

## Vector bionomics and malaria transmission along the Thailand-Myanmar border: a baseline entomological survey

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**ABSTRACT:** Baseline entomological surveys were conducted in four sentinel sites along the Thailand-Myanmar border to address vector bionomics and malaria transmission in the context of a study on malaria elimination. Adult *Anopheles* mosquitoes were collected using human-landing catch and cow-bait collection in four villages during the rainy season from May-June, 2013. Mosquitoes were identified to species level by morphological characters and by AS-PCR. Sporozoite indexes were determined on head/thoraces of primary and secondary malaria vectors using real-time PCR. A total of 4,301 anopheles belonging to 12 anopheline taxa were identified. *Anopheles minimus* represented >98% of the Minimus Complex members (n=1,683), whereas the *An. maculatus* group was composed of two dominant species, *An. sawadwongporni* and *An. maculatus*. Overall, 25 *Plasmodium*-positive mosquitoes (of 2,323) were found, representing a sporozoite index of 1.1% [95%CI 0.66-1.50]. The transmission intensity as measured by the EIR strongly varied according to the village (ANOVA, F=17.67, df=3, P<0.0001). Our findings highlight the diversity and complexity of the biting pattern of malaria vectors along the Thailand-Myanmar border that represent a formidable challenge for malaria control and elimination. *Journal of Vector Ecology* 42 (1): 84-93. 2017.

**Keyword Index:** Thailand-Myanmar border, malaria, vectors, *Plasmodium*, transmission, host seeking behavior.

### INTRODUCTION

The World Health Organization (WHO) reports that malaria continues to show ongoing transmission in 97 countries, leaving 3.2 billion people at risk. Africa traditionally has the highest burden with around 90% of the cases. Another region where malaria is a major public health problem is Southeast Asia (SEA), where over 1.3 billion people are at risk of malaria in ten malaria-endemic countries. The number of confirmed malaria cases decreased in the region from 2.9 to 1.6 million between 2000 and 2014. This is explained by several factors, including economic development, deforestation as well as preventive and curative strategies, including early diagnosis and prompt access to treatment, Artemisinin-based Combination Therapy (ACTs), and high coverage of long-lasting insecticidal-treated mosquito nets (LLINs). The SEA region has, however, become an area of major concern because of emerging resistance of *Plasmodium falciparum* to artemisinin derivatives and fear of the subsequent spread worldwide (Ashley et al. 2014, Tun et al. 2015).

In Thailand, malaria incidence has been reduced by 50-75% and the country is now entering the pre-elimination phase. Despite significant progress, malaria control remains difficult in foci located in forested areas and along the country borders with Myanmar and Cambodia due to complexities in scaling up malaria control interventions (Corbel et al. 2013). The Thailand-

Myanmar border accounts for 55% of malaria cases in Thailand, while Myanmar annually reports 20% of the total malaria cases in the SEA region. Malaria surveillance and control are difficult to implement due to the extensive population movements across the border, especially foreign workers who make disproportionate contributions to the malaria burden (Corbel et al. 2013). The mobile populations and remote locations make efforts much more challenging, especially if effective control measures are not appropriately deployed on both sides of the border (Carrara et al. 2013). The Thailand-Myanmar region is characterized by a forest and forest fringe area where local populations typically live in remote, hard-to-reach villages that place them in close proximity to very efficient anopheline vectors (Delacollette et al. 2009). At least 20 *Anopheles* species are known to play a role in malaria transmission along the border (Saeung 2012). Of these vectors, the most prominent belong to the Dirus and Minimus complexes and Maculatus group (Manguin et al. 2010). Within these complexes, the species that are deemed important malaria vectors are *An. dirus*, *An. baimaii*, *An. maculatus*, *An. sawadwongporni*, *An. aconitus*, *An. pseudowillmori*, and *An. minimus* (Muenworn et al. 2009, Tananchai et al. 2012, Tisgratog et al. 2012, Tainchum et al. 2015). There is also suspicion of potential secondary vectors including *An. epiroticus*, *An. barbirostris*, and *An. philippinensis* (Saeung 2012). The abundance and role of these secondary vectors is largely undetermined due to the focus on primary vectors.