Suprada Sukonthabhirom na Pattalung 2006: Gene Flow among *Aedes aegypti* (L.) Populations in Thailand. Doctor of Philosophy (Entomology), Major Field: Entomology, Department of Entomology. Thesis Advisor: Assistant Professor Apichai Daorai, Ph.D. 115 pages.

ISBN 974-16-1746-1

Twenty-four field populations of *Aedes aegypti* (L.) were compared using isozyme starch gel electrophoresis to estimate the gene flow rate between and within populations. *Aedes aegypti* were collected from the five leading dengue endemic provinces in Thailand: Bangkok, Chon Buri, Surat Thani, Nakhon Sawan and Nakhon Ratchasima. Four to five locations were sampled within each province based on recent dengue epidemiological data. From twenty enzyme systems, 31 loci with 19 polymorphisms were detected. Only small levels of genetic differentiation were observed when all populations were compared ($F_{ST} = 0.091$). The highest percent polymorphic loci was observed in an urban population from Bangkok (Huai Khwang), the smallest percent was seen in two urban populations from Chon Buri (Phanat Nikhom and Mueang Chon Buri) and two from Nakhon Ratchasima (Prathai and Sikhio). Gene flow within district populations varied from 4.5 to 9.4 reproductive migrants per generation, whereas those between different provinces ranged from 4.9 to 27.5. However, overall gene flow migration was only 2.5 when all populations were considered. Isolation by distance among all populations showed no correlation between genetic and geographical distance ($P > 0.05$). Details of findings and epidemiological ramifications are discussed herein.

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10 / May / 2006