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Levels and mechanisms of insecticide resistance in Southeast Asian *Aedes aegypti*: a scoping review

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Abstract

Purpose: To map published evidence on phenotypic insecticide resistance and resistance mechanisms in *Aedes aegypti* across Southeast Asia. **Methods:** This scoping review followed the JBI methodology and PRISMA-ScR reporting guidelines. PubMed, Scopus, and ProQuest were searched on September 11, 2025, for English-language primary studies published from January 1, 2015, to September 11, 2025. We included studies from Southeast Asian countries that used field or semi-field *Aedes aegypti* populations and reported WHO tube test or CDC bottle bioassay results, resistance mechanisms, or both. **Results:** We identified 416 records, removed 84 duplicates, screened 332 titles and abstracts, assessed 56 full texts, and included 26 studies from eight countries. Indonesia contributed 12 studies, and Malaysia, 6. Of the 20 studies that conducted WHO or CDC bioassays, all reported resistance to at least one insecticide, with outcomes varying by insecticide and site. Pyrethroids were the most frequently assessed class and the most commonly reported as resistant. Mechanisms were reported in 23 studies, most often VGSC *kdr* mutations V1016G (73.9%), F1534C (47.8%), and S989P (34.7%). Metabolic mechanisms were also reported, including elevated esterases (26.1%), oxidases or mixed-function oxidases (17.3%), cytochrome P450 monooxygenases (13%), and glutathione S-transferases (13%). No included studies reported cuticular or behavioral resistance. **Conclusion:** Insecticide resistance in Southeast Asian *Aedes aegypti* is widespread but heterogeneous, reflecting both target-site and metabolic mechanisms. Standardized, routine surveillance that links bioassays with mechanism testing is needed to guide insecticide choice, rotation, and integrated vector management.

Keywords: *Aedes aegypti*; insecticide resistance; scoping review; vector control

INTRODUCTION

Aedes aegypti mosquitoes are the principal vectors of several arboviral diseases, including chikungunya, dengue, Zika, and yellow fever, which have attracted global attention due to their rapid spread [1–3]. Highly anthropophilic and well adapted to man-made environments, *Aedes aegypti* flourishes in urban and suburban settings and remains deeply entrenched and widely distributed in disease-endemic regions[4]. In the absence of safe and widely available vaccines or specific antiviral treatments for most *Aedes aegypti*–borne diseases, vector control is the main strategy for preventing dengue transmission and managing outbreaks [3,4]. According to the World Health Organization, about half of the world's population is at

risk of dengue, and 100–400 million infections occur each year [5]. Dengue incidence has risen sharply worldwide, with cases reported to the WHO increasing from 505,430 in 2000 to over 14.6 million in 2024 [5]. In 2024, dengue reached a record high, affecting more than 100 countries across all continents [5]. Because most infections are asymptomatic or mild and self-managed, dengue is substantially underreported; in 2024, more than 12,000 dengue-related deaths were reported, and the Region of the Americas accounted for over 13 million cases [5]. Most countries in Southeast Asia have a high burden of dengue infection, with 3- to 5-year cyclical epidemics [6].

Effective *Aedes aegypti* control typically relies on a combination of approaches, including environmental management and elimination of breeding sites, biological control, and chemical insecticides [4]. In practice, however, insecticide-based interventions remain the most widely deployed tool because they can rapidly reduce adult mosquito populations and are relatively easy to implement at scale [4]. The major insecticide classes used in vector control include pyrethroids, organophosphates, carbamates, and organochlorines. Long-term and widespread use of these insecticides in dengue control has contributed to the development of resistance, making vector control operations more difficult [7]. The ability of a strain of an organism to withstand toxicant doses that would be fatal to most individuals in a normal population of the same species, due to physiological or behavioral adaptation, is known as resistance [8]. Insecticide resistance often leads to higher doses and more frequent applications, which can be detrimental to the environment [8].

Several resistance mechanisms have been identified, and these often occur concurrently. These include target-site (*kdr*) mutations in the voltage-gated sodium channel gene, such as V1016G/I, S989P, F1534C, and T1520I, which are strongly associated with pyrethroid resistance in Malaysia, Thailand, Indonesia, Singapore, and other regions [9–11]. Metabolic detoxification, mediated by increased activity of P450 monooxygenases (e.g., CYP9J27, CYP6CB1), glutathione S-transferases, and carboxylesterases, also contributes to resistance to pyrethroids and organophosphates [8,10,11]. Changes in cuticular penetration and mosquito behavior have likewise been described as components of resistance, although these mechanisms have been characterized less frequently and in less detail [8,9].

Several reviews have synthesized global or Asia-wide data on insecticide resistance in *Aedes* mosquitoes, including recent systematic reviews and meta-analyses [4,9,12]. However, many of these syntheses aggregate large geographic areas and may not examine resistance levels and mechanisms within Southeast Asia, as a distinct epidemiological and programmatic region, in depth [4,9,12]. Southeast Asia carries a substantial dengue burden and has long relied on insecticide-based vector control, suggesting that resistance is likely to be widespread and operationally important [3,4,9]. Unlike previous reviews that aggregated evidence at global or broader Asian levels, this scoping review specifically maps both bioassay-based resistance levels and reported resistance mechanisms of *Aedes aegypti* within the Southeast Asian context. Therefore, this scoping review aims to map the current evidence on insecticide resistance levels and resistance mechanisms in *Aedes aegypti* across Southeast Asia and to identify remaining evidence gaps to support surveillance and insecticide resistance management in the region.

METHODS

Study design, eligibility criteria, and framework

This scoping review followed the JBI methodology for scoping reviews and was reported in line with the PRISMA ScR guidelines [13]. To enhance transparency, the review protocol and supporting materials were deposited in OSF during peer-review revision: https://doi.org/10.17605/OSF.IO/V6PKC.

We developed the review questions using the Population-Concept-Context (PCC) framework. The population of interest was Aedes aegypti. The concept included phenotypic insecticide resistance levels, typically measured using World Health Organization (WHO) tube tests or Centers for Disease Control and Prevention (CDC) bottle bioassays, as well as the mechanisms underlying resistance. These mechanisms included target-site mutations in the voltage-gated sodium channel gene and metabolic resistance mechanisms. We also captured other mechanisms, such as cuticular changes and behavioral adaptations, when reported. The context was limited to Southeast Asian countries.

Eligible studies were primary research articles of any observational or experimental design that examined field or semi-field populations of Aedes aegypti from Southeast Asian countries. Studies were included if they reported at least one of the following: phenotypic insecticide resistance levels measured using WHO tube tests, CDC bottle bioassays, or other clearly described standardized bioassays; molecular resistance mechanisms, including knockdown resistance mutations; or biochemical/metabolic resistance mechanisms, including cytochrome P450 monooxygenases, esterases, glutathione S-transferases,

or carboxylesterase-related mechanisms. Studies involving multiple mosquito species were eligible only when data for Aedes aegypti were reported separately. Studies involving multiple countries were included if at least one study site was in Southeast Asia and relevant Aedes aegypti data could be extracted. Eligible articles were limited to full-text publications written in English and published between January 1, 2015, and September 11, 2025. This time frame was selected to capture contemporary evidence while retaining sufficient data for regional mapping, as insecticide resistance surveillance evidence in Southeast Asia is geographically scattered and not consistently reported annually.

Studies were excluded if they were reviews, meta-analyses, editorials, commentaries, letters, conference abstracts without full-text primary data, or modeling-only studies. Laboratory-only studies using long-established susceptible strains without field or semi-field mosquito populations were excluded. Studies were also excluded if results for Aedes aegypti could not be distinguished from those of other mosquito species, if resistance outcomes or mechanisms could not be extracted, or if the full text was not available in English.

Information sources, search strategy, and selection of evidence sources

A comprehensive literature search was conducted in PubMed, Scopus, and ProQuest on September 11, 2025. The same core search strategy was applied across databases, with database-specific syntax adapted as needed. The search terms were: ("Aedes aegypti") AND ("insecticide resistance") AND (kdr OR "knockdown resistance" OR "metabolic resistance"). Searches were limited to English-language records published from January 1, 2015, to September 11, 2025. No study design filters were applied. Grey literature, preprints, dissertations, and conference proceedings were not searched because this review focused on peer-reviewed primary research articles that were available in full text.

All retrieved records were exported to Mendeley for duplicate removal. The deduplicated library was then uploaded to Rayyan for title and abstract screening, followed by full-text assessment. Rayyan's duplicate detection feature was also used to identify any remaining duplicates. Titles and abstracts were screened against the eligibility criteria by the first reviewer. Potentially relevant articles were then assessed in full text. To reduce selection error, uncertain records and all exclusion decisions at the full-text stage were discussed with a second reviewer. Reasons for exclusion at the full-text stage were documented. Although two fully independent reviewers did not perform screening at all stages, the use of predefined eligibility criteria, discussion of uncertain records, and verification of full-text exclusion decisions helped strengthen consistency and reduce selection bias. The study selection process was documented using a PRISMA-ScR flow diagram. The flow diagram and detailed selection results are presented in the Results section.

Data collection, data analysis, and critical appraisal

In this process, the first author developed and completed a data-charting form in Microsoft Excel, which was reviewed by the second author and iteratively refined through discussion with the review team. The form included key information such as first author, year of publication, country, study location, study design, mosquito population source, bioassay method, insecticide class, specific insecticide tested, resistance level or mortality outcome, and reported resistance mechanism.

Extracted data were summarized descriptively using evidence-mapping tables and grouped by country, bioassay-based resistance level, and reported resistance mechanism. Because the included studies varied in bioassay methods, insecticide classes, diagnostic concentrations, mosquito life stages, population sources, and mechanism assays, quantitative pooling or meta-analysis was not performed. For descriptive mapping, WHO tube test results were interpreted using WHO mortality thresholds where applicable: 98–100% mortality as susceptible, 90–97% as possible or suspected resistance, and <90% as resistant. CDC bottle bioassay findings were summarized by mortality or survival at the diagnostic time reported in each study. Studies reporting multiple insecticides, sites, or mosquito populations could contribute to more than one resistance category or mechanism category. Reported mechanisms were grouped into target-site, metabolic, and other mechanisms, including cuticular or behavioral resistance when available.

A formal methodological quality appraisal was not conducted because this scoping review aimed to map the range and characteristics of available evidence rather than to assess risk of bias, determine intervention effectiveness, or generate pooled estimates. However, methodological differences across studies were considered during interpretation, particularly those in bioassay protocols, insecticides tested, diagnostic concentrations, mosquito populations, and outcome reporting.

RESULTS

A total of 416 records were identified from database searches. PubMed yielded 174 records, Scopus yielded 147 records, and ProQuest yielded 95 records. After 84 duplicate records were removed, 332 records were screened by title and abstract, and 276 records were excluded. A total of 56 full-text articles were sought for retrieval, and 56 articles were retrieved and assessed for eligibility. A total of 30 articles were excluded: 7 were conducted outside Southeast Asia, 11 did not address *Aedes aegypti* insecticide resistance, and 12 did not report resistance levels or mechanisms. Ultimately, 26 studies were included in the review (Figure 1).

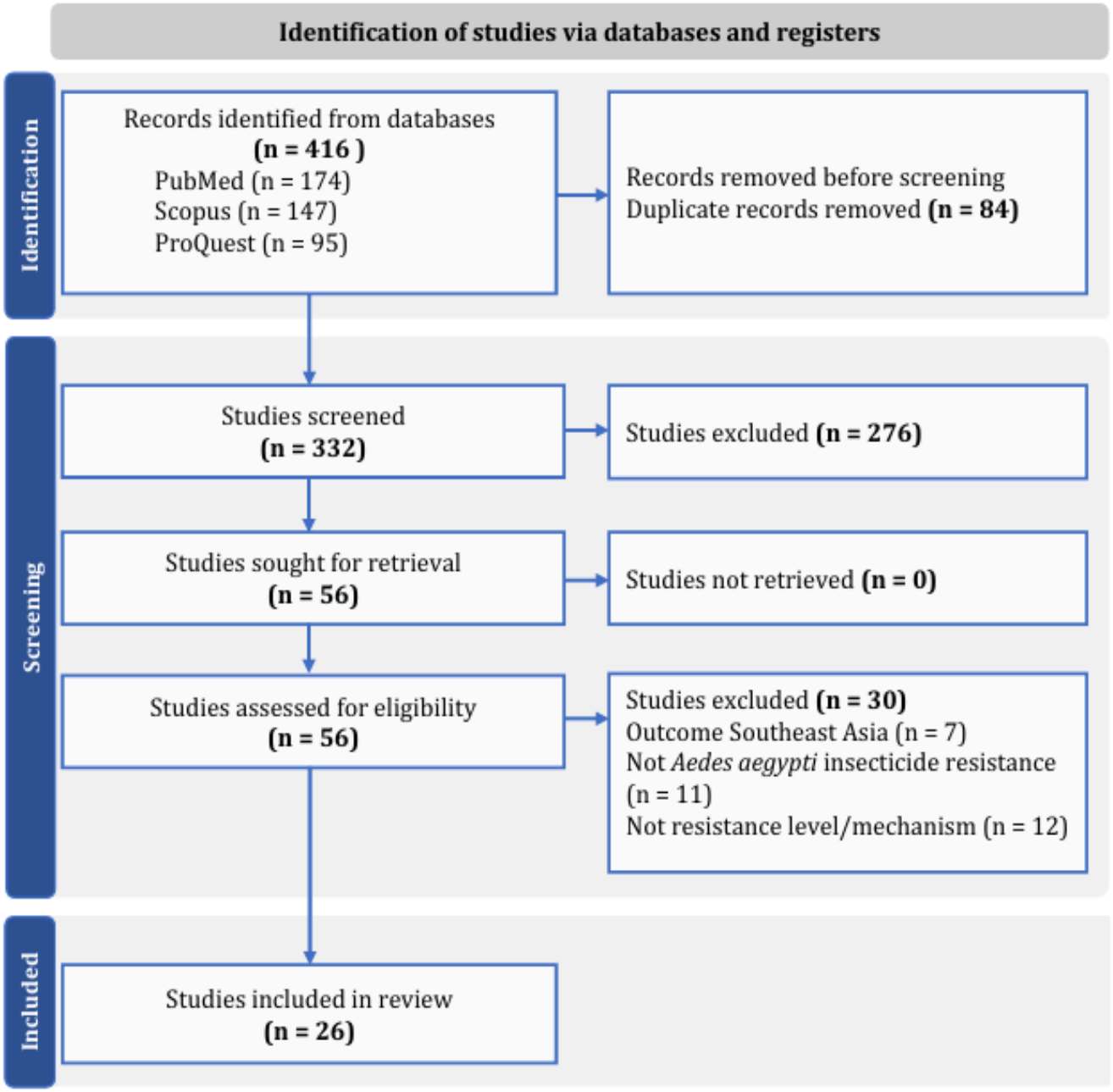

Figure 1. PRISMA flow diagram

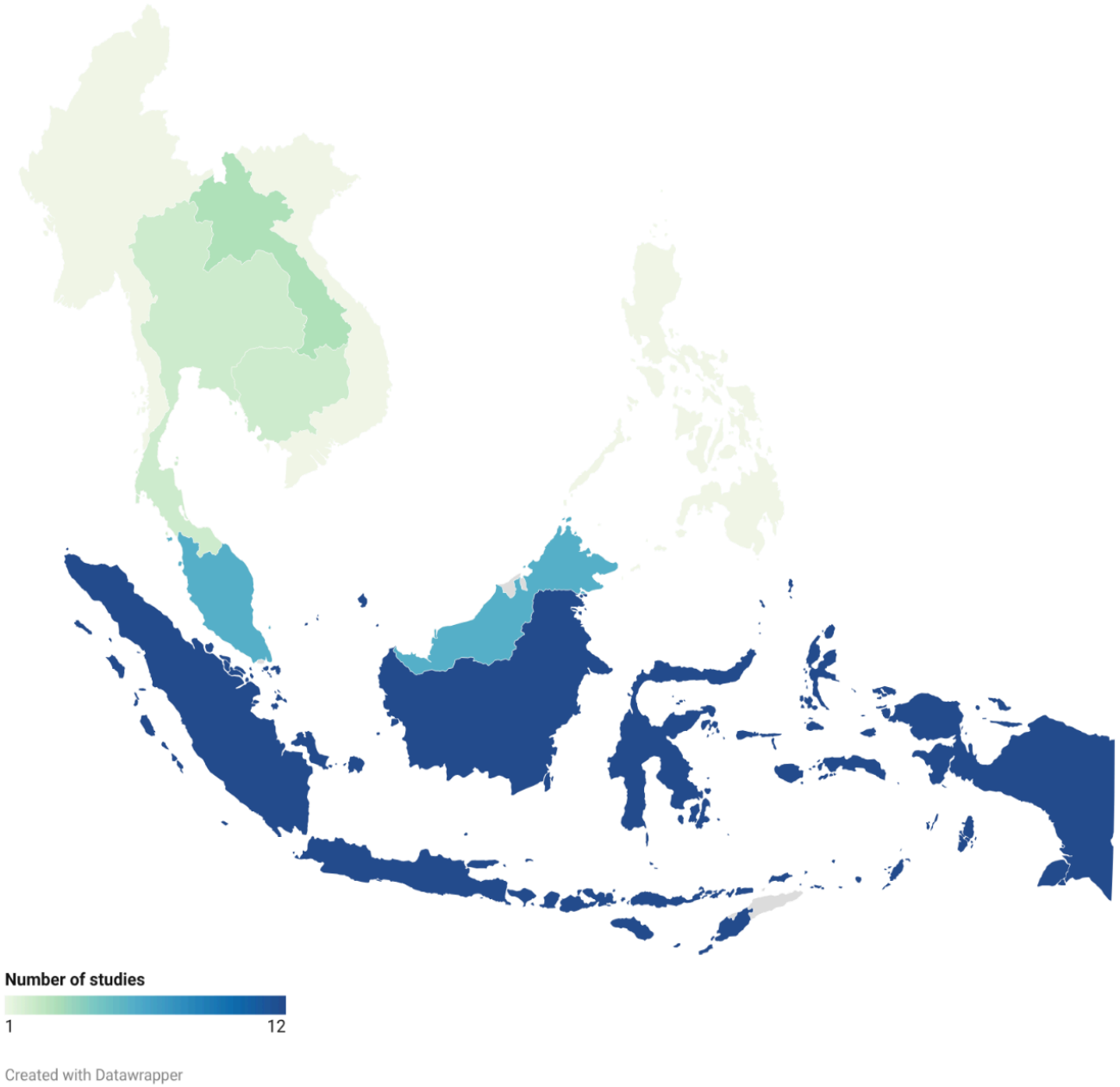

Figure 2. Geographic distribution of included studies on insecticide resistance in *Aedes aegypti* across Southeast Asia

Characteristics of the included articles

Table 1 summarizes the geographic distribution of the 26 included studies. The studies were conducted across eight Southeast Asian countries. The geographic distribution of included studies is further illustrated in Figure 2, showing that the evidence was concentrated mainly in Indonesia and Malaysia, with fewer studies from other Southeast Asian countries. Indonesia contributed the largest share of studies at 46.2%, followed by Malaysia at 23.1%. Smaller shares came from Laos at 11.5%. Cambodia and Thailand each accounted for 7.7%. Myanmar, the Philippines, and Vietnam each contributed one study, representing 3.8% of the total. All included studies reported laboratory-based assays using field-collected Aedes aegypti. One multi-country study included sites in Laos, Thailand, and Cambodia. As a result, the multi-country study is counted more than once in Table 1, although the total number of included studies remains 26.

Table 1. Characteristics of included studies by country

Country	Number of Studies	
	n	%
Cambodia [14,15]	2	7.7
Indonesia [16–27]	12	46.2
Laos [14,28,29]	3	11.5
Malaysia [1,30–34]	6	23.1
Myanmar [35]	1	3.8
Philippines [36]	1	3.8
Thailand [14,37]	2	7.7
Vietnam [38]	1	3.8

Notes: Study 14 was conducted in multiple countries (Cambodia, Laos, Thailand)

WHO/CDC-based resistance levels

Among the 20 studies that performed WHO tube tests or CDC bottle bioassays, all reported resistance to at least one insecticide. This finding suggests that *Aedes aegypti* populations are widely resistant in the sampled localities. Classification was harmonized for descriptive mapping. For WHO tube tests, 24 h post-exposure mortality was interpreted using WHO thresholds (98–100% susceptible, 90–97% possible or suspected resistance, and <90% resistant). For CDC bottle bioassays, mortality at the diagnostic time was used, where survival at the diagnostic time indicates resistance (Table 2).

Table 2. Bioassay-based insecticide resistance classification using harmonized WHO/CDC criteria among 20 studies

Level of resistance (WHO/CDC classification)	Number of studies	
	n	%*
Resistant (<90% mortality)	20	100
Possible/suspected resistance (90–97%)	4	20
Susceptible (98–100%)	7	35

Notes: *Percentages exceed 100% because studies could contribute to more than one category across insecticides and or sites; all 20 bioassay studies reported resistance to at least one insecticide.

Ten studies reported mixed phenotypic outcomes, meaning that the same study reported different bioassay-based resistance classifications across insecticides, study sites, or mosquito populations, ranging from resistant to possible/suspected resistance or susceptible. These patterns indicate variability within and between populations. Pyrethroids were the most frequently assessed insecticide class and the most commonly reported as resistant. The remaining six studies evaluated resistance mechanisms only using molecular or biochemical assays and were therefore not included in the phenotypic classification summary.

Mechanisms of insecticide resistance

A total of 23 studies reported molecular or biochemical mechanisms of insecticide resistance in *Aedes aegypti* (Table 3). Target site resistance was most frequently attributed to mutations in the voltage-gated sodium channel gene. The most commonly reported mutation was V1016G, found in 73.9% of studies, followed by F1534C at 47.8% and S989P at 34.7%. Less frequently reported markers included A1007G at 8.7%, T1520I at 4.3%, and L982W at 4.3%. One study also reported an insensitive acetylcholinesterase level of 4.3%, indicating an additional target-site mechanism relevant to organophosphate and carbamate resistance.

Metabolic resistance mechanisms were also reported. Elevated esterase or carboxylesterase activity was documented in six studies (26.1%), while increased mixed-function oxidase activity was reported in four studies (17.3%). Explicit reporting of cytochrome P450 monooxygenases appeared in three studies (13.0%), and glutathione S-transferases were also reported in three studies (13.0%). In addition, piperonyl butoxide synergist assays that indicated monooxygenase-mediated detoxification were reported in three studies, representing 13.0%. A specific metabolic mechanism, CCE cluster amplification, was reported in one study, representing 4.3%. Percentages may exceed 100% because many studies reported multiple mechanisms or multiple mutations. No included studies reported cuticular resistance or behavioral resistance mechanisms.

Table 3. Molecular and biochemical mechanisms reported (n = 23)

Mechanism category	Number of studies	
	n	%
Target-site mutations		
V1016G	17	73.9
F1534C	11	47.8
S989P	8	34.7
A1007G	2	8.7
T1520I	1	4.3
L982W	1	4.3
insensitive acetylcholinesterase (iAChE)	1	4.3
Metabolic mechanisms		
Esterase/COE activity	6	26.1
Mixed-function oxidase (MFO) / oxidase activity	4	17.3
Cytochrome P450 monooxygenase (P450)	3	13.0
Glutathione S-transferase (GST)	3	13.0
Synergist assay: piperonyl butoxide (PBO) (indicating monooxygenase/P450 involvement)	3	13.0
CCE cluster amplification	1	4.3

Notes: Percentages may exceed 100% because individual studies often reported more than one mechanism

DISCUSSION

Across Southeast Asia, pyrethroids are the most frequently studied and reported insecticide class in *Aedes aegypti* resistance literature, and resistance is commonly associated with *kdr* mutations in VGSC, particularly V1016G, F1534C, and S989P. This is operationally important because insecticide-based interventions remain widely used for *Aedes aegypti* control, and pyrethroid-based products are commonly deployed in household and public health applications [4,30].

Geographically, the evidence base in this review was uneven, with nearly half of the studies conducted in Indonesia and almost a quarter in Malaysia. At the same time, Myanmar, the Philippines, and Vietnam contributed only one study each. This is consistent with

Asia-wide evidence showing that there is no standardized protocol or system for monitoring insecticide resistance and that testing and reporting efforts vary by region, making reporting bias unavoidable [12]. Because vector-control strategies and insecticide-use patterns can differ substantially between countries, such gaps constrain region-wide inference and may obscure distinct local resistance profiles that require tailored responses. Therefore, strengthening standardized surveillance and research in underrepresented countries should be prioritized to improve regional inference [12].

Evidence from Indonesia illustrates both high pyrethroid resistance and plausible multi-source selection pressures. In Kalimantan, *Aedes aegypti* populations exhibited high resistance to deltamethrin and permethrin, and the authors noted that selection pressure may arise not only from vector control activities but also from broader insecticide use across sectors, thereby complicating control strategies [22]. Such multi-source pressure underscores the need to interpret resistance not solely as a consequence of vector control operations but within wider ecological and operational contexts [22].

The resistance patterns observed in this review are consistent with evidence that large-scale insecticide use for dengue vector control, often intensified during outbreaks, can contribute to the emergence of insecticide resistance and has become an important public health concern [9,12]. In our review, resistance outcomes varied across insecticides and sites, ranging from resistant to suspected-resistant to susceptible. This pattern is consistent with Asia-wide evidence that insecticide resistance is highly variable across space and time, and that resistance monitoring and reporting efforts vary by region, making some reporting bias unavoidable [12]. Importantly, cross-study comparability remains challenging because protocols and reporting are not always standardized; this can influence resistance classification and interpretation [12,30]. These issues highlight the need for harmonized surveillance and consistent reporting frameworks to strengthen evidence-based decision-making. *Kdr* mutations were commonly reported among studies assessing target-site mechanisms, particularly V1016G, F1534C, and S989P. These voltage-gated sodium channel substitutions are well-established contributors to pyrethroid resistance in *Aedes aegypti* [9]. Metabolic mechanisms have also been reported, including elevated cytochrome P450 monooxygenases, esterases, and GSTs, which may contribute to reduced insecticide susceptibility [9]. Field evidence from Selangor suggests that multiple resistance mechanisms may contribute, including metabolic detoxification (elevated MFO/GST), synergistic effects, and target-site (*kdr*) involvement [30].

From an operational perspective, widespread pyrethroid resistance, together with common *kdr* mutations and evidence of metabolic detoxification, suggests that the effectiveness of pyrethroid-based interventions may be reduced and may vary across settings [4,9,22,30]. Evidence suggests that *kdr* (V-GSC)-mediated resistance can confer cross-resistance between DDT and pyrethroids, with implications for insecticide selection and the interpretation of field performance [9]. Programmatic responses should therefore emphasize strengthened monitoring, evidence-based insecticide selection, and integrated vector management strategies [4,12,30]. Finally, combinations (co-occurrence) of VGSC mutations have been reported in Southeast Asia and have been associated with higher pyrethroid resistance than single mutations, reinforcing the importance of monitoring both mutation presence and co-occurrence patterns [4,9].

This review has limitations. We did not appraise methodological quality, so findings should be interpreted as a descriptive map of available evidence. One reviewer primarily conducted screening and the grey literature was not searched, which may have led to missed studies. We also limited inclusion to English-language publications and to the period January 1, 2015 — September 11, 2025. Finally, heterogeneity in study designs, bioassay protocols, and outcome reporting limited cross-study comparability and precluded quantitative pooling.

Future research should prioritize standardized longitudinal surveillance across underrepresented Southeast Asian countries, especially Myanmar, the Philippines, Vietnam, Cambodia, and Laos. Future studies should also report insecticide exposure history, diagnostic concentrations, mosquito generation, and site-level ecological context to improve comparability. Evidence on cuticular and behavioral resistance remains limited and should be incorporated into future surveillance frameworks.

CONCLUSION

Insecticide resistance in *Aedes aegypti* is widespread but heterogeneous across Southeast Asia, with pyrethroid resistance most frequently reported in the included studies. Evidence indicates that resistance is driven by multiple mechanisms, including target-site VGSC *kdr* mutations such as V1016G, F1534C, and S989P, as well as metabolic detoxification pathways. These findings are directly relevant to dengue vector control programs, suggesting that the effectiveness of

commonly used insecticides may vary across settings and may be reduced in some localities. Programmatically, this review highlights the need to strengthen routine resistance surveillance using standardized WHO/CDC bioassays, ensure consistent reporting across countries, and integrate phenotypic bioassays with mechanism testing to support decision-making. Vector control strategies should emphasize integrated vector management, including informed insecticide selection and rotation, alongside complementary nonchemical approaches to reduce reliance on any single insecticide class.

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Authors' contribution
I.E.: Conceptualization, Methodology, Data curation, Formal analysis, Writing—original draft. N.I.A.: Data verification writing—review & editing. H.S.S.: Supervision, Methodology, Writing—review & editing. M.S.A.: Supervision, Methodology, Writing—review & editing. All authors approved the final manuscript.

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Data availability
The data supporting the findings of this study are available from the corresponding author upon reasonable request.

Ethics statement
Ethical approval was not required because this study was a scoping review of previously published literature and did not involve human participants, animal subjects, or primary data collection.

Conflicts of interest
The authors declare no conflict of interest regarding the publication of this article.

Use of artificial intelligence (AI)
Portions of this manuscript were refined using ChatGPT for language editing and sentence structure improvement only. The tool was not used for data extraction, scientific analysis, interpretation of results, or the generation of core intellectual content. The authors reviewed and validated all outputs and take full responsibility for the accuracy, integrity, and originality of the final content.

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