

**UNIVERSITI TEKNOLOGI MARA**

**GENETIC VARIATIONS IN  
*Aedes albopictus*  
(DIPTERA: CULICIDAE) BASED ON  
*ND5* AND *CO1* MARKERS**

**NURUL ADILAH BINTI AMRANNUDIN**

Thesis submitted in fulfillment  
of the requirements for the degree of  
**Master of Health Sciences**  
**(Medical Laboratory Technology)**

**Faculty of Health Sciences**

February 2019

## ABSTRACT

*Ae. albopictus* is an invasive species that has expanded globally raising threats of arboviruses transmission and the re-emergence of dengue endemicity in Malaysia. Dengue transmission dynamics could be influenced by the distribution and genetic variation among vector species. Studies focusing on the genetic diversity of *Ae. albopictus* in local populations are currently lacking in the Malaysian setting, yet such studies are crucial to enhance the current vector control strategies. The present study was conducted to establish the genetic variability of maternally inherited mitochondrial DNA encoding the *nicotinamide adenine dehydrogenase subunit 5 (ND5)* and *cytochrome oxidase c subunit 1 (COI)* gene in *Ae. albopictus*. In order to achieve this, the genetic diversity, haplotype, phylogeography and phylogenetic analyses were performed. Twelve localities in the Subang Jaya municipality were selected based on temporal indices using 120 mosquito samples. Genetic polymorphism-based studies and phylogenetic analysis were conducted using local *Ae. albopictus* populations. Haplotype network and phylogram were used to determine the genetic relationship of sequences among groups of population in the Asian regions. Genotypic detection of all sampled localities was positive for both genes, with distinct genetic heterogeneity. *COI* gene polymorphisms revealed higher numbers of nucleotide diversity ( $\pi$ ) and haplotypes (h) compared to *ND5* gene in the studied samples, with indices values of 0.02803 and 55, respectively. Comparison of local *ND5* and *COI* sequences with sequences derived from other Asian countries revealed genetically distinct intrapopulation species of *Ae. albopictus*. Phylogenetic analysis of *Ae. albopictus* revealed that all local haplotypes descended from the same genetic lineage with the sequences from other Asian countries. This study revealed the discovery of 52 novel haplotypes of the *COI* gene and 7 novel haplotypes of the *ND5* gene within the local populations that have not been reported to date. The analysed *COI* gene identified substantial levels of genetic diversity among mosquitoes in the local populations and highlights the reliability of the long *COI* fragment to identify genetic divergence, which can be utilized in forthcoming studies. These findings demonstrate diverse patterns of genetic variation and establishment of gene flow of *Ae. albopictus*, which in turn could be used to aid the current vector surveillance strategies, both locally and regionally.

## ACKNOWLEDGEMENTS

In the name of Allah, the Most Gracious and the Most Merciful

First and foremost, Alhamdulillah. Greatest gratefulness and praise is to ALLAH, the Almighty, the greatest of all, on whom ultimately we depend for sustenance and guidance. I would like to thank Almighty Allah for giving me opportunity, determination and strength on completing my research. His continuous grace and mercy was with me throughout my life and ever more during the tenure of my research.

Now, I would like to thank and express my deep and sincere gratitude to my respected supervisor, Dr. Siti Nazrina Camalxaman for her continuous support, guidance, motivation and encouragement throughout these years. You have been an excellent supervisor and tremendous mentor for me. I appreciate all your contributions of time, support and ideas. Thanks also to my supportive co-supervisors, Associate Prof Rodziah Ismail, Prof Abu Hassan Ahmad and Dr. Nazri Che Dom for their valuable guidance and suggestions. Indeed, their constructive comments were really inspiring and helpful. May Almighty Allah bestow His blessing and mercy upon all of you.

Not forgotten, this study would have been impossible without the financial support of Fundamental Research Grant Scheme (FRGS/1/2014/SKK10/UITM/03/1) from the Ministry of Education (MOE), Malaysia. Special thanks also to Dr. Danielle Porretta (Department of Ecological and Biological Science, Tuscia University, Viterbo, Italy) and Dr. Daibin Zhong (College of Health Science, University of California, Irvine, USA) for their kind hearted in sharing the sequences data, which are very useful for me to complete my data analysis and finally support the findings of this study. I am also eternally grateful and thankful to the Vector Control Research Unit, Universiti Sains Malaysia (USM), Penang for providing the laboratory strain of *Aedes albopictus*. Many thanks also to Postgraduate Department for providing the research facilities, including staffs who had given technical assistances throughout the duration of this project.

Special appreciation dedicated to my beloved parents; Amrannudin Arbi and [REDACTED] [REDACTED] for their sincere supports and prayers. Their endless prayers kept me sustained and drive me throughout this study. I am sincerely grateful to my siblings; Mohammad Adil Akmal and Nurul Athirah for their continuous moral supports and motivations that they have given me through thick-and-thin. My love is eternally with all of you. Thank you so much!

My most heartfelt gratitude also goes to my fellow labmates and friends; Nurul Ain Ismail, Mayamin Hamsidi, Nabilah Amelia Mohammad, Muhammad Faiz Madzlan and Siti Nur Anis Hasnan for discussions, suggestions, ideas and helps on this research. My sincerest thanks extended to all my lecturers and postgraduate friends for their warm helps, encouragements and advices that motivates me to strive this journey. For those who are not mentioned but directly and indirectly involved in this study, I am truly appreciate your efforts and may Allah will bless and reward all of you for your generosity. Thank you.

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