Prin Phunngam 2012: Population Genetic Study of *Anopheles harrisoni* (Diptera: Culicidae) and Sequence-based Multilocus Phylogenetic Reconstruction of Malaria Vectors in Thailand. Master of Science (Genetics), Major Field: Genetics, Department of Genetics. Thesis Advisor: Miss Uraiwan Arunyawat, Dr.rer.nat. 149 pages.

Investigation of pattern and level of genetic diversity of malaria vector species are important for understanding the evolutionary history in order to achieve vector control. In this study, two *An. harrisoni* populations from Kanchanaburi province and one from north-western of Vietnam were collected and identified by molecular identification. Five putative neutral fragments on the X chromosome were chosen to amplify and sequence. The total length of the studied loci range from 245 bp to 609 bp. and average level of nucleotide variations (π) across all loci varies from 0.151 – 0.268 % based on single nucleotide polymorphism data. This result exhibited low level of nucleotide diversity for all three *An. harrisoni* populations. Moreover, the neutrality tests, e.g. Tajima's *D* and Fu and Li's *D* statistics, did not show significant deviation from standard neutral expectation suggesting that all populations are likely under mutation-random genetic drift equilibrium. Furthermore, no genetic differentiation was observed between Thai populations, while the genetic differentiation between Vietnam and Thai populations was high due to the geographical isolation between them.

An understanding the evolutionary and taxonomic status of closely related malaria vector species is the initial step in a malaria vector control program. In this study, four different approaches were performed to reconstruct phylogenetic trees for the main malaria vectors presented in Thailand based on the six DNA fragments from both the nuclear and mitochondrial regions. The results revealed clear evidence that *Anopheles* species separate into three distinct clades: Dirus group, Minimus group and Maculatus group. Interestingly, phylogenetic trees based on different reconstructed algorithms and different gene regions provided congruent phylogenetic status of the mosquito species studied. The phylogenetic relationships of these malaria vector species follow a pattern based on morphological identification. Moreover, estimation of the divergence time among the studied species inferred that *Anopheles* species probably existed around the Eocene and Miocene.

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