Genetic structure and gene flow of *Anopheles minimus* and *Anopheles harrisoni* in Kanchanaburi Province, Thailand

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ABSTRACT: Isozyme frequencies were compared in seven field collections of *Anopheles minimus* complex using starch gel electrophoresis. Mosquito collections were sampled from four districts in Kanchanaburi Province where malaria is endemic. From eight enzyme systems, nine loci and seven polymorphisms were detected, indicating limited genetic differentiation among the seven collections (F_{ST} = 0.061). The highest percent polymorphic loci were observed in Bong Ti Noi (BTN) Village (55.6%), whereas the least percent polymorphism was seen in Tha Kradan (TK) Village (22.2%). Comparing villages Pra Jedee (PJ) with Pu Teuy C (PTC) and Huai Khayeng (HK) with Pra Jedee (PJ), gene flow among collections varied from 3.72 to 62.25 reproductive migrants per generation. Among the seven collections, no correlation was seen between genetic and geographical distances ($P > 0.05$). *Anopheles minimus* (former species A) and *Anopheles harrisoni* (former species C) from Pu Teuy fit most closely in the same cluster, possibly indicating relatively recent divergence between taxa. The genetic and epidemiological ramifications of these findings are discussed. ***Journal of Vector Ecology* 33 (1) 158-165. 2008.**

Keyword Index: *Anopheles minimus, Anopheles harrisoni*, isozyme, genetic, gene flow, malaria, Thailand.

INTRODUCTION

In Thailand, malaria is still one of the most important infectious diseases despite decades of organized disease control in reducing both mortality and morbidity countrywide (WHO 2004). Seventy percent of the malaria cases are documented from the relatively undeveloped borders and hill region of eastern Myanmar where *Anopheles minimus* complex mosquitoes are common and represent important malaria vectors in Thailand (Reid 1968, Ismail et al. 1975).

The *An. minimus* complex, Theobald 1901, is composed of two formally named species, *An. minimus* (=species A) and *An. harrisoni* (=species C), and the informally designated *An. minimus* E (Harbach et al. 2006, 2007, Somboon et al. 2001, 2005).

Two sibling species within this complex, *An. minimus* and *An. harrisoni*, occur in Thailand along the Thai-Myanmar border (Sucharit et al. 1988, Baimai 1989, Green et al. 1990, Kengluecha et al. 2005, Garros et al. 2006, Sungvornyothin et al. 2006a, b). *Anopheles minimus* is the predominant member of the complex in the country and recognized as an important malaria vector, whereas *An. harrisoni* has only been reported from western Thailand and appears to play a minor role in transmission based on its limited distribution and greater zoophilic feeding predilection (Rwegoshora et al. 2002, Kengluecha et al. 2005, Trung et al. 2005, Sungvornyothin et al. 2006a).

In Kanchanaburi Province, sympatric collections of *An. minimus* and *An. harrisoni* have been identified from Pu Teuy Village, in Sai Yok District (Green et al. 1990, Sungvornyothin et al. 2006a, b) and in neighboring Sri Sawat District (Kengluecha et al. 2005). Larval habitats surveyed in Kanchanaburi Province found *An. minimus* in Pu Teuy where it had been reported previously undetectable or absent (Kengluecha et al. 2005). Rwegoshora et al. (2002) found sympatric populations of *An. minimus* and *An. harrisoni* present in a 1:3 ratio in Pu Teuy, and Sungvornyothin et al. (2006b) subsequently found relatively low frequency (4% based on molecular analysis) of *An. minimus* compared to *An. harrisoni* in the same study site during a two-year collection period. Both sympatric species described in this study are difficult to accurately distinguish on morphological characters alone, thus requiring molecular methods for precise identification (Rattanarithikul and Panthusiri 1994, Harrison 1980, Garros et al. 2004, 2006, Sungvornyothin et al. 2006b).

The reasons for the predominance of *An. harrisoni* in Pu Teuy are not clear but might be related to the prevailing environmental conditions that have preferentially favored this species by providing a competitive advantage over *An. minimus*. The natural evolutionary process is influenced by numerous environmental factors that account for varying rates of species adaptation or extinction that can lead to changes in species frequency over time (Dombeck and Jaenike 2004). Human activities in the province