

# **Mitochondrial variation in subpopulations of *Anopheles balabacensis* Baisas in Sabah, Malaysia (Diptera: Culicidae)**

## **ABSTRACT**

*Anopheles balabacensis*, the primary vector of *Plasmodium knowlesi* in Sabah, Malaysia, is both zoophilic and anthropophilic, feeding on macaques as well as humans. It is the dominant *Anopheles* species found in Kudat Division where it is responsible for all the cases of *P. knowlesi*. However there is a paucity of basic biological and ecological information on this vector. We investigated the genetic variation of this species using the sequences of *cox1* (1,383 bp) and *cox2* (685 bp) to gain an insight into the population genetics and inter-population gene flow in Sabah. A total of 71 *An. balabacensis* were collected from seven districts constituting 14 subpopulations. A total of 17, 10 and 25 haplotypes were detected in the subpopulations respectively using the *cox1*, *cox2* and the combined sequence. Some of the haplotypes were common among the subpopulations due to gene flow occurring between them. AMOVA showed that the genetic variation was high within subpopulations as compared to between subpopulations. Mantel test results showed that the variation between subpopulations was not due to the geographical distance between them. Furthermore, Tajima's *D* and Fu's *F<sub>s</sub>* tests showed that *An. balabacensis* in Sabah is experiencing population expansion and growth. High gene flow between the subpopulations was indicated by the low genetic distance and high gene diversity in the *cox1*, *cox2* and the combined sequence. However the population at Lipasu Lama appeared to be isolated possibly due to its higher altitude at 873 m above sea level.