

## Genetic structure among Thai populations of *Aedes aegypti* mosquitoes

Suprada Sukonthabhirom<sup>1,5</sup>, Seeviga Saengtharapip<sup>2</sup>, Nuananong Jirakanchanakit<sup>3</sup>, Pornpimol Rongnoparut<sup>4</sup>, Suthee Yoksan<sup>3</sup>, Apichai Daorai<sup>5</sup>, and Theeraphap Chareonviriyaphap<sup>5</sup>✉

<sup>1</sup>Office of Plant Protection Research and Development, Department of Agriculture, Ministry of Agriculture and Cooperatives, Bangkok, 10900, Thailand

<sup>2</sup>Office of Dengue Control, Department of Communicable Disease Control, Ministry of Public Health, Nonthaburi 11120, Thailand

<sup>3</sup>Center for Vaccine Development, Institute of Science and Technology for Research and Development, Mahidol University, Salaya, Nakhon Pathom 13140, Thailand

<sup>4</sup>Department of Biochemistry, Faculty of Science, Mahidol University, Bangkok 10900, Thailand

<sup>5</sup>Department of Entomology, Faculty of Agriculture, Kasetsart University, Bangkok 10900, Thailand

Received 11 June 2008; Accepted 9 December 2008

**ABSTRACT:** Thirty-one field populations of *Aedes aegypti* (L.) were compared using isozyme starch gel electrophoresis to characterize genetic variation between populations. *Ae. aegypti* were collected from seven provinces in Thailand. Thirty-one isozyme encoding loci, including 19 polymorphic loci, were characterized. Only small levels of genetic differentiation were observed among the 31 district populations in the seven provinces. Isolation by distance among populations from the seven provinces showed no correlation between genetic variation and geographical distance. *Journal of Vector Ecology* 34 (1): 43-49. 2009.

**Keyword Index:** *Aedes aegypti*, genetic structure, starch gel electrophoresis.

### INTRODUCTION

Dengue fever (DF) and dengue hemorrhagic fever (DHF) are the most common and important arboviral mosquito-borne diseases syndromes in the world (Gubler 1988). During the last decade, the number of dengue cases in Thailand has increased and disease transmission remains prevalent throughout the country. Each year, 50,000 to 200,000 dengue cases are reported annually in the country (Ministry of Public Health 2006). Currently, control of the mosquito vectors remains the most efficient method to prevent dengue virus transmission and avert dengue epidemics (Reiter and Gubler, 1997, World Health Organization 1999).

*Aedes aegypti* (L.), a predominately human-biting mosquito, is the primary vector world-wide and a common species throughout Thailand. It was first reported in Thailand in 1907 (Theobald, 1907) and is considered to be a polytypic species worldwide (Tabachnick 1991). Several population genetic studies of *Ae. aegypti* have been conducted in different regions of the world (Tabachnick and Powell 1979, Wallis et al. 1983, Apostol et al. 1996, Gorrochotegui-Escalante et al. 2000, Failloux et al. 2002, Mousson et al. 2002). Analyses of genetic variation among populations, established by comparing variability in isozyme encoding loci, have been used to estimate gene flow between different *Ae. aegypti* populations (Tabachnick 1991, Manguin et al. 1995). Relatively little is known about the genetic structure and gene flow among *Ae. aegypti* populations among cities in Thailand. Previous studies have shown that *Ae. aegypti* populations are genetically similar, with high levels of

gene flow between them in the city of Bangkok, in central Thailand (Sukonthabhirom et al. 2005). In other regions, for example, Chareonviriyaphap and Lerthusnee (2002) found no significant differentiation between *Ae. aegypti* mainland and Samui Island populations of the Surat Thani province in southern Thailand. Netthanomsak<sup>6</sup> reported low genetic variation of *Ae. aegypti* along the coastal area of Gulf of Thailand, covering six provinces. Mousson et al. (2002) confirmed high genetic differentiation among *Ae. aegypti* samples collected in different subdistricts from the Chiang Mai province in northern Thailand. Bosio et al. (2005) studied *Ae. aegypti* populations in Thailand from Chiang Mai in the north to the Songkhla province in the south and reported that *Ae. aegypti* in urban areas were relatively panmictic, while suburban / rural sites exhibited more restricted gene flow and there was no isolation by distance. The goal of the present study was to characterize the genetic structure of populations of *Ae. aegypti* in different provinces in Thailand using gene frequencies of isozyme encoding loci. Population genetic structure and the extent of gene flow between mosquito populations is fundamental information for developing more effective strategies to combat insecticide resistance and more effective and appropriate national programs to control *Ae. aegypti* in Thailand.

<sup>6</sup>Netthanomsak, S. 2004. Ecological significance and isozyme patterns of *Aedes aegypti* (Linnaeus), a vector of Dengue fever in Thailand. M.S. thesis, Kasetsart University, Bangkok, Thailand.