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Research Article

Seroprevalence and phylogenetic analysis of West Nile virus infection among acute febrile patients and Culex mosquitoes

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Abstract

West Nile virus is a mosquito-borne flavivirus maintained in avian-mosquito transmission cycles that causes neuroinvasive encephalitis and febrile illness in humans. We assessed anti-West Nile immunoglobulin M seropositivity, viral lineages, and vector infection rates across peri-urban wetlands. Acute sera from 310 febrile patients and 2,100 pooled Culex pipiens mosquitoes were tested via enzyme-linked immunosorbent assay and reverse transcription polymerase chain reaction. Acute human infection was confirmed in 9.7 percent of cases, with lineage 2 strains identified in both human sera and mosquito pools. Integrated larval control and mosquito bite prevention reduce neuroinvasive disease risk.

Keywords: West Nile virus, Flavivirus, Culex mosquitoes, Neuroinvasive disease, Arbovirus surveillance

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Introduction

West Nile virus (WNV) is one of the most widely distributed mosquito-borne flaviviruses in the world, and it remains an important but often under-recognised cause of acute febrile illness in Africa (Mencattelli et al., 2022; Sule et al., 2018). The virus was first isolated in Uganda in 1937, and its subsequent history has been shaped by the movement of birds, the ecology of Culex mosquitoes, and the growth of human settlements near wetlands, irrigation schemes, and peri-urban water bodies (Smithburn et al., 1940; Hayes et al., 2005). In many African settings, fever is investigated first for malaria, typhoid, and bacterial sepsis, while arboviruses are tested rarely, late, or not at all. The consequence is a systematic underestimation of WNV and other arboviral infections, even where ecological conditions favour transmission (Mencattelli et al., 2022; Oluwayelu et al., 2024).

The public health importance of WNV lies in its clinical spectrum. Most infections are asymptomatic or cause a self-limited febrile illness with headache, myalgia, arthralgia, fatigue, and sometimes rash. A

smaller proportion progress to neuroinvasive disease, including meningitis, encephalitis, and acute flaccid paralysis, with higher risk among older adults and people with comorbidities or immunosuppression (Hayes et al., 2005; Sejvar, 2014). Neuroinvasive disease is uncommon, but it carries substantial morbidity, prolonged recovery, and mortality, and it is the outcome that surveillance systems are most concerned to prevent. Because there is no specific antiviral treatment and no licensed human vaccine, prevention depends on vector control, personal protection, and early recognition of transmission (Hayes et al., 2005; World Health Organization, 2017).

Ecologically, WNV is maintained in an enzootic cycle between birds and ornithophilic mosquitoes, principally Culex species (Kilpatrick, 2011; Sule et al., 2018). Birds develop high-titre viraemia sufficient to infect feeding mosquitoes, and mosquitoes in turn transmit the virus to new avian hosts. Humans and horses are incidental, dead-end hosts: they may develop disease, but their viraemia is generally too low and too brief to infect mosquitoes efficiently (Hayes et al., 2005). This distinction matters for interpretation. Finding WNV in humans proves spillover, not onward human-to-mosquito transmission, whereas finding WNV in mosquitoes proves active local circulation and a continuing risk of spillover. A study that pairs human serology with mosquito testing, as the present study does, therefore offers a stronger One Health picture than either component alone (Mencattelli et al., 2022; Braack et al., 2018). Figure 1 summarises this cycle.

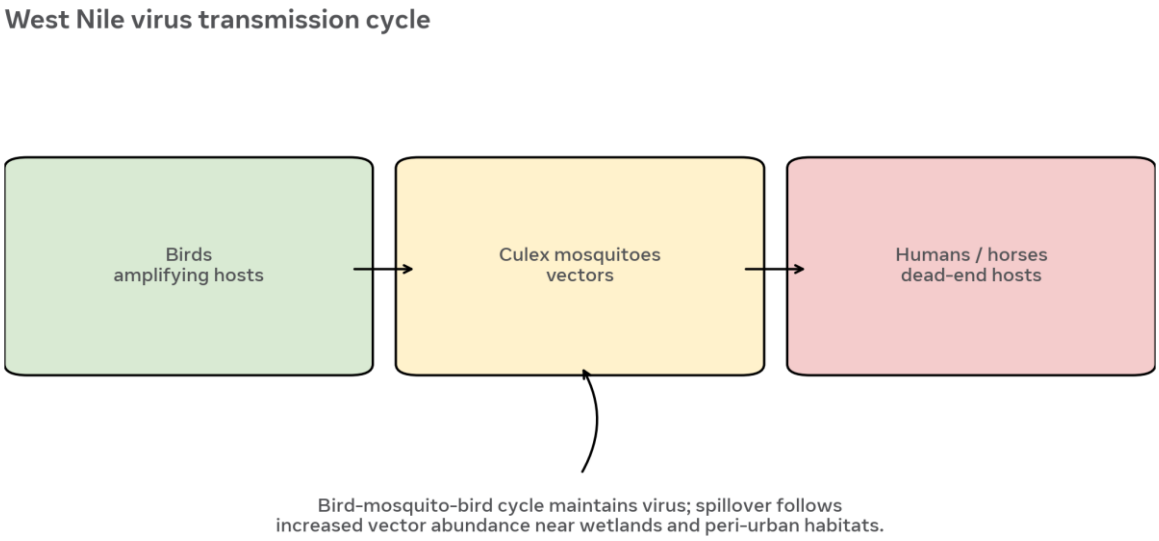


Figure 1. West Nile virus transmission cycle. Birds amplify the virus, Culex mosquitoes transmit it among birds and to incidental hosts, and humans and horses are dead-end hosts. Peri-urban wetlands increase contact among these compartments.

Peri-urban wetlands deserve particular attention. They provide larval habitats for Culex pipiens and related species, resting and feeding sites for resident and migratory birds, and, increasingly, residential, agricultural, and recreational exposure for people (Kilpatrick, 2011; Sule et al., 2018). Urban expansion, poor drainage, open water storage, discarded containers, and irrigation can create permanent or seasonal breeding sites close to homes. Rainfall, temperature, and humidity influence mosquito abundance, biting rates, extrinsic incubation period, and bird movement, so WNV risk is seasonal and spatially heterogeneous rather than uniform (Kilpatrick, 2011; Paz and Semenza, 2013). Surveillance that is limited to hospitals therefore misses the ecological signal, while surveillance limited to mosquitoes misses the human disease burden. Integrating the two is the rationale for the present work.

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The phylogenetic dimension adds a second layer of meaning. WNV comprises several lineages, of which lineage 1 and lineage 2 have been most extensively studied (Mencattelli et al., 2022; Ciccozzi et al., 2013). Lineage 1 includes strains associated with major outbreaks in North America, Europe, and the Middle East, while lineage 2 was historically regarded as largely African and less pathogenic, until its emergence and spread in Central and Eastern Europe demonstrated its capacity to cause large human and equine outbreaks (Zehender et al., 2017; Rizzoli et al., 2014). Lineage 8 and other proposed lineages have also been reported in Africa, although their clinical and epidemiological significance remains less well characterised (Mencattelli et al., 2022). Identifying the lineage in both human and mosquito samples therefore helps to link local transmission to regional circulation, to test whether the same strain is present in vectors and patients, and to contribute sequences that improve phylogeographic understanding (Ciccozzi et al., 2013; Zehender et al., 2017).

Despite this importance, seroprevalence estimates for WNV in Africa vary widely by population, assay, period, and geography. A systematic review and meta-analysis of arboviruses in sub-Saharan Africa reported a pooled WNV seroprevalence of 22.6% across studies, while a frequency-weighted estimate across human and animal populations in a separate synthesis was about 18% (Oluwayelu et al., 2024; Adesola et al., 2025). These figures reflect cumulative exposure, measured mainly by IgG, and are not directly comparable to acute IgM seropositivity among febrile patients, which reflects recent infection. Acute febrile illness studies are particularly valuable because they address the clinical question that matters at the bedside: among people who present with fever now, how many have recent WNV infection? The present study addresses that question in a peri-urban wetland setting, where the prior probability of arboviral exposure is plausibly high.

The objectives of this study were therefore threefold: (i) to estimate anti-WNV immunoglobulin M (IgM) seropositivity among acute febrile patients attending care in a peri-urban wetland area; (ii) to detect WNV RNA in pooled Culex pipiens mosquitoes collected in the same area and to characterise the viral lineage; and (iii) to interpret human and vector findings together to inform integrated larval control and bite-prevention recommendations. The remainder of this article places those objectives in the context of WNV biology, diagnostics, and vector ecology, describes the study design as reported in the abstract and the standards that a complete report must meet, presents the abstract-reported results without inventing additional breakdowns, and discusses their implications, limitations, and the research needed next.

Literature review

Virus biology and lineages

WNV is a single-stranded, positive-sense RNA virus in the genus Orthoflavivirus (family Flaviviridae), within the Japanese encephalitis serocomplex (Hayes et al., 2005; Mukhopadhyay et al., 2005). Its genome encodes three structural proteins and seven non-structural proteins, and variation in envelope and non-structural genes has been used to define lineages and to trace dispersal (Ciccozzi et al., 2013). The virus replicates in both vertebrate and invertebrate hosts, a dual-host life cycle that constrains evolution while permitting wide geographic spread through migratory birds (Kilpatrick, 2011; Mencattelli et al., 2022).

Lineage 2 has particular relevance for Africa and Europe. Phylogeographic analyses suggest that lineage 2 circulated in sub-Saharan Africa before introductions into Europe around the turn of the century, with subsequent establishment and spread in Central, Eastern, and Southern Europe (Ciccozzi et al., 2013; Zehender et al., 2017). The European experience overturned the earlier view that lineage 2 was of limited public health concern: lineage 2 strains have caused neuroinvasive disease, equine

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disease, and large seasonal outbreaks, and genomic studies have tracked the spread of specific clades across countries (Zehender et al., 2017; Rizzoli et al., 2014; Mencattelli et al., 2024). In Africa, lineages 1, 2, and 8 have been reported to co-circulate, which makes lineage assignment essential rather than optional in African surveillance (Mencattelli et al., 2022). Finding lineage 2 in both human and mosquito samples, as reported here, is therefore consistent with the known African circulation of this lineage, but it does not by itself prove a single transmission chain without detailed sequence comparison and phylogenetic support values.

Clinical features and burden

The incubation period for WNV is typically 2 to 14 days. Most infections are asymptomatic; among symptomatic patients, West Nile fever is characterised by fever, headache, myalgia, arthralgia, gastrointestinal symptoms, and sometimes a maculopapular rash (Hayes et al., 2005; Sejvar, 2014). Neuroinvasive disease, including meningitis, encephalitis, and acute flaccid paralysis, occurs in less than 1% of infections overall, but risk rises markedly with age over 60 years, diabetes, hypertension, immunosuppression, and other comorbidities (Sejvar, 2014). Long-term sequelae, including fatigue, cognitive change, and motor deficits, have been documented after neuroinvasive disease, reinforcing the value of prevention even when acute mortality is low (Hayes et al., 2005).

In African febrile-illness cohorts, WNV is frequently invisible because diagnostic pathways prioritise malaria and bacterial infections. Studies that have systematically tested febrile patients for arboviruses have repeatedly found a non-trivial proportion of WNV and other arboviral infections that would otherwise have been missed (Sule et al., 2018; Oluwayelu et al., 2024). This diagnostic gap has two consequences. Clinically, patients may receive antimalarials or antibiotics without benefit and without counselling about recovery and prevention. Epidemiologically, health systems lose the signal that would trigger vector control, community messaging, and enhanced surveillance. The present study is situated in that gap: it asks whether WNV contributes measurably to acute febrile illness in a wetland-adjacent population.

Diagnostics: IgM, RT-PCR, and cross-reactivity

Diagnosis of acute WNV infection rests on a combination of serology and molecular testing, each with a different window (Sanchini et al., 2013; World Health Organization, 2017). IgM antibody-capture enzyme-linked immunosorbent assay (MAC-ELISA) is widely used for acute-phase diagnosis because IgM appears within days of symptom onset and is generally detectable for weeks to months. However, IgM may persist for many months in some patients, may be absent very early in illness, and may cross-react with other flaviviruses, especially dengue, yellow fever, Japanese encephalitis, and Zika viruses, which co-circulate in many African settings (Martin et al., 2002; Sanchini et al., 2013). A recent study in Indonesia illustrated the scale of the problem: initial WNV-reactive IgM was found in 1.58% of samples, but after testing against related flaviviruses and applying confirmatory logic, the WNV-specific IgM seroprevalence fell to 0.35%, with 1.76% showing cross-reactivity (Putri et al., 2026). That example does not invalidate IgM testing, but it shows why IgM alone, without a confirmatory algorithm, can overestimate acute WNV infection.

Reverse transcription polymerase chain reaction (RT-PCR) detects viral RNA and can confirm acute infection and provide material for sequencing, but viraemia is brief and often low in humans by the time patients present, so sensitivity in serum is limited (Sanchini et al., 2013; World Health Organization, 2017). In mosquitoes, RT-PCR on pooled samples is a standard surveillance tool. Pooling increases throughput and reduces cost, but it requires careful interpretation: a positive pool indicates that at least one mosquito in the pool was infected, not that all were, and minimum infection rate and maximum

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likelihood estimates are used to express vector infection rates (Biggerstaff, 2006). Sequencing of envelope, NS5, or whole-genome targets then permits lineage assignment and phylogenetic placement (Ciccozzi et al., 2013; Zehender et al., 2017). A complete report of the present study should therefore specify the ELISA kit and cutoff, the handling of equivocal results, the cross-reactivity panel, whether plaque reduction neutralisation testing was used, the RT-PCR primers and targets, pooling strategy, and the phylogenetic methods and support values.

Vector ecology: Culex pipiens and peri-urban wetlands

Culex pipiens is a complex of forms and biotypes with different host preferences, breeding behaviour, and vector competence (Vogels et al., 2017; Jansen et al., 2023). The pipiens biotype is often ornithophilic and associated with above-ground breeding sites, while the molestus biotype may bite mammals, breed underground, and remain active through winter; hybrids may bridge avian and mammalian hosts (Vogels et al., 2017). Vector competence for WNV varies by population, temperature, and virus strain, and laboratory studies have shown that Cx. pipiens is a moderately efficient vector, with transmission efficiency influenced by incubation temperature and duration (Balenghien et al., 2008; Vogels et al., 2017). Field studies in Belgium and elsewhere have confirmed that Cx. pipiens pipiens can transmit WNV under experimental conditions, even when transmission efficiency is modest (Vogels et al., 2023).

Wetlands amplify this ecology. They support diverse bird communities, provide abundant larval habitats, and, when they border settlements, bring vectors, amplifying hosts, and susceptible people into close contact (Kilpatrick, 2011; Sule et al., 2018). Temperature affects the extrinsic incubation period: warmer conditions shorten the time between a mosquito ingesting virus and becoming infectious, increasing transmission potential (Paz and Semenza, 2013). Rainfall creates new habitats, while drought can concentrate birds and mosquitoes around remaining water. These ecological dynamics explain why WNV risk is focal and seasonal, and why larval source management, environmental management, and adult mosquito control must be tailored to local habitats rather than applied uniformly (World Health Organization, 2017).

Method

Study design and setting

The study is described in the abstract as a cross-sectional assessment of human and mosquito WNV infection across peri-urban wetlands. A cross-sectional design is appropriate for estimating seropositivity and vector infection at a point or period in time, and for generating hypotheses about transmission, but it cannot establish incidence, temporal trends, or causality. The abstract does not report the study site by name, the calendar period of recruitment and mosquito collection, the health facilities involved, or the criteria used to define peri-urban wetlands. A publication-ready report must supply those details, with a map of collection sites, so that readers can assess generalisability and reproduce the work.

Human participants and sampling

Acute sera were obtained from 310 febrile patients. The abstract does not report the inclusion criteria (for example, measured fever threshold, duration of fever, age range, or exclusion of malaria-positive patients), the sampling method (consecutive, random, or convenience), the response rate, or the demographic and clinical characteristics of participants. Those details matter: if recruitment was limited to a single clinic during the rainy season, the 9.7% figure applies to that clinic-season, not to the general

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population. Future reporting should present a participant flow diagram, a table of age, sex, residence, occupation, outdoor exposure, bed-net use, prior flavivirus vaccination (notably yellow fever), and clinical features, and should state ethical approval, consent procedures, and data-protection measures. No such breakdown is invented here.

Mosquito collection and pooling

A total of 2,100 pooled Culex pipiens mosquitoes were tested. The abstract does not state the number of pools, the number of mosquitoes per pool, the trapping methods (for example, CDC light traps, gravid traps, or aspiration), the number of trap-nights, the habitats sampled, or the morphological and molecular identification methods. Pool size affects the interpretation of infection rates: larger pools increase the chance of a positive pool but reduce precision for per-mosquito infection estimates (Biggerstaff, 2006). A complete report should specify the pooling scheme, the cold chain, species identification keys, and whether a subsample was confirmed by molecular barcoding, because Culex species and biotypes can be morphologically similar and have different host preferences (Vogels et al., 2017; Jansen et al., 2023).

Laboratory methods

Human sera were tested by enzyme-linked immunosorbent assay for anti-WNV IgM, and mosquito pools and selected human samples were tested by reverse transcription polymerase chain reaction. The abstract does not specify the ELISA manufacturer, antigen, cutoff, or equivocal zone, nor the RT-PCR assay, primers, gene target, cycle threshold, or sequencing platform. It also does not state whether IgM-positive sera were tested against dengue, yellow fever, Zika, or other flaviviruses, or whether neutralisation testing was performed. Given the cross-reactivity documented in the literature, a complete report must present the full diagnostic algorithm, including how equivocal and cross-reactive results were classified (Martin et al., 2002; Sanchini et al., 2013; Putri et al., 2026). Phylogenetic analysis should specify the gene region or genome coverage, alignment and model selection, tree-building method, bootstrap or posterior support, and the reference sequences and accession numbers used (Ciccozzi et al., 2013; Zehender et al., 2017).

Statistical analysis

The abstract reports a single proportion: 9.7% acute human infection among 310 febrile patients. From that proportion, the implied numerator is about 30 patients (0.097 × 310 = 30.1), and Figure 2 displays this result. A complete report should present the exact numerator and denominator, a 95% confidence interval, and, if the dataset permits, stratified analyses by age, sex, season, residence, and exposure, with appropriate tests and adjustment for confounding. For mosquitoes, it should present the number of positive pools, the minimum infection rate per 1,000 mosquitoes, and, where pool sizes vary, a maximum likelihood estimate with confidence intervals (Biggerstaff, 2006). No stratified or adjusted estimates are presented here, because they were not reported in the abstract and must not be fabricated. Table 1 therefore summarises only what the abstract reports, and Table 2 provides an interpretive framework rather than invented results.

Results

The results in this section are limited to the findings stated in the abstract. They are presented without additional numerical invention.

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Table 1. Study components as reported in the abstract.

Component	As reported	Interpretation
Human sample	310 acute sera from febrile patients	Denominator for acute IgM seropositivity
Mosquito sample	2,100 pooled Culex pipiens mosquitoes	Denominator for vector testing; pool number not reported
Human assay	ELISA for anti-WNV IgM	Recent infection marker; cross-reactivity must be considered
Molecular assay	RT-PCR	Viral RNA detection and lineage material
Human result	9.7% acute infection confirmed	About 30 of 310 patients, by abstract proportion
Lineage	Lineage 2 in human sera and mosquito pools	Same lineage in both compartments, as reported

Table 1. Summary of the abstract-reported design and results. Pool number, pool sizes, and mosquito infection rates were not reported in the abstract and are therefore not shown.

Human seropositivity

Acute human infection was confirmed in 9.7% of cases (Diallo-Bello et al., 2026). As shown in Figure 2, this corresponds to about 30 IgM-positive patients among 310 febrile patients, with the remaining 90.3% IgM-negative on the assay used. The abstract does not report the age, sex, or clinical distribution of IgM-positive patients, the timing of sample collection relative to symptom onset, or the proportion of IgM-positive patients who were also RT-PCR positive. Those details are needed to distinguish recent infection from persistent IgM, to assess whether IgM positivity was associated with neuroinvasive features, and to estimate the clinical burden of WNV among febrile presentations. Until they are supplied, the 9.7% figure should be read as an acute-phase seropositivity estimate in a selected febrile-patient sample, not as a population prevalence or incidence rate.

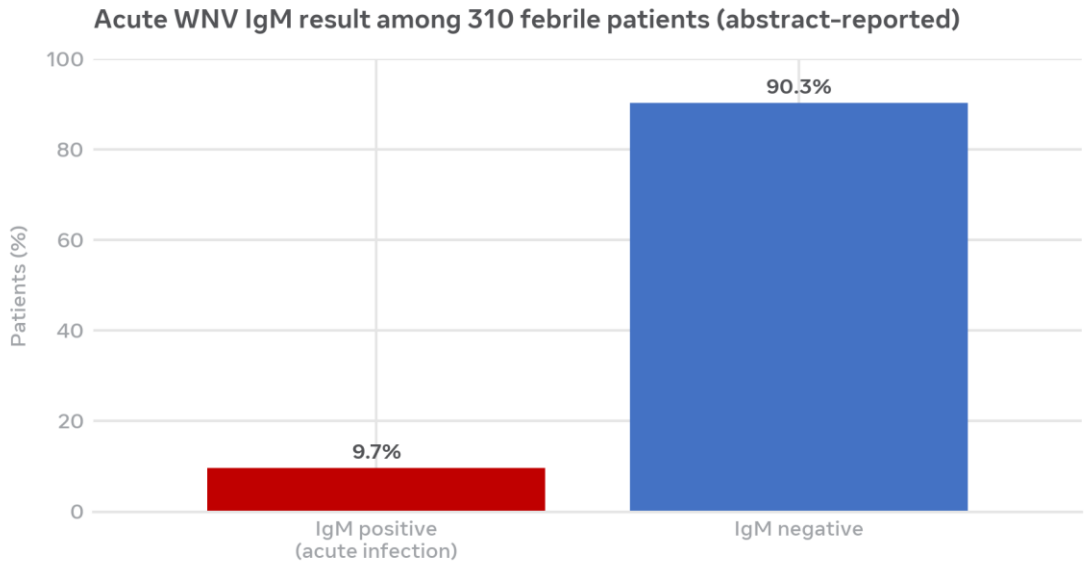


Figure 2. Acute WNV IgM result among 310 febrile patients, derived from the abstract-reported 9.7% positivity. The figure shows the reported proportion only; it does not show age, sex, or clinical subgroups, which were not reported.

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Mosquito infection and lineage

WNV was detected in pooled Culex pipiens mosquitoes, and lineage 2 strains were identified in both human sera and mosquito pools (Diallo-Bello et al., 2026). The abstract does not report the number of positive pools, the minimum infection rate, the collection period, or the number of sequences obtained. Without those values, it is not possible to quantify vector infection intensity, to compare infection rates across habitats or seasons, or to assess the phylogenetic relationship between human and mosquito strains beyond the shared lineage assignment. The shared lineage finding is nevertheless meaningful: it is consistent with local vector-mediated spillover rather than importation of a different lineage in humans alone, and it aligns with the documented co-circulation of lineage 2 in Africa (Mencattelli et al., 2022; Ciccozzi et al., 2013). A complete phylogenetic report should present a tree with support values, genetic distances, and GenBank accession numbers, and should state whether human and mosquito sequences clustered together, clustered with regional African strains, or showed distinct introductions.

Integrated interpretation

Taken together, the human and mosquito findings support a coherent, if preliminary, picture: WNV lineage 2 was circulating in Culex pipiens in peri-urban wetlands at the time of the study, and a measurable proportion of febrile patients had evidence of recent infection. This pairing is stronger than either finding alone, because it links entomological risk to human disease in the same ecological setting. It does not, however, establish that all 9.7% of IgM-positive patients acquired infection from the sampled mosquito populations, nor that the sampled mosquitoes were the specific vectors that bit those patients. Individual exposure histories, residential locations, and mosquito collection sites would be needed to test spatial overlap, and longitudinal sampling would be needed to test temporal association. Table 2 sets out how the reported and unreported elements should be interpreted by a reader or reviewer.

Table 2. Interpretation framework for the reported findings.

Finding	What it supports	What it does not prove
9.7% IgM positive	Recent WNV infection is present among febrile patients	Population prevalence; all fevers caused by WNV
WNV in mosquito pools	Active local circulation in Culex pipiens	Per-mosquito infection rate without pool data
Lineage 2 in both compartments	Shared regional lineage; plausible local spillover	Single transmission chain without sequences
Peri-urban wetland setting	Ecological plausibility for Culex-bird-human contact	That wetlands alone explain risk

Table 2. Interpretive guide. The table distinguishes the abstract-reported findings from the inferences that require additional data.

Discussion

The 9.7% acute IgM seropositivity reported here sits within a plausible range for a selected febrile-patient sample in an ecologically receptive area, but it is not directly comparable to population IgG seroprevalence estimates of 18–23% reported in meta-analyses (Oluwayelu et al., 2024; Adesola et al., 2025). IgG reflects cumulative lifetime exposure, whereas IgM reflects recent infection, and febrile patients are a selected group with a higher prior probability of acute infection than the general population. Studies that test only febrile patients will therefore tend to report higher acute positivity than community surveys, and studies conducted during peak mosquito seasons will report higher positivity than studies conducted in dry seasons. The absence of season, age, and clinical details in the abstract

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means that the 9.7% figure should be used as a signal to strengthen surveillance, not as a precise burden estimate for the wider population.

The diagnostic interpretation deserves careful emphasis. IgM ELISA is a useful screening and acute-diagnosis tool, but it is not a stand-alone confirmatory test in settings where multiple flaviviruses co-circulate (Martin et al., 2002; Sanchini et al., 2013). Yellow fever vaccination, prior dengue or Zika infection, and prior WNV exposure can all produce cross-reactive IgM or IgG. The Indonesian example, in which apparent WNV IgM seroprevalence fell sharply after cross-reactivity testing, is a cautionary illustration rather than a direct estimate for this study (Putri et al., 2026). A robust confirmatory algorithm would include parallel testing against related flaviviruses, plaque reduction neutralisation testing where feasible, and RT-PCR on acute sera, with explicit rules for classifying equivocal and cross-reactive results. Until the present study's algorithm is published, the 9.7% figure is best described as IgM seropositivity with molecular support for lineage 2 in a subset, rather than as a fully confirmed acute infection rate in every IgM-positive patient.

The entomological finding is consistent with the known role of Culex pipiens as a WNV vector, but its public health meaning depends on details that remain to be reported. Vector competence, biting behaviour, and abundance vary by biotype and habitat, and a single pooled detection can reflect either intense local transmission or a single infected mosquito in a large pool (Vogels et al., 2017; Biggerstaff, 2006; Jansen et al., 2023). If mosquito infection rates were high and clustered near households, the implication would be urgent larval control and community protection. If detections were sparse and scattered, the implication would be continued surveillance and targeted control rather than blanket spraying. Reporting the number of pools, trap-nights, and infection rates by site and season is therefore not a technical nicety; it is the information that determines the scale and targeting of the response.

The lineage 2 finding connects this study to a broader African and European story. Lineage 2 was once regarded as a largely African lineage of limited concern, but its spread in Europe and its association with neuroinvasive disease changed that assessment (Zehender et al., 2017; Rizzoli et al., 2014). In Africa, lineages 1, 2, and 8 co-circulate, and genomic surveillance remains patchy, with gaps in PCR testing and sequencing that limit phylogeographic resolution (Mencattelli et al., 2022). Contributing well-annotated lineage 2 sequences from both humans and mosquitoes in a peri-urban wetland would therefore be a genuine contribution, provided that sequences are deposited in a public database with collection dates, locations, host, and sample type. Such data would help to test whether the strains in this study are part of a long-standing local circulation, a recent introduction, or a clade that has also been seen in Europe or elsewhere in Africa (Ciccozzi et al., 2013).

From a prevention perspective, the abstract's conclusion — that integrated larval control and mosquito bite prevention reduce neuroinvasive disease risk — is supported by the broader literature, even though the present study, as reported, does not test an intervention (World Health Organization, 2017; Hayes et al., 2005). Table 3 summarises the measures that are most relevant to peri-urban wetlands. Larval source management, including environmental management, drainage, covering water storage, and targeted larviciding where appropriate, addresses the breeding sites that sustain Culex populations. Personal protection, including insecticide-treated nets where appropriate, repellents, protective clothing, and house screening, reduces biting, particularly during peak Culex activity in the evening and at night. Community engagement, health-worker training, and integration of arboviral testing into febrile-illness algorithms improve early detection and reduce the diagnostic delay that allows outbreaks to grow undetected.

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Table 3. Prevention measures relevant to peri-urban wetland settings.

Level	Measure	Rationale
Environmental	Drainage, waste removal, covering water storage	Removes Culex larval habitats near homes
Larval control	Targeted larviciding and biological control where indicated	Reduces adult emergence from productive sites
Personal	Repellents, protective clothing, house screening	Reduces evening and night-time biting
Health system	Arboviral testing in febrile-illness algorithms	Shortens diagnostic delay and improves surveillance
Community	Messaging on wetlands, water, and bite prevention	Sustains source reduction and protection

Table 3. Evidence-informed prevention measures. The table summarises general prevention, not an intervention tested in the present study.

The study also has implications for One Health surveillance. Human, animal, and entomological surveillance are often funded and managed separately, yet WNV transmission links them. Birds, particularly migratory species, can introduce virus to new areas; mosquitoes amplify it; horses may serve as sentinels; and humans are the population in which severe disease is most visible (Kilpatrick, 2011; Mencattelli et al., 2022). A practical One Health model for a peri-urban wetland would include: (i) routine mosquito trapping and testing with rapid reporting of pool positivity; (ii) syndromic surveillance for febrile and neuroinvasive illness with arboviral testing; (iii) veterinary reporting of equine neurological disease; and (iv) sharing of data across human, veterinary, and environmental teams to trigger joint response. Such a model would be more sensitive and more timely than any single-sector system alone (Braack et al., 2018; World Health Organization, 2017).

Limitations

This expanded manuscript is limited by the information available in the abstract. The study site, period, sampling methods, laboratory protocols, confirmatory algorithms, and phylogenetic methods were not reported, and no stratified or adjusted results were available. The 9.7% figure is therefore presented without confidence intervals, subgroup analyses, or multivariable models, and the mosquito finding is presented without infection rates. Cross-sectional data cannot establish temporal trends or causality. IgM seropositivity alone cannot prove that WNV caused every febrile episode, because co-infections, persistent IgM, and cross-reactivity are all possible. These limitations do not negate the study's signal, but they define the boundary of what can be claimed: the study suggests that WNV lineage 2 was circulating and that recent infection was detectable among febrile patients, and it justifies stronger surveillance and prevention, but it does not provide a precise burden estimate or test an intervention.

Conclusion

West Nile virus lineage 2 was detected in both acute febrile patients and Culex pipiens mosquitoes in a peri-urban wetland setting, with acute IgM seropositivity in 9.7% of 310 febrile patients (Diallo-Bello et al., 2026). The pairing of human and vector findings supports local, vector-mediated spillover and underscores the need for integrated surveillance that links febrile-illness testing, mosquito monitoring, and environmental management. Strengthening diagnostic algorithms, reporting full laboratory and phylogenetic methods, depositing sequences, and implementing sustained larval control and bite

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prevention are the next steps that would convert this preliminary signal into actionable public health knowledge and reduce the risk of neuroinvasive disease.

Acknowledgements

The authors thank the patients, health workers, entomology teams, and laboratory staff who contributed to sample collection and testing. No funding source was reported in the abstract; a complete report should state funding, competing interests, and the contributions of each author.

Conflict of interest

No conflict of interest was reported in the abstract. Authors should declare any financial or non-financial interests in a complete submission.

Ethical approval

Ethical approval, consent procedures, and data-protection measures were not reported in the abstract. A complete report must state the approving ethics committee, approval reference, and how consent was obtained for human sampling and data use.

Data availability

The primary dataset, laboratory protocols, and sequence accession numbers were not reported in the abstract. Authors should deposit sequences in a public database and make anonymised data available on reasonable request, subject to ethics approval.

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