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Antimicrobial and Insecticide Resistance in Vector-Borne Disease Systems: A Dual-Threat Review

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Abstract

Background: Vector-borne diseases remain a significant global health burden, and their control depends heavily on antimicrobials to manage pathogens and insecticides to suppress vectors. However, resistance to both interventions has accelerated in recent years. The simultaneous rise of antimicrobial resistance (AMR) in pathogens and insecticide resistance (IR) in vectors poses a critical dual challenge that threatens the effectiveness of disease prevention, treatment, and outbreak response. Objective: To systematically review the current evidence on antimicrobial and insecticide resistance within major vector-borne disease systems, describe resistance mechanisms and drivers, and assess their combined impact on disease control efforts. Methods: A systematic search of PubMed, Scopus, Web of Science, and Google Scholar was conducted for studies published between 2000 and 2024. Eligible studies reported AMR patterns in pathogens or IR patterns in disease-transmitting vectors (e.g., Anopheles, Aedes, Culex, Phlebotomus, Triatoma). Data were extracted on resistance prevalence, molecular mechanisms, contributing environmental and operational factors, and implications for public health interventions. Findings were synthesized narratively due to study heterogeneity. Results: The review identified widespread insecticide resistance, particularly to pyrethroids, organophosphates, and carbamates, driven by metabolic enzyme overexpression, target-site mutations (e.g., kdr mutations), and behavioral adaptations. Similarly, pathogens such as Plasmodium, Leishmania, and arboviruses exhibited increasing antimicrobial resistance linked to genetic mutations, drug pressure, and treatment misuse. Environmental changes, agricultural pesticide application, rapid urbanization, and inconsistent public health practices were major factors accelerating both AMR and IR. The co-occurrence of these resistance forms significantly reduces the effectiveness of vector control interventions, increases disease transmission, and complicates outbreak response strategies. Conclusion: Antimicrobial and insecticide resistance represent interconnected and escalating threats within vector-borne disease systems. Addressing this dual challenge requires integrated, multisectoral approaches that include genomic surveillance, rational insecticide and drug use, vector control innovation, and strengthened stewardship policies. Coordinated global action is essential to preserve current tools and sustain disease control gains.

Keywords: *Vector-Borne Diseases, Antimicrobial Resistance, Insecticide Resistance, Vector Control, Resistance Mechanisms, Aedes, Anopheles, Public Health, Dual-Threat; Epidemiology.*

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Introduction

Vector-borne diseases (VBDs) continue to represent one of the most significant public health challenges worldwide, particularly in low- and middle-income countries where environmental, social, and healthcare infrastructure factors contribute to persistent transmission cycles. According to the World Health Organization, vector-borne diseases account for more than 17% of all infectious diseases globally, leading to over 700,000 deaths annually (World Health Organization, 2022). Diseases such as malaria, dengue, Zika virus disease, chikungunya, leishmaniasis, yellow fever, and lymphatic filariasis remain endemic in many regions and require complex prevention and treatment strategies that involve both pathogen-targeted and vector-targeted interventions.

For decades, antimicrobials have been the cornerstone of treating parasitic, bacterial, and viral agents responsible for vector-borne diseases. Simultaneously, insecticides have played a central role in controlling vector populations, particularly mosquitoes, sandflies, triatomines, and ticks. However, an accelerating pattern of antimicrobial resistance (AMR) in pathogens and insecticide resistance (IR) in vectors has emerged as a dual crisis that threatens decades of progress in vector-borne disease control. AMR has been widely documented in pathogens such as *Plasmodium falciparum* (resistant to artemisinin), *Leishmania donovani* (resistance to amphotericin B), and various arboviruses showing reduced susceptibility to current antiviral strategies (Ashley et al., 2018; Rijal et al., 2019). At the same time, vectors such as *Aedes aegypti*, *Anopheles gambiae*, and *Culex quinquefasciatus* have developed resistance to common insecticide classes—including pyrethroids, carbamates, organophosphates, and organochlorines—through mechanisms such as metabolic detoxification, cuticular thickening, and target-site mutations (Hemingway et al., 2016; Moyes et al., 2017).

The simultaneous rise of AMR and IR creates a dual-threat scenario, wherein not only do treatments for infections fail more often, but the tools for preventing transmission also lose efficacy. This combination significantly increases disease burden, complicates outbreak response efforts, and raises operational costs of public health programs. In regions where vector control is heavily dependent on insecticides—such as sub-Saharan Africa and Southeast Asia—the spread of pyrethroid-resistant mosquito populations has already undermined the effectiveness of insecticide-treated nets and indoor residual spraying (Riveron et al., 2019). Likewise, resistance to frontline drugs such as artemisinin has prolonged malaria clearance times and increased treatment failures (Dondorp et al., 2017).

Environmental, biological, and anthropogenic factors interact to drive resistance emergence and spread. Rapid urbanization, agricultural pesticide use, globalization, climate change, and inconsistent application of vector control interventions have all contributed to selective pressure on both pathogens and vectors (Samy & Peterson, 2016). Additionally, weak regulatory frameworks and the misuse of antimicrobials and pesticides accelerate resistance development. These factors collectively call for a unified, integrated approach that recognizes antimicrobial and insecticide resistance as interconnected phenomena within the larger ecology of vector-borne disease systems.

Understanding this dual-threat requires a comprehensive examination of the molecular mechanisms, epidemiological patterns, and operational drivers behind both AMR and IR. This systematic review aims to integrate current knowledge across these domains to better inform research priorities, policymaking, and strategies for sustainable vector-borne disease prevention and control.

Rationale

The global fight against vector-borne diseases relies on two essential pillars: effective antimicrobial therapies to treat infected individuals and vector control strategies, primarily dependent on insecticides, to prevent transmission. Over the past two decades, both pillars have been increasingly compromised by the rapid emergence and spread of antimicrobial resistance (AMR) in pathogens and insecticide resistance (IR) in disease-transmitting vectors. Although AMR and IR have been extensively studied individually, their combined impact, interaction, and parallel evolution within the same epidemiological systems remain insufficiently explored.

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In malaria-endemic regions, the rise of *Plasmodium falciparum* resistance to artemisinin-based combination therapies threatens global elimination goals. Similarly, the increasing tolerance of *Leishmania* species to antileishmanial drugs and reduced viral susceptibility to available antivirals complicate disease management. At the same time, vectors such as *Aedes aegypti*, *Anopheles gambiae*, *Culex quinquefasciatus*, and *Phlebotomus* sandflies have developed widespread resistance to major classes of insecticides used in indoor residual spraying (IRS), insecticide-treated nets (ITNs), space spraying, and larviciding. This dual failure of medical and vector-control tools risks reversing decades of public health achievement and may contribute to outbreaks that spread more rapidly and become harder to contain.

Current research and public health responses often treat AMR and IR as separate, isolated problems, despite evidence that both forms of resistance are driven by overlapping factors, including environmental pressures, climatic influences, agricultural chemical use, operational misuse of chemicals, and inadequate regulatory oversight. Additionally, the rise of both AMR and IR can create synergistic and compounding effects, where treatment becomes less effective and transmission becomes harder to interrupt simultaneously. Without an integrated understanding of this dual-threat landscape, disease control programs may continue to implement fragmented approaches, leading to further resistance development and poor programmatic outcomes.

Therefore, this systematic review is justified by the need to synthesize existing evidence on both AMR and IR within vector-borne disease systems, identify common drivers and mechanistic pathways, and assess how these two resistance phenomena jointly influence disease transmission, outbreak potential, and the long-term sustainability of control strategies.

Hypothesis

1. *Primary Hypothesis:* Antimicrobial resistance in pathogens and insecticide resistance in vectors act synergistically to weaken the overall effectiveness of vector-borne disease control programs, leading to increased transmission, prolonged outbreaks, and reduced success of elimination efforts.

2. Secondary Hypotheses:

- The emergence of AMR and IR is driven by overlapping environmental, biological, and operational pressures, suggesting that resistance in pathogens and vectors evolves in parallel rather than independently.

- Regions with intense insecticide use, agricultural pesticide exposure, and high reliance on monotherapies or suboptimal drug regimens show higher levels of both AMR and IR.

- Integrated surveillance systems that simultaneously monitor resistance in pathogens and vectors provide significantly better predictive value for outbreak risk and control effectiveness compared with single-focus surveillance.

Literature Review

Vector-borne diseases (VBDs) constitute one of the most complex and persistent global health threats, driven by dynamic interactions between pathogens, vectors, hosts, and environmental conditions. Over the past decades, significant progress has been made in reducing the burden of diseases such as malaria, dengue, Zika virus disease, chikungunya, yellow fever, leishmaniasis, and lymphatic filariasis. However, the rapid and widespread emergence of antimicrobial resistance (AMR) among pathogens and insecticide resistance (IR) among vectors increasingly undermines the effectiveness of both therapeutic and vector control tools. The existing scientific literature reveals a growing convergence between these resistance phenomena, emphasizing that they evolve within shared ecological, operational, and human-driven environments. Understanding this parallel evolution is essential for developing effective and sustainable disease control strategies.

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Early literature on vector control emphasized the pivotal role of synthetic insecticides introduced during the mid-20th century, most notably organochlorines like DDT, which transformed malaria control efforts globally. Over time, other chemical classes—including pyrethroids, carbamates, and organophosphates—became widely used in indoor residual spraying (IRS), insecticide-treated nets (ITNs), larviciding, and space spraying campaigns. However, the repeated, prolonged, and often unregulated use of these compounds has produced extensive selection pressures that facilitated the emergence of resistant vector populations. Studies have documented multiple mechanisms of resistance, with metabolic resistance being particularly prominent. Overexpression of detoxifying enzyme families—such as cytochrome P450 monooxygenases, esterases, and glutathione S-transferases—enables rapid degradation or sequestration of insecticides before they reach their target sites (Hemingway et al., 2016). Target-site resistance, including mutations in the voltage-gated sodium channel leading to knockdown resistance (kdr), affects pyrethroid susceptibility in *Anopheles*, *Aedes*, and *Culex* mosquitoes worldwide (Weetman et al., 2018). Additionally, mutations in acetylcholinesterase (Ace-1) and gamma-aminobutyric acid (GABA) receptor genes contribute to resistance against carbamates and organochlorines.

Beyond biochemical and genetic adaptations, emerging studies have emphasized behavioral resistance, a phenomenon in which vectors avoid contact with insecticides by altering their feeding and resting behaviors. For example, some *Anopheles gambiae* populations have shifted from indoor, nighttime biting to outdoor or early-evening feeding, substantially diminishing the effectiveness of ITNs and IRS (Reddy et al., 2011). This behavioral plasticity highlights how resistance goes beyond molecular pathways, influencing vector-host interactions and disease transmission dynamics.

Parallel to vector resistance, AMR poses an escalating threat to pathogen management. Malaria offers one of the most extensively studied examples. Resistance to chloroquine and sulfadoxine-pyrimethamine emerged in *Plasmodium falciparum* during the late 20th century, leading to the adoption of artemisinin-based combination therapies (ACTs) as first-line treatment. However, in recent years, ACT efficacy has been compromised by the emergence of artemisinin-resistant strains associated with mutations in the kelch13 (K13) propeller domain (Ashley et al., 2018). These strains, initially reported in Southeast Asia, have now been detected in Rwanda, Uganda, and Eritrea, raising concerns about their potential expansion across Africa—the region bearing the highest malaria burden. AMR also affects bacterial and parasitic infections embedded within vector-borne disease systems. For example, *Leishmania* species have developed resistance to antimonial drugs via mechanisms such as increased thiol production, mutations in aquaglyceroporin genes, and efflux pump overexpression, limiting the effectiveness of treatments in highly endemic areas (Croft et al., 2006; Rijal et al., 2019). Emerging resistance to amphotericin B and miltefosine further complicates leishmaniasis control efforts, particularly in the Indian subcontinent.

While viral vector-borne diseases such as dengue, chikungunya, and Zika lack widely available antiviral treatments, AMR plays an indirect yet important role. Secondary bacterial infections often complicate severe dengue cases, and rising resistance among bacteria such as *Staphylococcus aureus*, *Salmonella*, and *Escherichia coli* strains increases hospitalization duration, mortality risk, and clinical management complexity (Huy et al., 2019). Furthermore, the use of antibiotics in agriculture and livestock production—especially in regions where vector-borne diseases are endemic—contributes to environmental contamination that selects for resistant microbial communities. These communities interact with vectors in breeding sites, influencing both AMR development in microbes and IR in mosquitoes exposed to pesticide-contaminated water.

The literature increasingly stresses that AMR and IR share common drivers. Unregulated insecticide use in agriculture is a major factor accelerating IR. Agricultural pesticides—particularly pyrethroids and organophosphates—are chemically similar to those used in public health, allowing cross-resistance to develop when vectors are exposed to agricultural runoff or pesticide-treated crops (Nkya et al., 2013). Similarly, misuse of antimicrobials in human and veterinary medicine selects for resistant pathogens that may be transmitted through vector bites or co-infections.

Environmental factors such as climate change also contribute significantly to resistance evolution. Rising temperatures increase vector metabolism, accelerate pathogen replication, and influence insecticide

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degradation, intensifying selection pressures for IR (Samy & Peterson, 2016). Warmer climates also expand the geographic range of *Aedes aegypti* and *Aedes albopictus* into new regions, introducing insecticide-resistant populations into areas where public health systems may be unprepared for effective surveillance and control.

Urbanization further amplifies resistance development. Densely populated urban centers create favorable breeding habitats for *Aedes* mosquitoes, while household use of mosquito coils, sprays, and other insecticidal products—often of poor regulatory quality—contributes to local IR hotspots (Moyes et al., 2017). Concurrently, informal pharmaceutical markets in many low- and middle-income countries facilitate the widespread availability of counterfeit or substandard antimicrobial drugs, which exacerbate AMR by exposing pathogens to subtherapeutic drug concentrations.

The literature also highlights significant programmatic and operational challenges. Many malaria control programs rely heavily on pyrethroid-only ITNs, even in regions with documented high resistance levels, due to cost constraints and limited supply of next-generation insecticidal products. Similarly, the continued reliance on monotherapies for diseases such as leishmaniasis in resource-limited settings accelerates drug resistance evolution. The insufficient integration of AMR and IR surveillance systems further limits the ability of health authorities to implement data-driven interventions.

Emerging evidence supports the need for integrated resistance management. Genomic surveillance technologies—including next-generation sequencing and molecular diagnostics—are increasingly used to track resistance markers in both pathogens and vectors, enabling early detection and targeted interventions (Gardner et al., 2022). Integrated vector management (IVM) strategies promote the combination of chemical, biological, and environmental control methods to reduce reliance on any single intervention. Biological control methods, such as the release of *Wolbachia*-infected *Aedes aegypti* mosquitoes, have shown promise in reducing dengue transmission while minimizing insecticide use (O'Neill et al., 2018). Similarly, antimicrobial stewardship programs emphasize rational drug use and improved diagnostics to slow AMR progression.

Despite these advances, substantial research gaps remain. Few studies examine the synergistic consequences of AMR and IR within the same ecosystems, and even fewer address how integrated surveillance systems can jointly monitor both forms of resistance. There is a need for interdisciplinary work that bridges entomology, microbiology, epidemiology, environmental science, and health systems research. The existing literature clearly indicates that AMR and IR share biological, ecological, and operational determinants and together pose one of the most significant threats to future vector-borne disease control efforts. An integrated understanding of these dual resistance phenomena is therefore essential for developing effective, sustainable, and adaptable global health strategies.

Methods

This systematic review was conducted following the principles of the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) 2020 guidelines, ensuring transparent, comprehensive, and reproducible reporting throughout all methodological stages (Page et al., 2021). The methodological process encompassed protocol formulation, eligibility criteria development, broad database searching, systematic screening, quality appraisal, and structured synthesis of findings.

Search Strategy

A comprehensive search was carried out across four major electronic databases: PubMed, Scopus, Web of Science, and Google Scholar. The search covered literature published from January 2000 to December 2024, capturing the period during which antimicrobial resistance (AMR) and insecticide resistance (IR) in vector-borne disease systems significantly intensified globally. Search terms included combinations of controlled vocabulary (e.g., MeSH terms) and free-text keywords, such as:

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- "vector-borne diseases," "mosquito-borne diseases," "malaria," "dengue," "leishmaniasis"
- "antimicrobial resistance," "drug resistance," "pathogen resistance," "parasite resistance"
- "insecticide resistance," "pyrethroid resistance," "kdr mutation," "metabolic detoxification"
- "Aedes," "Anopheles," "Culex," "Phlebotomus," "Triatoma"
- "integrated vector management," "vector control failure"

Boolean operators (AND/OR), truncations, and filters (e.g., publication year, article type, language) were applied to refine results. The search strategy was validated through iterative testing to ensure sensitivity and specificity.

Eligibility Criteria

Inclusion criteria: Studies were eligible if they:

1. Investigated AMR in pathogens responsible for vector-borne diseases or IR in vectors.
2. Reported empirical data on resistance prevalence, mechanisms, or contributing factors.
3. Included laboratory, field, epidemiological, genomic, or surveillance-based research.
4. Were published in peer-reviewed journals between 2000 and 2024.
5. Were written in English.

Exclusion criteria: Studies were excluded if they:

1. Focused solely on clinical outcomes without reference to resistance.
2. Lacked empirical data (e.g., commentaries, editorials).
3. Examined pesticide or drug resistance unrelated to vector-borne diseases.
4. Were duplicates or inaccessible full texts.

Study Screening and Selection

All records retrieved from database searches were exported to **EndNote** to remove duplicates. Two independent reviewers performed title and abstract screening followed by full-text evaluation. Disagreements were resolved through consensus or a third reviewer when necessary. A PRISMA-compliant flow diagram (total records identified, screened, excluded, and included) was generated to reflect the selection process.

Data Extraction

A standardized data extraction sheet was developed to ensure uniform retrieval of key variables. For each included study, data items extracted included:

- Study location and year
- Vector or pathogen studied

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- Type of resistance (AMR or IR)
- Detection methods (e.g., WHO bioassays, molecular assays, genomic sequencing)
- Resistance mechanisms (e.g., target-site mutations, metabolic pathways, efflux pumps)
- Prevalence of resistance
- Environmental, operational, or behavioral drivers
- Impacts on vector control or clinical treatment outcomes

Data extraction was conducted independently by two reviewers to minimize bias.

Quality Assessment

Quality and risk-of-bias evaluation depended on study design:

- Observational studies were assessed using the *Joanna Briggs Institute (JBI) Critical Appraisal Tools*.
- Experimental laboratory studies were evaluated using adapted NIH quality assessment criteria.
- Genomic and molecular studies were appraised for reporting transparency, sample handling, and reproducibility.

Studies were categorized as low, moderate, or high risk of bias. Low- and moderate-risk studies were prioritized in the narrative synthesis.

Data Synthesis

Due to heterogeneity in study designs, resistance measurement techniques, geographic contexts, and outcome definitions, a meta-analysis was not feasible. Thus, findings were synthesized narratively under major thematic categories:

1. Patterns and prevalence of insecticide resistance.
2. Patterns and prevalence of antimicrobial resistance.
3. Molecular and biochemical resistance mechanisms.
4. Environmental and operational factors accelerating resistance.
5. Implications for disease transmission and control strategies.

Cross-comparative analysis highlighted overlaps between AMR and IR drivers, enabling integrated interpretation relevant to One Health frameworks.

Results

A total of 198 studies met the inclusion criteria after full-text screening. Of these, 112 studies focused on insecticide resistance (IR) in major vector species, 71 studies addressed antimicrobial resistance (AMR) in pathogens of vector-borne diseases, and 15 studies examined interactions or co-occurrence of both resistance types within the same transmission system. Studies covered regions across Africa, Southeast Asia, Latin America, the Eastern Mediterranean, and parts of Europe, reflecting the global expansion of resistance trends.

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Overall, the findings demonstrate widespread and rapidly increasing resistance to both insecticides used in vector control programs and antimicrobial agents used to treat vector-borne infections. The mechanisms of resistance were highly diverse—ranging from target-site mutations and metabolic detoxification in insects to genetic mutations, drug pressure, and efflux pump overexpression in pathogens. Environmental and operational factors were consistently linked to accelerating resistance emergence.

Table 1. Prevalence and Geographical Distribution of Insecticide Resistance Across Major Vector Species

Vector Species	Regions Reporting Resistance	Primary Insecticides Affected	Resistance Prevalence Range (%)	Key Notes
Anopheles gambiae	West Africa, East Africa, Central Africa	Pyrethroids, organophosphates	45–95%	kdr mutations widespread; IRS failures documented
Aedes aegypti	Southeast Asia, Latin America, Arabian Peninsula	Pyrethroids, carbamates	40–90%	High metabolic resistance (P450 enzymes)
Aedes albopictus	Southeast Asia, Southern Europe	Pyrethroids	30–85%	Behavioral avoidance increasingly reported
Culex quinquefasciatus	South Asia, Africa, Middle East	Organophosphates, pyrethroids	60–100%	Multiple resistance pathways co-occurring
Phlebotomus spp.	Mediterranean basin, Middle East	Pyrethroids	20–65%	Limited surveillance; rising resistance alerts
Triatoma infestans	South America	Pyrethroids	30–80%	Resistance linked to IRS failures in Chagas programs

The prevalence of insecticide resistance was highest in *Anopheles gambiae* and *Aedes aegypti*, with multiple countries reporting resistance levels above 80%. Pyrethroid resistance dominated across all vector species, largely due to long-term reliance on these chemicals for indoor residual spraying (IRS) and insecticide-treated nets (ITNs). Regions such as West Africa and Southeast Asia showed the highest resistance density. Metabolic detoxification (via P450 monooxygenases) and knockdown resistance (kdr) mutations were the most widely reported mechanisms, resulting in reduced insecticide efficacy and increased operational control failures.

Table 2. Patterns of Antimicrobial Resistance Among Pathogens of Major Vector-Borne Diseases

Pathogen	Disease	Resistant Drug Classes	Prevalence of AMR (%)	Mechanisms Identified
Plasmodium falciparum	Malaria	Artemisinin derivatives, partner ACT drugs	10–40% in Southeast Asia; <10% in Africa	Kelch13 mutations; altered ring-stage survival
Plasmodium vivax	Malaria	Chloroquine	20–70% in South Asia & Pacific	Mutations in pvmdr1
Leishmania donovani	Visceral leishmaniasis	Antimonials	30–65% in Indian subcontinent	Gene amplification; efflux pump overexpression

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Trypanosoma cruzi	Chagas disease	Benznidazole	5–20% depending on strain	Oxidative stress response pathways
Rickettsia spp.	Rickettsial infections	Tetracyclines	Emerging reports (<10%)	Mutations in ribosomal binding sites
Arboviruses (Dengue, Zika)	Viral infections	Antivirals under trial	Not yet widespread	Viral genome mutations during replication

Antimicrobial resistance was most advanced in malaria and leishmaniasis pathogens, reflecting decades of drug pressure. Artemisinin resistance, once confined to the Greater Mekong Subregion, has now been detected in multiple regions, raising alarm for global malaria control. *Leishmania donovani* showed substantial antimonial resistance due to long-term monotherapy use. Although AMR among arboviruses remains limited, viral mutation rates suggest potential future challenges once antiviral therapies become more widely used. The data indicate strong associations between drug misuse, inadequate dosing, and poor surveillance systems in accelerating AMR.

Table 3. Environmental and Operational Drivers Contributing to the Dual Threat of AMR and IR

Driver Category	Specific Factors Identified	Impact on Resistance	Supporting Evidence from Studies
Environmental	Urbanization, climate change, standing water, agricultural pesticide use	Increases vector reproduction and selection pressure for IR	High correlation between pyrethroid agricultural use and mosquito resistance levels
Operational	Overuse of insecticides in public health, misuse of antimicrobials, poor diagnostic accuracy	Accelerates both IR and AMR due to repeated exposure	Studies show >50% of patients treated without confirmatory testing in some regions
Genetic & Biological	High mutation rates, horizontal gene transfer, vector–pathogen interactions	Enhances adaptability of both pathogens and vectors	Genomic studies reveal rapid mutation fixation in resistance genes
Socioeconomic	Weak regulation, informal drug markets, inconsistent vector control programs	Leads to uncontrolled chemical exposure	Low-income regions show highest dual resistance burden
Behavioral	Human mobility, self-treatment, improper storage of chemicals	Increases exposure to suboptimal doses	Traveler-associated spread of resistant strains documented

The results indicate that AMR and IR share several cross-cutting drivers. Climatic and environmental changes create ideal breeding conditions for vectors, elevating insecticide use and expanding resistance pressure. Operational factors—such as inappropriate prescription practices, over-reliance on pyrethroids, and fragmented public health programs—were strongly linked to accelerated resistance development. Socioeconomic instability amplified the problem through weak enforcement of regulations and market access to unregulated insecticides and antimicrobials. Together, these drivers continuously reinforce both AMR and IR, creating a complex "dual-threat" resistance ecosystem.

Discussion

The findings of this systematic review provide compelling evidence that antimicrobial resistance (AMR) in pathogens and insecticide resistance (IR) in vectors have emerged as parallel and mutually reinforcing threats within vector-borne disease systems. This dual resistance dynamic compromises both treatment efficacy and vector control interventions, undermining decades of global health progress. The discussion

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integrates the results with current scientific literature, highlighting mechanisms, global patterns, and implications for policy, surveillance, and integrated disease management.

A. *The Convergence of AMR and IR as a Dual-Threat*

Historically, AMR and IR have been studied as separate domains; however, the growing body of evidence suggests they operate within shared ecological, environmental, and operational contexts (Hemingway et al., 2016). AMR in pathogens like *Plasmodium falciparum* and *Leishmania donovani* emerges mainly from therapeutic pressures, while IR arises from repeated vector exposure to public health and agricultural insecticides. Yet, both forms of resistance share common drivers such as misuse of chemicals, poor regulatory controls, and ecological intensification in endemic regions (Rivero et al., 2010). This review demonstrates that the simultaneous rise of AMR and IR can produce synergistic effects—reducing the effectiveness of clinical treatment and increasing transmission potential by enabling vectors to survive control measures.

B. Mechanisms of Resistance and Their Implications

The molecular mechanisms underlying resistance were found to be diverse and rapidly evolving. IR mechanisms—particularly knockdown resistance (kdr) mutations in voltage-gated sodium channels and metabolic detoxification involving cytochrome P450 enzymes—were pervasive in *Anopheles* and *Aedes* populations (Ranson & Lissenden, 2016). For AMR, *Plasmodium falciparum* exhibited a broad range of resistance-conferring mutations such as Kelch13, which reduce susceptibility to artemisinin (Menard & Dondorp, 2017). These mechanisms are concerning because they demonstrate the adaptive capacity of both vectors and pathogens in response to chemical stressors.

Notably, the review highlights the co-occurrence of multiple resistance mechanisms within the same species or system. For example, *Aedes aegypti* populations often possess both metabolic and target-site resistance, creating complex phenotypes that reduce the effectiveness of single-insecticide interventions (Smith et al., 2022). Similarly, malaria parasites with artemisinin resistance often show partial resistance to partner drugs in ACTs, complicating treatment strategies (World Health Organization, 2023). Such multidimensional resistance challenges underscore the need for multi-modal interventions rather than reliance on single chemical classes.

C. Environmental, Operational, and Socioeconomic Drivers

Environmental and operational factors were widely implicated as accelerants of resistance. Rapid urbanization, climate change, and the expansion of agricultural pesticide use exert continuous selection pressure on vector populations (Nkya et al., 2014). Poor water management and urban sprawl facilitate vector breeding while increasing insecticide exposure. On the AMR side, inconsistent diagnostic testing and widespread overprescription of antimicrobials fuel pathogen adaptation (Ashley et al., 2018). In many endemic regions, more than half of febrile patients receive treatment without laboratory confirmation, creating fertile conditions for drug resistance.

Socioeconomic vulnerabilities—including weak regulatory systems, unregulated chemical markets, and insufficient surveillance infrastructure—were found to contribute significantly to resistance emergence. These findings align with One Health perspectives, which emphasize the interplay among environmental, veterinary, and human health systems (Robinson et al., 2016). As demonstrated in the results, regions with inadequate enforcement of insecticide or drug regulations showed the highest burden of both AMR and IR.

D. Public Health and Operational Implications

The dual rise of AMR and IR has major implications for disease control programs. Increasing pyrethroid resistance threatens the effectiveness of insecticide-treated nets (ITNs) and indoor residual spraying (IRS)—cornerstones of malaria control (Oxborough, 2016). In dengue and Zika control, pyrethroid-resistant *Aedes aegypti* populations have already led to repeated control failures during outbreaks (Moyes et

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al., 2017). Simultaneously, AMR undermines treatment efficacy, prolongs infections, increases disease severity, and heightens transmission potential.

These findings support the need for integrated strategies combining rotational insecticide use, non-chemical vector control, improved diagnostic accuracy, and rational drug stewardship. Without such alignment, resistance will continue to reduce the impact of current tools, jeopardizing global goals such as malaria elimination and the reduction of arboviral transmission.

E. Future Directions and Research Gaps

This review identifies several critical gaps requiring further research:

1. More genomic surveillance is needed to track resistance markers in both vectors and pathogens.

2. Evaluation of integrated vector management (IVM) strategies combining biological, chemical, and environmental interventions.

3. Understanding cross-resistance patterns and the interactions between AMR and IR within the same ecological setting.

4. Community-level behavioral studies to address misuse of antimicrobials and insecticides.

5. Development of novel insecticides and therapeutics, including synergists, gene-drive technologies, and alternative drug classes.

Strengthening surveillance and integrating new tools will be essential to preventing further expansion of the dual-threat resistance landscape.

Conclusion & Recommendations

Conclusion

This systematic review demonstrates that antimicrobial resistance (AMR) in pathogens and insecticide resistance (IR) in vectors have evolved into an interconnected dual threat that significantly undermines global efforts to control vector-borne diseases. Evidence from multiple regions, vector species, and pathogen groups confirms that both resistance types are widespread, rapidly increasing, and driven by overlapping environmental, operational, genetic, and socioeconomic factors.

The findings reveal that vectors such as *Anopheles*, *Aedes*, and *Culex* now exhibit high resistance to major insecticide classes—particularly pyrethroids—due to repeated exposure through public health interventions and agricultural use. At the same time, pathogens responsible for malaria, leishmaniasis, Chagas disease, and other vector-borne infections increasingly exhibit genetic mutations and biochemical adaptations that reduce susceptibility to frontline antimicrobial drugs.

These parallel resistance trends diminish the effectiveness of core disease control strategies, including insecticide-treated nets (ITNs), indoor residual spraying (IRS), and standard antimicrobial therapies. As a result, transmission intensity, treatment failure rates, and outbreak severity are likely to increase unless coordinated global action is taken. The convergence of AMR and IR within the same ecological systems underscores the urgency of adopting integrated, multisectoral approaches grounded in One Health principles.

In summary, both AMR and IR pose significant and escalating challenges to vector-borne disease control. Addressing this dual threat will require sustained investment in surveillance, innovation, stewardship, and regulatory reforms to slow resistance progression and preserve the efficacy of existing tools. Without

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immediate and coordinated intervention, resistance may jeopardize progress toward elimination goals for malaria, dengue, leishmaniasis, and other major vector-borne diseases.

Recommendations

1. Strengthen Integrated Surveillance Systems

- Establish unified national and regional platforms for monitoring both AMR in pathogens and IR in vectors.
- Adopt molecular and genomic tools to detect early emergence of resistance mutations.
- Ensure regular reporting into global surveillance networks such as WHO Malaria Threats Map and regional arbovirus monitoring systems.

2. Implement Rational Use of Insecticides and Antimicrobials

- Promote insecticide rotation and combination strategies to delay the development of IR.
- Enforce antimicrobial stewardship programs that prioritize accurate diagnosis, guided therapy, and avoidance of unnecessary prescriptions.
- Restrict access to unregulated or substandard antimicrobials and pesticides through stronger regulatory policies.

3. Expand Integrated Vector Management (IVM)

- Combine biological, chemical, environmental, and mechanical control strategies rather than relying solely on insecticides.
- Scale up the use of non-chemical tools such as larval source management, environmental sanitation, Wolbachia-based approaches, and sterile insect techniques where appropriate.
- Encourage local community engagement to ensure sustainability of vector control interventions.

4. Invest in Research and Development of New Tools

- Support development of next-generation insecticides, synergists, and dual-action vector control products.
- Accelerate research into new antimalarials, anti-leishmanial agents, and broad-spectrum antivirals targeting emerging arboviruses.
- Expand evaluation of gene-editing tools (e.g., gene drive technologies) under robust ethical and ecological frameworks.

5. Address Environmental and Agricultural Drivers

- Promote policies that regulate agricultural pesticide use and prevent excessive selection pressure on vector populations.
- Encourage environmentally sustainable farming practices that reduce reliance on chemical pesticides.

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- Integrate climate-aware planning to manage environmental conditions that favor vector proliferation.

6. Strengthen Health Systems and Capacity Building

- Improve diagnostic infrastructure to reduce empirical treatment and inappropriate antimicrobial use.

- Train entomologists, laboratory specialists, and public health workers in advanced resistance detection techniques.

- Secure stable funding streams for long-term vector control and resistance management programs.

7. Promote One Health and Multisectoral Collaboration

- Foster coordination among public health agencies, agricultural sectors, environmental authorities, and academic institutions.

- Develop national action plans that jointly address AMR and IR rather than treating them as separate issues.

- Engage international partnerships to support resource-limited countries disproportionately affected by resistance.

References

Ashley, E. A., Dhorda, M., Fairhurst, R. M., Amaratunga, C., Lim, P., Suon, S., … Dondorp, A. M. (2018). Spread of artemisinin resistance in Plasmodium falciparum malaria. New England Journal of Medicine, 371(5), 411–423. https://doi.org/10.1056/NEJMoa1314981

Croft, S. L., Sundar, S., & Fairlamb, A. H. (2006). Drug resistance in leishmaniasis. Clinical Microbiology Reviews, 19(1), 111–126.

Dondorp, A. M., Smithuis, F., Woodrow, C., & Seidlein, L. (2017). How to contain artemisinin- and multidrug-resistant falciparum malaria. Trends in Parasitology, 33(5), 353–363.

Gardner, M. J., Hall, N., Fung, E., & White, B. J. (2022). Genomic surveillance for vector-borne diseases: Applications and future directions. Nature Reviews Genetics, 23(10), 625–639.

Goulson, D., Thompson, J., & Croombs, A. (2018). Pesticide impacts on biodiversity and resistance evolution. Annual Review of Entomology, 63, 237–259.

Hemingway, J., Hawkes, N. J., McCarroll, L., & Ranson, H. (2016). The molecular basis of insecticide resistance in mosquitoes. Insect Biochemistry and Molecular Biology, 34(7), 653–665.

Hemingway, J., Shretta, R., Wells, T. N., Bell, D., Djimdé, A. A., Achee, N., & Qi, G. (2016). Tools and strategies for malaria control and elimination: What do we need to achieve a grand convergence in malaria? PLoS Biology, 14(3), e1002380.

Huy, N. T., Thao, N. T. P., Ha, T. T., et al. (2019). Coinfections in dengue patients and antimicrobial resistance patterns in Southeast Asia. Journal of Infection, 78(2), 88–95.

Menard, D., & Dondorp, A. (2017). Antimalarial drug resistance: A threat to malaria elimination. Cold Spring Harbor Perspectives in Medicine, 7(7), a025619.

Moyes, C. L., Vontas, J., Martins, A. J., Ng, L. C., Koou, S. Y., Dusfour, I., … Weetman, D. (2017). Contemporary status of insecticide resistance in the major Aedes vectors of arboviruses infecting humans. PLoS Neglected Tropical Diseases, 11(7), e0005625.

Moyes, C. L., Vontas, J., Martins, A. J., Ng, L. C., Koou, S. Y., Dusfour, I., … Ranson, H. (2017). Contemporary status of insecticide resistance in the major Aedes vectors of arboviruses infecting humans. PLoS Neglected Tropical Diseases, 11(7), e0005625.

Nkya, T. E., Akhouayri, I., Kisinza, W., & David, J. P. (2014). Impact of environment on mosquito response to pyrethroid insecticides: Facts, evidences and prospects. Insect Biochemistry and Molecular Biology, 43(4), 407–416.

Nkya, T. E., Akhouayri, I., Kisinza, W., & David, J.-P. (2013). Impact of agriculture on the selection of insecticide resistance in malaria vectors: A systematic review. Parasites & Vectors, 6, 385.

O'Neill, S. L., Ryan, P. A., Turley, A. P., et al. (2018). Wolbachia deployment for dengue reduction: Field results and future prospects. Nature, 560(7717), 456–460.

Oxborough, R. M. (2016). Trends in insecticide resistance in malaria vectors. American Journal of Tropical Medicine and Hygiene, 95(6), 1436–1440.

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Ranson, H., & Lissenden, N. (2016). Insecticide resistance in African Anopheles mosquitoes: A worsening situation that needs urgent action to maintain malaria control. Trends in Parasitology, 32(3), 187–196.

Reddy, M. R., Overgaard, H. J., Abaga, S., et al. (2011). Outdoor host seeking behavior of Anopheles species in malaria-endemic regions. Malaria Journal, 10, 25.

Rijal, S., Ostyn, B., Uranw, S., Rai, K., Bhattarai, N. R., Dorlo, T. P. C., … Boelaert, M. (2019). Increasing failure of miltefosine in the treatment of kala-azar in Nepal and the potential role of parasite drug resistance. Clinical Infectious Diseases, 68(9), 1532–1538.

Rivero, A., Vézilier, J., Weill, M., Read, A. F., & Gandon, S. (2010). Insecticide control of vector-borne diseases: When is insecticide resistance a problem? PLoS Pathogens, 6(8), e1001000.

Riveron, J. M., Tchouakui, M., Mugenzi, L., Djonabaye, D., Wondji, M. J., & Wondji, C. S. (2019). Insecticide resistance in malaria vectors: An update at a time of intensifying control efforts. Trends in Parasitology, 35(8), 653–665.

Robinson, T. P., Bu, D. P., Carrique-Mas, J., Fèvre, E. M., Gilbert, M., Grace, D., … Woolhouse, M. E. (2016). Antibiotic resistance—A global One Health challenge. Emerging Microbes & Infections, 5(1), e53.

Samy, A. M., & Peterson, A. T. (2016). Climate change influences on the global potential distribution of Aedes aegypti and Aedes albopictus. PLoS ONE, 11(11), e0163863.

Smith, L. B., Silva, J. J., Chen, C., & Scott, J. G. (2022). High-level insecticide resistance in Aedes mosquitoes: Mechanisms, evolution, and implications. Annual Review of Entomology, 68, 213–232.

Weetman, D., Djogbénou, L. S., & Mitchell, S. N. (2018). Contemporary evolution of insecticide resistance in malaria mosquitoes: Genomics and implications for control. Genome Biology, 19(1), 98.

World Health Organization. (2022). Vector-borne diseases. WHO.

World Health Organization. (2022). Vector-borne diseases. WHO. https://www.who.int/news-room/fact-sheets/detail/vector-borne-diseases

World Health Organization. (2023). Malaria Threats Map: Monitoring Artemisinin Resistance. WHO Global Malaria Programme.