egger's weighted regression method were used to test for publication bias.

3 Results

3.1 Identification of Studies

Studies were selected as shown in the PRISMA flow chart (Fig. 1). Initially, a total of 1956 studies were identified through the database search and additional references. From these, 616 studies were removed due to duplication. The remaining 1340 studies were screened based on the title and abstract, and 1247 were excluded due to ineligibility. A review of the full articles was carried out on the remaining 93 studies, of which 29 met the inclusion criteria, representing a total of 90,668 individuals (Fig. 1; Table 1). The largest study was among blood donors with a sample size of 68,404 [18], while the smallest study was among patients presenting with jaundice with a sample size of 84 [19]. Whereas all studies reported the prevalence of HCV based on the presence of HCV-Ab, seven studies (sample size of 574) also reported HCV viremia using HCV RNA polymerase chain reaction (PCR). Among these seven studies, only one screened all the individuals for both HCV-Ab and HCV RNA [20]. The remaining six studies initially screened for HCV-Ab and then performed HCV RNA on the HCV-Ab-positive samples [21–26]. Eight studies reported HCV-Ab prevalence in the low-risk category, which included blood
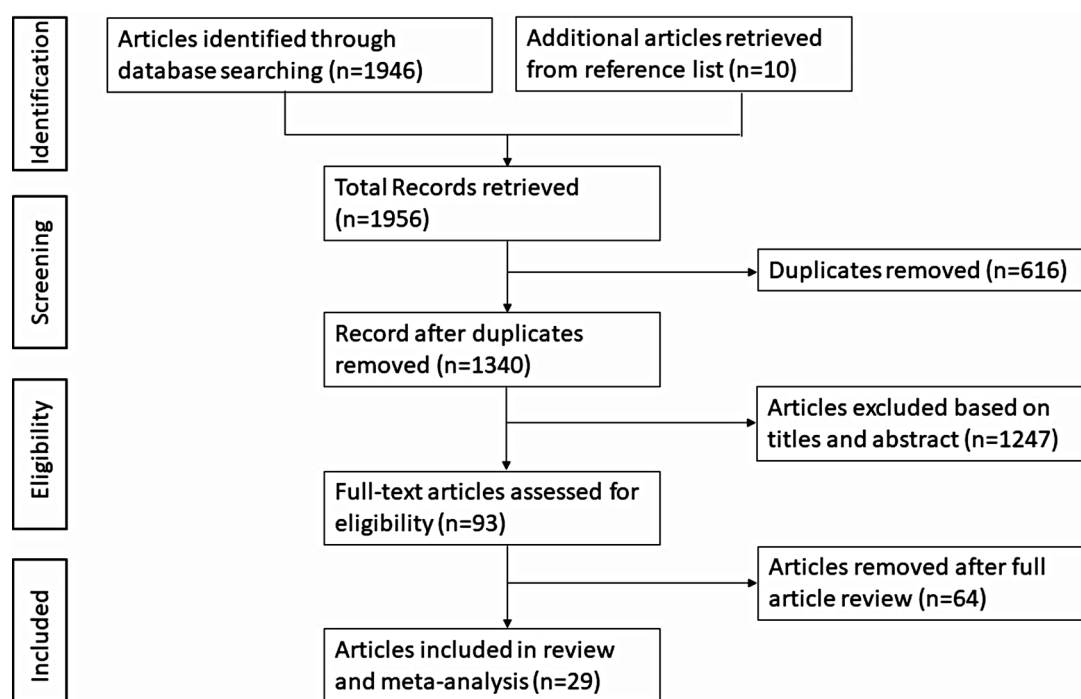
Fig. 1 PRISMA flow diagram of the process of study identification and selection

donors and the general population (total number of participants = 75308) [18, 22, 27–32], thirteen studies in the intermediate-risk category which included HIV-infected individuals, a mixed special population, patients with acute hepatitis, kidney disease, and ovarian cancer (total number of participants = 9210) [20, 25, 33–43], and eight studies in the high-risk category which included patients presenting with jaundice and drug users and their partners (total number of participants = 6150) [19, 21, 23, 24, 26, 44–46]. Five studies reported HCV genotype data from the individuals who tested positive for HCV RNA [21, 23–26].

3.2 Geographical Distribution of HCV Seroprevalence Data

21 of the 29 studies reported data from only one of the country's eight regions. The remaining 8 studies included data from two or more regions (Table 1). A total of 52 data points for individual regions were collected from the 29 studies. Nairobi, which is the capital city and most populous region of the country, had the highest representation at 17 data points (32.7%), followed by the Rift Valley and Coast regions at 9 (17.3%), the Nyanza region at 8 (15.4%), the Western and Eastern regions at 3 (5.8%), the Central region at 2 (3.8%), and the North Eastern region at 1 data point (1.9%) (Fig. 2). Only one study reported data from all eight of the regions [22], which was a national survey encompassing both rural and urban populations of HIV-negative individuals (Table 1). One other study included data from seven

of the eight regions [39]. In terms of studies per individual region, Rift Valley was the best represented, with an overall sample size of 69,559 (Table 1).

3.3 Prevalence of HCV

The prevalence of HCV in the studies ranged between 0.2% and 43.9%, depending on the study population, with the lowest prevalence in an HIV-infected population [25], and the highest prevalence among drug users [44]. The studies were of significant heterogeneity in the populations represented; less than a third reported HCV in the general population. On these grounds, the studies were divided into three groups representing populations with differing risks of testing positive for HCV infection. The pooled estimate for HCV prevalence using the random effects model in the low-risk group was 2.0% (95% CI: 1.0-3.3) (Fig. 3a), compared with 3.5% (95% CI: 0.8–7.7%) in the intermediate-risk group (Fig. 3b), and 15.5% (95% CI: 11.4–20.1) in the high-risk group (Fig. 3c). We note that the confidence interval of this estimate is very wide for the intermediate-risk group. Heterogeneity was also significant ($I^2 > 50\%$) within each category and was highest in the intermediate and low-risk sub-groups ($I^2 = 98\%$, $p < 0.01$). Among the studies that assessed HCV viremia, the average HCV RNA positivity rate in the HCV-Ab samples was 70.7%, ranging from 93% [26] to 0% [22].

Table 1 Summary of the characteristics of all studies included in the systematic review and meta-analysis of the prevalence and genotype distribution of HCV in Kenya, 2000–2022

Author	Publication Year	Design	Region	Population	Study Year	Age (group/mean/Median)	Sample size	HCV Ab + (%)	Test Method	JBI score
Otedo	2003	Cross-sectional	Nairobi	Kidney Patients	1998	44.3	100	5	MEIA	7
Atina	2004	Cross-sectional	Nairobi	Jaundice Patients	2000	0-67	84	7.1	ELISA	8
Harania	2008	Prospective	Nairobi	HIV-1+ Patients	NA	13-65	378	1.1	ELISA	7
Muasya	2008	Prospective	Nairobi	Drug Users	2000	15-55	333	22.2	ELISA/PCR	6
Njeru	2009	Cross-sectional	Nairobi	Blood Donors	NA	16-54	400	1	ELISA	9
Muchiri	2012	Cross-sectional	Nairobi	Acute hepatitis patients	2007-2008	16-83	100	5	ELISA/PCR	8
Muriuki	2013	Cross-sectional	Nairobi	HIV-1+ Patients	2009	Apr-59	300	10.3	ELISA	8
Kerubo	2015	Cross-sectional	Nairobi	General Population	2006-2007	15-54 (29.3)	1308	0.76	Rapid/ELISA	8
Ndombi	2015	Cross-sectional	Coast	Drug Users	NA	>18	123	43.9	Rapid	6
Mwatelah	2015	Cross-sectional	Coast	Drug Users	NA	33	152	16.4	Rapid/PCR	6
Wambani	2015	Cross-sectional	Rift Valley	HIV-1+ Patients	2014	18-60 (43)	124	1.6	ELISA	8
Wairimu	2016	Retrospective	Central	Blood Donors	2004	16-55	250	3.2	ELISA	8
Maina	2017	Cross-sectional	Rift Valley	HIV-1+ Patients	2015	36.7	190	4.2	ELISA	8
Okoth	2017	Cross-sectional	Rift Valley	HIV-1+ Patients	2009	39.3	247	1.6	ELISA	8
Wamamba	2017	Retrospective	Nyanza	Blood Donors	2015	30	2046	2.3	Rapid/ELISA	8
Karoney	2018	Retrospective cross-sectional study	Rift Valley	Blood Donors	2010-2012	16-60	68,404	0.26	ELISA	8
Ly	2018	Retrospective	National	General Population	2007	15-64	1091	4.4	ELISA/PCR	8
Too	2018	Cross-sectional	4 regions	HIV-1+ Patients	NA	>18	140	5.7	Rapid Test/PCR	6
Onyango	2018	Cross-sectional	Nyanza	Blood Donors	2015-2016	16-65	1215	3.2	ELISA	9
Oyaro	2018	Cross-sectional	3 regions	Drug Users	2011-2012	>18	672	6.5	ELISA	8
Bartonjo	2019	Cross-sectional	Rift Valley	Blood Donors	2011-2012	16-65	594	3.2	ELISA	8
Mwangi	2019	Cross-sectional	7 regions	HIV-1+ Patients	NA	>14	1829	14	Rapid/ELISA	7
Akiyama	2019	Retrospective	3 regions	Drug Users	2015-2017	>18	2188	13	ELISA/PCR	8
Loarec	2019	Retrospective	2 regions	HIV-1+ Patients	2014-2016	>18	4851	0.23	Rapid/ELISA/PCR	7
Maiyo	2020	Cross-sectional	Nairobi	Drug Users	2016-2017	33.6	212	13.7	ELISA/PCR	7
Onyango	2021	Cross-sectional	Nyanza	HIV-1+ Patients	2018	3-76 (38.2)	225	4	Rapid Test	9
Mwangi	2022	Cross-sectional	3 regions	High Risk Groups	NA	18-65	640	1.3	Rapid	7

Table 1 (continued)

Author	Publication Year	Design	Region	Population	Study Year	Age (group/mean/Median)	Sample size	HCV Ab + (%)	Test Method	JBI score
Sambai	2022	Cross-sectional	2 regions	Partners of PWID	2018-2020	>18	2386	12.4	Rapid	8
Wanyama	2022	Cross-sectional	Nairobi	Ovarian Cancer Patients	2018-2020	19-91	86	1.2	ELISA	7

HCV prevalence data distribution in Kenya
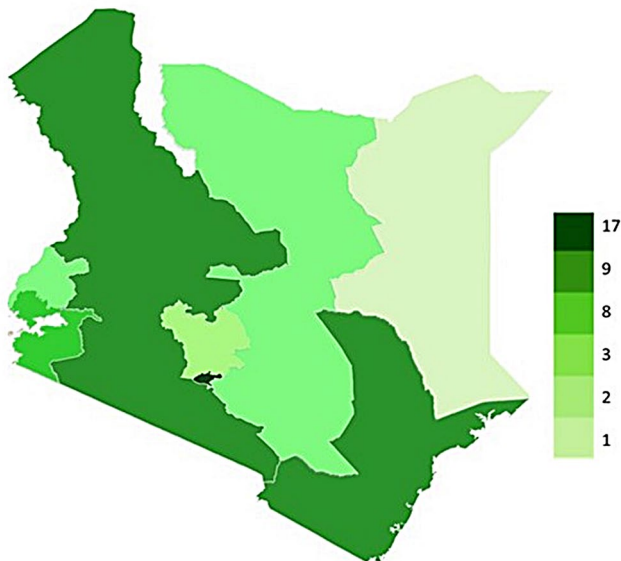
Fig. 2 Map of Kenya showing the geographical distribution of all data points included in the studies, 2000–2022

3.4 Assessment of Study Quality

The quality of studies investigating HCV prevalence in Kenya was assessed using the JBI Critical Appraisal Checklist for Studies Reporting Prevalence Data (S2 File) for risk of bias in inclusion. The studies scored a median of 8 (range 5–9) using JBI's nine items of risk bias (Table 1). Four (14%) studies had a quality score of 6 or less, whereas the remaining 25 (86%) studies scored greater than 6, indicating a low risk of bias. All studies used valid diagnostic methods for HCV-Ab detection, with seven studies including testing for HCV RNA, and the prevalence was measured in a standardized way. In terms of study type, twenty-one studies were cross-sectional, two studies included prospectively collected data, and six included retrospectively collected data (Table 1).

3.5 HCV Genotypes and Subtypes

The five studies that reported HCV genotypes were performed either among drug users [21, 23, 24, 26] or HIV-infected individuals [25], with a total of 267 individuals. HCV genotype 1/1a was predominant, representing 52% of the identified strains, followed by genotype 4/4a at 42% (Fig. 4). Other genotypes reported were genotype 2 (0.4%) [23], genotype 6 (1.5%), genotype 5 (0.7%), and geotype 3 (0.4%) [26]. Whereas all the studies involving drug users reported the presence of both genotype 1 and genotype 4, the study involving HIV-infected individuals reported the presence of only genotype 4. Most HCV-viremic individuals were infected with a single strain of the virus but one study reported the presence of mixed genotypes of 1a and 2a or 1a and 4a [24]. Moreover, another study reported the presence of genotypes of unknown strains [26] (Fig. 4).
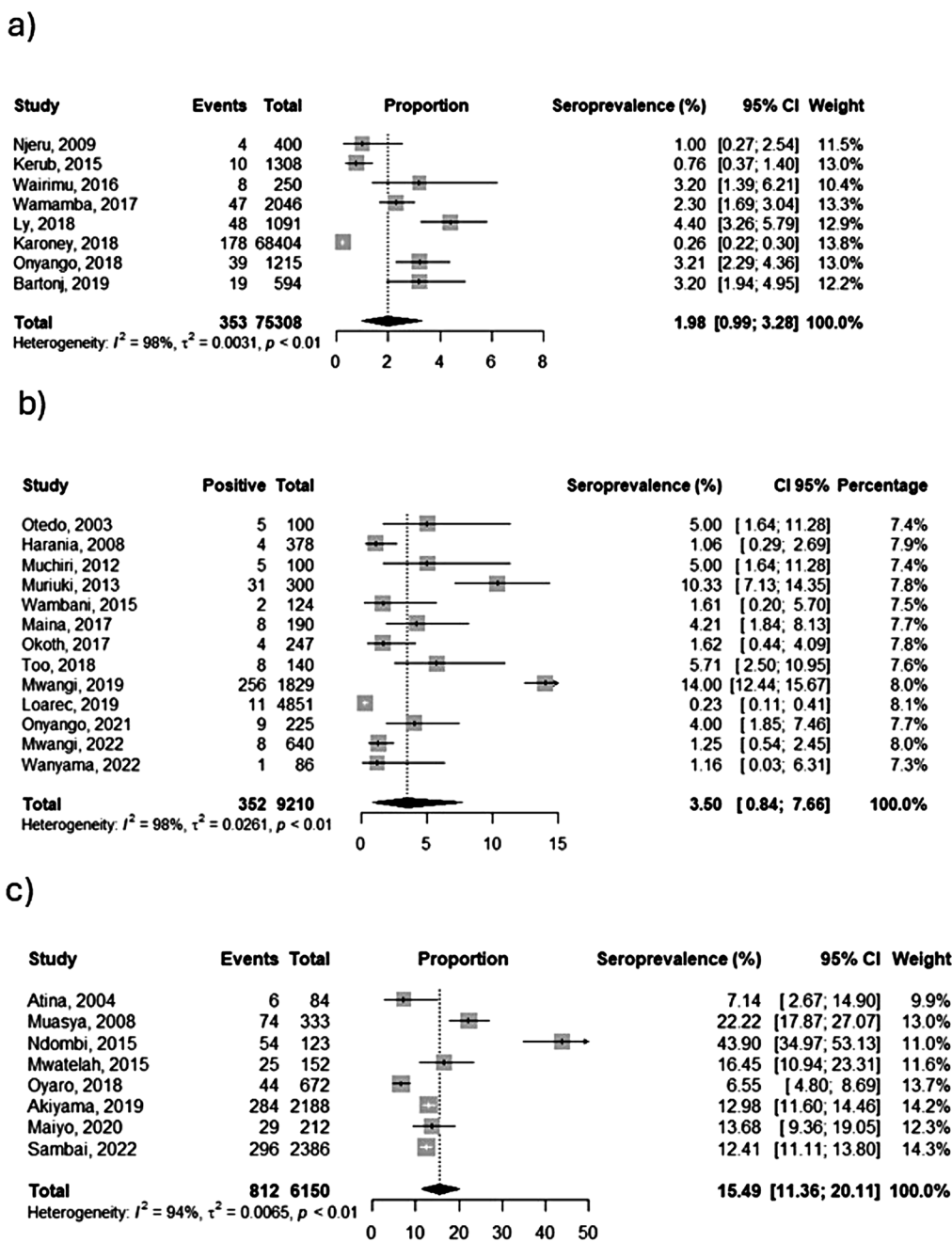
3.6 Sensitivity Analysis

Sensitivity analysis was performed by removing the study with the largest (low-risk category) or the smallest (intermediate- and high-risk category) sample size and assessing the effect based on the remaining studies. The overall pooled prevalence rate before omission for the low-, intermediate- and high-risk category was 2.0% (95% CI: 1.0-3.3, $I^2 = 98\%$, $p > 0.01$), 3.5% (95% CI: 0.8–7.7, $I^2 = 98\%$, $p > 0.01$), and 15.5% (95% CI: 11.4–20.1, $I^2 = 94\%$, $p > 0.01$), respectively. After the omission, the pooled prevalence rate increased slightly to 2.4% (95% CI: 1.4–3.6, $I^2 = 87\%$, $p > 0.01$), 3.7% (95% CI: 0.9–8.2, $I^2 = 98\%$, $p < 0.01$), and 16.6% (95% CI: 0.8–7.7), $I^2 = 94.9\%$, $p > 0.01$, respectively (Fig. 5). Thus, the calculated pooled prevalence for each category was not significantly affected by a single influential study, suggesting that the results are robust.

3.7 Publication Bias

Whereas the intermediate-risk category included 13 studies, the low- and high-risk categories had only 8 studies each. Tests for publication bias are not recommended when there are fewer than 10 studies because test power is usually too

a)

Study	Events	Total	Proportion	Seroprevalence (%)	95% CI	Weight
Njeru, 2009	4	400		1.00	[0.27; 2.54]	11.5%
Kerub, 2015	10	1308		0.76	[0.37; 1.40]	13.0%
Wairimu, 2016	8	250		3.20	[1.39; 6.21]	10.4%
Wamamba, 2017	47	2046		2.30	[1.69; 3.04]	13.3%
Ly, 2018	48	1091		4.40	[3.26; 5.79]	12.9%
Karoney, 2018	178	68404		0.26	[0.22; 0.30]	13.8%
Onyango, 2018	39	1215		3.21	[2.29; 4.36]	13.0%
Bartonj, 2019	19	594		3.20	[1.94; 4.95]	12.2%
Total	**353**	**75308**		**1.98**	**[0.99; 3.28]**	**100.0%**

Heterogeneity: $I^2 = 98\%$, $\tau^2 = 0.0031$, $p < 0.01$
0   2   4   6   8

b)

Study	Positive	Total	Seroprevalence (%)	CI 95%	Percentage
Otedo, 2003	5	100	5.00	[1.64; 11.28]	7.4%
Harania, 2008	4	378	1.06	[0.29; 2.69]	7.9%
Muchiri, 2012	5	100	5.00	[1.64; 11.28]	7.4%
Muriuki, 2013	31	300	10.33	[7.13; 14.35]	7.8%
Wambani, 2015	2	124	1.61	[0.20; 5.70]	7.5%
Maina, 2017	8	190	4.21	[1.84; 8.13]	7.7%
Okoth, 2017	4	247	1.62	[0.44; 4.09]	7.8%
Too, 2018	8	140	5.71	[2.50; 10.95]	7.6%
Mwangi, 2019	256	1829	14.00	[12.44; 15.67]	8.0%
Loarec, 2019	11	4851	0.23	[0.11; 0.41]	8.1%
Onyango, 2021	9	225	4.00	[1.85; 7.46]	7.7%
Mwangi, 2022	8	640	1.25	[0.54; 2.45]	8.0%
Wanyama, 2022	1	86	1.16	[0.03; 6.31]	7.3%
Total	**352**	**9210**	**3.50**	**[0.84; 7.66]**	**100.0%**

Heterogeneity: $I^2 = 98\%$, $\tau^2 = 0.0261$, $p < 0.01$
0   5   10   15

c)

Study	Events	Total	Proportion	Seroprevalence (%)	95% CI	Weight
Atina, 2004	6	84		7.14	[2.67; 14.90]	9.9%
Muasya, 2008	74	333		22.22	[17.87; 27.07]	13.0%
Ndombi, 2015	54	123		43.90	[34.97; 53.13]	11.0%
Mwatelah, 2015	25	152		16.45	[10.94; 23.31]	11.6%
Oyaro, 2018	44	672		6.55	[4.80; 8.69]	13.7%
Akiyama, 2019	284	2188		12.98	[11.60; 14.46]	14.2%
Maiyo, 2020	29	212		13.68	[9.36; 19.05]	12.3%
Sambai, 2022	296	2386		12.41	[11.11; 13.80]	14.3%
Total	**812**	**6150**		**15.49**	**[11.36; 20.11]**	**100.0%**

Heterogeneity: $I^2 = 94\%$, $\tau^2 = 0.0065$, $p < 0.01$
0   10   20   30   40   50

Fig. 3 Forest plot of the pooled prevalence estimate of HCV in the low- (**a**), intermediate- (**b**) and high- (**c**) risk populations of Kenya, 2000–2022

low to distinguish chance from real asymmetry [47]. Therefore, only the intermediate risk category was assessed for potential publication bias using Egger's weighted regression and Beggs's rank correlation tests. Neither test revealed evidence of publication bias (p-value = 0.3330, and 0.4260, respectively). This is depicted graphically in Begg's funnel plot comparing the effect size of each study (expressed as the proportion) on the x-axis, versus the standard error of proportion (on the y axis) for the prevalence of HCV

(Fig. 6). The symmetry about the pooled proportion line is consistent with the absence of publication bias.

4 Discussion

A recent global analysis of the prevalence of HCV reported the highest prevalence from the African continent at 7.1% [48]. While most studies included in the above review were from the Northern part of Africa, the results are alarming

HCV genotype distribution in Kenya
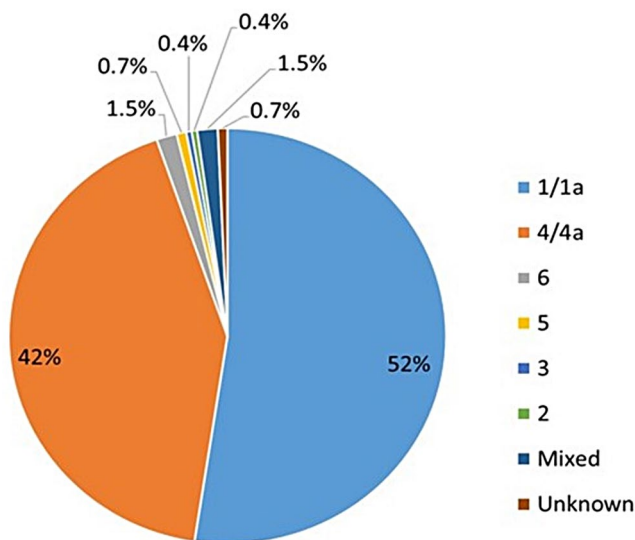
Fig. 4 Graphical representation of HCV genotype distribution in Kenyan populations, 2000–2022

and call for increased efforts to characterize the epidemiology and disease burden in a continent where viral hepatitis has long been neglected as a public health problem. We systematically reviewed all studies relating to the prevalence of HCV and the genotype distribution in Kenya for the past two decades. The study included 29 articles published between 2000 and 2022. Whereas each of the studies reported the prevalence of HCV by antibody testing, seven studies also included data on HCV RNA, with a positivity rate of 71% of the HCV-Ab positive samples. By stratifying cohorts as low-, intermediate-, or high-risk, we characterized the HCV epidemiology with the goal of informing an elimination policy. We report a low pooled prevalence estimate of 2% in blood donors and the general population (low-risk) but a higher pooled prevalence in other risk populations, which remains at 3.5% and 15% for the intermediate- (HIV-infected individuals, a mixed special population, patients with acute hepatitis, kidney disease, and ovarian cancer), and high-risk (patients presenting with jaundice and drug users and their partners) categories, respectively. The data shows that HCV infection might be increasingly concentrated in specific high-risk groups, particularly people who inject drugs, their partners, and HIV-infected individuals.

The prevalence of HCV in East Africa, which includes Kenya, was previously estimated at 3.0% [49]. However, half the studies included in that review focused on specific groups of people such as those co-infected with HIV, other high-risk groups, and patients with chronic illnesses. On the other hand, our results for the low-risk group, which largely represents the status in the general population, are close to

those of a worldwide review where the overall prevalence of HCV was reported at 1.8% in the general population [48]. Considering that less than 30% of the studies in the meta-analysis were from the general population, the seroprevalence of HCV could be higher due to a lack of sufficient data. In Kenya, testing for HCV is not routinely performed except at blood donor centers for transfusion purposes, and only a few hospitals conduct tests for HCV in clinical settings [50]. Indeed, it was reported that there is still little knowledge regarding the burden of HCV infection in the general population in many other countries in Africa, such as Nigeria [51]. However, a few serological studies have been carried out in selected population groups. The ready availability of data from these specific groups could be due to the increased accessibility of HCV screening among these individuals, given that they are already engaged in the healthcare system and likely come for follow-up visits. Interventions in these groups can have a significant impact on reducing transmission events. The WHO elimination plan for viral hepatitis including HCV requires national planning, appropriate resource allocation, and the political will to expedite unrestricted access to screening, care, and treatment for all individuals.

As in two recent reviews concerning the prevalence of HBV, another major hepatitis virus in Kenya that we and others have reported [52, 53], we observed that data on HCV prevalence from the Northern part of the country was scanty, as only one data point was reported among all the studies. This region is of particular interest as it lies along the border with Somalia, a country in which the prevalence of HCV is substantially higher, at an estimated 4.8% [54]. Due to the recently increasing influx of immigrants from such nearby countries [55], this region is likely to have a higher prevalence of HCV in the general population than the rest of the country. However, it is also important to note that the population density in this region is considerably lower than in the other regions [53].

Screening patients for HCV can be done using laboratory-based antibody detection methods. If the tests are positive, confirmation is required via HCV-RNA nucleic acid testing to establish active viremia [56]. Seven studies in this review screened for HCV RNA using PCR in addition to the serology tests. From a clinical standpoint, it is worth recalling that HCV antibody carriage is not evidence of chronic infection, as it has been found that the proportion of viremic individuals among those having HCV antibodies ranges between 54% and 86% [57]. In our analysis, the positivity rate of HCV-Ab samples for HCV RNA was 71%, which is similar to a demographic health survey done in Egypt where 67.7% of the individuals positive for HCV-Ab were viremic [58]. Therefore, approximately two-thirds of antibody carriers are likely to be chronically infected in countries in which
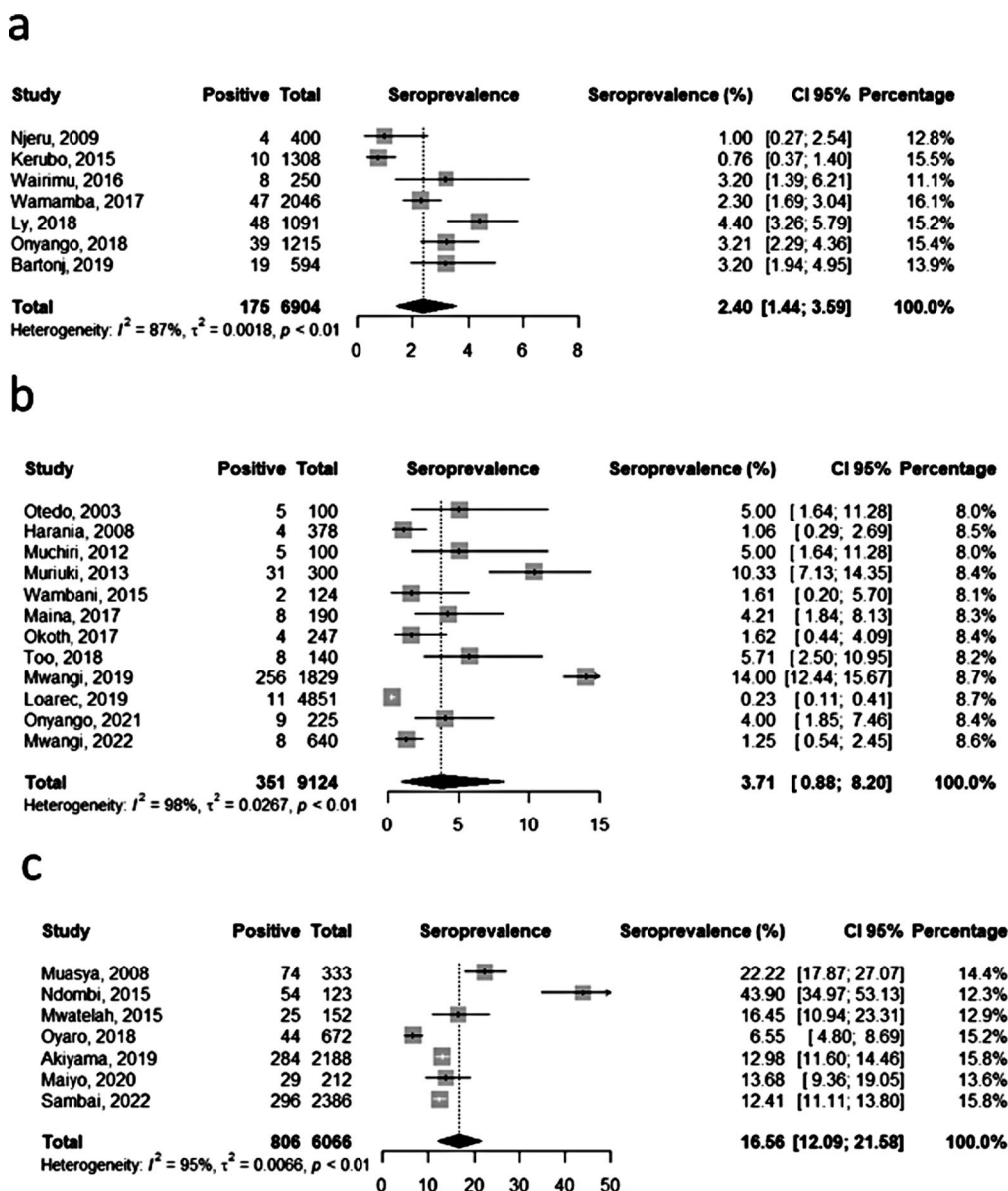
Fig. 5 Sensitivity analysis after omission of one study in the pooled prevalence estimate of HCV in the low- (**a**), intermediate- (**b**) and high- (**c**) risk populations of Kenya, 2000–2022

treatment is not routinely available. Automatic HCV RNA testing on all HCV antibody-reactive samples will increase the percentage of patients with current HCV infection who are linked to care and receive curative antiviral therapy.

Due to the shared mode of transmission, which includes parenteral, sexual, and vertical transmission, people living with HIV (PLHIV) are frequently co-infected with HBV and or HCV [59]. The current prevalence of HIV infection in Kenyan adults is 4.5% [60]. Nine (31%) of the studies in our analysis reported HCV prevalence in PLHIV, with a pooled HCV prevalence of 3.8% (95% CI: 0.5–9.8). Even though the pooled prevalence found in this study is lower than that obtained previously in SSA (5.4%), it is higher than that

of the general Kenyan population, which we estimated at 2.0%. We therefore conclude that the prevalence of HCV increases with HIV coinfection. It is noteworthy that this population was the highest included individual risk group in our analysis because screening for HCV or other related infections is easier to offer to individuals already accessing healthcare for HIV monitoring and treatment. In addition to the fact that over 70% of PLHIV reside in SSA [61], many of them are likely HCV-coinfected, suggesting a substantial burden of coinfection in this resource-poor setting. Coinfection of HIV with HCV and or HBV significantly impacts the survival of PLHIV and requires establishing measures

Funnel plot with pseudo 95% confidence limits
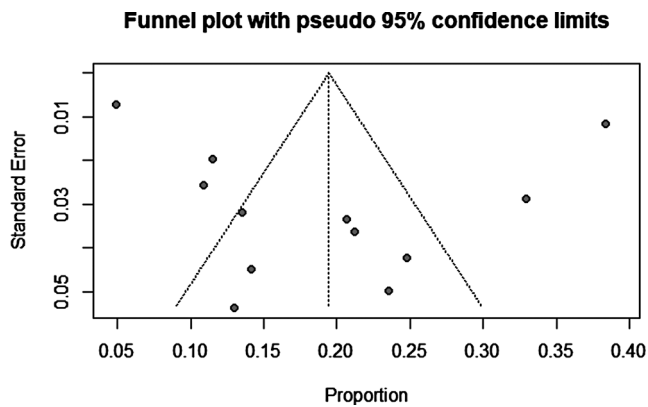
Fig. 6 A bias assessment funnel plot of the studies reporting HCV prevalence in the intermediate-risk populations of Kenya, 2000–2022

to reduce the risks of liver-related complications such as cirrhosis and hepatocellular carcinoma.

People who inject drugs (PWID) are of particular concern due to an increased risk for HCV transmission. Moreover, since they constitute the group with the highest HCV prevalence in many countries, they are central to HCV elimination efforts [24]. Globally, around 18% of PWID are living with HIV, and more than 50% have been infected with HCV, which is roughly 8·2 million PWID [62]. In Kenya, 22% of PWID were reported to be HCV-Ab positive, out of whom 81% were viremic [24]. Since this rate is lower than the global rates, earlier intervention could prevent the more widespread, established epidemics observed among PWID in higher-income settings. With the release of direct-acting antiretrovirals (DAAs), which are over 90% effective in treating HCV within other PWID settings, HCV elimination is achievable and has shown promising, cost-effective results when incorporated into existing harm reduction and HIV programs for PWID [63]. Within Kenya, DAA access has been largely cost-prohibitive, with few HCV prevention resources, and there is limited evidence on current PWID knowledge and perceptions of HCV, which can contribute to future HCV programs and services. The government should consider as urgent the need for all PWID to be screened for HCV. Moreover, evidence-based interventions centered on testing and linkage to affordable DAA treatments should be scaled upwards.

HCV genotype evaluation is necessary in understanding the natural history, transmission chains, and treatment responses to HCV infection. The genetic diversity of HCV has hampered the development of a successful vaccine, which is crucial for viral elimination [51]. Whereas only five studies assessed HCV genotype in our meta-analysis, with genotype 1 the most common at 52%, the results seem to agree with previous reports from Africa. For instance, a review by Sonderup et al., showed that the distribution of HCV genotypes across SSA was variable, but genotype 1

predominated overall [7]. Moreover, Azevedo et al. showed that HCV genotype 1 predominated among HIV-infected individuals in Africa [64]. On the other hand, results from a previous study carried out on HCV-Ab-positive blood samples in Kenya showed a genotype distribution of 1a (10%) and 2b (90%), although only 10 samples were analyzed [50]. Since the two study populations are different, the latter consisting of HIV-infected individuals and drug users, it is most likely that HCV genotypes among blood donors could be more diverse than those in such specialized groups. Sharing of needles and close association among individuals injecting drugs could contribute to the over-representation of specific genotypes within the group, whereas this may not be the case in the diverse population from which blood donations are normally obtained. Although only a few samples were sequenced, because information on HCV genotypes is scarce, the results of this study provide crucial data on HCV genotype distribution, not only in Kenya but throughout this region as well.

A strength of our study is that HCV epidemiology was characterized among several populations: the general population, blood donors, PLHIV, drug users, and patients with different diseases including liver diseases. Such outcomes provide empirical evidence for planning appropriate and comprehensive public health interventions, such as prevention of transmission, screening, care, and treatment of infected individuals. However, the study was limited by the lack of epidemiological data among children, as our pooled estimates were among adults only. Since adults make up 52% of the overall population in SSA [49], the total number of HCV cases is likely to be higher. This is supported by a study of HCV prevalence in children which showed a lower prevalence of 0.9% globally but a higher prevalence of 3.0% in Africa [65]. Thus, an overall seroprevalence that includes children would likely be higher than the pooled adult prevalence estimate. Finally, we do not fully account for the frequency of active, viremic infection, due to limited data on this variable. Caution should be exercised when interpreting only serological data with regard to the presented evidence on the state of exposure (acute or chronic). Nevertheless, our findings offer a timely update on the burden of HCV in Kenya, together with genetic information that will directly impact the choice of treatment. We recommend that the Kenyan government expands the number of people diagnosed and treated for HCV and put more focus on the named key populations. Subsidies in the cost and affordability of treatments for HCV will be important to achieve the targets set for disease elimination.

5 Conclusion

We present the first systematic review of its kind in Kenya that assimilates all published data on HCV seroprevalence for the past two decades. Our data demonstrates that there is a higher prevalence of HCV in key populations such as HIV-infected individuals and drug users than in the general population. HCV genotypes 1 and 4 were the most common genotypes. The significant heterogeneity we observed calls for more studies in the future, especially in the general population and in children to provide a single pooled estimate for the country.

Declarations

Ethical Approval As this is a systematic review and meta-analysis of published literature, ethical approval was not sought.

Conflict of Interest The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

References

1. Mafirakureva N et al. Feb., Cost-effectiveness of screening and treatment using direct-acting antivirals for chronic Hepatitis C virus in a primary care setting in Karachi, Pakistan. J Viral Hepat. 2021;28(2):268–278. https://doi.org/10.1111/JVH.13422

2. Stasi C, Silvestri C, Voller F. Update on Hepatitis C Epidemiology: Unaware and Untreated Infected Population Could Be the Key to Elimination. SN Compr Clin Med. 2020;2(12):2808–2815. https://doi.org/10.1007/S42399-020-00588-3

3. Global Hepatitis Programme. Accessed: Mar. 05, 2024. [Online]. Available: https://www.who.int/teams/global-hiv-hepatitis-and-stis-programmes/hepatitis/strategic-information

4. Global health sector strategy on viral hepatitis 2016–2021. Towards ending viral hepatitis. Accessed: Mar. 05, 2024. [Online]. Available: https://www.who.int/publications/i/item/WHO-HIV-2016.06

5. Karoney MJ, Siika AM. Hepatitis C virus (HCV) infection in Africa: a review. Pan Afr Med J. 2013;14. https://doi.org/10.11604/PAMJ.2013.14.44.2199.

6. Heath K, Hill A. WHO Hepatitis C elimination targets: the global equity challenge. Lancet Gastroenterol Hepatol. 2024;9:1–3. https://doi.org/10.1016/s2468-1253(23)00408-9.

7. Sonderup MW, et al. Hepatitis C in sub-saharan Africa: the current status and recommendations for achieving elimination by 2030. Lancet Gastroenterol Hepatol. 2017;2(12):910–9. https://doi.org/10.1016/S2468-1253(17)30249-2.

8. Mokdad AA, et al. Liver cirrhosis mortality in 187 countries between 1980 and 2010: a systematic analysis. BMC Med. 2014;12(1):1–24.https://doi.org/10.1186/s12916-014-0145-y.

9. Rao VB, Johari N, du Cros P, Messina J, Ford N, Cooke GS. Hepatitis C seroprevalence and HIV co-infection in sub-saharan Africa: a systematic review and meta-analysis. Lancet Infect Dis. 2015;15(7):819–24. https://doi.org/10.1016/S1473-3099(15)00006-7.

10. Riou J, et al. Hepatitis C virus seroprevalence in adults in Africa: a systematic review and meta-analysis. J Viral Hepat. 2016;23(4):244–55. https://doi.org/10.1111/jvh.12481.

11. Cooke GS, et al. Accelerating the elimination of viral hepatitis: a Lancet Gastroenterology & Hepatology Commission. Lancet Gastroenterol Hepatol. 2019;4(2):135–84.https://doi.org/10.1016/S2468-1253(18)30270-X.

12. Palayew A, Razavi H, Hutchinson SJ, Cooke GS, Lazarus JV. Do the most heavily burdened countries have the right policies to eliminate viral hepatitis B and C? Lancet Gastroenterol Hepatol. 2020;5(10):948–953. https://doi.org/10.1016/S2468-1253(20)30011-X

13. Schiavo JH. PROSPERO: An International Register of Systematic Review Protocols, Med Ref Serv Q.2019; 38(2):171–180.https://doi.org/10.1080/02763869.2019.1588072

14. Page MJ et al. The PRISMA 2020 statement: an updated guideline for reporting systematic reviews, https://doi.org/10.1136/bmj.n71

15. Checklist for Systematic Reviews and Research Syntheses Critical Appraisal Checklist for Systematic. Reviews Res Syntheses 2, 2017.

16. R. The R Project for Statistical Computing. Accessed: Mar. 05, 2024. [Online]. Available: https://www.r-project.org/

17. Kulinskaya E, Dollinger MB. An accurate test for homogeneity of odds ratios based on Cochran's Q-statistic. BMC Med Res Methodol. 2015;15(1):1–19. https://doi.org/10.1186/S12874-015-0034-X/FIGURES/16.

18. Jelangat M, Karoney A, Koskei Z, Rugut F, Faraj, Gardner A. Sero-prevalence of hepatitis B virus, hepatitis c virus and human immunodeficiency virus infections among blood donors in Western Kenya: A cross sectional study. East Afr Med J.Dec. 2018; 95(12): 2181–2188

19. Atina JO, Ogutu EO, Hardison WG, Mumo J. Prevalence of hepatitis A, B, C and human immunodeficiency virus seropositivity

among patients with acute icteric hepatitis at the Kenyatta National Hospital, Nairobi. East Afr Med J. 2004;81(4):183–7. https://doi.org/10.4314/eamj.v81i4.9152.

20. Muchiri I, Okoth FA, Ngaira J, Tuei S. Seroprevalence of HAV, HBV, HCV, and HEV among acute hepatitis patients at Kenyatta National Hospital in Nairobi, Kenya. East Afr Med J. 89(6):199–205.

21. Muasya T, et al. Prevalence of hepatitis C virus and its genotypes among a cohort of drug users in Kenya. East Afr Med J. 2008;85:318–25. https://doi.org/10.4314/eamj.v85i7.9649.

22. Ly TE, Kim KN, Drobeniuc AA, Kodani J, Montgomery M, Fields JM. The prevalence of hepatitis c virus antibody in HIV-Negative persons in Kenya, 2007. Am J Trop Med Hyg. 2018;98(6):1876–9.

23. Oyaro M, Wylie J, Chen CY, Ondondo RO, Kramvis A. Human immunodeficiency virus infection predictors and genetic diversity of hepatitis B virus and hepatitis C virus co-infections among drug users in three major Kenyan cities. South Afr J HIV Med. 2018;19(1):1–9. https://doi.org/10.4102/sajhivmed.v19i1.737.

24. Akiyama MJ, Cleland CM, Lizcano JA, Cherutich P, Kurth AE. Prevalence, estimated incidence, risk behaviours, and genotypic distribution of hepatitis C virus among people who inject drugs accessing harm-reduction services in Kenya: a retrospective cohort study. Lancet Infect Dis.Nov. 2019 19(11):1255–1263.https://doi.org/10.1016/S1473-3099(19)30264-6

25. Loarec A et al. Feb., Extremely low hepatitis C prevalence among HIV co-infected individuals in four countries in sub-Saharan Africa. Aids 2019;33(2):353–355.https://doi.org/10.1097/QAD.0000000000002070

26. Maiyo AK, Odari EO, Kinyua J, Songok EM. Sero-prevalence and genotypes of hepatitis c among people who inject drugs in Nairobi Kenya. J Hum Virol Retrovirol. 2020;8(3):86–92. https://doi.org/10.15406/jhvrv.2020.08.00225.

27. Njeru DG, Mwanda WO, Kitonyi GW, Njagi EC. Prevalence of cytomegalovirus antibodies in blood donors at the National Blood Transfusion Centre, Nairobi., East Afr Med J. 2009;86(12):58–61.https://doi.org/10.4314/eamj.v86i12.62903

28. Kerubo G et al. Jun., Hepatitis B, hepatitis C and HIV-1 coinfection in two informal urban settlements in Nairobi, Kenya. PLoS One. 2015;10(6):1–9. https://doi.org/10.1371/journal.pone.0129247

29. Wairimu KM, Herbert K, John M. Prevalence of Transfusion Transmissible Infections Among Blood Donated At Nyeri Satellite Transfusion Centre In Kenya Kamande Magdaline Wairimu. Kibebe Herbert and Mokua John. 2016;6(2):20–30.

30. Wamamba D et al. Nov., Transfusion transmissible infections among walk-in blood donors at Kisumu regional blood transfusion centre, Kisumu County, Kenya, 2015, Lab Medicine. 2017;48(4):362–366. https://doi.org/10.1093/labmed/lmx059

31. Onyango CG, et al. Seroprevalence and determinants of transfusion transmissible infections among voluntary blood donors in Homabay, Kisumu and Siaya counties in western Kenya. BMC Res Notes. 2018;11(1):1–6. https://doi.org/10.1186/s13104-018-3276-y.

32. Bartonjo G, Oundo J, Ng'ang'a Z. Prevalence and associated risk factors of transfusion transmissible infections among blood donors at regional blood transfusion center nakuru and tenwek mission hospital, Kenya. Pan Afr Med J. 2019;34:1–13. https://doi.org/10.11604/pamj.2019.34.31.17885.

33. Harania RS, Karuru J, Nelson M, Stebbing J. HIV, Hepatitis B and Hepatitis C coinfection in Kenya. Aids. 2008;22(10):1221–2. https://doi.org/10.1097/QAD.0b013e32830162a8.

34. Muriuki BM, Gicheru MM, Wachira D, Nyamache AK, Khamadi SA. Prevalence of hepatitis B and C viral co-infections among HIV-1 infected individuals in Nairobi, Kenya. BMC Res Notes. 2013;6(1):1–6. https://doi.org/10.1186/1756-0500-6-363.

35. Wambani N, Ogola RJ, Makori PE AW and, DW BM, Lihana R, Hepatitis B, Co-Infections C. among HIV-1 Infected Patients Attending the Academic Model Providing Access to Healthcare Clinic, Kenya, 2014.Journal of Infectious Diseases and Diagnosis.2016; 1(1): 1–4.https://doi.org/10.4172/2576-389x.1000102

36. Maina DN, Nyerere AK, Gicho RW, Mwangi JM, Lihana RW. Prevalence and factors Associated with Hepatitis B and C Co-infection among HIV-1-Infected patients in Kenya. East Afr Health Res J. 2017;1(2):73–9. https://doi.org/10.24248/EAHRJ-D-16-00334.

37. Okoth SB, Rehmani OF, Karoney MJ, Diero L, Ayuo PO, SERO PREVALENCE OF HEPATITIS B AND C VIRUSES AMONG HIV INFECTED PATIENTS IN A HIV CARE PROGRAM IN KENYA.: A CROSS SECTIONAL STUDY. 2017; 94(4):266–73.

38. Too OW, Wamunyokoli B, Okendo F, Oketch J, Okwaro J, Lihana Wekesa A, Ogutu R. Viral Hepatitis B and Hepatitis C co-infections of HIV-1 infected patients in Kenya. East Afr Med J. 2018;95(7):1776–84.

39. Joseph M, Mpoke S. Sero-Mapping of HBV, HCV, HSV2 and Syphilis Across regions in Kenya. J Biol Agric Healthc. 2019;9(12):51–60. https://doi.org/10.7176/jbah/9-12-06.

40. Onyango KO, Nyamache AK, Kasera GO, Mabeya SN, Nonoh JO. Hepatitis B and C virus co-infections and genetic diversity among HIV-1 infected individuals in Siaya County, Kenya. East Afr Med J. 2021;98(2):3508–18.

41. Joseph M, et al. What are the missed opportunities in Prevention interventions for HBV, HCV and HIV among Key populations along the Northern Transport Corridor in Kenya? J Infect Dis Epidemiol. 2022;8(2):6–11. https://doi.org/10.23937/2474-3658/1510249.

42. Otedo AEO, Mc'Ligeyo SO, Okoth FA, Kayima JK. Seroprevalence of hepatitis B and C in maintenance dialysis in a public hospital in a developing country. South Afr Med J. 2003;93(5):380–4.

43. Wanyama FM, Tauber R, Mokomba A, Nyongesa C, Blanchard V, The Burden of Hepatitis B, Hepatitis C. and Human Immunodeficiency Viruses in Ovarian Cancer Patients in Nairobi, Kenya. Infect Dis Rep. 2022;14(3):433–445.https://doi.org/10.3390/idr14030047

44. Ndombi EM, et al. Serum adiponectin in HIV-1 and Hepatitis C virus mono- and coinfected Kenyan injection drug users. Endocr Connect. 2015;4(4):223–32. https://doi.org/10.1530/EC-15-0071.

45. Mwatelah RS, et al. Co-infection burden of hepatitis C virus and human immunodeficiency virus among injecting heroin users at the Kenyan coast. PLoS ONE. 2015;10(7):1–13. https://doi.org/10.1371/journal.pone.0132287.

46. Sambai BC et al. Dec., Characteristics associated with HIV and hepatitis C seroprevalence among sexual and injecting partners of HIV positive persons who inject drugs in Nairobi and coastal Kenya.BMC Infect Dis. 2022;22(1):1–15.https://doi.org/10.1186/s12879-022-07036-8

47. Sterne professor JAC, Sutton professor AJ. Recommendations for examining and interpreting funnel plot asymmetry in meta-analyses of randomised controlled trials, https://doi.org/10.1136/bmj.d4002

48. Salari N, Kazeminia M, Hemati N, Ammari-Allahyari M, Mohammadi M, Shohaimi S. Global prevalence of hepatitis C in general population: A systematic review and meta-analysis, Travel Med Infect Dis, vol. 46, no. April 2021, p. 102255, 2022, https://doi.org/10.1016/j.tmaid.2022.102255

49. Mora N, et al. A synthesis of Hepatitis C prevalence estimates in Sub-saharan Africa: 2000–2013. BMC Infect Dis. 2016;16(1):1–8. https://doi.org/10.1186/s12879-016-1584-1.

50. Mwangi J, et al. Hepatitis C virus genotypes in Kenya. Arch Virol. 2016;161(1):95–101. https://doi.org/10.1007/S00705-015-2623-8/FIGURES/1.

51. Anejo-Okopi J, Okojokwu OJ, Audu O, Virus HC. Molecular Epidemiology, Treatment and Diagnosis Challenges in Sub-Saharan Africa (SSA).Hosts and Viruses. 2020;7(3).https://doi.org/10.17582/journal.hv/2020/7.3.43.49

52. Makokha GN, Zhang P, Hayes CN, Songok E, Chayama K. The burden of Hepatitis B virus infection in Kenya: a systematic review and meta-analysis. Front Public Health.2023;11. https://doi.org/10.3389/FPUBH.2023.986020/FULL.

53. Downs LO, et al. A systematic review of Hepatitis B virus (HBV) prevalence and genotypes in Kenya: data to inform clinical care and health policy. PLOS Global Public Health. 2023;3(1):e0001165. https://doi.org/10.1371/JOURNAL.PGPH.0001165.

54. Hassan-Kadle MA, Osman MS, Ogurtsov PP. Epidemiology of viral hepatitis in Somalia: systematic review and meta-analysis study. World J Gastroenterol. 2018;24:3927–57. https://doi.org/10.3748/wjg.v24.i34.3927.

55. Kenya's Dadaab struggles with new influx of Somalis fleeing drought| UNHCR. Accessed: Apr. 09, 2024. [Online]. Available: https://www.unhcr.org/news/stories/kenya-s-dadaab-struggles-new-influx-somalis-fleeing-drought

56. Kim MH, Kang SY, Lee WI, Lee MY. Evaluation of HCV RNA by PCR and signal-to-cutoff ratios of HCV antibody assays for diagnosis of HCV infection. Lab Med. 2021;52(3):240–4. https://doi.org/10.1093/LABMED/LMAA074.

57. Seeff LB. Natural history of chronic hepatitis C, Hepatology. 2002;36(5) Suppl 1. https://doi.org/10.1053/JHEP.2002.36806

58. Guerra J, Garenne M, Mohamed MK, Fontanet A. HCV burden of infection in Egypt: results from a nationwide survey, J Viral Hepat. 2012;19(8):560–567. https://doi.org/10.1111/J.1365-2893.2011.01576.X

59. Mohammadi M, et al. Survey of both hepatitis B virus (HBsAg) and hepatitis C virus (HCV-Ab) coinfection among HIV positive patients. Virol J. 2009;6. https://doi.org/10.1186/1743-422X-6-202.

60. Mwaniki SW, Kaberia PM, Mugo PM, Palanee-Phillips T. HIV prevalence and associated risk factors among young tertiary student men who have sex with men (MSM) in Nairobi, Kenya: a respondent-driven sampling survey.AIDS Res Ther. 2023;20(1):1–11.https://doi.org/10.1186/S12981-023-00502-6/TABLES/2

61. Parker E, et al. HIV infection in Eastern and Southern Africa: highest burden, largest challenges, greatest potential. South Afr J HIV Med. 2021;22(1). https://doi.org/10.4102/SAJHIVMED.V22I1.1237.

62. Artenie A, et al. Incidence of HIV and Hepatitis C virus among people who inject drugs, and associations with age and sex or gender: a global systematic review and meta-analysis. Lancet Gastroenterol Hepatol. 2023;8(6):533–52. https://doi.org/10.1016/S2468-1253(23)00018-3.

63. Ludwig-Barron NT, et al. Barriers and facilitators of HIV and Hepatitis C care among people who inject drugs in Nairobi, Kenya: a qualitative study with peer educators. Harm Reduct J. 2021;18(1):133. https://doi.org/10.1186/S12954-021-00580-7.

64. Azevedo TCL, Zwahlen M, Rauch A, Egger M, Wandeler G. Hepatitis C in HIV-infected individuals: a systematic review and meta-analysis of estimated prevalence in Africa. J Int AIDS Soc. 2016;19(1):1–8. https://doi.org/10.7448/IAS.19.1.20711.

65. Melikoki V, Kourlaba G, Kanavaki I, Fessatou S, Papaevangelou V. Seroprevalence of Hepatitis C in Children without identifiable Risk-Factors: a systematic review and Meta-analysis. J Pediatr Gastroenterol Nutr. 2021;72(6):E140–8. https://doi.org/10.1097/MPG.0000000000003099.