

DEVELOPING A SYSTEM TO DETERMINE ENTOMOLOGICAL RISK FACTORS FOR DENGUE TRANSMISSION IN KAMPHAENG PHET PROVINCE, THAILAND

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Infection with dengue virus remains a serious threat for human health throughout Thailand. We present how the most important (local) entomological risk factors of dengue virus transmission can be determined through the integration of entomological, serological and clinical data. Recently infected and clinically ill children are actively located at their homes in Kamphaeng Phet Province, Thailand. This is followed by intensive entomological and serological sampling in the immediate surroundings of the dengue case (≤ 100 m; a 'cluster survey'). Virus transmission by the mosquito vector is then terminated by spraying BP-300, a non-residual pyrethroid, and the application of 1% Abate™ in water containers. This enables us to link in time and space entomological, serological and clinical factors with the actual infection. In preparation for the cluster studies, we initiated a cross-sectional survey among 535 households in the GIS mapped study area of 4,368 households during the hot dry season (February - April). This survey indicated that immature as well as adult vector densities were high (range Breteau Index: 188 - 320; range adult female *Ae. aegypti* per house: 0 - 20). All immature indices exceeded control targets as defined by the Thai Ministry of Public Health. We present how these data provide important information on the spatial structure of the vector population and how this type of data can be used to define spatial and temporal dengue risk.

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DEVELOPMENT OF MICROSATELLITE DNA MARKERS IN *ANOPHELES MINIMUS*, A MAJOR MALARIA VECTOR IN THAILAND

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Anopheles minimus is a principal malaria vector in Thailand. Two species, A and C, are recognized within *An. minimus* s.l. Species A is found throughout the country, whereas species C is confined to Kanchanaburi Province. Little is known about genetic structure of this malaria vector. Knowledge of the genetic structure on gene dispersal patterns will benefit for predicting spread of insecticide resistance genes in vector control strategy. Microsatellite DNA markers were developed to determine extent of gene flow among populations of *Anopheles dirus* and *Anopheles maculatus* in Thailand. However, there are no microsatellite sequence data available for *An. minimus*. *Anopheles minimus* laboratory colony was maintained in Entomology Department, AFRIMS. To develop the microsatellite marker, *An. minimus* genomic DNA was digested with MboI restriction enzyme and probed with (AC)₁₄, (AG)₁₄, (AT)₁₄ and (CG)₁₄ to preliminarily assess the abundance of microsatellite sequences using Southern blot analysis. The results showed relatively

high abundance of (AC)_n and (AG)_n sequences in the *An. minimus* genome. A partial genomic DNA library of *An. minimus* was generated and the recombinant clones containing sequences that hybridized to each (AC)₁₄ or (AG)₁₄ probe were obtained and sequenced. Most clones contained sizes of insert ranging 200-1,200 base pairs. From the amount of positive clones determined, (AC)_n dinucleotide microsatellite was found predominately distributed in the genome of *An. minimus*, comparing to (AG)_n.

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EVALUATION OF CANDIDATE TRAPS AS TOOLS FOR CONDUCTING SURVEILLANCE FOR ANOPHELES MOSQUITOES IN A MALARIA-ENDEMIC AREA IN WESTERN THAILAND

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The effectiveness of five mosquito traps at sampling anopheline mosquitoes was compared with landing/biting (L/B) collections in western Thailand. Traps evaluated included a CDC style light trap (CDC LT) with dry ice, the American Biophysics Corporation (ABC) standard light trap (ABC LT) with dry ice and octenol, the ABC counterflow geometry (CFG) trap with dry ice and octenol, the ABC mosquito magnet (MM) trap with octenol, and the Nicosia and Reinhardt Company Mosquito Attractor Device (N & R trap). Mosquito numbers captured in landing-biting collections were 5.2, 7.0, 7.3, 31.1, and 168.8 times greater than those collected in the ABC LT, MM, CDC LT, CFG, and N & R traps, respectively, for *Anopheles minimus* Theobald, the predominant malaria vector in the region. Similar results were obtained for the secondary malaria vectors *Anopheles maculatus* Theobald and *Anopheles sawadwongporni* Rattanarithikul & Green. Only *Anopheles kochi* Doenitz was collected in significantly greater numbers in the CDC LT, ABC LT, and MM traps compared with L/B collections. Although none of the traps were as effective as L/B collections, the ABC LT, MM, and CDC LT were the best alternatives to human bait for the collection of anopheline malaria vectors in Thailand.

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EVIDENCE FOR ARBOVIRUS DISSEMINATION CONDUITS FROM THE MOSQUITO (DIPTERA: CULICIDAE) MIDGUT

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The mechanism by which arboviruses bypass the basal lamina of mosquito midgut cells and enter the body cavity has been unclear. Experiments using Venezuelan equine encephalitis