



## Original Article

Genetic variation of *Aedes aegypti* mosquitoes across Thailand based on nuclear DNA sequencesPimnapat Parimittr,<sup>a</sup> Theeraphap Chareonviriyaphap,<sup>c</sup> Michael J. Bangs,<sup>c, d</sup> Uraiwan Arunyawat<sup>a, b, \*</sup><sup>a</sup> Department of Genetics, Faculty of Science, Kasetsart University, Bangkok, 10900, Thailand<sup>b</sup> Center for Advanced Studies in Tropical Natural Resources, Kasetsart University, Bangkok, 10900, Thailand<sup>c</sup> Department of Entomology, Faculty of Agriculture, Kasetsart University, Bangkok, 10900, Thailand<sup>d</sup> Public Health & Malaria Control Dept., PT Freeport Indonesia/International SOS, Kuala Kencana, 99920, Papua, Indonesia

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## ABSTRACT

The *Aedes aegypti* L. mosquito is the primary vector of dengue viruses in Thailand, where dengue disease is a major public health problem in both urban and rural areas. Understanding the genetic variation of *Ae. aegypti* populations can help to understand the distribution, population structure and gene flow of this species. Single nucleotide polymorphism (SNP) markers were used to analyze the genetic variation of 21 *Ae. aegypti* populations collected across six geographic locations in Thailand. Nuclear DNA sequences of four putative neutral fragments located on different chromosomes were examined. An average of 14 SNPs per kb was detected per population. Tajima's D statistical test showed no significant deviation from the neutral equilibrium model in the majority of populations, suggesting that the detected patterns of variation were under random mutation and genetic drift equilibrium. Relatively low genetic differentiation was detected between all mosquito populations.

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## Introduction

Dengue is the most common and widespread mosquito-borne viral infection in the world (Gubler, 2002; Bhatt et al., 2013). Dengue viruses, the cause of dengue fever and more severe disease, are transmitted to humans by the infective bite of the female *Aedes aegypti* (L.) mosquito, the most important species among potential natural vectors in the subgenus *Stegomyia* and moreover, this mosquito species is also responsible for transmitting chikungunya and Zika viruses throughout Southeast Asia, Africa and the Americas (Higgs and Vanlandingham, 2015; Paixão et al., 2016). In Thailand, *Ae. aegypti* was first reported in 1907 and is believed to have spread from Southeast Asia into the Pacific Region during World War II (Gubler, 1998). This mosquito species is widespread in urban and rural areas of Thailand and is a major public health threat and contributor to disease burden in communities (Bureau of Epidemiology, Department of Disease Control, 2014).

The study of population genetics involves the comparison and estimation of temporal heredity changes for describing patterns of genetic diversity in natural populations and developing genotypic maps. Data from population genetic studies of *Ae. aegypti* are useful for a better understanding of the epidemiology of dengue transmission and improving vector control. Genetic structure analysis allows identification of genetic differentiation between individuals in subpopulations across areas (Brown et al., 2011; Gloria-Soria et al., 2016).

Mitochondrial DNA (mtDNA) is a commonly used genetic marker for studying molecular diversity in animals. However, the appearance of nuclear mitochondrial pseudogenes (Numt) in the nuclear genome of *Ae. aegypti* may result in over amplification of mtDNA, or even the targeting of actual mtDNA sequences (Hlaing et al., 2009), potentially causing serious complications when analyzing population genetic studies using mtDNA alone (Hazkani-Covo et al., 2010). The use of nuclear DNA is intended to overcome this potential problem with *Ae. aegypti*. As others have demonstrated, the use of nuclear DNA for studying *Ae. aegypti* population genetics appears an acceptable alternative for avoiding some inherent limitations with using mtDNA (Crawford et al., 2017; Pless et al., 2017).

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