



اَوْنِوَسِيْتِي تِيكْنُوْلُوْجِي مَارَا
UNIVERSITI
TEKNOLOGI
MARA

**HAPLOTYPE ANALYSIS OF *Cytochrome oxidase (COI)* GENE of *Aedes albopictus*
ISOLATED FROM TAWAU, SABAH: AN ASIAN PERSPECTIVE**

By

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**Thesis Submitted in Partial Fulfilment of the Requirement for Bachelor of Medical
Laboratory Technology (Hons), Faculty of Health Sciences, Universiti Teknologi
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2017

DECLARATION

I hereby declare that this thesis is my original work and has not been submitted previously or currently for any other degree at UiTM or any other institutions.

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ACKNOWLEDGEMENTS

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

Alhamdulillah, all praises to Allah SWT for His countless blessings, the good health, strength and guidance for me to finish this entire journey upon completing the thesis. First of all, I would like to thank the Dean of the Faculty of Health Sciences, UiTM Puncak Alam for providing fund and necessitate laboratory facilities for this project completion. Not forgotten, this study was partially funded by Fundamental Research Grant Scheme 600-RMI/FRGS 5/3 (28/2014).

My greatest gratitude highly expressed to my beloved supervisor, Dr. Siti Nazrina Camalxaman, for your patient guidance, help and continuous support all the way through this research. I am enormously grateful to be under your supervision and indebted to you for the knowledge you have passed on and all the sacrifices that you did to me. Only the Almighty Allah SWT could can repay and devotes you with His blessing hereafter.

Next, I wish to express my sincere thanks to Dr. Wan Mazlina Md Saad, the Head of the Medical Laboratory Technology Centre, all lecturers especially my co-supervisors Mr. Mohd Fahmi Mastuki as well as Dr. Nazri Che Dom from the Centre of Environmental Health and Safety and to all laboratory personnel for their invaluable help and contributions in various aspects throughout this project.

I also owed my profound debt to the respected postgraduate students, Nur Mayamin Hamsidi, Nurul Adilah Amrannudin and Nurul Ain Ismail for their accountable help and advices on both theory and practical skills from the beginning until now. Thank you for all the knowledge, guidance and sharing of experiences. My deep gratitude goes to my research partner, Fatin Hannani binti Yusoff and also my fellow colleagues Mario Joseph and Nurlina Yasmin binti Zulkifli for their thoughtful helps and comforts. A million thanks to my beloved parents and family for their limitless prayer, love, motivation and strength because without them on my back through my thick and thin, none of this would have been possible.

Last but not least, I would like to thank my fellow friends and all those who had given directly or indirectly helps and contributions during this study. May God bless all of us and all the best for our future undertaking.

TABLE OF CONTENT

DECLARATION	iii
ACKNOWLEDGEMENTS	vii
TABLE OF CONTENT	viii
LIST OF TABLES	x
LIST OF FIGURES	xi
LIST OF SYMBOLS	xiii
LIST OF ABBREVIATIONS	xiv
ABSTRACT	xv
CHAPTER 1	1
INTRODUCTION	1
1.1 Background of the study	1
1.2 Problem statement	3
1.3 Objective of the study	3
1.3.1 General objective	3
1.3.2 Specific objectives	3
1.4 Significance of the study	4
CHAPTER 2	5
LITERATURE REVIEW	5
2.1 <i>Aedes</i> mosquito – <i>Aedes albopictus</i>	5
2.1.1 Taxonomy classification of <i>Ae. albopictus</i>	5
2.1.2 Morphological characteristics of <i>Ae. albopictus</i>	6
2.1.2.1 <i>Ae. albopictus</i> versus <i>Ae.aegypti</i>	6
2.1.2.1 Male versus female <i>Ae. albopictus</i>	8
2.2 Life cycle of <i>Ae. albopictus</i>	10
2.2.1 Egg phase	10
2.2.2 Larval phase	10
2.2.3 Pupal phase	11
2.2.4 Adult phase	11
2.3 Natural habitat of <i>Ae. albopictus</i>	13
2.4 Feeding behavior of <i>Ae. albopictus</i>	13
2.5 Origin and population expansion of <i>Ae. albopictus</i>	14
2.6 <i>Aedes albopictus</i> as a vector	14
2.7 Molecular study of <i>Ae. albopictus</i> on <i>C01</i> gene	15
CHAPTER 3	17
MATERIALS AND METHOD	17
3.1 Sampling	17
3.1.1 Study area	17
3.1.2 Sampling collection	17
3.1.3 Rearing process	19
3.1.4 Morphological identification of <i>Ae. albopictus</i>	22
3.1.5 Fixation	22

ABSTRACT

HAPLOTYPE ANALYSIS OF *Cytochrome oxidase (COI)* GENE of *Aedes albopictus* ISOLATED FROM TAWAU, SABAH: AN ASIAN PERSPECTIVE

The spread and the rise of *Ae. albopictus* population from its native range in Southeast Asia was resulting in increasing of dengue outbreak and dengue cases reported in Malaysia. Present vector control programs seems to become ineffective and lose their potential to combat the rapid expansion of *Ae. albopictus* mosquitoes in all over the nation. Studies on *Ae. albopictus* population genetic structure and genetic diversity was considered as the best option for better understanding on this mosquito species origin and its evolutions from time to time. Thus, this study was conducted to analyze and identify the genetic diversity among *Ae. albopictus* isolated from Tawau, Sabah in Malaysia using a mitochondrial DNA (mtDNA) marker, *Cytochrome oxidase (COI)* gene. Molecular study started with genomic DNA extraction of three individual adult female *Ae. albopictus* mosquitoes isolated from Tawau, Sabah and three USM laboratory strains (USM LS) followed by the amplifications of the extracted samples using three different sets of *COI* primer. PCR products were sent for sequencing and the obtained sequenced were subjected to BioEdit software for concatenation process, involving the joining of the three fragments that have been amplified. BLAST analysis revealed high similarities between the samples with the reference sequences obtained from NCBI GenBank database proved the used of *Ae. albopictus* in this study. Subsequently, the concatenated sequences were aligned using ClustalX2.1 together with another 12 reference sequences from NCBI GenBank representing four Asian countries (China, Taiwan, Japan and Singapore). Haplotype network and haplotype analysis of all the samples was constructed using TCS network via PopART and DNasp software respectively. This study disclosed an interesting finding whereby 18 different haplotypes from the total of 18 samples tested, with haplotype (gene) diversity (Hd value) of 1.000 was detected. In conclusion, the finding in this study revealed the merit of using the concatenated *COI* gene as a genetic marker. A longer fragment of *COI* gene was amplified and sequenced (1420bp), which helped the polymorphisms determination within Tawau samples.

Keywords: *Aedes albopictus*; Mosquito; *COI* gene; Haplotype; Malaysia