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Epidemiology of arboviruses in humans and livestock in Ethiopia: a systematic review and meta-analysis

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Abstract

Background Arbovirus infections are a global public health threat, accounting for approximately 73% of the total emerging and re-emerging human infections, where the burden is worsened in sub-Saharan Africa, including Ethiopia. However, the surveillance system has been still challenged, and their burden and magnitude are not well estimated due to underestimates of true arbovirus burdens by passive case detections. To support targeted evidence-based public health decision-making, comprehensive evidence of arbovirus prevalence is crucial. Thus, the aim of this study was to assess the prevalence of arboviruses in humans and livestock in Ethiopia.

Method Articles were extensively searched in bibliographic databases and gray literatures using entry terms or phrases. PRISMA 2020 flow diagram was used and data among studies meeting eligibility criteria extracted in MS Excel sheet and exported into STATA-17 software for analysis. A random-effects model was used to compute the pooled magnitude of arboviruses in humans and livestock. The heterogeneity was quantified using the I^2 value. Publication bias was assessed using a funnel plot and Egger's test. Sensitivity analysis, subgroup analysis and meta-regression were performed to explore heterogeneity.

Result Of the 1957 studies identified, 39 human and 6 livestock studies were eligible for meta-analysis. The overall pooled sero-epidemiology of arboviruses in humans using anti-IgG and anti-IgM was 15.43% (95% CI: 12.11-18.76) and 10.04% (95% CI: 6.46-13.62), respectively. The molecular prevalence of arboviruses in humans was 38.42% (95% CI: 21.77-55.08). The pooled prevalence of arboviruses in livestock was 15.77% (95% CI: 0.45, 31.08). Dengue virus, Yellow fever virus, Zika virus, Rift valley fever, West Nile virus, and chikungunya virus in humans and Rift valley fever, West Nile virus, and Schmallenberg virus in livestock were reported.

Conclusion The magnitude of arboviruses in humans and livestock in Ethiopia alarms the need for immediate multi-sectoral interventions such as strengthening laboratory diagnostic capacities, undertaking an integrated regular national surveillance, and implementation of one-health initiatives and a planetary health approach.

Keywords Arboviruses, Ethiopia, Human, Livestock, Systematic review and meta-analysis

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Background

Globally, arbovirus infect millions of individuals and pose a significant emerging and re-emerging public health threats. These viruses account for approximately 73% of all newly identified human infections [1]. Arboviral diseases affect over half of the world's population, resulting hundreds of millions of cases annually. For instance, the dengue virus alone is responsible for more than 390 million infections each year [2], while yellow fever caused 84,000–170,000 severe cases and 29,000–60,000 deaths in Africa in 2013 [1]. The global economic burden is estimated at $8–9 billion per year, encompassing costs related to illness and vector control. This burden is expected to increase as climate change affects transmission dynamics [3]. The cumulative reported cost of arboviral diseases was estimated to be $87.3 billion from 1975 to 2020 [4] and the costs of vector control programs was ranged from 5.62 to 73.5 million USD [5].

The predominant arboviruses co-circulating in the African region includes Yellow fever virus (YFV), dengue virus (DENV), Chikungunya virus (CHIKV), Rift Valley fever (RVF), West Nile virus (WNV), and Zika virus (ZIKV) [6]. In sub-Saharan Africa (SSA), these arboviral diseases impose enormous health and economic burdens, leading to increased mortality, morbidity, and disability in the region [7, 8]. Thus, there is an urgent need to strengthen epidemiological characterization and enhance control capabilities [7, 8].

Global trends such as climate change, population growth, and human activities like increased travel and trade connectivity, are facilitating the geographic expansion and evolution of arboviruses, altering vector life cycles and viral transmission dynamics, which heightens the risk of disease outbreaks [1, 9, 10]. On the contrary, surveillance systems continue to face significant challenges due to different factors. Passive case detection often underestimates the true arbovirus burdens due to the non-specific clinical presentations of DENV, CHIKV, and ZIKV [2]. Additionally, limited diagnostic capacities in resource limited countries hinder effective epidemiological analyses and response monitoring [11]. The lack of viability for confirmatory testing of surveillance samples [12] as well as integrated vector surveillance, is rarely sustained, yet critical for outbreak preparedness.

Moreover, these infections are associated with loss of productivity and increased healthcare costs as a result of prolonged illness and disability from infections. Emerging outbreaks might occur due to the invasion of naïve populations by Chikungunya's, which leads to escalating demand for services [13]. The problem is also certainly higher in rural communities where farming and livestock are carried out. In forested areas, the risk of yellow fever is higher, particularly in immunologically naive travelers and workers. However, knowledge of circulating virus strains involved in transmission remains limited in high-risk areas of the African region.

Despite the substantial burden of arboviral diseases in SSA, critical gaps remain in generating comprehensive evidence necessary for targeted public health decision-making. Although some initiatives have improved certain research aspects, the lack of integrated, multidisciplinary investigations hampers our understanding of the dynamic relationships driving local transmission [14]. Furthermore, up-dated and comprehensive evidence is needed for outbreak preparedness; however, comprehensive data of cocirculating strains of arboviruses in Ethiopia is lacking. This review aims to address this gap by enhancing our understanding of arbovirus epidemiology in Ethiopia, providing a foundation for evidence-based decision-making in integrated disease prevention and control from human and animal health dimensions. Therefore, the aim of this systematic review and meta-analysis (SRMA) is to determine the overall pooled magnitude of arboviruses among humans and livestock in Ethiopia.

Methods

Protocol registration and guidelines

This SRMA was developed and reported according to the Preferred Reporting Items for Systematic Reviews and Meta-Analyses Guidelines (PRISMA) [15] as indicated in Supplementary File 1. The protocol for this review was originally registered in the International Prospective Register of Systematic Reviews (PROSPERO) database with registration identification number CRD42024561271, available from: https://www.crd.york.ac.uk/prospero/display_record.php?ID=CRD42024561271.

Data source, search strategy and selection of studies

A systematic and comprehensive search of the existing literature was carried out using multiple electronic databases, including PubMed/Medline, Epistimonikos, and Embase. Additionally, grey literature such as Wiley Online Library, Science Direct, Research Gate, African Journal Online (AJOL), Google Scholar, and Web of Sciences were used to retrieve potentially eligible studies reporting the prevalence of the common arboviruses (Dengue virus, Yellow fever virus, West Nile virus, Zika virus, Chikungunya virus, Rift valley fever, and Schmallenberg virus) among humans and livestock in Ethiopia. In order to include additional relevant studies omitted during electronic database searches, a snowball search was conducted using the bibliographies of the identified studies. Generally, the search was conducted from April 20, 2024, to May 20, 2024.

An extensive comprehensive search strategy was employed using the condition, context, population, and outcome of interest (CoCoPop) framework to formulate research questions [16]. The research question was formulated as "What is the prevalence of arboviral infections in humans and livestock's' of Ethiopia?". Moreover, the CoCoPop framework was condition (arboviral infections), context (Ethiopia), and population (humans and livestock's). To access all eligible studies, Medical Subject Headings (MeSH) terms and combination key words including "prevalence", "outbreak", "sero-prevalence", "Sero-positivity", "detection", "epidemiology", "burden", "magnitude", "Arbovirus", "Dengue virus", "Zika virus", "West Nile Virus", Yellow fever virus", "Chikungunya virus", "Chikungunya fever", "Schmallenberg virus", "YFV", "DENV", "RVF", "ZIKV", "CHIKV", "SBV", and "Ethiopia" were employed. Boolean operators such as "OR" and "AND" were used as necessary in the advanced search databases. Furthermore, the bibliographies of included studies were reviewed for additional articles, and authors were contacted to obtain any missing papers. Duplicates were removed after the search results were organized using Endnote 20 software (Clarivate Analytics USA). Three independent reviewers (AG, MAB, and EA) identified the articles from databases and other sources and removed duplicates. Subsequently, two independent reviewers (HD, LW) screened the titles and abstracts of all retrieved studies, cross-checked by a third reviewer (MT), followed by assessment of the full texts of potentially eligible studies against inclusion criteria by two reviewers (AS and MT), verified by a third reviewer (HE), and added to the extraction collection. Disagreements during each screening stage were resolved through consensus between the two reviewers and/or intervention of a third reviewer (MT).

Eligibility criteria

All articles published in peer-reviewed journals or grey literature in English language and reporting the prevalence of arbovirus infection and/or its genetic variants were included in this SRMA. Moreover, all laboratory-based observational studies, including cross-sectional studies, case-control, and cohort studies using laboratory detection methods such as polymerase chain reaction (PCR) and enzyme-linked immunosorbent assays (ELISA) for detecting arboviruses such as RNA, IgG, IgM, Non-structural protein-1 and plaque reduction neutralization tests (PRNT) from clinical specimens and livestock in Ethiopia until April 30, 2024, were included. However, reviews, qualitative studies, author replies, letters to the editor, case reports and commentaries were excluded from this SRMA.

Risk of bias assessment

The quality of studies included in this SRMA was evaluated by three authors (ZM, MAB and BK) using the Joanna Briggs Institute (JBI) quality appraisal tool designed for prevalence studies [17]. The critical appraisal checklist was used to evaluate the methodological quality of studies included in the SRMA. Finally, studies with an average quality score of 50% or more were considered to be high quality (low risk of bias) and consequently included in the analysis. The evaluation involved screening studies at the title, abstract, and full text levels. A supplementary file provides further details on the critical appraisal process and scoring (Supplementary File 2).

Outcome measurement

The primary outcome variable of this SRMA was the pooled prevalence of arboviral infections in humans and livestock in Ethiopia.

Data extraction, synthesis and statistical analysis

The data extraction of eligible studies was performed by four reviewers (SS, BE, MMT, and NKM) using a Microsoft Excel worksheet. The extracted data includes authors names, publication year, region, study area, setting, study design, approach, population type, laboratory diagnosis method, diagnostic marker, sample size, number and type of arboviruses. The three reviewers meticulously reviewed and verified their extraction results, resolving any discrepancies through discussions and cross-verification of data (Supplementary File 3).

The meta-analysis was performed using STATA version 17.0 software (Stata Corp., College Station, TX). The point estimate and 95% confidence interval of the pooled prevalence of arbovirus was computed. A random-effects model of analysis was used to estimate the pooled prevalence of arboviruses [18]. Cochrane's Q test and I^2 statistics were used to assess heterogeneity between studies [19], in which an I^2 of more than 75% was considered substantial heterogeneity. A p value of >0.05 was used to declare that the effect was homogeneous. Therefore, to adjust the observed variability, a random effect model was used. The presence of heterogeneity was further analyzed for its source using subgroup analysis, which was computed based on region, study design, approach, type of arbovirus, setting, population type, laboratory diagnostic method, and diagnostic markers. Likewise, meta-regression was also conducted to identify the possible source of heterogeneity. Finally, a sensitivity analysis was performed to evaluate the impact of individual studies on the overall pooled estimate using a leave-one-out analysis to examine the influence of a single study on the overall

estimate of arboviruses. Furthermore, publication bias was assessed using visual inspection of the symmetry of the funnel plot and Egger's test statistics [20–22].

Result

Literature search and eligible studies

During the initial electronic search and manual search of reference lists, a total of 1957 articles were retrieved. Approximately 541 articles were excluded because of duplication, 1346 studies were excluded by reviewing their title, abstract and body, and 22 articles were excluded because they were not related to the objective or outcome of this study. Finally, after methodological quality assessment, 52 human studies and 6 livestock studies were included in this systematic review, however, seven studies were excluded in the quantitative synthesis or meta-analysis due to their sample size being lower than 30. Thus, 41 and 6 studies among humans and livestock were included in the final analysis, respectively (Figure 1).

Study characteristics

The studies were conducted from 2014 to 2023 in nine national regional states and the two city administrations of Ethiopia. Considering the districts where the studies were conducted in SNNRP (Arba Minch Zuria, South Omo Zone, Mareka district) and the Somalia region (Kabradihar, Dollo, Dollo ado, Adadle, Godey) (Figure 2, Table 1). Only six human studies were case-control, while all animal studies were cross-sectional, and all are published in English. PCR, ELISA, IFT, and PRNT were employed for the detection of arboviruses targeting the RNA of the virus, its antigen, and antibodies (IgG and IgM), however, ELISA was found to be the commonly used method. The maximum sample size from the included studies was 41,162. In all the studies included in the systematic review, a total of 56,057 humans and 3639 livestock were involved. Of the included participants, 2,584 humans were positive by either of PCR, ELISA, IFT, NS1, PRNT, anti-IgG, and anti-IgM, and 980 livestock were positive by anti-IgG antibodies of arboviruses. In human studies, six arboviruses (DENV, YFV, ZIKV, RVF, WNV, and CHIKV) from the three families (Flaviviridae, Bunyaviridae, and Togaviridae) and three genera (Flavivirus, Phlebovirus, and Alphavirus) were reported, while among livestock studies, three arboviruses (RVF, WNV, and SBV) from two families (Bunyaviridae and Flaviviridae) and three genera (Flavivirus, Phlebovirus, and Orthobunyavirus) were reported. The overall risk of bias assessment score of included studies was 82.44% (Table 1).

Epidemiology of Arboviruses in Ethiopia

After the qualitative synthesis, studies with fewer than 30 participants (eight studies) were excluded from quantitative analysis (meta-analysis). Regardless of the diagnostic markers, the overall pooled prevalence of arboviruses was 11.96% (95% CI: 10.82%, 13.09%), and 15.77% (95% CI: 0.45, 31.08%), respectively in human (Figure 3) and livestock (Figs 4, 5). The existence of heterogeneity between studies was assessed by visual (subjective) techniques using the Galbraith plot to check whether all the points lie within the 95% confidence bounds and the Forest plot to check whether the confidence intervals of studies (the summary effects) overlap with each other. To avoid the subjective nature of visual techniques, the I^2 test was used. Consequently, there was substantial heterogeneity between the included studies in human and livestock studies with an I^2 value of 98.65% and 99.59%, respectively. Therefore, we have used certain strategies to address heterogeneity, such as carrying-out the meta-analysis using the random effect model, followed by exploring the sources of heterogeneity using sensitivity analysis, subgroup analysis, and meta regression. Thus, Galbraith plot revealed the presence of studies that were outside of the 95% confidence interval in human studies and livestock studies. However, in the leave one-out meta-analysis (sensitivity) analysis, none of the omitted analyses were lies outside the confidence interval for combined analysis. As a result, the result was analyzed considering stratification variables through setting, diagnostic methods and markers, approaches used and the type of viruses reported as reported in the following sections.

Arboviruses epidemiology based on diagnostic markers and methodology among humans

A total of 46 prevalence studies for different arboviruses using different diagnostic methods were identified in humans, of which 10 estimated seroprevalence prospectively from 2018 to 2022. The studies covered 6 of the regional states of Ethiopia with an estimated seroprevalence of 2.7% to 22.53%. Furthermore, the overall seroprevalence of IgM in humans was 10.02% (95% CI: 6.44%, 13.61%), with a significant level of heterogeneity (I^2 = 95.72%). Among eighteen [18] studies that were reported arboviruses in humans using IgG detection, 11 were conducted at the community level and all of the 18 studies were prospective studies published from 2018 to 2021 with an estimated seroprevalence of 3.47% to 49.52%. The overall sero-prevalence of IgG in humans was 15.43% (95% CI: 12.11%, 18.75%), with a significant level of heterogeneity (I^2 = 98.02%). Additionally, seven studies with 232 cases were reported arboviruses in two regional

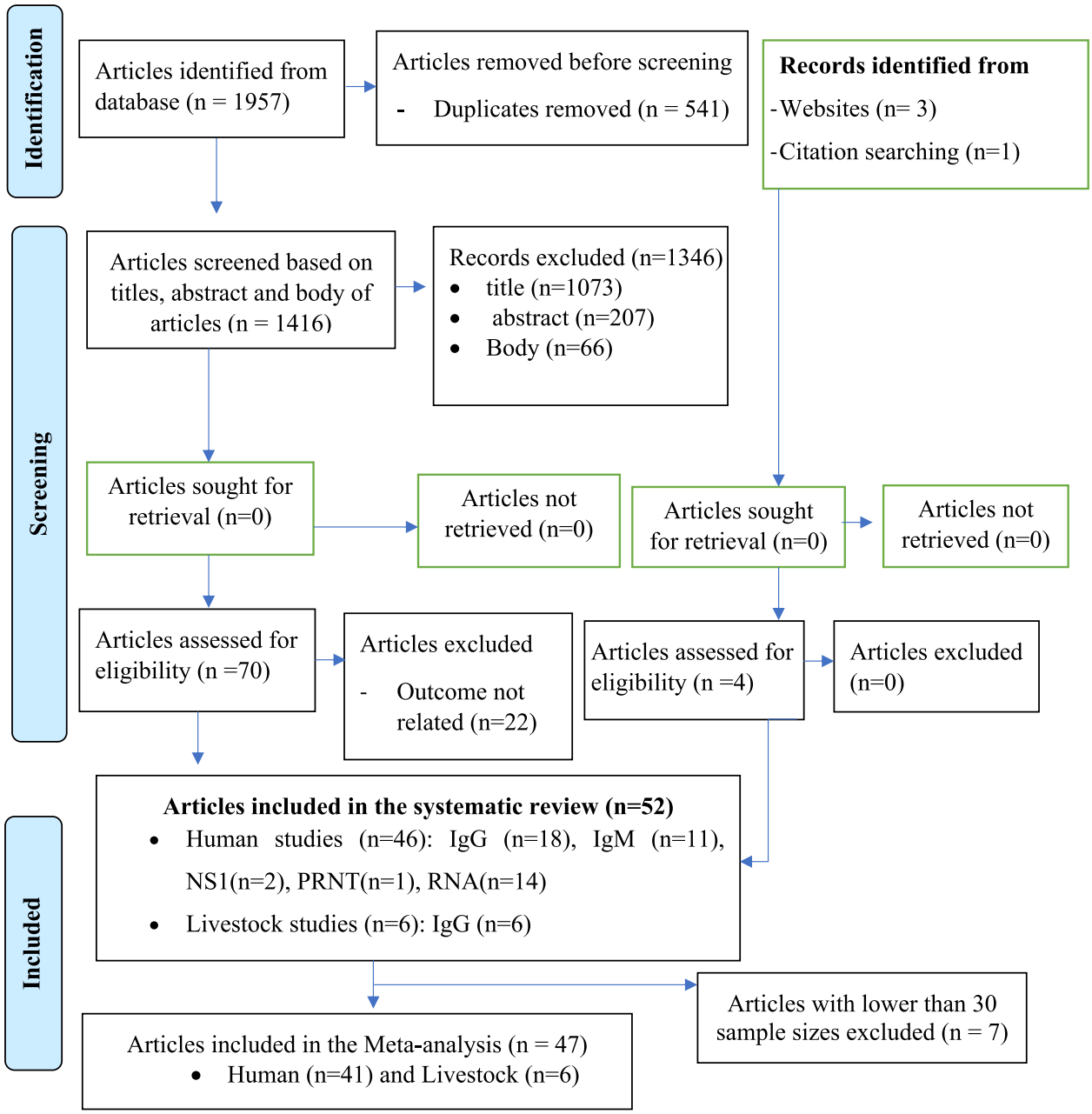

Fig. 1 Flow diagram for the selection process of eligible studies

states (Afar and Somalia) and one city administration (Dire Dawa) of Ethiopia. The estimated prevalence was reported from 12.3% in 2020 to 67.74% in 2019. The overall pooled prevalence of arboviral RNA was 36.82% (95% CI: 14.82%,58.81%) with a similar substantial heterogeneity of serological markers (I^2 = 97.73%). Furthermore, two studies estimated arboviruses using NS1 detection in 2022 and 2023 with an overall pooled prevalence of arboviruses in humans using NS1 detection was 21.45% (95% CI: −16.75%,59.63%). One the other hand, a single study was performed using PRNT and reported four different arboviruses from the genus Flaviviruses (i.e., DENV, ZIKV, YFV and WNV (Table 2, Figure 6).

Considering the diagnostic methods used for the detection of arboviruses, the predominancy was observed in molecular methods (36.82%) followed by ELISA (17.09%) and IFT (10.44%). Almost all human studies were cross-sectional studies employed a

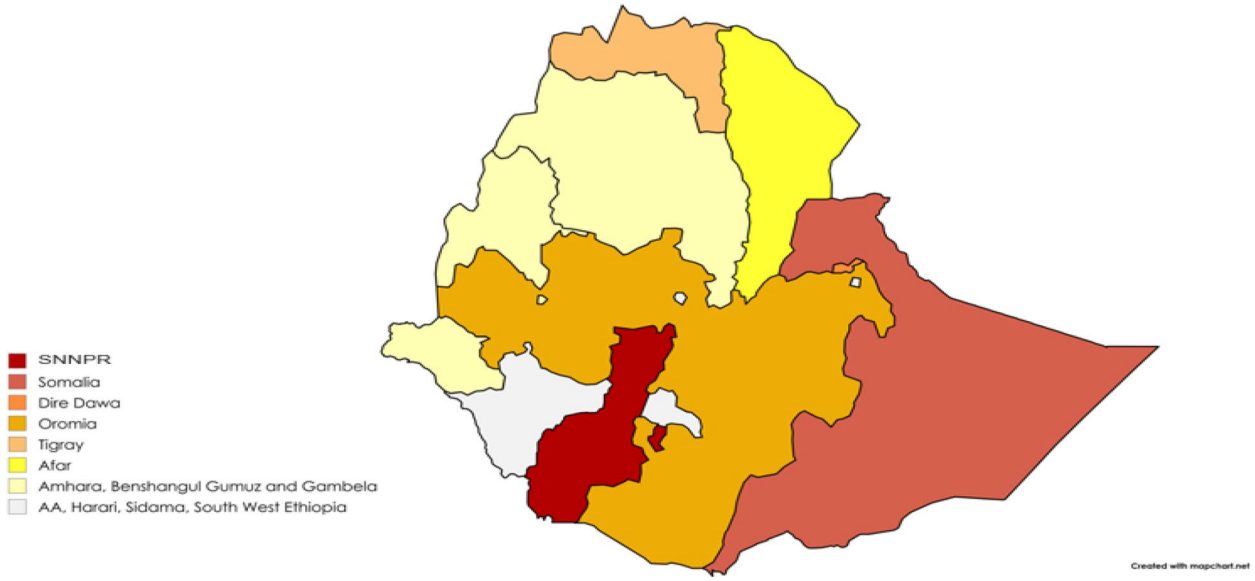

Fig. 2 Map showing Ethiopian regions for which data were included in the systematic review and meta-analysis created using https://www.mapchart.net/world-subdivisions.html. The depth of different color shading indicates the number of studies performed in each region of SNNPR the country.

prospective approach however, their pooled effect was not statistically varied. Furthermore, there was a significant difference (P <0.001) in the epidemiology of arbovirus between studies conducted at the clinical settings (17.91%) and the community level (8.49%) (Figure 6). However, all of livestock studies were a prospective and cross-sectional studies conducted at the community level (Table 1).

Geographic distribution and trends of arboviruses among humans and livestock in Ethiopia

Arboviruses among humans were reported in multiple regions of Ethiopia particularly in hottest areas and boundaries of neighboring countries such as Metema and Humera, Dire Dawa, Somalia and Gambella (Figure 7). According to the cumulative meta-analysis, there was a variability of prevalence of arboviruses ranged from 0.04% to 57.9%. It showed that the arbovirus prevalence can vary considerably across different populations, geographical regions, and study settings (Figure 8). The former studies (i.e., studies of 2014 and 2016 were single) but showing the peak level of arbovirus. Likewise, the peak level of arbovirus in humans pooled from multiple studies was reported in 2022(27.68%), 2019 (23.72%), and 2023 (21.71%) (Figure 9).

Among livestock, arboviruses were reported from camels, goats, sheep, and cattle (Table 1). The subgroup analysis for revealed that majority of studies were conducted at SNNRP and Gambella regional states with a pooled prevalence of 4.91% and 6.4%, respectively. Two families and three genera were reported in livestock studies (Table 3).

Types of arboviruses among humans and livestock in Ethiopia

Regardless of the type of diagnostic methods and diagnostic markers used, the overall pooled prevalence of CHIKV, DENV, RVF, WNV, YFV, and ZIKV was 16.69% (7.0%, 26.39%), 23.41% (19.02%, 27.79%), 13.2% (8.39%, 18.01%), 4.43% (1.78%, 7.07%), 10.48% (6.58%, 14.37%), and 7.18% (2.72%, 11.65%), respectively. Three genus and families of arboviruses were reported in humans, of which, the predominant genus/families were Flaviviruses/Flaviviridae, which was found to be reported in 34 studies with an overall pooled prevalence of 12.62% (11.08%, 14.15%; P<0.001) (Figure 10). However, in livestock studies the most frequently reported arboviruses were the Bunyaviridae family, with a pooled prevalence of 21.1% (−2.09%, 44.3%). Half of the studies were RFV, with a pooled prevalence of 9.26%. Moreover, the three reported viruses among livestock were detected using IgG (Table 3). Furthermore, DENV was predominantly reported among 3 studies from Dire Dawa and Tigray region with a pooled prevalence of 48.67% (95% CI: 21.71%−75.63%) and 26.49% (13.11%−39.87%), respectively, while it was reported with high frequency from a single study from both Somalia and Afar region with a prevalence of 57.89% and 41.56%, respectively. Yellow fever was most common in SNNRP reported from four

Table 1 Characteristics of included studies for assessing the epidemiology of Arboviruses among humans and livestock in Ethiopia

	Authors	Publication year	Region	District/s	Study Design	Approach	Study setting	Diagnostic technique	Group	Sample size	Number of cases reported						Arbovirus type	Quality
											RNA	IgM	IgG	IgG +IgM	NS1	PRNT		
1	Woyessa et al. [23]	2014	Dire Dawa	Dire Dawa	CS	Prospective	Clinical	PCR	Human	88	50						DENV	Medium
2	Ahmed et al. [24]	2016	Somali	Godey	CS	Retrospective	Clinical	PCR	Human	57	33						DENV	High
3	Ferede et al. [25]	2018	Tigray	Humera and Metema	CS	Prospective	Clinical	ELISA	Human	600		114	126	40			DENV	High
				Humera	CS	Prospective	Clinical	ELISA	Human	320		55	51	17				
				Metema	CS	Prospective	Clinical	ELISA	Human	280		60	75	23				
4	Geleta et al [26]	2019	Oromia	Borena	CS	Prospective	Clinical	IFT	Human	519		41	119				DENV	High
5	Eshetu et al. [27]	2020	SNNRP	Arba Minch Zuria	CS	Prospective	Clinical	IFT	Human	529		42	133				DENV	High
6	Gutu et al. [28]	2021	Somali	Kabradihar	CC	Prospective	Clinical	PCR	Human	21	15						DENV	Medium
7	Akelew et al. [29]	2022	Amhara	Gondar	CS	Prospective	Clinical	ELISA	Human	200		41					DENV	High
8	Sisay et al. [30]	2022	Dire Dawa	Dire Dawa	CS	Prospective	Clinical	PCR	Human	60	13						DENV	High
9	Mekuriaw et al. [31]	2022	Afar	Gewane	CS	-	Clinical	PCR	Human	12	6						DENV	High
10	Mesfin et al. [32]	2022	Somali	Dollo	CC	-	Clinical	PCR	Human	20	6						DENV	High
11	Biru et al [33]	2020	Dire Dawa	Dire Dawa	CC	Prospective	Clinical	PCR	Human	10	6						DENV	High
12	Shimelis et al. [34]	2023	SNNRP	Hawassa	CS	Prospective	Clinical	ELISA	Human	407					9		DENV	High
13	Tsegaye et al [35]	2018	Amhara, Oromia, SNNRP, Somalia, BG	Multiple	CS	Prospective	Community	ELISA	Human	1643			57			9	DENV	High
14	Sisay et al. [36]	2023	Afar	Multiple	CS	Prospective	Clinical	PCR	Human	154	64						DENV	Medium
15	Degifie [37]	2019	Dire Dawa	Dire Dawa	CS	Prospective	Clinical	PCR	Human	62	42						DENV	High

Table 1 (continued)

	Authors	Publication year	Region	District/s	Study Design	Approach	Study setting	Diagnostic technique	Group	Sample size	Number of cases reported						Arbovirus type	Quality
											RNA	IgM	IgG	IgG +IgM	NS1	PRNT		
16 17	Ferede et al. [38]	2023	Tigray	Humera and Metema	CS	Prospective	Clinical	ELISA	Human	114 60					17 49		DENV	High
	Nigussie et al [39]	2020	Oromia	Borena	CS	Prospective	Clinical	IFT	Human	519		38	65				YFV	High
18	Endale et al [40]	2020	SNNRP	South Omo Zone	CS	Prospective	Community	ELISA	Human	313			155				YFV	High
19	Lilay [41]	2017	SNNRP	South Omo Zone	CS	Retrospective	Clinical	ELISA	Human	21		7					YFV	High
20	Eshetu et al. [42]	2020	SNNRP	Gamo Gofa zone	CS	Prospective	Clinical	IFT	Human	529		38	79				YFV	High
21	Asebe et al [43]	2021	Gambella	Lare and Itang	CS	Prospective	Community	ELISA	Human	135			4				YFV	High
22	Mulchandani et al [44]	2019	SNNRP	South Omo Zone	CS	Prospective	Community	ELISA	Human	165		6					YFV	Medium
23	Tsegaye et al [35]	2018	Amhara, Oromia, SNNRP, Somalia, BG	Multiple	CS	Prospective	Community	PRNT	Human	1643			112			10	YFV	High
24	Tsegaye et al [35]	2018	Amhara, Oromia, SNNRP, Somalia, BG	Multiple	CS	Prospective	Community	PRNT	Human	1643			91			15	WNV	High
25	Eshetu et al. [45]	2020	SNNRP	Arba Minch Zuria	CS	Prospective	Clinical	IFT	Human	529		24	39				WNV	High
26	Nigussie et al [46]	2021	Oromia	Borena	CS	Prospective	Clinical	IFT	Human	519		14	38				WNV	High
27	Tsegaye et al [35]	2018	Amhara, Oromia, SNNRP, Somalia, BG	Multiple	CS	Prospective	Community	PRNT	Human	1643			65			7	ZIKV	High
28	Asebe et al [43]	2021	Gambella	Lare and Itang	CS	Prospective	Community	ELISA	Human	150			41				ZIKV	High
29	Ibrahim et al [47]	2021	Somali	Adadle	CS	Prospective	Community	ELISA	Human	190			25				RVF	High

Table 1 (continued)

	Authors	Publication year	Region	District/s	Study Design	Approach	Study setting	Diagnostic technique	Group	Sample size	Number of cases reported						Arbovirus type	Quality
											RNA	IgM	IgG	IgG +IgM	NS1	PRNT		
30	Asebe et al [43]	2021	Gambella	Lare and Itang	CS	Prospective	Community	ELISA	Human	90			14				CHIKV	High
31	Endale et al [40]	2020	SNNRP	South Omo Zone	CS	Prospective	Community	ELISA	Human	360			157				CHIKV	High
32	Geleta et al [48]	2020	Dire Dawa	Dire Dawa	CS	Retrospective	Clinical	PCR	Human	41162	16						CHIKV	Medium
33	Ferede et al. [49]	2021	Tigray	Humer-Metema	CS	Prospective	Clinical	ELISA	Human	586		132	31	28			CHIKV	High
				Metema	CS	Prospective	Clinical	ELISA	Human	274		82	18	16			CHIKV	High
				Humera	CS	Prospective	Clinical	ELISA	Human	312		50	13	12			CHIKV	High
34	Takele et al [50]	2020	Somali	Dolo ado	CC	Prospective	Clinical	PCR	Human	99	14						CHIKV	Medium
	Aassefa et al [51]	2020	SNNRP	Mareka district	CC	Prospective	Clinical	PCR	Human	14	8						CHIKV	High
35	Alayu et al [52]	2020	Somali	Kebridhar City	CC	Prospective	Clinical	PCR	Human	5	3						CHIKV	High
36	Asebe et al [53]	2020	Gambella	Lare	CS	Prospective	Community	ELISA	Livestok[1]	368			28				RFV	High
37	Endale et al [54]	2021	SNNRP	South Omo Zone	CS	Prospective	Community	ELISA	Livestok[1]	397			20				RFV	High
38	Asebe et al [53]	2020	Gambella	Lare	CS	Prospective	Community	ELISA	Livestok[1]	368			20				WNV	High
39	Endale et al [54]	2021	SNNRP	South Omo Zone	CS	Prospective	Community	ELISA	Livestok[1]	397			19				WNV	High
40	Sibhat et al [55]	2018	AA, Oromia, SNNRP	Multiple	CS	Prospective	Community	ELISA	Livestok[1]	1379			780				SBV	Medium
41	Ibrahim et al [47]	2021	Somali	Adadle	CS	Prospective	Community	ELISA	Livestok[1]	108			19				RFV	High
									Livestok[2]	141			60				RFV	High
									Livestok[3]	252			15				RFV	High
									Livestok[4]	229			17				RFV	High
										59696	276	744	2445	136	58	41		

CC Case Control, *CS* Cross-sectional, *ELISA* Enzyme-Linked Immunosorbent Assay, *IFT* Immune Fluorescent Test, *PCR* Polymerase Chain Reaction, *PRNT* Plaque Reduction Neutralization Test, *SNNRP* Southern Nations Nationalities and People's Region, Livestok[1]: Cattle; Livestok[2]: Camel; Livestok[3]: Goat; Livestok[4]: Sheep; CHIKV: Chikungunya Virus; DENV: Dengue Fever Virus; RFV: Rift Valley Fever; SBV: Schmallenberg virus; WNV: West Nile Virus; YFV: Yellow Fever Virus; ZIKV: Zika Virus

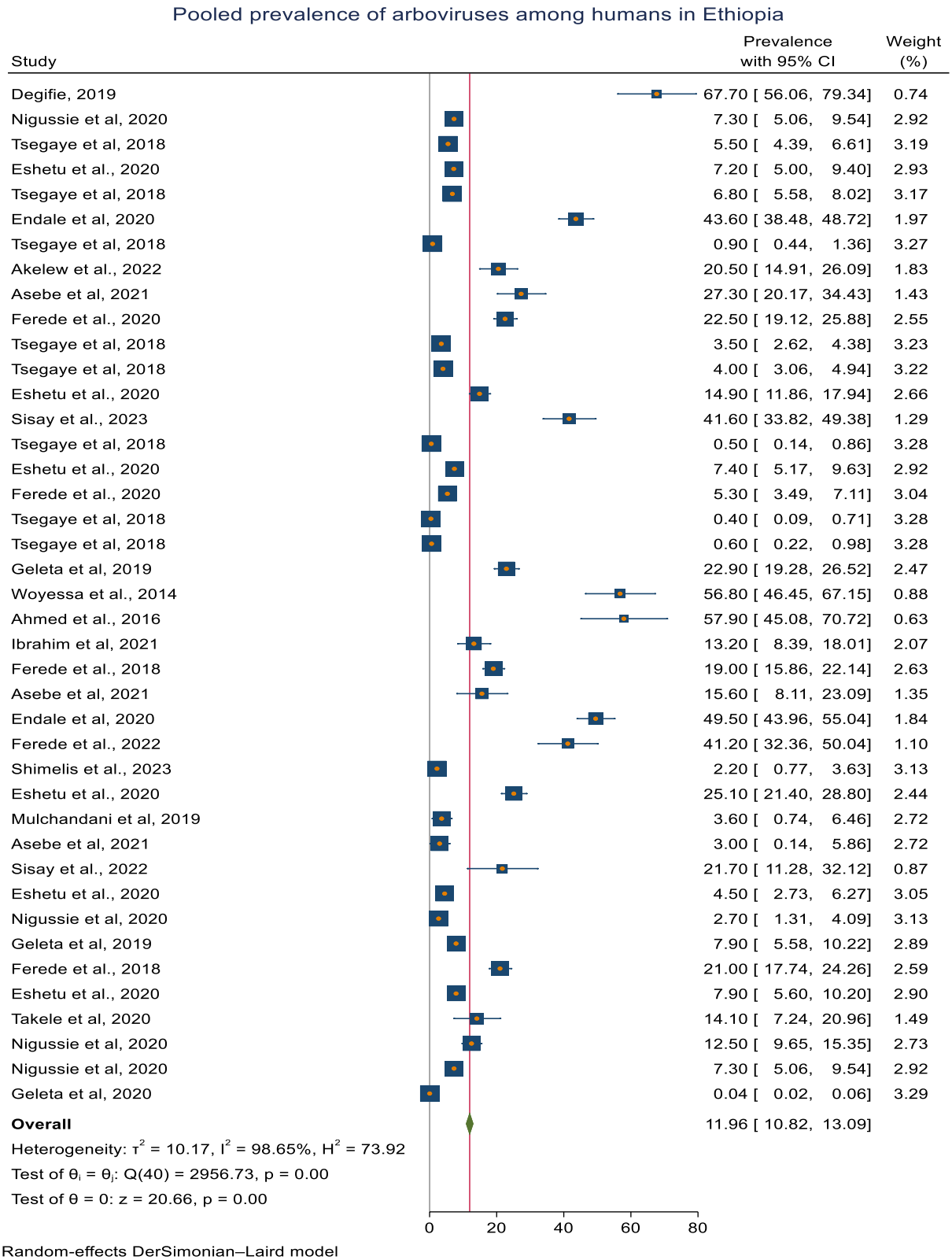

Fig. 3 Forest plot showing pooled prevalence of arboviruses among humans in Ethiopia

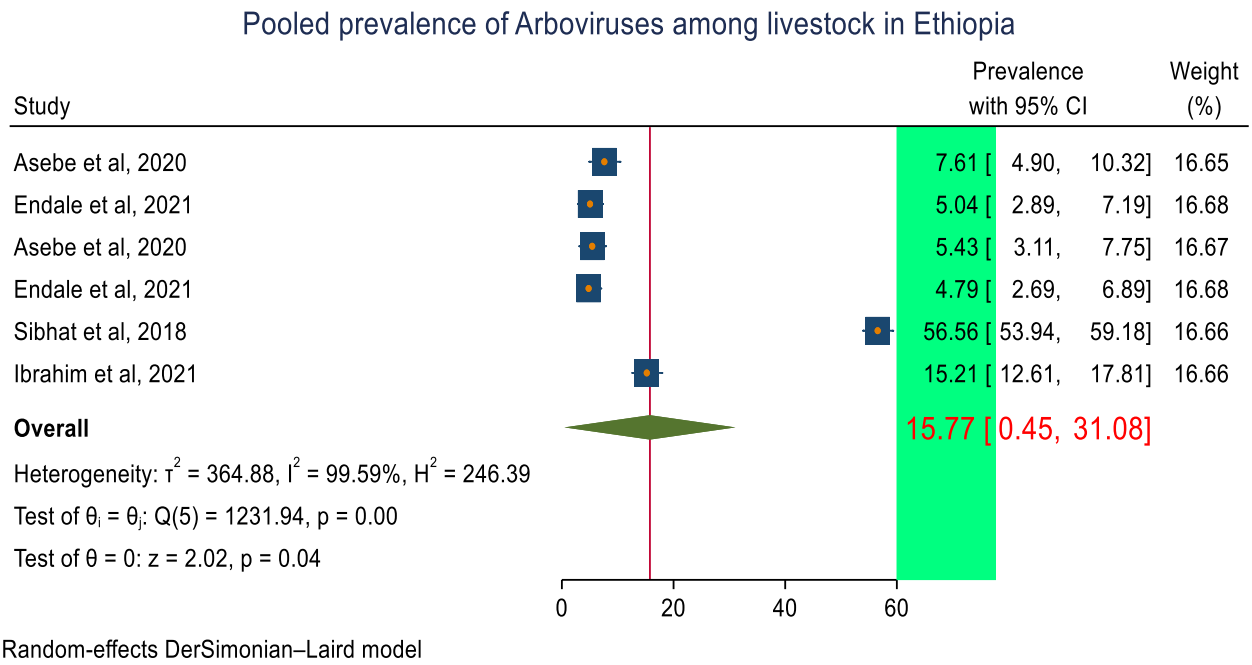

Fig. 4 Forest plot showing pooled prevalence of arboviruses IgM seroprevalence among livestock in Ethiopia

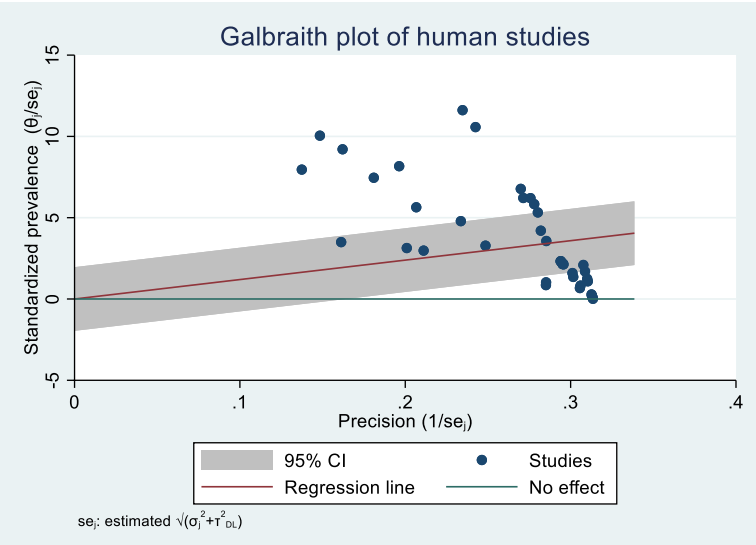

Fig. 5 Forest plot showing pooled prevalence of arboviruses IgM seroprevalence among livestock in Ethiopia

studies with a pooled prevalence of 18.71%, and CHIKV virus was most frequently reported from SNNRP, Gambella and Somalia respectively. Additionally, WNV was predominant in SNNRP and Oromia with a pooled prevalence of 5.86% and 4.92%, respectively.

Meta-regression analyses

To investigate the impacts of active potential factors in the heterogeneity of prevalence of arboviruses in Ethiopia, a random-effects meta-regression test has been done using the DerSimonian–Laird method. Furthermore, meta-regression analysis was computed with each potential factors and covariates individually with the effect size. Diagnostic markers (R^2 = 1.90%), quality of studies (R^2 =

Table 2 Pooled prevalence of arboviruses among humans in Ethiopia using different diagnostic markers

Arbovirus markers	Number of studies	Number of cases	PP (95% CI)	I^2	H	*p*-value
Humans						
- IgG seroprevalence	18	1465	15.43(12.11, 18.75)	98.02	50.52	**<0.001**
- IgM seroprevalence	11	136	10.02(6.44, 13.61)	95.72	23.34	**<0.001**
- NS1	2	58	21.45(−16.77, 59.66)	98.63	72.86	**<0.001**
- PRNT	1*	41	0.56(0.37, 0.75)	7.36	1.08	0.36
- Viral RNA prevalence	7	232	36.82(14.82,58.81)	97.73	44.07	**0.001**
Livestock						
- IgG seroprevalence	6	980	15.77(0.45, 31.08)	99.59	246.39	**<0.001**

1*: one article assessed four viruses (DENV, ZIKV, YFV and WNV), *PRNT* plaque reduction neutralization tests, *NS1* Non-structural protein-1, *PP* pooled prevalence, *CI* confidence interval, *H* Cochrane Q, chi square for heterogeneity, *Ig* immunoglobulin; *P*<0.01: Significant heterogeneity.

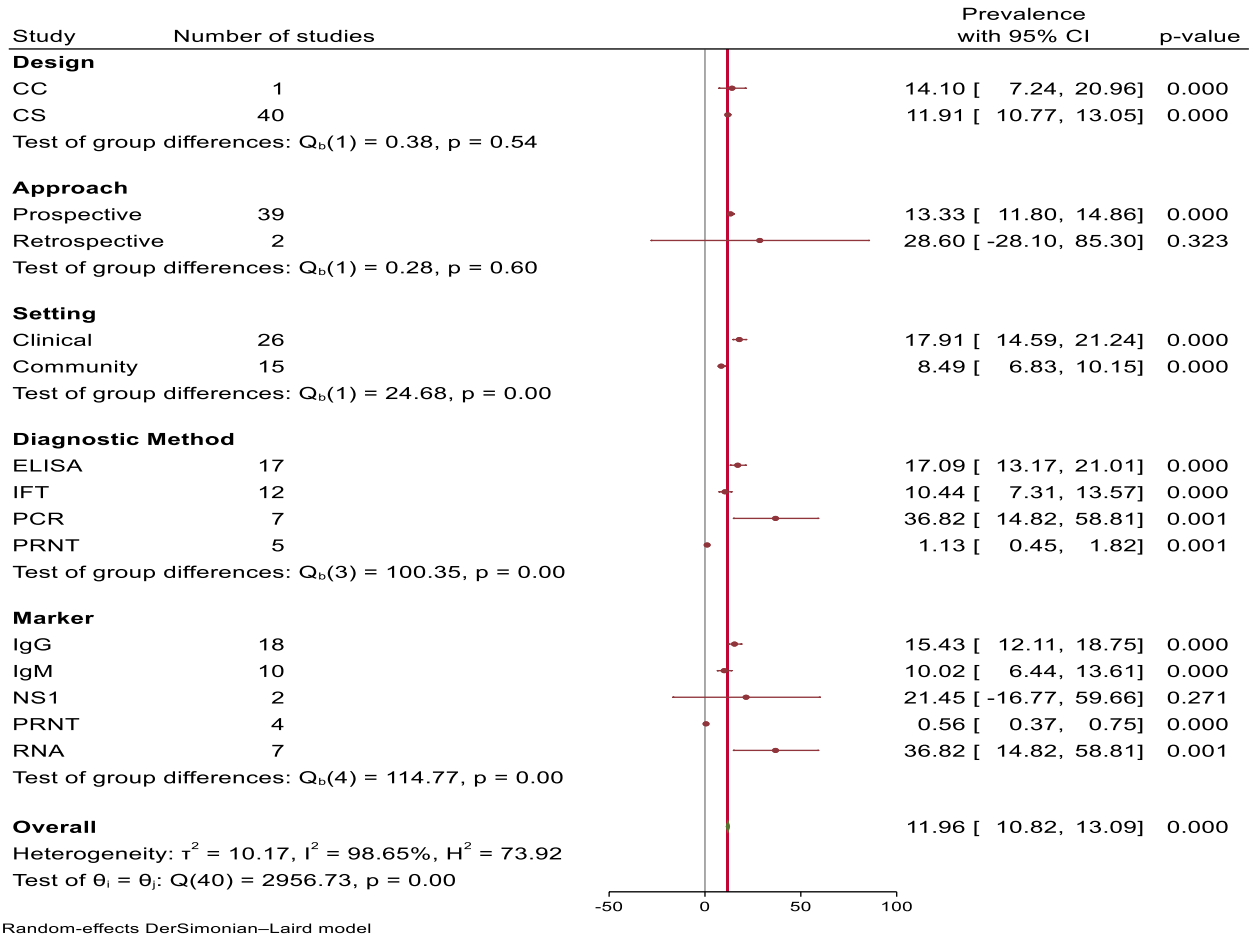

Fig. 6 Forest plot showing subgroup analysis of arboviruses by study design, approach, diagnostic method and markers among humans in Ethiopia

64.72%), publication year (R^2 = 59.70%), sample size (R^2 = 62.11%), approaches used (R^2 = 63.48%), setting (R^2 = 72.92%), and type of viruses (R^2 = 42.66%) were significantly explained (*P*<0.005) heterogeneity between studies among humans. Furthermore, in livestock studies, heterogeneity was statistically explained by the two covariates (publication year and sample size) and one factor (quality of studies) with an R^2 of greater than 89% (Table 4).

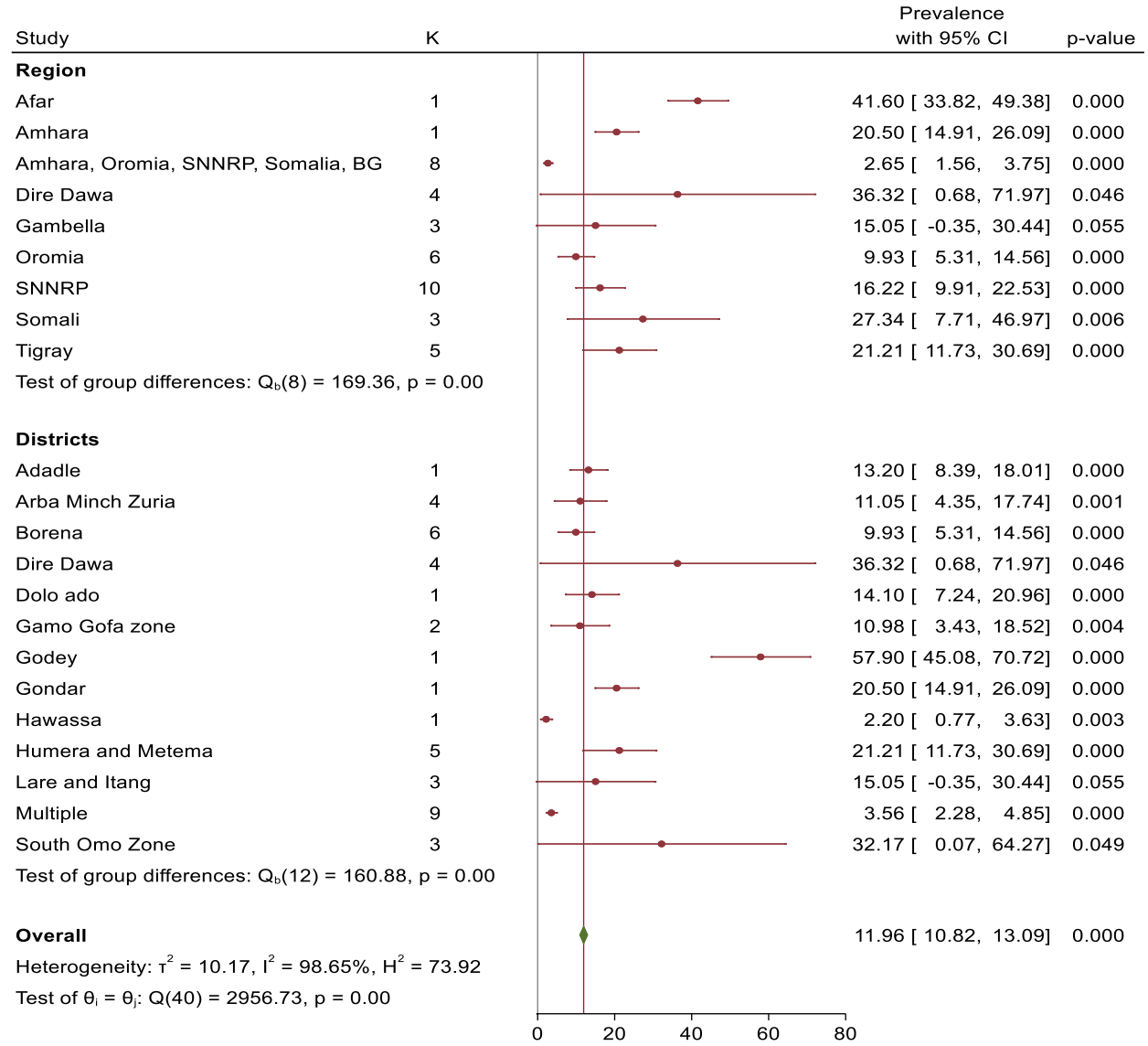

Fig. 7 Forest plot showing distribution of arboviruses among humans in Ethiopia by region and districts

Publication bias

To check the publication bias, funnel plot analysis was performed. The asymmetry of the funnel plot in the figure below indicates the presence of publication bias (Supplementary file-4). To avoid the subjective nature of visual inspection of the asymmetric distribution of the studies, Egger's test statistics was performed, and the presence of publication bias was confirmed for both humans and livestock studies with *p*-value of less than 0.001 and 0.024, respectively. Thus, the non-parametric trim and fill analysis was performed. Four additional articles were imputed in humans yielding the total number of articles to be 45 with a pooled prevalence of 12.72% (95% CI: 10.67%, 14.01%). Similarly, in livestock studies, two articles were imputed and the total number of studies reached 8 with a pooled prevalence of 21.2% (7.72%, 34.68%). Fortunately, the pooled prevalence of the final model (observed and imputed) wasn't significantly differed from the observed value (Table 5).

Discussion

Arbovirus infections have continued to be a global burden of climate-sensitive vector borne infectious diseases, particularly in resource-limited countries, including Ethiopia, where sufficient diagnostic facilities aren't available. The increased prevalence rate of arbovirus infections

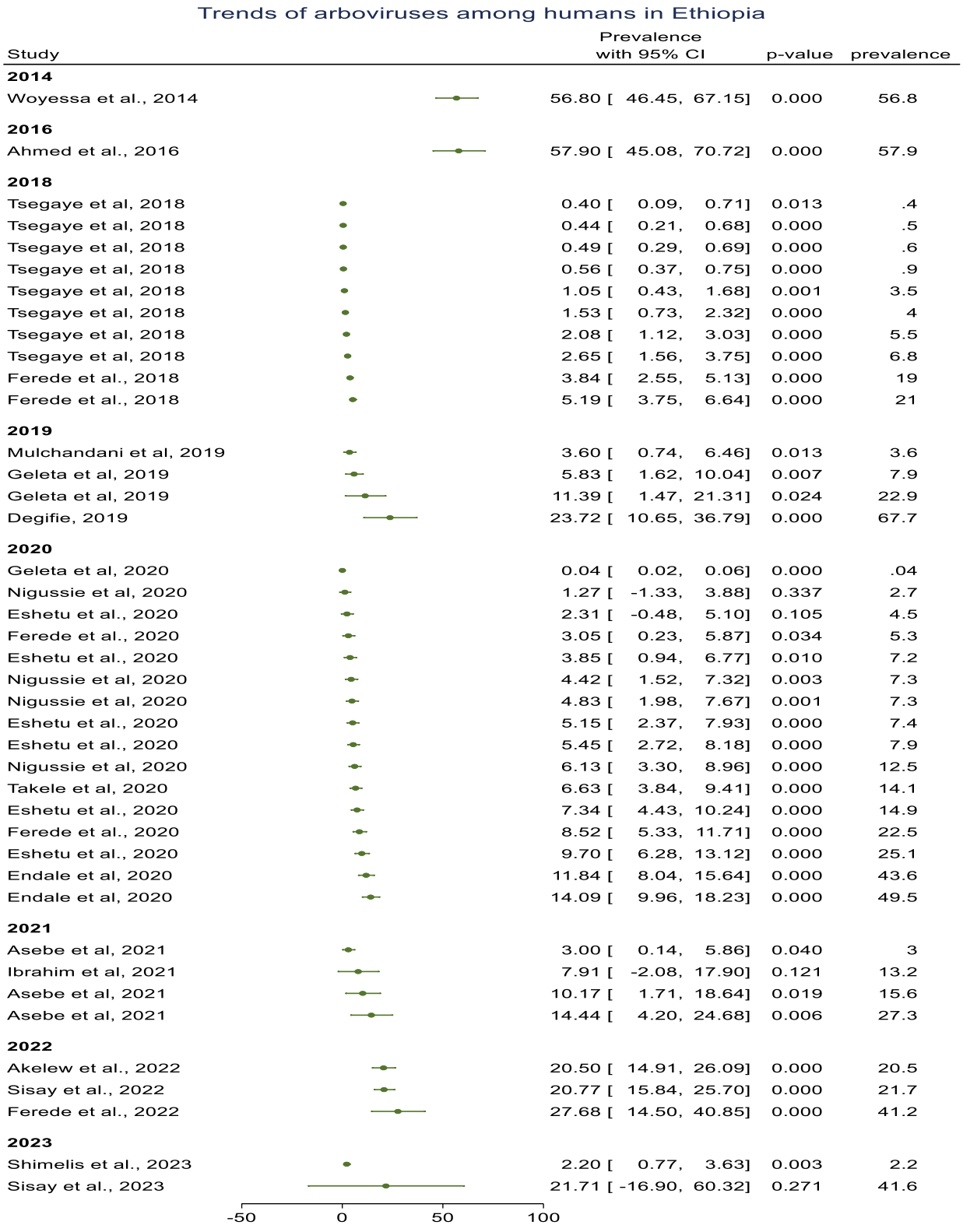

Fig. 8 Forest plot showing cumulative meta-analysis of arboviruses among humans in Ethiopia

Table 3 Subgroup analysis of arboviruses among livestock in Ethiopia

Arbovirus markers	Category	Number of studies	PP (95% CI)	I^2	*p*-value
Regions	AA, Oromia and SNNRP	1	56.56(53.94, 59.18)	0.0	**0.87**
	Gambella	2	6.4(4.28, 8.53)		
	SNNRP	2	4.91(3.41, 6.41)		
	Somalia	1	15.21(12.61, 17.81)		
Viruses	RVF	3	9.26(3.21, 15.31)	78.25	0.048
	SBV	1	56.56(53.94, 59.18)		
	WNV	2	5.08(3.52, 6.63)		
Quality	High	5	7.57(3.94, 11.2)	91.59	**<0.001**
	Medium	1	56.56(53.94, 59.18)		

AA Addis Ababa, *RFV* Rift Valley Fever, *SBV* Schmallenberg virus, *SNNRP* Southern Nations Nationalities and People's Region, *WNV* West Nile Virus

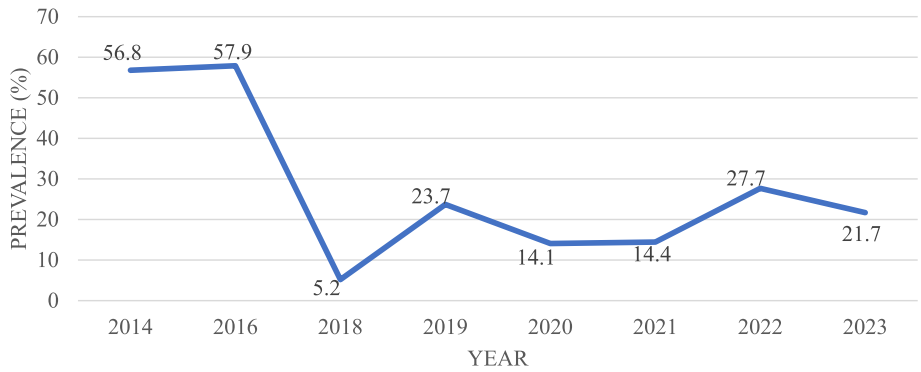

Fig. 9 Prevalence of arboviruses in humans over time in Ethiopia. The graph is created by chart.js library.

alarms the need for immediate intervention strategies from the interface of human and animal health. Thus, this systematic review and meta-analysis provides a comprehensive overview of the epidemiology of arboviruses in humans and livestock in Ethiopia. This study provides critical insights into the dynamics of these zoonotic diseases and further highlights the significant burden and widespread distribution of arboviruses in both humans and animals across the different regions of the country. A cross-sectional study design coupled with a prospective methodological approach was the most commonly employed design in the included studies. The geographical distribution spanned multiple regions, indicating that arboviruses pose a nationwide public health threat in Ethiopia, however, the most frequent studies were reported from the SNNRP and Somalia regions. Six different arboviruses (DENV, YFV, ZIKV, RVF, WNV, CHIKV) were reported in humans and three in livestock (RVF, WNV, SBV), representing the diverse viral families and genera.

In this SRMA, the pooled prevalence of arboviral RNA, IgG, and IgM sero-prevalence among humans was 38.42%, 15.43%, and 10.04%, respectively. This indicates that for every six, ten and three suspected individuals, at least one individual can have an arboviral infections based on IgG, IgM and viral RNA detection. Moreover, this finding implies that there is a need for robust and nationwide surveillance and early warning systems; expansion of diagnostic capacities or facilities for early detection of arboviruses across the region; integrated vector control programs tailored to the local ecological contexts; integrated multi-sectoral collaborations working in the same vein as the One Health approach; and climate change consideration. Therefore, the national-level public health policies should focus on evidence-based integrated arbovirus surveillance and control, explore the potential of cross-border transmission dynamics of arboviruses, and international collaboration for integrated control. Moreover, a planetary health approach could be an important approach to control anthropogenic activities such as urbanization, land use change, and deforestation, all of which aggravate the extent of climate change and the circulation of arboviruses [1, 7]. On the other hand, the wide spread distribution of arboviruses suggests a significant economic burden on the healthcare system and the affected individuals. Thus, for an integrated arbovirus prevention and control program, funding is crucial,

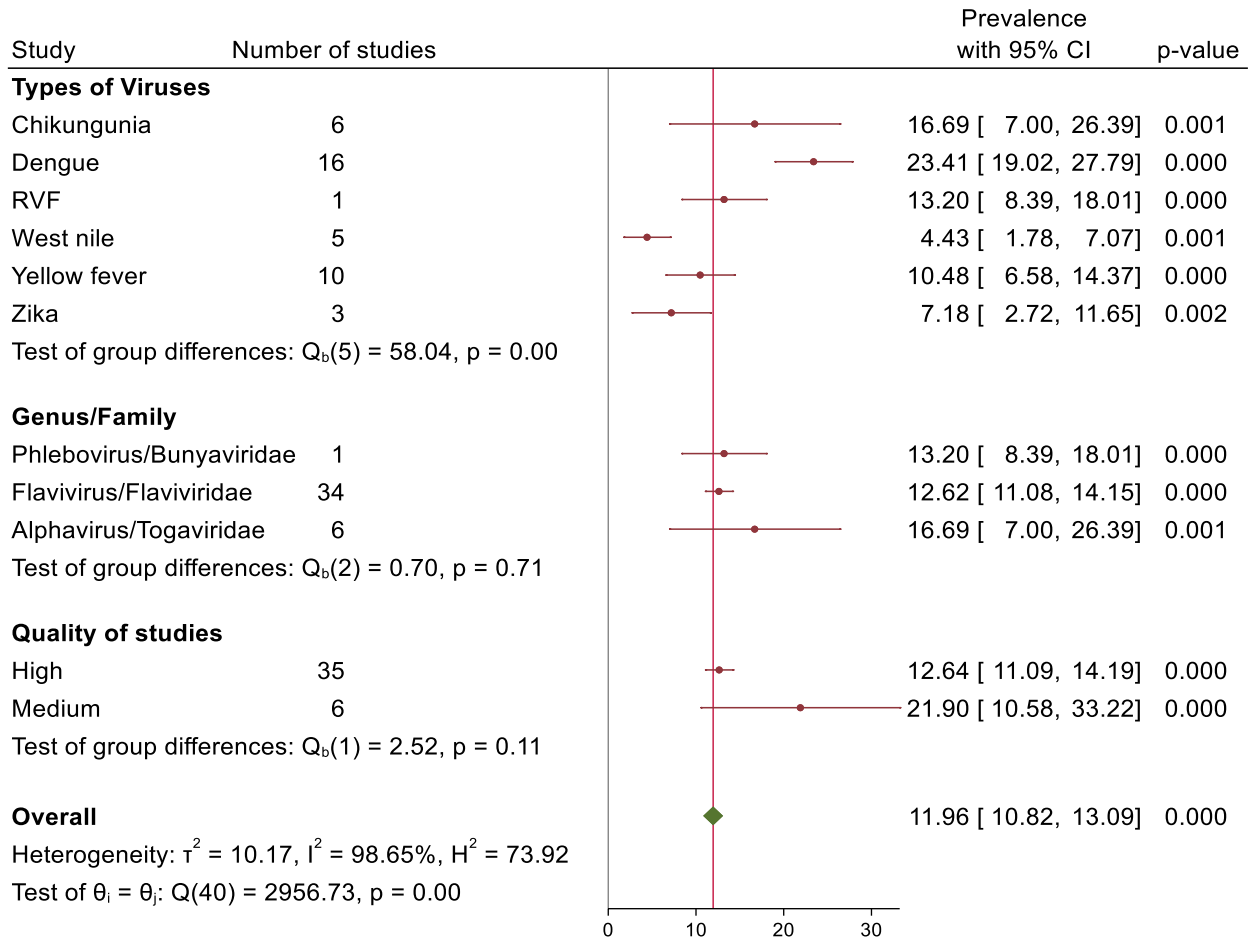

Fig. 10 Forest plot showing distribution of arboviruses among humans in Ethiopia by type of pathogen and quality of studies

Table 4 Meta-regression analysis of potential factors and covariates of Arboviruses among humans and livestock in Ethiopia

Category	Covariates	Coefficient	95% CI	R^2 (%)	I^2	P
Arboviruses in humans	**Quality of studies**	**8.805708**	**4.96269, 12.64873**	**64.72**	**100.0**	**<0.001**
	Publication year	**−1.069989**	**−1.91126, −0.22873**	**59.70**	**100.0**	**0.013**
	Sample size	**0.264783**	**0.100145, 0.34176**	**62.11**	**100.0**	**0.025**
	Approach	**18.69573**	**12.28022, 25.11125**	**63.48**	**100.0**	**<0.001**
	Study area/district	−0.1736615	−0.3621052, 0.0147821	70.56	100.0	0.071
	Setting	**−8.574682**	**−11.04537, −6.103994**	**72.92**	**100.0**	**<0.001**
	Diagnostic marker	**3.702445**	**2.213595, 5.191295**	**1.9**	**100.0**	**<0.001**
	Virus type	**−3.672766**	**−4.724589, −2.620943**	**42.66**	**100.0**	**<0.001**
	Region	0.8667409	−0.0464061, 1.779888	24.20	100.0	0.063
IgG seroprevalence in Livestock	**Quality of studies**	48.99059	40.03358, 57.9476	**95.7**	**91.59**	**<0.001**
	Publication year	−15.19463	−23.06647, −7.322777	**70.24**	**98.67**	**<0.001**
	Sample size	0.0496674	0.54115613, 0.0577735	**96.65**	**89.41**	**<0.001**
	Region	−11.56939	−25.74781, 2.609022	21.59	99.05	0.110
	Study area/district	−0.2885099	−15.80802, 15.231	0.0	99.67	0.971
	Virus type	−15.99024	−49.60642, 17.62594	0.0	99.61	0.351
	Family/genus	0.389662	−18.88995, 19.66927	0.0	99.67	0.968

Table 5 Nonparametric trim- and -fill analysis of publication bias for assessing arboviruses in humans and livestock in Ethiopia

	Prevalence of Arboviral in human's	Seroprevalence in livestock
Iteration and pooling Model: Random effects	Observed =41	Observed =6
Iteration and pooling Method: DerSimonian-Laird	Imputed = 4	Imputed = 2
	Total studies = 45	Total studies = 8
Pooled result after trim-and -fill analysis		
Number of studies	Prevalence (95% CI)	Prevalence (95% CI)
Observed	11.96(10.82, 13.09)	15.77(0.45, 31.8)
Observed + Imputed	12.72(10.67, 14.01)	21.2 (7.72, 34.68)

which knocks the door of national and international organizations.

ELISA and IFT were the most frequently used diagnostic methods for arbovirus detection, while PCR and PRNT weren't commonly used in Ethiopia. This might be due to the fact that serological tests are easy to use, sensitive, cheap, readily available, and important for understanding population exposures in the past, however, their epidemiological application is limited by the potential for cross-reactivity with antibodies of different arboviruses because of the molecular mimicry of nucleotide homology they share and can be affected by history of vaccination [56–58]. Furthermore, nucleic acid-based tests aren't easily applicable and require sophisticated resources and well-trained expertise unlikely to serological tests. Hence, real-time (quantitative) polymerase chain reaction (qPCR) and plaque reduction neutralization test (PRNT) are required to validate the findings of these serologic assays [59], and confirm outbreaks, but not for routine screening techniques in resource-limited countries like Africa [60].

Subgroup analyses regarding the epidemiological profile of arboviruses were conducted in this study. The most commonly reported arboviruses in humans were DENV, CHIKV, and YFV. The overall pooled IgG seroprevalence of DENV (18.07%) and CHIKV (21.45%) was consistent with the global seroprevalence of Dengue virus (24%) and Chikungunya virus (21.6%) in blood donors [60], however, the present findings of DENV was lower than the pooled seroprevalences of DENV (38%) [61]. This difference might be due to the variations in the time period and number of articles included in the meta-analysis, where it includes 133 articles from 44 countries published from 2000, while the present study articles published from 2014 were included.

The epidemics of YFV in Ethiopia were reported between 1960 and 1962, with an estimate of 100,000 cases and 30,000 deaths [62]. This meta-analysis also documented that the burden of YFV was 14.77% and 6.76%, respectively in IgG and IgM seroprevalence in humans, which was consistent with previously reported 9.4% pooled prevalence of YFV in SSA [63]. This finding revealed that the burden consistently existed across the African region, suggesting ongoing challenges in managing and preventing the disease in the region. Furthermore, considering the cross-border risk of the disease, the finding highlights the urgent need for regional collaboration in the control and prevention of arboviruses in general and YFV in particular.

The overall pooled IgG seroprevalence of ZIKV among humans was 15.37%. The present finding was consistent with the global seroprevalence of ZIKV, 21% in 2024 and 18% in 2021 [61, 64], which further indicates that ZIKV is an existing global burden found in Ethiopia. Moreover, the overall pooled IgG seroprevalence of ZIKV in our study was slightly higher than the seroprevalence of ZIKV, 5.1% [60] and 1.02% [65] among blood donors, which could be varied by their degree of risk exposure differences. Additionally, studies included in this meta-analysis were carried-out among suspected cases, which might contribute to the presence of a slight increment of ZIKV compared to blood donors.

In our meta-analysis, the overall pooled IgG and IgM seroprevalence of WNV in humans was 7.35% and 3.53%, respectively; these pooled values were lower than those met-analysis study reported 76.5% and 7.1% anti-IgG and anti-IgM seroprevalences of WNV in Nigeria [56]. Moreover, the pooled IgG seroprevalence of WNV among livestock in this study (5.08%) was lower than the pooled seroprevalence of WNV (8%) among equids from 16 European countries [66]. This variation might be due to the variations of livestock, where the livestock included in this meta-analysis were only cattle, sheep, goats and camels. This also further suggests the effective surveillance and control measures across the human and animal domains in order to reduce the transmission dynamics of YFV.

RVF (9.26%) was predominantly reported in multiple studies of livestock, but a single report was found in humans. The burden of RVF in livestock's' of the present

meta-analysis was consistent with the 9.3% report of RVF in animals reported from Africa [67]. The existing burden of RVF might have a socio-economic impact both at national and international levels [68] with direct costs of morbidity and death in both humans and animals, which further leads to an economic crisis. Additionally, animal losses can have knock-on effects altering herd dynamics [69].

Meta-regression analysis was used to explore the sources of heterogeneity. Hence, sample size was found to explain the largest source of heterogeneity in IgG seroprevalence studies both in humans and livestock. Likewise, in IgM and viral RNA prevalence, type of viruses was found the influential factors for explaining the sources of heterogeneity between studies. Furthermore, Publication bias was assessed by using the visual funnel plots and statistical Egger's test. Both methods confirmed the presence of publication bias. Thus, non-parametric trim-and -fill analysis was performed but there was no statistical difference between the observed value and final trim- and -fill analysis (observed and imputed) of pooled prevalence of arboviruses in humans and livestock.

Future studies shall focus on circulating arboviruses coupled with vector distribution and association and vaccination status and effectiveness. This study has certain limitations. Thus, caution must be applied when generalizing the pooled estimates to the target population. Although I^2 is not an absolute measure of heterogeneity, high heterogeneity was observed. This variation might not be solely attributed to publication bias; rather, it might be due to variations in the sample size, diagnostic methodology and markers, and variations in types of arboviruses. Therefore, the random effect model was used to limit the influence of the study heterogeneity, and subgroup analyses, sensitivity analyses, and meta-regression were performed to rule out study variability. The meta-regression finding revealed types of diagnostic method, sample size, family/genus, type of viruses and district explained the heterogeneity between studies at different levels.

Conclusion and recommendation

The overall national pooled prevalence of arbovirus infections in humans and livestock in Ethiopia was notable, which alarms the need for immediate multi-sectoral interventions. DENV, CHIKV, and YFV in humans and RVF and WNV in livestock were the most commonly reported arboviruses. The most commonly employed diagnostic methods for arbovirus infections were serological tests (i.e., ELISA and IFT). Therefore, targeted evidence-based public health interventions are essential to mitigate the risk of arboviral outbreaks. This requires implementing national surveillance systems to monitor the long-term impact of these interventions, and fostering a coordinated, multi-sectoral One Health initiative that integrates human, animal, and environmental health to optimize vector control strategies in light of climate change, alongside the national immunization programs. Anthropogenic activities are blamed to be associated with an increased circulation of arboviruses. Therefore, planetary health, which is a holistic approach encompassing multisystem and multilateral strategies, could be crucial. This approach promotes collaboration among personnel and organizations at various level globally, helping to maintain ecological balance and strengthen arboviral prevention and control programs.

Abbreviations

CC	Case Control
CS	Cross-sectional
CHIKV	Chikungunya Virus
DENV	Dengue Fever Virus
ELISA	Enzyme-Linked Immunosorbent Assay
IFT	Immune Fluorescent Test
IgG	Immunoglobulin G
IgM	Immunoglobulin M
NS1	Non-structural protein-1
PCR	Polymerase Chain Reaction
PRISMA	Preferred Reporting Items for Systematic Review and Meta-analysis
PRNT	Plaque Reduction Neutralization Test
RVF	Rift Valley Fever
SBV	Schmallenberg Virus
SNNPR	Southern Nations, Nationalities, and People Region
SSA	Sub-Saharan Africa
WNV	West Nile Virus
YFV	Yellow Fever Virus
ZIKV	Zika Virus

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s12879-025-10824-7.

Supplementary file 1. PRISMA Checklist

Supplementary file 2. Quality assessment

Supplementary file 3. Dataset

Supplementary file 4. Funnel plot for assessing the publication bias

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Clinical trial number

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Authors' contributions

Gedefie A, Debash H, Kassaw AB, Belete MA, Desale S, Sebsibe S, Tilahun M, Mulatie Z, Shibabaw A, Tesfaye M. involved in the conception and design, data collection, analysis, and interpretation of the data. Gedefie A, Mankelki G, Metaferia Y, Eshetu B, Kassa Y, Ebrahim H, Alemayehu E, Woretaw L, Kebede L, Temesgen MM, and Msganew NK took part in drafting the article or revising it critically for important intellectual content. Finally, all authors read and approve the final manuscript before submission.

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Data availability
All the datasets used and/or analyzed during the current study are available in the manuscript.

Declarations

Ethics approval and consent to participate
Not applicable.

Consent for publication
Not applicable.

Competing interests
The authors declare no competing interests.

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