GSC Advanced Research and Reviews
eISSN: 2582-4597 CODEN (USA): GARRC2
Cross Ref DOI: 10.30574/gscarr
Journal homepage: https://gsconlinepress.com/journals/gscarr/

(REVIEW ARTICLE)

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Evolution of phenotypic and molecular insecticide resistance in malaria vectors in Burkina Faso (2016-2025): A systematic review and quantitative synthesis

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GSC Advanced Research and Reviews, 2026, 28(01), 264–275

Publication history: Received on 16 June 2026; revised on 25 July 2026; accepted on 28 July 2026

Article DOI: https://doi.org/10.30574/gscarr.2026.28.1.0177

Abstract

Insecticide-based vector control remains central to malaria prevention in Burkina Faso, but its effectiveness is increasingly threatened by intense and multi-mechanistic resistance in malaria vectors. This review synthesizes evidence generated between 2016 and 2025 on phenotypic resistance, resistance intensity, molecular markers, metabolic mechanisms and emerging genomic signatures in *Anopheles* populations from Burkina Faso. A systematic review and quantitative synthesis were conducted following PRISMA principles. Eligible sources reported insecticide susceptibility bioassays, resistance-intensity assays, synergist assays, target-site mutations, metabolic indicators or genomic resistance markers in malaria vectors from Burkina Faso. Because studies differed in design, insecticide panels, vector species and reporting formats, findings were summarized through structured quantitative synthesis rather than formal pooled meta-analysis. The final evidence base included 73 studies or reports, including 29 records with detailed structured extraction and 42 usable pyrethroid mortality estimates. Pyrethroid resistance was consistently reported across Sahelian, Sudano-Sahelian and Sudanian settings. In the broadest sentinel survey, mean mortality in *Anopheles gambiae* s.l. was 33.2% for deltamethrin, 24.5% for permethrin and 19.0% for alpha-cypermethrin. Resistance intensity was frequently high. Vgsc-L1014F/L995F and Vgsc-L1014S/L995S were widespread but heterogeneous, while genomic evidence indicated diversification through additional VGSC variants, ace-1/ace1 signals and copy-number variation in detoxification gene families. PBO synergist assays often increased pyrethroid mortality but rarely restored full susceptibility, indicating multifactorial resistance. Chlorfenapyr susceptibility was largely retained where tested. Between 2016 and 2025, malaria vectors in Burkina Faso shifted from widespread pyrethroid resistance toward more complex resistance systems combining target-site, metabolic and genomic mechanisms. Resistance management should prioritize mechanism-aware surveillance, chlorfenapyr-based dual-active-ingredient nets in high-resistance areas, targeted PBO-net deployment and preservation of organophosphate susceptibility through rotation and genomic monitoring.

Keywords: Burkina Faso; Malaria vectors; Insecticide resistance; Pyrethroids; *Anopheles gambiae* complex; Metabolic resistance

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1. Introduction

Malaria remains a major public-health burden in Burkina Faso, where transmission persists across ecological settings ranging from the northern Sahelian zone to the Sudano-Sahelian transition belt and the more humid Sudanian landscapes of the south-west [1–3]. Transmission is sustained by members of the *Anopheles gambiae* complex, principally *An. gambiae* s.s., *An. coluzzii* and *An. arabiensis*, with *An. funestus* group and secondary vectors such as *An. coustani* contributing locally in specific ecological contexts [3–5]. This heterogeneous vector system complicates national malaria control because species differ in behavior, seasonal dynamics, larval ecology and resistance profiles [2,6,7]. Vector control in Burkina Faso relies mainly on long-lasting insecticidal nets (LLINs), complemented in selected settings by indoor residual spraying (IRS) and other targeted interventions [8–10]. For more than two decades, pyrethroids have been the dominant active ingredient in LLINs because of their rapid knockdown effect, relative safety and historical affordability [9,11]. However, the large-scale deployment of pyrethroid-based LLINs, combined with insecticide use in agriculture, has created sustained selection pressure on mosquito populations [12–14]. This pressure is particularly important in cotton-, rice- and vegetable-growing areas of western and south-western Burkina Faso, where public-health and agricultural insecticide exposure may act jointly on the same vector populations [14–16]. Insecticide resistance in malaria vectors is not a single biological event but a multi-layered evolutionary process [11,17]. Target-site resistance reduces insecticide binding to its molecular target, most notably through knockdown resistance mutations in the voltage-gated sodium channel (VGSC), including L1014F/L995F and L1014S/L995S [18,19]. Resistance to carbamates and organophosphates may involve acetylcholinesterase variants or ace-1/ace1 copy-number changes [20]. In parallel, metabolic resistance enhances detoxification through cytochrome P450 monooxygenases, glutathione S-transferases and carboxylesterases [13,15,21]. Additional mechanisms, including cuticular changes and behavioral avoidance, may further reduce insecticide contact or penetration [12,22,23].

Burkina Faso is regarded as a West African setting where pyrethroid resistance is among the most severe [13,24,25]. By the start of the 2016-2025 review period, resistance to pyrethroids and DDT had already been documented in several vector populations, and subsequent studies increasingly moved beyond simple detection toward quantification of resistance intensity and characterization of molecular mechanisms [3,9,13]. Nationwide sentinel surveillance, local bioassay studies, experimental-hut evaluations, longitudinal genotyping and whole-genome sequencing have since provided a richer but fragmented evidence base [7–9,20]. The period 2016-2025 is particularly important because it captures a transition in the resistance landscape. Phenotypic evidence shows persistent low mortality to deltamethrin, permethrin and alpha-cypermethrin, while molecular and genomic data indicate that resistance is diversifying beyond classical kdr alleles [7,9,12,20]. Longitudinal evidence from Goden and western Burkina Faso points to species-specific trajectories, with changes in L1014F/L995F, persistence of L1014S/L995S and emergence or expansion of additional VGSC variants such as V402L, I1527T and N1570Y [7,20,21]. These patterns suggest that resistance surveillance based only on diagnostic-dose mortality or a single kdr marker is no longer sufficient [19,21]. The operational response to resistance has also evolved. PBO-synergist nets were introduced to counter cytochrome P450-mediated metabolic resistance, while dual-active-ingredient nets containing chlorfenapyr offer a non-pyrethroid mode of action that can bypass sodium-channel-based resistance [8,9,26]. IRS with organophosphates, particularly pirimiphos-methyl, remains an important option where susceptibility is retained [4,10]. These tools require local evidence on the relative contribution of target-site, metabolic and genomic mechanisms, because their effectiveness is likely to vary among ecological zones, vector species and local selection environments [9,15,21]. Despite this growing body of work, evidence remains dispersed across site-specific studies, national surveillance reports, genomic investigations and studies of residual transmission [9,13,27]. A consolidated synthesis is needed to clarify the temporal evolution, geographic distribution and mechanistic complexity of insecticide resistance in Burkina Faso, and to identify the operational implications for LLIN procurement, IRS management, resistance monitoring and future research priorities [19,21,28]. This review therefore aimed to synthesize evidence on the evolution of phenotypic and molecular insecticide resistance in malaria vectors in Burkina Faso between 2016 and 2025. Specifically, it sought to describe patterns of phenotypic susceptibility by insecticide class; summarize temporal and geographic trends in pyrethroid mortality; characterize target-site, metabolic and genomic resistance mechanisms; and draw practical implications for mechanism-aware vector-control decision-making.

2. Materials and methods

2.1. Study design and reporting approach

This study was conducted as a systematic review and quantitative synthesis of evidence on insecticide resistance in malaria vectors in Burkina Faso during 2016-2025. The review was structured according to the PRISMA 2020 principle of transparent identification, screening, eligibility assessment and inclusion [29]. Because the included studies varied

substantially in design, species, insecticides, bioassay protocols and reporting formats, the synthesis combined structured narrative interpretation with quantitative summaries of extractable mortality estimates and reported resistance-marker frequencies.

2.2. Search strategy and information sources

Candidate sources were identified using Elicit-assisted searches complemented by manual searches, reference-list screening, citation tracking and updates for recent publications. Search concepts combined Burkina Faso, malaria vectors, *Anopheles*, insecticide resistance, susceptibility, resistance intensity, kdr, metabolic resistance, PBO, Chlorfenapyr and genomic resistance. The search strategy was designed to capture phenotypic bioassay studies, molecular studies, genomic studies, experimental hut evaluations and surveillance reports relevant to malaria vector resistance in Burkina Faso.

2.3. Eligibility criteria

Sources were eligible if they reported malaria vector taxa sampled in Burkina Faso and provided at least one outcome related to insecticide resistance. Eligible outcomes included WHO tube-test mortality, CDC bottle-bioassay mortality, resistance-intensity assays, synergist bioassays, target-site mutations, metabolic indicators, detoxification-gene evidence or genomic resistance markers. Studies conducted outside Burkina Faso, studies not involving malaria vectors, studies without resistance-relevant outcomes and duplicate records without additional extractable data were excluded from the primary synthesis. Background regional or methodological references were retained only when they supported interpretation.

2.4. Study selection

Records were screened by title and abstract, followed by full-text assessment for potentially eligible reports. The final PRISMA workflow identified 750 candidate records, retained 268 reports after title and abstract screening, assessed 155 full-text reports and included 73 studies or reports in the final synthesis. Where multiple publications used overlapping datasets, the most informative source was prioritized for quantitative extraction while related papers were used to interpret mechanisms or context. The study-selection process is summarized in Figure 1.

2.5. Data extraction

Extracted variables included author and year, study design, sampling period, study localities, current administrative region assignment, vector species, life stage, insecticide tested, bioassay method, mortality estimate, resistance classification, resistance intensity, molecular markers, metabolic assays, genomic findings and main conclusions. Detailed structured extraction was available for 29 study-level records, and 42 pyrethroid mortality estimates were sufficiently complete and comparable for quantitative trend description.

2.6. Outcomes and definitions

The primary phenotypic outcome was 24 h mortality after standardized insecticide exposure. Resistance interpretation followed WHO thresholds where these were explicitly reported, with mortality below 90% interpreted as confirmed resistance, 90-97% as possible resistance requiring confirmation and 98% or higher as susceptibility [30]. Molecular outcomes included reported frequencies of Vgsc-L1014F/L995F, Vgsc-L1014S/L995S, ace-1 or ace1-related markers, and genomic indicators such as copy-number variation in detoxification gene families. Metabolic evidence was inferred from synergist assays and detoxification-gene findings.

2.7. Quantitative synthesis

Quantitative synthesis focused on estimates that were sufficiently comparable across studies. For pyrethroids, mortality estimates were grouped by year and insecticide to describe temporal changes in deltamethrin, permethrin and alpha-cypermethrin mortality. For resistance markers, reported values were summarized as representative frequencies rather than pooled meta-analytic estimates because studies differed in species composition, sampling design, genotyping targets and denominator definitions. No universal pooled estimate was calculated across all outcomes because of substantial methodological heterogeneity.

2.8. Geographic information handling

Study localities were retained as reported in the original sources and extracted for descriptive geographic interpretation. Where available, locality names and GPS coordinates were recorded during data extraction to support interpretation of the spatial distribution of evidence. Because several localities were clustered within urban or peri-

urban settings and some coordinates required field-level validation, geographic information was used descriptively rather than to produce a definitive map in the main manuscript.

2.9. Quality and interpretation considerations

Evidence was interpreted with attention to study design, sampling period, vector species, insecticide concentration, bioassay protocol and denominator size. Greater weight was given to standardized multi-site surveillance, longitudinal studies and studies combining phenotypic and molecular evidence. Single-site and single-season studies were considered informative for local patterns but were not overgeneralized to national trends.

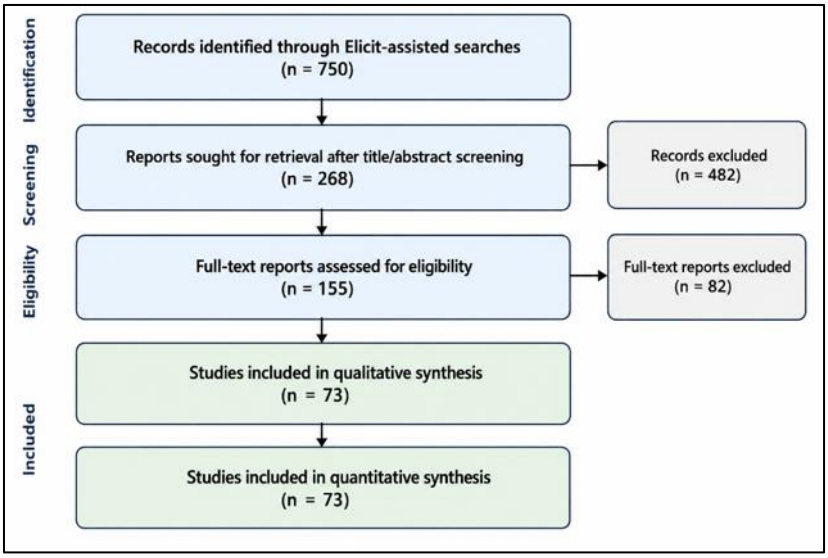

Figure 1 PRISMA 2020 flow diagram showing identification, screening, eligibility assessment and inclusion of studies

3. Results

3.1. Study selection and evidence base

The final synthesis included 73 studies or reports. Detailed structured extraction was available for 29 records, while 42 usable pyrethroid mortality estimates were available for quantitative trend description. The evidence base included nationwide surveillance, district-level longitudinal monitoring, experimental hut evaluations, seasonal entomological studies, studies around ecological features such as dams and irrigated areas, and molecular or genomic investigations [3,7–9,20]. Most detailed field evidence was concentrated in western and south-western Burkina Faso, with additional data from central, northern and multi-zone surveillance settings [12,13,16,31]. The main characteristics of the evidence base are summarized in Table 1.

3.2. Characteristics of included evidence

The included sources covered the main malaria vector taxa reported in Burkina Faso, including *An. gambiae* s.l., *An. gambiae* s.s., *An. coluzzii*, *An. arabiensis*, *An. funestus* group and *An. coustani* [2–5]. Bioassay approaches included WHO tube tests, CDC bottle bioassays, resistance-intensity assays, PBO synergist assays and experimental hut trials [8,9,15]. The most frequently tested insecticides were pyrethroids, particularly deltamethrin, permethrin and alpha-cypermethrin. Evidence was also available for DDT, bendiocarb, pirimiphos-methyl, chlorfenapyr and synergist-based combinations [4,9,13].

3.3. Geographic distribution of study sites

Study localities were distributed across several ecological and administrative contexts, with a high concentration of evidence in western and south-western Burkina Faso and additional records from central, northern and eastern localities. This concentration reflects the high number of studies conducted in agro-ecological settings such as Bobo-Dioulasso, Banfora, the Vallée du Kou, Diébougou, Dano, Gaoua and neighbouring localities, where agricultural insecticide exposure and vector-control interventions may jointly influence resistance dynamics. Locality names and available coordinates were retained during data extraction and used only for descriptive geographic interpretation.

3.4. Phenotypic resistance to pyrethroids

Pyrethroid resistance was the most consistent finding across the review. Nationwide sentinel surveillance reported mean diagnostic-dose mortality in *An. gambiae* s.l. of 33.2% for deltamethrin, 24.5% for permethrin and 19.0% for alpha-cypermethrin [9]. These values are far below the WHO susceptibility threshold and indicate severe resistance. Local and district-level studies similarly reported very low mortality in several settings, including Bobo-Dioulasso, Diébougou, Dano, Banfora, Gaoua and Soum-related localities [3,16,31,32].

3.5. Resistance intensity and temporal evolution

Resistance was not limited to diagnostic-dose failure. Intensity assays showed that several vector populations survived elevated pyrethroid concentrations, with mortality remaining below the 98% susceptibility threshold at 5x or 10x concentrations in multiple studies. In localities currently assigned to the Tannounyan region, formerly the Cascades region, deltamethrin mortality declined from approximately 38% in 2016 to approximately 17% in 2018, indicating rapid intensification of pyrethroid resistance [12]. In south-western Burkina Faso, district-level monitoring from 2019 to 2021 showed persistently low deltamethrin mortality, with some areas showing further declines under continued selection pressure [32]. The temporal evolution of pyrethroid mortality estimates is presented in Figure 2.

3.6. Non-pyrethroid insecticides and synergist evidence

Evidence for non-pyrethroid insecticides was more heterogeneous but operationally important. Bendiocarb and pirimiphos-methyl often retained higher efficacy than pyrethroids, although carbamate resistance was reported in some local contexts. Chlorfenapyr susceptibility was largely preserved where tested, with most sites showing 98-100% mortality at 24 h in bottle bioassays [9]. PBO synergist assays repeatedly increased mortality after pyrethroid exposure, implicating oxidase-mediated metabolic resistance, but complete restoration of susceptibility was uncommon. This pattern suggests that metabolic resistance is important but often coexists with target-site and other mechanisms.

3.7. Molecular resistance markers

Target-site resistance was widespread but heterogeneous. Vgsc-L1014F/L995F was common in the *An. gambiae* complex, while Vgsc-L1014S/L995S was also detected across several species and localities. Nationwide surveillance reported mean frequencies of 0.71 for Vgsc-L1014F and 0.13 for Vgsc-L1014S in *An. gambiae s.s.*, with a minority of individuals carrying both alleles [9]. In Bobo-Dioulasso, kdr-West frequencies were high in *An. arabiensis*, while kdr-East was detected at lower but non-negligible frequencies [31]. At Goden, longitudinal genotyping revealed divergent trajectories between *An. coluzzii* and *An. arabiensis*, highlighting the importance of species-specific dynamics [7].

3.8. Metabolic and genomic resistance evidence

Metabolic resistance was supported by both synergist assays and molecular evidence. PBO pre-exposure increased pyrethroid mortality in several studies, and detoxification pathways involving P450s, GSTs and esterases were reported in local populations [8,13,15]. Genomic evidence further suggests that resistance is evolving through structural and regulatory mechanisms. Whole-genome analyses identified multiple VGSC variants, ace1-related changes and copy-number variation in detoxification gene families, including P450 clusters associated with pyrethroid resistance [20,21]. The main resistance mechanisms and representative evidence are summarized in Table 2, and selected molecular and genomic indicators are shown in Figure 3.

3.9. Integrated interpretation of the decade 2016-2025

Taken together, the evidence indicates a transition from widespread diagnostic-dose pyrethroid resistance to more complex and intense resistance phenotypes [9,12,16,31]. The decade was characterized by geographic expansion, increasing resistance intensity, persistence of kdr alleles, growing evidence for metabolic resistance, and the emergence of genomic signatures that may affect future intervention performance [7,13,20,21]. These trends support the need for resistance surveillance that is both geographically representative and mechanistically detailed [19,21]. The integrated conceptual pathway linking selection pressure, resistance mechanisms, vector heterogeneity and operational response is presented in Figure 4.

Table 1 Summary characteristics of the evidence base included in the review

Characteristic	Summary
Final evidence corpus	73 studies/reports included in the final synthesis.
Detailed structured extraction available	29 study-level records with detailed structured extraction available.
Pyrethroid mortality estimates	42 usable pyrethroid mortality estimates available for quantitative trend description.
Study period	2016-2025 (with a small number of background/historical references retained for context).
Main vector taxa	**Anopheles gambiae* s.l.*, **An. gambiae* s.s.*, **An. coluzzii**, **An. arabiensis**, **An. funestus* group*, **An. funestus* s.s.* and **An. coustani**.
Main insecticide classes	Pyrethroids, organochlorines, carbamates, organophosphates, chlorfenapyr and synergist-based exposures (PBO + pyrethroids).
Main bioassay methods	WHO tube tests, CDC bottle bioassays, intensity assays at 5x/10x concentrations, experimental hut trials and synergist assays.
Main resistance mechanisms	Target-site mutations (Vgsc-L1014F/L1014S or L995F/L995S), ace-1/ace1 amplification, metabolic detoxification (P450s, GSTs, esterases), and genomic variants/CNVs.
Geographic coverage	Western, south-western, central, northern and eastern Burkina Faso, with strongest representation in western and south-western agro-ecological settings.

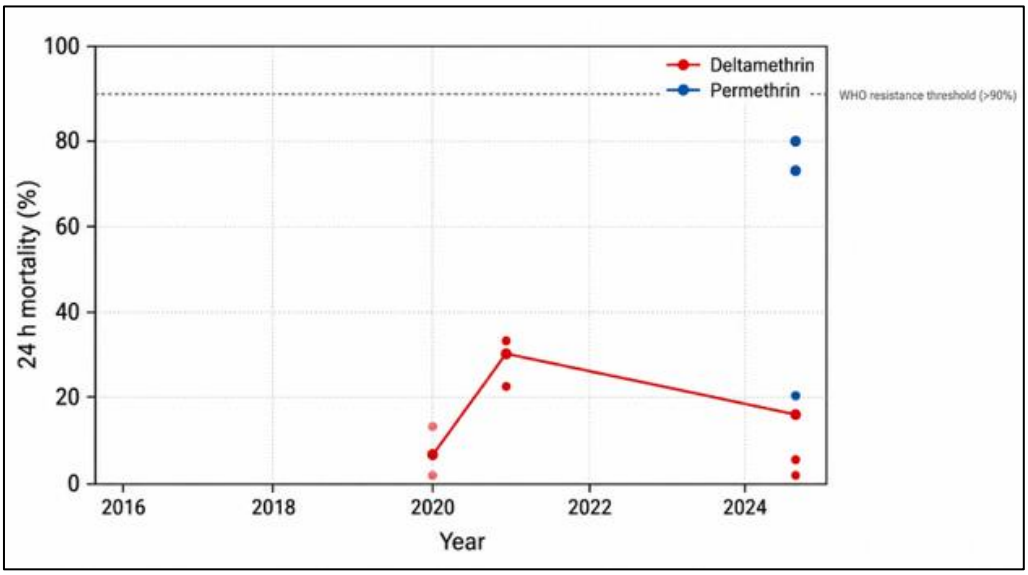

Figure 2 Temporal evolution of pyrethroid mortality estimates in malaria vectors in Burkina Faso (*Points represent extracted estimates; lines indicate annual means by insecticide*)

Table 2 Summary of resistance mechanisms reported in malaria vectors in Burkina Faso

Mechanism category	Marker/indicator	Evidence level	Representative evidence	Key studies
Target-site resistance	Vgsc-L1014F/L995F	High	Common but heterogeneous; mean L1014F frequency ~0.71 in *An. gambiae* s.s. in nationwide surveillance.	[7,9,18]
Target-site resistance	Vgsc-L1014S/L995S	High	Widespread nationally and detected in multiple species, with lower mean frequency than L1014F.	[7,9,18]
Acetylcholinesterase-related resistance	ace-1 / ace1-G280S and amplification	Moderate to emerging	Low frequencies in some phenotypic studies but genomic time-series evidence suggests amplification and rising frequencies in western Burkina Faso.	[20]
Metabolic resistance	PBO synergist response / oxidase involvement	High	PBO pre-exposure repeatedly increased pyrethroid mortality, although complete restoration was uncommon.	[8,9,16,31]
Metabolic resistance	Cytochrome P450s, GSTs, esterases	High	Detoxification enzyme pathways and GSTE2 signals reported in multiple populations and colony-based profiles.	[13,15,22]
Genomic adaptation	CNVs, detoxification clusters, signatures of selection	Emerging but important	Whole-genome studies identify novel variants, CNVs in P450 clusters and selection signals associated with resistance evolution.	[20,21]
Alternative chemistry susceptibility	Chlorfenapyr bottle bioassays	High where tested	Most sites showed 98-100% mortality at 24 h with chlorfenapyr 100 ug/bottle.	[9,32]

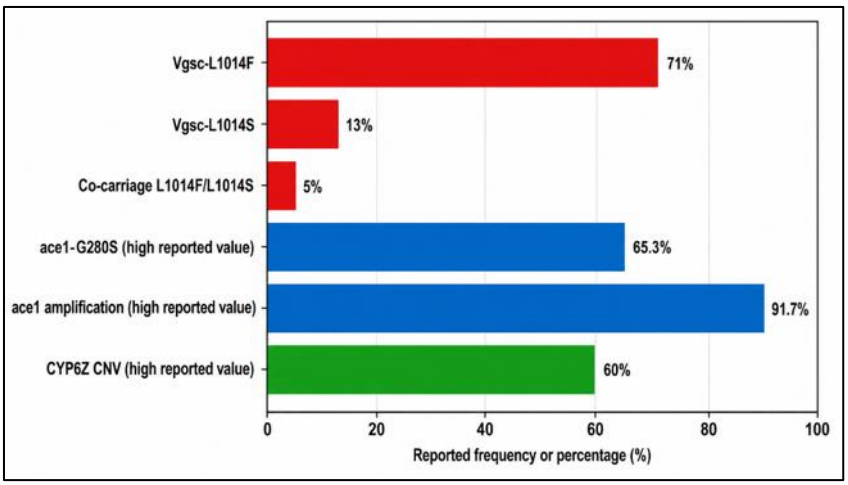

Figure 3 Selected molecular and genomic resistance indicators reported in Burkina Faso (*Values represent extracted estimates from included studies)*

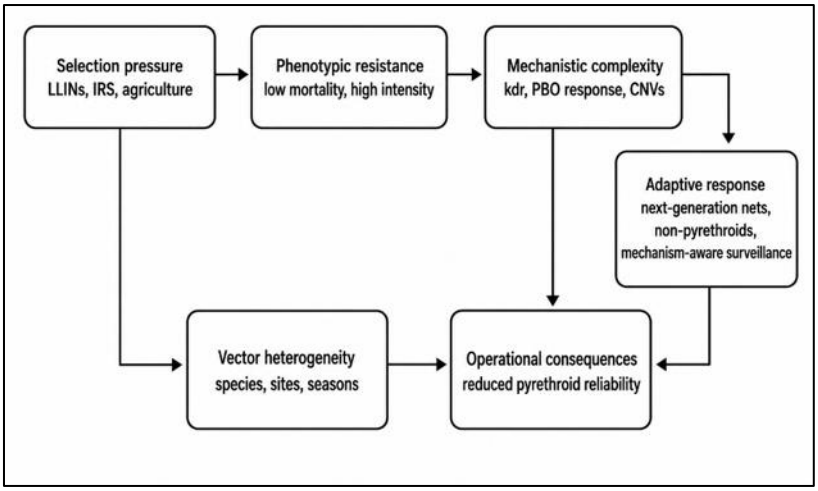

Figure 4 Conceptual framework of insecticide resistance evolution in malaria vectors in Burkina Faso (2016-2025)

4. Discussion

This systematic review and quantitative synthesis indicate that insecticide resistance in malaria vectors in Burkina Faso has progressed from widespread pyrethroid resistance to a more complex evolutionary system involving resistance intensity, target-site diversification, metabolic detoxification and emerging genomic adaptation [9,13,15,20]. The central message is therefore not only that resistance is present, but that it has become biologically entrenched and operationally consequential across multiple ecological contexts [12,16,27].

4.1. Geographic saturation and increasing resistance intensity

A major finding is the broad geographic distribution of pyrethroid resistance. Nationwide surveillance and site-specific studies consistently reported low diagnostic-dose mortality to deltamethrin, permethrin and alpha-cypermethrin across Sahelian, Sudano-Sahelian and Sudanian settings [3,9,13]. The national mean mortality estimates of 33.2% for deltamethrin, 24.5% for permethrin and 19.0% for alpha-cypermethrin indicate resistance levels far below the WHO susceptibility threshold [9,30]. Such values are not compatible with an interpretation of localized resistance; rather, they suggest countrywide saturation of pyrethroid resistance in the *An. gambiae* complex [9,18,24]. The resistance-intensity data further strengthen this conclusion. Survival at 5x and 10x diagnostic concentrations indicates that several populations can tolerate insecticide doses far above those used for standard susceptibility testing [9,15]. This distinction is operationally important because diagnostic-dose assays confirm the presence of resistance, whereas intensity assays better approximate the depth of resistance and therefore the potential risk of reduced performance of pyrethroid-only interventions [12,30]. The evidence from Banfora, Gaoua, Kaya, Bobo-Dioulasso, the Soum agropolis and other sites shows that the resistance problem is not only widespread but frequently intense [9,12,16,31].

4.2. Evolution from classical kdr resistance to diversified target-site architecture

The molecular evidence shows that target-site resistance remains a core component of the resistance landscape, but it is no longer adequately described by L1014F/L995F alone. Vgsc-L1014F/L995F is widespread and often occurs at high frequency, while L1014S/L995S is also detected in several species and sites [7,9,18]. However, longitudinal and genomic studies indicate that the target-site architecture is diversifying through additional VGSC variants, including V402L, I1527T and N1570Y [7,20,21]. This diversification helps explain why high phenotypic resistance may persist even where classical kdr trajectories differ among species [20,21]. Species-specific trajectories are particularly important. In *An. coluzzii*, some studies suggest that L1014F may decline while other VGSC variants increase, whereas in *An. arabiensis* L1014F can rise sharply over time [7,20]. These patterns imply that resistance evolution is species-dependent and may involve introgression, local selection and multi-locus haplotypes rather than a single mutation sweeping uniformly through all vector populations [7,21,33]. Surveillance programmes that monitor only L1014F risk underestimating the actual genetic complexity of pyrethroid resistance [19,21].

4.3. Metabolic resistance and the limits of PBO restoration

Target-site resistance alone cannot explain the observed phenotypes. PBO synergist assays repeatedly increased pyrethroid mortality, demonstrating an important contribution of cytochrome P450-mediated metabolic resistance

[8,9,16]. Nevertheless, full restoration of susceptibility was uncommon, and some sites showed only partial or weak recovery after PBO pre-exposure [9,15]. This pattern suggests that P450s are important but not exclusive drivers of resistance [13,21]. Genomic and biochemical evidence supports this interpretation. Detoxification pathways involving cytochrome P450s, glutathione S-transferases and carboxylesterases appear to act together, and copy-number variation in detoxification gene families points to an expanding metabolic resistance repertoire [13,15,20,21]. The implication is that PBO-pyrethroid nets may be useful where P450-mediated resistance predominates, but their benefit will be limited where resistance is driven by combined target-site mutations, non-P450 metabolic pathways, cuticular changes or behavioral avoidance [12,22,23]. This reinforces the need for local synergist testing before interpreting PBO nets as a universal solution [8,26].

4.4. Non-pyrethroid tools and the need to preserve organophosphate susceptibility

The retained activity of non-pyrethroid chemistries is one of the most important operational findings of this review. Chlorfenapyr susceptibility was largely preserved where tested, supporting the deployment of chlorfenapyr-based dual-active-ingredient LLINs in areas of intense pyrethroid resistance [9,32,34]. Because chlorfenapyr acts through oxidative phosphorylation rather than the sodium channel, it is mechanistically well suited to settings where kdr-mediated resistance is common [9,35]. Organophosphates also remain valuable, with pirimiphos-methyl, chlorpyrifos-methyl, malathion and fenitrothion generally producing high mortality in tested populations [4,13,16]. However, this apparent phenotypic susceptibility should not lead to complacency. Emerging ace-1/ace1 signals and gene-copy changes reported in genomic studies are early warnings that resistance to carbamates and organophosphates could develop if selection pressure increases [20,21]. IRS programmes should therefore be accompanied by annual monitoring of acetylcholinesterase markers and by rotation strategies that avoid replacing one exhausted insecticide class with another [10,36].

4.5. Ecological drivers and the role of agricultural co-selection

The resistance landscape in Burkina Faso is shaped by overlapping selection pressures. LLINs and IRS exert direct selection on adult mosquitoes, while agricultural insecticides can select larvae and adults in breeding sites and agro-ecosystems [13,14,23]. This interaction is particularly plausible in cotton-, rice- and vegetable-growing zones of western and south-western Burkina Faso [14,15]. Evidence of very low pyrethroid mortality in agro-pastoral or irrigated settings, and fine-scale heterogeneity within Bobo-Dioulasso and around the Soum agropolis, supports the hypothesis that local land use, pesticide exposure and vector ecology jointly influence resistance intensity [16,27,31]. These ecological drivers also explain why resistance management cannot be based only on national averages. Local differences in species composition, agricultural exposure, LLIN coverage, larval habitat type and biting behavior can produce distinct resistance profiles over short distances [2,7,23]. The Bobo-Dioulasso cluster, the Vallée du Kou, Banfora, Diébougou-Dano, Goden and Soum agropolis illustrate the need for geographically resolved surveillance capable of linking phenotypic, molecular and environmental data [3,9,16,31].

4.6. Secondary vectors and residual transmission

Another important implication is that resistance monitoring should not be limited to the primary *An. gambiae* complex. Evidence that *An. coustani* from the Vallée du Kou shows resistance to permethrin indicates that insecticide selection pressure can extend to secondary vectors [5]. In addition, *An. funestus* remains epidemiologically relevant in south-western Burkina Faso, where residual transmission may persist even under high intervention coverage [3,4,27]. As next-generation LLINs are deployed, resistance and behavior in secondary vectors should be incorporated into routine monitoring because these species may sustain residual transmission when primary vector populations are partially controlled [5,27].

4.7. Programmatic implications for resistance management

The evidence supports a mechanism-aware vector-control strategy. First, chlorfenapyr-based dual-active-ingredient LLINs should be prioritized in areas where pyrethroid resistance intensity is high and PBO restoration is incomplete [9,32,34]. Second, PBO nets should be targeted to areas where synergist assays demonstrate substantial improvement in mortality, rather than deployed solely on the assumption that metabolic resistance is P450-dominated [8,26]. Third, organophosphate-based IRS remains an important tool but should be protected through insecticide rotation and genomic surveillance of ace-1/ace1 variants [10,20,37]. Fourth, routine surveillance should combine diagnostic-dose assays, intensity assays, PBO synergist tests, species identification and molecular markers, including both classical kdr mutations and emerging VGSC variants [7,19,21].

4.8. Strengths, limitations and future research priorities

This review integrates phenotypic, molecular, metabolic and genomic evidence over a decade during which resistance monitoring in Burkina Faso became more mechanistically informative [9,13,20,21]. Its strengths include the combination of national sentinel data, localized field studies, longitudinal genotyping and genomic evidence. The review also distinguishes structured quantitative synthesis from formal pooled meta-analysis, which is important given the heterogeneity of species, insecticide panels, test protocols, denominators and reporting formats. The main limitations are the uneven geographic distribution of studies, incomplete denominator reporting in some sources, variation in bioassay methods and limited longitudinal data from several ecological zones. The south-west and western regions are better represented than the northern, eastern and some central areas. In addition, many studies report aggregated mortality or allele frequencies without complete site-, species- and year-specific denominators, limiting the ability to conduct robust pooled modelling. Future research should prioritize a harmonized national resistance database linking georeferenced sites, species, bioassay denominators, mortality estimates, resistance-intensity results, synergist assays, kdr/VGSC markers, ace-1/ace1 indicators, metabolic gene expression and agricultural pesticide exposure. Such a platform would allow Burkina Faso to move from descriptive resistance monitoring toward predictive resistance management, enabling vector-control decisions to be matched to local resistance mechanisms and ecological risk.

5. Conclusion

The decade 2016-2025 marked a transition in Burkina Faso from widespread pyrethroid resistance to increasingly complex resistance systems involving interacting target-site, metabolic and genomic mechanisms in malaria vectors. Pyrethroid resistance is now geographically widespread and frequently intense, while resistance mechanisms are diversifying beyond classical kdr mutations to include additional VGSC variants, detoxification pathways and emerging genomic signatures. The evidence supports a shift toward mechanism-aware vector control. Chlorfenapyr-based dual-active-ingredient LLINs should be prioritized where pyrethroid resistance intensity is high, PBO-pyrethroid nets should be targeted where synergist assays show clear benefit, and organophosphate IRS should be protected through rotation and genomic monitoring of ace-1/ace1 markers. Sustained national surveillance integrating phenotypic assays, molecular diagnostics, genomic tools and agricultural pesticide-use data is essential to preserve insecticide efficacy and guide adaptive malaria vector control in Burkina Faso.

Compliance with ethical standards

Disclosure of conflict of interest

No conflict of interest to be disclosed.

References

[1] Dambach P, Schleicher M, Korir P, Ouedraogo S, Dambach J, Sié A, et al. Nightly Biting Cycles of *Anopheles* Species in Rural Northwestern Burkina Faso. Journal of medical entomology. 2018. doi:10.1093/jme/tjy043

[2] Epopa PS, Collins C, North AR, Millogo A, Benedict M, Tripet F, et al. Seasonal malaria vector and transmission dynamics in western Burkina Faso. Malaria Journal. 2019. doi:10.1186/s12936-019-2747-5

[3] Soma DD, Poda S, Hien A, Namountougou M, Sangare I, Sawadogo J, et al. Malaria vectors diversity, insecticide resistance and transmission during the rainy season in peri-urban villages of south-western Burkina Faso. Malaria Journal. 2021. doi:10.1186/s12936-020-03554-5

[4] Soma DD, Zogo B, Hien DDF, Hien A, Kaboré DA, Kientega M, et al. Insecticide resistance status of malaria vectors *Anopheles gambiae* (s.l.) of southwest Burkina Faso and residual efficacy of indoor residual spraying with microencapsulated pirimiphos-methyl insecticide. Parasites & Vectors. 2020. doi:10.1186/s13071-020-04563-8

[5] Hien DDF, Badiel ABS, Bayili K, Diabaté A, Bilgo E. Insecticide selection pressure extends to the secondary malaria vector *Anopheles coustani* in the Vallée du Kou, Burkina Faso. Sciences de la Santé. 2025. doi:10.64707/revstss.v48i2.1980

[6] Zouré A, Noel G, Sombié A, Somda Z, Badolo A, Francis F. Genetic analysis and population structure of *Anopheles gambiae* complex (Diptera: Culicidae) from different ecological zones of Burkina Faso. Infection, Genetics and Evolution. 2020. doi:10.1016/j.meegid.2020.104261

[7] Perugini E, Pichler V, Guelbéogo W, Micocci M, Poggi C, Manzi S, et al. Longitudinal survey of insecticide resistance in a village of central region of Burkina Faso reveals co-occurrence of 1014F, 1014S and 402L mutations in *Anopheles coluzzii* and *Anopheles arabiensis*. Malaria Journal. 2024. doi:10.1186/s12936-024-05069-9

[8] Toe KH, Müller P, Badolo A, Traore A, Sagnon N, Dabiré RK, et al. Do bednets including piperonyl butoxide offer additional protection against populations of *Anopheles gambiae* s.l . that are highly resistant to pyrethroids? An experimental hut evaluation in Burkina Fasov. Medical Vet Entomology. 2018;32(4):407–16. Located at: Crossref. doi:10.1111/mve.12316

[9] Hien A, Soma DD, Maiga S, Coulibaly D, Diabaté A, Belemvire A, et al. Evidence supporting deployment of next generation insecticide treated nets in Burkina Faso: bioassays with either chlorfenapyr or piperonyl butoxide increase mortality of pyrethroid-resistant *Anopheles gambiae*. Malaria Journal. 2021. doi:10.1186/s12936-021-03936-3

[10] Bayili K, Ki H, Bayili B, Sow B, Ouattara A, Small G, et al. Laboratory and experimental hut trial evaluation of VECTRON ™ T500 for indoor residual spraying (IRS) against insecticide resistant malaria vectors in Burkina Faso [version 2; peer review: 3 approved]. Gates Open Research. 2022.

[11] Ranson H, Lissenden N. Insecticide Resistance in African *Anopheles* Mosquitoes: A Worsening Situation that Needs Urgent Action to Maintain Malaria Control. Trends in parasitology. 2016;32(3):187–96. doi:10.1016/j.pt.2015.11.010

[12] Sanou A, Nelli L, Guelbéogo W, Cissé F, Tapsoba M, Ouédraogo P, et al. Insecticide resistance and behavioural adaptation as a response to long-lasting insecticidal net deployment in malaria vectors in the Cascades region of Burkina Faso. Scientific Reports. 2021. doi:10.1038/s41598-021-96759-w

[13] Namountougou M, Soma DD, Kientega M, Balboné M, Kaboré DPA, Drabo S, et al. Insecticide resistance mechanisms in *Anopheles gambiae* complex populations from Burkina Faso, West Africa. Acta Tropica. 2019. doi:10.1016/j.actatropica.2019.105054

[14] Hien A, Soma DD, Héma O, Bayili B, Namountougou M, Gnankiné O, et al. Evidence that agricultural use of pesticides selects pyrethroid resistance within *Anopheles gambiae* s.l. populations from cotton growing areas in Burkina Faso, West Africa. PLoS ONE. 2017. doi:10.1371/journal.pone.0173098

[15] Williams J, Ingham V, Morris M, Toé KH, Hien A, Morgan J, et al. Sympatric Populations of the *Anopheles gambiae* Complex in Southwest Burkina Faso Evolve Multiple Diverse Resistance Mechanisms in Response to Intense Selection Pressure with Pyrethroids. Insects. 2022. doi:10.3390/insects13030247

[16] Ilboudo H, Traore FA, Bayili K, Hien DDF, Sanon EDG, Hansson H, et al. Insecticide resistance in *Anopheles gambiae* in villages around the Soum agropolis in the Center-West Region of Burkina Faso. Malaria Journal. 2025. doi:10.1186/s12936-025-05562-9

[17] Alout H, Roche B, Dabiré R, Cohuet A. Consequences of insecticide resistance on malaria transmission. PLoS Pathogens. 2017. doi:10.1371/journal.ppat.1006499

[18] Somda Z, Zanré N, Wangrawa DW, Toé HK, Sombié A, Saiki E, et al. High pyrethroid resistance is associated with high frequencies of 1014F and 1014S kdr mutations in *Anopheles arabiensis* (Diptera: Culicidae) from Ouagadougou, Burkina Faso. Journal of medical entomology. 2024. doi:10.1093/jme/tjae135

[19] Hancock P, Lynd A, Wiebe A, Devine M, Essandoh J, Wat'senga F, et al. Modelling spatiotemporal trends in the frequency of genetic mutations conferring insecticide target-site resistance in African mosquito malaria vector species. BMC Biology. 2022. doi:10.1186/s12915-022-01242-1

[20] Kientega M, Clarkson CS, Traoré N, Hui TYJ, O'Loughlin S, Millogo A, et al. Whole-genome sequencing of major malaria vectors reveals the evolution of new insecticide resistance variants in a longitudinal study in Burkina Faso. Malaria Journal. 2024. doi:10.1186/s12936-024-05106-7

[21] Kientega M, Kaboré H, Sawadogo G, Hui TYJ, Traoré N, Millogo A, et al. Genomic insights into the spread and evolution of insecticide resistance in *Anopheles gambiae* s.l. from Burkina Faso. Research Square. 2025. doi:10.21203/rs.3.rs-8172434/v1

[22] Ingham V, Anthousi A, Douris V, Harding NJ, Lycett G, Morris M, et al. A sensory appendage protein protects malaria vectors from pyrethroids. Nature. 2019. doi:10.1038/s41586-019-1864-1

[23] Taconet P, Soma DD, Zogo B, Mouline K, Simard F, Koffi A, et al. Physiological and behavioural resistance of malaria vectors in rural West-Africa : a data mining study to address their fine-scale spatiotemporal heterogeneity, drivers, and predictability. bioRxiv. 2024. doi:10.1101/2022.08.20.504631

[24] 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

[25] 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

[26] Hien A, Maiga S, Bayili K, Ouattara AY, Soma DD, Bationo R, et al. The Entomological Efficacy of Piperonyl Butoxide (PBO) Combined with a Pyrethroid in Insecticide-Treated Nets for Malaria Prevention: A Village-Based Cohort Study Prior to Large-Scale Deployment of New Generation Mosquito Nets in Burkina Faso. Advances in Entomology. 2024. doi:10.4236/ae.2024.123018

[27] Kouadio KWU, Amara MF, Soma DD, Dabiré R, Diabaté A, Gnankiné O, et al. Residual Malaria Transmission in Western Burkina Faso: Vector Behavior, Insecticide Resistance, and the Efficacy Limits of Next-Generation LLINs. Acta Tropica. 2025. doi:10.1016/j.actatropica.2025.107824

[28] Ngaffo KL, Soma DD, Hien AS, Delphine KO, Maiga S, Kaboré DPA, et al. Impact of combined vector control interventions on *Anopheles gambiae* sensu lato resistance dynamics in a high pyrethroid resistance settings in Southwestern Burkina Faso. Malaria Journal. 2025. doi:10.1186/s12936-025-05702-1

[29] 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

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

[31] Amara MF, Namountougou M, Konaté H, Kouadio KWU, Yaméogo KB, Kagoné ST, et al. Insecticide resistance and malaria transmission indicators in *Anopheles gambiae* s.l. in Bobo-Dioulasso, Burkina Faso: implications for vector control strategies. Tropical Medicine and Health. 2025. doi:10.1186/s41182-025-00853-y

[32] Tapsoba M, Guelbéogo W, Sanou A, Zongo S, Gogue C, Debe S, et al. Differential effects of dual and synergist-based insecticide-treated bed nets on pyrethroid resistance and L995F/S knockdown resistance mutation dynamics in *Anopheles gambiae* s.l. populations in south-western Burkina Faso. Parasites & Vectors. 2025. doi:10.1186/s13071-025-07190-3

[33] Hanemaaijer MJ, Higgins H, Eralp I, Yamasaki Y, Becker N, Kirstein OD, et al. Introgression between *Anopheles gambiae* and *Anopheles coluzzii* in Burkina Faso and its associations with kdr resistance and *Plasmodium* infection. Malar J. 2019;18(1):127. doi:10.1186/s12936-019-2759-1

[34] Tapsoba M, Guelbéogo W, Sanou A, Zongo S, Gogue C, Debe S, et al. Three-year trends in malaria transmission parameters under deployment of Interceptor®G1, Interceptor®G2 and PermaNet®3.0 insecticide-treated bed nets in South-Western Burkina Faso. Malaria Journal. 2025. doi:10.1186/s12936-025-05732-9

[35] Alzain HM, Alkhunaizi HA. Efficacy of Interceptor® G2 Long-Lasting Insecticidal Net Against Pyrethroid-Resistant Malaria Vector *Anopheles gambiae* s.l.: A Systematic Review and Meta-Analysis. International journal of research and review. 2025. doi:10.52403/ijrr.20251011

[36] Sherrard-Smith E, Griffin J, Winskill P, Corbel V, Pennetier C, Djènontin A, et al. Systematic review of indoor residual spray efficacy and effectiveness against *Plasmodium falciparum* in Africa. Nature Communications. 2018. doi:10.1038/s41467-018-07357-w

[37] Soma DD, Zogo B, Somé A, Tchiekoi BN, Hien DDF, Pooda HS, et al. *Anopheles* bionomics, insecticide resistance and malaria transmission in southwest Burkina Faso: A pre-intervention study. PLoS ONE. 2020. doi:10.1371/journal.pone.0236920