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REVIEW

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Current epidemiological status of mosquito-borne arboviruses in Gulf countries: a systematic review and meta-analysis

Khalid Hajissa[1,2,3*], Mutiat Hammed-Akanmu[4], Hussain Omar Alfaqih[5], Ahmad A. Alshehri[6], Mohammed Dauda Goni[3] and Maha Al-Asmakh[7,8]

Abstract

Background Mosquito-borne viral (MBV) infections caused by dengue virus (DENV), Rift Valley fever virus (RVFV), West Nile virus (WNV), and chikungunya virus (CHIKV) pose a significant global public health concern. The aim of this systematic review is to summarise the reported prevalence data for these viruses in Gulf countries.

Methods A web search in four electronic databases (Scopus, PubMed, Google Scholar, and Web of Science) was conducted, and forty-four eligible studies were fulfilled the selection criteria and were therefore included in this study. The Pooled prevalence of MBVs was estimated using a random-effects model. The heterogeneity was assessed using Cochrane Q test and I^2 test, while publication bias was evaluated using Egger's test.

Results Using meta-analysis of proportions, the pooled prevalence of MBVs in Gulf countries among 34,367 human and 19,062 Animal samples was estimated to be 22.5% (95% CI: 13.7–31.4) and 11.6% (95% CI: 0.5 − 22.7%), respectively. In human, DENV was the most predominant virus reported in 19 studies, with an overall pooled prevalence of 32.4%, followed by RVFV in 9 studies, with an infection rate of 10.1%, while WNV and CHIKV were only reported in two studies, with overall prevalence rates of 6.4% and 2.4%, respectively. On the other hand, the overall prevalence of WNV and RVFV in animals was estimated to be 27.7% and 1.5%, respectively.

Conclusion This review revealed that MBVs are highly prevalent among humans in Gulf countries but relatively low in animals. As a result, additional therapeutic and preventive measures are required. However, the study highlights the need for further studies and surveillance to precisely monitor the burden of these viruses in the region.

Keywords Arboviruses, Mosquito-borne, Dengue, Chikungunya, Rift Valley fever, West Nile virus, Gulf countries

*Correspondence:
Khalid Hajissa
khalid541983@yahoo.com
[1]Department of Medical Microbiology and Immunology, College of Medicine and Health Sciences, United Arab Emirates University, Al Ain, United Arab Emirates
[2]Department of Zoology, Faculty of Science and Technology, Omdurman Islamic University, Omdurman, Sudan
[3]Faculty of Veterinary Medicine, Universiti Malaysia Kelantan, Kota Baru, Pengkalan Chepa 16100, Kelantan, Malaysia
[4]Department of Biomedicine, School of Health Sciences, Universiti Sains Malaysia, Kubang Kerian 16150, Kelantan, Malaysia
[5]Faculty of Medicine, Cairo University, Al-Saray Street, El Manial, Cairo 11956, Egypt
[6]Department of Clinical Laboratory Sciences, College of Applied Medical Sciences, Najran University, P.O. Box 1988, Najran, Saudi Arabia
[7]Department of Biomedical Sciences, College of Health Sciences, QU Health, Qatar University, Doha, Qatar
[8]Biomedical Research Center, Qatar University, Doha, Qatar

Introduction

The blood-feeding habit of some mosquito species is a key factor in the transmission of several medically important viruses. With an estimated 80% of the world's population living in areas threatened by mosquito-borne viruses, the prevalence of these viruses is constantly worsening, raising serious threats to human life and health [1, 2]. Over the last three decades, a dramatic spread of many mosquito-borne viruses (MBVs) has been documented worldwide, despite centuries of prevention and control efforts [3]. Among mosquito-borne viruses, arbovirus infections are gaining ground and emerging faster than expected, causing widespread outbreaks.

Arboviruses as a cause of pandemic is a global problem and are especially the common cause of disabling fever syndrome globally. The infections range from asymptomatic infection to devastating and undifferentiated feverish illnesses [4]. The disease can also progress congenital maladies and severe secondary conditions. These may lead to long-term physical disability, cognitive injury or early death [2]. There have been global efforts of countries to control the spread of mosquito borne arboviruses [3]. The spread of these viruses had been associated with accelerated urbanization, global warming, intensified intercontinental trade and travel, the adaptation and co-evolution of pathogens and mosquito vectors and the development of insecticides resistance. Mosquitoes belonging to Aedes and culex species are vectors for arboviral diseases. Aedes sp. transmit Chikungunya virus (CHIKV), Dengue virus (DENV), Yellow Fever virus (YFV), and Zika virus (ZIKV) [2, 3], while Culex sp. transmits West Nile virus [5]. Notably, Rift Valley fever virus (RVFV) is transmitted by both Culex and Aedes mosquitoes [6]. CHIKV, DENV, ZIKV have shown high global incidence due to the widespread distribution of their vector.

The MBVs are classified into 14 families. Among them, *Flaviviridae*, *Togaviridae*, and *Bunyaviridae* being the most significant families affecting humans. Viruses from the *Flaviviridae* family, such as DENV, WNV, ZIKV, and YFV, are now widely distributed around the world, with over 400 million infections annually [2, 5]. Meanwhile, CHIKV a member of the *Togaviridae* family, has spread to more than 100 countries across Asia, the Americas, and Europe [6]. In contrast, the RVFV, which belongs to the *Bunyaviridae* family, was identified in 1931 during an epidemic outbreak in Kenya [7]. The disease symptoms range from uncomplicated acute febrile illness to hepatitis, retinitis, meningoencephalitis, renal failure, severe haemorrhagic disease, and death [8, 9]. In recent RVFV outbreaks, about 950 death cases were recorded, representing a mortality rate of approximately 19.5% [10].

Despite the establishment of a number of communicable disease surveillance and control programs, the aforementioned viruses continue to pose a serious public health threat in the Arabian Gulf countries, with several outbreaks reported over the last 20 years [11–13]. Yet, the current burden of MBV's overall prevalence in Arabian Gulf countries remains unknown. Accordingly, numerous observational studies have attempted to determine the prevalence of DENV, RVFV, WNV, and CHIKV in Gulf countries, with varying findings that may have been influenced by factors such as study designs and different diagnostic methods.

The main objective of this study is to estimate the prevalence of MBVs in Gulf countries through a comprehensive systematic review and meta-analysis (SRMA) of the available literature. The findings may provide insight into the regional disease burden, help develop arbovirus surveillance in areas where data is scarce, and guide future studies while prioritizing research initiatives.

Methods

Search strategy

This SRMA was conducted in accordance with the Preferred Reporting Items for Systematic Reviews and Meta-analysis (PRISMA) guidelines [14]. The protocol has been registered in the Prospective Register of Systematic Reviews (PROSPERO) database under the number CRD42024497476. A systematic search was conducted in Scopus, PubMed, Google Scholar, and Web of Science databases to retrieve all published studies that potentially reported the prevalence of MBVs in Gulf Countries from January 2003 to the last week of May 2024 using MBVs specific keywords. Supplementary Table S2 displays the detailed search strategy applied to all databases.

Inclusion and exclusion criteria

To be eligible for inclusion in this SRMA, a published study must meet the following criteria: (1) conducted in one of the Gulf Countries and published between January 2003 to May 2024; (2) provide original quantitative data on the prevalence of MBVs in humans and/or Animals. On the other hand, studies were excluded if they reported data from outside the Arabian Gulf region or did not publish between January 2003 and May 2024. Furthermore, clinical trials, non-original papers (reviews, short communications, case reports, theses, conference abstracts), and studies on other viruses were also excluded.

Definition of MBV infection and outcome measures

This study defined the MBV infection as detecting one or more of the following arboviruses:

DENV, RVFV, WNV, and CHIKV. The primary outcome was to estimate the pooled prevalence of MBVs in Gulf countries. An individual was considered to have

MBV infection, if any of the above-mentioned viruses were detected either alone or in combination.

Study selection

The identified studies and citations were exported from each database to Endnote reference manager (Thomson Reuters, USA). Duplicate records were then removed, and the remaining studies were exported into a Microsoft Word document. Two independent authors (K.H and H.M) assessed titles and abstracts to identify studies that were eligible for full-text review. Two additional reviewers (H.O.A. and M.D.G.) then evaluated the full-text against inclusion criteria. A fourth independent reviewer (A.A.A.) made the final decision, if necessary, after discussing inconsistencies regarding inclusion and reaching a consensus.

Data extraction

Three authors (K.H., H.M., and H.O.A.) worked collaboratively to extract the relevant information using a standardized data extraction Excel form, with a fourth author (M.A.) double-checked the extracted data when necessary. The following key information were recorded from each study: The first author's name, publication year, country, recruitment time and location, species, target population, age, gender, sample size, detection method, detected biological marker, reported virus, and number of positive cases.

Quality assessment

Studies included in this SRMA were assessed for quality based on the Joana Briggs Institute's (JBI) quality assessment checklist for prevalence studies. Two reviewers (K.H. and H.M.) independently evaluated the quality of the studies. Any notable discrepancy in the assessment results was resolved through consensus. The JBI tool uses nine items with each item being answered yes', 'no', 'unclear' or 'not applicable'. The final evaluation of each study was calculated based on the proportion of 'yes' answers. Consequently, three categories were established. Study quality was classified as low if the score is ≤ 49%, moderate if the score is 50–69%, and high if the score is ≥ 70% [15, 16].

Statistical analysis

Meta-analysis was conducted using Metaprop commands in the meta and metafor packages of R software in RStudio [17]. Using a random effects model, the overall prevalence estimates for MBVs in the Gulf countries were calculated and presented as proportions with 95% confidence intervals (CI). The heterogeneity, which is commonly utilized to express the variability among the included studies in systematic reviews, was assessed using Cochran's Q-test and the I^2 statistic, with I^2 statistic values of 25, 50, and 75% denoting low, medium, and high levels of heterogeneity. Publication bias was visually assessed by funnel plot as well as Egger's test which was applied to objectively validate the funnel plot's asymmetry. Egger's test for publication bias was significant with $p < 0.05$.

Results

Study selection

In this SRMA, a total of 921 potentially relevant records were identified from the four online databases PubMed ($n = 222$), Scopus ($n = 385$), Google scholar ($n = 227$) and Web of Science ($n = 87$). After removing 175 duplicate records, the titles, and abstracts of 746 studies were assessed resulting in the exclusion of 532 non-relevant studies. Subsequently, the full text of 214 articles were reviewed for eligibility criteria. Finally, 44 eligible studies were included (Fig. 1).

Study characteristics

Forty-four studies published between 2003 and 2023 and reported prevalence data on MBVs in Gulf countries were eligible for inclusion in this SRMA. Of them 70.5% ($n = 31$) were conducted among human subjects, 22.7% ($n = 10$) involved domestic animal samples, and 6.8% ($n = 3$) with both human and animal samples. Based on the study locations, 40 of the included studies were conducted in Saudi Arabia, while three were conducted in Qatar and one in Oman. Unexpectedly, no studies met the inclusion criteria in Bahrain, the United Arab Emirates, or Kuwait. ELISA was the predominant diagnostic test used for detecting MBV infections in 31 studies. Table 1 provides additional information about the main characteristics of the included studies.

The overall prevalence of MBVs among humans and animals

The pooled prevalence estimates of the overall and subgroup analysis for the selected MBV infections are presented in Table 2. A total of 34,367 human and 19,062 Animal samples were examined for the presence of MBV during the period under review, of which 8,993 and 455 samples were laboratory-confirmed for one or more species of MBV respectively, yielding an overall prevalence of 22.5% (95% CI: 13.7–31.4) in Human and 11.6% (95% CI: 0.5 – 22.7%) in Animal (Figs. 2 and 3). The heterogeneity between the eligible studies was substantial ($I^2 = 100\%$ for humans and 99% for animals). In subgroup analysis considering the country where the studies were conducted, Saudi Arabia had a higher prevalence of MBV among human subjects (22.3%) than Oman (67.7%) or Qatar (3.8%). Among animals, the meta-analysis revealed a pooled prevalence of 12.6% in Saudi Arabia and 0.0% in Qatar. The visual inspection of the Funnel plots generated

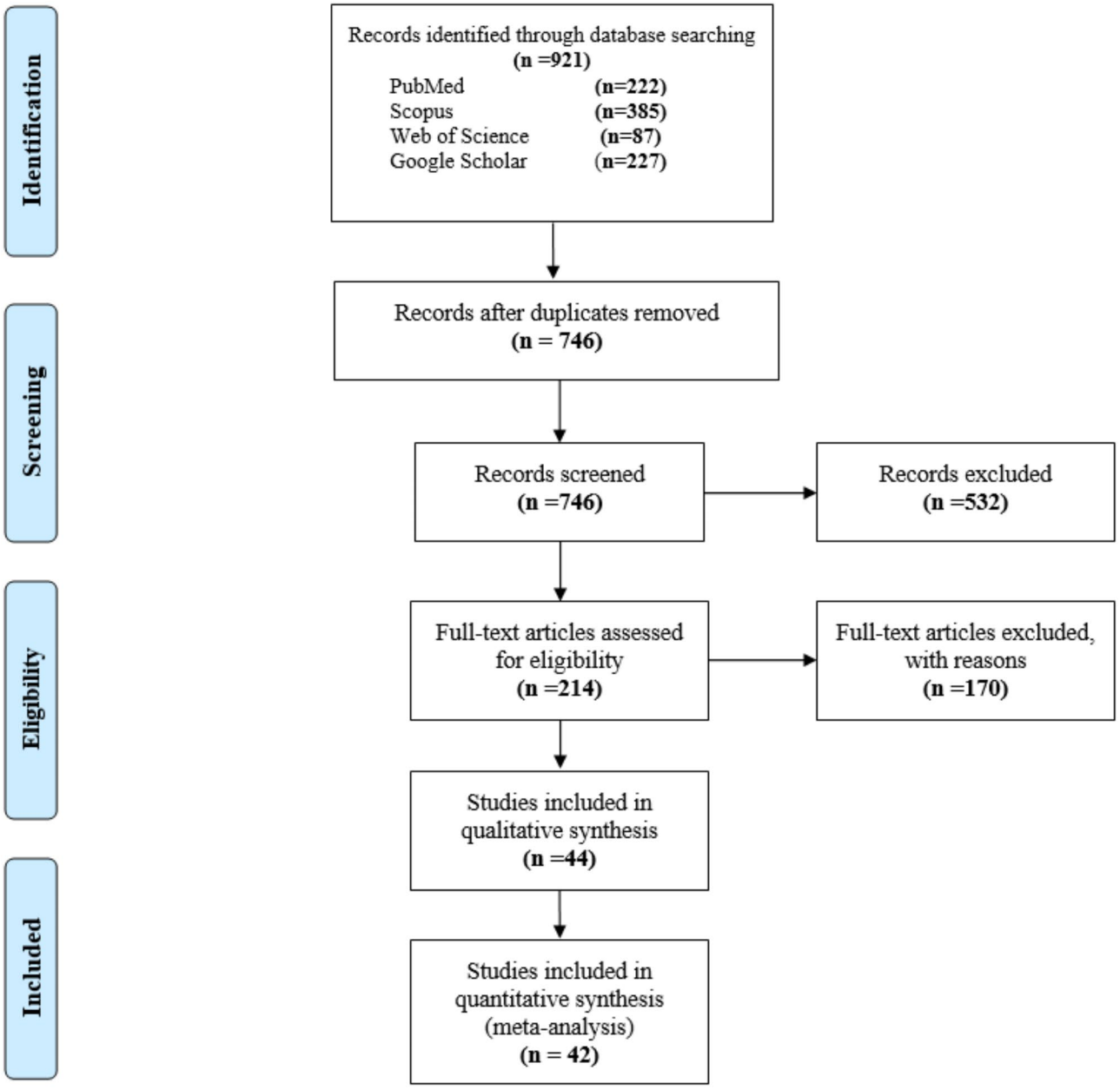

Fig. 1 The PRISMA diagram showing the study selection process

to explore the publication bias for humans and animal studies revealed asymmetrical graphs, which was objectively confirmed by Egger's tests ($p < 0.05$) (Figure S1).

DENV

After pooling the results of the primary studies using the random effect model, the overall prevalence of DENV infection in human was estimated to be 32.4% (95% CI: 22.6 – 42.1%, $n = 24133$, 19 studies, I^2:100%, $p < 0.0001$), while the pooled prevalence of laboratory-confirmed DENV infection based on detection of anti-DENV IgM, anti-DENV IgG, and the viral RNA were 17.7% (95% CI: 7.4 – 28.1%), 26.3% (95% CI: 17.1 – 35.5%) and 37.0% (95% CI: 18.7 – 55.2%), respectively.

RVFV

Fifteen studies reporting prevalence data on RVFV were eligible for inclusion in this study, 46.7% of which were conducted among human subjects, 40% involved domestic animal samples, and 13.3% with both human and animal samples. The overall prevalence of RVFV among humans was estimated to be 10.1% (95% CI: 0.0 – 27.8%, $n = 8053$, 9 studies, I^2:100%, $p < 0.0001$). The seroprevalence of IgM and IgG antibodies against RVFV was 10.5%

Table 1 Major characteristics of the included studies

Study ID [references]	Country	Study Period	Species	Sample size	Detection Method	Target antigen/antibodies/RNA	Reported Virus
Al-Ghamdi, 2014 [18]	Saudi Arabia	2007	Horses	63	ELISA	Anti-WNV	WNV
Al Azraqi 2013 [19]	Saudi Arabia	2008	Human	389	ELISA	Anti-RVFV IgG and IgM	RVFV
Al Balushi 2023 [20]	Oman	1 Feb. to 15 April 2022	Human	250	ELISA and RT-PCR	DENV-NS1, Anti-DENV IgM and IgG, viral RNA	DENV
Al-Afaleq 2012 [21]	Saudi Arabia	NR	Sheep, Goat, Cattle and Camel	3,480	ELISA	Anti-RVFV IgG	RVFV
Al-Azraqi 2012 [22]	Saudi Arabia	NR	Human	2322	ELISA	Anti-RVFV IgG and IgM	RVFV
Al-Azraqi 2013 [23]	Saudi Arabia	2008	Human	62	ELISA	Anti-RVFV IgG and IgM	RVFV
Al-Azraqi 2013 [24]	Saudi Arabia	NR	Human	965	ELISA	DENV-specific IgG	DENV
Alguridi 2023 [25]	Saudi Arabia	2018	Human	21	RT-PCR	Viral RNA	CHIKV
Alhaj 2015 [26]	Saudi Arabia	Aug. 2013 to Dec. 2013	Sheep and Goats	4930	ELISA	Anti-RVFV IgG and IgM	RVFV
Alhaj 2019 [27]	Saudi Arabia	2004 to 2018	Sheep and Goats	330	ELISA	Anti-RVFV IgG and IgM	RVFV
Alkharsah 2021 [28]	Saudi Arabia	2014 to 2017	Human, Pigeons and Horses	752	ELISA	Anti-WNV IgG	WNV
Almasri 2019 [29]	Saudi Arabia	Oct. 2013	Human	80	RT-PCR	Viral RNA	RVFV
Alqahtani 2020 [30]	Saudi Arabia	Nov. 2016 and July 2017	Human	410	ELISA, RT-PCR	Anti-DENV IgG, viral RNA	DENV
Alqahtani 2020 [31]	Saudi Arabia	March to Nov. 2017	Horses	92	ELISA	Anti-WNV IgM and IgG	WNV
Al-Raddadi 2019 [32]	Saudi Arabia	Sept. 2016 to Jan. 2017	Human	6,397	ELISA	Anti-DENV IgG	DENV
Al-Saeed 2017 [33]	Saudi Arabia	Jan. 2010 and Dec. 2015	Human	690	RT-PCR	Viral RNA	DENV
Alshabi 2022 [34]	Saudi Arabia	2012 to 2020	Human	6637	RT-PCR	Viral RNA	DENV
Ashshi 2015 [35]	Saudi Arabia	Jan. to April 2014	Human	100	ELISA	DENV-NS1, IgM and IgG	DENV
Ashshi 2017 [36]	Saudi Arabia	March 2015 and Aug. 2016	Human	910	ELISA	DENV-NS1, IgM and IgG	DENV
Ayyub 2006 [37]	Saudi Arabia	May 2004 to April 2005	Human	80	ELISA	Anti-DENV IgM and IgG	DENV
Azhar 2010 [38]	Saudi Arabia	2006 to 2008	Human	233	CC, RT-PCR, IFA	Virus isolation, Viral RNA	DENV
Azhar 2010 [39]	Saudi Arabia	2004 to 2006	Human	2476	ELISA	Anti-RVFV IgG	RVFV
Boshra 2015 [40]	Saudi Arabia	2007 and 2013 to 2014	Sheep and Goats	685	VNT	Anti-RVFV antibodies	RVFV
Dafalla 2021 [41]	Saudi Arabia	2020	Human	192	RT-PCR	Viral RNA	DENV
Dafalla 2023 [42]	Saudi Arabia	2019	Human	482	RT-PCR	Viral RNA	DENV
Dargham 2021 [43]	Qatar	2013 to 2016	Human	1948	ELISA	Anti-WNV IgM and IgG	WNV
EL Mekki 2014 [44]	Saudi Arabia	2013	Human	965	ELISA	Anti-DENV IgM	DENV
El-Badry 2014 [45]	Saudi Arabia	2008 to 2009	Human	1,578	ELISA, RT-PCR	Anti-DENV IgM and IgG, viral RNA	DENV
Elfadil 2006 [46]	Saudi Arabia	Aug. to Oct. 2004	Sheep and Goats	6143	ELISA	Anti-RVFV IgM and IgG	RVFV
Elsheikh 2011 [47]	Saudi Arabia	2009 to 2010	Humans and Animals	2850	ELISA	Anti-RVF IgM and IgG	RVFV
Gamil 2014 [48]	Saudi Arabia	April 2010 to March 2011	Human	553	ELISA	DENV-NS1, Anti-DENV IgM and IgG	DENV
Hakami 2018a [49]	Saudi Arabia	NR	Human	123	RT-PCR	Viral RNA	DENV
Hakami 2018b [50]	Saudi Arabia	2017 and 2018	Human	189	ELISA, RT-PCR	Viral RNA, DENV-NS1, Anti-DENV IgM and IgG	DENV
Hakami 2021 [51]	Saudi Arabia	Dec. 2019 and Feb. 2020	Human	40	ELISA, RT-PCR	AntiCHIKV IgG, viral RNA	CHIKV
Haroun 2017 [52]	Qatar	2006 and 2014	Horses	260	ELISA	Anti-WNV IgM	WNV
Hemida 2019 [53]	Saudi Arabia	2013 to 2015	Horses	200	ELISA and MNT	NR	WNV
Humphrey 2019 [54]	Qatar	June 2013 to June 2016	Human	1992	ELISA	Anti-DENV and anti-CHIKV IgG	CHIKV and DENV
Jamjoom 2016 [55]	Saudi Arabia	NR	Human	1939	ELISA	Anti-DENV IgG	DENV

Table 1 (continued)

Study ID [references]	Country	Study Period	Species	Sample size	Detection Method	Target antigen/antibodies/RNA	Reported Virus
Madani 2003 [56]	Saudi Arabia	Aug. 2000 to Sept. 2001	Human	834	ELISA	Anti-RVFV IgM, RVFV antigen	RVFV
Memish 2015 [57]	Saudi Arabia	2012	Human	350	ELISA, RT-PCR	Anti-RVFV IgG and viral RNA	RVFV
Mohamed 2011 [58]	Saudi Arabia	Nov. 2009	Sheep and Goats	580	ELISA	Anti-RVFV IgM and IgG	RVFV
Mohamed 2014 [59]	Saudi Arabia	Nov. 2011	Human, Sheep and Goats	600	ELISA	Anti-RVFV IgM and IgG	RVFV
Organji 2017 [60]	Saudi Arabia	NR	Human	25	RT-PCR	Viral RNA	DENV
Zailayee 2008 [61]	Saudi Arabia	April to Aug. 2007	Human	305	CC, ELISA, IFA, RT-PCR	Viral RNA, anti-DENV IgM and IgG	DENV

Key: NR: Not Reported, IFA: Indirect Immunofluorescent Assay, ELISA: Enzyme-linked Immunosorbent Assay, RT-PCR: Real-time Reverse Transcriptase Polymerase Chain Reaction, VNT: Virus Neutralization Testing, MNT: Microneutralization Tests and CC: Cell Culture Immunoassay

Table 2 Overall pooled estimates of MBV infection in different subgroups

Subgroups	Prevalence [95% CIs] (%)	Number of studies analysed	Total number of subjects	Heterogeneity		Publication Bias, Egger's test (*p*-value)
				I^2	*p*-value	
MBV in Human						
Total	22.5 [13.7; 31.4]	31	34,367	100%	< 0.0001	0.0003
Reported Virus						
DENV	32.4 [22.6; 42.1]	19	24,133	100%	< 0.0001	0.0556
RVFV	10.1 [0.0; 27.8]	9	8053	100%	< 0.0001	NA
WNV	6.4 [0.4; 12.3]	2	2141	92%	< 0.01	NA
CHIKV	2.4 [0.0; 6.4]	2	2032	81%	0.02	NA
Country						
Saudi Arabia	22.3 [13.2; 31.3]	28	30,307	100%	< 0.0001	0.0009
Qatar	3.8 [3.2; 4.4]	2	3810	0%	0.34	NA
Oman	67.7 [61.4; 73.4]	1	250	NA	NA	NA
MBV in Animal						
Total	11.6 [0.5; 22.7]	13	19,062	99%	< 0.01	0.0137
Reported Virus						
RVFV	1.5 [0.0; 3.7]	8	18,018	90%	< 0.01	NA
WNV	27.7 [3.8; 51.6]	5	1044	100%	< 0.01	NA
Country						
Saudi Arabia	12.6 [0.6; 24.5]	12	18,802	99%	< 0.01	NA
Qatar	0.0 [0.0; 1.4]	1	260	NA	NA	NA

CIs: Confidence intervals; NA: Not applicable

(95% CI: 0.0 – 31.1%) and 4.3% (95% CI: 0.9 – 7.7%), respectively.

On the other hand, eight studies tested animal samples for RVFV infection and found that the infection rate is relatively low, with six studies reporting a prevalence rate of less than 0.05%. The pooled prevalence of RVFV among animals in Gulf countries was 1.5% (95% CI: 0.0 – 3.7%, $n = 18018$, 8 studies, I^2:90%, $p < 0.01$). Furthermore, four studies reported on anti-RVFV IgM ($n = 13523$) with an overall seroprevalence of 0.4%, and anti-RVFV IgG was detected in 15.5% of the 17,003 examined animal samples.

WNV

Seven studies reported laboratory findings of WNV in Gulf countries, with five based on data from animal subjects, one on humans, and one on both human and animal participants. Accordingly, the overall prevalence of WNV among animals, as estimated by pooling the findings of six studies was 27.7% (95% CI: 3.8 – 51.6%), with substantial heterogeneity ($I^2 = 100\%$; $p < 0.01$). The pooled anti-WNV IgM and IgG seroprevalence was 0.0% (95% CI: 0.0 – 0.5%) and 37.4% (95% CI: 0.0 – 80.8%), respectively. Nevertheless, the estimated pooled prevalence of WNV in humans was 6.4% (95% CI: 0.4 – 6.4%). In the pooled human studies, there were 64 (3.5%) and 234 (10.3%) anti-WNV IgM and anti-WNV IgG positive cases.

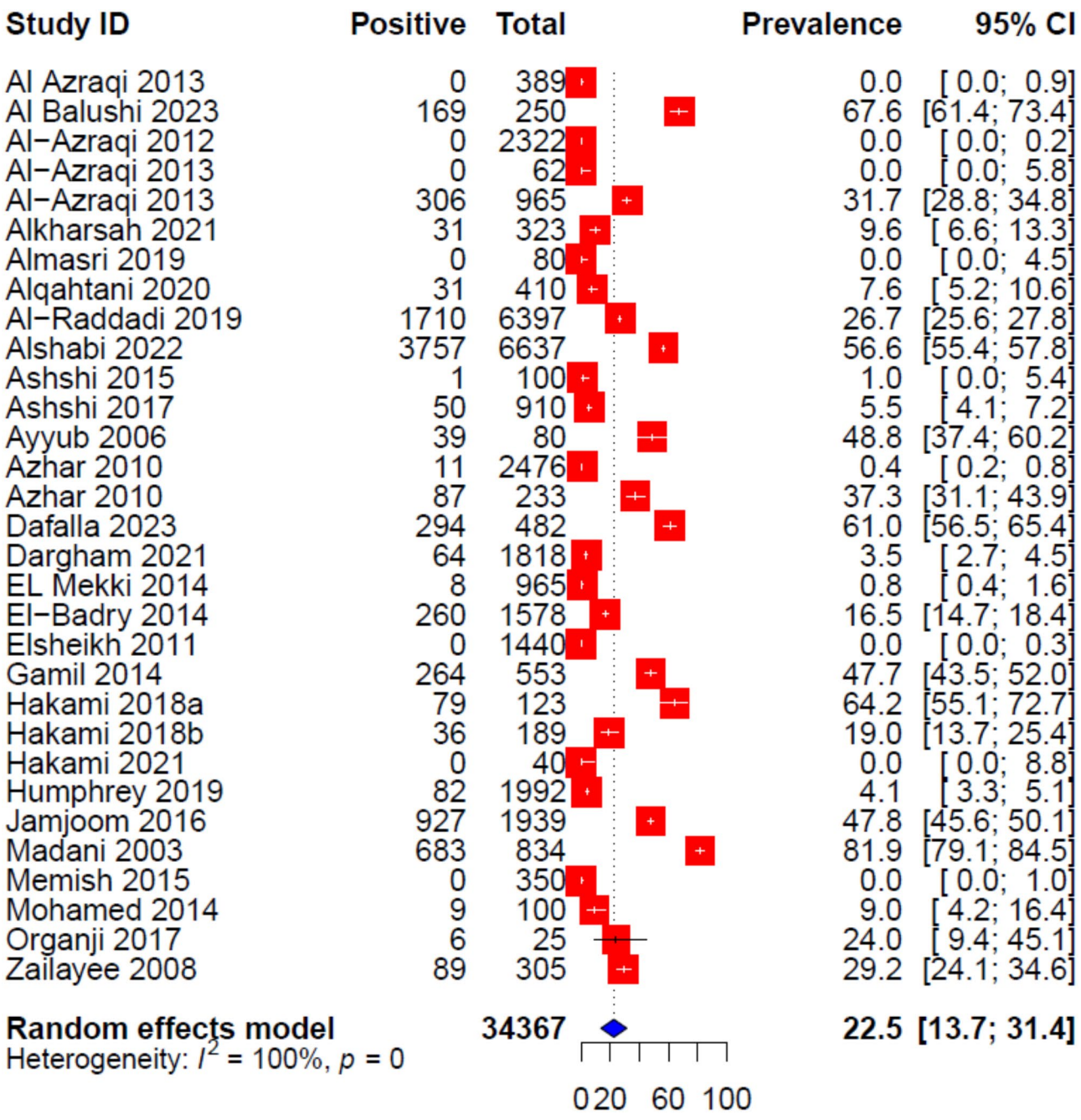

Fig. 2 The overall prevalence of MBVs among humans in Gulf countries

CHIKV

Relevant information about CHIKV in Gulf countries was reported in three eligible articles, two of which included prevalence data and were conducted on humans with a total sample size of 2032 participants. The meta-analysis showed that the pooled prevalence of CHIKV among human was 2.4% (95% CI: 0.0 – 6.4%). The subgroup analysis based on the detected biomarker revealed that the overall anti-CHIKV IgG seroprevalence was 4.1% (95% CI: 3.2–4.9), whereas the pooled prevalence of CHIKV based on viral RNA detection was 0.0% (95% CI: 0.0-8.8).

Discussion

Indeed, several observational studies have been carried out over the last two decades to determine the prevalence of MBVs in Gulf countries. However, there has been no SRMA that compiles all available information on the status of MBVs in these countries. To our knowledge, the current study is the first to provide up-to-date and

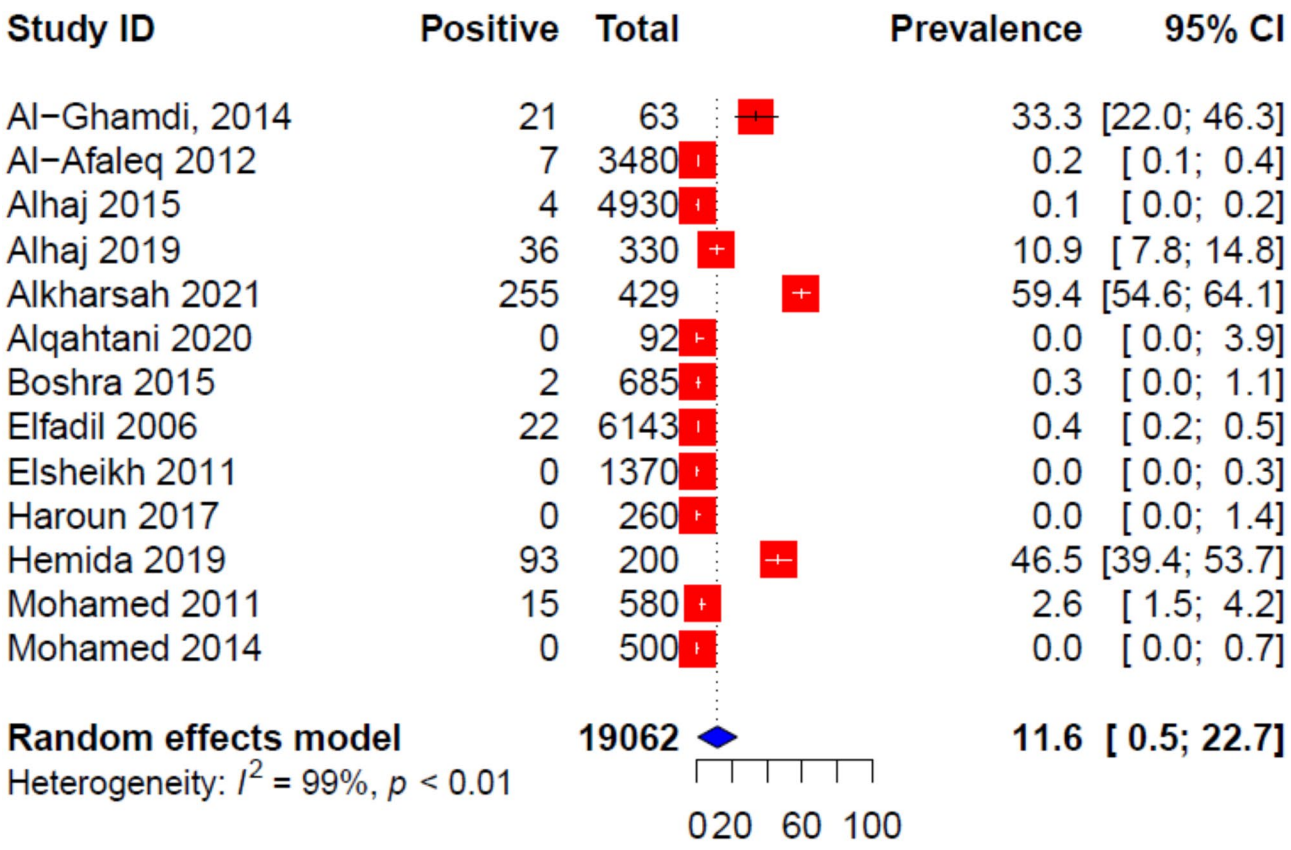

Fig. 3 The overall prevalence of MBVs among animals in Gulf countries

comprehensive evidences on the prevalence of MBVs in the Arabian Gulf region. The overall prevalence of MBVs was estimated from 34,367 human and 19,062 animal participants, based on data from 34 observational studies conducted between 2000 and 2022. However, there are notable variations among Gulf countries in terms of the number of studies and data availability. Limited datasets were available for CHIKV and WNV, and no study on yellow fever virus met the selection criteria. Besides, no studies from Bahrain, the UAE, and Kuwait were eligible for inclusion.

The prevalence of DENV, RVFV, CHIKV and WNV as examples of mosquito-borne viral infections in Gulf countries were reported in this systematic review. Despite the considerable heterogeneity, the overall prevalence of MBV infections was estimated to be 22.5% in humans and 11.6% in animals. In general, the risk of MBVs in Gulf countries is high because of virus circulation and the presence of mosquito vectors in the area. Furthermore, climate conditions and increased population movement to the region, particularly to Saudi Arabia, where millions of people visit annually for Hajj and Umrah activities are also factors that favour the dissemination of these viruses.

The meta-analysis results revealed that DENV had the highest pooled prevalence of 32.4% compared to RVFV, WNV, and CHIKV with 10.1%, 6.4%, and 2.4%, respectively. For DENV infection, the pooled estimate of 32.4% was based on data from 24,133 individuals across 19 studies. Likewise, the prevalence of IgM (17.7%) and IgG (26.3%) antibodies against dengue virus and DENV-RNA (37.0%) was relatively high. The high prevalence of DENV infection in this SRMA was similar to that found in a previous systematic review without meta-analysis conducted in Saudi Arabia and reported a prevalence rate ranging from 31.7 to 56.9% [62]. However, the overall prevalence obtained in this study is significantly higher than the 14% reported in studies from Africa [63]. The variation could be attributed to the fact that DENV prevalence varies greatly around the world and is often inconsistent across studies within a single country. On the other hand, the significantly higher prevalence of DENV than other MBVs could be linked primarily to the large number of included studies that reported DENV infection (19 out of 31), compared to 9 for RVFV and only 4 for WNV and CHIKV (2 each). Furthermore, the overall prevalence was estimated by pooling the findings of individual studies, regardless of the measured viral marker, which may have contributed to the high prevalence and significant

heterogeneity. As a result, the true burden of DENV infection in this study might be overestimated.

Using the available data on RVFV from 8053 participants in this study, the pooled prevalence of RVFV in humans was estimated to be 10.1%. This was slightly higher than the estimate of a recent SRMA, which found infection rates of 7.8% among 102,427 African participants [64]. It was also considerably higher than the reported 5.9% pooled prevalence of RVFV in Africa [65]. However, both studies reported a higher prevalence of RVFV among animals than the 1.5% prevalence rate found in this SRMA. This could be attributed to the fact that only livestock were examined, and none of the included studies reported prevalence data for wildlife. Indeed, the lack of epidemiological data for RVFV in wildlife may hinder understanding the overall picture of virus circulation in the region. Despite previous evidence suggesting that some wildlife species act as RVFV reservoirs, investigating the burden of the virus in wildlife remains a neglected area of research in Gulf countries [66]. Such investigations are required to better understand the role of wildlife animals in viral maintenance, potential spillover into livestock animals, and cross-species transmission.

Despite the aim of this SRMA being to provide baseline data on the prevalence of CHIKV and WNV in Gulf countries, only a few studies have tested human or animal samples for both viruses. Surprisingly, this study included only three CHIKV studies, all of which were conducted on humans, while only two studies met the selection criteria for WNV infection in humans. The meta-analysis of two studies with 2,032 participants resulted in a pooled prevalence of CHIKV infection of 27.7%, 4.1%% and 0% for overall, IgG and viral RNA, respectively. In comparison to other reports, the pooled estimate found in this SRMA was in the range of a similar meta-analysis conducted for population-based studies worldwide [67]. However, the seroprevalence of anti-CHIKV IgM and IgG in this study was significantly lower than the 26.7% anti-CHIKV IgM and 29.3% anti-CHIKV IgG reported in Nigeria [68]. Nonetheless, it was remarkably higher than the estimates reported by Simo et al. [69], who analysed data on the prevalence of CHIKV infection in Africa. Indeed, variations in the prevalence of CHIKV infection may be due to various factors such as ecological, economic, and climatic factors, variability of the detection methods, differences in clinical presentation, and participant recruitment time [70, 71]. In addition, the burden of CHIKV infection is typically high in areas where periodic outbreaks have been reported [72, 73]. Hence, the findings of this study should be interpreted with caution due to the scarcity of documented data on CHIKV prevalence. Therefore, future medical and veterinary studies could significantly contribute to a better understanding of the region's CHIKV endemicity, allowing for more targeted control measures.

This study provides useful epidemiological information for better understanding the prevalence and distribution of MBVs in Gulf countries. However, this SRMA review is not without limitations. First, there was no prevalence data from three Gulf countries (Bahrain, the UAE, and Kuwait), and the remaining countries did not have an adequate representation of eligible studies. Second, there have been few prevalence studies on CHIKV and WNV, so the overall prevalences of both viruses may be either underestimated or overestimated. Third, most of the eligible studies were hospital-based and enrolled suspected patients, with a limited number of community-based studies, which might bias the overall prevalence. Fourth, only peer-reviewed studies were included, and it is possible that articles indexed in databases other than the ones used or non-indexed studies could have provided additional information to this review.

Conclusion

In conclusion, this study revealed that MBVs are highly prevalent among humans in Gulf countries but relatively low in animals. The meta-analysis results showed that DENV had the highest prevalence among humans (32.4%). Despite the low prevalence of RVFV, WNV, and CHIKV, these cases should not be underestimated. This prompted us to propose that more therapeutic and preventative measures are required to reduce the transmission of these viruses. However, the review highlights the need for further studies and surveillance to precisely monitor the burden of these viruses in the region.

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s40794-025-00247-2.

Supplementary Material 1

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Author contributions

Conceptualization, K.H, and M.A; methodology, K.H, H.M and A.H.O.; software, K.H.; validation, A.A.A.; formal analysis, K.H.; data curation, M.D.G.; writing—original draft preparation, K.H.; writing—review and editing, M.A. and A.A.A.; supervision, M.A. and M.D.G.

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Data availability

No datasets were generated or analysed during the current study.

Declarations

Ethics approval and consent to participate
Not applicable.

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