International Journal of Health Geographics

RESEARCH

Open Access

Spatial eco-climatic gradients drive adaptive 2La chromosomal inversion polymorphism in *Anopheles coluzzii*, a major malaria vector in Nigeria

Adedapo O. Adeogun[1,2*†], Oluwakemi Adetunji[1*†], Ayodele S. Babalola[1*†], Romoke T. Izekor[1†], Tolulope A. Oyeniyi[1], Oluwaseun Adesoye[3], Jasini Wahedi[4], Lateef O. Busari[5], George Aniekeme[6], Seun Ajayi[7], Joseph Chabi[8] and Samson T. Awolola[1]

Abstract

Background Chromosomal inversions are important genetic mechanisms that facilitate local adaptation, ecological flexibility, and behavioural variation in mosquito populations. In *Anopheles coluzzii*, a dominant malaria vector in West Africa, the 2La inversion has been associated with desiccation tolerance, thermal resistance, and insecticide resistance. Despite Nigeria's ecological diversity and substantial malaria burden, the spatial distribution and clinal dynamics of 2La inversion polymorphism in *An. coluzzii* remain poorly characterized. This study investigated the distribution of 2La inversion karyotypes across major Nigerian ecozones and examined their association with climatic gradients.

Methods Larvae of *Anopheles* mosquitoes were sampled across 12 states representing Nigeria's southern, central, and northern ecological zones. Species identification was conducted morphologically and confirmed with PCR diagnostics. The 2La inversion was determined using established molecular assays, and allele frequencies were analyzed with respect to ecozone and climatic gradients. Spatial distribution maps and statistical analyses, including correlation and clinal trend assessment, were done in R version 4.4.

Results A clear geographic structuring of 2La inversion polymorphism was observed in *An. coluzzii* populations. The 2La/2La homokaryotype was strongly predominant in the northern Sahelian and Sudan savanna ecozones, reflecting adaptation to hot and arid conditions. In contrast, the standard 2La+/2La+ arrangement was predominant in humid southern forest and mangrove regions. The heterokaryotype (2La/2La+) occurred at intermediate frequencies within

---

†Adedapo O. Adeogun, Oluwakemi Adetunji and Ayodele S. Babalola contributed equally to this work.

*Correspondence:
Adedapo O. Adeogun
dapoadeogun@hotmail.com
Oluwakemi Adetunji
adesalukemi@gmail.com
Ayodele S. Babalola
ayodelebabalola2011@gmail.com

Full list of author information is available at the end of the article

the central transitional belt, where ecological gradients overlap. Karyotype frequencies exhibited a pronounced latitudinal cline, with heterozygosity peaking in central Nigeria. The spatial patterns indicate that climatic pressures, particularly aridity and humidity, might be a major determinant of inversion distribution in *An. coluzzii* from Nigeria.

Conclusion This study provides the first detailed nationwide characterization of 2La inversion polymorphism in *An. coluzzii* across Nigeria's ecological zones. The strong alignment between inversion frequency and eco-climatic gradients highlights the role of chromosomal rearrangements in promoting vector survival and ecological fitness. These adaptive patterns have significant implications for malaria control, as inversion-mediated adaptability may influence resting behaviour, insecticide response, and vector persistence under climate change. Integrating chromosomal inversion surveillance into entomological monitoring frameworks will be essential for designing ecologically tailored vector control strategies in Nigeria.

Keywords *An. coluzzii*, 2La chromosomal inversion, Ecological adaptation, Climatic gradients, Malaria vector, Nigeria

Background

Malaria remains a persistent and devastating public health problem across sub-Saharan Africa (WHO, 2024). Members of the *Anopheles gambiae* species complex, including *Anopheles gambiae* s.s., *Anopheles coluzzii*, and *Anopheles arabiensis* are the primary malaria vectors in Nigeria [1]. Mosquito distribution, survival, and vectorial capacity in tropical regions are strongly influenced by climatic factors (temperature, rainfall, and relative humidity) all of which fluctuate markedly across seasons [2, 3]. Ongoing climate change further intensifies these fluctuations, creating selective pressures that favour mosquito populations with greater physiological tolerance and adaptive potential, while disadvantaging less tolerant populations [4, 5]. In West Africa, malaria vectors are often exposed to substantial seasonal shifts, from cooler, rainy months to prolonged dry periods characterized by high temperatures and low humidity [6]. Such environmental heterogeneity drives natural selection and local adaptation, enabling mosquito populations to survive even under harsh ecological conditions [7, 8]. Moreover, it has been reported that during extended dry seasons, shortened mosquito generation times can increase the transmission potential of malaria, dengue, yellow fever, chikungunya, West Nile, and Japanese encephalitis viruses [9, 10, 11, 12].

Chromosomal inversions constitute one of the major genomic mechanisms that facilitate these adaptive responses. By suppressing recombination within the inverted region, inversions preserve advantageous allelic combinations and promote phenotypic flexibility across environmental gradients [8, 13, 14]. Among these structural changes, paracentric inversions are particularly important drivers of local adaptation, ecological divergence, and incipient speciation (Kirkpatrick et al., 2010). They have played a central role in the evolutionary radiation of the *Anopheles gambiae* complex, enabling its members to colonize diverse habitats across sub-Saharan Africa [13].

An. coluzzii, a major malaria vector in West Africa including Nigeria, is notable for its ecological adaptability and propensity for metabolic insecticide resistance [2, 15]. Within this species, the 2La chromosomal inversion represents one of the most ecologically significant polymorphisms. The inversion, with alternative arrangements 2La and 2La+, is widely distributed in West Africa and displays strong geographic structuring resulting from varying climatic conditions [16, 17]. The 2La arrangement is typically associated with arid and semi-arid environments, conferring traits such as enhanced desiccation resistance, thermotolerance, and improved survival under xeric conditions [18, 19]. In contrast, the standard 2La+ arrangement predominates in humid forested regions where stable moisture levels favour mosquitoes adapted to mesic habitats [16, 19]. The predictable association between inversion frequencies and environmental gradients indicates strong climatic selection maintaining these polymorphisms.

Beyond climatic adaptation, the 2La inversion has been linked to larval habitat specialization, resting and biting behaviour, vector competence, and insecticide resistance [17, 20, 21]. In Nigeria, this inversion has been implicated in dieldrin resistance [22] and in shaping permethrin resistance in Sahelian populations through shifts in 2La/ 2La+ allele balance [8]. These associations buttress the importance of chromosomal inversions as markers of vector adaptability, with direct implications for malaria control.

Nigeria's ecological gradient, from humid southern mangrove forests to hot, arid Sahelian savannas, offers an ideal framework for assessing inversion-driven adaptation. Despite the country's exceptionally high malaria burden, comprehensive investigations of inversion polymorphism in *An. coluzzii* remain limited. Understanding how inversion frequencies vary across ecozones, and how they relate to environmental selective pressures, is essential for predicting vector behaviour, tracking insecticide resistance evolution, and optimizing vector control strategies.

This study therefore characterizes the spatial distribution and ecological correlates of the 2La inversion in *An. coluzzii* across the major ecological zones of Nigeria.

Methods

Study area and larvae collection

The study was conducted across 12 states representing Nigeria's major ecological zones, spanning humid coastal forests, Guinea savannah, and Sudan–Sahel savannah regions (Fig. 1). These zones differ markedly in rainfall, vegetation structure, humidity, and seasonality, creating distinct ecological conditions for *Anopheles* breeding and survival [2].

Southern sites are characterized by high annual rainfall (approximately 1,300–2,500 mm), perennial surface water, and semi-permanent larval habitats embedded within mangrove and rainforest ecosystems. In contrast, northern sites receive lower annual rainfall (approximately 600–1,000 mm), with breeding habitats that are largely seasonal and closely linked to rainfall patterns (Coluzzi, 1979). The central Guinea savannah zone represents a transitional environment with intermediate ecological characteristics [2].

Larvae were collected between June and October 2024 using the standard dipping method (Ibrahim et al., 2014). Collections were conducted directly from typical *Anopheles* breeding habitats, including puddles, tyre tracks, footprints, shallow pools, and temporary ponds [22]. These habitats reflect local hydrological and climatic conditions and are known to support *Anopheles* development across ecological gradients. All sampling locations and their corresponding ecological classifications are presented in Fig. 1.

Mosquito rearing and species identification

Larvae were collected from diverse aquatic habitats across 12 Nigerian states and reared to adult under standard insectary conditions (70–80% RH; 25–27 °C; 12:12 h light–dark cycle). Adults were maintained on 10% sucrose solution and morphologically identified as members of the *Anopheles gambiae* complex using standard taxonomic keys [23]. Genomic DNA from a subset of adults was extracted following the Scott method and subjected to species-specific SINE200 PCR for molecular identification of sibling species [24, 25].

2La/2La+ Inversion karyotyping

A subset of *An. coluzzii* specimens was genotyped for the 2La inversion using PCR-based chromosomal karyotyping [25]. Amplification employed primers 23A2 (universal reverse), 27A2 (2La-specific), and DPCross5 (2La+-specific). PCR reactions were performed in a total reaction

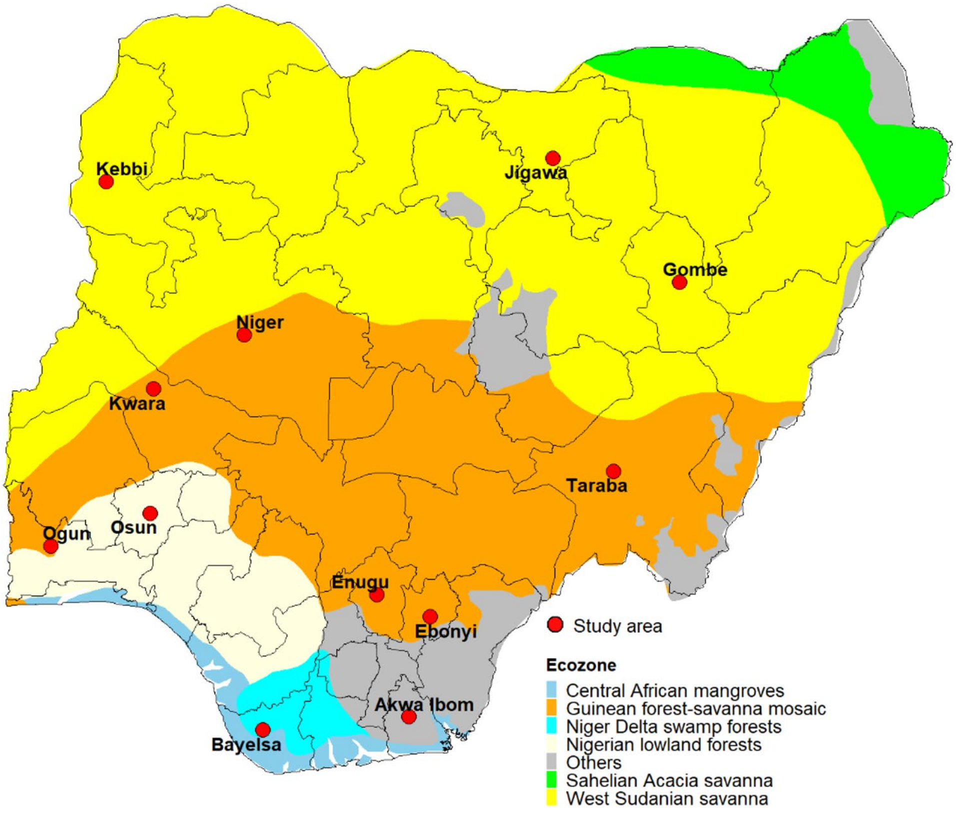

Fig. 1 Map of Nigeria showing major ecotypes and the study sites

volume of 12 µl volume using DreamTaq polymerase with cycling conditions of 94 °C for 2 min; 35 cycles of 94 °C for 30 s, 60 °C for 30 s, 72 °C for 45 s; and final extension at 72 °C for 10 min. Amplicons were resolved on 1.5% agarose gels. Diagnostic fragment sizes were 492 bp (2La) and 207 bp (2La+); heterozygotes produced both bands.

Data analysis

Karyotype frequencies (2La/2La, 2La/ 2La+, and 2La+/ 2La+) were calculated for each state as the proportion of individuals exhibiting each genotype relative to the total number of successfully genotyped specimens. Allele frequencies for 2La and 2La+ were derived from genotype counts using standard population genetic formulas under diploid inheritance assumptions. Departures from Hardy–Weinberg equilibrium (HWE) were assessed separately for each state using chi-square goodness-of-fit tests comparing observed and expected genotype frequencies. Expected frequencies were calculated under the assumptions of random mating, large population size, no selection, no mutation, and no migration. A significance threshold of $P < 0.05$ was applied. To assess spatial clinal structure, linear regression models were fitted to evaluate the association between state-level inversion frequency (dependent variable) and latitude (independent variable). Latitude was treated as a continuous predictor representing the south–north ecological gradient. Model assumptions (including linearity, homoscedasticity, and normality of residuals) were evaluated using diagnostic plots. The coefficient of determination (R^2) was used to quantify the proportion of variance in inversion frequency explained by latitude. Spatial distribution maps of karyotype and allele frequencies were generated using the sf and ggplot2 packages in R version 4.4. All statistical analyses were conducted in R version 4.4 (R Core Team, 2024).

Results

Spatial distribution of 2La inversion frequencies in *An. coluzzii* across Nigerian states

A total of 1163 *Anopheles gambiae* s.l. were morphologically identified from 1200 specimens collected. PCR-based sibling species identification revealed *An. gambiae* 447(38.4%), *An. coluzzii* 600(51.6%), and *An. arabiensis* 116(10.0%). The diagnostic amplicons for the 2La inversion are shown in Supplementary file 1, and the karyotyped allele frequencies are summarized in Table 1. In this study, only *An. coluzzii* was tested for 2La.

Across the 12 sampled states, clear geographic structuring of 2La inversion karyotypes was observed. The inverted homokaryotype (2La/2La) predominated in northern states, reaching very high frequencies in Jigawa (0.98) and occurring at moderate to high levels across other Sahel and savannah locations, but was absent in the coastal state of Akwa Ibom. In contrast, the standard homokaryotype (2La+/ 2La+) was most frequent in southern states such as Ogun and Akwa Ibom (up to 0.70), but was not detected in several northern states, including Kebbi, Jigawa, Gombe, and Taraba. The heterokaryotype (2La/ 2La+) occurred at lower to intermediate frequencies across sites, ranging from absence in Kebbi to 0.38 in Osun.

Notably, 2La+/ 2La + was entirely absent from the driest northern states (Kebbi, Jigawa, Gombe, Taraba), while 2La/2La was undetected in the coastal state of Akwa Ibom (Table 1).Choropleth maps (Fig. 2) revealed distinct spatial structuring of inversion frequencies. The 2La/2La arrangement predominated in the northern savanna belt, with Kebbi, Jigawa, Gombe, and Taraba showing frequencies > 0.8. Conversely, the 2La+/2La+ arrangement was concentrated in the humid southern ecozones; particularly Bayelsa, Akwa Ibom, and Ogun, where frequencies are higher (0.59 to 0.7). The heterozygous 2La/2La+ form was more pronounced (though with frequency < 0.5)

Table 1 Observed numbers and frequencies of 2La karyotypes in *An.coluzzi* from the sampled localities of Nigeria

No. assigned to locality	Locality name from south to north	No. karyotyped	Allele frequency per state		
			2La+/2La+	**2La/2La+**	**2La/2La**
1	Bayelsa	41	24(0.59)	15(0.37)	2(0.05)
2	Akwa Ibom	53	37(0.70)	16(0.30)	0(0.00)
3	Enugu	48	27(0.56)	13(0.27)	8(0.17)
4	Ebonyi	56	23(0.41)	20(0.36)	13(0.23)
5	Ogun	50	35(0.70)	10(0.20)	5(0.10)
6	Osun	52	24(0.46)	20(0.38)	8(0.15)
7	Kwara	39	0(0.00)	7(0.18)	32(0.82)
8	Niger	54	8(0.15)	9(0.17)	37(0.69)
9	Kebbi	58	0(0.00)	0(0.00)	58(1.00)
10	Jigawa	55	0(0.00)	1(0.02)	54(0.98)
11	Gombe	46	0(0.00)	5(0.11)	41(0.89)
12	Taraba	48	0(0.00)	4(0.08)	44(0.92)
		600	**178(0.30)**	**120(0.20)**	**302(0.50)**

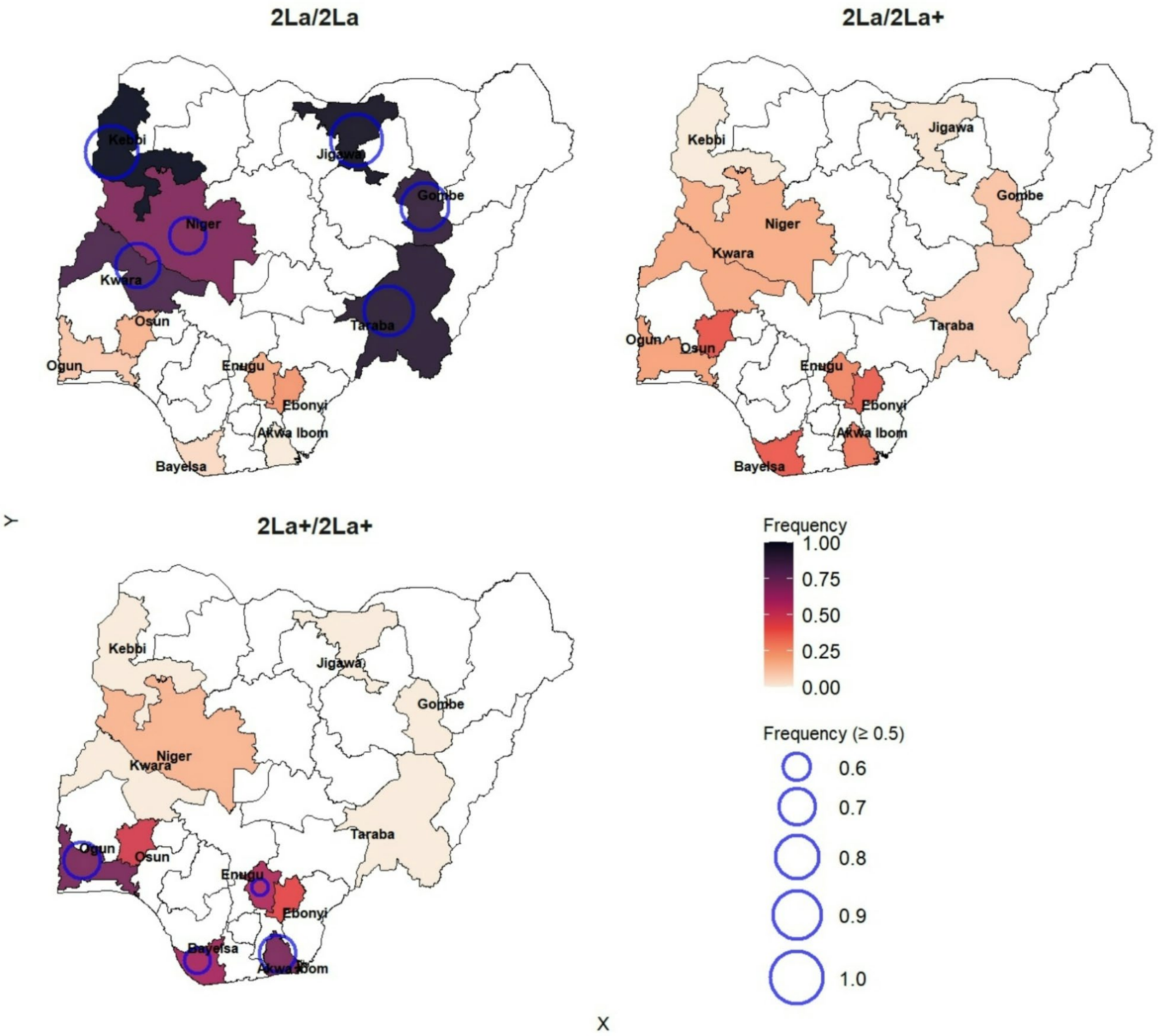

Fig. 2 Spatial distribution of *An. coluzzii* 2La inversion karyotypes across 12 surveyed Nigerian states. Each map represents the frequency of one karyotype: 2La/2La, 2La+/2La+, and 2La/2La+. Frequency gradients show local variation in allele distribution, with darker shades representing higher frequencies. Larger red circles indicate states with frequencies ≥ 0.5. The maps highlight a clear north–south differentiation, with 2La/2La predominating in northern states and 2La+/2La+ more frequent in southern ecozones

in central transition zone (Osun), however, similar frequency range were also recorded in *An. coluzzii* from the more humid southern part of the country (Ebonyi, and Bayelsa) (Fig. 2).

Figure 3 revealed a clear ecological partitioning in inversion polymorphism when mapped against ecological regions. 2La/2La was strongly associated with the Sahelian and West Sudanian savannas, reflecting adaptation to arid and semi-arid environments. In contrast, 2La+/2La+ arrangement was more frequent in the lowland rainforest, mangrove swamps, and coastal humid zones. These spatial patterns reveal the adaptive differentiation of *An. coluzzii* populations along Nigeria's ecological gradient.

Latitudinal clines of 2La inversion frequencies in *An. coluzzii*.

A ridge plot illustrating allele frequencies along a south–north transect (Fig. 4) demonstrated a pronounced latitudinal cline. The frequency of 2La/2La increased sharply with latitude, while 2La+/2La+ decreased in the opposite direction. The inflection zone, located approximately between Osun and Taraba, corresponded to Nigeria's major ecological transition from humid forest to dry savanna. This zone also exhibited slightly elevated frequencies of the heterokaryotype 2La/2La+, reflecting a transitional population structure. However, the Southern part of the country seems to exhibit slightly elevated

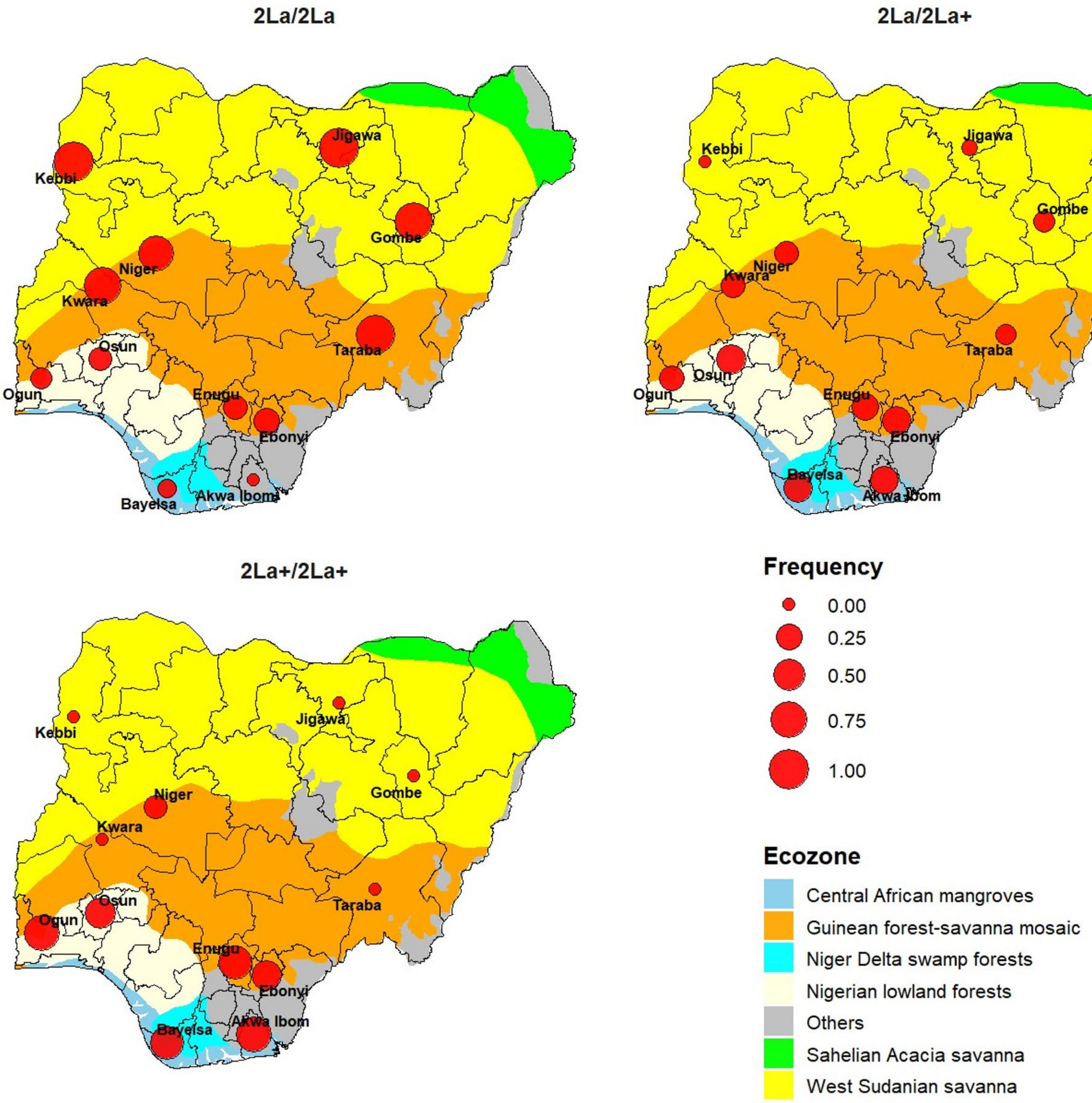

Fig. 3 Chromosomal inversion frequencies of *An. coluzzii* over Nigerian ecozones. State-level frequencies of *An. coluzzii* 2La inversion karyotypes overlaid on Nigeria's ecozones. Background colors represent major ecological regions derived from the national ecozone classification. Red circles mark state centroids, with size proportional to inversion frequency. The 2La/2La arrangement dominates arid northern ecozones (Sahelian and West Sudanian savanna), while 2La+/2La+ is concentrated in humid southern and coastal regions (Guinean forest and mangroves). The spatial alignment between inversion frequency and ecozone distribution indicates strong ecological selection along climatic gradients

frequencies for the heterokaryotype 2La/2La+ compared with the Northern part (Fig. 4).

Regression plots (Fig. 5) further quantified these patterns. The inverted 2La/2La arrangement showed a strong positive association with latitude ($R^2 = 0.80$), indicating increasing prevalence in northern, arid environments. The standard 2La+/2La+ arrangement declined significantly with latitude ($R^2 = 0.72$), consistent with adaptation to southern humid ecozones. The heterokaryotype 2La/2La+ though with low frequencies also show a negative trend ($R^2 = 0.74$), decreasing towards the North.

Hardy–Weinberg equilibrium (HWE) tests indicated no significant departures from equilibrium in most states ($P > 0.05$). However, significant deviations were detected in Enugu, Ogun, and Niger (Table 2), suggesting departures from random mating expectations. Such deviations may arise from localized selection, population sub-structuring (Wahlund effect), gene flow, assortative mating, or demographic processes, including recent expansion or drift. Further fine-scale population genetic analyses would be required to disentangle these potential mechanisms (Table 2).

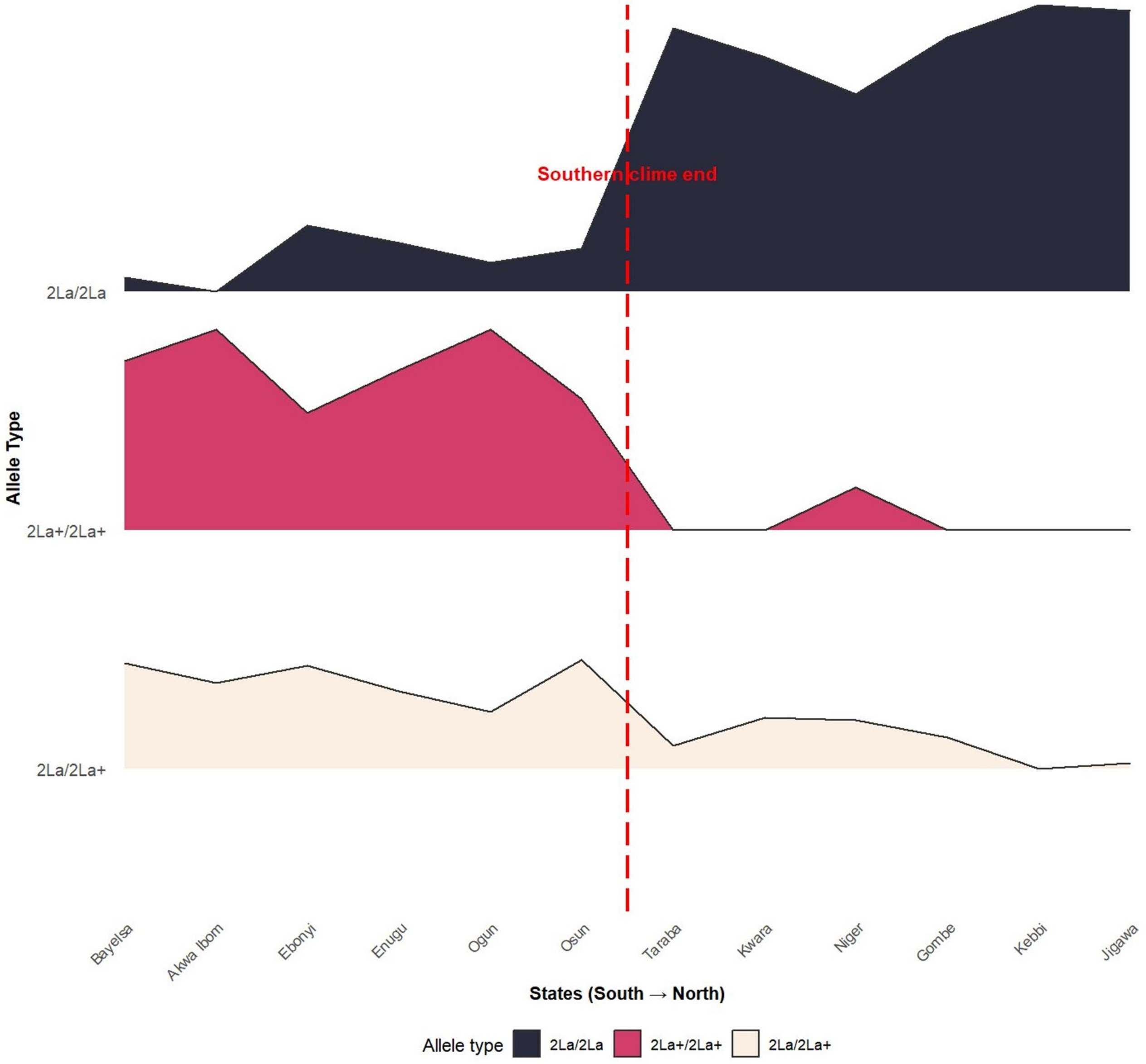

Fig. 4 Ridge plot showing latitudinal patterns of 2La inversion frequencies along a south–north cline. Ridge plot showing the latitudinal progression of *An. coluzzii* 2La inversion frequencies from southern to northern Nigeria. Each panel represents a distinct karyotype: 2La/2La, 2La+/2La+, and 2La/2La+. The dashed vertical red line marks the approximate boundary between southern and northern climes (Osun–Taraba representing central Nigeria / forest-savanna transition zone). Frequencies of 2La/2La increase sharply toward the north, while 2La+/2La+ declines, suggesting a strong climatic gradient influencing karyotype distribution across ecozones

Discussion

This study provides the first nationwide assessment of the 2La inversion polymorphism in *An. coluzzii* across Nigeria and demonstrates strong ecological structuring consistent with the country's unique climatic gradient. Chromosomal inversions are well-established drivers of local adaptation in African malaria vectors, maintaining co-adapted gene complexes under reduced recombination and enabling populations to persist under heterogeneous environmental pressures [16, 21, 26]. The study findings confirm that the 2La inversion remains a major axis of ecological differentiation in *An. coluzzii*, shaping population structure and adaptive potential across Nigeria's ecozones.

A clear latitudinal cline was observed, with the 2La/2La arrangement nearly fixed in the arid Sahelian and Sudan savanna states. These regions are characterized by extreme temperatures, low rainfall, and prolonged dry seasons (Adeogun et al., 2025), conditions under which the 2La arrangement has been shown to confer significant adaptive advantages, including enhanced desiccation tolerance, thermal resilience, and larval survival

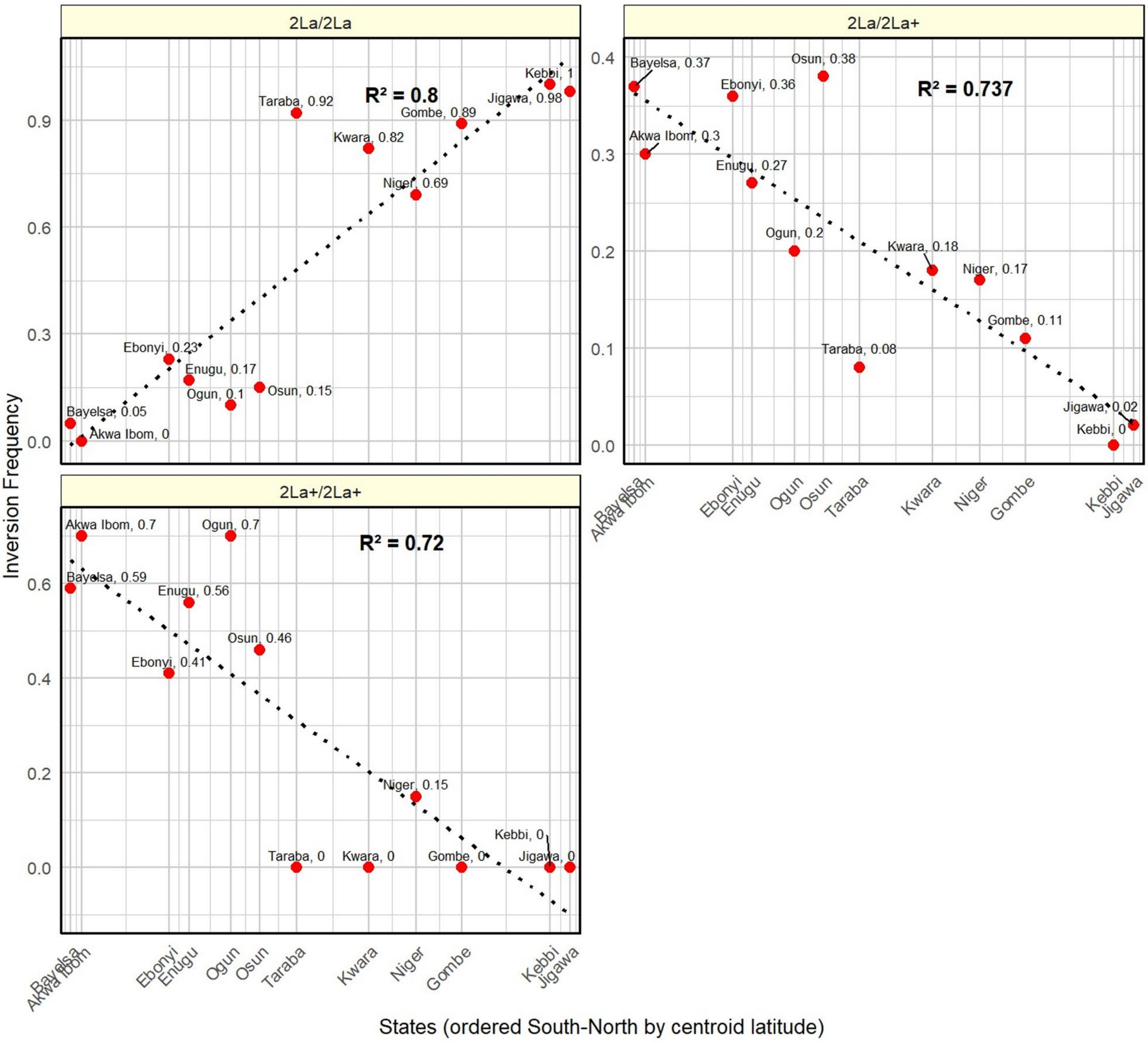

Fig. 5 South–north cline and correlation of inversion frequency with latitude. Regression analysis of *An. coluzzii* 2La inversion frequencies ordered by latitude. Each scatterplot shows the relationship between inversion frequency and south–north position across 12 states for 2La/2La, 2La+/2La+, and 2La/2La+. Dotted lines represent linear fits with corresponding coefficients of determination (R^2). A strong positive correlation for 2La/2La (R^2 = 0.80) and negative correlation for 2La+/2La+ (R^2 = 0.72) indicate a clear latitudinal cline, reflecting adaptation of inversion forms to distinct environmental conditions

in transient habitats [8, 17]. Conversely, the standard 2La+/2La+ arrangement predominated in the humid southern forest and mangrove zones, reflecting adaptation to cooler, mesic conditions with stable breeding habitats [16, 18, 27]. These patterns reinforce the key role of climatic selection in maintaining inversion polymorphism along environmental gradients.

The transitional forest–savanna mosaic in central Nigeria exhibited the highest frequencies of the heterokaryotype (2La/2La+), suggesting strong balancing selection in this ecotone where wet and dry conditions alternate seasonally. Heterozygosity in inversion polymorphisms has previously been associated with increased ecological flexibility and stability in fluctuating environments [28, 29]. Interestingly, our results also show elevated heterozygosity in two humid southern states (Ebonyi and Bayelsa) despite their high rainfall and moisture availability. This unexpected pattern suggests that factors beyond macroclimate may influence inversion dynamics.

Possible drivers of the observed karyotype pattern include localized ecological disturbance and human-mediated processes. In Bayelsa, an oil-producing state in the Niger Delta, extensive petroleum exploration and infrastructure development have resulted in habitat

Table 2 Observed and Expected (Hardy-Weinberg) karyotype frequencies for polymorphic chromosome inversion 2La + and 2La in *An. coluzzii* from the sampled localities in Nigeria

Localities	**Counts**	**Allele frequency per state**			**χ2**	***P* value**
		2La+/2La+	**2La/2La+**	**2La/2La**		
Bayelsa	No. Observed	24	15	2	0.031	0.984^{NS}
	Expected H-W	24.2	14.6	2.2		
Akwa-Ibom	No. Observed	37	16	0	1.675	0.433^{NS}
	Expected H-W	38.21	13.58	1.21		
Enugu	No. Observed	27	13	8	6.141	0.044^{S}
	Expected H-W	23.38	20.24	4.38		
Ebonyi	No. Observed	23	20	13	3.85	0.146$^{\mathbf{NS}}$
	Expected H-W	19.45	27.11	9.45		
Ogun	No. Observed	35	10	5	7.031	0.030^{S}
	Expected H-W	32	16	2		
Osun	No. Observed	24	20	8	1.175	0.556^{NS}
	Expected H-W	22.23	23.54	6.23		
Kwara	No. Observed	0	7	32	0.379	0.827^{NS}
	Expected H-W	0.31	6.37	32.31		
Niger	No. Observed	8	9	37	15.258	< 0.001$^{\mathbf{S}}$
	Expected H-W	2.89	19.21	31.89		
Kebbi	No. Observed	58	0	58	ND	ND
	Expected H-W	-	-	-		
Jigawa	No. Observed	0	1	54	0.004	0.998^{NS}
	Expected H-W	0	0.99	54.1		
Gombe	No. Observed	0	5	41	0.152	0.927^{NS}
	Expected H-W	0.14	4.73	41.14		
Taraba	No. Observed	0	4	44	0.091	0.956^{NS}
	Expected H-W	0.08	3.83	44.08		

NS – Values not significant at 95%CI

S – Values significant at 95%CI

fragmentation, wetland modification, gas flaring, and peri-urban settlement expansion. These activities may alter larval habitat availability and microclimatic conditions, potentially favouring karyotypes adapted to humid but anthropogenically disturbed environments. Increased population mobility associated with oil industry activities may also facilitate gene flow from other regions, reshaping local allele frequencies.

In addition, agricultural expansion and peri-urban farming practices can create heterogeneous breeding sites and localized insecticide exposure, generating selective pressures on inversion-linked traits. Although no study from this zone has directly demonstrated a correlation between 2La heterozygosity and insecticide resistance spread, previous studies in Nigeria have reported associations between 2La arrangements and resistance to permethrin and dieldrin [8, 22]. Therefore, elevated heterozygosity in this region may, in part, reflect responses to vector control insecticides and agricultural pesticide exposure, although this remains speculative and requires further investigation. Routine vector control interventions, including widespread LLIN distribution and indoor residual spraying, may further contribute to differential survival of behavioural phenotypes associated with specific karyotypes. Human movement between northern, central, and southern states (through trade routes, seasonal labour migration, and urbanization) could facilitate admixture and contribute to deviations from expected equilibrium patterns. Together, these geographically and socially structured processes may help explain the unexpected distribution of the 2La inversion in this setting.

Elevated heterozygosity in southern Nigeria may reflect increased gene flow and population admixture associated with high human population density, urbanization, and extensive transport networks. Greater connectivity can facilitate mixing between ecologically differentiated populations, maintaining heterokaryotypes through admixture rather than selection alone. Additionally, heterogeneous urban and peri-urban environments may support diverse larval habitats, favouring the persistence of both inversion arrangements within the same region.

The increasing heterozygosity observed in central Nigeria, combined with its moderate presence in some southern sites, indicates that these regions may serve as genetic convergence zones where divergent lineages interact. Such mixing could enhance adaptive potential, including responses to climatic fluctuations and insecticide pressure. Inversion polymorphism has been linked to multiple ecologically important traits in *An. coluzzii*, including resting and biting behaviour, larval habitat specialization, thermal tolerance, and insecticide resistance [17, 20, 21]. In Nigeria, 2La has been associated with resistance to dieldrin [22] and with shifts in permethrin resistance patterns in the Sahel driven by changes in 2La/ 2La+ allelic distribution [8]. Populations with high heterozygosity, particularly in central Nigeria, may have an increased capacity for rapid adaptation, including the potential emergence or spread of resistance alleles linked to the inversion region. The presence of comparable heterozygosity in southern states suggests that these populations may also be poised for greater adaptive shifts than previously recognized.

These inversion-mediated adaptive traits may also explain the recent range expansion of *An. coluzzii* across Nigeria and West Africa, as reported by Adeogun et al., [2]. The ability to maintain polymorphic combinations of 2La and 2La+ likely enhances ecological versatility, enabling *An. coluzzii* to colonize new environments, exploit both temporary and permanent larval habitats, and persist under increasing climatic variability. The inversion polymorphism documented in this study provides a genetic mechanism that may partly explain this expansion, providing insight into why *An. coluzzii* is becoming more geographically widespread in Nigeria [2].

The observed patterns may have implications for malaria control. Northern populations with higher frequencies of the 2La arrangement could be associated with increased exophilic or exophagic tendencies [30], which may influence exposure to indoor interventions such as indoor residual spraying (IRS) and long-lasting insecticidal nets (LLINs). Conversely, southern populations enriched for the 2La+ arrangement may exhibit behavioural profiles more compatible with indoor-based control measures. The central zone, where heterokaryotypes occur at moderate frequencies, may represent an area of greater genetic variability, which could facilitate ecological or behavioural flexibility. These dynamics underscore the importance of context-specific vector control strategies supported by continued entomological and genomic surveillance.

Overall, this nationwide analysis demonstrates that the 2La inversion is a major determinant of ecological adaptation, geographic distribution, and possibly range expansion in *An. coluzzii* across Nigeria. The combination of climatic selection, microhabitat variation, lineage mixing, and widespread heterozygosity emphasizes the need for ecozone-specific malaria vector control strategies. Continued genomic surveillance is essential, particularly in transitional regions and emerging heterozygosity hotspots, to anticipate adaptive shifts that may undermine current malaria control tools.

Conclusion

This study provides the first detailed nationwide characterization of 2La inversion polymorphism in *An. coluzzii* across Nigeria's ecological zones. The strong alignment between inversion frequency and eco-climatic gradients highlights the role of chromosomal rearrangements in promoting vector survival and ecological fitness. These adaptive patterns have significant implications for malaria control, as inversion-mediated resilience may influence resting behaviour, insecticide response, and vector persistence under climate variability. Integrating chromosomal inversion surveillance into entomological monitoring frameworks will be essential for designing ecologically tailored vector control strategies in Nigeria.

Abbreviations

WHO	World Health Organization
LLIN	Long–lasting insecticide net
IRS	Indoor residual pray
NMSP	Nigeria National Malaria Strategic Plan
NIMR	Nigerian institute of medical research
DNA	Deoxyribose nucleic acid
PCR	Polymerase chain reaction
IMP	Intentional mismatch primer
MgCl	Magnessium chloride
dNTP	Dinitrogen triphosphate
Taq	Thermus aquaticus
Bp	Base pair
DDT	Dichloro–diphenyl–trichloroethane

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s12942-026-00465-7.

Supplementary Material 1

Acknowledgements

The authors extend their appreciation to the numerous entomological technicians and mosquito collectors for their efforts during the nation-wide mosquito breeding sites sampling. We also appreciate the project staff at the molecular and vector control laboratory, Nigerian Institute of Medical Research for their assistance during the molecular analysis.

Author contributions

Conceptualization – AOA, OA, ASBSupervision – AOA, ASB, TAOInvestigation – AOA, OA, ASB, TAO, RTISoftware and visualization – ASBData collection – OA, OA, JW, LOB, RTIFormal analysis – ASB, AOAWriting original draft – AOA, OA, ASBWriting review and editing – AOA, OA, ASB, RTI, TAO, OA, JW, LOB, GA, SA, JC, STA.

Funding

The authors declare that this study was not funded.

Data availability

All data generated and analyzed during this study are included in this published article. The raw datasets are available from the corresponding author upon reasonable request.

Declarations

Ethics approval and consent to participate

Ethical clearance for this study was obtained from the Ethics review committee, Federal Ministry of Health (NG-23-011). All methods including mosquito larva collection and breeding, laboratory analysis and data management were performed in accordance with the 1964 Declarations of Helsinki.

Consent for publication

Not applicable.

Competing interests

The authors declare no competing interests.

Author details

[1]Molecular Entomology and Vector Control Unit, Nigerian Institute of Medical Research, Yaba, Lagos, Nigeria
[2]Department of Animal and Environmental Biology, Faculty of Basic and Applied Sciences, College of Science, Engineering and Technology, Osun State University, Osogbo, Nigeria
[3]Department of Biological Sciences, University of Abuja, Abuja, Nigeria
[4]Department of Zoology, Adamawa State University, Mubi, Adamawa State, Nigeria
[5]Department of Biological Sciences, College of Natural and Applied Sciences, Fountain University, Oke-Osun, Osogbo, Osun State, Nigeria
[6]Oxford Vaccine Group, Centre for Clinical Vaccinology and Tropical Medicine, Department of Paediatrics, University of Oxford, Churchill Hospital, Old Road, Headington, Oxford OX3 7LE, UK
[7]Centre for Tropical Medicine and Global Health, Nuffield Department of Medicine, University of Oxford, New Richards Building, Old Road Campus, OX3 7LG Oxford, UK
[8]Vector Research Group, Department of Parasitology, Noguchi Memorial Institute for Medical Research, University of Ghana, Legon, Accra, Ghana

Received: 28 November 2025 / Accepted: 9 March 2026

References

1. World Health Organization. World Malaria Report 2024. Geneva: WHO; 2024.
2. Adeogun AO, Babalola AS, Okoko OO, Oyeniyi TA, Omotayo A, Izekor RT, et al. Spatial distribution and ecological niche modeling of geographical spread of *Anopheles gambiae* complex in Nigeria using real-time data. Sci Rep. 2023;13:14412. https://doi.org/10.1038/s41598-023-40929-5.
3. Babalola AS, Adeogun AO, Thabet HS, TagEldin RA, Oyeniyi T, Adekunle O, et al. Geospatial modeling of geographical spread of *Aedes* species, in relation to climatic and topographical factors in Lagos State, Nigeria. PLoS Negl Trop Dis. 2025;19(2):e0012860. https://doi.org/10.1371/journal.pntd.0012860.
4. Love RR, Redmond SN, Pombi M, Caputo B, Petrarca V, Torre AD, et al. In silico karyotyping of chromosomally polymorphic malaria mosquitoes in the *Anopheles gambiae* complex. G3 (Bethesda). 2019;9(10):3249–62.
5. Liang J, Rose NH, Brusentsov II, Besansky NJ, Hahn MW. Chromosomal inversions and their potential impact on the evolution of arboviral vector *Aedes aegypti*. Genome Biol Evol. 2025;17(7):evaf118.
6. Kiam BC, Bouopda-Tuedom AG, Mbida Mbida JA, et al. Diversity of anopheline species and malaria transmission dynamics in high-altitude areas of western Cameroon. Malar J. 2025;24:251. https://doi.org/10.1186/s12936-025-05480-w.
7. Sinka ME, Bangs MJ, Manguin S, Coetzee M, Mbogo CM, Hemingway J, et al. The dominant Anopheles vectors of human malaria in Africa, Europe and the Middle East: occurrence data, distribution maps and bionomic précis. Parasit Vectors. 2010;3:117.
8. Ibrahim SS, Mukhtar MM, Muhammad A, Wondji CS. 2La paracentric chromosomal inversion and overexpressed metabolic genes enhance thermotolerance and pyrethroid resistance in the major malaria vector Anopheles gambiae. Biology (Basel). 2021;10(6):518.
9. Yi H, Devkota BR, Yu J-s, Oh K-c, Kim J, Kim H-J. The new strategies for mosquito control. Entomol Res. 2014;44:215–35. https://doi.org/10.1111/1748-5967.12084.
10. Reinhold JM, Lazzari CR, Lahondère C. Effects of the Environmental Temperature on Aedes aegypti and Aedes albopictus Mosquitoes: A Review. Insects. 2018;9(4):158. https://doi.org/10.3390/insects9040158.
11. Carbone G, Boiardi G, Infantino C, Cunico D, Esposito S. Vectors on the Move: How Climate Change Fuels the Spread of Arboviruses in Europe. Microorganisms. 2025;13(9):2034. https://doi.org/10.3390/microorganisms13092034.
12. Roy K, Basu R, Basu A. Climate change and neurotropic vector-borne viruses: addressing emerging threats through a One Health approach. mBio. 2025;16(11):e0088625. https://doi.org/10.1128/mbio.00886-25.
13. Ayala D, Acevedo P, Pombi M, Dia I, Boccolini D, Costantini C, et al. Chromosome inversions and ecological plasticity in the main African malaria mosquitoes. Evolution. 2017;71(3):686–701.
14. Adeogun AO, Popoola KOK, Brooke BD, Olakiigbe AK, Awolola ST. Polymorphic inversion 2La frequencies associated with ecotypes in populations of *Anopheles coluzzii* from Southwest Nigeria. Sci Afr. 2021;12:e00746.
15. Zoh DD, Yapi A, Adja MA, Guindo-Coulibaly N, Kpan DMS, Sagna AB, Adou AK, Cornelie S, Brengues C, Poinsignon A, Chandre F. Role of Anopheles gambiae s.s. and Anopheles coluzzii (Diptera: Culicidae) in Human Malaria Transmission in Rural Areas of Bouaké, in Côte d'Ivoire. J Med Entomol. 2020;57(4):1254–61. https://doi.org/10.1093/jme/tjaa001.
16. Coluzzi M, Sabatini A, Petrarca V, Di Deco MA. Chromosomal differentiation and adaptation to human environments in the *Anopheles gambiae* complex. Trans R Soc Trop Med Hyg. 1979;73(5):483–97.
17. Fouet C, Gray E, Besansky NJ, Costantini C. Adaptation to aridity in the malaria mosquito *Anopheles gambiae*: chromosomal inversion polymorphism and body size influence resistance to desiccation. PLoS ONE. 2012;7(4):e34841.
18. Rocca KA, Gray EM, Costantini C, Besansky NJ. 2La chromosomal inversion enhances desiccation resistance in. Anopheles gambiae Malar J. 2009;8:215.
19. Cassone BJ, Molloy MJ, Cheng C, et al. Divergent transcriptional response to thermal stress by *Anopheles gambiae* larvae carrying alternative arrangements of inversion 2La. Mol Ecol. 2011;20:2567–80.
20. Toure YT, Petrarca V, Traoré SF, Coulibaly A, Maiga HM, Sankaré O, et al. Ecological genetic studies in the chromosomal form Mopti of *Anopheles gambiae* s.str. in Mali, West Africa. Genetica. 1994;94(2–3):213–23.
21. Riehle MM, Guelbeogo WM, Gneme A, Eiglmeier K, Holm I, Bischoff E, et al. A cryptic subgroup of *Anopheles gambiae* is highly susceptible to human malaria parasites. Science. 2017;347(6220):989–93.
22. Adeogun AO, Olakiigbe AK, Popoola KOK, Awolola ST. Insecticide resistance and 2La inversion polymorphism in *Anopheles gambiae* populations from Nigeria. J Vector Borne Dis. 2019;56(3):222–8.
23. Coetzee M. Key to the females of Afrotropical Anopheles mosquitoes (Diptera: Culicidae). Malar J. 2020;19(1):70. https://doi.org/10.1186/s12936-020-3144-9.
24. Scott JA, Brogdon WG, Collins FH. Identification of single specimens of the Anopheles gambiae complex by the polymerase chain reaction. Am J Trop Med Hyg. 1993;49(4):520–9. https://doi.org/10.4269/ajtmh.1993.49.520.
25. White BJ, Santolamazza F, Kamau L, Pombi M, Grushko O, della Torre A, et al. Molecular karyotyping of the 2La inversion in *Anopheles gambiae*. Am J Trop Med Hyg. 2007;76(2):334–9.
26. Brooke BD, Kloke G, Hunt RH, Koekemoer LL, Taylor ME, Small G, et al. Insecticide resistance in the malaria vector *Anopheles gambiae*: chromosomal inversion 2La and resistance to pyrethroids. Med Vet Entomol. 2002;16(3):287–94.
27. Cheng C, Tan JC, Hahn MW, Besansky NJ. Systems genetic analysis of inversion polymorphisms in the malaria mosquito Anopheles gambiae. Proc Natl Acad Sci USA. 2018;115(30):E7005–14.
28. Kenig B, Kurbalija Novičić Z, Patenković A, Stamenković-Radak M, Anđelković M. Adaptive Role of Inversion Polymorphism of Drosophila subobscura in Lead Stressed Environment. PLoS ONE. 2015;10(6):e0131270. https://doi.org/10.1371/journal.pone.0131270.
29. Reeve J, Butlin RK, Koch EL, Stankowski S, Faria R. Chromosomal inversion polymorphisms are widespread across the species ranges of rough periwinkles (Littorina saxatilis and L. arcana). Mol Ecol. 2024;33(24):e17160. https://doi.org/10.1111/mec.17160.
30. Michelle MR, Tullu B, Awa G, et al. The *Anopheles* gambiae 2La chromosome inversion is associated with susceptibility to *Plasmodium falciparum* in Africa. eLife. 2017;6:e25813.

Publisher's note