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Marker-specific seroprevalence and epidemiological patterns of dengue virus in Nigeria: a systematic review and meta-analysis

Justin Onyebuchi Nwofe

justin.nwofe@gmail.com

Nasarawa State University

Sunday Alapetei Gbeyedobo

Nasarawa State University

Monday Tarshi

Nasarawa State University

Queensly Onah

Nasarawa State University

Praise Danson

Nasarawa State University

Aisha Bisallah Aburke

Nasarawa State University

Ogechukwu Nwakaego Onyebuchi

Nasarawa State University

Adamu Ishaku Akyala

Nasarawa State University

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Abstract

Background

Dengue virus (DENV) is an increasingly recognized cause of febrile illness in sub-Saharan Africa, yet its epidemiology in Nigeria remains incompletely defined because of fragmented surveillance, underdiagnosis, and heterogeneous diagnostic practices. This systematic review and meta-analysis synthesized marker-specific evidence on dengue virus burden in Nigeria and examined geographic variation, environmental correlates, and reported seasonal transmission patterns between 2014 and 2024.

Methods

A systematic search of PubMed, Scopus, Web of Science, EMBASE, Google Scholar, and African Index Medicus was conducted in accordance with PRISMA guidelines. Studies reporting laboratory-confirmed dengue infection in human populations in Nigeria were eligible for inclusion. Random-effects meta-analysis was used to estimate pooled marker-specific prevalence and pooled odds ratios (ORs) with 95% confidence intervals (CIs). Between-study heterogeneity was assessed using the I^2 statistic, and subgroup analyses explored variation by diagnostic marker, population group, and geographic region.

Results

Thirty-three studies met the inclusion criteria. The pooled prevalence of recent dengue infection measured by IgM antibodies was 20.9% (95% CI: 13.0–30.1; I^2 = 98.6%), while IgG seroprevalence indicating past exposure was 19.9% (95% CI: 11.6–29.7; I^2 = 97.7%). Acute infection markers showed lower pooled estimates, with NS1 antigen positivity of 8.9% (95% CI: 2.3–19.1) and PCR-confirmed infection of 7.3% (95% CI: 3.9–11.5; I^2 = 25.8%). Significant geographic variation was observed for both IgM ($p = 0.0179$) and IgG ($p = 0.0030$), with higher pooled estimates in southeastern Nigeria and lower estimates in the Southsouth region.

Environmental exposures associated with dengue seropositivity included proximity to refuse dumpsites (OR = 9.39, 95% CI: 7.44–11.84) and open household water storage (OR = 2.18, 95% CI: 1.65–2.89), while mosquito-treated bed net use (OR = 0.29, 95% CI: 0.19–0.44) and indoor insecticide spraying (OR = 0.26, 95% CI: 0.15–0.47) were associated with reduced odds of seropositivity. All four DENV serotypes were reported, and several studies described higher transmission during rainy periods.

Conclusions

This study provides the first integrated marker-specific quantitative synthesis demonstrating discordance between serologic and molecular dengue detection patterns in Nigeria, suggesting that dengue transmission is broader than routine confirmed diagnosis indicates. The findings reveal substantial underrecognized dengue burden, important geographic heterogeneity, and recurrent environmental exposure associations relevant to surveillance and control. Strengthening diagnostic

integration within febrile illness management and expanding arboviral surveillance capacity will be critical for improving dengue detection and response in Nigeria.

Background

Dengue virus (DENV), a mosquito-borne flavivirus transmitted primarily by *Aedes aegypti* and *Aedes albopictus*, has become one of the most rapidly expanding arboviral threats worldwide. Global dengue incidence has increased markedly over recent decades, driven by rapid urbanization, population growth, intensified human mobility, and climate change, all of which enhance vector proliferation and viral spread (1, 2). The World Health Organization estimates that approximately 3.9 billion people in over 128 countries are at risk of dengue infection, with an estimated 390 million infections occurring annually, including 96 million clinically apparent cases (3, 4). Although dengue has historically been concentrated in Southeast Asia, the Western Pacific, and the Americas, its geographic range is expanding across Africa, where surveillance remains comparatively limited (3).

Dengue is caused by four antigenically distinct but closely related serotypes (DENV-1 to DENV-4), all of which can circulate simultaneously within endemic regions. Infection with one serotype confers lifelong immunity only to that serotype, while secondary infection with a heterologous serotype may increase the risk of severe disease through antibody-dependent enhancement (5–9). Environmental conditions associated with rapid urbanization including inadequate drainage systems, poor waste management, unplanned housing expansion, and widespread household water storage create ideal breeding habitats for *Aedes* mosquitoes and facilitate sustained dengue transmission (2, 10–12). Increasing regional travel and population mobility further contribute to viral dissemination across ecological zones (13–16).

Despite growing recognition of dengue as an emerging public health threat, its epidemiology in sub-Saharan Africa remains incompletely characterized. In Nigeria, dengue is likely underrecognized because febrile illnesses are commonly presumed to be malaria or typhoid in routine clinical practice, given substantial overlap in presenting symptoms and limited access to confirmatory arboviral diagnostics (17–22). Studies across West Africa have reported variable dengue seroprevalence, suggesting ongoing but under detected transmission in multiple ecological settings (23–26). However, fragmented surveillance systems, inconsistent laboratory capacity, and heterogeneous reporting frameworks continue to impede accurate assessment of dengue burden.

Nigeria presents ecological and demographic conditions highly favorable for dengue transmission. Rapid urban expansion, dense population centers, seasonal rainfall variability, and widespread peri-domestic mosquito breeding habitats support persistent vector circulation (27–29). Published Nigerian studies report markedly variable dengue prevalence estimates across regions, reflecting differences in study populations, sampling periods, and diagnostic approaches, including IgM, IgG, NS1 antigen assays, reverse transcription polymerase chain reaction (RT-PCR), and plaque reduction neutralization testing (30–35). Recent molecular investigations have also documented circulation of multiple dengue

serotypes in Nigeria and neighboring West African countries, supporting the possibility of sustained endemic transmission rather than isolated outbreaks (36–38).

An important but insufficiently synthesized dimension of dengue epidemiology in Nigeria is the divergence between serologic and molecular evidence of infection. Serologic markers such as IgM and IgG reflect recent and past exposure, whereas NS1 antigen and PCR indicate acute or active infection. Comparing these markers quantitatively can generate new epidemiologic insight into transmission dynamics, diagnostic under ascertainment, and surveillance blind spots. In addition, seasonal variation and environmental exposures including rainfall-associated vector amplification, refuse accumulation, household water storage, and vector control behaviors may influence transmission risk but have not been systematically integrated across Nigerian studies.

Given these gaps, a comprehensive synthesis of available evidence is needed to clarify the epidemiologic profile of dengue virus infection in Nigeria. Unlike prior narrative summaries, marker-specific meta-analysis enables differentiation between recent, past, acute, and molecularly confirmed infection, thereby allowing interpretation of diagnostic discordance and hidden surveillance gaps. Therefore, this study conducted a systematic review and meta-analysis of laboratory-confirmed dengue infections reported in Nigeria between 2014 and 2024 to: (1) estimate marker-specific pooled prevalence across diagnostic categories; (2) evaluate reported environmental and demographic associations through pooled effect-size analysis; and (3) characterize geographic and seasonal patterns relevant to dengue transmission. By consolidating fragmented evidence into an integrated epidemiologic framework, this study aims to inform dengue surveillance strengthening, improve recognition of dengue within febrile illness management, and support evidence-based vector control strategies in Nigeria.

Methods

Study design and reporting framework

This study was conducted as a systematic review and meta-analysis to synthesize available evidence on the epidemiology of dengue virus (DENV) infection in Nigeria, with emphasis on marker-specific seroprevalence, environmental correlates, and reported seasonal transmission patterns between January 2014 and August 2024. The review protocol was prospectively registered in the International Prospective Register of Systematic Reviews (PROSPERO; CRD420261328923), and no amendments were made after registration. Reporting adhered to the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) 2020 guidelines (39). (Supplementary file 1).

Eligibility criteria

Studies were eligible if they reported laboratory-confirmed dengue infection among human populations residing in Nigeria and provided sufficient data to calculate prevalence estimates or effect sizes. Acceptable diagnostic methods included IgM antibody detection, IgG antibody detection, NS1 antigen

assays, plaque reduction neutralization tests (PRNT), and reverse transcription polymerase chain reaction (RT-PCR). Eligible study designs included cross-sectional, cohort, case-control, and surveillance-based observational studies. Studies conducted outside Nigeria, vector-only investigations without human infection data, editorials, commentaries, reviews, conference abstracts without accessible full text, and studies lacking laboratory confirmation of dengue infection were excluded.

Search strategy and study selection

A comprehensive literature search was conducted in PubMed, Scopus, Web of Science, EMBASE, Google Scholar, and African Index Medicus for studies published between January 2014 and August 2024. Search strategies combined controlled vocabulary terms, including Medical Subject Headings (MeSH), with free-text keywords related to dengue, dengue virus, seroprevalence, epidemiology, and Nigeria, using Boolean operators adapted to each database. (Supplementary File 2).

All retrieved records were imported into Covidence for duplicate removal and screening. Two reviewers independently screened titles and abstracts, followed by full-text review of potentially eligible studies. Disagreements were resolved through discussion and, where necessary, consultation with a third reviewer.

Data extraction

Data were extracted using a standardized form in Covidence. The primary outcome was laboratory-confirmed dengue infection categorized according to diagnostic marker: IgM as an indicator of recent infection, IgG as evidence of past exposure, NS1 antigen as a marker of acute infection, RT-PCR as molecular confirmation of active infection, and PRNT as confirmatory neutralizing antibody evidence. For each diagnostic marker, the number of positive cases and total sample size were extracted to generate marker-specific prevalence estimates. Where studies reported multiple diagnostic markers, data were extracted separately for each marker to preserve epidemiologic distinction.

For environmental and behavioral exposures, two-by-two contingency table data were extracted, including exposed cases, exposed total, unexposed cases, and unexposed total, to permit pooled odds ratio estimation. Additional extracted variables included author, publication year, geographic region, study design, study setting, population characteristics, diagnostic methods, and serotype data where available. Data extraction was performed independently by two reviewers, and discrepancies were resolved by consensus. No imputation of missing data was performed (Supplementary File 3).

Risk of bias assessment

Methodological quality of included studies was assessed using the Joanna Briggs Institute (JBI) Critical Appraisal Checklist for Studies Reporting Prevalence Data (40). This tool evaluates domains including

sampling methodology, representativeness, validity of diagnostic measurement, and appropriateness of statistical analysis. Risk of bias assessments were conducted independently by two reviewers, with disagreements resolved through consensus (Supplementary File 4).

Statistical analysis

All statistical analyses were performed in R software (version 4.5.2) using the meta package. Separate meta-analyses were conducted for each diagnostic marker to account for differences in biologic interpretation and diagnostic performance. Random-effects meta-analysis was used to estimate pooled prevalence and pooled odds ratios using the inverse variance method. Between-study variance was estimated using the DerSimonian–Laird method, and Hartung–Knapp adjustment was applied to derive confidence intervals. For prevalence pooling, Freeman–Tukey double arcsine transformation was used to stabilize variance.

Between-study heterogeneity was assessed using Cochran's Q statistic and quantified using the I^2 statistic. Because substantial heterogeneity was anticipated, prediction intervals were calculated to estimate the range of true effects expected in comparable future settings. Forest plots were generated to visualize study-specific and pooled estimates.

Subgroup analyses

Subgroup analyses were conducted to explore sources of heterogeneity according to geographic region and population group, including febrile or clinical populations, community-based populations, and special populations such as pregnant women and individuals living with HIV. Statistical differences between subgroups were evaluated using chi-square tests for subgroup interaction.

Risk-factor meta-analysis

For environmental and behavioral exposures, pooled odds ratios with 95% confidence intervals were estimated using random-effects meta-analysis of extracted two-by-two contingency data. Because these analyses were based on aggregated observational study data, findings were interpreted as epidemiological associations rather than causal relationships. Sensitivity analyses using leave-one-out procedures were performed to assess the influence of individual studies on pooled effect estimates.

Publication bias assessment

Publication bias was assessed using funnel plot inspection and Egger's regression test when at least ten studies were available within a marker-specific analysis (41).

Serotype distribution

Due to limited and heterogeneous molecular reporting, dengue serotype data were summarized descriptively using aggregated counts across reporting studies rather than pooled quantitative synthesis.

Analytical rationale

This marker-specific analytical framework enabled comparison of recent, past, acute, and molecularly confirmed dengue burden in Nigeria, allowing identification of diagnostic discordance and providing insight into potential surveillance gaps in routine febrile illness detection systems.

Results

Study selection

The literature search identified 211 records, of which 132 remained after duplicate removal. Following title and abstract screening, 54 articles underwent full-text review. Thirty-three studies met the eligibility criteria and were included in the quantitative synthesis (Fig. 1).

Study characteristics

The included studies were published between 2014 and 2024 and were predominantly cross-sectional in design. Most were conducted in hospital-based settings, although several community-based studies were also included. Study populations were heterogeneous and comprised febrile patients, apparently healthy individuals, pregnant women, and people living with HIV. Diagnostic methods varied across studies and included enzyme-linked immunosorbent assays for IgM and IgG antibodies, NS1 antigen detection, rapid diagnostic tests, plaque reduction neutralization testing (PRNT), and RT-PCR. Detailed study characteristics are summarized in Table 1.

Marker-specific pooled prevalence

IgM seroprevalence (recent infection)

Twenty-six studies comprising 7,736 participants and 1,478 IgM-positive cases were included in the IgM meta-analysis. The pooled random-effects IgM seroprevalence was 20.5% (95% CI: 12.6–29.7), with substantial between-study heterogeneity ($I^2 = 98.6\%$, $\tau^2 = 0.0617$, $p < 0.001$) (Fig. 2). The wide prediction interval indicates marked variability in recent dengue transmission across study settings. (Supplementary fig 2).

IgG seroprevalence (past exposure)

Seventeen studies involving 4,861 participants and 831 IgG-positive cases contributed to the IgG analysis. The pooled random-effects IgG seroprevalence was 19.9% (95% CI: 11.6–29.7), with high heterogeneity ($I^2 = 97.7\%$, $\tau^2 = 0.0474$, $p < 0.001$) (Fig. 3), indicating substantial variation in cumulative dengue exposure across populations.

NS1 antigen prevalence (acute infection)

Eleven studies comprising 3,078 participants and 389 NS1-positive cases were included. The pooled prevalence of NS1 antigen positivity was 8.9% (95% CI: 2.2–19.4), with substantial heterogeneity (I^2 = 98.5%, τ^2 = 0.0500, $p < 0.001$) (Fig. 4).

PCR-confirmed infection

Three studies including 323 participants and 25 PCR-confirmed dengue cases, were analyzed. The pooled prevalence of PCR-confirmed infection was 7.3% (95% CI: 3.9–11.5), with low to moderate heterogeneity (I^2 = 25.8%, $p = 0.26$) (Fig. 5).

PRNT-confirmed neutralizing antibody detection

Only one study reported PRNT results, with a prevalence estimate of 18.2% (95% CI: 14.9–21.7). Because only one dataset was available, pooled meta-analysis was not performed.

Comparison across diagnostic markers

There were statistically significant differences in pooled prevalence across diagnostic markers (χ^2 = 21.55, df = 4, $p = 0.0002$), indicating that dengue burden estimates varied according to diagnostic method and infection stage (Table 2). The divergence between serologic and molecular markers suggests discordance between cumulative exposure burden and routine laboratory confirmation of acute infection.

Population and geographic variation

Population-group variation

Subgroup analyses demonstrated variation in prevalence across population categories. Community-based populations generally showed higher pooled prevalence than febrile clinical populations, while special populations such as pregnant women and people living with HIV showed variable estimates. However, substantial heterogeneity remained within all population strata (Table 3).

Geographic variation

Regional subgroup analysis revealed significant geographic variation for both IgM (χ^2 = 13.66, $p = 0.0179$) and IgG (χ^2 = 17.92, $p = 0.0030$). For IgM, pooled prevalence ranged from approximately 8% in the Southsouth region to 37% in the Southeast. IgG estimates ranged from 9% to 36% across regions. These findings indicate spatial heterogeneity in dengue exposure across Nigeria, although differences in study populations and diagnostic methods limit interpretation as nationally representative gradients.

Environmental and behavioral correlations

Environmental and behavioral exposures demonstrated consistent associations with dengue seropositivity. Proximity to refuse dumpsites was associated with markedly increased odds of dengue infection (OR = 9.39, 95% CI: 7.44–11.84; I^2 = 0%). Open household water storage was also associated with increased odds of seropositivity (OR = 2.18, 95% CI: 1.65–2.89; I^2 = 0%).

Protective associations were observed for mosquito-treated bed net use (OR = 0.29, 95% CI: 0.19–0.44; I^2 = 0%) and indoor insecticide spray use (OR = 0.26, 95% CI: 0.15–0.47; I^2 = 0%). These associations were consistent across included studies (Table 4).

Occupational exposures

Occupational exposures showed variable associations with dengue seropositivity. Farming was associated with increased odds of infection (OR = 3.19, 95% CI: 1.44–7.06), as was hunting activity (OR = 1.76, 95% CI: 1.32–2.36). Mechanic work showed an elevated pooled odds ratio (OR = 2.81, 95% CI: 0.87–9.08), although this association did not reach statistical significance and was based on a limited number of studies (Table 4).

Serotype distribution

Among studies reporting serotype data, all four dengue virus serotypes (DENV-1 to DENV-4) were identified. DENV-1 and DENV-3 were most frequently reported, followed by DENV-2 and DENV-4. However, serotype reporting was limited and inconsistent across studies.

Seasonal patterns

Several studies reported higher dengue prevalence during rainy seasons compared with dry periods, suggesting seasonal amplification of transmission during periods favorable for vector breeding. Because seasonal data were not uniformly collected or reported, no pooled quantitative synthesis was performed, and these findings are interpreted descriptively.

Publication bias and sensitivity analysis

Funnel plot inspection for IgM seroprevalence suggested mild asymmetry; however, Egger's regression test did not demonstrate statistically significant evidence of small-study effects ($t = 1.47$, $p = 0.156$). Leave-one-out sensitivity analyses showed that removal of individual studies did not materially alter pooled prevalence estimates, indicating that no single study disproportionately influenced the overall findings.

The persistently wide prediction intervals and substantial heterogeneity across marker-specific analyses indicate considerable variability between study settings. Accordingly, pooled estimates should be interpreted as summaries of reported study-level evidence rather than precise national prevalence estimates.

Discussion

This systematic review and meta-analysis provide the first integrated marker-specific synthesis of dengue virus epidemiology in Nigeria, demonstrating substantial dengue burden across diverse ecological and population settings while revealing important discordance between serologic and molecular indicators of infection. The pooled IgM and IgG estimates indicate both ongoing recent transmission and substantial cumulative population exposure, whereas lower NS1 and PCR prevalence suggest that acute laboratory-confirmed dengue is less frequently detected in routine practice. This divergence between serologic and molecular findings provides new epidemiologic insight into probable under ascertainment of acute dengue infection in Nigeria and highlights surveillance blind spots within routine febrile illness detection systems. Similar patterns have been reported across other sub-Saharan African settings, where dengue remains underrecognized because of overlapping clinical presentation with malaria and other febrile illnesses, limited diagnostic infrastructure, and inconsistent arboviral surveillance systems (42–45).

The marked geographic variation observed across Nigerian regions suggests that dengue transmission is spatially heterogeneous and shaped by local ecological and demographic conditions. Higher pooled prevalence in southeastern Nigeria compared with lower estimates in the Southsouth region may reflect differences in urban density, waste disposal practices, rainfall patterns, vector habitat suitability, and population mobility. Comparable subnational clustering has been described in other African countries, where dengue transmission often occurs in focal ecological hotspots rather than uniformly across regions (46, 47). Nigeria's rapid urban expansion, especially in densely populated peri-urban areas with inadequate drainage and waste management systems, likely contributes to persistent breeding opportunities for *Aedes* mosquitoes and sustained viral transmission (27, 35, 48, 49).

The environmental correlations identified in this review reinforce the importance of peri-domestic transmission dynamics in dengue epidemiology. Proximity to refuse dumpsites and open household water storage were strongly associated with increased odds of dengue seropositivity, while mosquito-treated bed net use and indoor insecticide spraying were associated with reduced odds. These findings are biologically plausible and consistent with established evidence that unmanaged refuse accumulation and water storage create productive larval habitats for *Aedes aegypti*, particularly in urban environments lacking reliable sanitation infrastructure (50–52). Because these associations were derived from aggregated observational data, they should be interpreted as epidemiological correlates rather than causal determinants. Nevertheless, their consistency across studies suggests that environmental management remains a critical component of dengue prevention in Nigeria.

Occupational exposures showed less consistent but potentially important associations. Farming and hunting were associated with increased odds of dengue seropositivity, possibly reflecting greater exposure to mosquito breeding environments in rural or peri-forest settings. Mechanic work showed an elevated but statistically imprecise pooled estimate, likely reflecting small sample size and limited

contributing studies. These findings remain exploratory and highlight the need for more rigorous occupational exposure studies using standardized definitions and larger sample sizes.

Seasonal patterns reported across included studies suggest that dengue transmission intensifies during rainy periods, when rainfall increases vector breeding habitats and humidity enhances mosquito survival. Similar climate-linked amplification has been documented across tropical African settings, where rainfall variability strongly influences arboviral transmission dynamics (53, 54). However, seasonal data in the included studies were inconsistently measured and insufficiently standardized for pooled quantitative analysis. As such, the seasonal findings should be interpreted as descriptive evidence supporting recurrent temporal transmission amplification rather than definitive seasonal effect estimates.

The identification of all four dengue serotypes across reporting studies provides further evidence that dengue in Nigeria reflects sustained endemic circulation rather than isolated importation events. Co-circulation of multiple serotypes is epidemiologically important because sequential infection with heterologous serotypes may increase the risk of severe disease through antibody-dependent enhancement, as documented in endemic settings elsewhere (5–9). However, inconsistent molecular reporting and limited genomic surveillance restricted more detailed interpretation of serotype-specific transmission patterns and lineage movement.

A central contribution of this review lies in demonstrating diagnostic discordance across marker categories. Serologic markers capture broader evidence of recent and past exposure, whereas NS1 antigen and PCR identify narrower windows of acute infection. The lower pooled prevalence of molecular confirmation relative to serologic burden suggests that dengue transmission in Nigeria may be substantially broader than routine laboratory-confirmed case counts indicate. This pattern likely reflects limited access to molecular diagnostics, delayed presentation after peak viremia, and under integration of dengue testing into routine febrile illness evaluation. Similar diagnostic gaps have been reported across endemic low-resource settings, where dependence on syndromic clinical diagnosis contributes to persistent under detection of arboviral disease (43–45).

The consistently high heterogeneity observed across IgM, IgG, and NS1 analyses reflects the complexity of dengue epidemiology in Nigeria. Variation in study populations, geographic regions, diagnostic assays, case definitions, and sampling periods likely contributed substantially to between-study dispersion. Wide prediction intervals further demonstrate that dengue prevalence can differ markedly between settings. Accordingly, pooled estimates should not be interpreted as nationally representative prevalence values but rather as summaries of heterogeneous study-level evidence reflecting context-specific transmission dynamics.

These findings have important implications for public health practice. First, dengue should be more systematically integrated into routine febrile illness surveillance and differential diagnosis in Nigeria, particularly in malaria-endemic settings where arboviral infections are frequently overlooked. Second, strengthening laboratory infrastructure for molecular diagnosis and expanding access to standardized confirmatory testing are essential for improving case detection. Third, vector control strategies should

prioritize modifiable environmental exposures identified in this review, including waste management, water storage practices, and peri-domestic mosquito control.

This review has several limitations. The included studies were highly heterogeneous in design, population characteristics, and diagnostic methods, limiting comparability. Most were cross-sectional and hospital-based, which may reduce generalizability to broader community populations. Diagnostic variability, including potential serologic cross-reactivity with other flaviviruses, may also have influenced prevalence estimates. In addition, seasonal and serotype data were inconsistently reported, limiting detailed secondary analyses. At the review level, reliance on aggregated study-level data precluded adjustment for individual-level confounding, and publication bias assessment has limited interpretability under extreme heterogeneity.

Conclusion

This systematic review and meta-analysis demonstrate that dengue virus is a widely circulating but underrecognized cause of febrile illness in Nigeria, with evidence of both recent transmission and cumulative past exposure across diverse populations and geographic regions. The coexistence of all four dengue serotypes and the marked regional variation in seroprevalence support the presence of sustained endemic transmission rather than isolated episodic outbreaks.

A key finding of this study is the discordance between substantial serologic burden and comparatively lower molecular confirmation, suggesting that dengue transmission in Nigeria is broader than routine confirmed case detection currently indicates. This gap highlights important weaknesses in diagnostic integration and arboviral surveillance systems, where dengue remains frequently overlooked because of overlap with malaria and other febrile illnesses.

Although pooled estimates provide valuable epidemiologic insight, they should be interpreted as summaries of heterogeneous study-level evidence rather than precise national prevalence estimates, given the substantial variability in study populations, diagnostic approaches, and sampling contexts. The observed associations with refuse accumulation, household water storage, and vector control practices further emphasize the importance of peri-domestic environmental conditions in shaping dengue transmission risk.

Strengthening laboratory capacity, expanding access to standardized molecular and serologic diagnostics, and integrating dengue testing into routine febrile illness surveillance are essential for improving case detection and outbreak response in Nigeria. Future efforts should also prioritize longitudinal surveillance, expanded genomic monitoring, and targeted vector control.

Declarations

Ethics approval and consent to participate

Not applicable. This study is a systematic review and meta-analysis of previously published data and did not involve collection of primary data from human participants or animals.

Consent for publication

Not applicable.

Data Availability Statement

The extracted study-level dataset used for meta-analysis, 2×2 contingency tables for risk-factor analyses, and analytic code (R script) are provided as Supporting Information files (S2–S5 Files). The review protocol is publicly available via PROSPERO (CRD420261328923). No individual participant data was used in this review.

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Author Contributions

Conceptualization: Justin Onyebuchi Nwofe
Data curation: Justin Onyebuchi Nwofe, Sunday Gbeyedobo, Monday Tarshi, Queensly Onah, Praise Danson, Aisha Bisallah Aburke, Ogechukwu Nwakaego Onyebuchi
Formal analysis: Justin Onyebuchi Nwofe
Investigation: Justin Onyebuchi Nwofe, Sunday Gbeyedobo, Monday Tarshi, Queensly Onah, Praise Danson, Aisha Bisallah Aburke, Ogechukwu Nwakaego Onyebuchi
Methodology: Justin Onyebuchi Nwofe
Software: Justin Onyebuchi Nwofe
Validation: Sunday Gbeyedobo, Monday Tarshi, Queensly Onah, Praise Danson, Aisha Bisallah Aburke, Ogechukwu Nwakaego Onyebuchi
Supervision: Adamu Ishaku Akyala
Visualization: Justin Onyebuchi Nwofe
Writing – original draft: Justin Onyebuchi Nwofe, Sunday Gbeyedobo, Monday Tarshi, Queensly Onah, Praise Danson, Aisha Bisallah Aburke, Ogechukwu Nwakaego Onyebuchi
Writing – review & editing: Justin Onyebuchi Nwofe, Adamu Ishaku Akyala

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Conflict of Interest

The authors declare that they have no competing interests.

Trial registration

Not applicable. This study is a systematic review and meta-analysis and does not involve a clinical trial.

Clinical Trial Number

Not applicable

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Tables

Table 1 to 4 are available in the Supplementary Files section.

Figures

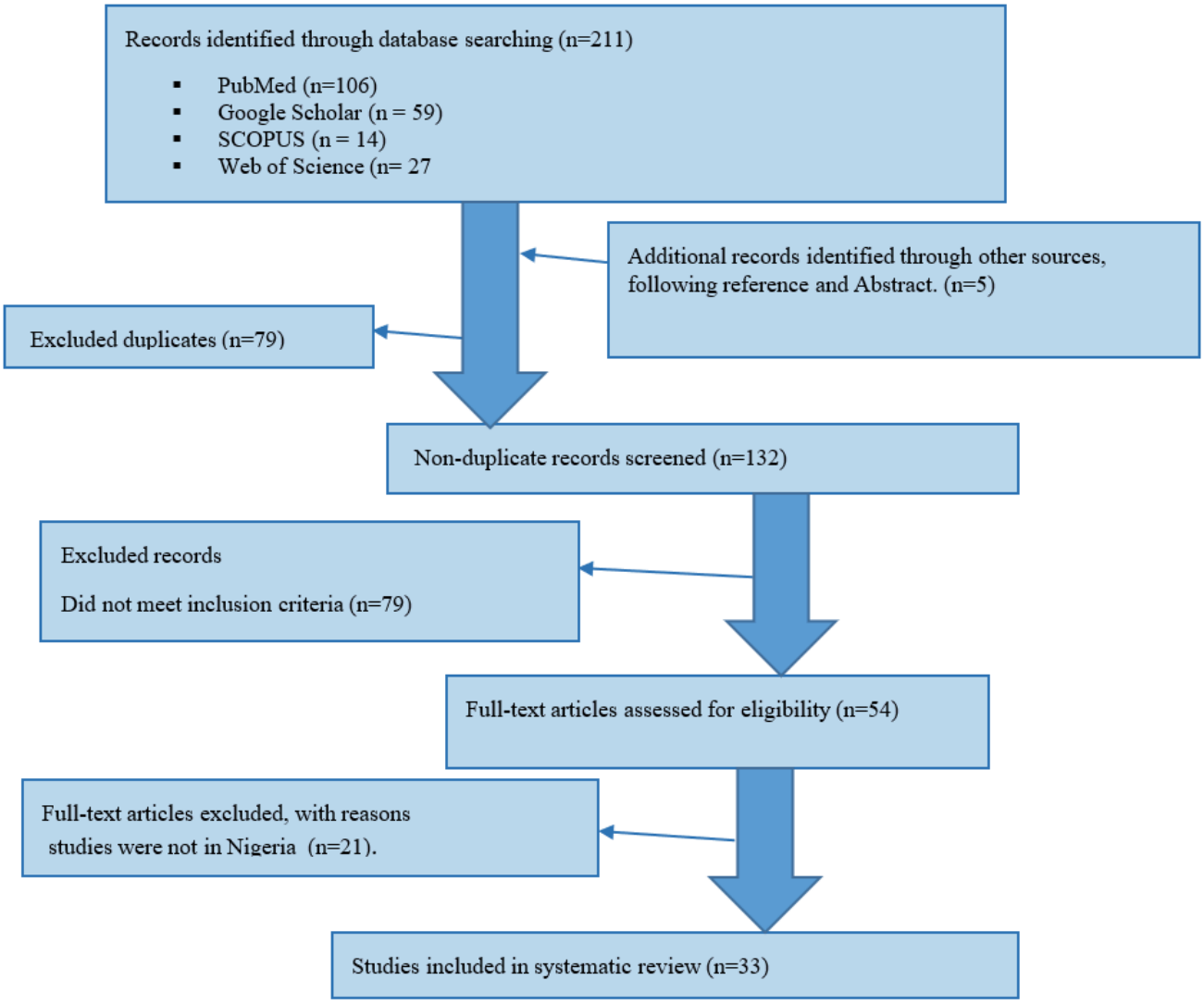


Figure 1

PRISMA Flow chart showing process for selection of included studies

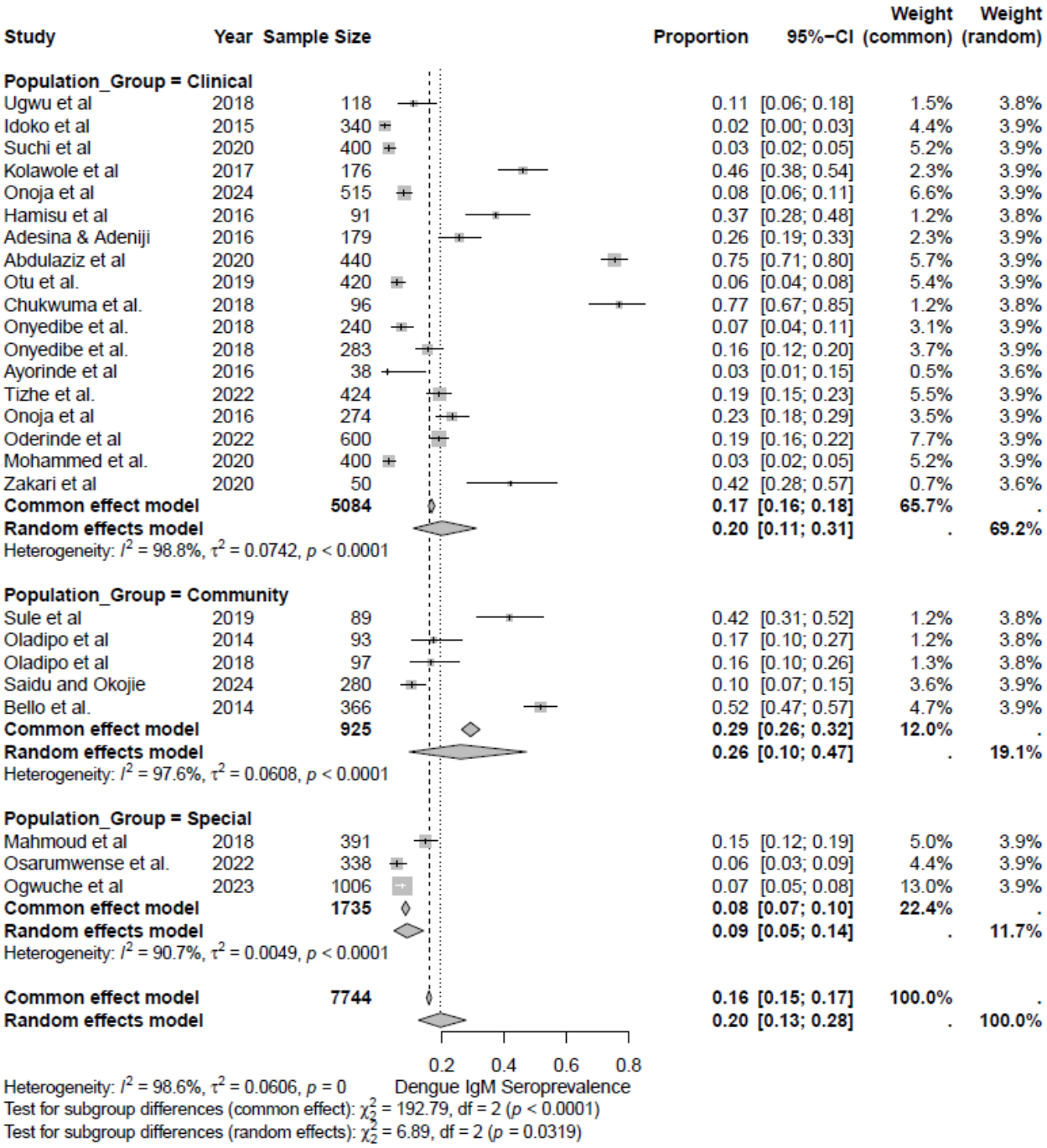


Figure 2

Forest plot of IgM seroprevalence estimates of dengue virus infection across included studies in Nigeria.

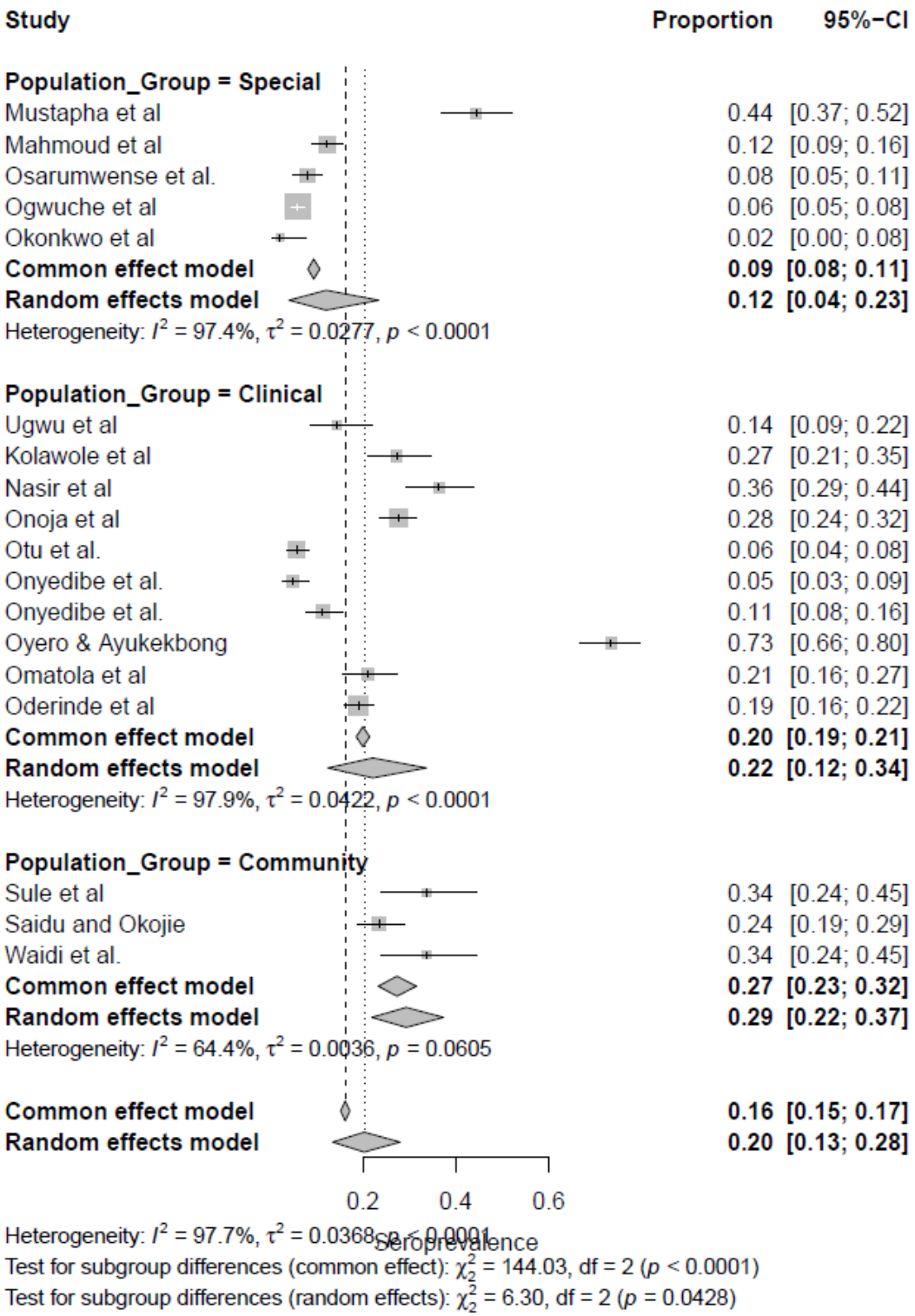


Figure 3

Forest plot of IgG seroprevalence estimates of dengue virus infection across included studies in Nigeria.

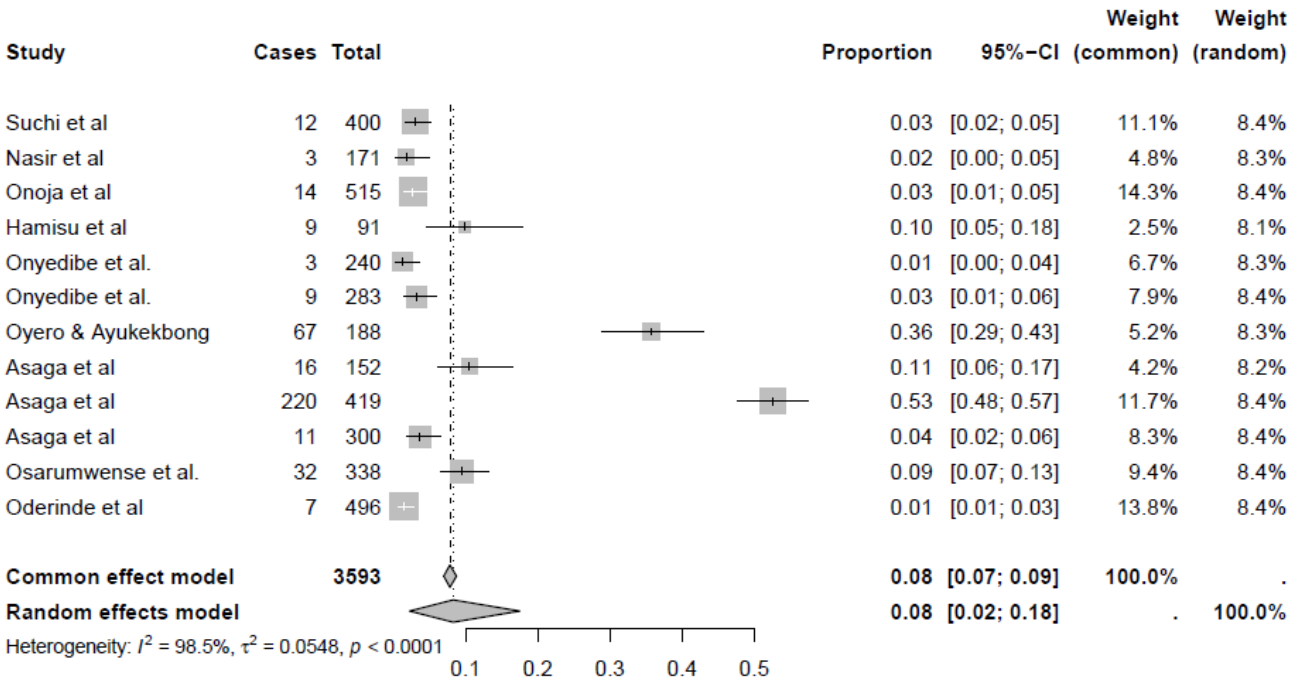


Figure 4

Forest plot of NS1 antigen prevalence of dengue virus infection across included studies in Nigeria.

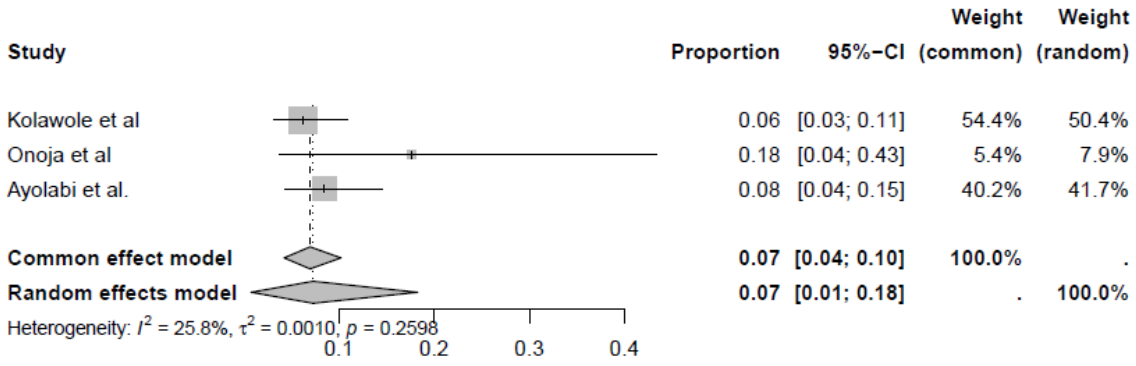


Figure 5

Forest plot of PCR prevalence of dengue virus infection across included studies in Nigeria.

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- Table1CharacteristicsofIncludedStudies.xlsx
- Table2MarkerSpecificMetaanalysis.docx
- Table3SubgroupAnalysis.docx
- Table4RiskFactorsofDengueSeroprevalence.docx
- SupplementaryTable3DengueStudyDataExtraction.xlsx
- SupplementaryTable4RiskofBiasAssessment.xlsx
- SupplementaryTable1PRISMA2020checklist.docx
- SupplementaryFigure1LeaveOneOutMetaAnalysisIgGInfluence.pdf
- Supplementaryfigure2LeaveOneOutMetaAnalysisIgMInfluence.pdf
- SupplementaryFile2SearchStrategies.docx