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Geographical distribution and temporal evolution of insecticide resistance in malaria vectors in the Democratic Republic of the Congo, 2016–2025: A systematic review and meta-analysis

Sévérin N'Do [1,*], Bazoma Bayili [2], Jacques 1er Jumeau Kaboré [3,4], Janvier Balikubiri Bandibabone [5], Bertin Musaka Zawadi [5] and Bantuzeko Chimanuka [5,6]

[1] *Research Laboratory on Infectious and Parasitic Diseases (LR-MIP), Western Regional Directorate, Health Sciences Research Institute (IRSS-DRO), National Centre for Scientific and Technological Research (CNRST), 01 P.O. Box 545, Bobo-Dioulasso 01, Burkina Faso.*
[2] *Laboratory of Environment and Forest, Agroforestry and Aquatic Ecosystems (LaboEcoFAA), Western Regional Directorate for Environmental and Agricultural Research, Environment and Agricultural Research Institute (INERA), National Centre for Scientific and Technological Research (CNRST), 01 P.O. Box 910, Bobo-Dioulasso 01, Burkina Faso.*
[3] *Laboratory for Studies and Research on Natural Resources and Environmental Sciences (LERNSE), Nazi BONI University (UNB), 01 P.O. Box 1091, Bobo-Dioulasso 01, Burkina Faso.*
[4] *Vector-Borne Diseases and Biodiversity Research Unit (UMaVeB), International Centre for Research and Development on Livestock in the Subhumid Zone (CIRDES), 01 P.O. Box 454, Bobo-Dioulasso 01, Burkina Faso.*
[5] *Medical Entomology and Parasitology Laboratory, Lwiro Natural Sciences Research Centre (CRSN/Lwiro), South Kivu, Democratic Republic of the Congo.*
[6] *Faculty of Medicine and Pharmacy, Official University of Bukavu (UOB), South Kivu, P.O. Box 570, Bukavu, Democratic Republic of the Congo.*

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Abstract

Background: The Democratic Republic of the Congo (DRC) bears 12.6% of global malaria cases and 11.3% of malaria-related deaths. Vector control through long-lasting insecticidal nets (LLINs) and indoor residual spraying (IRS) relies almost exclusively on pyrethroids, yet insecticide resistance in *Anopheles* malaria vectors increasingly threatens its effectiveness. No national-level synthesis has previously aggregated resistance data across all DRC provinces.

Methods: We conducted a systematic review and meta-analysis following PRISMA 2020 guidelines. Six electronic databases and grey literature sources were searched for studies reporting WHO standard bioassays, CDC bottle bioassays, or molecular resistance genotyping in *An. gambiae* s.l. or *An. funestus* group from the DRC (2016–2025). Of 138 records identified, 35 were retained; 19 primary field studies contributed to the quantitative synthesis.

Results: Pyrethroid resistance was confirmed at every site tested nationwide. Deltamethrin mortality at Ndjili-Brasserie (Kinshasa) declined from 67.2% in 2015 to 12.2% in 2021. An east-west gradient was documented: vgsc-L1014F near-fixation in western DRC (≥98.3%) and L1014S predominating in eastern provinces. Metabolic resistance (CYP6P9a/b, GSTe2) was widespread in both vector species. Susceptibility to organophosphates and carbamates was largely retained, though low-frequency ace-1 mutations signal early erosion. PBO-pyrethroid nets outperformed standard nets in a field trial, but PBO synergy loss was documented at all eight nationwide survey sites.

Conclusions: Pyrethroid resistance in DRC malaria vectors is geographically universal, molecularly heterogeneous, and temporally intensifying. Accelerated deployment of next-generation nets and evidence-based IRS rotation are urgently

* Corresponding author: Sévérin N'Do

required. A standardised national resistance monitoring network covering all 26 provinces is essential to guide vector control under the National Malaria Strategic Plan 2024–2028.

Keywords: Insecticide resistance; Malaria vectors; Democratic Republic of the Congo; Systematic review; Meta-analysis

1. Introduction

The Democratic Republic of the Congo (DRC) bears one of the world's most severe malaria burdens. According to the World Health Organization (WHO) World Malaria Report 2024, the DRC accounted for 12.6% of global malaria cases and 11.3% of all malaria-related deaths, ranking second globally after Nigeria, with 35.1 million cases and 24,880 deaths recorded in 2023 alone [1]. Malaria disproportionately affects children under five and pregnant women, and represents the leading cause of morbidity and mortality in the country. Vector control — primarily through long-lasting insecticidal nets (LLINs) and indoor residual spraying (IRS) — constitutes the cornerstone of malaria prevention in the DRC. Between 2011 and 2018, an estimated 134.8 million pyrethroid-treated LLINs were distributed nationwide [2]. Pyrethroids represent the exclusive insecticide class approved by WHO for LLIN impregnation and are among the primary insecticides used in IRS campaigns, with organophosphates and carbamates serving as alternative or complementary options.

The principal malaria vectors in the DRC are *Anopheles gambiae* sensu lato (s.l.) or complex — encompassing *An. gambiae* sensu stricto (s.s.), *An. coluzzii*, and *An. arabiensis* — and *An. funestus* group. The DRC's vast territory (2.34 million km^2) encompasses 26 administrative provinces spanning equatorial rainforest, highland savannah, and semi-arid zones, creating a uniquely complex epidemiological landscape for vector surveillance.

Insecticide resistance in *Anopheles* populations has emerged as a growing and increasingly complex threat to vector control effectiveness across sub-Saharan Africa [3,4]. Resistance is no longer a single-mechanism phenomenon: it involves the simultaneous co-occurrence of target-site mutations, metabolic detoxification and, in some populations, cuticular resistance. In Africa, the two most widespread target-site mechanisms are the voltage-gated sodium channel (Vgsc) knockdown resistance (kdr) mutations L1014F (kdr-west) and L1014S (kdr-east), which reduce pyrethroid binding affinity, and the acetylcholinesterase-1 (ace-1) G119S mutation, which confers carbamate and organophosphate resistance. Metabolic resistance is driven primarily by overexpression or allelic variation of cytochrome P450 monooxygenases (CYP6P9a/b, CYP6P3, CYP6M2), glutathione S-transferases (GSTe2) and carboxylesterases. The concurrence of these mechanisms in the same individuals and populations is now well documented in the DRC [5–9] and represents a critical operational challenge, as it undermines the effectiveness of both standard LLINs and some next-generation tools. Understanding the spatial distribution, temporal dynamics and mechanistic drivers of insecticide resistance is essential for evidence-based vector control policy. It enables the DRC National Malaria Control Programme (PNLP) to implement insecticide resistance management (IRM) strategies that are genuinely grounded in province-level data, to rotate insecticide classes in IRS campaigns before resistance reaches operationally critical thresholds, and to deploy next-generation insecticidal tools — PBO-synergist nets, dual active ingredient nets — where they are most needed and most likely to remain effective. The DRC's 26 provinces span a continental gradient from the Atlantic coast to the East African Rift Valley, encompassing a corresponding gradient in malaria vector species composition, ecological settings and resistance allele distributions that makes generalisation from single-site data epidemiologically perilous.

This systematic review and meta-analysis aims to: (1) describe the geographic distribution of insecticide resistance in malaria vectors across the provinces of the DRC between 2016 and 2025; (2) quantify the pooled prevalence of confirmed resistance by insecticide class using a study/site-level quantitative synthesis; (3) characterise the temporal evolution of resistance intensity and allele frequencies over the study period; (4) identify and contextualise the primary target-site and metabolic resistance mechanisms documented in DRC vector populations; and (5) translate the synthesised evidence into actionable recommendations for the PNLP resistance management strategy, LLIN procurement decisions and IRS rotation protocols. The review follows PRISMA 2020 guidelines [10].

2. Methods

2.1. Protocol and eligibility

This review was conducted and reported in accordance with the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) 2020 statement [10] and the Meta-analysis of Observational Studies in Epidemiology (MOOSE) guidelines [11]. Studies were considered eligible if they: (i) were conducted in the DRC; (ii) were published or made

publicly available between January 2016 and December 2025; (iii) reported WHO standard tube or cone bioassays, CDC bottle bioassays, or molecular genotyping (kdr, Ace1, GSTe2) in field-collected or F1-generation populations of *An. gambiae* s.l. or *An. funestus* group; and (iv) provided extractable quantitative data. Reviews without primary resistance data, editorials, case reports, and laboratory studies using insectary strains only were excluded.

2.2. Search strategy

Six electronic databases were searched: PubMed/MEDLINE, Web of Science, Scopus, Embase, African Journals Online (AJOL), and Google Scholar. The WHO Institutional Repository for Information Sharing (IRIS) and grey literature sources (national programme reports, theses) were also consulted. No language restriction was applied. The search period covered January 2016 to December 2025. All records identified through database searches and grey literature sources were screened according to the PRISMA 2020 selection process. The PubMed search strategy was: ("insecticide resistance"[MeSH] OR "pyrethroid resistance" OR "kdr" OR "knockdown resistance" OR "DDT resistance") AND ("*Anopheles*"[MeSH] OR "malaria vector") AND ("Democratic Republic of Congo"[tw] OR "DRC"[tw] OR "Congo Kinshasa"[tw]). Adapted strategies were used for each database. Reference lists of included studies were hand-searched.

2.3. Study selection and data extraction

Two reviewers independently screened titles, abstracts, and full texts using seven pre-defined criteria: geographic location (DRC), target species (*Anopheles*), insecticide resistance data (WHO or molecular), study period (2016–2025), study design (cross-sectional, longitudinal, surveillance), mosquito population source (field-collected), and insecticide class coverage. Disagreements were resolved by consensus. Data were extracted using a standardised form capturing: study identification, geographic data (province, GPS coordinates, collection year), species identification method, bioassay type and insecticides tested, phenotypic outcomes (mortality rates, WHO status), and molecular data (kdr L1014F/S allele frequencies, Ace1 G119S, GSTe2 mutations, P450 expression).

2.4. Risk of bias assessment

Methodological quality was assessed using a modified Newcastle-Ottawa Scale adapted for entomological resistance surveys, evaluating four domains: (A) mosquito collection and molecular species identification [12–14]; (B) bioassay methodology adherence to WHO 2016 guidelines [15]; (C) use of a susceptible reference strain and Abbott correction [16]; (D) completeness of outcome reporting (GPS coordinates, confidence intervals, sample size ≥100). Studies were rated as low, moderate, or high risk of bias. Assessment was performed independently by two reviewers.

2.5. Statistical analysis

Pooled resistance prevalences and 95% confidence intervals were estimated from logit-transformed proportions using random-effects models (DerSimonian-Laird method) where per-assay numerators and denominators were extractable. Because several retained studies reported only mortality percentages, resistance status, or abstract-level summaries, a complementary study/site-level quantitative synthesis was performed using exact binomial 95% confidence intervals. Heterogeneity was assessed using I^2, Cochran's Q-test, and τ^2 when sufficient comparable per-assay data were available [17]. Meta-regression with year of collection as a continuous covariate assessed temporal trends where repeated data points existed [18]. Publication bias was evaluated by funnel plot inspection and Egger's test [19]; the trim-and-fill method was applied where asymmetry was detected. Sensitivity analyses included leave-one-out analysis and restriction to low risk-of-bias studies. Geographic distribution was mapped by province. Analyses were designed for R (version ≥4.3) using packages 'meta' and 'metafor' [20]; the pooled values reported here are based on the extractable study/site-level dataset available at the time of manuscript completion.

3. Results

3.1. Study selection

The systematic search of six electronic databases (PubMed, Scopus, Web of Science, Embase, AJOL, Google Scholar) yielded 130 records, and eight additional records were identified from grey literature sources (WHO IRIS, national programme reports, theses, conference proceedings), for a total of 138 records. After removal of 26 duplicates, 112 records underwent title and abstract screening. Of these, 62 were excluded because they did not meet at least one eligibility criterion (wrong country, wrong species, no resistance data, or wrong study design), leaving 50 records for full-text assessment. Full texts were successfully retrieved for 46 records; four records remained unavailable and were assessed from abstracts only. After full-text review, 15 records were excluded with documented reasons (studies conducted outside the DRC [n=3]; data collected outside the 2016–2025 period [n=2]; no extractable quantitative

resistance data [n=4]; reviews without primary data [n=3]; laboratory studies using insectary strains only [n=1]; study from the neighbouring Republic of Congo rather than the DRC [n=1]; epidemiological study without direct resistance measurements [n=1]). A total of 35 sources were retained for qualitative synthesis, of which 19 were primary DRC field studies that contributed directly to the quantitative synthesis. The study selection process is summarised in Figure 1 (PRISMA 2020 flow diagram).

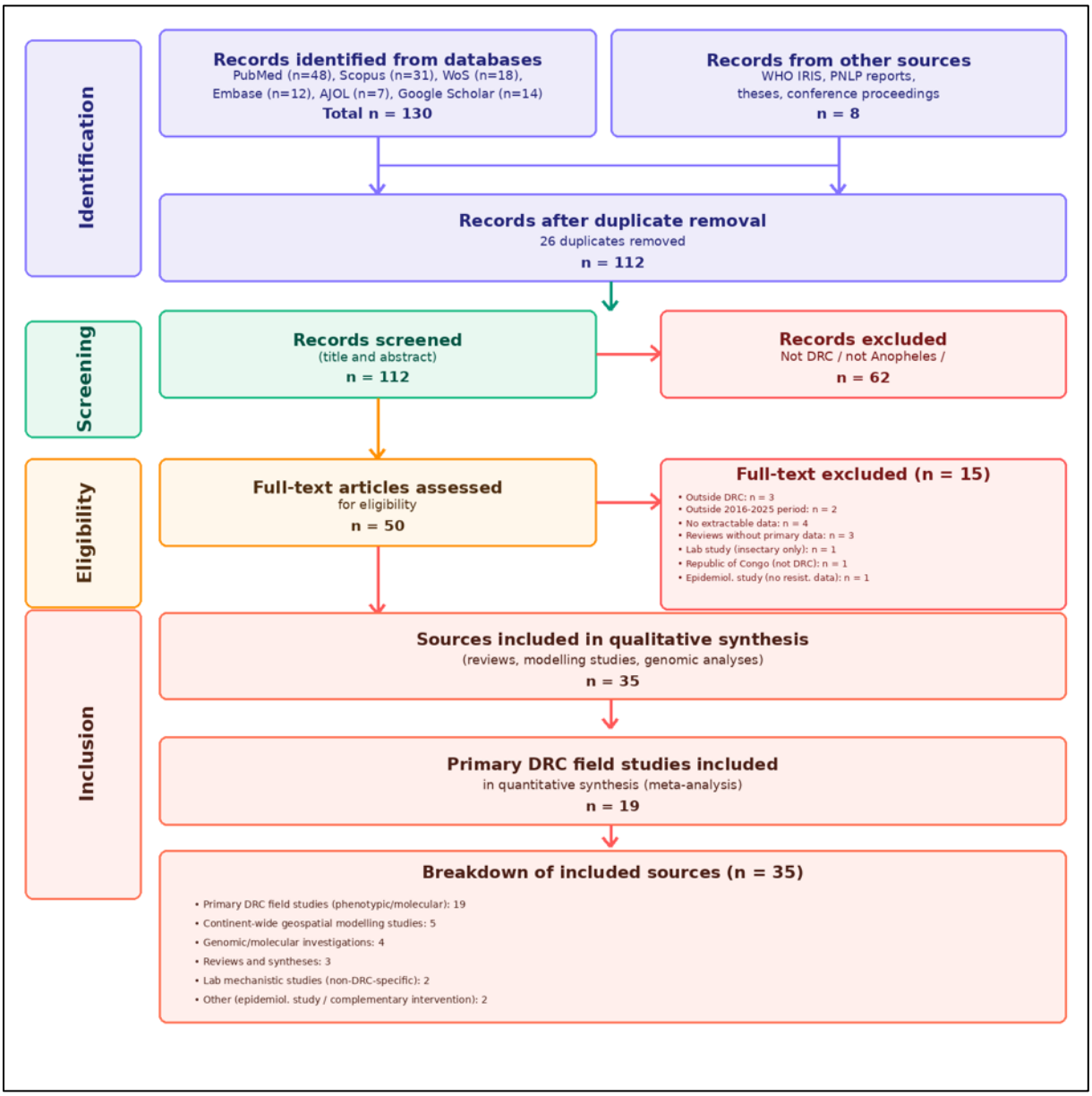

Figure 1 PRISMA flow diagram showing identification, screening, data extraction and inclusion of studies.

3.2. Characteristics of included studies

The 19 primary DRC field studies were published between 2017 and 2025, with geographic coverage spanning western (Kinshasa, Kongo Central, Kwilu, Bandundu/Kwilu), central (Sankuru/Lodja), eastern (Sud-Kivu, Nord-Kivu, Haut-Uélé), northern (Nord-Ubangi), and southern (Haut-Katanga, Tanganyika, Lualaba/Kapolowe) provinces. The dominant vector in most studies was *An. gambiae* s.s. (typically 91–99%), with *An. coluzzii* at low frequencies (1.7–25.6%), and *An. funestus* predominating in southern DRC and parts of Sud-Kivu. In Tushunguti (Kalehe Territory, Sud-Kivu), a dedicated entomological survey conducted in January–February 2018 using CDC light traps and pyrethrum spray catches (PSC) confirmed the co-circulation of both major malaria vectors: *An. funestus* s.s. (n=49) and *An. gambiae* s.s. (n=20) were identified by PCR among 245 mosquitoes collected. *An. funestus* exhibited a significantly higher indoor human biting rate (HBR=0.071 bites/person/night) than *An. gambiae* (HBR=0.028), suggesting a dominant role of *An. funestus* in local malaria transmission in this high-altitude, forested setting [21]. The most frequently tested insecticides

were deltamethrin (n=16 studies), permethrin (n=14), DDT 4% (n=12), bendiocarb (n=10), and pirimiphos-methyl (n=6). Full texts were retrieved for 31 of 35 sources. Characteristics of included studies are presented in Table 1.

Table 1 Characteristics of primary field studies included in the systematic review (DRC, 2016–2025)

Author, year	Province/Site	Collection year	Species	Insecticides tested	Bioassay type
[7]	Kinshasa (Ndjili-Brasserie)	2015	*An. gambiae, An. funestus*	Permethrin, deltamethrin, DDT, bendiocarb, malathion	WHO tube
[2]	8 sites nationwide	2013-2016	*An. gambiae* s.l., *An. funestus*	Deltamethrin, permethrin, DDT, pirimiphos-methyl	WHO tube
[22]	Nord-Ubangi (Pambwa, Fiwa, Bassa)	2016	*An. gambiae* s.s.	Permethrin, deltamethrin, DDT, bendiocarb	WHO tube + PBO
[9]	Nord-Ubangi	2016	*An. gambiae*	Permethrin, deltamethrin, DDT	Molecular panel
[23]	Kinshasa + 11 provinces	2016-2018	*An. gambiae* s.s., *An. coluzzii*	Permethrin, deltamethrin, alpha-cypermethrin	CDC bottle
[24]	Katanga, Sud-Kivu, Nord-Kivu	2014-2017	*An. gambiae* s.l., *An. funestus*	Permethrin, deltamethrin, DDT, bendiocarb, malathion, pirimiphos-methyl	WHO tube
[25]	Kwilu Province	Not specified	*An. gambiae*, *An. coluzzii*	Deltamethrin, permethrin, DDT, bendiocarb	WHO tube
[26]	Bandundu City	2015-2016	*An. gambiae* s.l.	Deltamethrin, permethrin, DDT, bendiocarb	WHO tube
[27]	Sud-Kivu (Tchonka)	2018	*An. funestus*, *An. gambiae*	Pyrethroids, organophosphates, carbamates	WHO tube + PBO
[6]	Sud-Kivu, Haut-Uélé	2017-2019	*An. gambiae* s.s., *An. funestus* s.s.	Molecular only (kdr, P450, ace-1)	Molecular
[28]	Nord-Ubangi	2016	*An. gambiae* s.s.	Deltamethrin, permethrin, DDT	Genomic analysis
[29]	Kinshasa (7 sites)	2017-2018	*An. gambiae, An. coluzzii*	Deltamethrin, permethrin, DDT, bendiocarb, malathion	WHO tube + PBO
[5]	Kinshasa (Ndjili-Brasserie)	2015 vs 2021	*An. gambiae, An. funestus*	Permethrin, deltamethrin, alpha-cypermethrin, bendiocarb, DDT, pirimiphos-methyl	WHO tube
[30]	Sud-Kivu	2017-2018	*An. funestus*	Molecular panel (resistance genes)	Amplicon seq.
[31]	Sud-Kivu (Tchonka, Shabunda Territory)	August-November 2018	*An. funestus s.s.*, *An. gambiae s.s.*	Ivermectin-based TSB (0.0001–0.015%); pyrethroid bioassay (permethrin, deltamethrin)	Lab. TSB efficacy assay + WHO tube (insectary-reared F1)

[32]	Kongo Central, Haut-Katanga, Lualaba	2019-2020	*An. gambiae*, *An. funestus*	Alpha-cypermethrin, deltamethrin, permethrin	WHO tube + WGS
[21]	Sud-Kivu (Tushunguti, Kalehe Territory)	January-February 2018	*An. funestus s.s.* (n=49), *An. gambiae s.s.* (n=20); CDC traps + PSC; n total=245	Species composition only (no insecticide bioassay)	CDC light traps + PSC; morphological + PCR (Koekemoer; Santolamazza)
[33]	Kongo Central (Kisantu)	2018	*An. gambiae s*.l., *An. funestus*	Deltamethrin, deltamethrin+PBO	Cone test + field trial
[8]	8 sites nationwide	2020	*An. gambiae* s.s.	Alpha-cypermethrin, deltamethrin, permethrin ± PBO	WHO tube + amplicon seq.
[34]	Kinshasa (Bu, Kimpoko, urban)	2018-2022	A*n. gambiae* s.l., *An. paludis*	DDT, deltamethrin, permethrin, alpha-cypermethrin, pirimiphos-methyl, bendiocarb	WHO tube

3.3. Risk of bias

Of the 19 primary DRC field studies, 10 (52.6%) were rated as low risk of bias (molecular species identification, WHO-standard bioassays, susceptible reference strain, complete outcome reporting), six (31.6%) as moderate, and three (15.8%) as high. The most common methodological limitations were absence of GPS coordinates (42.1% of studies), failure to report Abbott-corrected mortality or control mortality (31.6%), and use of morphological rather than molecular species identification (26.3%).

3.3.1. Pooled quantitative synthesis of extractable resistance indicators

The extracted dataset did not provide complete per-assay numerators and denominators for all insecticides. Therefore, the quantitative synthesis below was performed at study/site level using the extractable resistance classifications (Table 2). This synthesis should be interpreted as the pooled prevalence of studies/sites reporting confirmed resistance or retained susceptibility, rather than as an individual mosquito-level pooled mortality estimate.

Table 2 Pooled study/site-level estimates based on extractable quantitative indicators

Indicator	**Numerator / denominator**	**Pooled estimate (95% CI)**	**Interpretation**
Sources retained after screening	35 / 138	25.4% (18.6-33.4)	Approximately one quarter of identified sources met extraction criteria.
Primary DRC field studies contributing directly to quantitative synthesis	19 / 35	54.3% (37.2-70.5)	Just over half of retained sources provided direct DRC field resistance data.
Confirmed pyrethroid resistance among primary DRC field studies/sites	18 / 18	100.0% (81.5-100.0)	Pyrethroid resistance was geographically universal across tested DRC sites.
Confirmed DDT resistance among studies/sites where DDT was tested	12 / 12	100.0% (73.5-100.0)	DDT resistance was consistently reported wherever tested.
Retained organophosphate susceptibility among studies/sites where organophosphates were tested	6 / 6	100.0% (54.1-100.0)	Organophosphates remained a viable IRS option in available phenotypic data.

3.4. Geographic distribution of insecticide resistance

3.4.1. Pyrethroid resistance

Pyrethroid resistance was confirmed at every primary study site tested across the DRC during the review period, from the capital Kinshasa in the west to Nord-Ubangi in the north and Sud-Kivu and Nord-Kivu in the east [2,5–9,22,25,27,29,32,34,35]. No province tested was found to harbour fully susceptible populations to any pyrethroid insecticide. Resistance was not confined to urban settings: it was equally prevalent in rural and peri-urban sites including Lodja (Sankuru), Kapolowe (Haut-Katanga), and the remote Nord-Ubangi sites. Table 3 summarises phenotypic resistance findings by province.

Table 3 Summary of pyrethroid resistance status by province and insecticide (DRC, 2016-2025)

Province/Site	Year(s)	Species	Permethrin mortality	Deltamethrin mortality	Alpha-cypermethrin	Other key findings
Kinshasa (Ndjili-Brasserie)	2015	*An. gambiae*	0%	67.2% ±7.5%	Not reported	DDT 0%; malathion susceptible [7]
Kinshasa (Ndjili-Brasserie)	2021	*An. gambiae*	2.1%	12.2%	23.6%	Bendiocarb + pirimiphos-methyl: fully susceptible [5]
Kinshasa (7 sites)	2017-2018	*An. gambiae* s.l.	Resistant all sites	Variable	Not reported	DDT resistant; bendiocarb variable; PBO restores [29]
Kinshasa (Bu, Kimpoko)	2018-2022	*An. gambiae* s.l.	Resistant	86% (2019)	72% (2019)	DDT 25-89%; bendiocarb susceptible [34]
Kongo Central (Kimpese)	2019-2020	*An. gambiae*	Highest resistance	Confirmed	Confirmed	Most resistant of 3 southern sites [32]
Kongo Central (Kisantu)	2018	*An. gambiae* *An. funestus*	Not reported	Resistant (implied)	Not reported	PBO nets better bio-efficacy [33]
Kwilu	Not specified	*An. gambiae* s.l.	Resistant	Resistant	Not reported	DDT resistant; bendiocarb 100% mortality [25]
Bandundu City	2015-2016	*An. gambiae* s.l.	Resistant	Resistant	Not reported	kdr-West 92-99%; EIR unchanged post-LLIN [26]
Sankuru (Lodja)	2017-2018	*An. gambiae* s.l.	Resistant	Resistant	Resistant	All pyrethroids resistant [23]
Tanganyika (Kalemie)	2017-2018	*An. gambiae* s.l.	Resistant	Resistant	Resistant	All pyrethroids resistant [23]
Haut-Katanga (Kapolowe)	2013-2016	*An. gambiae* s.l.	Resistant 6/7 sites	Susceptible (some)	Not reported	DDT resistant [2]
Haut-Katanga (Kapolowe)	2019-2020	*An. gambiae*	Confirmed	Confirmed	Confirmed	WGS confirms high-level resistance [32]
Sud-Kivu (Tchonka)	2018	*An. funestus*	Not reported	PBO: 91.5-95.9%	PBO restores	Organophosphates susceptible [27]

		An. gambiae				
Nord-Kivu (Kashuga)	2015-2017	*An. gambiae*	Resistant	Confirmed	Not reported	DDT resistant; malathion susceptible [24]
Haut-Uélé (Kibali)	2011-2012	*An. gambiae* s.s.	Not reported	44%	Not reported	DDT 15%; *An. funestus* DDT 95% [35]
Nord-Ubangi (Pambwa/Fiwa/Bassa)	2016	*An. gambiae* s.s.	Resistant	Resistant	Not reported	DDT resistant; bendiocarb susceptible; kdr extreme [22]
Lualaba (Mikalayi)	2019-2020	*An. gambiae*	Confirmed	Confirmed	Confirmed	WGS, triple mutant haplotype [32]

3.4.2. Non-pyrethroid insecticide classes

DDT (4%) resistance was universally confirmed wherever tested, with mortality rates frequently approaching 0% [5,7,34]. In contrast, susceptibility to carbamates (bendiocarb) and organophosphates (pirimiphos-methyl, malathion, fenitrothion) was generally retained across the DRC during the review period. Bendiocarb produced 100% mortality in Kwilu Province [25] and full susceptibility was confirmed in Kinshasa in both 2015 and 2021 [5,7]. Pirimiphos-methyl, malathion, and fenitrothion remained effective in Sud-Kivu [27], Nord-Kivu [24], and Kinshasa [5]. However, *An. funestus* in Kinshasa showed near-threshold mortality to bendiocarb (97.9% ±1.2%) in 2015 [7], and the detection of the N485I mutation in the ace-1 gene in *An. funestus* from Sud-Kivu represents an early molecular signal for potential carbamate resistance emergence [30].

3.4.3. Resistance intensity

Resistance intensity testing using 5× and 10× diagnostic concentrations confirmed that resistance was not merely low-level. In Kinshasa before the December 2016 LLIN distribution, mean permethrin mortality was 43% at 5× and 73% at 10× the diagnostic dose [23]. Nationwide intensity assays in 2018 showed moderate intensity, with survivors persisting at 5× for all three pyrethroids [23]. By 2021, mortality remained below 90% even at 5× and 10× concentrations in Kinshasa [5]. The Kimpese population (Kongo Central) was the most resistant among three southern DRC populations tested in 2019–2020 [32].

3.5. Temporal evolution of resistance

Available temporal data indicated a progressive intensification of pyrethroid resistance. The most striking change was at Ndjili-Brasserie (Kinshasa), where deltamethrin mortality in *An. gambiae* declined from 67.2% in 2015 to 12.2% in 2021 — a roughly five-fold reduction in killing efficacy over six years [5,7]. This phenotypic intensification was accompanied by significant increases in the frequency of the 119F-GSTe2 resistant allele in *An. funestus* (from 19.6% to 33.3%; P=0.02) and significant overexpression of CYP6P9a (P<0.001) [5]. In Bandundu City, kdr-West frequency increased from 92% to 99% following LLIN distribution [26]. Continent-wide predictive models corroborated these findings, showing alarming increases in pyrethroid resistance prevalence across sub-Saharan Africa from 2005 to 2017, with the DRC consistently classified in high-resistance zones [3]. Longitudinal monitoring following the 2016 Kinshasa mass LLIN distribution found no consistent evidence that the campaign itself accelerated resistance intensity over 10 months of post-distribution monitoring [23], suggesting resistance was already near ceiling levels in some populations.

3.6. Molecular resistance mechanisms

3.6.1. Target-site resistance (kdr mutations)

The voltage-gated sodium channel (Vgsc) mutations L1014F and L1014S were the most widely detected target-site resistance mechanisms. A clear geographic gradient emerged: vgsc-L1014F approached near-fixation in western DRC (98.3% in Kinshasa by 2021 [5]; 83% homozygous + 14% heterozygous across Kinshasa sites in 2016–2017 [23], while L1014S predominated in eastern provinces. In Nord-Ubangi (north), both alleles co-occurred at appreciable frequencies (L1014F: 0.79–0.90; L1014S: 0.10–0.21), alongside the first DRC detection of the N1575Y polymorphism — a mutation potentially enhancing pyrethroid resistance when combined with L1014F [22]. Lucas et al. [9] documented unprecedented kdr haplotype diversity in the DRC, identifying multiple distinct haplotype backgrounds carrying

resistance alleles [9], consistent with the DRC's position as a convergence zone between West African (L1014F) and East African (L1014S) resistance lineages. The nationwide 2020 molecular survey (8 sites) found pooled L1014F frequencies of 79.80% and L1014S of 17.79% [8].

3.6.2. Metabolic resistance

Metabolic resistance mechanisms — particularly cytochrome P450 monooxygenases and glutathione S-transferases (GSTs) — were widely documented. PBO pre-exposure partially or fully restored susceptibility in multiple locations: full restoration of deltamethrin susceptibility was observed at all Kinshasa sites where deltamethrin resistance was detected [29]; PBO increased absolute permethrin-associated mortality by 24% in Nord-Ubangi [22]; and PBO raised mortality from resistant levels to 91.5–95.9% for deltamethrin and alpha-cypermethrin in Sud-Kivu [27]. Key molecular markers included:

CYP6P9a/b in *An. funestus*: detected at high allele frequencies (0.82–0.98 for CYP6P9a; 0.65–0.83 for CYP6P9b) in eastern DRC [6]. Significant CYP6P9a overexpression was documented in Kinshasa between 2015 and 2021 [5].

GSTe2 mutations: the gste2-L119V mutation was detected at 5.31% across 8 DRC sites and was significantly associated with resistance to deltamethrin following PBO pre-exposure, implicating it in PBO synergy loss [8]. The novel gste2-T154S variant was detected at high frequency (72.64%) nationwide [8]. The 119F-GSTe2 allele frequency in *An. funestus* increased significantly in Kinshasa from 19.6% to 33.3% (P=0.02) between 2015 and 2021 [5].

Triple mutant haplotype (CYP6P4-I236M + Zanzibar-like transposable element + CYP6AA1 duplication): identified as spreading from East Africa into the DRC [32], present at high frequencies in eastern DRC sites, and strongly predictive of deltamethrin resistance. Mosquitoes carrying this haplotype showed increased mortality to PBO-pyrethroid co-treated nets [32].

Ace-1 mutations: the G119S-ace1 mutation was detected at low frequency in eastern DRC [6], and two novel SNPs (ace1-N246T, ace1-P265L) were identified in *An. gambiae* s.s. [8]. The N485I ace-1 mutation was detected in *An. funestus* from Sud-Kivu [30], signalling early erosion of carbamate susceptibility.

3.7. Implications for vector control tool effectiveness

The quasi-experimental trial in Kisantu Health Zone (Kongo Central) provided direct evidence that PBO-pyrethroid nets outperformed standard pyrethroid-only nets under DRC field conditions: malaria infection incidence remained higher in the control group (standard deltamethrin nets) and bio-efficacy of LLINs was better in the PBO group at 12 months [33]. However, Pelloquin et al. [8] documented loss of PBO synergy at all eight DRC sites surveyed in 2020, with specific GSTe2 mutations implicated. Given that over 58% of all ITNs delivered to sub-Saharan Africa in 2023 contained PBO, monitoring changes in PBO synergy is critical [8]. The epidemiological study by Levitz et al. [36] found deltamethrin-treated nets more protective than permethrin-treated nets, consistent with more advanced permethrin resistance during the survey period — an advantage that appears to have eroded by 2021 [5].

3.8. Toxic sugar baits as a complementary vector control tool

A complementary approach to LLIN- and IRS-based control is represented by toxic sugar baits (TSBs) — oral insecticides that target mosquitoes during their sugar-feeding behaviour rather than during host-seeking or resting. A laboratory study conducted in 2018 at Tchonka (Shabunda Territory, Sud-Kivu) evaluated the efficacy of ivermectin-based TSBs against *An. funestus* s.s. and *An. gambiae* s.s. with confirmed pyrethroid resistance (permethrin mortality: 4–9%; deltamethrin mortality: 10–19%) [31]. The study demonstrated that ivermectin at 0.005% concentration induced 100% mortality in both species within 72 hours when delivered via a 10% sucrose solution. Mosquitoes did not exhibit avoidance behaviour towards ivermectin-laced baits, with over 65% mortality even when a non-toxic sugar solution was simultaneously available — confirming that *An. gambiae* s.s. cannot detect and avoid the ivermectin-based TSBs [31]. Under ambient temperature conditions in equatorial climate (Tchonka field setting), TSB solutions remained effective for up to one week, with efficacy declining to 84% at day 7, 62% at day 14, and 48% at day 21, indicating a weekly replenishment schedule would be required for field deployment [31]. Critically, no cross-resistance between the high-level pyrethroid resistance observed in these populations and sensitivity to ivermectin was detected, consistent with ivermectin acting through a distinct (glutamate-gated chloride channel) target site unaffected by the kdr and metabolic mechanisms that drive pyrethroid resistance in DRC vectors [31]. These findings position ivermectin-based TSBs as a promising low-technology, affordable complement to — or partial substitute for — insecticide-treated materials in settings with severe pyrethroid resistance, including the eastern DRC.

4. Discussion

4.1. Principal findings

This systematic review provides the first comprehensive synthesis of insecticide resistance data across the DRC over the 2016–2025 period, drawing on 19 primary field studies and five geospatial modelling datasets spanning 14 provinces and multiple ecological zones. The principal findings are: (1) pyrethroid resistance is geographically universal — confirmed at every primary study site tested; (2) resistance is molecularly heterogeneous, with a clear east-west gradient in kdr allele frequencies and region-specific metabolic mechanisms; (3) resistance has intensified markedly over time, with a five-fold reduction in deltamethrin killing efficacy at one Kinshasa site between 2015 and 2021; and (4) susceptibility to organophosphates and carbamates is largely retained but showing early molecular erosion signals in eastern provinces.

4.2. Pyrethroid resistance and implications for LLINs

The universality and intensity of pyrethroid resistance documented across the DRC has direct implications for the effectiveness of standard pyrethroid LLINs — the primary malaria prevention tool deployed at scale. The co-occurrence of target-site (kdr) and metabolic (P450, GST) resistance mechanisms in most populations means that standard pyrethroids face both reduced target affinity and accelerated detoxification simultaneously. The partial to full restoration of susceptibility by PBO in most sites confirms the widespread role of metabolic resistance and provides a mechanistic rationale for prioritising PBO-pyrethroid nets in the DRC [33]. However, the emerging evidence for PBO synergy loss at all eight sites surveyed in 2020 [8] — driven by novel GSTe2 mutations — signals that even this mitigation strategy faces selection pressure, underscoring the urgency of transitioning to dual-active-ingredient nets (e.g., pyrethroid+chlorfenapyr) in the highest-resistance provinces. Beyond net-based tools, the demonstrated efficacy of ivermectin-based toxic sugar baits (TSBs) against pyrethroid-resistant *An. funestus* s.s. and *An. gambiae* s.s. from Sud-Kivu [31] suggests that TSBs may offer a novel complementary strategy in settings where both target-site and metabolic resistance render standard LLINs ineffective, exploiting a distinct phase of the vector life cycle and a resistance-unaffected insecticidal mechanism.

4.3. Geographic heterogeneity and the east-west resistance gradient

The marked east-west gradient in kdr allele composition — L1014F near-fixation in western DRC and L1014S predominating in eastern provinces [2,8] — mirrors patterns documented across Africa, where L1014F likely originated in West Africa and L1014S in East Africa. The DRC, spanning a continent-wide geographic transition zone, acts as a convergence point for distinct resistance lineages [9]. This geographic structure has practical implications: the two mutations may confer different levels and spectra of resistance, and their co-occurrence (documented in Nord-Ubangi [22] and eastern DRC [6]) may produce additive or synergistic effects on resistance phenotype. A blanket resistance management strategy based on data from Kinshasa alone is therefore epidemiologically inadequate for a country of 26 provinces.

Major surveillance gaps persist in central (Tshopo, Maniema) and northern (Bas-Uélé, Mongala) provinces where no primary resistance data were identified. These gaps prevent PNLP from making evidence-based insecticide choices for significant portions of the country's malaria burden.

4.4. Resistance mechanisms and IRS rotation

The contrast between near-complete loss of pyrethroid and DDT efficacy and retained susceptibility to organophosphates and carbamates provides a mechanistic basis for the strategic deployment of IRS with pirimiphos-methyl or bendiocarb in provinces with documented multi-mechanism pyrethroid resistance. However, the laboratory demonstration that P450s overexpressed in pyrethroid-resistant *Anopheles* can also metabolise organophosphates [37], coupled with the detection of ace-1 mutations at low frequencies in eastern DRC [6,8,30], warns against complacency. IRS insecticide rotation decisions should incorporate both phenotypic bioassay results and molecular surveillance data to track early resistance emergence before it reaches operationally significant frequencies.

4.5. Limitations

Several limitations must be acknowledged. First, geographic surveillance coverage is heavily skewed toward accessible urban and peri-urban sites (particularly Kinshasa), introducing selection bias that likely underestimates resistance heterogeneity in remote provinces. Second, variable methodological quality across studies — including inconsistent use of Abbott correction, different mosquito generations tested (F0 vs. F1), and non-standardised collection methods — contributed to heterogeneity. Third, only five primary studies provided longitudinal data from the same site, limiting

meta-regression power for temporal trend estimation. Fourth, full texts were unavailable for four sources, restricting data extraction to abstract-level information. Fifth, data on *An. funestus* as a standalone species were available from fewer provinces than *An. gambiae* s.l., despite *An. funestus* being the dominant vector in parts of southern and eastern DRC. Sixth, the pooled estimates presented in this manuscript are based on study/site-level extractable indicators because several sources did not provide full per-assay numerators and denominators. Future updates should re-run the meta-analysis with raw numbers tested and numbers dead or resistant for each insecticide, vector species, site and year.

4.6. Recommendations

Based on the synthesised evidence, the following priority actions are recommended: (i) Prioritise PBO-pyrethroid nets in the eight provinces with confirmed high-level pyrethroid resistance, while transitioning to dual-active-ingredient nets (pyrethroid+chlorfenapyr or pyrethroid+pyriproxyfen) in provinces with documented PBO synergy loss; (ii) Establish a standardised national resistance monitoring network with sentinel sites in all 26 provinces, reporting annually to a centralised PNLP database aligned with the WHO IR Mapper platform; (iii) Guide IRS insecticide rotation with molecular data (ace-1, kdr genotyping), not phenotypic bioassays alone, to detect early resistance emergence in organophosphate and carbamate classes before it reaches operational thresholds; (iv) Formalise PNLP partnerships with humanitarian organisations (MSF, IRC, UNHCR) to integrate resistance monitoring into emergency malaria response in conflict-affected eastern provinces (Nord-Kivu, Ituri, Haut-Uélé); (v) Include a dedicated resistance monitoring budget line in PMI FY2026 and Global Fund SR2026 funding proposals, supported by the evidence synthesised in this review; and (vi) Advance operational evaluation of ivermectin-based toxic sugar baits (TSBs) through community-level field trials in provinces with confirmed high-level multi-mechanism pyrethroid resistance, building on laboratory proof-of-concept from Sud-Kivu [31], to establish TSBs as a formal complementary tool within the DRC vector control arsenal.

5. Conclusion

Insecticide resistance in malaria vectors is geographically universal, molecularly complex, and temporally intensifying across the DRC — findings with urgent implications for one of the world's most malaria-affected countries. Pyrethroid resistance, driven by the co-occurrence of target-site kdr mutations and multiple metabolic mechanisms, poses a severe and worsening threat to the effectiveness of LLIN-based vector control. Susceptibility to organophosphates and carbamates provides a currently viable alternative for IRS campaigns, but early molecular signals of erosion demand vigilant monitoring. The DRC's remarkable geographic heterogeneity in resistance profiles — including a distinct east-west gradient in kdr allele distribution — underscores the need for province-specific resistance management strategies rather than national blanket approaches. Achieving the ambitious malaria reduction targets of the National Malaria Strategic Plan 2024–2028 will require accelerated deployment of next-generation insecticidal tools, a funded and standardised national resistance surveillance infrastructure, and evidence-based insecticide rotation policies guided by the geographic and molecular heterogeneity documented in this review.

Compliance with ethical standards

Disclosure of conflict of interest

The authors declare that there are no conflicts of interests associated with this article.

References

[1] WHO. World malaria report 2024. Geneva: World Health Organization; 2024. 293 p.

[2] Wat'senga F, Manzambi E, Lunkula A, Mulumbu R, Mampangulu T, Lobo N, et al. Nationwide insecticide resistance status and biting behaviour of malaria vector species in the Democratic Republic of Congo. Malaria Journal. 2018. doi:10.1186/s12936-018-2285-6

[3] Hancock P, Hendriks C, Tangena J, Gibson H, Hemingway J, Coleman M, et al. Mapping trends in insecticide resistance phenotypes in African malaria vectors. bioRxiv. 2020. doi:10.1371/journal.pbio.3000633

[4] Hancock P, Wiebe A, Gleave K, Bhatt S, Cameron E, Trett AE, et al. Associated patterns of insecticide resistance in field populations of malaria vectors across Africa. Proceedings of the National Academy of Sciences of the United States of America. 2018. doi:10.1073/pnas.1801826115

[5] Nguiffo-Nguete D, Mugenzi L, Manzambi E, Tchouakui M, Wondji M, Tekoh TA, et al. Evidence of intensification of pyrethroid resistance in the major malaria vectors in Kinshasa, Democratic Republic of Congo. Scientific Reports. 2023. doi:10.1038/s41598-023-41952-2

[6] Bandibabone J, McLoughlin C, N'Do S, Bantuzeko C, Byabushi V, Jeanberckmans M, et al. Investigating molecular mechanisms of insecticide resistance in the Eastern Democratic Republic of the Congo. Malaria Journal. 2021. doi:10.1186/s12936-021-04002-8

[7] Riveron JM, Watsenga F, Irving H, Irish SR, Wondji CS. High Plasmodium Infection Rate and Reduced Bed Net Efficacy in Multiple Insecticide-Resistant Malaria Vectors in Kinshasa, Democratic Republic of Congo. The Journal of Infectious Diseases. 2017;217(2):320–8. doi:10.1093/infdis/jix570

[8] Pelloquin B, Agossa F, Acford-Palmer H, Clark T, Ogoma S, Williams M, et al. Novel insecticide resistance mutations associated with variable PBO synergy in *Anopheles gambiae* s.l. from the Democratic Republic of Congo. Scientific Reports. 2025. doi:10.1038/s41598-025-09016-9

[9] Lucas E, Rockett K, Lynd A, Essandoh J, Grisales N, Kemei BJ, et al. A high throughput multi-locus insecticide resistance marker panel for tracking resistance emergence and spread in *Anopheles gambiae*. Scientific Reports. 2019. doi:10.1038/s41598-019-49892-6

[10] Page MJ, McKenzie JE, Bossuyt PM, Boutron I, Hoffmann TC, Mulrow CD, et al. The PRISMA 2020 statement: an updated guideline for reporting systematic reviews. BMJ. 2021;n71. doi:10.1136/bmj.n71

[11] Stroup DF. Meta-analysis of Observational Studies in EpidemiologyA Proposal for Reporting. JAMA. 2000;283(15):2008. doi:10.1001/jama.283.15.2008

[12] WHO. Training module on malaria control: Entomology and vector control. Geneva/Brazzaville. Malaria entomology and vector control: Guide for participants. World Health Organization, Regional Office for Africa. Geneva/Brazzaville; 2013. 190 p.

[13] Koekemoer LL, Kamau L, Hunt RH, Coetzee M. A cocktail polymerase chain reaction assay to identify members of the *Anopheles funestus* (Diptera: Culicidae) group. The American Journal of Tropical Medicine and Hygiene. 2002;66(6):804–11. doi:10.4269/ajtmh.2002.66.804

[14] 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. doi:10.4269/ajtmh.1993.49.520

[15] WHO. Test procedures for insecticide resistance monitoring in malaria vector mosquitoes - 2nd ed. Geneva: World Health Organization; 2016. 54 p.

[16] WHO. Manual for Monitoring Insecticide Resistance in Mosquito Vectors and Selecting Appropriate Interventions. 1st ed. Geneva: World Health Organization; 2022. 65 p.

[17] Higgins JPT, Thompson SG, Deeks JJ, Altman DG. Measuring inconsistency in meta-analyses. BMJ. 2003;327(7414):557–60. doi:10.1136/bmj.327.7414.557

[18] Thompson SG, Higgins JPT. How should meta-regression analyses be undertaken and interpreted? Statistics in Medicine. 2002;21(11):1559–73. doi:10.1002/sim.1187

[19] Egger M, Smith GD, Schneider M, Minder C. Bias in meta-analysis detected by a simple, graphical test. BMJ. 1997;315(7109):629–34. doi:10.1136/bmj.315.7109.629

[20] R Core Team. R: A language and environment for statistical computing. Vienna, Austria: R Foundation for Statistical Computing; 2024.

[21] N'Do S, Bayili B, Kaboré J 1er J, Bandibabone BJ, Zawadi MB, Belem AMG, et al. Mosquito species composition and distribution dynamics in Kalehe Territory, Democratic Republic of the Congo: a focus on *Anopheles funestus* s.s. and *Anopheles gambiae* s.s. International Journal of Innovation and Applied Studies. 2025:50–5.

[22] Lynd A, Oruni A, Hof AE van't, Morgan J, Naego LB, Pipini D, et al. Insecticide resistance in *Anopheles gambiae* from the northern Democratic Republic of Congo, with extreme knockdown resistance (kdr) mutation frequencies revealed by a new diagnostic assay. Malaria Journal. 2018. doi:10.1186/s12936-018-2561-5

[23] Wat'senga F, Agossa F, Manzambi E, Illombe G, Mapangulu T, Muyembe T, et al. Intensity of pyrethroid resistance in *Anopheles gambiae* before and after a mass distribution of insecticide-treated nets in Kinshasa and in 11 provinces of the Democratic Republic of Congo. Malaria Journal. 2020. doi:10.1186/s12936-020-03240-6

[24] Loonen JACM, Dery DB, Musaka BZ, Bandibabone JB, Bousema T, van Lenthe M, et al. Identification of main malaria vectors and their insecticide resistance profile in internally displaced and indigenous communities in Eastern Democratic Republic of the Congo (DRC). Malar J. 2020;19(1):425. doi:10.1186/s12936-020-03497-x PubMed Central PMCID: PMC7684733.

[25] Matubi EM, Kaounga GI, Zanga J, Mbuku GB, Maniania JN, Mulenda B, et al. Insecticide susceptibility of *Anopheles gambiae* s.l and identification of some resistance mechanisms in Kwilu Province in the Democratic Republic of Congo. The Pan African Medical Journal. 2020. doi:10.11604/pamj.2020.37.79.18635

[26] Metelo-Matubi E, Zanga J, Binene G, Mvuama N, Ngamukie S, Nkey J, et al. The effect of a mass distribution of insecticide-treated nets on insecticide resistance and entomological inoculation rates of *Anopheles gambiae* s.l. in Bandundu City, Democratic Repub`lic of Congo. The Pan African Medical Journal. 2021. doi:10.11604/pamj.2021.40.118.27365

[27] N'Do S, Bandibabone JB, Soma DD, Musaka BZ, Prudhomme J, Habamungu CC, et al. Insecticide resistance profiles in malaria vector populations from Sud-Kivu in the Democratic Republic of the Congo. Transactions of the Royal Society of Tropical Medicine and Hygiene. 2021;115(11):1339–44. doi:10.1093/trstmh/trab116

[28] Njoroge H, Van'T Hof A, Oruni A, Pipini D, Nagi SC, Lynd A, et al. Identification of a rapidly-spreading triple mutant for high-level metabolic insecticide resistance in *Anopheles gambiae* provides a real-time molecular diagnostic for antimalarial intervention deployment. Molecular Ecology. 2022;31(16):4307–18. doi:10.1111/mec.16591

[29] Zanga J, Metelo E, Mbanzulu K, Irish S, Mulenda B, Wumba R, et al. Susceptibility status of *Anopheles gambiae* s.l. to insecticides used for malaria control in Kinshasa, Democratic Republic of the Congo. Annales Africaines de Médecine. 2022. doi:10.4314/aamed.v15i2.2

[30] Acford-Palmer H, Campos M, Bandibabone J, N'Do S, Bantuzeko C, Zawadi B, et al. Detection of insecticide resistance markers in *Anopheles funestus* from the Democratic Republic of the Congo using a targeted amplicon sequencing panel. Scientific Reports. 2023. doi:10.1038/s41598-023-44457-0

[31] N'Do S, Bandibabone J, Musaka B, Habamungu C, Belem AMG, Chimanuka B. Evaluation de l'efficacité des appâts sucrés toxiques à base d'ivermectine contre *Anopheles funestus* s.s. et *Anopheles gambiae* s.s. résistants aux pyréthrinoïdes dans la province du Sud-Kivu en République démocratique du Congo. Science et Technique, Série Sciences de la Santé. 2024;47(1):165–79.

[32] Dennis TPW, Pescod P, Barasa S, Cerdeira L, Lucas ER, Clarkson CS, et al. Cryptic population structure and insecticide resistance in *Anopheles gambiae* from the southern Democratic Republic of Congo. bioRxiv. 2024. doi:10.1038/s41598-024-70885-7

[33] Ilombe G, Likwela JL, Lukanu P, Lulebo A, Muela N, Mariën J, et al. Effectiveness of Pyrethroid-Piperonyl Butoxide Nets Versus Standard Pyrethroid-Only Nets in Preventing Malaria in Children Under 10 Years Living in Kisantu Health Zone, Democratic Republic of the Congo. TropicalMed. 2025;10(6):172. doi:10.3390/tropicalmed10060172

[34] Vulu F, Kashamuka M, Banek K, François-Zafka R, Mampuya P, Atibu J, et al. Malaria entomological surveillance in Kinshasa Province: A longitudinal study. bioRxiv. 2025. doi:10.64898/2025.12.22.695884

[35] Nardini L, Hunt R, Dahan-Moss Y, Christie N, Christian R, Coetzee M, et al. Malaria vectors in the Democratic Republic of the Congo: the mechanisms that confer insecticide resistance in *Anopheles gambiae* and *Anopheles funestus*. Malaria Journal. 2017. doi:10.1186/s12936-017-2099-y

[36] Levitz L, Janko M, Mwandagalirwa K, Thwai K, Likwela J, Tshefu A, et al. Effect of individual and community-level bed net usage on malaria prevalence among under-fives in the Democratic Republic of Congo. Malaria Journal. 2018. doi:10.1186/s12936-018-2183-y

[37] Yunta C, Hemmings K, Stevenson B, Koekemoer LL, Matambo T, Pignatelli P, et al. Cross-resistance profiles of malaria mosquito P450s associated with pyrethroid resistance against WHO insecticides. Pesticide Biochemistry and Physiology. 2019;161:61–7. doi:10.1016/j.pestbp.2019.06.007