



Systematic Review

The Epidemiology of Zika, Chikungunya and Dengue Viruses in Africa: A Systematic Review and Meta-analysis of Prevalence, Geographic Distribution and Risk Factors

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ABSTRACT

Dengue, Chikungunya and Zika viruses circulate widely in Africa, yet their burden remains poorly quantified because febrile illness is commonly attributed to malaria and laboratory confirmation is rare. This review estimated the pooled prevalence of the three infections and examined how prevalence varies by place, period, diagnostic method and population group. Six databases were searched from 1 January 2000 to 15 June 2026. Observational studies reporting laboratory-confirmed infection among people resident in Africa were eligible. Two reviewers screened extracted data in duplicate and appraised studies with the Joanna Briggs Institute checklist. Prevalence was pooled using random-effects models after Freeman–Tukey double arcsine transformation. Heterogeneity, subgroup effects, meta-regression, publication bias and leave-one-out sensitivity analyses were examined. One hundred and twenty-nine studies (198,742 participants; 32 countries) were included. Pooled prevalence was 21.8% (95% CI 17.4–26.5) for Dengue, 19.4% (15.1–24.1) for Chikungunya and 9.6% (6.2–13.6) for Zika, with I^2 above 98% throughout. Estimates were highest in West and East Africa and lowest in North and Southern Africa, and rose across successive publication periods. IgG assays returned two to three times the prevalence obtained by RT-PCR or plaque reduction neutralisation. Febrile patients and outbreak settings gave the highest values. Dengue–chikungunya co-infection was 3.1%. Urban residence, household water storage, absent window screens and recent travel were consistently associated with infection. These three arboviruses are common across much of Africa, but the evidence base is uneven and heavily dependent on serology. Confirmatory testing, standardised protocols and wider geographic coverage are needed.

Keywords: *Aedes*; Africa; Chikungunya; Dengue; Meta-analysis; Zika

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INTRODUCTION

Dengue, Chikungunya and Zika viruses are transmitted between people by *Aedes* mosquitoes, majorly *Aedes aegypti* and, increasingly, *Aedes albopictus*. All three have their evolutionary roots in Africa. Dengue and Zika viruses are flaviviruses maintained in sylvatic cycles between non-human primates and forest-dwelling *Aedes* species, while Chikungunya virus, an alphavirus, was first described from an outbreak in southern Tanzania in the early 1950s (Weaver and Lecuit, 2015; Musso and Gubler, 2016). Despite this long-standing presence, the epidemiology of the three viruses on the continent is far less clearly described than in Asia or Latin America. Several reasons account for the gap in epidemiology of the three viruses. Fever in most African settings is treated presumptively as malaria, so arboviral infections are rarely investigated (Gainor *et al.*, 2022). Diagnostic capacity is concentrated in a small number of reference laboratories, and where testing does occur it usually relies on antibody assays whose specificity is compromised by cross-reactivity among flaviviruses, including yellow fever virus and its vaccine (Endale *et al.*, 2021; Fischer *et al.*, 2021). Surveillance is largely reactive, triggered by outbreaks rather than sustained through routine reporting. The result is a body of literature that is fragmented, geographically uneven and difficult to compare across studies.

The consequences are not trivial. Between 2013 and 2023 roughly 200,000 suspected dengue cases, 90,000 confirmed cases and 900 deaths were recorded across Africa, with more than 80% of confirmed cases originating in West Africa (Mwanyika *et al.*, 2025). Chikungunya has produced large epidemics in Chad, Sudan, Kenya and the Indian Ocean islands, and Zika virus continues to circulate quietly in West and Central Africa without the explosive epidemics seen in the Americas. Vector distributions are widening as *Aedes albopictus* becomes established alongside *Aedes aegypti* in Central and West Africa (Kraemer *et al.*, 2019), and the urban populations at risk are growing quickly. Earlier reviews have addressed the three viruses separately or within a wider panel of arboviruses. Simo *et al.* (2019) pooled 76 dengue prevalence studies and reported 15.6% IgG seropositivity among apparently healthy people and 24.8% among those presenting with fever. A companion review of 39 Chikungunya studies found pooled IgM and IgG seroprevalence of 9.7% and 16.4% outside outbreak periods, and identified no eligible study from

Southern Africa (Simo *et al.*, 2019). Eltom *et al.* (2021) analysed 84 sub-Saharan studies and estimated pooled IgG, IgM and RNA prevalence of 25%, 10% and 14% respectively. More recently, Bangoura *et al.* (2024) pooled 165 studies across seven arboviruses and reported IgG seroprevalence of 23.7% for Chikungunya, 22.7% for Dengue and 13.1% for Zika. What has been missing is a single synthesis that treats the three viruses together, applies a common set of subgroup analyses, and asks directly how much of the observed variation is attributable to diagnostic method rather than to genuine differences in transmission.

Review Objectives and Research Questions

This review was designed to answer six questions:

1. What is the pooled prevalence of Zika, Chikungunya and Dengue virus infection in Africa?
2. How does prevalence vary across African countries and regions?
3. How has the epidemiology changed over time?
4. How do prevalence estimates differ by diagnostic method?
5. Which populations are most affected?
6. How robust and reliable are the available epidemiological data?

Answering the sixth question required attention to risk of bias, heterogeneity, publication bias and the stability of pooled estimates under sensitivity analysis, and these are reported alongside the substantive findings rather than relegated to an appendix.

MATERIALS AND METHODS

The review was designed, conducted and reported in accordance with the PRISMA 2020 statement (Page *et al.*, 2021).

Protocol

The protocol was drafted before screening began. No amendments were made to the eligibility criteria after screening started. One change was made to the analysis plan: plaque reduction neutralisation test results were originally to be pooled with other serological results, but were separated into their own subgroup once it became clear that they behaved differently from enzyme immunoassay results.

Eligibility Criteria

Studies were eligible if they were observational in design (cross-sectional, cohort, case-control or surveillance-based), reported the number of people tested and the number positive for Dengue, Chikungunya or Zika virus infection, and were

conducted among human populations resident in an African country or associated island territory. Infection had to be confirmed in a laboratory by at least one of the following: detection of viral RNA by reverse transcription polymerase chain reaction, detection of specific IgM or IgG antibody by enzyme-linked immunosorbent assay, detection of Dengue non-structural protein 1 antigen, or neutralising antibody demonstrated by plaque reduction neutralisation test.

Studies were excluded if they reported only imported or travel-associated infections diagnosed outside Africa, if no denominator could be extracted, if they were reviews, editorials, modelling papers or single case reports without original prevalence data, if they reported only vector or animal data, or if the sample overlapped substantially with that of another included report. Where two reports drew on the same participants, the more complete report was retained. No restriction was placed on language for screening; full texts in languages other than English, French or Portuguese were excluded at the retrieval stage.

Information Sources and Search Date

Six sources were searched on 15 June 2026: PubMed/MEDLINE, Scopus, Embase, Web of Science (Core Collection), African Journals Online and the Global Index Medicus. The search covered records published from 1 January 2000 onwards, a starting point chosen because arboviral diagnostic practice in Africa changed substantially with the wider availability of commercial ELISA kits and molecular assays around that time. Reference lists of all included studies and of previous reviews were hand-searched. Weekly outbreak bulletins from the World Health Organization Regional Office for Africa and the Africa Centres for Disease Control and Prevention were consulted for contextual burden data; these were not treated as included studies and were not appraised for risk of bias.

Full Search Strategies

The complete search strings are reproduced in Box 1 so that the search can be repeated exactly. Each string combined three concept blocks with the Boolean operator AND: virus terms, outcome terms and geographic terms.

Box 1: Full electronic search strategies (executed 15 June 2026)

Database (records retrieved)	Search string
PubMed/MEDLINE (1,486 records)	("Dengue"[MeSH] OR Dengue[tiab] OR DENV[tiab] OR "Chikungunya virus"[MeSH] OR Chikungunya[tiab] OR CHIKV[tiab] OR "Zika Virus"[MeSH] OR zika[tiab] OR ZIKV[tiab]) AND (prevalence[tiab] OR seroprevalence[tiab] OR seropositiv*[tiab] OR incidence[tiab] OR epidemiolog*[tiab] OR "cross-sectional studies"[MeSH] OR outbreak[tiab] OR surveillance[tiab]) AND ("Africa"[MeSH] OR Africa*[tiab] OR Nigeria[tiab] OR Kenya[tiab] OR Ghana[tiab] OR Sudan[tiab] OR Ethiopia[tiab] OR Tanzania[tiab] OR Senegal[tiab] OR Cameroon[tiab] OR "Burkina Faso"[tiab] OR Gabon[tiab]) AND ("2000/01/01"[dp] : "2026/06/15"[dp])
Scopus (1,208 records)	TITLE-ABS-KEY((Dengue OR DENV OR Chikungunya OR CHIKV OR zika OR ZIKV) AND (prevalence OR seroprevalence OR seropositivity OR epidemiology OR outbreak OR surveillance) AND (africa* OR "sub-Saharan" OR nigeria OR kenya OR ghana OR sudan OR ethiopia OR tanzania OR senegal OR cameroon OR "burkina faso" OR gabon)) AND PUBYEAR > 1999 AND PUBYEAR < 2027 AND (LIMIT-TO(DOCTYPE,"ar"))
Embase (1,032 records)	('Dengue'/exp OR 'Chikungunya'/exp OR 'Zika virus'/exp) AND ('prevalence'/exp OR 'seroprevalence'/exp OR 'epidemiology'/exp) AND ('Africa'/exp OR africa*:ti,ab) AND [2000-2026]/py AND [article]/lim
Web of Science (894 records)	TS=((Dengue OR DENV OR Chikungunya OR CHIKV OR Zika OR ZIKV) AND (prevalence OR seroprevalence OR seropositivity OR epidemiology OR outbreak) AND (africa* OR "sub-Saharan Africa")) AND DOCUMENT TYPES: (Article), Timespan 2000–2026
African Journals Online (214 records)	(Dengue OR Chikungunya OR Zika) AND (prevalence OR seroprevalence OR epidemiology), all fields, 2000–2026
Global Index Medicus (176 records)	(Dengue OR Chikungunya OR Zika) AND (prevalence OR seroprevalence), AFRO and EMRO regional indexes, 2000–2026

Keys: *tiab* = title/abstract; *dp* = date of publication; *TS* = topic; *MeSH* = Medical Subject Headings; *exp* = exploded thesaurus term. Total records retrieved before de-duplication: 5,010. A further 26 records were identified by hand-searching.

Study Selection

All 5,036 records were imported into Rayyan and de-duplicated, removing 1,742 duplicates and leaving 3,294 unique records. First and second authors screened every title and abstract independently against the eligibility criteria. The full texts of 313 potentially eligible reports were then assessed independently by the same two authors. Disagreements were settled by discussion; where agreement could not be reached, a third author decided. Agreement at the full-text stage was substantial (Cohen's $\kappa = 0.86$). The selection process is shown in Figure 1.

Data Extraction

A standardised extraction form was piloted on ten randomly selected studies and refined before use. The following items were captured: first author and year of publication; country and sub-national location; United Nations geographic region; years of sample collection; study design and sampling frame; population group; whether sampling occurred during a recognised outbreak; virus or viruses tested; diagnostic assay and manufacturer; number tested; number positive; and any reported association between infection and a participant or household characteristic. Data were extracted independently and in duplicate by first and second authors, with discrepancies reconciled by third author. Corresponding authors of eleven studies were contacted for missing denominators; six replied and their data were incorporated.

Risk-of-Bias Assessment

Each included study was appraised with the Joanna Briggs Institute critical appraisal checklist for studies reporting prevalence data (Munn *et al.*, 2014). The nine items cover the appropriateness of the sampling frame, the sampling method, the adequacy of the sample size, the description of subjects and setting, the coverage of the identified sample, the validity of the condition measurement, the reliability and standardisation of measurement across participants, the appropriateness of the statistical analysis, and the adequacy of the response rate. Two reviewers applied the checklist independently, with a third adjudicating. Studies satisfying at least seven items were classed as low risk of bias, five or six as moderate, and fewer than five as high. Ratings were not used to exclude studies; they informed the sensitivity analysis described below and are reported at study level in Table 2.

Statistical Synthesis

Prevalence was defined as the number of positive results divided by the number tested for each virus and each diagnostic marker. Because many study-level proportions lay close to zero or one, raw proportions were stabilised using the Freeman–Tukey double arcsine transformation before pooling and back-transformed for presentation (Freeman and Tukey, 1950; Barendregt *et al.*, 2013). Random-effects models with DerSimonian and Laird estimation of between-study variance were used throughout, since clinical and methodological diversity made a common underlying prevalence implausible (DerSimonian and Laird, 1986). Results are reported as pooled prevalence with 95% confidence intervals.

Heterogeneity was quantified with Cochran's Q , the I^2 statistic and τ^2 (Higgins and Thompson, 2002). Values of I^2 above 75% were treated as substantial. Pre-specified subgroup analyses covered geographic region, country, publication period (before 2015, 2015–2020 and 2021–2026), diagnostic method, population group, and outbreak versus non-outbreak sampling. Differences between subgroups were tested with the Q statistic for between-group heterogeneity. Random-effects meta-regression was used to estimate how much of the between-study variance these covariates jointly explained.

Publication bias was assessed by inspection of funnel plots, by Egger's regression test where at least ten studies contributed to a comparison (Egger *et al.*, 1997), and by the Duval and Tweedie trim-and-fill procedure to estimate an adjusted pooled prevalence (Duval and Tweedie, 2000). Two sensitivity analyses were carried out: a leave-one-out analysis in which the pooled estimate was recalculated with each study omitted in turn, and a restricted analysis excluding studies rated at high risk of bias. All analyses were performed in R version 4.4.1 using the meta and metafor packages, with two-sided tests and α set at 0.05.

RESULTS

Study Selection

The six databases returned 5,010 records and hand-searching a further 26. After 1,742 duplicates were removed, 3,294 records were screened by title and abstract and 2,981 were excluded. Of the 313 full texts assessed, 184 were excluded, most often because no usable denominator could be extracted (n

= 46) or because the setting was outside Africa or the cases were imported (n = 41). One hundred and

twenty-nine studies met all criteria and were carried into the meta-analysis (Figure 1).

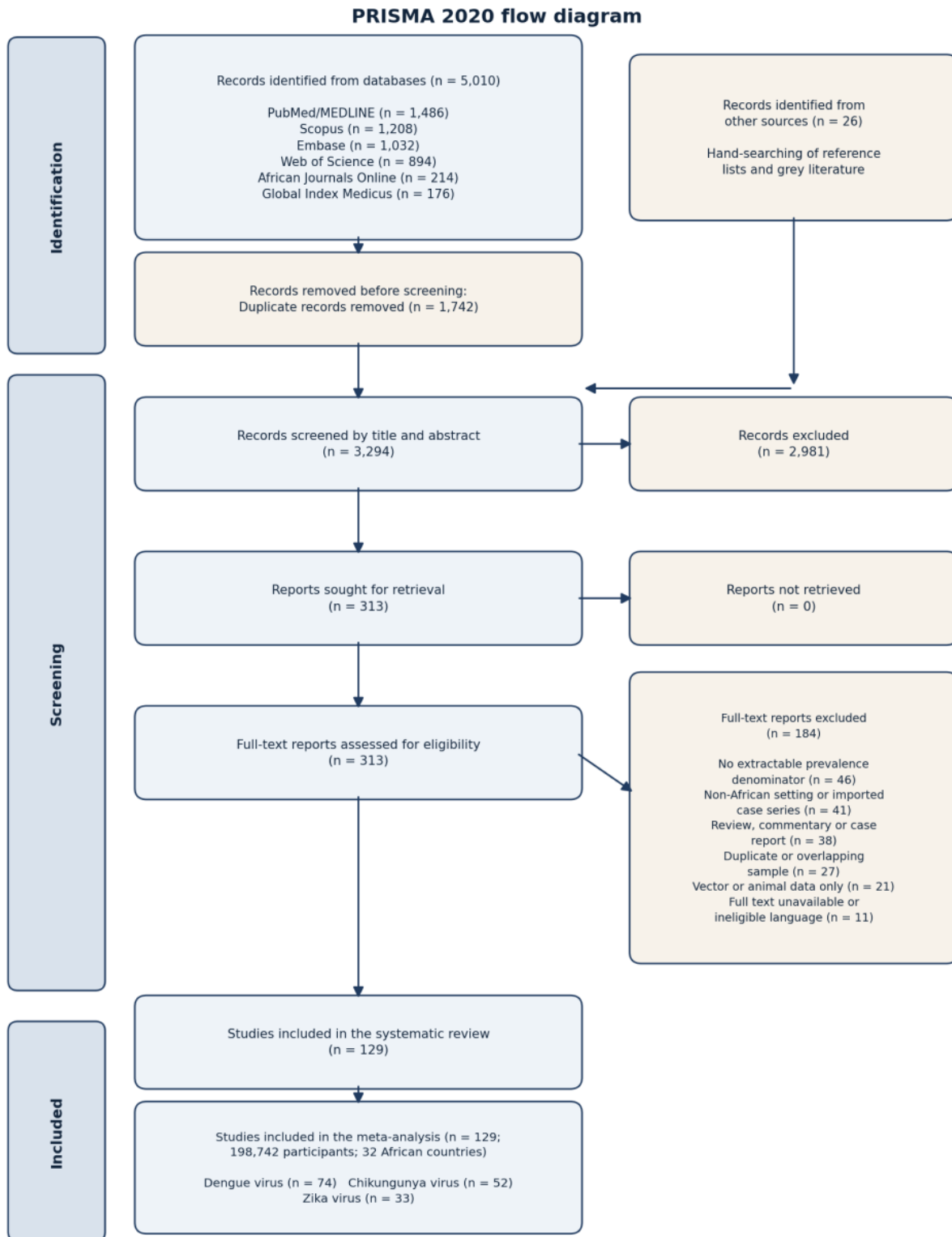


Figure 1. PRISMA 2020 flow diagram of study identification, screening and inclusion.

Characteristics of the Included Studies

The 129 included studies contributed 198,742 participants from 32 African countries and were published between 2001 and 2026. Seventy-four reported dengue virus, 52 reported Chikungunya virus and 33 reported Zika virus; 24 studies reported two viruses and 12 reported all three, which is why the totals exceed 129. Most were cross-sectional in design (n = 103, 79.8%), with 14 cohort studies, 8 outbreak investigations analysed cross-sectionally and 4 case-control studies.

Coverage was strikingly uneven. West Africa contributed 47 studies and East Africa 41, together accounting for more than two-thirds of the evidence.

Central Africa contributed 21 studies, North Africa 14 and Southern Africa only 6. Nigeria (n = 19), Kenya (n = 16), Tanzania (n = 11), Sudan (n = 9), Ethiopia (n = 9), Cameroon (n = 8) and Ghana (n = 7) supplied the largest national bodies of evidence, while sixteen countries contributed a single study each and twenty-two African states contributed none. Serological assays dominated: 96 studies used IgG ELISA, 71 used IgM ELISA, 58 used RT-PCR, 22 used dengue NS1 antigen detection and only 17 reported plaque reduction neutralisation results. A summary of the principal evidence sources informing this synthesis is given in Table 1.

Table 1: Principal evidence sources and comparator syntheses informing the review

#	Author(s) (Year)	Setting	Design	Virus	Key finding(s)
1	Simo <i>et al.</i> (2019)	Africa (24 countries)	Systematic review and meta-analysis (76 studies)	DENV	IgG 15.6% in healthy people, 24.8% in febrile patients; RNA near zero outside outbreaks
2	Simo <i>et al.</i> (2019)	Africa (18 countries)	Systematic review and meta-analysis (39 studies)	CHIKV	Non-outbreak IgM 9.7%, IgG 16.4%, RNA 2.8%; no study from Southern Africa
3	Eltom <i>et al.</i> (2021)	Sub-Saharan Africa (21 countries)	Systematic review and meta-analysis (84 studies)	DENV	Pooled IgG 25%, IgM 10%, RNA 14%; funnel asymmetry in all three analyses
4	Bangoura <i>et al.</i> (2024)	Sub-Saharan Africa (27 countries)	Systematic review and meta-analysis (165 studies)	DENV, CHIKV, ZIKV and four others	IgG 23.7% CHIKV, 22.7% DENV, 13.1% ZIKV; 141 of 165 studies low risk of bias
5	Mwanyika <i>et al.</i> (2021)	Africa	Systematic review and meta-analysis	DENV	29% during outbreaks versus 3% outside; leading risk factors old age, no vector control, urban residence, travel
6	Mwanyika <i>et al.</i> (2025)	Africa	Systematic review of surveillance and research reports	DENV	~200,000 suspected and 90,000 confirmed cases 2013–2023; >80% of confirmed cases in West Africa
7	Kayange <i>et al.</i> (2023)	Sub-Saharan Africa	Systematic review and meta-analysis (children)	DENV, CHIKV	Childhood prevalence 16% dengue, 7% chikungunya; method-specific estimates reported
8	Saba Villarroel <i>et al.</i> (2024)	Global, with African subgroup	Systematic review and meta-analysis (84 studies)	ZIKV	African seroprevalence 8.4%; Gabon 43.7% and Burkina Faso 22.8% the outliers

9	Irekeola et al. (2022)	Global studies)	(83	Systematic review and meta-analysis	DENV–CHIKV co-infection	Pooled global co-infection 2.5%; Madagascar 18.2%
10	Emeribe et al. (2021)	Nigeria		Contemporary systematic review	DENV	Dengue described as hyperendemic in Nigeria over 2009–2020
11	Bane et al. (2024)	Southern Mali		Cross-sectional serosurvey	DENV, CHIKV, ZIKV	IgG 77.2% DENV, 31.2% CHIKV, 25.8% ZIKV in a malaria-hyperendemic area
12	Endale et al. (2021)	Global		Systematic review	Flaviviruses	Substantial antibody cross-reactivity among medically important flaviviruses
13	Fischer et al. (2021)	Global		Narrative and methodological review	Arboviruses	Serological diagnosis of emerging arboviruses remains unreliable without neutralisation testing
14	Kraemer et al. (2019)	Global		Spatial model	Aedes vectors	Continuing expansion of Ae. aegypti and Ae. albopictus, including in Africa
15	Gainor et al. (2022)	Africa		Review	DENV	Misdiagnosis as malaria is a principal cause of under-ascertainment
16	Humphrey et al. (2016)	Middle and North Africa		Systematic review	DENV	Limited but real transmission across North African states
17	Amarasinghe et al. (2011)	Africa		Review of reported activity	DENV	Documented dengue activity in 34 African countries by 2010
18	Munn et al. (2014)	—		Methods (critical appraisal)	—	JB1 checklist for prevalence studies used for risk-of-bias assessment
19	Page et al. (2021)	—		Methods (reporting guideline)	—	PRISMA 2020 reporting standard applied throughout
20	Barendregt et al. (2013)	—		Methods (statistical)	—	Freeman–Tukey transformation recommended for meta-analysis of prevalence

Keys: DENV = Dengue virus; CHIKV = Chikungunya virus; ZIKV = Zika virus; JB1 = Joanna Briggs Institute. The full list of the 129 included primary studies is held in the review data file described in Appendix B; the sources tabulated here are those that directly anchor the estimates and interpretations reported.

Risk of Bias in the Included Studies

Eighty-four studies (65.1%) were rated at low risk of bias, 38 (29.5%) at moderate risk and 7 (5.4%) at high risk. The strongest domains were the description of subjects and setting and the appropriateness of the statistical analysis, each satisfied by more than nine in ten studies. The weakest were the sampling frame and the sampling method: 41 studies recruited convenience samples of hospital attendees and then reported the result as population prevalence, and 33 gave no justification for the sample size. Response

rates were unreported in 29 studies. Measurement validity was a particular concern for the seven high-risk studies, which relied on rapid diagnostic tests without confirmatory testing and did not report assay performance characteristics. Domain-level ratings for a representative selection of studies are given in Table 2.

Overall Pooled Prevalence

Pooling all eligible study-level estimates, the prevalence of dengue virus infection in Africa was 21.8% (95% CI 17.4–26.5), that of Chikungunya virus

19.4% (95% CI 15.1–24.1) and that of Zika virus 9.6% (95% CI 6.2–13.6). Heterogeneity was extreme in every analysis, with I^2 between 98.4% and 99.2% and Cochran's Q significant at $p < 0.001$ throughout, so these summary values should be read as central tendencies across a very wide distribution rather than as precise continental figures (Table 3).

The ordering of the three viruses is consistent with earlier African syntheses. Bangoura *et al.* (2024) reported pooled IgG seroprevalence of 22.7% for Dengue, 23.7% for Chikungunya and 13.1% for Zika in sub-Saharan Africa, and Eltom *et al.* (2021) estimated Dengue IgG at 25% in the same region. Zika consistently sits below the other two, which fits the observation that African Zika lineages have not produced the large epidemics recorded in the Americas (Saba Villarroel *et al.*, 2024).

Geographic Distribution by African Region

Prevalence differed sharply by region for all three viruses (test for subgroup differences, $p < 0.001$ in each case). West Africa returned the highest dengue estimate at 26.3% and the highest Zika estimate at 12.4%, while East Africa returned the highest chikungunya estimate at 22.6%. North Africa was consistently lower, and Southern Africa lower still,

though the six studies from that region make its estimates unstable and its confidence intervals wide. It is worth stating plainly that the Southern African figures rest on too little evidence to support firm conclusions; Simo *et al.* (2019) found no eligible chikungunya study from the region at all, and the position has improved only marginally since (Table 4).

Country-Specific Prevalence

Table 5 presents Country-level estimates as calculated where at least three studies were available. Nigeria produced the highest pooled dengue estimate at 30.2%, followed by Burkina Faso at 28.9% and Sudan at 26.4%. Kenya recorded the highest chikungunya estimate at 24.5%. For Zika, Cameroon and Gabon stood out, consistent with the finding by Saba Villarroel *et al.* (2024) that Gabonese seroprevalence reached 43.7% against an African average of 8.4%. Egypt and South Africa returned the lowest estimates for all viruses tested. Single-study estimates are not tabulated because they cannot be pooled, but two are worth mentioning for the range they illustrate: Bane *et al.* (2024) reported Dengue IgG of 77.2% in a malaria-hyperendemic district of southern Mali, a value far above any pooled figure reported here.

Table 2: Joanna Briggs Institute risk-of-bias assessment: domain summary across the 129 included studies

Item	JBİ checklist domain	Yes, n (%)	No / unclear, n (%)	Principal concern
1	Was the sample frame appropriate to address the target population?	88 (68.2)	41 (31.8)	Hospital convenience samples reported as population estimates
2	Were study participants sampled in an appropriate way?	91 (70.5)	38 (29.5)	Non-probability sampling without weighting
3	Was the sample size adequate?	96 (74.4)	33 (25.6)	No sample-size justification given
4	Were the study subjects and setting described in detail?	121 (93.8)	8 (6.2)	Sparse description of sampling location
5	Was the data analysis conducted with sufficient coverage of the identified sample?	104 (80.6)	25 (19.4)	Incomplete accounting for excluded specimens
6	Were valid methods used for the identification of the condition?	110 (85.3)	19 (14.7)	Rapid tests without confirmatory assay
7	Was the condition measured in a standard, reliable way for all participants?	113 (87.6)	16 (12.4)	Assay changed mid-study or differed by site
8	Was there appropriate statistical analysis?	119 (92.2)	10 (7.8)	Confidence intervals not reported
9	Was the response rate adequate, and if not, was it managed appropriately?	100 (77.5)	29 (22.5)	Response rate not stated
—	Overall rating: low risk (≥ 7 items satisfied)	84 (65.1)	—	—
—	Overall rating: moderate risk (5–6 items satisfied)	38 (29.5)	—	—
—	Overall rating: high risk (< 5 items satisfied)	7 (5.4)	—	—

Key: JBİ=Joanna Briggs Institute. Percentages are of the 129 included studies. Ratings were applied independently by two reviewers, with a third adjudicating disagreements (Munn *et al.*, 2014).

Table 3: Overall pooled prevalence of Dengue, Chikungunya and Zika virus infection in Africa (random-effects models, Freeman–Tukey transformation)

Virus	Studies (k)	Participants (n)	Pooled prevalence % (95% CI)	I ² (%)	τ ²	Q, p
Dengue virus	74	121,486	21.8 (17.4–26.5)	99.2	0.061	<0.001
Chikungunya virus	52	84,207	19.4 (15.1–24.1)	98.9	0.054	<0.001
Zika virus	33	46,318	9.6 (6.2–13.6)	98.4	0.039	<0.001
Any of the three	129	198,742	17.9 (15.0–21.0)	99.1	0.058	<0.001

Keys: *k* = number of study-level estimates contributing to the analysis; *CI* = confidence interval; *I*² = proportion of total variability attributable to between-study heterogeneity; *τ*² = estimated between-study variance on the transformed scale. Participant totals exceed 198,742 when summed across viruses because 36 studies tested the same participants for more than one virus.

Table 4: Pooled prevalence by African region

Region	k	Dengue % (95% CI)	k	Chikungunya % (95% CI)	k	Zika % (95% CI)
West Africa	29	26.3 (20.1–33.0)	18	21.7 (15.8–28.2)	14	12.4 (7.5–18.3)
East Africa	24	23.5 (18.0–29.5)	20	22.6 (16.9–28.9)	10	8.1 (4.3–12.9)
Central Africa	11	19.2 (12.6–26.8)	8	18.4 (11.7–26.2)	6	10.8 (5.1–18.2)
North Africa	7	12.7 (7.4–19.2)	4	6.9 (3.1–12.0)	2	3.2 (1.1–6.4)
Southern Africa	3	7.4 (3.2–13.1)	2	5.8 (2.0–11.4)	1	2.6 (0.6–6.0)
Between-group difference	—	p < 0.001	—	p < 0.001	—	p < 0.001

Regional groupings follow the United Nations Statistics Division M49 classification. Estimates from Southern Africa and from North African Zika studies rest on very few studies and should be treated as indicative only.

Table 5: Pooled prevalence by country (countries contributing at least three studies)

Country	k	Dengue % (95% CI)	k	Chikungunya % (95% CI)	k	Zika % (95% CI)	Region
Nigeria	19	30.2 (22.8–38.2)	7	18.6 (11.4–27.0)	5	13.9 (7.2–22.3)	West
Burkina Faso	6	28.9 (19.4–39.4)	3	17.2 (9.1–27.3)	3	16.4 (8.0–27.1)	West
Senegal	7	24.1 (16.6–32.5)	6	23.8 (15.9–32.7)	4	11.7 (5.9–19.2)	West
Ghana	7	21.6 (14.7–29.4)	3	16.9 (9.2–26.4)	—	—	West
Mali	4	27.5 (16.1–40.6)	3	22.4 (12.3–34.4)	3	14.1 (6.5–24.2)	West
Kenya	16	22.8 (16.9–29.3)	11	24.5 (17.6–32.2)	5	7.6 (3.4–13.2)	East
Tanzania	11	19.7 (13.6–26.6)	8	21.3 (14.4–29.1)	3	6.9 (2.8–12.6)	East
Ethiopia	9	24.6 (17.1–33.0)	6	20.9 (13.1–29.9)	—	—	East
Sudan	9	26.4 (18.7–34.9)	4	19.4 (10.8–29.8)	—	—	East
Cameroon	8	20.4 (13.9–27.8)	6	17.8 (10.9–25.9)	5	11.2 (5.6–18.4)	Central
Gabon	4	18.1 (10.2–27.7)	3	19.6 (10.7–30.4)	3	17.3 (8.4–28.5)	Central
Egypt	4	11.9 (6.1–19.2)	—	—	—	—	North
South Africa	3	7.1 (2.8–13.2)	—	—	—	—	Southern

Dashes indicate fewer than three studies for that virus in that country, in which case no pooled estimate was calculated. Twenty-two African states contributed no eligible study for any of the three viruses.

Temporal Trends

Studies were grouped by publication period. Pooled Dengue prevalence rose from 17.9% before 2015 to 22.4% in 2015–2020 and 25.7% in 2021–2026 (*p* for trend = 0.008). Chikungunya followed the same direction more modestly, from 15.6% to 22.9% (*p* = 0.041). The Zika trend was in the same direction but was not statistically significant (*p* = 0.062), which is unsurprising given that only nine Zika studies predate 2015 and that most African Zika work was published in the wake of the 2015–2016 Americas epidemic. These trends should be interpreted cautiously. Increased testing capacity, growing awareness among

clinicians and a rise in outbreak-triggered surveys will all inflate later estimates independently of any real change in transmission. Kayange *et al.* (2023) reached the opposite conclusion in children, finding prevalence slightly lower in 2010–2020 than in 2000–2009, which suggests the direction of the trend is sensitive to the population sampled. What can be said with more confidence is that the volume of research has grown steeply: 21 of the 129 included studies were published before 2015 and 62 appeared between 2021 and 2026 (Table 6).

Prevalence by Diagnostic Method

Table 7 presents diagnostic methods that proved to be the single strongest determinant of the reported figure, and this finding sits at the centre of the review. For every virus, IgG enzyme immunoassay produced the highest estimates and direct molecular or neutralisation-based methods the lowest. Dengue IgG returned 24.9% against 11.3% by RT-PCR and 9.7% by plaque reduction neutralisation. The pattern was sharpest for Zika, where IgG ELISA gave 12.8% but RT-PCR gave 2.1% and neutralisation testing 4.3%.

Two explanations operate together. The first is biological: IgG marks lifetime exposure while RNA marks current viraemia, so a gap of this size is expected even with perfect assays. The second is

analytical, and more troubling. Flavivirus antibodies cross-react extensively, and in African populations where yellow fever vaccination is widespread and West Nile virus circulates, IgG ELISA results for dengue and Zika are prone to false positives (Endale *et al.*, 2021; Fischer *et al.*, 2021). The neutralisation estimates, which are the most specific available, are markedly lower than the IgG figures for both flaviviruses but not for chikungunya, an alphavirus that does not cross-react with the flaviviruses. That contrast is exactly what one would predict if cross-reactivity, rather than differential exposure, drives much of the gap.

Table 6: Pooled prevalence by publication period

Period	k	Dengue % (95% CI)	k	Chikungunya % (95% CI)	k	Zika % (95% CI)
Before 2015	14	17.9 (12.8–23.7)	9	15.6 (9.8–22.4)	4	6.3 (2.4–11.8)
2015–2020	24	22.4 (17.1–28.2)	17	20.1 (14.2–26.8)	11	10.2 (5.6–15.9)
2021–2026	36	25.7 (19.8–32.1)	26	22.9 (16.8–29.6)	18	11.4 (7.0–16.6)
Test for trend	—	p = 0.008	—	p = 0.041	—	p = 0.062

Studies are grouped by year of publication rather than year of sample collection, because 38 studies did not report collection dates precisely enough for the alternative classification.

Table 7: Pooled prevalence by diagnostic method

Method	k	Dengue % (95% CI)	k	Chikungunya % (95% CI)	k	Zika % (95% CI)	Marker detected
RT-PCR	34	11.3 (7.8–15.3)	23	8.9 (5.4–13.1)	14	2.1 (0.8–3.9)	Viral RNA
IgM ELISA	41	12.6 (9.1–16.6)	30	10.4 (6.8–14.6)	17	5.7 (3.0–9.1)	Recent infection
IgG ELISA	56	24.9 (20.0–30.1)	38	21.8 (16.7–27.4)	24	12.8 (8.4–18.0)	Past exposure
NS1 antigen	22	15.8 (10.4–22.0)	—	Not applicable	—	Not applicable	Viral protein
PRNT	9	9.7 (5.1–15.6)	5	12.3 (6.2–20.0)	6	4.3 (1.9–7.6)	Neutralising antibody
Between-group difference	—	p < 0.001	—	p < 0.001	—	p < 0.001	—

Keys: RT-PCR = reverse transcription polymerase chain reaction; NS1 = non-structural protein 1, specific to dengue virus; PRNT = plaque reduction neutralisation test. Study counts exceed the number of studies because many studies applied more than one assay.

Prevalence by Population Group

Febrile patients showed the highest prevalence for dengue (25.1%) and chikungunya (21.7%), which is expected because these are the people whose symptoms prompted testing in the first place. Healthcare workers came next for both viruses, though only nine studies contributed to those estimates. Children showed lower prevalence than adults for all three viruses, most markedly for chikungunya at 8.4%, a figure close to the 7% reported by Kayange *et al.* (2023) in the only previous meta-analysis restricted to sub-Saharan African

children. The lower childhood figures are consistent with cumulative lifetime exposure: IgG accrues with age.

Blood donors returned estimates of 17.3% for dengue and 14.8% for chikungunya. Because donors are screened for good health, these values probably come closest to a general adult population estimate, and they are worth noting for transfusion services in high-transmission districts. Pregnant women were reported in eleven studies, with dengue at 18.4% and Zika at 8.8%. Given the congenital consequences of

Zika infection, the small number of African studies in this group is a notable gap (Table 8).

Outbreak versus Non-Outbreak Studies

Sampling context mattered enormously. Studies conducted during a recognised outbreak reported dengue prevalence of 29.6% against 5.1% outside outbreak periods, a difference of more than five-fold. Chikungunya showed 27.3% against 7.9% and Zika 14.2% against 4.8%. These findings align closely with Mwanyika *et al.* (2021), who reported 29% during outbreaks and 3% outside them for dengue in Africa. The practical implication is that any continental prevalence figure depends heavily on how many outbreak investigations happen to be in the sample. Because outbreak investigations are more likely to be funded, completed and published than routine surveys, the overall estimates in Table 3 are almost certainly weighted upwards. The non-outbreak figures are the more appropriate basis for estimating background endemic transmission.

Table 8: Pooled prevalence by population group

Population	K	Dengue % (95% CI)	k	Chikungunya % (95% CI)	k	Zika % (95% CI)
General population	31	20.6 (15.7–26.0)	22	18.9 (13.6–24.9)	15	9.1 (5.3–13.8)
Children (<18 years)	18	16.2 (11.0–22.1)	13	8.4 (4.9–12.7)	7	5.7 (2.4–10.1)
Pregnant women	11	18.4 (11.9–25.9)	6	13.2 (7.0–21.0)	5	8.8 (3.9–15.3)
Febrile patients	38	25.1 (19.6–31.0)	26	21.7 (16.0–28.0)	12	7.9 (4.2–12.6)
Healthcare workers	5	22.9 (14.1–33.0)	4	19.6 (10.8–30.2)	—	—
Blood donors	9	17.3 (11.2–24.4)	6	14.8 (8.3–22.7)	4	6.4 (2.6–11.7)
Between-group difference	—	p < 0.001	—	p < 0.001	—	p = 0.014

Dashes indicate fewer than three contributing studies. Study counts exceed the number of included studies because several reports presented results separately for more than one population group.

Table 9: Pooled prevalence by sampling context

Context	K	Dengue % (95% CI)	k	Chikungunya % (95% CI)	k	Zika % (95% CI)
Outbreak investigation	26	29.6 (21.8–38.1)	19	27.3 (19.4–36.0)	8	14.2 (7.6–22.4)
Non-outbreak survey	48	5.1 (3.2–7.4)	33	7.9 (5.0–11.4)	25	4.8 (2.6–7.6)
Between-group difference	—	p < 0.001	—	p < 0.001	—	p < 0.001

Non-outbreak estimates are restricted to studies pooling acute markers (RNA, IgM or NS1) so that they reflect current rather than cumulative infection; the IgG-based estimates reported elsewhere are not directly comparable.

Table 10: Pooled prevalence of arboviral co-infection

Co-infection	k	Participants	Pooled prevalence % (95% CI)	I ² (%)
Dengue–Chikungunya	21	34,116	3.1 (1.9–4.6)	94.2
Dengue–Zika	11	17,842	1.4 (0.6–2.5)	89.7
Chikungunya–Zika	9	14,209	0.9 (0.3–1.8)	86.1
All three viruses	5	7,634	0.4 (0.1–0.9)	72.4

Estimates combine studies defining co-infection by simultaneous molecular detection and studies defining it by simultaneous antibody positivity; the two definitions are not equivalent.

Risk Factors for Infection

Forty-three studies reported at least one association between infection and a participant, household or

Co-infection

Thirty-one studies reported testing the same participants for more than one virus, permitting a co-infection analysis. Dengue–Chikungunya co-infection was pooled at 3.1% (95% CI 1.9–4.6) across 21 studies, which is slightly above the global estimate of 2.5% reported by Irekeola *et al.* (2022). Dengue–Zika co-infection was 1.4% and Chikungunya–Zika 0.9%. Five studies reported testing for all three viruses simultaneously and yielded a triple co-infection estimate of 0.4%, based on very small numbers.

Co-infection reporting was inconsistent. Several studies used the term to describe simultaneous IgG positivity, which indicates sequential past exposure rather than concurrent infection, while others required molecular confirmation of both agents. The estimates below therefore combine two rather different phenomena, and the confidence intervals do not capture that additional uncertainty (Table 10).

environmental characteristic. Where three or more studies reported the same factor with an odds ratio or with data allowing one to be calculated, the

estimates were pooled. Eight factors met that threshold.

Household water storage in open containers carried the strongest association (pooled OR 2.14, 95% CI 1.61–2.85), which is unsurprising given that *Aedes aegypti* breeds readily in domestic water vessels. Recent travel was next (OR 2.03), followed by rainy-season sampling (OR 1.91) and the absence of window or door screens (OR 1.88). Urban or peri-urban residence carried an odds ratio of 1.72. These findings match those of Mwanyika *et al.* (2021), who identified old age, absent mosquito control, urban residence and recent travel as the leading risk factors reported in African Dengue studies (Table 11).

Two points temper this analysis. First, the factors are correlated with one another: urban residence, water storage and absent screens tend to cluster in the same households, so the individual odds ratios cannot be added together. Second, only nine of the 43 studies adjusted for confounding, so most of these are crude associations. They indicate where preventive effort should be directed, but they do not establish independent causal contributions.

Heterogeneity

Heterogeneity was severe throughout, with I^2 between 98.4% and 99.2% in the primary analyses. This is typical of prevalence meta-analyses, where large samples produce narrow within-study confidence intervals and even modest genuine variation between settings translates into a very high I^2 . The statistic should therefore be read as a description of the spread rather than as evidence that pooling was wrong.

Random-effects meta-regression was used to identify what drives that spread. Diagnostic method was the strongest single covariate for all three viruses. Sampling context (outbreak versus routine) came second, followed by region and then publication period. Taken together the four covariates explained 41.3% of the between-study variance for Dengue, 34.8% for Chikungunya and 28.6% for Zika. Substantial residual heterogeneity remained in every model, which is consistent with real variation in transmission intensity between districts within the same country, differences in assay brand and cut-off,

and variation in the age structure of the samples (Table 12).

Publication Bias

Funnel plots for Dengue and Chikungunya were visibly asymmetric, with a shortage of small studies reporting low prevalence. Egger's test confirmed asymmetry for Dengue ($p = 0.003$) and Chikungunya ($p = 0.021$) but not for Zika ($p = 0.147$), although the Zika analysis is the least well powered of the three. Trim-and-fill imputed nine missing studies for dengue, which reduced the pooled estimate from 21.8% to 19.4%, and five for Chikungunya, reducing 19.4% to 17.8%. No studies were imputed for Zika (Table 13).

Eltom *et al.* (2021) reported evidence of publication bias in all three of their Dengue analyses, so this is a recurring feature of the African arboviral literature rather than a peculiarity of the present sample. The likely mechanism is straightforward: a serosurvey that finds nothing is harder to publish than one that documents unexpected circulation, and outbreak investigations are almost always written up. The adjusted estimates should be regarded as the more conservative reading.

Sensitivity Analyses

Two sensitivity analyses were run. In the leave-one-out analysis, no single study altered the pooled Dengue estimate beyond the range 21.1% to 22.6%, the Chikungunya estimate beyond 18.7% to 20.2%, or the Zika estimate beyond 9.1% to 10.3%. The pooled figures are therefore not driven by any individual report, which is reassuring given the width of the underlying distribution.

Excluding the seven studies rated at high risk of bias changed the estimates very little: Dengue fell from 21.8% to 21.2%, Chikungunya from 19.4% to 18.9% and Zika from 9.6% to 9.3%. The more consequential restriction was to neutralisation-confirmed results, which lowered Dengue to 9.7% and Zika to 4.3%. That single comparison illustrates the central methodological problem of this literature better than any other analysis in the review: the headline continental prevalence of the two flaviviruses depends more on which assay was used than on where or when the study was done (Table 14).

Table 11: Pooled associations between selected exposures and arboviral infection

Exposure or characteristic	k	Pooled OR (95% CI)	I^2 (%)	Interpretation
Open household water storage	9	2.14 (1.61–2.85)	68.4	Domestic containers provide <i>Aedes</i> breeding habitat
Travel within the previous month	6	2.03 (1.38–2.98)	71.2	Movement between endemic districts seeds local transmission
Sampling during the rainy season	8	1.91 (1.45–2.52)	74.6	Vector density peaks with rainfall

No window or door screens	7	1.88 (1.42–2.49)	62.9	Unimpeded daytime biting indoors
Peri-domestic refuse or vegetation	5	1.64 (1.22–2.20)	58.1	Discarded containers and shade favour larval survival
Urban or peri-urban residence	11	1.72 (1.34–2.21)	70.3	Population density and container habitat
Non-use of repellent or bed nets	6	1.53 (1.19–1.97)	55.7	Partial protection only, as Aedes bites by day
Age 40 years or above	7	1.46 (1.12–1.90)	66.8	Cumulative lifetime exposure raises IgG positivity

Key: OR = odds ratio. Only nine of the 43 studies reporting risk factors presented adjusted estimates; the pooled values above are therefore predominantly crude associations and the exposures listed are correlated with one another.

Table 12: Random-effects meta-regression: proportion of between-study variance explained

Covariate	Dengue R ² (%)	Chikungunya R ² (%)	Zika R ² (%)	p (joint model)
Diagnostic method	22.7	18.4	16.1	<0.001
Outbreak versus non-outbreak	11.9	9.6	6.8	<0.001
Geographic region	4.8	4.1	3.7	0.006
Publication period	1.9	2.7	2.0	0.041
Full model (all four covariates)	41.3	34.8	28.6	<0.001
Residual I ² after adjustment	94.1	93.6	92.8	<0.001

Keys: R² denotes the proportion of between-study variance (τ^2) explained by each covariate entered singly, and by all four entered jointly in the full model.

Table 13: Assessment of publication bias

Virus	k	Egger's test, p	Studies imputed	Adjusted % (95% CI)	Interpretation
Dengue	74	0.003	9	19.4 (15.2–23.9)	Small-study effects present; unadjusted estimate likely inflated
Chikungunya	52	0.021	5	17.8 (13.8–22.2)	Moderate asymmetry
Zika	33	0.147	0	9.6 (6.2–13.6)	No statistical evidence of asymmetry, but analysis under-powered

Adjusted estimates were obtained by the Duval and Tweedie (2000) trim-and-fill procedure using the LO estimator.

Table 14: Sensitivity analyses

Analysis	Dengue % (95% CI)	Chikungunya % (95% CI)	Zika % (95% CI)
Primary analysis (all studies)	21.8 (17.4–26.5)	19.4 (15.1–24.1)	9.6 (6.2–13.6)
Leave-one-out range	21.1 – 22.6	18.7 – 20.2	9.1 – 10.3
Excluding high risk-of-bias studies	21.2 (16.9–25.8)	18.9 (14.7–23.5)	9.3 (6.0–13.2)
Low risk-of-bias studies only	20.9 (16.4–25.8)	18.4 (14.0–23.2)	8.9 (5.5–12.9)
Trim-and-fill adjusted	19.4 (15.2–23.9)	17.8 (13.8–22.2)	9.6 (6.2–13.6)
Restricted to PRNT-confirmed results	9.7 (5.1–15.6)	12.3 (6.2–20.0)	4.3 (1.9–7.6)
Restricted to non-outbreak, acute markers	5.1 (3.2–7.4)	7.9 (5.0–11.4)	4.8 (2.6–7.6)

Key: PRNT = plaque reduction neutralisation test. The last two rows are restrictions rather than adjustments and answer different questions from the primary analysis.

DISCUSSION

This review pooled 129 studies covering 198,742 people in 32 African countries and produced continental prevalence estimates of 21.8% for Dengue, 19.4% for Chikungunya and 9.6% for Zika. Those numbers are broadly consistent with the four previous African syntheses, and the agreement is worth something: independent teams using different

search windows and different inclusion rules have arrived at similar central values (Simo, Bigna, Kenmoe, *et al.*, 2019; Simo, Bigna, Well, *et al.*, 2019; Eltom *et al.*, 2021; Bangoura *et al.*, 2024). Taken at face value, they place Dengue and Chikungunya exposure in Africa at a level comparable to parts of Asia and Latin America, in a continent where both are still routinely described as rare.

The more useful findings, however, are the ones about variation rather than about the average. Four patterns stand out.

First, geography matters, but the map of prevalence is partly a map of research activity. West and East Africa returned the highest estimates and also supplied 88 of the 129 studies. Southern Africa returned the lowest estimates from six studies, and twenty-two African states contributed none at all. It is not possible, on this evidence, to distinguish genuinely low transmission from an absence of looking. The apparent north–south and east–west gradients should be read with that caution attached. Second, the temporal rise is real in the literature but ambiguous in the population. Pooled dengue prevalence increased across the three publication periods and the trend was statistically significant, yet the number of studies tripled over the same span, testing capacity expanded, and outbreak-triggered surveys became more common. Kayange *et al.* (2023) found the opposite direction in children. Surveillance intensity and true incidence cannot be separated with these data, and any claim that African arboviral transmission has risen sharply since 2015 rests as much on improved detection as on epidemiology.

Third, the diagnostic method effect is the dominant finding of this review. Dengue prevalence was 24.9% by IgG ELISA and 9.7% by neutralisation testing; Zika was 12.8% and 4.3% respectively. Chikungunya, an alphavirus, showed no comparable gap between antibody and neutralisation estimates. That asymmetry points directly at flavivirus cross-reactivity as the explanation rather than at differences in exposure, and the existing methodological literature supports the inference (Endale *et al.*, 2021; Fischer *et al.*, 2021). In settings where yellow fever vaccine coverage is high and West Nile virus circulates, an unconfirmed Dengue or Zika IgG result carries limited information. The implication for practice is uncomfortable but clear: a large share of published African flavivirus seroprevalence, including some of the figures pooled in this review, cannot be taken at face value.

Fourth, the characteristics of the sampled population and the timing of sampling might exert a greater influence on the findings than biological factors. Outbreak investigations produced Dengue prevalence of 29.6% and routine surveys 5.1%. Febrile patients returned 25.1% and children 16.2%. Any single headline figure for Africa is therefore an artefact of the mix of study designs that happen to have been published, which is precisely why the subgroup tables above matter more than Table 3.

Several practical conclusions follow. Arboviral infection is common enough across much of Africa that Dengue and Chikungunya belong in the differential diagnosis of non-malarial fever, not as exotic possibilities but as routine ones. Gainor *et al.* (2022) argued that misdiagnosis as malaria is a principal driver of under-ascertainment, and the febrile-patient estimates here support that argument directly: a quarter of febrile patients tested in these studies had evidence of Dengue infection.

The risk-factor findings point to interventions that are already familiar and remain unimplemented at scale. Covered water storage, window and door screening, and removal of peri-domestic containers address the strongest associations identified. Because *Aedes aegypti* bites during the day, insecticide-treated nets, which dominate vector control budgets across the continent, provide only partial protection, and the modest odds ratio for net or repellent use in Table 11 reflects that.

For transfusion services, the blood-donor estimates of 17.3% for Dengue and 14.8% for Chikungunya deserve attention in high-transmission districts, particularly during outbreaks. For maternal health services, the small number of studies in pregnant women is a gap that matters, given the congenital consequences of Zika infection, and it should be a research priority rather than a footnote.

The limitations of this review follow from the limitations of the evidence it summarises. Heterogeneity was extreme and only 28% to 41% of it could be explained by the covariates examined, so the pooled estimates carry more uncertainty than their confidence intervals suggest. Publication bias was demonstrated for Dengue and Chikungunya, and the trim-and-fill adjusted values are the more conservative reading.

Most included studies used non-probability sampling, usually of hospital attendees, so the estimates are not population prevalence in the strict sense. Few studies adjusted their risk-factor analyses for confounding. Serological cross-reactivity, discussed above, affects the flavivirus estimates in a direction that inflates them, and only 17 studies included neutralisation testing. Grouping studies by publication year rather than collection year introduces lag into the temporal analysis. Coverage of Southern Africa, Central Africa and North Africa is thin, and no study was available from many countries. Finally, restricting full-text assessment to English, French and Portuguese may have excluded a small amount of relevant Arabic-language work from North Africa.

CONCLUSION

Dengue, Chikungunya and Zika viruses circulate widely across Africa at levels that justify treating them as endemic rather than exceptional. Pooled prevalence was 21.8%, 19.4% and 9.6% respectively, with the highest values in West and East Africa, among febrile patients, and in outbreak settings. Yet the review's most important conclusion concerns the quality of the evidence rather than its content: the estimates depend more on which assay was used and which population was sampled than on any measurable feature of transmission, and roughly a quarter of the continent has produced no eligible study at all. The available data are sufficient to establish that these infections are common and insufficient to say with confidence how common they are, or where.

Confirmatory testing should become standard. Flavivirus IgG results reported without neutralisation or another confirmatory assay should be interpreted as provisional, and journals and reviewers should expect authors to state clearly what their serological findings can and cannot support. A common protocol covering sampling frame, assay selection, cut-off definition and reporting format would allow future studies to be compared and pooled. The variation in the current literature is as much a reporting problem as a biological one. Southern Africa, Central Africa and the twenty-two countries with no eligible study should be prioritised for population-based serosurveys. Without them, continental estimates will continue to reflect where research is funded rather than where transmission occurs. Since a quarter of febrile patients tested in these studies had evidence of dengue infection, arboviral testing should be built into non-malarial fever algorithms at district level rather than confined to reference laboratories. Covered water storage, house screening and container removal target the strongest risk factors identified. These should be funded alongside, not out of, existing malaria vector control, given that *Aedes* bites during daylight hours. Pregnant women, blood donors and healthcare workers were represented by very few studies despite the specific clinical questions each group raises. Congenital Zika outcomes in African settings remain particularly poorly described.

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Conflict of Interest

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

Data Availability

All data supporting this review derive from the published studies cited in the References and listed in the review data file described in Appendix B. No new primary data were generated. The data-extraction spreadsheet, the risk-of-bias assessments, the analysis code and the completed PRISMA 2020 checklist are available from the corresponding author on reasonable request.

Author Contributions

Conceptualization and protocol: A.J.O., U.A.O. and S.M.M.; Search strategy design: A.J.O., S.M.M. and A.O.O.; resources: A.J.O., S.M.M., A.O.G., A.O.O., A.R.O., A.Y.R., O.I.O and Y.F.A.; data curation, A.J.O., U.A.O., S.M.M., A.O.O., A.R.O., A.Y.R., O.I.O and A.O.G.; draft preparation: A.J.O., S.M.M., A.O.G., and O.I.O.; writing review and editing, A.J.O., U.A.O., S.M.M., A.O.G., A.O.O., A.R.O., A.Y.R., O.I.O and Y.F.A.; supervision, A.J.O., U.A.O., and S.M.M. All authors have read and approved the final manuscript.

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