

Review

Malaria Vectors and Species Complexes in Thailand: Implications for Vector Control

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There are seven *Anopheles* species incriminated as important (primary) malaria vectors in Thailand. These vectors belong to species complexes or are in closely related groups that are difficult to separate morphologically. Precise species identification, using molecular methods, enables control operations to target only important vectors and to increase understanding of their specific ecological requirements, bionomic characteristics, and behavioral traits. This review focuses on adult mosquito behavior, vector transmission capacity, and geographical distribution of malaria vectors in Thailand identified using genetic and molecular identification methods between 1994 and 2019. A better understanding of *Anopheles* biodiversity, biology, behavior, vector capacity, and distribution in Thailand and neighboring countries in the Greater Mekong Subregion (GMS) will facilitate more effective and efficient vector-control strategies and consequently contribute to a further decrease in the malaria burden.

Status of Malaria and Its Vectors

Among mosquito-borne diseases, malaria remains the most prevalent and a major public health priority in many tropical and subtropical regions. An estimated 3.7 billion people in 90 endemic countries and territories are at risk [1]. In 2018, over 200 million cases of malaria were reported worldwide, resulting in an estimated 429 000 deaths. Over 90% of morbidity and mortality occurred in sub-Saharan Africa, with deaths predominantly among children under 5 years of age and pregnant women [1]. The Southeast Asian region accounted for around 5% of the estimated global morbidity/mortality burden [1]. Since 2010, the Southeast Asian countries, collectively, have seen significant reductions in the overall malaria burden, with 59% and 54% decreases in reported malaria cases and mortality, respectively [1,2]. Today, **malaria elimination** (see Glossary) is a primary strategic goal for many countries, including Thailand [3], the aim being to achieve a complete interruption of all autochthonous transmission in defined geographic areas. Yet the incidence of malaria remains stubbornly high in some locations and countries despite substantial efforts and resources used to combat it [1]. Specific strategies for achieving elimination vary by country and locality, and are influenced by multiple epidemiological, financial, and political factors [4].

Typically, four species of *Plasmodium* infect humans in the Southeast Asian region, with *Plasmodium falciparum* and *Plasmodium vivax* being predominant, followed by sporadic cases of *Plasmodium malariae* and *Plasmodium ovale*. More recently, *Plasmodium knowlesi*, a zoonotic Asian simian malaria parasite, has been found to infect humans with increasing frequency [5]. Malaria parasites are naturally transmitted to humans by the bite of the infective female *Anopheles* mosquitoes. Of the currently known *Anopheles* species, of which at least 540 are described or are as yet to be formally named, approximately 80 are considered important public health vectors of malaria and lymphatic filariasis [6]. Of these, 41 species are deemed 'dominant' or primary malaria

Highlights

Enhanced molecular methods have facilitated the identification of members within the *Anopheles* isomorphic sibling species 'complexes' present in Thailand and other countries comprising the Greater Mekong Subregion (GMS) in Southeast Asia.

Molecular identification methods augment the greater malaria vector-control challenge in the context of outdoor malaria transmission in Thailand and the GMS.

Utilizing accurate vector species identification techniques allows greater focus on remaining gaps in the understanding of key vector mosquito behavior and interrelated human behaviors in malaria endemic countries.

Malaria vector distribution, bionomics, and vector capacity are critical for identifying and implementing targeted and more effective vector-control strategies in Thailand and the GMS.

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