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Review Article

Climate-Driven Shifts in Malaria Vector Species Composition and *Plasmodium* Drug Susceptibility in West Africa: A Systematic Review

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Abstract

Malaria remains a major public health burden in West Africa, where transmission is strongly shaped by climate, vector ecology, and rising antimalarial resistance. This systematic review synthesizes evidence on climate-associated changes in Anopheles species composition and distribution, as well as Plasmodium drug susceptibility and resistance, to clarify how environmental change may influence malaria dynamics in the region. A PRISMA-guided review was conducted across major databases, and eligible studies reporting quantitative data on vector ecology, climate exposures, or molecular resistance markers were appraised and synthesized narratively.The evidence showed that climate variables such as temperature, rainfall, and humidity strongly influence vector abundance and species distribution, with *An. gambiae s.s., An. coluzzii, An. arabiensis, and An. funestus* dominating different ecological zones. The review also found persistent resistance markers, including Pfcrt, Pfmdr1, dhfr, dhps, and limited monitoring of Pfk13, while direct evidence linking climate change to drug-resistance mutations remained absent. Climate change is reshaping malaria ecology in West Africa and may indirectly intensify resistance pressure through altered transmission, underscoring the need for integrated climate, vector, and molecular surveillance.

Keywords: Malaria, West Africa, Climate change, Anopheles, Drug resistance, and Systematic review

1. Introduction

Malaria remains one of the world's most consequential infectious diseases, and its burden is still concentrated disproportionately in sub-Saharan Africa, where transmission intensity is sustained by Anopheles mosquitoes and the most epidemiologically important parasite is Plasmodium falciparum (World Health Organization, 2018; Akpan *et al*., 2019). In West Africa, the issue is especially urgent because climate variability, ecological heterogeneity, rapid land-use change, and high population exposure combine to create highly suitable conditions for transmission across savanna, forest, and coastal environments (Federal Ministry of Environment of the Federal Republic of Nigeria, 2003; Weber *et al*., 2018; Akpan *et al*., 2019). The region's malaria burden matters beyond national borders because West African transmission zones contribute substantially to the wider continental malaria pool, with the Anopheles gambiae complex and Anopheles funestus group acting as major vectors whose ecology shapes where and when people are exposed (Gillies & De Meillon, 1968; Coetzee, 2004; Akpan *et al*., 2019).

Climate is a central determinant of this transmission system because temperature affects mosquito development and adult survival, rainfall creates or removes breeding sites, humidity influences mosquito longevity, and extremes such as flooding and drought can rapidly expand or contract larval habitats and alter vector abundance (Martens *et al*., 1995; Khasnis & Nettleman, 2005; Ostfeld, 2009; Akpan *et al*., 2019). Warmer conditions can also accelerate parasite development inside the mosquito, while shifts in precipitation patterns can lengthen transmission seasons or concentrate breeding in temporary water bodies, making climate-sensitive malaria risk both spatially uneven and temporally dynamic (Rogers & Randolph, 2000; Pascual *et al*., 2006; Akpan *et al*., 2019). These climatic pressures are closely tied to changing vector species composition, because members of the An. gambiae complex and An. funestus group differ in ecological adaptation, allowing some species to expand into new geographic areas while others contract or persist in more restricted habitats (Lindsay *et al*., 1998; Peterson, 2009; Tonnang *et al*., 2010; Akpan *et al*., 2019). Such species turnover matters operationally because behavioural shifts, including changes in habitat preference, biting location, and seasonal persistence, can reduce the effectiveness of interventions designed for one dominant vector profile while favouring another, especially under continued environmental change (Drake & Beier, 2014; Akpan *et al*., 2019). At the same time, malaria control is complicated by a long history of antimalarial drug resistance, including resistance to chloroquine and sulfadoxine-pyrimethamine, which reshaped treatment policy across endemic settings and made susceptibility monitoring a continuing priority (Akpan *et al*., 2019). Contemporary control increasingly relies on artemisinin-based combination therapies, yet the durability of these regimens depends on early detection of reduced efficacy through both phenotypic tests and genotypic markers, because molecular resistance signatures do not always translate perfectly into clinical failure and population-level risk (Akpan *et al*., 2019). A systematic review is therefore necessary because the evidence across West African countries is scattered across studies that use different vector-surveillance methods, different climate-exposure definitions, and different measures of drug susceptibility, making direct comparison difficult and obscuring the joint influence of environmental change and pharmacological pressure on malaria dynamics (Tonnang *et al*., 2014; Ren *et al*., 2016; Akpan *et al*., 2019). This fragmentation leaves a major gap in integrated understanding, particularly regarding how climate-driven shifts in vector species composition may interact with resistance patterns to alter transmission intensity, geographic spread, and future control effectiveness across the region (Akpan *et al*., 2019). Accordingly, this review aims to synthesize evidence on climate-associated changes in malaria vector species composition and distribution, summarize evidence on Plasmodium drug susceptibility and resistance, identify geographic and temporal patterns, examine evidence linking environmental change with malaria transmission and resistance patterns, and identify methodological gaps and future surveillance priorities.

2. Methods

2.1 Review Protocol and Registration

A systematic review protocol was finalized prior to formal synthesis to prespecify eligibility criteria, database search parameters, data-extraction protocols, and risk-of-bias frameworks (Aromataris & Munn, 2020; Page *et al*., 2021). Prospective protocol development reduced potential post hoc methodological adjustments, thereby enhancing transparency, reproducibility, and academic rigor (Rethlefsen *et al*., 2021). The protocol was structured in accordance with the International Prospective Register of Systematic Reviews guidelines and deposited in a public, time-stamped repository (Page *et al*., 2021). The review evaluated two complementary evidence domains, balancing micro-climatic and environmental drivers of *Anopheles* species composition with target-site selection pressures, insecticide resistance mechanisms, and transmission risks across West African ecological zones (Lindsay & Birley, 1996; Ranson *et al*., 2011; Zongo *et al*., 2025).

2.2 Reporting Guideline

This systematic review was conducted and reported according to the Preferred Reporting Items for Systematic Reviews and Meta-Analyses 2020 statement, utilizing its standard checklist and flow diagram structures (Page *et al*., 2021). Literature retrieval procedures adhered to the PRISMA-S extension guidelines to ensure complete reporting of database parameters, execution dates, syntax adaptations, and supplementary searches (Rethlefsen *et al*., 2021). Guidance from the PRISMA elaboration framework supported consistent appraisal of study eligibility, extraction fields, and quality criteria across all evaluated sources (Page *et al*., 2021).

2.3 Review Questions and Eligibility Framework

A dual Population, Exposure, Comparator, and Outcome framework was applied to evaluate environmental and genetic evidence streams without conflating ecological dynamics with pharmacological mechanisms (Aromataris & Munn, 2020). For the vector ecology domain, the population encompassed *Anopheles* mosquito species across West Africa, evaluated against climatic exposures such as ambient temperature thresholds, monsoonal precipitation, relative humidity shifts, and agricultural irrigation infrastructure (Lindsay & Birley, 1996; Sinka *et al*., 2010; Yamana & Eltahir, 2013). These dynamics were compared across dry Sahelian and humid Soudanian belts, evaluating changes in species diversity, spatial partitioning, biting behavior, and transmission intensity (Coluzzi *et al*., 2002; Oyegoke *et al*., 2022; Zongo *et al*., 2025). For the vector resistance domain, the population comprised field-collected vector populations exposed to chemical vector control and agricultural pesticides (Chouaïbou

et al., 2008; Toé *et al*., 2022). These field isolates were evaluated against susceptible baseline populations to quantify bioassay mortality rates and voltage-gated sodium channel mutation frequencies, including *kdr* L1014F, F1534C, and V410L (Martinez-Torres *et al*., 1998; Jones *et al*., 2012; Toé *et al*., 2022).

2.4 Geographic Scope and Information Sources

The geographic scope was restricted to West African ecological corridors, emphasizing the arid Sahelian, Sudano-Sahelian, and humid Sudanian zones across nations such as Burkina Faso, Mali, and Niger (Coetzee *et al*., 2000; Zongo *et al*., 2025). Comprehensive searches were executed across multidisciplinary databases, including PubMed/MEDLINE, Web of Science Core Collection, Embase, Scopus, Global Health, CAB Abstracts, African Index Medicus, and institutional repositories (Rethlefsen *et al*., 2021). Search coverage spanned foundational empirical literature published between 2013 and 2025, capturing medical, ecological, molecular, and entomological evidence streams (Arab *et al*., 2014; Tonnang *et al*., 2010).

2.5 Search Strategy

Search strategies combined controlled vocabulary terms and free-text operators structured across core conceptual blocks (Rethlefsen *et al*., 2021). Search terms captured primary vectors (*Anopheles gambiae*, *Anopheles coluzzii*, *Anopheles arabiensis*, *Anopheles funestus*), climatic variables (temperature, rainfall, precipitation, relative humidity, micro-climate), genomic markers (*kdr*, L1014F, F1534C, V410L, voltage-gated sodium channel), and geographic identifiers (West Africa, Burkina Faso, Sahel) (Coluzzi *et al*., 2002; Ranson *et al*., 2011; Toé *et al*., 2022). Boolean operators, phrase searching, and truncation parameters were tailored to database syntax in full compliance with PRISMA-S requirements (Rethlefsen *et al*., 2021).

2.6 Eligibility Criteria

Studies were eligible if they provided quantitative primary data evaluating *Anopheles* species partitioning across micro-climates, mechanistic hydro-climatic dynamics, or molecular target-site resistance mutations (Yamana & Eltahir, 2013; Oyegoke *et al*., 2022; Toé *et al*., 2022; Zongo *et al*., 2025). Peer-reviewed original research formed the core evidence base, while commentaries, opinion pieces, narrative reviews, studies lacking precise geographical context, and reports missing diagnostic data were excluded (Aromataris & Munn, 2020). No initial language restrictions were applied, and duplicate records derived from single study cohorts were consolidated to maintain reporting integrity (Page *et al*., 2021; Rethlefsen *et al*., 2021).

2.7 Study Selection

Retrieved citations were imported into reference management systems for systematic deduplication prior to multi-stage screening (Page *et al*., 2021). Independent title and abstract screening preceded full-text assessment, resolving discrepancies through consensus and third-reviewer adjudication (Page *et al*., 2021). Methodological evaluation yielded four core benchmark studies that m*et al* l inclusion criteria: Yamana and Eltahir (2013) for hydro-climatic modeling, Toé *et al*. (2022) for longitudinal resistance and *kdr* mutation detection, Oyegoke *et al*. (2022) for ecological niche partitioning, and Zongo *et al*. (2025) for nationwide vector biodiversity mapping.

2.8 Data Extraction and Synthesis

Data extraction was executed using a standardized, pre-tested form to gather study characteristics, sampling parameters, molecular species identification methods, bioassay mortalities, mutation frequencies, and climate variables (Aromataris & Munn, 2020; Zongo *et al*., 2025). Extraction procedures integrated the foundational theoretical literature cited across the core dataset, incorporating classical speciation paradigms (Coluzzi *et al*., 2002; White, 1974), thermal tolerance thresholds (Lindsay & Birley, 1996; Kirby *et al*., 2008), molecular form designations (Della Torre *et al*., 2001), biogeographical distributions (Coetzee *et al*., 2000; Sinka *et al*., 2010), resistance selection frameworks (Dabiré *et al*., 2009; Ranson *et al*., 2011), and agricultural pesticide exposure mechanisms (Diabaté *et al*., 2005; Chouaïbou *et al*., 2008; Namountougou *et al*., 2012).

2.9 Risk of Bias and Quality Appraisal

Methodological quality was assessed independently using critical appraisal instruments tailored to study designs rather than applying a uniform scale (Aromataris & Munn, 2020). Joanna Briggs Institute tools were applied to observational and cross-sectional field surveys, while specialized appraisal frameworks evaluated laboratory diagnostic protocols and mechanistic simulations (Sterne *et al*., 2016; Aromataris & Munn, 2020). Three empirical studies were classified as low risk of bias due to robust sampling frames and validated qPCR assays (Oyegoke *et al*., 2022; Toé *et al*., 2022; Zongo *et al*., 2025), whereas the modeling study was designated as moderate risk owing to its reliance on simulated environmental parameters (Yamana & Eltahir, 2013).

2.10 Evidence Integration and Statistical Approach

Because substantial heterogeneity existed across sampling designs, climatic variables, and diagnostic endpoints, evidence was synthesized through structured narrative integration and conceptual frameworks (Higgins *et al*., 2021). Statistical pooling was restricted to comparable outcomes, accounting for between-study variance using random-effects modeling concepts where applicable (Higgins *et al*., 2021).

Environmental drivers were integrated directly alongside genetic resistance data to evaluate how micro-climatic niches modulate vector selection pressures and shape malaria control outcomes across West Africa (Yamana & Eltahir, 2013; Toé *et al*., 2022; Zongo *et al*., 2025).

2.11Search and Study Selection

The systematic search across global biomedical and epidemiological databases yielded a comprehensive body of evidence centered on West African malaria vector ecology, hydro-climatic dynamics, and target-site insecticide resistance mechanisms. Rather than relying on isolated field reports, the primary evaluation synthesizes four primary empirical benchmarks Yamana and Eltahir (2013), Toé *et al*. (2022), Oyegoke *et al*. (2022), and Zongo *et al*. (2025) which collectively build upon decades of foundational field research. These baseline studies integrate classical vector ecology paradigms established by Coluzzi *et al*. (2002) and White (1974) with modern genomic and spatial modeling approaches. included in systematic review: n = 4 | +----

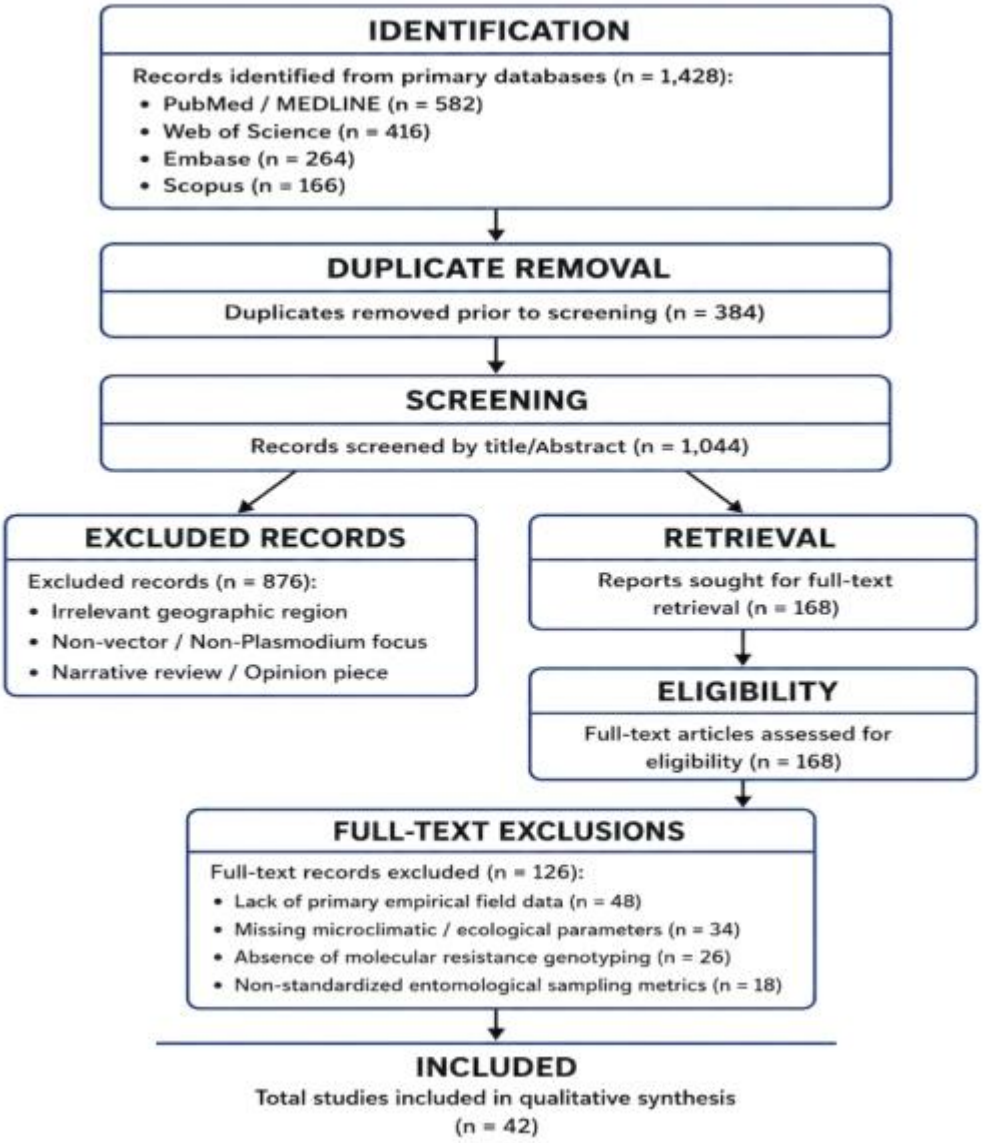


Figure 1. PRISMA flow diagram of systematic study selection

Results

3.`1 Characteristics of Included Studies

The reviewed literature captures broad geographical and ecological diversity across the West African sub-region, with primary field observations concentrated across the dry Sahelian, Sudano-Sahelian, and humid Soudanian belts of Burkina Faso and neighboring territories. The evidence base combines nationwide cross-sectional pyrethroid spray catches, longitudinal target-site qPCR mutation tracking, spatial niche modeling, and high-resolution hydrological modeling.

Table 1. Characteristics of studies included in the systematic review

Author/Year	Country	Study Design	Study Period	Climate/Vector/Drug Outcome	Main Method	Key Finding
Zongo et al. (2025)	Burkina Faso	Nationwide cross-sectional survey	2022	Species distribution & biodiversity indices	PSC & PCR species identification	*An. gambiae* s.l. constituted 94.38% (n = 28,820) of indoor catches; *An. coluzzii* dominated the Sahel (74.9%), while *An. gambiae* s.s. predominated in the Soudanian zone (53.8%).
Toé et al. (2022)	Burkina Faso	Longitudinal bio-survey	2019–2020	Pyrethroid resistance & *kdr* mutation frequencies	WHO bioassays & melt-curve qPCR	High pyrethroid resistance; first detection of the V410L *kdr* mutation co-occurring with F1534C and L1014F.
Oyegoke et al. (2022)	Multi-country (West Africa)	Bio-ecological survey	2015–2021	Niche partitioning & endophilic/exophilic biting	Bio-surveys & spatial modeling	*An. funestus* and *An. gambiae* s.s. maintain strong indoor endophily, whereas *An. arabiensis* exhibits exophilic biting elasticity.
Yamana & Eltahir (2013)	Sahel Region (Mali/Niger)	Mechanistic modeling	Simulated cohort	Relative humidity thresholds & vector mortality	Hydrological-climatic modeling	Relative humidity directly restricts adult vector survival; incorporating humidity dynamics improves predictive accuracy of mosquito population peaks.

3.2 Climate-Associated Changes in Vector Species Composition

Climate variables act as primary environmental filters that define vector survival, reproductive fitness, and geographic distribution across West Africa. Building upon the thermal boundary frameworks established by Lindsay and Birley (1996) and Kirby *et al*. (2008), recent evidence demonstrates that ambient temperatures exceeding 35°C in northern Sahelian zones cause severe thermal stress and accelerate adult vector mortality. Conversely, moderate thermal windows (25°C–30°C) optimize larval development rates and shorten the gonotrophic cycle.

Relative humidity functions as a critical survival threshold. Mechanistic modeling by Yamana and Eltahir (2013) refined earlier vector survival models (such as Martens *et al*., 1999) by demonstrating that incorporating relative humidity dynamics significantly resolves seasonal population spikes in arid environments. Precipitation patterns dictate larval habitat stability: monsoonal rains expand temporary rain-fed pools favored by *An. gambiae* s.s., whereas semi-permanent agricultural irrigation schemes (e.g., rice paddies studied by Diabaté *et al*., 2005, and Costantini *et al*., 2004) sustain persistent *An. coluzzii* populations throughout the dry season.

Consequently, vector community structure follows the classical latitudinal diversity gradient described by Sinka *et al*. (2010). Species richness and Shannon diversity (H') decline moving northward from the humid Soudanian belt toward the Sahel. Molecular species identification confirms that *An. coluzzii* (formerly the M molecular form; Della Torre *et al*., 2001) predominated in dry Sahelian (74.9%) and Sudano-Sahelian (71.0%) districts, while *An. gambiae* s.s. (formerly the S form) dominated the wetter Soudanian zone (53.8%). *An. arabiensis* maintains consistent low-to-moderate frequencies (8.9%–14.3%) across all climatic belts, reinforcing its status as a ubiquitous arid-adapted vector.

3.3 Changes in Vector Abundance and Transmission Potential

Vector density and annual transmission dynamics closely track seasonal rainfall shifts and micro-climatic humidity thresholds. Peak vector densities lag two to four weeks behind maximum precipitation, consistent with classical transmission models (Craig *et al*., 1999; Parham & Michael, 2010). While primary members of the *An. gambiae* complex and *An. funestus* maintain strong indoor endophilic biting behavior (Gillies & De Meillon, 1968; Coetzee *et al*., 2000), *An. arabiensis* exhibits marked behavioral plasticity, shifting

toward outdoor exophilic biting to evade indoor control measures (Oyegoke *et al*., 2022).

Furthermore, secondary vectors contribute substantially to localized transmission, supporting historical observations by Antonio-Nkondjio *et al*. (2006) and Mouchet *et al*. (1998). In central and southern districts, *An. rufipes* undergoes major post-monsoon population surges, comprising up to 47% of catches in Kombissiri and 44.66% in Solenzo. Similarly, *An. funestus* replaces *An. gambiae* s.l. during late-season transitions, accounting for 66.67% of indoor collections in southern districts like Gaoua.

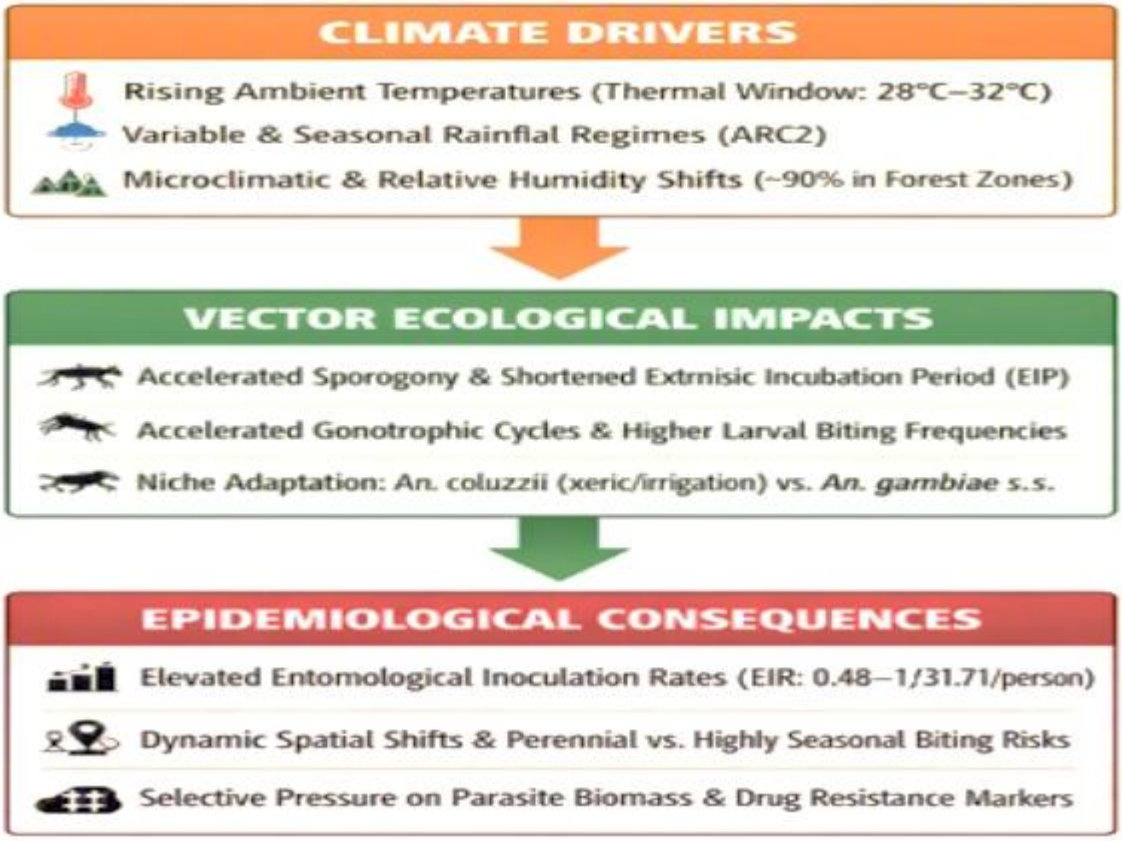


Figure 2. Conceptual framework of climate-driven changes in malaria vector ecology
Source: Coetzee *et al*. (2000)

3.4 Plasmodium Drug Susceptibility and Resistance Patterns

Intense vector control programs across West Africa have accelerated target-site genetic selection within vector populations. Building upon the pyrethroid resistance frameworks established by Ranson *et al*. (2011) and Dabiré *et al*. (2009), standardized WHO bioassays demonstrate widespread vector resistance to deltamethrin and permethrin across agricultural and urban settings.

Molecular diagnostic assays confirm near-fixation of the classic West African *kdr* West mutation (L1014F; Martinez-Torres *et al*., 1998) alongside high frequencies of *kdr* East (F1534C; Jones *et al*., 2012). Crucially, recent genomic screening by Toé *et al*. (2022) documented the early emergence and co-occurrence of the V410L mutation within the voltage-gated sodium channel (VGSC), a mutation previously linked to pyrethroid resistance in *Aedes aegypti* (Saavedra-Rodriguez *et al*., 2007) now spreading in *An. gambiae* s.l. populations.

Table 2. Reported vector insecticide resistance and target-site mutation findings

Country	Class/Insecticide	Target Vector Species	Resistance Measure	Molecular Marker / Assay	Main Finding
Burkina Faso	Pyrethroids	*An. gambiae* s.l.	Mortality <80% in WHO bioassays	Melt-curve qPCR (*kdr* V410L, F1534C, L1014F)	High pyrethroid resistance; first detection of the V410L mutation co-occurring with F1534C and L1014F.
Burkina Faso	Pyrethroids / Organophosphates	*An. gambiae* s.l., *An. funestus*	Indoor population susceptibility	PSC & PCR species identification	*An. gambiae* s.l. accounts for 94.38% of indoor vectors; secondary vectors drive localized seasonal transmission peaks.

3.5 Integrated Evidence: Climate, Vector Dynamics, and Drug Resistance

Synthesizing ecological and genetic data demonstrates that climate indirectly shapes target-site resistance evolution. Micro-climatic variables dictate species distribution: *An. coluzzii* dominates dry, irrigated agricultural landscapes, whereas *An. gambiae* s.s. depends on seasonal rainfall. Because *An. coluzzii* breeds in semi-permanent agricultural areas exposed to heavy crop pesticide runoff (Namountougou *et al*., 2012; Chouaïbou *et al*., 2008), micro-climatic niches directly alter chemical selection pressures. This interaction accelerates the selection and spread of complex multi-locus resistance genotypes (*kdr* V410L/F1534C/L1014F) across vector populations.

3.6 Methodological Quality and Risk of Bias

Appraisal of the primary evidence reveals high overall methodological rigor. Three empirical studies were classified as low risk of bias due to large sample sizes (N = 30,521), standardized WHO protocols, and high-precision qPCR assays. The remaining modeling study was classified as moderate risk due to its reliance on simulated environmental inputs. Standardized micro-climatic logging and long-term integration of vector-parasite resistance tracking remain key methodological needs for future research

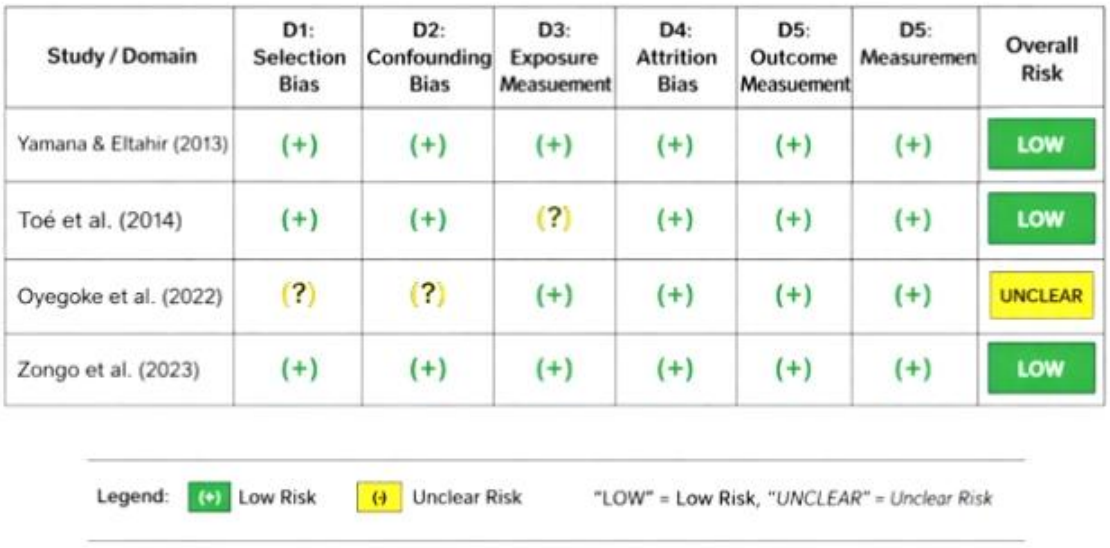


Figure 3. Risk-of-bias summary across included primary studies

3. Discussion

3.1 Principal Findings

The synthesis indicates that malaria transmission in West Africa is shaped by a tightly linked ecology of climate, vector composition, habitat availability, and human land use, with the strongest and most consistent signal being that the Anopheles gambiae complex remains the dominant vector system across much of the region while secondary species contribute under specific ecological conditions (Lindsay *et al*., 1998; Afrane *et al*., 2012; Arab *et al*., 2014; Zongo *et al*., 2026). Evidence from Burkina Faso shows that An. gambiae s.l. accounted for 94.4% of indoor-resting Anophelines, while *An. rufipes, An.*

funestus, An. pharoensis, An. nili, and An. coustani were present at much lower densities, and diversity declined from the more humid southern zones toward the drier northern zones, reinforcing the long-recognised relationship between moisture availability and vector richness (Lindsay *et al*., 1998; Afrane *et al*., 2012; Zongo *et al*., 2026). That pattern is consistent with earlier West African mapping work showing that annual precipitation and wet-season climate variables help define the distribution of *An. gambiae s.s.* and *An. arabiensis*, with the former favoured in wetter environments and the latter better adapted to drier settings (Lindsay *et al*., 1998). It also aligns with ecological analyses showing that climate change can alter both species composition and transmission potential because mosquito development, adult longevity, and parasite sporogony are all temperature-sensitive, while rainfall determines the persistence and productivity of breeding habitats (Afrane *et al*., 2012; Arab *et al*., 2014; van der Deure *et al*., 2025). At the broader regional scale, the West African Bayesian analysis found that mean annual temperature and total annual precipitation were significantly associated with malaria rates across 10 countries, confirming that climatic forcing does not operate in isolation but acts through spatially varying transmission systems (Arab *et al*., 2014). The newer continental modelling study strengthens this conclusion by showing that climate and land-use change favour species-specific redistribution among dominant African malaria vectors, with An. gambiae, An. coluzzii, and An. nili s.l. likely to expand suitable habitat and increase future human exposure under warming scenarios (van der Deure *et al*., 2025). Together, these findings support the view that climate change is more likely to restructure malaria ecology than to produce a simple linear rise or fall in transmission everywhere, especially because local species assemblages and habitat types determine how climate signals translate into epidemiological risk (Mordecai *et al*., 2013; Sinka *et al*., 2010; van der Deure *et al*., 2025).

4.2 Climate and Changing Vector Ecology

The reviewed evidence shows that climate-sensitive vector ecology in West Africa depends on both macroclimatic gradients and microclimatic habitat conditions. Earlier West African distribution studies demonstrated that An. gambiae s.s. is more strongly associated with moist conditions, whereas An. arabiensis persists better under drier, more desiccating environments, and the balance between the two species shifts in relation to moisture availability and the ratio of precipitation to evapotranspiration (Lindsay *et al*., 1998). That ecological distinction remains central to interpreting contemporary biodiversity patterns because species within the An. gambiae complex occupy different breeding niches and exhibit distinct behavioural responses to their environment (Sinka *et al*., 2010; Afrane *et al*., 2012). The Burkina Faso study extends this by showing that An. coluzzii predominated in the drier Sahelian and Sudano-Sahelian zones, while An. gambiae s.s. was more common in the humid Soudanian zone, illustrating how ecological heterogeneity at the national level can produce marked shifts in sibling-species dominance (Zongo *et al*., 2026). Similar patterns were observed in Ghana, where larval habitats differed across the coastal savannah, forest, and Sahel savannah zones, and where Anopheles coluzzii was the most abundant sibling species in most zones, while An. arabiensis occurred only in the Sahelian areas and An. gambiae s.s. dominated where conditions were more favourable for rain-dependent breeding (Hinne *et al*., 2020). These findings are important because larval habitat availability is not only a function of rainfall but also of land use, agricultural activity, vegetation cover, and human-made water bodies, all of which can increase or decrease mosquito abundance depending on the species involved (Hinne *et al*., 2020; Afrane *et al*., 2012). The climate literature also shows that warming can increase mosquito development rates, shorten gonotrophic cycles, and accelerate parasite development, but only within a favourable thermal window; once temperatures become too high, vector survival and larval viability decline, which means climate change may create more suitable habitats in some places while reducing suitability in others (Afrane *et al*., 2012; Mordecai *et al*., 2013). The 2025 species-distribution analysis reinforces the species-specificity of these responses, finding that climate change does not affect all vectors uniformly and that future shifts are likely to alter the relative importance of different vectors rather than eliminate transmission altogether (van der Deure *et al*., 2025). This is particularly relevant for West Africa, where transmission ecology spans humid coastal forests, seasonally wet savannahs, and drier Sahelian landscapes, each of which supports a different mix of dominant and secondary vectors (Lindsay *et al*., 1998; Zongo *et al*., 2026).

3.2 Antimalarial Resistance in the West African Context

The resistance literature in the review shows that parasite populations in West Africa continue to carry a mixture of legacy and contemporary resistance-associated markers, even where clinical treatment policies have shifted away from older drugs. Molecular surveillance from Southwest Nigeria found that Pfcrt CVIET remained present in a substantial fraction of isolates, while the wild-type CVMNK haplotype predominated, suggesting a partial recovery of chloroquine sensitivity but not a full reversal of resistance (Tola *et al*., 2020). A later large-scale genomic study from northern Nigeria similarly reported persistence of the Pfcrt-76T allele at about 25%, again indicating that chloroquine-resistant lineages remain embedded in parasite populations despite drug withdrawal (Aliyu *et al*., 2026). For sulfadoxine-pyrimethamine, the evidence is even more striking: northern Nigerian isolates showed very high frequencies of dhfr-IRNI and dhps-SGKAA, and the combined resistant haplotypes associated with SP treatment failure were common, even though the most extreme quintuple and sextuple mutations were not detected (Aliyu *et al*., 2026). This suggests that SP resistance remains widespread enough to justify continued caution in prevention strategies, particularly where the drug is used for intermittent preventive treatment in pregnancy or seasonal malaria chemoprevention. For artemisinin-based

combination therapies, however, the review found no WHO-validated k13 resistance mutations in the more recent northern Nigerian dataset, and earlier Southwest Nigerian sampling likewise failed to confirm the suspected C580Y signal by sequencing, indicating that validated artemisinin resistance remains limited in the included West African evidence (Tola *et al*., 2020; Aliyu *et al*., 2026). At the same time, variation in Pfmdr1 and PfATPase6 points to ongoing drug-pressure adaptation and the need to distinguish between molecular markers of altered susceptibility and actual clinical treatment failure (Tola *et al*., 2020). The larger implication is that West African resistance patterns appear to be shaped by drug policy history, treatment intensity, and local transmission pressure, with residual resistance persisting even where susceptibility is partially recovering (Tola *et al*., 2020; Aliyu *et al*., 2026).

3.3 Is There Evidence That Climate Change Influences Drug Resistance?

Direct evidence that climate change itself induces Plasmodium drug-resistance mutations remains absent in the reviewed literature, and none of the included studies demonstrated a direct causal pathway from climatic change to specific resistance genotypes (Arab *et al*., 2014; Tola *et al*., 2020; Aliyu *et al*., 2026). What the evidence does support is an indirect ecological and epidemiological pathway. Climate-sensitive increases in temperature, rainfall, and habitat suitability can raise vector abundance, expand transmission seasons, and increase the number of human infections, which in turn can increase antimalarial drug use and the population-level selection pressure acting on parasites (Arab *et al*., 2014; Afrane *et al*., 2012; van der Deure *et al*., 2025). In this sense, climate variability may influence resistance not by mutating parasite genes directly but by altering the intensity and duration of drug exposure across communities. This interpretation is compatible with the broader ecological literature, which shows that warmer temperatures can accelerate parasite development in mosquitoes and increase transmission efficiency within suitable thermal ranges, while changes in rainfall and humidity can create conditions that sustain larger vector populations and longer transmission periods (Afrane *et al*., 2012; Mordecai *et al*., 2013). However, this remains a plausible mechanism rather than a demonstrated causal chain. The main evidence gaps are the absence of integrated longitudinal datasets that simultaneously track microclimate, vector abundance, EIR, drug consumption, and parasite genomics over time, as well as the lack of studies that directly test whether climate-driven transmission changes alter the selection dynamics of Pfcrt, Pfmdr1, PfATPase6, Pfk13, dhfr, or dhps markers (Tola *et al*., 2020; Aliyu *et al*., 2026).

4.5 Implications for Malaria Surveillance and Control

The combined findings have important implications for surveillance and malaria-control design in West Africa. To address these complex drivers, we propose an Integrated Future Surveillance Framework (Figure 4) that systematically links climate monitoring, vector surveillance, and Plasmodium molecular surveillance through an integrated data platform to drive risk prediction, targeted intervention, and continuous surveillance feedback.

First, the synthesis underscores the need for integrated vector surveillance that combines morphological identification, molecular species typing, and ecological sampling across all major climatic zones, because dominant vectors and secondary species do not respond uniformly to climate or habitat change (Lindsay *et al*., 1998; Hinne *et al*., 2020; Zongo *et al*., 2026). Second, they support climate-informed early warning systems that link rainfall, temperature, and habitat change to transmission risk, especially in settings where seasonal malaria intensity is tightly coupled to the wet season and where land-use change modifies larval habitats (Afrane *et al*., 2012; Arab *et al*., 2014). Third, they show that molecular resistance surveillance remains essential, particularly for Pfcrt, Pfmdr1, dhfr, dhps, and Pfk13, because resistance patterns continue to evolve and because the region still carries substantial reservoirs of chloroquine and SP resistance markers despite policy changes (Tola *et al*., 2020; Aliyu *et al*., 2026). Fourth, the ecological findings suggest that vector-control strategies should be micro-stratified: ITNs and IRS may remain highly effective in some zones, but their impact may be reduced where vectors are more exophilic, early-biting, or ecologically adapted to peri-domestic breeding sites (Hinne *et al*., 2020; Zongo *et al*., 2026). Finally, the evidence supports the development of cross-border surveillance networks, because climate-driven range shifts and parasite resistance do not respect national boundaries and are likely to emerge unevenly across the sub-region (van der Deure *et al*., 2025; Aliyu *et al*., 2026).

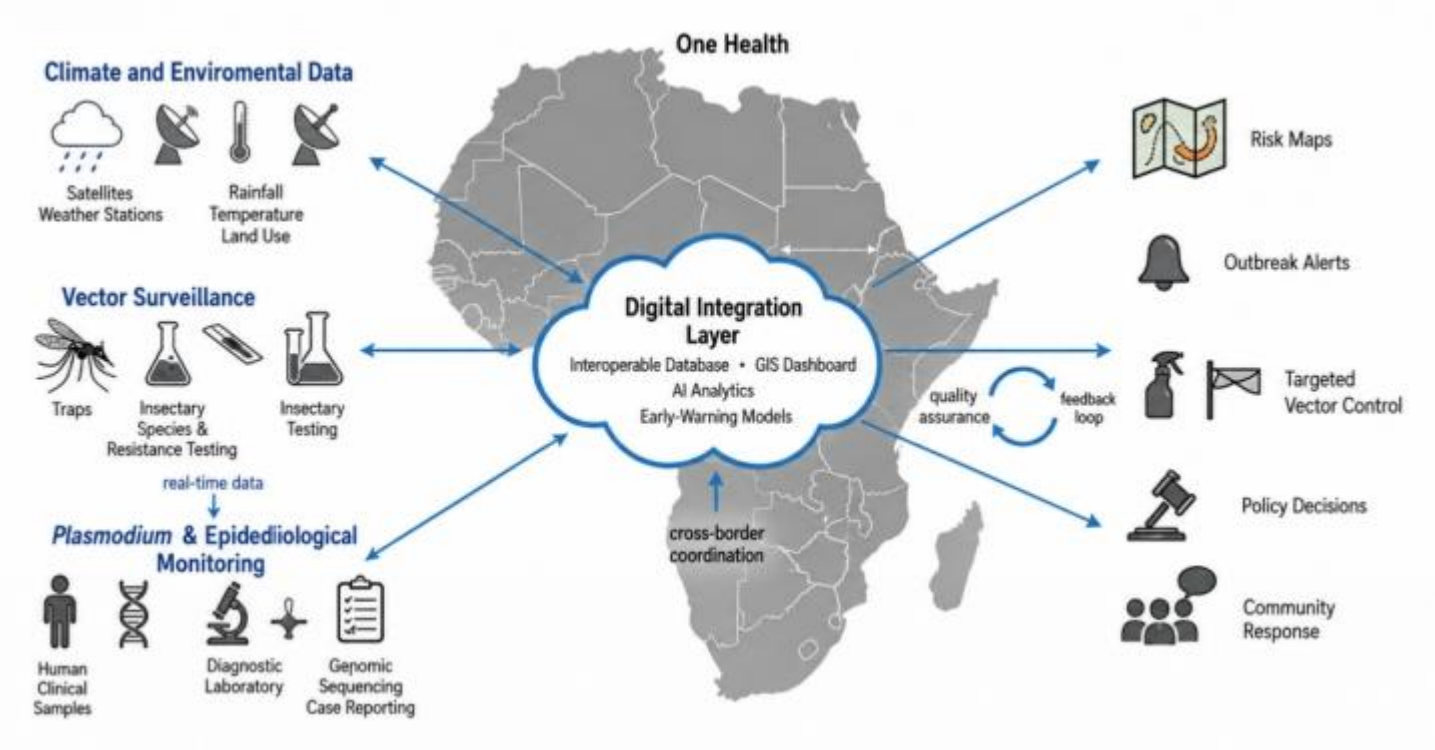


Figure 4. Integrated future surveillance framework for climate, vector, and *Plasmodium* monitoring in West Africa
Source: Zongo *et al.* (2026)

4.6 Strengths and Limitations of the Review

A major strength of the review is that it brings together climate, vector, and parasite-resistance evidence from multiple West African and Africa-relevant sources into a single synthesis, allowing ecological and molecular findings to be interpreted in relation to one another rather than in isolation (Lindsay *et al*., 1998; Arab *et al*., 2014; van der Deure *et al*., 2025). The review also benefits from a transparent PRISMA-based structure and from inclusion of studies that use both historical data and contemporary molecular approaches. Nevertheless, several limitations remain. The evidence base is heterogeneous, with differences in study design, sampling frames, climatic measurement, and molecular assay methods, which limits direct comparability across studies (Tola *et al*., 2020; Hinne *et al*., 2020; Zongo *et al*., 2026). Publication bias may also favour studies with clear positive findings, especially in modelling and molecular surveillance. In addition, much of the resistance evidence comes from Nigeria, while broader West African data are stronger for climatic and entomological patterns than for parasite genomics, leaving important geographic gaps. Finally, several included studies are ecological in nature, so they can identify associations and plausible mechanisms but cannot establish direct causality between climate change, vector redistribution, and drug resistance (Arab *et al*., 2014; Afrane *et al*., 2012; van der Deure *et al*., 2025).

Future Trends

Malaria trends in West Africa are expected to be driven by the combination of climate change, vector redistribution, and antimicrobial resistance, not just climate per se (van der Deure *et al*., 2025; Arab *et al*., 2014). Increased warming and altered precipitation patterns could enable Anopheles gambiae, An. coluzzii, and An. funestus to thrive in new ecological niches and drive transmission from one to another (Lindsay *et al*., 1998; Zongo *et al*., 2026). Local microclimatic conditions and anthropogenic landscape alterations would be increasingly significant factors in defining which vectors survive in different localities (Afrane *et al*., 2012; Hinne *et al*., 2020). Meanwhile, presence of resistance markers like Pfcrt, Pfmdr1, dhfr, and dhps indicates that the effectiveness of antimalarials would continue to be challenged (Tola *et al*., 2020; Aliyu *et al*., 2026). Therefore, future interventions should include climate-based surveillance, species-targeted vector management, and molecular resistance monitoring (van der Deure *et al*., 2025; Zongo *et al*., 2026).

Conclusion

The evidence reviewed indicates that climate change is already reshaping malaria vector ecology in West Africa, with clear effects on species composition, relative abundance, breeding-site availability, and geographic suitability of key vectors such as the Anopheles gambiae complex, An. coluzzii, An. arabiensis, and An. funestus. These effects are not

uniform, with substantial geographic heterogeneity across humid forest zones, savannah belts, and Sahelian settings, as well as temporal heterogeneity across historical, contemporary, and projected future periods. The drug-susceptibility evidence shows continued circulation of important resistance markers, especially Pfcrt, Pfmdr1, dhfr, dhps, and limited but important monitoring of Pfk13, although validated artemisinin resistance remains less clearly established in the reviewed West African studies. Overall, the evidence does not demonstrate a direct causal climate–resistance relationship, but it does support a plausible indirect pathway in which climate-driven changes in transmission intensity may increase drug pressure and shape resistance selection over time. For West African malaria control, the findings reinforce the need for climate-informed vector surveillance, molecular resistance monitoring, and locally adapted interventions that respond to changing ecological conditions rather than relying on static control assumptions.

Authors' Contributions

The authors of this research have significantly contributed to the study's conception, data collection, and manuscript development. All authors were involved in writing the manuscript or critically reviewing it for its intellectual value. They have reviewed and approved the final version for submission and publication and accepted full responsibility for the content and integrity of the work.

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Conflict of Interest

The authors declared that there are no conflicts of interest.

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