Current Research in Parasitology & Vector-Borne Diseases 9 (2026) 100360

Contents lists available at ScienceDirect

Current Research in Parasitology & Vector-Borne Diseases

journal homepage: www.sciencedirect.com/journal/current-research-in-parasitology-and-vector-borne-diseases

A systematic review and meta-analysis of mosquito arboviral infections detected through xenosurveillance in Africa: A focus on West Nile, Rift Valley fever, and chikungunya virus infections

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ARTICLE INFO

Keywords:
Arboviruses
Africa
Mosquito vectors
Prevalence
Meta-analysis
Xenosurveillance

ABSTRACT

This systematic review and meta-analysis comprehensively evaluated the mosquito arboviral infections with West Nile virus (WNV), Rift Valley fever virus (RVFV), and chikungunya virus (CHIV), detected through xenosurveillance, reported in mosquito vectors across Africa in the last 25 years (2000–2024). The study analysed xenosurveillance data from 45 studies conducted with over 115,000 mosquito specimens, and incorporated moderator analyses to assess the influence of trap type, seasonality, regional location, settlement type, and screening methods on virus detection rates. The estimated pooled prevalence of WNV was 1.18% (95% CI: 0.60–3.43%), with higher rates observed in *Culex quinquefasciatus* and *Culex pipiens*, particularly in Northern Africa. RVFV prevalence was 2.00% (95% CI: 0.96–4.52%), with notable detections in *Cx. tritaeniorhynchus* and *Aedes mcintoshi* in Eastern Africa. Pooled prevalence was highest for CHIV (8.00%, 95% CI: 2.92–22.25%), primarily in *Ae. aegypti* and *Ae. albopictus* in Central and Eastern Africa. In meta-regression analysis, qRT-PCR and indirect immunofluorescence were identified as screening methods associated with higher WNV detection, while wet season sampling and CDC light traps were linked to elevated RVFV prevalence. There was substantial heterogeneity ($I^2 > 97\%$) in regional and methodological approaches. The disparities underscore the need for standardised xenosurveillance protocols, region-specific strategies, and enhanced diagnostics to mitigate arboviral risks in Africa. Limitations included sparse CHIV data and underrepresentation of studies from Southern and Central Africa, emphasising the need for expanded longitudinal and geographically inclusive research.

1. Introduction

The emergence of vector-borne diseases (VBDs) and their impact on human and animal health require that resources and strategies be in place to combat them (de Souza and Weaver, 2024). It is estimated that approximately 80% of the world's population is at risk of exposure to at least one VBD-causing pathogen and that these infections result in an estimated 700,000 deaths annually (WHO, 2017; Cuervo et al., 2023). Among VBDs, mosquito-borne arboviruses remain of particular concern due to their expanding geographical range, climate-driven shifts in vector suitability, and the increasing frequency of outbreaks in previously unaffected areas (Chala and Hamde, 2021; Parhizgari et al., 2021). In Africa, the ecological conditions, as well as vector and host diversity, support the transmission of West Nile virus (WNV), Rift Valley fever virus (RVFV), and chikungunya virus (CHIV), amongst other arboviruses (Braack et al., 2018; Weetman et al., 2018). WNV (*Orthoflavivirus nilense*) is a *Flavivirus* from the family *Flaviviridae*; RVFV (*Phlebovirus riftense*), a *Phlebovirus*, belongs to the family *Bunyaviridae*; and CHIV, an *Alphavirus*, is part of the family *Togaviridae* (Braack et al., 2018). These zoonotic pathogens pose a significant threat to public health in both urban and rural settings in Africa, as they are transmitted by mosquitoes predominantly from the genera *Aedes*, *Culex*, and *Anopheles*.

WNV is maintained and amplified by certain birds (ornithophilic) and primarily transmitted by mosquitoes of the genus *Culex* (Campbell et al., 2002; Heidecke et al., 2023). WNV consists of two lineages that are well established and have been found to cause significant infections in both animals and humans. Lineage 1 was found in Central to Northern Africa, while Lineage 2 was found in the Southern part of Africa, with

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https://doi.org/10.1016/j.crpvbd.2026.100360
Received 1 September 2025; Received in revised form 4 February 2026; Accepted 11 February 2026
Available online 12 February 2026

some traces in Europe (dos Santos et al., 2011). The other minor lineages were found in Russia (Lineage 3 and 4), India (Lineage 5), and Spain (Lineage 6) (Kukreti et al., 2009; Manakkadan et al., 2013). However, their importance remains unclear as taxonomically, WNV falls within the Japanese Encephalitis Virus (JEV) sero-complex (Khare and Kuhn, 2022). It is thought that JEV replaces WNV in areas that are dominated by WNV minor lineages, due to climate constraints that impact efficient replication of WNV in vectors (Khare and Kuhn, 2022).

Ever since WNV was first isolated in Uganda in 1937, progression of its transmission has been exacerbated by climate change (increase in temperature), global travel, international distribution of *Culex* species and invasion of birds like *Passer domesticus* (Paz and Semenza, 2013). Mosquito infection patterns are strongly influenced by temperature, vector species composition, and migratory bird movements, which play a key role in viral dispersal across continents (Sule et al., 2018). This has improved the source-vector-maintenance host relationships in a conducive and permissive environment (Weaver and Reisen, 2010). In Africa, birds have been incriminated as the primary hosts (source) of the virus; their circum-global migration has contributed to global dispersal of the virus (Sule et al., 2018). The virus mostly affects equids, with 80% of the infections being asymptomatic, and 20% presenting as neurological disorders (like tremors), with a 30% mortality rate (Sule et al., 2018). Additional clinical manifestations include febrile illness, neurologic illness and poliomyelitis-like syndromes (Sejvar, 2014).

RVFV was first described in Kenya in 1931 and has since been detected across Africa, Madagascar, and the Arabian Peninsula (Kokernot et al., 1957; Sang et al., 2010). This *Phlebovirus* of the family *Bunyaviridae* causes significant outbreaks, particularly affecting livestock such as sheep, goats, and cattle. RVF causes a viral disease primarily affecting livestock, but can also infect humans (Peters and Linthicum, 2017; Kwaśnik et al., 2021). The outbreaks are closely associated with environmental factors, particularly rainfall patterns. Notable historical outbreaks include the 1950–1951 outbreak in South Africa, which resulted in over 100,000 sheep deaths and 500,000 abortions (McMillen and Hartman, 2018). Another outbreak occurred in Egypt (1977–1978) that led to approximately 200,000 human infections and 598 fatalities (McMillen and Hartman, 2018). Furthermore, in 1997, the largest outbreak recorded in East Africa occurred in Kenya, resulting in approximately 27,500 human infections and nearly 200 deaths in the Carissa District (Woods et al., 2002).

RVFV is known for causing high abortion rates and mortality in newborn ruminants (Hartman, 2017). While human cases are typically mild, presenting as febrile illness with symptoms like malaise, headache, and nausea, serious complications and fatalities can occur (Anywaine et al., 2022). Historical outbreaks have shown significant impacts on both livestock and human populations, highlighting the zoonotic potential of RVFV. The virus has been isolated from various mosquito species in the genera *Aedes*, *Culex* and *Mansonia*. These include *Ae. mcintoshi/Ae. circumluteolus*, *Ae. ochraceus*, *Ae. pembaensis*, *Cx. poicilipes*, *Cx. bitaeniorhynchus*, *Cx. quinquefasciatus*, *Cx. univittatus*, *An. squamosus*, *Mansonia africana*, *Mansonia uniformis* (Sang et al., 2010; Linthicum et al., 2016). The transmission cycle involves early-season infections initiated by flood-water *Aedes* mosquitoes, with *Culex* species amplifying the spread in favourable environmental conditions (Linthicum et al., 2016). RVFV has shown the ability to survive in mosquito populations through transovarial transmission, with eggs capable of enduring drought conditions (Kwaśnik et al., 2021). The virus has adapted to seasonal breeding patterns, with mathematical and climate models developed to predict potential outbreaks (Chemison et al., 2024; Mulwa et al., 2025). The ongoing presence of RVFV in sylvatic contexts, along with its capacity for intercontinental spread, poses future public health challenges.

CHIV, belonging to the family *Togaviridae*, is a re-emerging mosquito-borne alphavirus and causes chikungunya fever. The term “chikungunya” is derived from the Makonde language, meaning “that which bends up”, referring to the contorted posture of patients suffering from severe joint pain (Charrel et al., 2007; Caglioti et al., 2013). The virus was first identified during an outbreak in Tanzania in 1952 and has since caused numerous outbreaks across Africa and Southeast Asia (Weaver and Forrester, 2015). A notable mutation in its genome has increased its replication in mosquito vectors, significantly enhancing its transmission capabilities (Tsetsarkin et al., 2007; Lwande et al., 2022). Three CHIV genotypes are recognized: East/Central/South African, West African, and Asian (Charrel et al., 2007). Starting in 2004, CHIV led to global outbreaks affecting millions, including significant cases in La Reunion (2005–2006) and India (2006–2007) (Bessaud et al., 2006; Braack et al., 2018b). It subsequently spread to the Americas, where it was first reported in the Caribbean in December 2013, rapidly affecting over 43 countries with over 1.1 million suspected cases (Lobkowicz, 2020). To date, CHIV has been identified in nearly 40 countries, with significant outbreaks occurring in India (1.4–6.5 million cases in 2006–2007) and the Indian Ocean islands (300,000 cases in 2005–2006) (Caglioti et al., 2013). The virus has further re-emerged in various locations, including Kinshasa, Congo (50,000 cases in 1999–2000), Indonesia (2001–2003), Italy (2007, 161 cases; 2017, 414 cases), and Malaysia and Thailand (3000 and 42,000 cases in 2009, respectively) (Poletti et al., 2011; Caglioti et al., 2013; Guzzetta et al., 2020; Chala and Hamde, 2021). Recently, CHIV was reported in more seven African countries with La Reunion, France, reporting 47,500 cases with 12 deaths (NICD, 2025).

The incubation period of CHIV is usually 2–4 days before symptoms appear, with some infections being asymptomatic (Bhatia et al., 2015). CHIV targets various tissues, including lymphoid tissue, liver, central nervous system, and joints (Tritsch, 2021). The acute phase of the disease is characterised by a pro-inflammatory response (Kayange et al., 2023). Some patients, especially the elderly, are at higher risk for chronic symptoms, including persistent joint pain (Chala and Hamde, 2021; Kayange et al., 2023). Once the infection has been established, consequent symptoms are fever, rash, arthralgia, myalgia, headache, and potential severe manifestations like neurological disease or multi-organ failure in rare cases (Chala and Hamde, 2021). Initially maintained in a sylvatic cycle involving wild primates and *Aedes* mosquitoes, it has evolved into urban transmission cycles involving humans (Kraemer et al., 2015). *Aedes aegypti* and *Ae. albopictus* are the main vectors, with *Ae. albopictus* as the most significant vector in temperate regions due to a genetic mutation increasing its transmissibility to this species (Kraemer et al., 2015; Kalyanasundram et al., 2024).

In response to the outbreaks, a multidisciplinary approach has been adopted, involving virologists, epidemiologists, and clinicians to study and manage CHIV (Abdul-Ghani et al., 2020). This approach has focused on understanding the epidemiology, physiopathology, and virology of the infection (Braack et al., 2018). Nevertheless, CHIV remains a significant public health challenge with potential for severe outbreaks. Continued research and surveillance are critical for effective management and mitigation of the impacts of this virus. Understanding its transmission, clinical presentation, and long-term effects will aid in developing strategies for prevention and treatment.

The detection of pathogens in vector populations, xenosurveillance, is a crucial component of integrated public health efforts for arbovirus management, complementing human and animal disease surveillance (Grubaugh et al., 2015). Detecting arboviruses in mosquito vectors, as opposed to solely monitoring clinical cases, provides an early warning system for transmission risk and helps delineate the geographical spread of active vector-virus cycles. Xenosurveillance enables early detection of virus circulation, identification of competent or potentially involved vector species, assessment of ecological and seasonal drivers of arbovirus activity, and improved outbreak forecasting in high-risk settings (Grubaugh et al., 2015). It also offers a cost-effective and biologically grounded complement to human or livestock case reporting, especially for low-income countries (Grubaugh et al., 2015). The interpretation of xenosurveillance findings, however, requires careful consideration of the vector-virus relationship. This includes species competence, feeding

behaviour, and the specific tissues tested (e.g. whole mosquito *vs* head/thorax), which determine whether a positive result represents a competent vector or merely a mosquito with a recent infected blood meal (Fauver et al., 2017). Furthermore, mosquito infection data across Africa remain fragmented across countries, ecotypes, and surveillance programmes. Differences in sample processing (e.g. whole mosquito *vs* head/thorax only), trapping methods, and diagnostic protocols further complicate cross-study comparisons.

Although dengue virus (DENV) and yellow fever virus (YFV) are epidemiologically important, they were excluded because their transmission cycles, surveillance frameworks, and existing systematic reviews differ from those of WNV, RVFV, and CHIV, which share overlapping ecologies and xenosurveillance approaches (Hartman, 2017; WHO, 2017; Braack et al., 2018). Surveillance for these viruses relies mainly on human case detection, serology, and, for YFV specifically, vaccination monitoring, rather than routine mosquito testing (McMillen and Hartman, 2018). As a result, very few studies report mosquito infection metrics in formats suitable for quantitative synthesis. Ecological factors also limit comparable data; YFV circulates mainly in sylvatic cycles with forest-dwelling vectors, and DENV rarely has standardised vector infection assays reported (Asish et al., 2023; Baranowski et al., 2024). In contrast, WNV, RVFV, and CHIV have extensive, detailed mosquito-based datasets that support robust pooled analyses.

Despite the significant burden of WNV, RVFV, and CHIV across Africa, there remains a critical knowledge gap regarding regional pooled estimates of mosquito infection rates and transmission patterns. Although numerous xenosurveillance studies have documented the presence of these viruses in mosquito populations across Africa, there is a paucity of synthesised evidence quantifying their overall prevalence (Gedefie et al., 2025). A systematic review and meta-analysis of such studies is crucial to understand the spatial and temporal patterns of these viruses in African mosquito vectors. This systematic review and meta-analysis seek to (i) quantify the prevalence of these arboviruses in African-collected mosquito populations, (ii) identify key ecological and geographical determinants of infection rates, and (iii) provide evidence to guide targeted xenosurveillance and control programmes. By synthesising three decades of xenosurveillance data, this study addresses an urgent need for standardised risk assessment across diverse African ecologies where these zoonotic pathogens overlap. Such insights are vital for guiding integrated vector xenosurveillance, informing risk assessment models, and strengthening preparedness for future outbreaks. Therefore, quantifying mosquito infection prevalence provides direct evidence of the circulation risk independent of human/animal symptomatic cases, which is the primary focus and novelty of this systematic review and meta-analysis.

2. Materials and methods

2.1. Study design

This study was conducted as a systematic review and meta-analysis following the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines (Page et al., 2021) (Supplementary Table S1). The aim was to determine the pooled prevalence of WNV, RVFV, and CHIV infections in mosquito populations trapped across Africa. This review is registered with PROSPERO, a registry for international systematic reviews and their protocols, whereby upon registration, a unique registration number is issued for the review, and the record is made publicly available. The registration ID of this review is CRD420250651004, and with a similar title.

2.2. Search strategy

A comprehensive literature search was performed across multiple electronic databases, including African Journal Online, African Index Medicus, PubMed, Scopus, Embase, Ovid, and Google Scholar. PICo ("P", participants; "I", phenomenon of interest; "Co", context) was used as a model for the search terms and approach. In this review, "P" alluded to mosquito population; "I" referred to CHIV, WNV and/or RVFV infection; and "Co" meant African countries. The search terms were combined using Boolean operators, "OR", within the same domain, and "AND" between the domains of PICo in an exclusive database requirement. Search keywords included medical subject headings (MeSH) terms and other terms relevant to the approach model for this review, as detailed in the search terms (Supplementary Table S2). Manual screening of the references of the selected papers was performed to establish additional relevant studies.

2.3. Eligibility criteria, study selection and data extraction

This study involved cross-sectional studies that used WNV, CHIV, and RVFV screening, isolation, and detection techniques in mosquitoes collected from the field. Specifically, it includes studies published in English from January 2000 to December 2024 undertaken in at least one African country.

The articles were searched independently by all three investigators (MM, AB, and DPT) on international databases. Each investigator screened all retrieved articles based on their titles and abstracts and created an Excel spreadsheet with the following details of the eligible studies: year, journal, title, and abstract. The three Excel files were compared, and any discrepancies regarding duplicates, inclusion, or exclusion of studies between any two investigators were resolved by consensus or by considering the third investigator (AB) as the final arbiter. The references of the included studies were screened by MM and DPT to identify any potentially missed studies not captured in the databases. Thereafter, MM and DPT conducted data extraction. AB compared the extracted data of the included studies from MM and DPT, resolved discrepancies, and randomly selected one study per region to validate the correctness and completeness of data extraction.

Studies were included if they reported original research on mosquitoes collected in Africa and tested for the presence of WNV, RVFV, or CHIV using validated molecular assays (e.g. RT-PCR, qRT-PCR) or antigen- or antibody-based assays when used for detecting evidence of infection. Essentially, each study had to provide sufficient data to calculate prevalence (number of infected mosquitoes/total tested).

Studies were excluded if they: (i) focused on experimental infections in laboratory mosquitoes; (ii) data were insufficient or unavailable to bear out sound prevalence estimation or calculation; (iii) were reviews, commentaries, abstracts, or case reports; (iv) studies that did not investigate for WNV, CHIV or RVFV, or if they did, it was on other organisms besides mosquitoes; and (v) studies that collected mosquitoes outside of Africa, regardless of where the laboratory testing occurred.

All included studies were compiled into a single final Excel spreadsheet, recording the following details: author names; article title; journal title; year of publication; country of sampling; geographical region; settlement type; year of sampling; season(s) of sampling; mosquito collection method; method of mosquito species identification; mosquito species; virus detection method; number of mosquitoes tested; and number of mosquitoes infected with WNV, CHIV, and/or RVFV.

2.4. Quality assessment

Each included study was assessed for methodological quality using a modified version of the Joanna Briggs Institute (JBI) checklist for prevalence studies (Munn et al., 2023). This tool was used to assess the trustworthiness, relevance, and results of each study. Parameters included sample representativeness, reliability of diagnostic tools, and appropriateness of statistical analysis, amongst others. Reviewers MM and DPT conducted the assessment for each study. Each assessing question of the criteria amounted to a score of either one if the answer was "Yes" or zero if the answer was "No". Any discrepancy that surfaced

in the overall assessment of each study between reviewer DPT and MM was resolved by consensus after discussion or, if needed, by consultation with AB. The ten parameters or measures established the critical scoring of each study, such that articles with a score of 50% or above were considered to have a low risk of bias. Supplementary Table S3 provides the detailed appraisal parameters for every study involved.

2.5. Study outcome

The primary outcome of this systematic review/meta-analysis was the pooled mosquito infection rate, prevalence, as statistical proportions of WNV, CHIV, and RVFV in mosquitoes collected in African countries. Prevalence was determined as the number of mosquito pools that tested positive divided by the total number of mosquito pools tested. As some studies included in this review tested or detected viruses in individual mosquitoes, each mosquito was regarded as a separate pool. Therefore, a pool, according to this study, was regarded as one or more mosquitoes combined as a unit for detection and analysis (Maneerattanasak et al., 2024).

2.6. Statistical analysis

Meta-analysis was conducted using a random-effects model, specifically the DerSimonian and Laird method, to account for heterogeneity among studies. The primary outcome was the pooled prevalence, presented as a percentage (%), of WNV, CHIV, and RVFV infections among mosquitoes, and their corresponding 95% confidence intervals (CI) were also computed. Heterogeneity was assessed using the I^2 statistic and Cochran's Q test, whereby and I^2 of $> 75\%$ or Cochran's Q-test $P < 0.1$ indicated heterogeneity. All estimated prevalence values were transformed to logit units for analysis and back-transformed for ease of 95% CI interpretation. Furthermore, subgroup analyses were executed based on geographical regions to investigate sources of heterogeneity and delineate differences in prevalence among distinct participant groups. For the visualization of each study's data, the forest plot was created, which depicted each study's average effect size, 95% CI and weight. Likewise, to determine the source of heterogeneity, the restricted maximum-likelihood method was employed to conduct meta-regression of the predictors. A significance threshold of $P < 0.05$ will be established for statistical relevance. A random intercept logistic regression model was also adopted for univariate analysis. Publication bias was evaluated using funnel plots and Egger's test, where applicable. All analyses were conducted using R software version 4.2.2 (packages *meta* and *metafor*) (Viechtbauer, 2010; Balduzzi et al., 2019).

The predictors used in this review were abbreviated for the meta-regression analysis, and are described as follows:

- For geographical region: U, urban; R, rural; Co, conservancy, and the mixed symbols of the above, e.g. UR, urban and rural;
- For collection method: CLT, CDC light trap; CLTC, CO_2-baited CDC light trap; BST, BG-sentinel trap; BSTB, BG-sentinel trap baited with BG-lure; A, aspirators; MN, mosquito nets; ABT, animal-baited traps; and others that are sparingly included in the study and will be explained in Section 3;
- For screening method (virus): RT-PCR, reverse-transcription polymerase chain reaction; qRT-PCR, quantitative/real-time RT-PCR; ii, indirect immunofluorescence;
- For study region: NAFR, Northern Africa; WAFR, Western Africa; EAFR, Eastern Africa; SAFR, Southern Africa; and CAFR, Central Africa;
- For seasons: D, dry; W, wet; WD, both wet and dry.

3. Results

3.1. Study characteristics

A total of 3245 studies were identified, and citation manual screening was performed, as depicted in Fig. 1, with more records retrieved from Embase ($n = 1063$). After removing duplicates and applying the inclusion/exclusion criteria, 343 studies were included in the qualitative synthesis, and 45 records were deemed eligible for this review (Fig. 1; see Supplementary Table S4 for details). The risk of bias was assessed for all included records, and all studies fell into the low-risk bias category at a range of 7–10. The average (± standard deviation, SD) score of the studies was 9.81 ± 0.55, indicating a low risk of bias.

Therefore, this synthesis is based on data from distinct xenosurveillance surveys investigating WNV, RVFV and CHIV prevalence among field-caught mosquitoes from across Africa. The publication years of the 45 studies spanned from 2000 to 2024, and represented diverse ecological zones and study regions across Africa (Supplementary Fig. S1). Most of the studies were conducted in Eastern Africa (31/45, 68.9%) and Western Africa (12/45, 26.7%). The remainder were conducted in Northern Africa (10/45, 22.2%), Central Africa (5/45, 11.1%), and Southern Africa (4/45, 8.8%). The collection time varied across studies, with most studies capturing data equally during wet (W) and dry (D) seasons at a rate of 44.4% (20 out of 45 studies) for each. Five of the 45 studies (11.1%) were conducted both during the wet and dry seasons.

Mosquitoes were primarily and predominantly collected using CO_2-baited light traps (CCLTC) (14 out of 45 studies, 31.1%). Some studies employed aspirators, BG-sentinel traps (baited or unbaited), nets, human-landing collections, or a combination thereof. The screening methods included conventional RT-PCR (16 out of 45 studies, 35.6%) and qRT-PCR (10 out of 45 studies, 22.2%). Although molecular studies were commonly used, some studies employed immunological techniques, such as indirect immunofluorescence. For most of the 45 studies (24 studies, 53.3%), mosquitoes were collected in rural areas (R), and 26.7% (12 out of 45 studies) in both urban and rural areas (UR). The remaining data were collected from urban areas (U), conservancies (Co), or both urban and conservancies (UCo). The collection periods ranged from less than 10 days to continuous or unspecified periods.

3.2. Mosquito vectors of WNV, CHIV, and RVFV

The included mosquitoes were collected across Northern, Western, Southern, Eastern, and Central Africa between 2000 and 2024. Most studies collected species of *Aedes* and *Culex*, with CHIV detected predominantly in *Ae. aegypti*, WNV in *Cx. quinquefasciatus*, and RVFV in both *Aedes* and *Culex* species. Table 1 presents details of the vector diversity in this study, wherein 90,468 mosquitoes were collected for WNV, 15,426 for RVFV, and 10,252 for CHIV. In Western Africa, 6.27% (26 out of 415) of *Culex neavei* and 0.27% of *Culex poicilipes* (1 out of 368) tested positive for WNV. In the same region, 8.2% (36 out of 439) and 0.1% (5 out of 3566) mosquito pools of *Cx. poicilipes* and *Anopheles pharoensis* tested positive for RVFV. Additionally, *Anopheles domicola* and *Anopheles coustani* tested positive for CHIV, with positivity rates of 7.1% (1 out of 14) and 0.4% (1 out of 235), respectively. *Aedes vittatus* did not test positive for CHIV (0 out of 589).

WNV was prevalent in Eastern Africa in *Cx. neavei* (0.16%, 1 out of 615), *Aedes sudanensis* (0.04%, 1 out of 2651), and *Culex* spp. (23.81%, 15 out of 63). More diverse mosquito species were collected and screened for RVFV and CHIV in this region; however, most species tested negative for these viruses. RVFV was detected from *Culex tritaeniorhynchus* (20.83%, 5 out of 24) and *Cx. quinquefasciatus* (0.67%, 1 out of 149). CHIV was detected in *Ae. aegypti* and *Cx. quinquefasciatus* with a positivity rate of 5.6% (9 out of 161) and 1.6% (4 out of 243), respectively.

No studies on CHIV have been reported in Northern Africa. Nevertheless, WNV was detected in *Cx. pipiens* (10.17%, 129 out of 1268) and

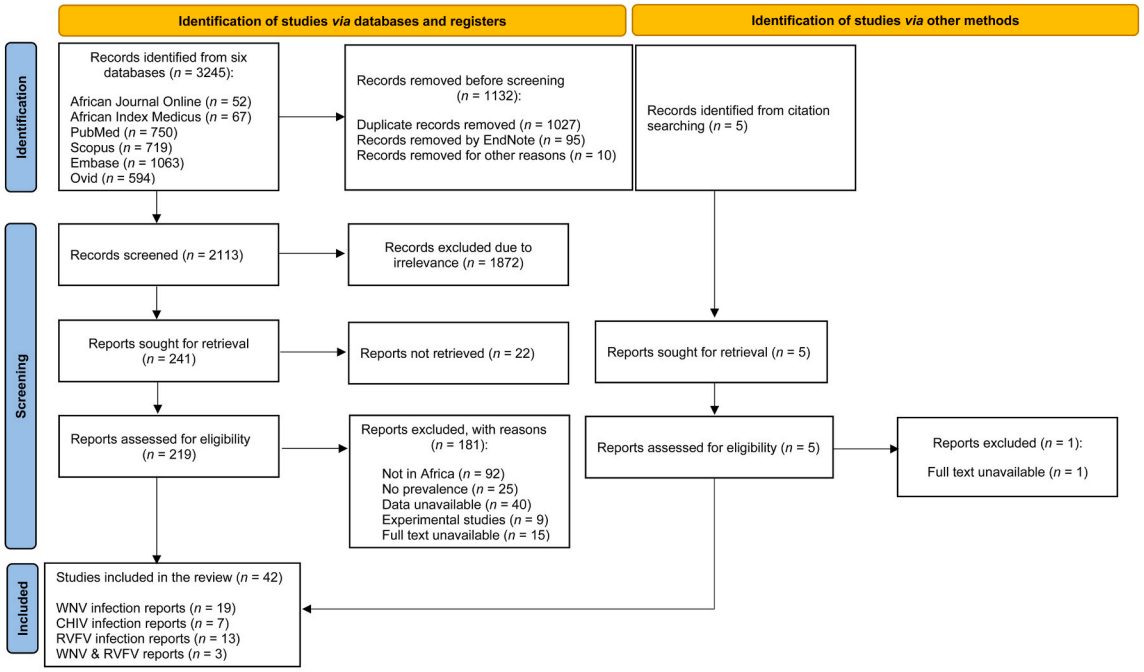

Fig. 1. PRISMA flow diagram for systematic reviews, which includes searches of databases, registers and other sources.

Culex antennatus (0.19%, 5 out of 2691). However, *An. pharoensis* (0 out of 145) and *Anopheles tenebrosus* (0 out of 245) did not test positive for WNV. RVFV in Northern Africa was prevalent in *An. coustani* and *Cx. poicilipes* with positivity rates of 16.7% (3 out of 18) and 3.3% (1 out of 30), respectively. In Central Africa, WNV was detected in 25% (5 out of 20) pools of *Aedes* spp., and CHIV was detected in *Ae. albopictus* (4.39%, 48 out of 1094) and *Ae. aegypti* (12.39%, 14 of 113). No RVFV was detected in this region. In Southern Africa, only WNV was detected in different species, such as *Cx. pipiens* (16.27%, 2 out of 12), *Cx. poicilipes* (2%, 1 out of 50) and *Cx. univittatus* (0.7%, 8 out of 1135). RVFV was detected in *Aedes durbanensis* from this region with a positivity rate of 0.95% (1 out of 103).

3.3. Pooled prevalence for WNV, RVFV, and CHIV

The forest plots (Figs. 2–4; Supplementary Tables S5–S7) illustrate the pooled prevalence of WNV, RVFV, and CHIV infections in mosquito vectors across all African regions. A total of 19 studies were used to assess the prevalence of WNV infection in mosquitoes, and the pooled prevalence was 1.18% (95% CI: 0.60–3.43%), according to the meta-analysis based on the random-effects model (Fig. 2). Further analysis revealed significant heterogeneity among these studies, with an I^2 statistic value of 98.7%, indicating substantial variability in WNV prevalence estimates across regions. Based on subgroup analysis, Northern Africa had the highest prevalence rate of 3.37% (95% CI: 0.60–16.73%; 8 studies), and the random-effects model of the region showed high heterogeneity ($I^2 = 99.1\%$). This was followed by Western Africa (12.3%, 95% CI: 0.38–3.90%; 4 studies), Southern Africa (6.1%, 95% CI: 0.22–1.67%; 3 studies), and lastly, Eastern Africa (0.22%, 95% CI: 0.01–3.62%; 4 studies). Significant heterogeneity was observed in Eastern Africa ($I^2 = 98.4\%$), more so in Western Africa ($I^2 = 98.2\%$), and minimal in Southern Africa ($I^2 = 63.7\%$) (Supplementary Table S5).

The pooled prevalence of CHIV was 8.49% (95% CI: 2.92–22.25%), with high heterogeneity between studies ($I^2 = 97.4\%$) (Fig. 3). Subgroup analysis revealed that CHIV prevalence was highest in Central Africa (23.32%, 95% CI: 6.72–56.20%; 4 studies), followed by Eastern Africa (5.71%, 95% CI: 1.07–25.31%; 3 studies), and lastly, Western Africa (2.72%, 95% CI: 0.50–13.39%; 3 studies) (Supplementary Table S6).

The pooled prevalence of RVFV was 2.10% (95% CI: 0.96–4.52%), with high heterogeneity between studies across regions (Fig. 4). Subgroup analysis revealed the highest and lowest prevalence of RVFV in Eastern Africa (3.44, 95% CI: 1.64–7.10%; 7 studies) and Western Africa (0.44%, 95% CI: 0.07–2.57%; 5 studies) (Supplementary Table S7).

3.4. Meta-regression

Six meta-regression models were tested to explore the heterogeneity in WNV prevalence across African mosquito studies (Supplementary Table S8). Each model used a different intercept to evaluate the influence of the individual moderators. Model 6, which included screening method, collection method, and study region, was selected as the best fit model (QM = 104.82, $P < 0.0001$), with the lowest residual heterogeneity ($\tau^2 = 0.60$), and biological relevance. The highest prevalence was associated with the use of indirect immunofluorescence and qRT-PCR screening methods, whereas the lowest prevalence was linked to traps employing CO_2-baited CDC light traps (CLTC). The prevalence was also significantly higher in the Northern African group (Supplementary Table S9). These findings highlight the importance of methodological and geographical variations in interpreting arboviral surveillance data.

Although Model 3 had the lowest AIC (100.39), it was limited in scope and focused primarily on the collection method. Model 6, while having a slightly higher AIC (107.01), was selected as the final model due to its inclusion of key biological and methodological moderators (screening method, study region, and collection method), offering a more comprehensive explanation of heterogeneity across studies. The AIC difference was modest and did not outweigh the interpretative value of Model 6 (Supplementary Table S8).

Likewise, a mixed-effects meta-regression (Model 5) was conducted to assess the influence of seasonality, mosquito collection method, and regional differences on the prevalence of RFVF in African mosquito populations (Supplementary Table S10). This model showed a strong performance among the other six, with a low AIC (97.61), indicating a good model fit with minimal residual heterogeneity ($\tau^2 = 0$; $I^2 = 0\%$). Significant positive predictors of RVFV prevalence included collections during the wet season (SeasonW: $\beta = 2.82$, $P < 0.0001$), and studies conducted in Northern Africa ($\beta = 1.94$, $P = 0.0113$). For collection methods, there were more than one positive significant predictors; the use of CDC light traps only (CLT: $\beta = 1.64$, $P = 0.0698$), and when

Table 1
Distribution of mosquito vectors infected with WNV, RVFV, and CHIV across African regions and species.

Virus	Study region	Mosquito species	Total no. positive	Total no. tested	Prevalence (%)
WNV	Northern Africa	*Aedes caspius*	32	17,209	0.19
		Aedes detritus	19	190	10.00
		Aedes vexans	1	2	50.00
		Anopheles maculipennis	1	5	20.00
		Anopheles multicolor	0	5	0
		Anopheles pharoensis	0	145	0
		Anopheles tenebrosus	0	245	0
		Culex antennatus	5	2691	0.19
		Culex perexiguus	23	9011	0.26
		Culex pipiens	149	1954	7.63
		Culex poicilipes	0	16,889	0
		Culex quinquefasciatus	769	10,906	7.05
		Culex univittatus	4	6	66.67
		Uranotaenia unguiculata	0	30	0
		Total	1003	59,288	1.69
	Western Africa	*Aedes dalzieli*	1	104	0.96
		Anopheles rufipes	1	32	3.13
		Culex antennatus	3	198	1.52
		Culex neavei	26	415	6.27
		Culex perfuscus	1	101	0.99
		Culex poicilipes	1	368	0.27
		Culex quinquefasciatus	1	101	0.99
		Culex tritaeniorhynchus	3	372	0.81
		Mansonia uniformis	30	517	5.80
		Total	67	2208	3.03
	Eastern Africa	*Aedes* spp.	3	4	75.00
		Aedes sudanensis	1	2651	0.04
		Culex neavei	1	615	0.16
		Culex spp.	15	63	23.81
		Total	20	3333	0.60
	Southern Africa	*Aedes* spp.	1	1	100
		Anopheles gambiae	1	1	100
		Anopheles spp.	2	2	100
		Culex bitaeniorhynchus	1	1	100
		Culex pipiens	2	12	16.67
		Culex poicilipes	1	50	2
		Culex simpsoni	1	4	25.00
		Culex theileri	1	5	20.00
		Culex univittatus	8	1135	0.70
		Total	18	1211	1.49
RVFV	Western Africa	*Aedes fowleri*	0	10	0
		Aedes ochraceus	1	184	0.54
		Aedes ochraceus	1	437	0.23
		Aedes vexans	0	17	0
		Anopheles gambiae	5	295	1.69
		Anopheles pharoensis	5	3566	0.14
		Anopheles pretoriensis	0	33	0
		Anopheles rufipes	0	63	0
		Culex neavei	0	31	0
		Culex poicilipes	36	439	8.20
		Mansonia uniformis	0	517	0
		Total	48	5592	0.86
	Northern Africa	*Aedes aegypti*	10	24	41.67
		Aedes detritus	0	1	0
		Aedes mcintoshi	0	4	0
		Aedes vexans	0	2	0
		Anopheles coustani	3	18	16.67
		Anopheles gambiae arabiensis	300	400	75.00
		Anopheles pharoensis	0	17	0
		Anopheles tennebrosus	0	41	0
		Culex antennatus	3	218	1.38
		Culex perexiguus	0	3	0
		Culex pipiens	29	527	5.50
		Culex poicilipes	1	30	3.33
		Total	346	1285	26.93
	Central Africa	*Aedes* spp.	5	20	25.00
		Anopheles spp.	0	3	0
		Culex spp.	0	6	0
		Total	5	29	17.24
	Eastern Africa	*Aedes aegypti*	0	1	0
		Aedes albopictus	1	18	5.56
		Aedes albothorax	0	2	0

(*continued on next page*)

Table 1 (*continued*)

Virus	Study region	Mosquito species	Total no. positive	Total no. tested	Prevalence (%)
		Aedes argenteopunctatus	2	10	20.00
		Aedes circumluteolus	0	2	0
		Aedes cumminsii	0	14	0
		Aedes dentatus	0	6	0
		Aedes domesticus	0	6	0
		Aedes gibbinsi	1	72	1.39
		Aedes mcintoshi	26	678	3.83
		Aedes neomelaniconion	0	3	0
		Aedes ochraceus	33	1011	3.26
		Aedes pembaensis	1	65	1.54
		Aedes phylolabis	0	2	0
		Aedes simpsoni	0	1	0
		Aedes spp.	2	48	4.17
		Aedes (*Stegomyia*) spp.	0	2	0
		Aedes sudanensis	1	38	2.63
		Aedes tarsalis	0	2	0
		Aedes tricholabis	0	35	0
		Anopheles coustani	20	53	37.74
		Anopheles funestus	0	1	0
		Anopheles gambiae	12	28	42.86
		Anopheles implexus	0	4	0
		Anopheles maculipalpis	0	3	0
		Anopheles mascarensis	9	121	7.44
		Anopheles pharoensis	0	2	0
		Anopheles spp.	3	17	17.65
		Anopheles squamosus	15	322	4.66
		Anopheles gambiae	1	10	10.00
		Anopheles ziemanni	2	17	11.76
		Coquilletidia fuscopennata	1	41	2.44
		Coquillettidia aurites	0	5	0
		Coquillettidia fraseri	0	1	0
		Coquillettidia metallica	0	10	0
		Coquillettidia pseudoconopas	0	2	0
		Coquillettidia spp.	0	62	0
		Coquillettidia versicolor	0	4	0
		Culex annulioris	0	22	0
		Culex antennatus	14	339	4.13
		Culex bitaeniorhynchus	3	48	6.25
		Culex decens	2	44	4.55
		Culex duttoni	0	2	0
		Culex ethiopicus	0	7	0
		Culex neavei	0	7	0
		Culex perfuscus	0	3	0
		Culex poicilipes	3	252	1.19
		Culex quinquefasciatus	1	149	0.67
		Culex rubinotus	0	1	0
		Culex simpsoni	0	8	0
		Culex spp.	9	125	7.20
		Culex tigripes	0	1	0
		Culex trifilatus	0	4	0
		Culex tritaeniorhynchus	5	24	20.83
		Culex univitattus	1	49	2.04
		Culex quinquefasciatus	3	296	1.01
		Culiciomyia nebulosus	0	1	0
		Finlaya ingrami	0	4	0
		Hodgesia spp.	1	11	9.09
		Mansonia africana	2	341	0.59
		Mansonia spp.	3	22	13.64
		Mansonia uniformis	21	836	2.51
		Mansonioides nigerrima	0	8	0
		Mansonioides uniformis	0	2	0
		Metalutzia tigripes	0	3	0
		Neomelaniconion circumluteolus	0	4	0
		Oculeomyia annulioris	0	5	0
		Orthopodomyia spp.	0	3	0
		Stegomyia simpsoni	0	1	0
		Uranotaenia spp.	1	7	14.29
		Total	199	5348	3.72
	Southern Africa	*Aedes durbanensis*	1	105	0.95
		Total	1	105	0.95
CHIV	Western Africa	*Aedes aegypti*	1	187	0.53
		Aedes africanus	2	40	5.00
		Aedes centopuntatus	1	28	3.57
		Aedes dalzeili	4	338	1.18

(*continued on next page*)

Table 1 (*continued*)

Virus	Study region	Mosquito species	Total no. positive	Total no. tested	Prevalence (%)
		Aedes furcifer	16	612	2.61
		Aedes hirsutus	1	58	1.72
		Aedes luteocephalus	5	363	1.38
		Aedes metallicus	1	80	1.25
		Aedes spp.	6	27	22.22
		Aedes tylori	5	213	2.35
		Aedes vittatus	0	589	0
		Anopheles coustani	1	235	0.43
		Anopheles domicola	1	14	7.14
		Anopheles funestus	1	147	0.68
		Culex poicilipes	1	30	3.33
		Mansonia uniformis	1	116	0.86
		Other moqsuitoes	0	1160	0
		Total	47	4237	1.11
	Eastern Africa	*Aedes aegypti*	9	161	5.59
		Aedes africanus	1	6	16.67
		Aedes africanus	0	1	0
		Aedes albopictus	0	3	0
		Aedes natalensis	0	1	0
		Aedes pembaensis	0	7	0
		Aedes simpsoni	0	1	0
		Aedes simpsoni	0	1	0
		Aedes spp.	0	17	0
		Aedes tricholabis	0	6	0
		Aedes vittatus	0	74	0
		Anopheles gambiae	0	2	0
		Culex annulioris	0	13	0
		Culex poicilipes	0	1	0
		Culex quinquefasciatus	4	243	1.65
		Culex spp.	0	2	0
		Culex univittatus	0	5	0
		Culex vansomereni	0	5	0
		Culex zombaensis	0	26	0
		Eretmapodites chrysogaster	0	3	0
		Mansonia africana	0	2	0
		Mansonia uniformis	0	3	0
		Total	14	583	2.40
	Central Africa	*Aedes aegypti*	14	113	12.39
		Aedes albopictus	48	1094	4.39
		Aedes simpsoni	0	3	0
		Total	62	1210	5.12

combined with BG-sentinel traps baited with BG-lure (CLT + BSTB: $\beta = 3.18$, $P < 0.0001$. It is also worth noting that the use of animal-baited traps (TP: $\beta = 2.39$, $P = 0.0008$) also showed to be a positive significant predictor. Conversely, collections conducted in both wet and dry seasons (WD: $\beta = -1.41$, $P = 0.0015$) and the use of heavy-duty EVS traps (HDET) ($\beta = -3.75$, $P = 0.0048$) were associated with significantly lower RVFV prevalence.

Among the six models, Model 4, which focused on the study region, also performed strongly (AIC = 97.61), identifying significantly lower RVFV prevalence in Western Africa and Southern Africa than in the other areas (see Supplementary Table S11). However, Model 5 offers a more integrative perspective and better interpretive value by combining seasonal, regional, and methodological factors.

For CHIV, the multivariable meta-regression was not performed due to sparsity and multicollinearity of its data. Univariate meta-regression was performed for this virus; however, none of the predictors demonstrated significance.

4. Discussion

This systematic review and meta-analysis comprehensively evaluated mosquito-borne arboviral infections, specifically, those caused by WNV, RVFV, and CHIV, in mosquito vectors across Africa between 2000 and 2024. The study is based on xenosurveillance data from 45 studies and over 100,000 mosquito specimens. Unlike prior reviews, this study incorporated moderator analyses that evaluated trap type, seasonality, and screening method, revealing their substantial influence on detection rates in Africa. Therefore, the study provides the most up-to-date and geographically inclusive synthesis of the prevalence of these mosquito-borne arboviruses in Africa, with a robust methodological framework that incorporates mixed-effects models. Thus, the value of this synthesis is providing pooled prevalence estimates for risk assessment. The inclusion of nearly 120,000 mosquito samples comprising over 100 species and five African regions enabled fine-scale ecological interpretation and helped explain inconsistencies reported in past literature. These methodological differences may explain some of the inconsistencies reported in earlier literature regarding arboviral prevalence in mosquitoes.

The analysis revealed important epidemiological patterns and methodological heterogeneity with implications for mosquito-based arboviral disease surveillance. WNV was the most widely detected virus, with a pooled prevalence of 1.18% (95% CI: 0.40–3.43%), predominantly in *Cx. quinquefasciatus* and *Cx. pipiens*, especially in Northern Africa. *Cx. pipiens* has traits of higher dissemination and transmission rates and has also been implicated as a WNV vector (Fall et al., 2014; Kalmouni et al., 2024). *Culex. quinquefasciatus*, *Cx. univittatus*, and *Culex vansomereni* are also competent vectors of WNV (Amraoui et al., 2012; Kalmouni et al., 2024). RVFV exhibited a slightly higher prevalence of 2.10% (95% CI: 0.96–4.52%), with notable detections in *Cx. tritaeniorhynchus* and *Ae. mcintoshi* in Eastern Africa. CHIV showed the highest pooled prevalence (8.49%, 95% CI: 2.92–22.25%), predominantly in *Ae. aegypti* and *Ae. albopictus*, especially in Central and Eastern Africa.

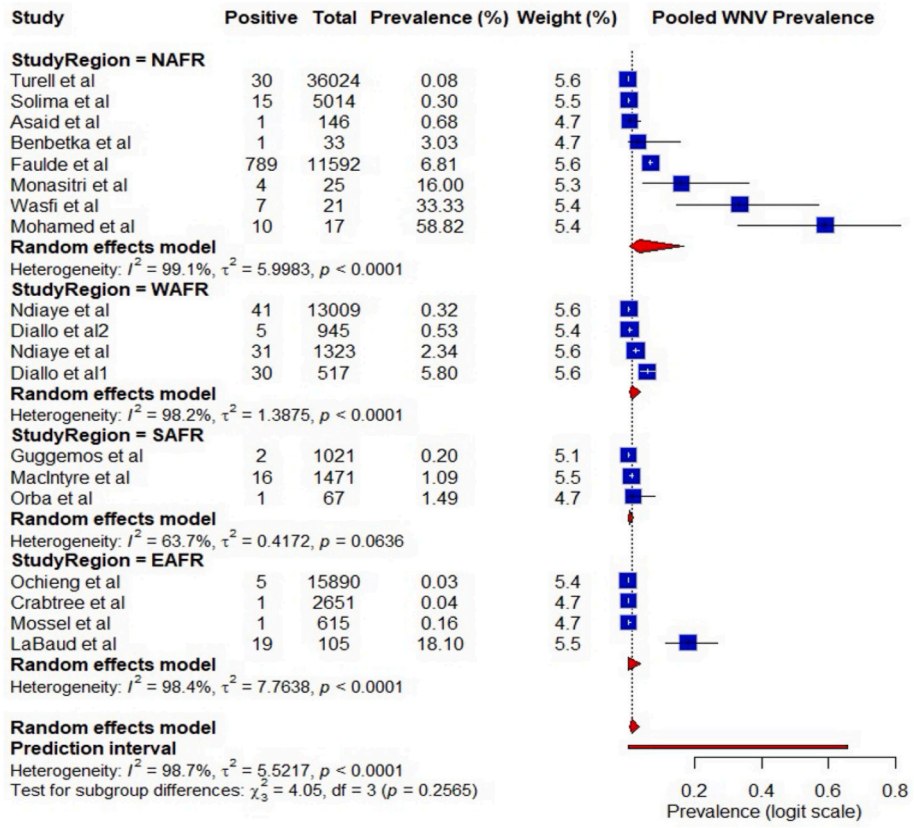

Fig. 2. Forest plot of West Nile virus (WNV) prevalence in mosquitoes across African regions. Squares represent individual study estimates, with horizontal lines indicating 95% confidence intervals (CIs). The red diamonds summarize the pooled prevalence for each region, with its width representing the CI. Heterogeneity statistics (I^2, τ^2, P) are provided for each subgroup.

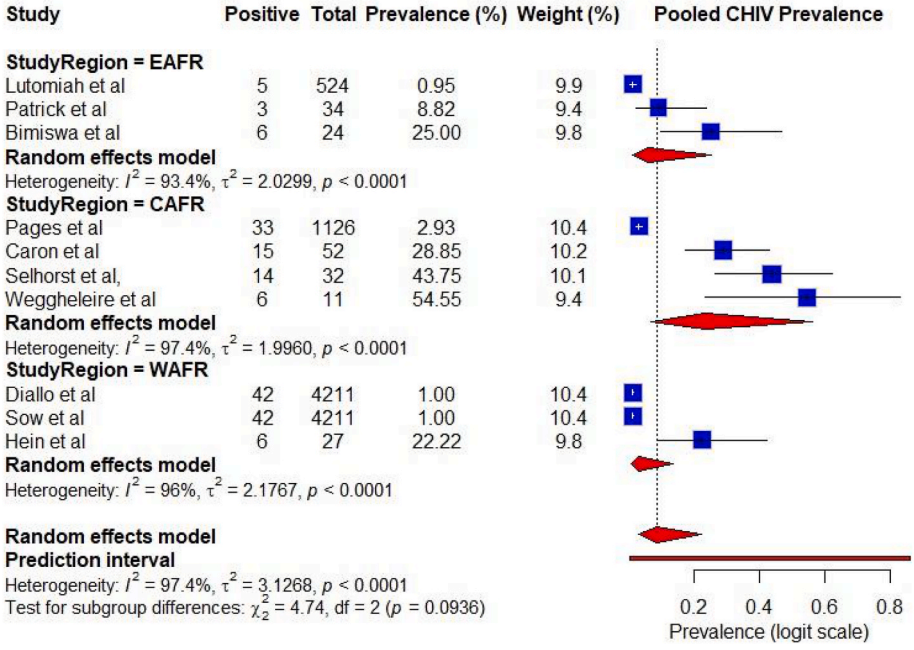

Fig. 3. Forest plot of CHIV prevalence in mosquitoes across African regions. Squares represent individual study estimates, with horizontal lines indicating 95% confidence intervals (CIs). The diamonds summarize the pooled prevalence for each region, with its width representing the CI. Heterogeneity statistics (I^2, τ^2, P) are provided for each subgroup.

Our findings are consistent with earlier reports identifying *Culex* spp. and flood-water *Aedes* spp. as primary vectors of RVFV, particularly in rural regions (Tchouassi et al., 2014). *Aedes* (*Stegomyia*) spp. are efficient vectors for CHIV due to their anthropophilic behaviours (Tchouassi

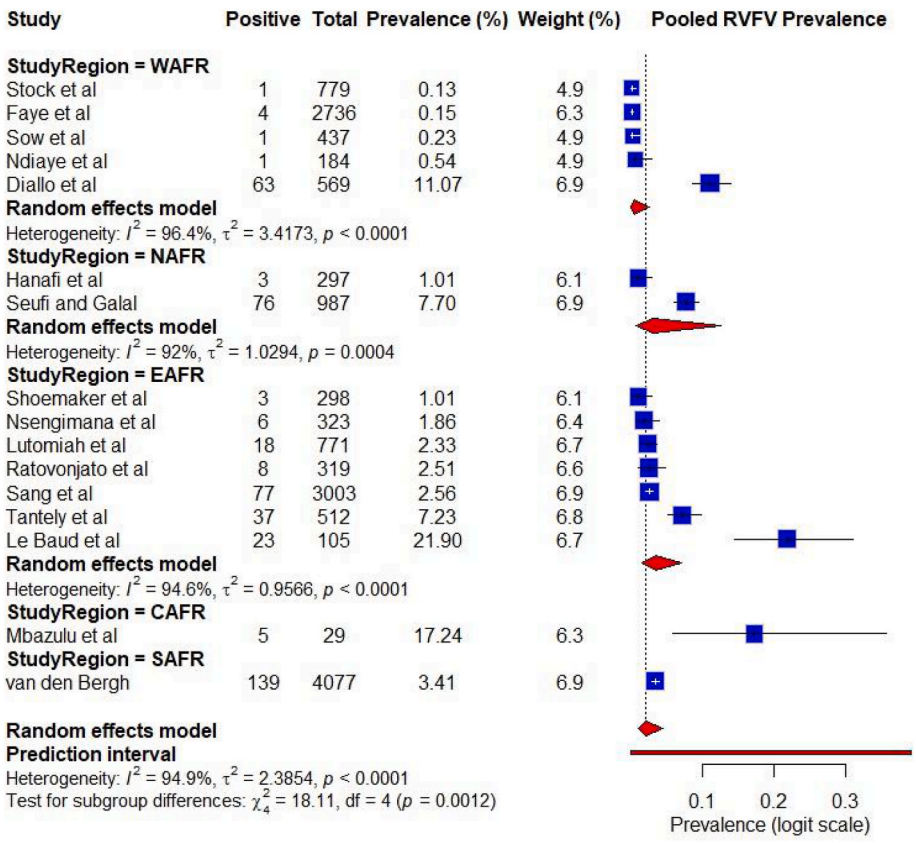

Fig. 4. Forest plot of RVFV prevalence in mosquitoes across African regions. Squares represent individual study estimates, with horizontal lines indicating 95% confidence intervals (CIs). The diamonds summarize the pooled prevalence for each region, with its width representing the CI. Heterogeneity statistics (I^2, τ^2, P) are provided for each subgroup.

et al., 2022; Cottis et al., 2023; Gardela et al., 2024). Moreover, the detection of CHIV in *Cx. quinquefasciatus* in Eastern Africa (1.6%, 4/243) is notable as this species is not typically considered a competent vector for CHIV. This finding may result from the detection of non-infective viral RNA, a recent infected blood meal, or pooled sampling methodology, rather than evidence of efficient vector competence. *Aedes aegypti* and *Ae. albopictus* remain the primary competent vector for CHIV (Kalyanasundram et al., 2024).

Substantial statistical heterogeneity was observed across studies for all three viruses ($I^2 > 97\%$), attributed to differences in study region and season, collection methods, and screening techniques. To address the observed heterogeneity in WNV and RVFV prevalence, meta-regression models were applied to explore the influence of potential moderators. For WNV, the best-fit model identified screening method and trapping technique as important determinants of virus detection rates. Screening method, as a moderator, showed significant predictors of WNV prevalence, indicating that differences in diagnostic approaches contribute to heterogeneity across studies. Studies employing molecular techniques (RT-PCR and qRT-PCR) generally reported higher detection rates compared to serological or immunofluorescent methods. This is consistent with the greater sensitivity and specificity of molecular assays, which directly detect viral RNA and therefore reflect current infections (Wang and Pang, 2024). Conversely, CO_2-baited CDC light traps (CLTC) were associated with lower detection probabilities, suggesting variability in trap efficacy for different species. Based on the trapping technique, methodological bias relates to trap efficiency and selectivity in collecting target vectors, but also the proportion of newly emerged to gravid cohorts in the traps. Traps that maximise gravid cohorts increase the likelihood of virus detection (Adhiambo et al., 2024). Additionally, Northern Africa emerged as the region with significantly elevated prevalence, highlighting a geographical hotspot. Northern Africa has extensive wetland systems, favourable bird migratory routes on top of its hotter climates with seasonal rainfall that may facilitate virus amplification and circulation (García-Carrasco et al., 2023). In Africa, it has already been determined that WNV has been predominantly isolated from mosquitoes rather than serologically detected from vertebrates, thereby highlighting mosquitoes as the transmitting agent (Mencattelli et al., 2022). Moreover, most of these mosquitoes were collected from North African countries like Morocco, Tunisia, and Egypt. qRT-PCR is efficient in detecting WNV across different samples like culture medium, human serum, vertebrate tissue, among others. Even though other methods like immunofluorescent techniques are being used, qRT-PCR is being routinely used throughout the world as a tool with enhanced sensitivity towards WNV detection (Kauffman et al., 2003; Fall et al., 2014; Ivănescu et al., 2024).

For RVFV, Model 5 that integrated the effects of season, collection method, and study region, yielded the best model fit. Key predictors of higher RVFV prevalence included sampling during the wet season, use of tent traps (TP), CDC light traps (CLT) alone, and in combination with BG-sentinel traps baited with lure (CLT + BSTB), and studies conducted in Northern Africa. An abnormal amount of rainfall has been associated with the high-risk period of RVF disease (Sang et al., 2016). The rainy season also coincides with higher abundance periods of the primary driving vectors, flood-water *Aedes* mosquitoes and also the secondary *Culex* vectors (Sang et al., 2016; Firaol and Rebuma, 2024). RVFV is transmitted by mosquitoes in the genera *Aedes* and *Culex*, and they are also known to have a high affinity towards CDC light traps (Goi et al., 2022). Furthermore, CDC light traps are known to collect mosquito populations with the highest species diversity (Adhiambo et al., 2024; Lee et al., 2024). In contrast, collection during both dry and wet seasons, as well as the use of heavy-duty EVS traps (HDET), were significantly associated with lower prevalence.

For CHIV, meta-regression was not performed due to sparse data and multicollinearity. Univariate analyses showed no significant associations with the tested predictors; this highlights the importance of methodological standardisation and increased region-specific surveillance approaches in enhancing comparability and accurately assessing CHIV transmission risk.

In this review, DENV and YFV were excluded from quantitative synthesis due to major limitations in the availability and quality of mosquito-based infection data across Africa. Nevertheless, both viruses remain epidemiologically important, particularly in urban DENV outbreaks and sylvatic YFV spill-over events. However, exhaustive screening of the literature revealed that xenosurveillance for these viruses is sparse, inconsistent, and rarely reported in a manner that supports meta-analysis. For YFV, transmission is maintained predominantly in *Aedes africanus* and other forest-dwelling vectors within sylvatic ecosystems, and outbreaks are typically detected through human clinical surveillance and vaccination programme monitoring rather than routine mosquito infection screening (Weaver and Reisen, 2010; Braack et al., 2018; Garcia-Oliveira et al., 2023). Similarly, although DENV transmission is increasingly recognized in African urban and peri-urban centres and is driven mainly by *Ae. aegypti* and *Ae. albopictus*, studies employing standardised mosquito pool testing or species-specific viral detection methods are limited on the continent (Kraemer et al., 2015). As a result, mosquito infection data for DENV and YFV are insufficient, heterogeneous, and unsuitable for pooled prevalence estimation or meta-regression.

Despite the comprehensive meta-analysis this study provides, limitations exist. First, CHIV data were too sparse (especially the absence of reported studies in Northern Africa) and characterized by multicollinearity, severely limiting the ability to perform a multivariable meta-regression and reliably analyse its moderators. Secondly, some mosquito species were aggregated under broad categories (e.g. "*Culex* spp."), potentially obscuring species-specific trends. Furthermore, most studies were not wide enough to include other information about species-feeding behaviour, like blood-meal analysis, amongst others. Therefore, even though there has been a significant prevalence of viruses in mosquitoes, there is no direct evidence that those mosquitoes ever fed or interacted with the dead-end hosts where they transmit the virus. Fourthly, for data analysis and reporting, only those mosquitoes with more than ten individuals tested or screened for arboviruses were included. Finally, studies from Southern and Central Africa were significantly underrepresented (8.8% and 11.1% of studies, respectively), which limits the statistical power of the pooled prevalence estimates and their generalizability for those regions.

The present findings reinforce the need for targeted xenosurveillance tailored to regional ecological contexts. High WNV prevalence in Northern Africa and CHIV in Central Africa suggests the potential for emergent outbreaks in areas not traditionally considered high-risk. This may be due to climate change, and consequently, the change in vector ecology (Merle et al., 2018). Xenosurveillance systems should incorporate standardised diagnostic protocols (favouring qRT-PCR) and employ trap combinations with proven efficacy (e.g. BG-sentinel traps with lure). Moreover, the significant influence of seasonality and trap type on RVFV detection advocates for seasonally adaptive xenosurveillance strategies that emphasise the wet season when transmission risk is elevated. Cross-training in molecular diagnostics and harmonised protocols for mosquito identification and virus detection are essential for improving inter-study comparability and outbreak preparedness.

Future research should prioritise longitudinal mosquito xenosurveillance to capture seasonal dynamics, and the integration of remote sensing data (e.g. NDVI, land cover, rainfall patterns) to predict risk zones and vector abundance. Expanded CHIV monitoring, particularly in under-sampled regions (Northern and Southern Africa), to clarify its geographical range, is also essential. Furthermore, future studies should incorporate blood-meal analysis for infected mosquito pools to establish the virus-vector-host transmission links, which is currently a major knowledge gap in African arbovirus xenosurveillance. Lastly, a major barrier to conducting more refined analyses of arbovirus infection status in mosquito vectors is the persistent lack of standardization in how studies report the anatomical components used for viral screening. Most studies included in this review did not specify whether diagnostic assays were performed on whole mosquitoes, head-thorax tissues, abdomens, or saliva expectorates. This omission prevents meaningful differentiation among infection, dissemination, and transmission stages and limits the ability to accurately classify vector competence across species and regions.

5. Conclusions

This systematic review and meta-analysis synthesised 25 years of African entomological evidence and confirms ongoing detection of WNV, RVFV, and CHIV in mosquito vectors across diverse ecological settings. However, the very high between-study heterogeneity indicates that methodological differences, including trapping strategies, seasonal sampling, and diagnostic approaches, strongly influence observed prevalence patterns. This limits comparability across regions and can obscure true spatiotemporal transmission risk. The key implication is the need to move from opportunistic, method-variable surveys to harmonised, region-adapted surveillance that prioritises sensitive molecular diagnostics and seasonally optimised sampling. In the context of climate-driven shifts in rainfall and vector ecology, integrating standardised entomological surveillance with environmental/climate intelligence within a One Health framework is critical to support policy-relevant early warning, targeted control, and preparedness for outbreaks affecting both humans and livestock.

Ethical approval

Not applicable.

CRediT authorship contribution statement

Mxolisi Mgongoma: Conceptualization, Methodology, Formal analysis, Investigation, Data curation, Writing - original draft, Visualization. **Armanda Bastos:** Writing - review & editing, Supervision. **Abel Ramoelo:** Writing - review & editing, Supervision.**David P. Tchouassi:** Validation, Writing - review & editing.

Funding

This research was supported by the Council for Scientific and Industrial Research in partnership with the Department of Science, Technology, and Innovation (DSTI), South Africa.

Declaration of competing interests

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Acknowledgements

We would like to extend our gratitude to Belelani N. Pepeta for his contribution to the modelling and structuring of this manuscript.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.crpvbd.2026.100360.

Data availability

The data supporting the conclusions of this article are included within the article and its supplementary file.

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