

# Genetic Structure and Gene Flow Among *Aedes aegypti* (Diptera: Culicidae) Populations from Central Thailand

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**ABSTRACT** Isozymes from five wild-caught populations of *Aedes aegypti* (L.) were compared using starch gel electrophoresis to estimate rates of gene flow between and among geographically close mosquito populations. *Ae. aegypti* were collected from five different locations in Bangkok, Thailand. One collection was obtained from central Bangkok (Huai-Khwang); the other four samples were obtained from surrounding areas (Districts Latkrabang, Ratburana, Laksi, and Bangkok Noi). Based on 24 loci (17 enzyme systems), only minor genetic differentiation was observed between all five populations. The highest percentage of polymorphic loci (34.3) was observed from the central Bangkok population; the least percentage of polymorphism (20.0) was seen from Laksi (north Bangkok). This study indicates that a large effective migration rate exists among all five populations. No fixed genetic differences were detected.

**KEY WORDS** *Aedes aegypti*, isozymes, genetics, gene flow, Thailand

DENGUE FEVER and dengue hemorrhagic fever are the most important mosquito-borne viral diseases affecting humans throughout the tropical and subtropical world (Gubler 1988). Annually, >50 million cases are reported and tens of thousands die from this disease. In Thailand, between 50,000 and 200,000 dengue-related illnesses are reported each year (Communicable Disease Control 1995–2004). Furthermore, significant population growth, demographic movement to urban residential areas, and an increase in tourism-based facilities are deemed major factors involved in the dengue resurgence in the country. The four virus serotypes responsible for human disease are transmitted primarily by the mosquito, *Aedes aegypti* (L.), a vector with an unusually close relationship with humans, their dwellings, and immediate surroundings. This species is found virtually everywhere in Thailand and is the primary day-biting mosquito in urban areas.

Relatively little is known about the genetic structure and gene flow among *Ae. aegypti* populations within large metropolitan areas such as Bangkok. Knowledge of population structure can help estimate migration between vector populations, provide insights into the epidemiology and transmission of dengue viruses, and help develop more responsive and

effective vector control. We measured the genetic relationship of five different urban populations of *Ae. aegypti* in and around Bangkok by using isozyme electrophoresis to evaluate gene frequencies to assess gene flow and effective migration rates between populations.

## Materials and Methods

**Mosquito Populations.** *Ae. aegypti* mosquitoes were sampled from five locations in Bangkok, Thailand (Fig. 1). One collection was obtained from central Bangkok (Huai-Khwang), whereas the other four samples were collected peripherally in Districts Bangkok Noi (western), Laksi (northern), Ratburana (southern), and Latkrabang (eastern). Further details of all five field sites are given in Table 1.

All *Ae. aegypti* samples were collected as larvae or pupae and reared to adults in a protected insectary at the Department of Entomology, Kasetsart University. Approximately 100 larvae were sampled per site. Strict segregation of field specimens was maintained in the insectary to prevent potential contamination from other *Ae. aegypti* colonies present. Mosquitoes were reared and adults were either tested immediately or frozen (–70°C) before processing. An average of 30 adults (equal number of males and females) from each population were processed and tested by electrophoresis.

**Starch Gel Electrophoresis.** Electrophoresis was used to analyze 17 enzyme systems, aconitase (ACON, EC 4.2.1.3), adenylate kinase (AK, EC 2.7.4.3), aldehyde oxidase (AO, EC 1.2.3.1), arginine kinase (ARGK, EC

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