Volume 10, Issue 10, October – 2025 International Journal of Innovative Science and Research Technology
ISSN No:-2456-2165 https://doi.org/10.38124/ijisrt/25oct222

Prevalence of Asymptomatic Malaria Infection in Malaria-Endemic Areas of Southeast Asia: A Scoping Review

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Publication Date: 2025/11/04

Abstract: Asymptomatic malaria remains a hidden barrier to elimination efforts in Southeast Asia. Individuals without symptoms often serve as undetected reservoirs of infection, making them difficult to capture through symptom-based surveillance. Understanding prevalence, species distribution, at-risk populations, and diagnostic approaches is essential to inform evidence-based interventions. The reported prevalence of asymptomatic malaria ranged from 1.03% to 88.6%, with the highest found in Southern Papua. Molecular methods such as PCR, qPCR, nested PCR and HVUSqPCR known for higher sensitivity, detected submicroscopic infections and reported prevalence up to 80% compared with RDTs and Microscopy. Among species, *P. vivax* showed the highest prevalence at 81%, followed by *P. knowlesi, P. falciparum, P. ovale, P. cynomolgi*, and *P. malariae*. High-risk groups is in border areas, forests, or highly mobile communities. The findings emphasize the need for active surveillance, sensitive diagnostics, and targeted interventions to address asymptomatic reservoirs and support evidence-informed elimination strategies in Southeast Asia.

Keywords: *Malaria Asymptomatic, Prevalence, Southeast Asia, Plasmodium Spp.*

How to Cite: Ilyas M.; Fauzi Muh; Martini (2025) Prevalence of Asymptomatic Malaria Infection in Malaria-Endemic Areas of Southeast Asia: A Scoping Review. *International Journal of Innovative Science and Research Technology*, 10(10), 2241-2247. https://doi.org/10.38124/ijisrt/25oct222

I. INTRODUCTION

Malaria remains a global public health threat, with an estimated 247 million cases and 619,000 deaths reported in 2021[1]. Southeast Asia including countries such as Indonesia, Thailand, Myanmar, Vietnam, Cambodia, Laos, Malaysia, and the Philippines continues to bear a high malaria burden. Although some countries have made progress in reducing incidence rates, malaria elimination targets still face major challenges, one of which is asymptomatic malaria infections that often go undetected by symptom-based surveillance systems[2].

Asymptomatic infections complicate elimination strategies because infected individuals do not exhibit symptoms but can still transmit the parasite through *Anopheles* mosquito bites[3]. This mode of transmission is difficult to detect through symptom-based control programs, particularly in areas with low transmission or nearing elimination. Studies across Southeast Asia have shown a wide variation in the prevalence of asymptomatic malaria, ranging from less than 2% to over 80%[2],[4], depending on geographic location, diagnostic approach, and population characteristics. Other research has demonstrated that such infections may remain transmissible even when undetected by routine methods[5].

A key factor influencing this variation is the diagnostic method used. Microscopy and rapid diagnostic tests (RDTs), which are commonly used in routine surveillance, have limited ability to detect low-density parasitemia. Global studies report that submicroscopic infections account for over 50% of total infections in low- to moderate-endemic areas [6]. In contrast, molecular techniques such as PCR and qPCR offer higher sensitivity in detecting submicroscopic infections[7],[8]. Furthermore, ultra-sensitive qPCR and loop-mediated isothermal amplification (LAMP) are emerging as promising field-deployable technologies for detecting latent infections[9],[10]. Thus, diagnostic differences contribute to variations in prevalence estimates across studies and may affect the effectiveness of elimination interventions.

High-risk populations such as border communities, forest workers, and mobile groups are often underserved by healthcare services and excluded from surveillance. These populations, however, may act as reservoirs that sustain ongoing transmission[11], [12]. Therefore, mapping scientific evidence on the prevalence and characteristics of asymptomatic malaria is essential for designing evidence-based and targeted malaria elimination policies.

Therefore, this scoping review aims to evaluate and map the scientific evidence on the prevalence of asymptomatic malaria in Southeast Asia from 2015 to 2025. The review covers aspects such as geographic distribution studies, sensitivity of diagnostic methods that used, asymptomatic malaria prevalence, *Plasmodium* species prevalence and risk factor or characteristics of the studied populations. It is anticipated that the findings of this review will provide a comprehensive overview to support more targeted and effective malaria elimination policies in the region.

II. METHODS

This scoping review was conducted based on the methodological framework proposed by Arksey and O'Malley, refined by Tricco et al. (2018) and guided by the Preferred Reporting Items for Systematic Reviews and Meta-Analyses extension for Scoping Reviews (PRISMA-ScR)[13], [14].

The objective of this review is to describe the available scientific evidence regarding the prevalence of asymptomatic malaria in Southeast Asia over the period from 2015 to 2025. A systematic literature search was performed across three databases: Scopus, PubMed, and Google Scholar. The search strategy incorporated a combination of keywords and Boolean operators: ("asymptomatic malaria" OR "subclinical malaria") AND ("prevalence") AND ("Southeast Asia" OR "Indonesia" OR "Thailand" OR "Vietnam" OR "Cambodia" OR "Laos" OR "Myanmar" OR "Malaysia" OR "Philippines" OR "Timor Leste" OR "Brunei"). The search was limited to articles published between 2015 and 2025, written in English, and freely available in full text.

Inclusion criteria were as follows: (1) observational studies (cross-sectional, cohort, or surveillance studies); (2) conducted in Southeast Asian countries; (3) reported the prevalence of asymptomatic malaria and *Plasmodium* species; (4) employed diagnostic methods such as microscopy, rapid diagnostic tests (RDT), or molecular techniques (PCR/LAMP); (5) published between 2015 and 2025; and (6) available in full-text English versions. Exclusion criteria included: (1) reviews, commentaries, protocols, or case reports; (2) animal or laboratory-based experimental studies; (3) studies not reporting the prevalence of asymptomatic malaria; (4) studies conducted outside Southeast Asia; or (5) articles not available in full text.

All retrieved articles were imported into Mendeley Reference Manager for de-duplication. Two independent reviewers screened the titles and abstracts for initial selection. Potentially relevant articles were assessed in full-text format. Any discrepancies between reviewers were resolved through discussion. Data from eligible studies were extracted using a Microsoft Excel data charting form, including the following information: author(s), year of publication, study country, study design, sample size, population characteristics, prevalence rate, *Plasmodium* species identified, and diagnostic method used.

The extracted data were analyzed descriptively and presented through thematic narrative synthesis and summary tables. The PRISMA-ScR flow diagram was used to illustrate the study selection process (Fig. 1).

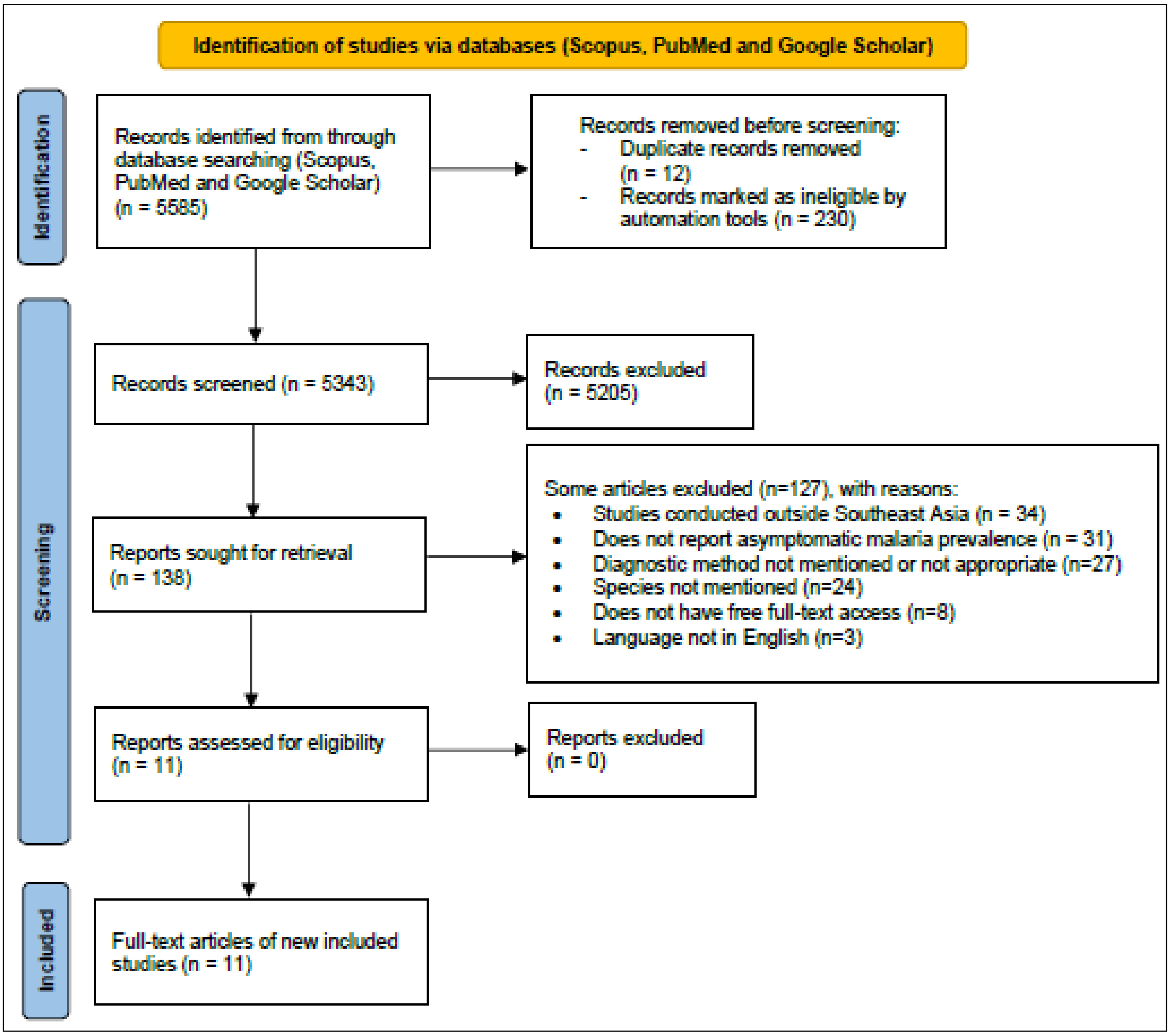

Fig. 1 PRISMA ScR Flowchart of Selection Process

III. RESULTS

The literature search conducted across Scopus, PubMed, and Google Scholar yielded a total of 5,585 articles. After the deduplication process, which removed 242 duplicate records, 5,343 articles remained for title and abstract screening. Of these, 138 articles were retrieved for full-text review, and 128 were excluded for un-met the inclusion criteria in terms of publication year, study location, or failure to explicitly report the prevalence of asymptomatic malaria. Ultimately, 11 studies were included in the final synthesis. The study selection process is illustrated in the PRISMA Scoping Review (ScR) flow diagram (Figure 1) and the summary of the key characteristics and findings from the included studies is presented in Table 1.

➢ *Geographic Distribution of Studies*

A total of 11 studies analyzed in this review originated from seven Southeast Asian countries: Indonesia, Vietnam, Laos, Myanmar, Cambodia, Malaysia, and Thailand. Countries such as Indonesia, Vietnam, and Laos were represented in more than one study, while Myanmar, Malaysia, and Thailand were each represented by a single study. Additionally, one cross-border study was conducted in the border regions of Thailand–Myanmar, Cambodia, and Vietnam. Areas with specific ecosystems such as forests, highlands, and border zones were predominantly studied due to their role as persistent transmission hotspots[2], [7], [15]. The absence of studies from Brunei Darussalam, Timor-Leste, and Singapore indicates a surveillance gap that may hinder effective coordination in regional malaria elimination efforts.

➢ *Diagnostic Methods*

The majority of studies employed molecular methods such as PCR, nested PCR, qPCR, and HVUSqPCR to detect submicroscopic infections. These methods have demonstrated higher sensitivity compared to conventional microscopy and rapid diagnostic tests (RDTs). For instance, ultra-sensitive qPCR was able to detect malaria cases that went undetected by RDTs within the same population[7]. Studies relying on RDTs and microscopy generally reported lower prevalence rates, reflecting the limitations of conventional methods in identifying low-density parasitemia[8]. Although RDTs are known for their low sensitivity, such findings may also reflect high local transmission intensity or methodological differences between studies. The use of loop-mediated isothermal amplification (LAMP) was also noted in several studies and has shown promise as a field-deployable molecular diagnostic tool[16].

➢ *Prevalence of Asymptomatic Malaria*

The prevalence of asymptomatic malaria ranged from 1.03% to 88.6%, depending on the diagnostic methods used, study location, and population characteristics. The highest prevalence (88.6%) was reported in a study conducted in southern Papua, Indonesia using PCR[15] while the lowest (1.03%) was found in Kanyah State, Myanmar using RDT[12]. These findings underscore the critical importance of selecting appropriate diagnostic methods to identify hidden reservoirs of infection that contribute to sustained malaria transmission.

➢ *Plasmodium Species Prevalence*

The most frequently detected Plasmodium species were *Plasmodium vivax* and *Plasmodium falciparum*. In addition, non-falciparum species such as *Plasmodium knowlesi*, *Plasmodium malariae*, *Plasmodium ovale*, and *Plasmodium cynomolgi* were also reported, primarily through species specific molecular methods. In Malaysia, *P. knowlesi* was identified as the dominant species in a community-based study[17]. In Cambodia, *Plasmodium cynomolgi* was detected among high-risk populations using an active surveillance approach[18], while *Plasmodium malariae* was reported in Vietnam[19]. The detection of the zoonotic *Plasmodium knowlesi* highlights the need for accurate species-level diagnosis to prevent misclassification and ensure appropriate case management[15], [20]. The highest prevalence that detected is *P. vivax* (81%), followed by *Plasmodium knowlesi*, *Plasmodium. falciparum*, *Plasmodium ovale*, *Plasmodium cynomolgi*, and *Plasmodium malariae.*

➢ *Risk Factors and Population Characteristics*

The most frequently studied populations were those residing in rural, forested, and border areas, particularly farmers, forest workers, and communities with high mobility. These groups often have limited access to healthcare services. Key risk factors identified included sleeping outdoors, not using insecticide-treated bed nets, and engaging in nighttime forest activities[7], [12], [21]. Children and women were also included in several studies, although the majority of participants were adults and male. These populations are critical targets for active case detection programs due to their potential role as undetected reservoirs of infection that are not captured by symptom-based passive surveillance systems.

Table. 1 Results of Included Studies

No	Author/ Year	Location	Study type	Sample numbers	Diagnostic test (% asymptomatic)	Plasmodium spp. Prevalence	Risk factors/ Characteristics respondent
1	Shimizu et al. / 202222	Surat Thani province, Thailand	Cross-sectional	9418	Nested-PCR. The prevalence of malaria infection was 0.45% (32 7034) in January and 0.61% (53 8671) in May 2019	P. falciparum: 15/32 (47%, January) and 14/53 (26%, May). P. vivax: 11 (34%, January) and 18 (34%, May). P. knowlesi: 1 (3%, January) and 2 (4%, May).	Staying outdoors during night-time and being males were the only common significant risk factor for malaria infection in both surveys.
2	Zaw et al. / 201712	Kayah State, Myanmar	Cross-sectional	1303	RDT, Microscopy and Qpcr. RDT: 1.03% Microscopy: 1.44% and Qpcr: is 2.3%	P. falciparum: 27.3% (3/11) P. vivax: 72.7% (8/11)	Men were at greater risk of infection by Plasmodium spp. than women. Individuals who worked as farmers or wood and bamboo cutters had an increased risk of infection
3	Phommasone et al. / 20167	Thapangthong and Nong Districts of Savannakhet Province, Laos	Cross-sectional	888	RDT and Upcr. RDT: 2 % (18/888). Upcr: 20% (175/888)	P. falciparum: 3.6 % (32/888) P. vivax: 11.1 % (99/888) P. falciparum + P. vivax 1.6 % (14/888) undetermined species 3.4 % (30/888).	Males were more likely to have P. vivax infections, while older villagers were at lower risk for parasitaemia.
4	Bouwe et al. / 202516	Nong District, Savannakhet Province, Laos	Cross-sectional	622	LAMP detected 1.8% (11/622).	– Plasmodium vivax 15.4% (2/13).	Participants reported not using mosquito bed nets in the forest and also the participants had been to the forest were nighttime as forest workers

5	Imwong et al. / 20152	Thailand–Myanmar border areas, Cambodia, and Vietnam	Cross-sectional	7355	RDT, Light microscopy and HVUSqPCR. RDT: 4 % (224/5008), microscopy 5 % (229/5111) and HVUSqPCR 20 % (988/4975).	– P. falciparum: 7% (357) – P. vivax: 1% (56) – mixed infections P. falciparum and P. vivax 8% (411)	history of fever, male sex, and age equal or older 15 years were independently and significantly associated with parasitaemia
6	Doum et al. / 202318	Mondulkiri, Cambodia	Cross-sectional	1030	PCR detected 6.7% (87/1301)	- P. vivax 81% - P. falciparum 9% - Plasmodium cynomolgi 3% - undetermined species 7%.	Forest rangers, forest goers, and forest dwellers was associated with malaria prevalence. Male participants having higher odds of malaria infection than female participants
7	Quang et al. / 202123	Dak Nong province, Vietnam	Cross-sectional	2.809	RT-qPCR Dak Buk So 1.7% (22/1,328), Dak Ngo 3.5% (31/890) and Quang Truc 12.2% (72/591)	- P. falciparum: 32.0% (40/125) - P.vivax: (3/125)	Higher malaria prevalence is amongs forest rangers, using bed nets rarely, going to the forest and sleeping in the forest under a bed net
No	Author/ Year	Location	Study type	Sample numbers	Diagnostic test (% asymtomatic)	Plasmodium spp. Prevalence	Risk factors/ Characteristics respondent
8	Pava et al. / 201615	Southern Papua, Indonesia.	Cross-sectional	2.830	Microscopy and PCR. Microscopy: 12.8% (357/2,796) PCR: 88.6% (2,476/2,796)	P. falciparum: 15.4% (396/2567) P. vivax 18.3% (471/2567).	There was a higherrisk of submicroscopic infections in females compared to males and in those who did not own a bed net.
9	Istiana et al. / 20218	South Kalimantan, Indonesia	Cross-sectional	107	RDT and Microscopy. RDT: 38 (35.5%) Microscopy: 9 (17.75%).	P. falciparum 9 (47.36%) P. vivax 5 (26.32%) mixed infections of P. falciparum and P. vivax 5 (26.32%)	House factors that influence the prevalence of malaria were the condition of the walls that are open or not tight, the roof is made of plastic, and the presence of animal cage around the house.
10	Noordin et al. / 202017	Johor, Pahang, Kelantan, and Selangor,Malaysia	Cross-sectional	585	Nested PCR 3.3% (19/585)	Plasmodium knowlesi 52.6% (10) Plasmodium vivax 42.1% (8) Plasmodium ovale 5.3% (1).	Army personel who frequented forests during training had been reported also respondents did visit forest or agricultural areas.
11	San et al. / 202219	Gia Lai province, Vietnam	Cross-sectional	3.283	PCR and RDT. PCR: 1.74% (57/3283). RDT 0.06% (2/3283)	P. falciparum 1.07%, P. vivax 0.40%, P. malariae 0.15% mixed infections 0.12%)	Female being from an ethnic minority group, farming or residing indicated an increased risk of malaria infections

IV DISCUSSION

The prevalence of asymptomatic malaria in Southeast Asia shows considerable variation, ranging from 1.03% in Kayah State, Myanmar to 88.6% in Southern Papua, Indonesia[12], [15]. This disparity highlights that, beyond geographic differences, local transmission intensity and socio-ecological conditions greatly influence the burden of latent infection.

Diagnostic methods also significantly impact reported prevalence rates. Studies employing molecular techniques (PCR, nested PCR, qPCR) tend to report higher prevalence compared to those using microscopy or rapid diagnostic tests (RDTs). For instance, a PCR-based study in Southern Papua, Indonesia reported an 88.6% prevalence[15], whereas another study in South Kalimantan found only 35.5% of cases with PCR and 17.75% with microscopy[8]. This gap reflects the varying sensitivity of detection tools. Runge et al. (2022) demonstrated that qPCR could identify latent infections that RDT and microscopy missed[24]. Ultra-sensitive qPCR technology is increasingly adopted in active surveillance due to its high precision in detecting submicroscopic infections[9]. Inconsistencies in methods between studies may introduce bias in estimating disease burden and affect intervention policy design.

Plasmodium species prevalence reported that the highest is *Plasmodium vivax* (81%) studied at Mondulkiri, Cambodia[18]. A study in Malaysia reported a dominance of *Plasmodium knowlesi* in the community, with *Plasmodium knowlesi* accounting for 52.6% of infections[17], Meanwhile, in Vietnam dan Laos, *Plasmodium vivax* was more frequently found, with proportions such as 18.3%, 11.1%, and 0.4% across different studies, and *Plasmodium falciparum* ranged from 3.6%, 1.07% down to 0.15%[19], [23]. *Plasmodium ovale, Plasmodium cynomolgi and Plasmodium malariae* also reported but in low prevalence such as 5.3%, 3% and 0,15%[17], [18], [19]. From the all of the studied that *P. vivax* and *P. falciparum* frequently detected and reported. The presence of zoonotic species such as *P. knowlesi* and *P. cynomolgi* adds complexity to malaria control, especially in areas with exposure to wild primates[21], [25].

Identified risk factors were consistent across study locations. Approximately 81% of studies involved populations in border areas, forests, or highly mobile communities such as farmers, forest workers, and rangers[7], [18], [21]. A study in Myanmar found that men working outdoors had higher infection risks[12], and a study in Cambodia reported a significant prevalence of asymptomatic cases among forest rangers[18]. In Southern Papua, submicroscopic infections were significantly associated with anemia and other clinical risks[15]. Several studies also noted that behaviors such as sleeping outdoors, not using insecticide-treated nets, and engaging in nighttime forest activities increased infection risk[7], [22].

These findings underscore that asymptomatic malaria remains a major challenge to elimination efforts in Southeast Asia. Symptom-based detection is insufficient to capture the hidden reservoir of latent infections. Therefore, more sensitive diagnostic tools such as PCR and LAMP should be integrated into active surveillance systems[16]. A study by Chen et al. (2021) demonstrated that LAMP could serve as an efficient field-based alternative for detecting *P. vivax* in low-transmission settings[10]. Cross-border collaboration, data harmonization, and risk-based mapping are essential strategies to address current surveillance gaps and accelerate progress toward malaria elimination in the region.

FUNDING

This study was funded by the Research and Community Service Program managed by the Directorate of Research and Community Service 2025 (DPPM – Penelitian Tesis Magister).

AUTHOR CONTRIBUTION

All authors actively contributed to all stages of the research and the writing of this article. MI conducted the literature search, data extraction, and thematic analysis. FM and MM provided scientific supervision, reviewed the extracted findings, and contributed to the writing and editing of the manuscript. All authors read and approved the final manuscript

ACKNOWLEDGMENT

The authors express their gratitude to the Master of Epidemiology Study Program, Faculty of Public Health, Unviversitas Diponegoro for the academic support provided. Appreciation is also extended to the Department of Epidemiology and Tropical Diseases for their valuable insights and supervision. The authors acknowledge the hard work of colleagues and administrative staff who assisted in the data extraction and documentation process. Special thanks are also extended to the editor and reviewers for their constructive feedback on this manuscript.

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