Chikungunya virus in Nigeria: A re-emerging threat obscured by diagnostic gaps

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ABSTRACT

Chikungunya virus (CHIKV) is re-emerging in Nigeria, but diagnostic and surveillance gaps obscure its true burden. A narrative review of literature and surveillance data (1969–2024) identified consistent serologic and entomologic evidence of CHIKV circulation, yet limited molecular confirmation and exclusion from national surveillance impede detection. We summarise epidemiology, diagnostic challenges, and policy implications, recommending CHIKV inclusion in Nigeria's Integrated Disease Surveillance and Response (IDSR), strengthening laboratory capacity, and enhancing clinician awareness.

Introduction

Chikungunya virus (CHIKV) is a mosquito-borne alphavirus belonging to the *Togaviridae* family, genus *Alphavirus*. It was first isolated in 1952–1953 from the Makonde Plateau in Tanzania, with its name derived from the *Kimakonde* phrase meaning "that which bends up," describing the severe arthralgia typical of infection [1,2]. CHIKV transmission occurs primarily through *Aedes aegypti* and *Aedes albopictus* mosquitoes, which sustain both urban and sylvatic cycles [3]. The sylvatic cycle involves non-human primates and forest-dwelling mosquitoes, while the urban cycle is human–mosquito–human.

Clinically, chikungunya fever manifests as an abrupt onset of high fever, rash, headache, and incapacitating polyarthralgia that may persist for months [2,4]. The illness overlaps with dengue and malaria, complicating clinical diagnosis in endemic areas. Although CHIKV rarely causes death, its debilitating arthropathy and productivity loss generate a significant socioeconomic burden [4].
Since 2004, mutations such as E1-A226V have facilitated adaptation to *Aedes albopictus*, expanding global outbreaks to more than 100 countries [2,3]. In West Africa, CHIKV circulation has been reported in Nigeria, Senegal, Côte d'Ivoire, and Cameroon, but Nigeria exhibits one of the largest populations at risk due to high urban density, poor waste management, and weak vector control. Despite this, CHIKV remains under-recognized and largely excluded from national reporting systems.

Rationale

Nigeria's ecological and demographic diversity, from tropical rainforests to savannah zones, creates ideal habitats for *Aedes* mosquitoes. Rapid urbanization, unplanned settlements, and inadequate water management amplify mosquito breeding. Human movement between rural and urban areas facilitates virus spread, while limited laboratory capacity and reliance on syndromic diagnosis blur the true burden of arboviral diseases.
The Integrated Disease Surveillance and Response (IDSR) strategy, adopted by Nigeria for epidemic-prone diseases, prioritizes pathogens such as malaria, Lassa fever, and yellow fever but does not explicitly include CHIKV [6]. This omission stems from both policy prioritization and infrastructural limitations, leading to under-reporting. The absence of CHIKV in national notifiable disease lists, coupled with scarce molecular diagnostic platforms, results in misdiagnosis as malaria or dengue [5,8]. Understanding diagnostic gaps and surveillance weaknesses is therefore critical to inform evidence-based policy and enhance preparedness for arboviral threats.

Methods

A narrative literature review was conducted to synthesize evidence on CHIKV epidemiology, vectors, and diagnostic challenges in Nigeria from 1969 to 2024. Searches were performed in PubMed, Scopus, AJOL and Google Scholar using combinations of the keywords *"Chikungunya Nigeria," "Aedes aegypti Nigeria," "arbovirus surveillance Nigeria,"* and *"CHIKV diagnostics."* Peer-reviewed articles, surveillance reports, and entomological studies involving Nigerian populations or mosquito samples were included. Non-Nigerian data, non-arboviral reports, duplicates, and non-English sources were excluded. Information extracted included study location, diagnostic method, seroprevalence, vector species, and surveillance context. Findings were qualitatively integrated to identify diagnostic gaps and policy implications.

Results

Epidemiologic and Diagnostic Evidence

CHIKV circulation in Nigeria has been consistently documented since the 1969 Ibadan outbreak (Table 1), which was confirmed by virus isolation and serology [7]. Subsequent studies report high IgG seroprevalence rates of up to 69.5% in the central region and 41.3% across Abuja, Ibadan, and Jos [5,8]. However, most surveys relied on IgG assays without molecular confirmation, limiting interpretation due to possible cross-reactivity with other alphaviruses [2].

Recent surveillance (2019–2024) detected CHIKV RNA in *Aedes* mosquitoes across nine of sixteen surveyed states, confirming active vector circulation [10]. Both *Aedes aegypti* (51%) and *Aedes albopictus* (42%) were identified, with dominance varying seasonally and regionally. Urban overcrowding and poor sanitation enhance *Aedes* breeding, while surveillance remains sporadic and reactive.

Despite mounting serologic and entomologic evidence, Nigeria's diagnostic capacity is heavily

skewed towards malaria and yellow fever testing. Studies show that up to 65% of CHIKV-positive individuals also tested positive for malaria antigen, reflecting frequent clinical misclassification [5]. The limited use of RT-PCR or IgM ELISA tests hinders accurate case confirmation, as few laboratories maintain molecular capacity outside reference centres.

Limitations and Data Gaps

Serologic studies dominate CHIKV research in Nigeria, but cross-reactivity and inconsistent methodology hinder comparability. Few studies include children or asymptomatic carriers, and none provide longitudinal data to establish incidence trends. Vector studies rarely correlate mosquito infection with human cases, leaving gaps in understanding transmission intensity. Moreover, regional heterogeneity is underexplored: northern Nigeria shows sporadic seropositivity, while southern and central zones report higher IgG prevalence, possibly linked to rainfall and vector abundance. Such variability underscores the need for geographically stratified surveillance.

The overlap of CHIKV with malaria, dengue, and Zika in clinical presentation challenges frontline diagnosis. Most health centres lack arboviral rapid diagnostic tests (RDTs), forcing clinicians to treat all febrile cases presumptively as malaria. Updating diagnostic algorithms to incorporate CHIKV differentials, especially during malaria-negative febrile illness, is crucial.

Way forward

To address surveillance and diagnostic gaps, a tiered implementation approach is proposed.

Short-term (1–2 years):

- Include CHIKV in Nigeria's IDSR list for formal reporting.
- Train clinicians and laboratory staff to recognize and test for arboviral infections.
- Incorporate CHIKV awareness into malaria and dengue diagnostic protocols.

Medium-term (3–5 years):

- Expand RT-PCR and IgM ELISA testing in regional laboratories.
- Establish sentinel surveillance in hospitals and border regions.
- Initiate early-warning surveillance for potential reservoir hosts (non-human primates) in forested areas to monitor sylvatic transmission cycles.
- Strengthen entomological surveillance and *Aedes* mapping to predict outbreak risk zones.

Long-term (>5 years):

- Develop integrated arboviral surveillance platforms linking human, vector, and animal data.
- Promote regional collaboration across West Africa to monitor cross-border CHIKV movement.
- Encourage vaccine and diagnostic research partnerships within Nigeria's academic and public-health institutions.

Feasibility challenges such as laboratory infrastructure, human-resource limitations, and funding constraints should be acknowledged. Nonetheless, integrating CHIKV monitoring into existing IDSR and malaria programmes is both achievable and cost-efficient.

Conclusion

Serologic and vector evidence suggest endemic CHIKV transmission in Nigeria, but diagnostic limitations and exclusion from national reporting systems obscure its true magnitude. Addressing laboratory capacity, clinician awareness, and vector surveillance is critical for early detection and response. Integrating CHIKV into Nigeria's IDSR, improving RT-PCR access, and enhancing training will help bridge diagnostic gaps. Proactive inclusion of reservoir host monitoring and regional coordination can further strengthen preparedness for arboviral threats.

What is already known about the topic

- CHIKV is an arbovirus causing fever, rash, and arthralgia, often misdiagnosed as malaria or dengue.
- Nigeria has historical CHIKV outbreaks (e.g., 1969 Ibadan).
- *Aedes aegypti* and *Aedes albopictus* are primary vectors in Nigeria.

What this study adds

- High IgG seroprevalence (up to 69.5%) indicates endemic CHIKV in Nigeria.
- Exclusion from IDSR and limited molecular diagnostics cause underdiagnosis.
- Recommendations include adding CHIKV to IDSR and enhancing surveillance.

Competing Interest

The authors of this work declare no competing interests.

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Authors´ contributions

M.M. Hamman: conceptualization, data curation, writing (original draft). F.A. Oluwadare: methodology, writing (review). A.M. Lateef: writing (review). V.I. Agbajelola: methodology, writing (review), supervision. All authors approved final manuscript.

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Table 1: Summary of Key Studies on CHIKV in Nigeria, 1969–2024				
Study/Source	**Type**	**Location**	**Findings**	**Limitations**
Moore et al., 1974 [7]	Serosurvey (HI/NT)	Nationwide	CHIKV antibodies in 40-60% humans/monkeys; early evidence of sylvatic cycle.	No molecular; pre-ELISA era; limited to 1960s-70s samples
Mac et al., 2023 [5]	IgG seroprevalence	Kaduna (North), Abia (South), Nasarawa (Central)	IgG positivity up to 69.5% (central); 65.1% CHIKV seropositive also malaria-positive	No IgM or RT-PCR testing; hospital bias; cross-reactivity possible
Ekong et al., 2022 [8]	IgG seroprevalence	Abuja, Ibadan, Jos	41.3% IgG seropositivity; age-associated, malaria co-exposure noted	Limited to IgG, no RT-PCR; convenience samples from 2010-2018
Ogwuche et al., 2023 [9]	IgM/ELISA/NT	North-central Nigeria (Jos)	11.8% acute CHIKV (IgM+ incl. co-infectionss); 31.1% arbovirus infections asymptomatic; birth outcome links	Limited confirmatory testing; pregnancy-only cohort; low mono-infections
Nwangwu et al., 2024 [10]	Vector RT-qPCR	16 states (positives in 9)	CHIKV RNA in 9/127 Aedes pools; Ae. aegypti (51%), Ae. albopictus (42%) dominant	No linkage to human cases; outbreak-focused (2017-2020); no DENV/ZIKV found
Legend: This table summarizes key evidence of CHIKV transmission in Nigeria, highlighting seroprevalence, co-occurrence with malaria, vector presence, and diagnostic limitations. Data from 1969–2024 show high seropositivity and Aedes vectors but limited molecular confirmation, underscoring surveillance gaps.				