

GENETIC DIFFERENTIATION OF *Aedes aegypti* MAINLAND AND ISLAND POPULATIONS FROM SOUTHERN THAILAND

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ABSTRACT. Isozymes of 5 wild-caught collections of *Aedes aegypti* were compared by using starch gel electrophoresis. All collections were collected from Surat-Thanee Province, southern Thailand, an area considered to be a hyperendemic zone for dengue virus. One collection was from Donsak Harbor, whereas the other 4 collections were from 4 districts of Samui Island. The percent polymorphic loci (24.2–33%) in the 4 island collections was lower than in the mainland collection (36.4%). This study revealed a large effective migration rate among all 5 collections. No fixed differences were detected. No significant differentiation was found among the 5 collections from Surat-Thanee Province.

KEY WORDS *Aedes aegypti*, isozyme analysis, genetics, mainland and island populations, Thailand

INTRODUCTION

Dengue fever (DF) and dengue hemorrhagic fever (DHF), which are mosquito-borne viral diseases, commonly occur throughout Asia (Gubler 1988). *Aedes aegypti* (L.), an urban mosquito species in Asia, is known to be an important dengue virus vector in Thailand (Bhamarapravati 1990). This species is considered to be a polytypic species worldwide because of morphological, physiological, and geographical variations (Craig and VandeHey 1962, Gouck 1972, McClelland 1974, Trpis and Hausermann 1975, Leahy et al. 1978, Tabachnick et al. 1979, Tabachnick and Powell 1979, Trpis et al. 1995). Thousands of cases of DF and DHF are reported worldwide annually (Henchal and Putnak 1990, Monath 1994, Gubler 1997).

Samui Island is located approximately 740 km from Bangkok and 30 km east of Donsak Harbor in Surat-Thanee Province, southern Thailand (Fig. 1). Samui Island is the 3rd largest island of Thailand, with an area of approximately 280 km² and a population of 35,000 inhabitants. Presently, little is known concerning the spread of *Ae. aegypti* between the mainland and Samui Island. Therefore, in this study, we compared genetic profiles of *Ae. aegypti* by using starch gel electrophoresis to determine if any significant differences occurred between mainland and island collections of *Ae. aegypti* in Surat-Thanee Province, southern Thailand.

MATERIALS AND METHODS

Mosquito collections: Five collections of *Ae. aegypti* were made from 2 different geographical

zones. One collection was from the mainland from Donsak Harbor and the other 4 collections were from Mae-Nam, Na-Thon, Ma-Ret, and Taling-Ngam districts on Samui Island (Fig. 1). Mosquitoes were collected as larvae or pupae and reared to adults. An average of 30 adults from each collection was stored at -70°C while awaiting electrophoretic analyses.

Starch gel electrophoresis: Starch gel electrophoresis was used to analyze 24 enzyme systems according to Harris and Hopkinson (1976), Manguin et al. (1995), and Lerdthusnee and Chareonviriyaphap (1999).

Data analysis: Analysis of allele frequencies, heterozygosity, conformity to the Hardy-Weinberg equilibrium, and genetic distance were calculated by using BIOSYS-1 (Swofford and Selander 1989). Differentiation among collections was reported by using F_{ST} (Wright 1978). The effective migration rate (N_m) among the collections was estimated from F_{ST} with equation $N_m \approx (1 - F_{ST})/4F_{ST}$ (Wright 1978) and N_m values were compared between collections. Nei's (1978) unbiased genetic distance was used for the cluster analysis by unweighted pair group method averaging (UPGMA) to produce a phenogram.

RESULTS

Of 24 enzyme systems screened, 33 putative loci were detected (Table 1). The number of allelic polymorphic loci was 20 in the mainland-Donsak collection, whereas 14, 15, 11, and 16 loci were detected in 4 island collections of Mae-Nam, Na-Thon, Ma-Rat, and Taling-Ngam, respectively (Table 2). Nine loci (*Est-3*, *Hk-1*, *Idh-1*, *Lap-2*, *Mdh-1*, *Mdh-2*, *Pgd-1*, *Pgm-1*, and *Pk-2*) showed allelic polymorphism in all collections, whereas the other 13 loci (*Aox-1*, *Est-1*, *Est-2*, *Fum-1*, *G6p-1*, *Gpd-1*, *Gcd-1*, *Got-2*, *G3p-1*, *Mez-1*, *Mpi-1*, *Tpi-1*, and *Xdh-1*) were monomorphic in all collections. The frequency of polymorphic loci was also significantly higher ($P < 0.05$) for the mainland-Donsak collection (36.4%) than in 4 island collections (24.2 for Mae-Nam, Na-Thon, and Ma-Ret and 33.3 for

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