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HAPLOTYPE ANALYSIS OF FIELD COLLECTED *Aedes albopictus* FROM TAMAN BUKIT KINRARA, SELANGOR USING THE NADH DEHYDROGENASE SUBUNIT 5 (*ND5*) MARKER

By

NOR ADIRA BINTI ABDUL KHALID

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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.

Signature :

Name : Nor Adira Binti Abdul Khalid
Matric Number : 2013483628
Date : 18th July 2016

TABLE OF CONTENTS

Page

CHAPTER

1 INTRODUCTION

2 LITRATURE REVIEW

3 MATERIALS AND METHODS

ABSTRACT

HAPLOTYPE ANALYSIS OF FIELD COLLECTED *Aedes albopictus* FROM TAMAN BUKIT KINRARA, SELANGOR USING THE NADH DEHYDROGENASE SUBUNIT 5 (*ND5*) MARKER

Recent spread of *Ae. albopictus* from its native range in Southeast Asia has been implicated in the increasing numbers of dengue cases in Malaysia. Dengue is a public health concern and Malaysia needs to implement effective vector control programs. However, existing programs has proven ineffectual with the worldwide expansion of *Ae. albopictus* mosquitoes. Studies examining the population genetics structure of *Ae. albopictus* based on mitochondrial DNA *ND5* marker has not been elucidated at the local settings, despite its importance. Hence, this study was conducted to evaluate the intrapopulation and interpopulation genetic diversity among *Ae. albopictus* from Taman Bukit Kinrara, Selangor, a dengue cluster areas in Malaysia using a mitochondrial DNA marker. The genomic DNA of ten individual adult female *Ae. albopictus* mosquitoes and ten USM laboratory strains (USM LS)was extracted and analysed for DNA polymorphism based on the mitochondrial *ND5* marker. 450 bp of amplified PCR products was obtained and sequenced. BLAST analysis showed high similarities with reference sequences from NCBI GenBank. Subsequently, the multiple nucleotide sequences were aligned using ClustalX2.1. Haplotype network was constructed using TCS network in PopART software. Haplotypes generated was analyzed using DNaSP. Our findings revealed that *Ae. albopictus* population from Taman Bukit Kinrara, Selangor are genetically related at intrapopulation and interpopulation levels with low genetic variation with Hd values of 0.4368 and 0.5869 respectively. This study highlights the generation of 11 haplotypes from 49 sequences at 11 different polymorphic sites. The data obtained from this study may provides new fundamental knowledge regarding the genetic structure of local *Ae. albopictus* that could be utilised in forthcoming studies.

Keywords: *Aedes albopictus*, Malaysia, *ND5*, haplotype analysis, genetic diversity

CHAPTER 1
INTRODUCTION

1.1 Background of the study

The Asian tiger mosquito, *Aedes albopictus*, is otherwise known as *Stegomyia albopicta sensu* is considered to be the one of the most invasive mosquito species in the world (Medlock et al., 2012; Zhong et al., 2013). This species stands out as a model species for invasive disease vector studies. Native to Southeast Asia, *Ae. albopictus* has spread throughout the world in the past three decades and it is now found on every continent except Antartica (Goubert, Minard, Vieira, & Boulesteix, 2016). *Ae. albopictus* is a day-time biting mosquito that transmits a variety of viruses such as dengue virus (DENV) and Chikunguya virus (CHIKV) through aggressive biting anthropophilic adult females (Zawani, Abu, Sazaly, Zary, & Darlina, 2014; Zhong et al., 2013). Because its primary role in recent DENV and CHIKV outbreaks and its competence for numerous other arboviruses and pathogens such as the Zika virus causes worldwide concern (Bonizzoni, Gasperi, Chen, & James, 2013; Goubert et al., 2016).

Ae. albopictus has a wide distribution. The distribution and invasion history of *Ae. albopictus* has been reviewed by (Hawley, 1988). This species is thought to have originated in the Asian forests and is distributed throughout temperate and tropical regions of America, Africa, Europe and a number of locations in the Pacific and Indian oceans (Kamgang, Nchoutpouen, Simard, & Paupy, 2012; Paupy, Delatte, Bagny, Corbel, & Fontenille, 2009; Rai, 1991). The geographical spread of this invasive mosquito has dramatically shifted during the past decades following the spread of *Aedes aegypti* and *Culex piplens*. The spread of *Ae. albopictus* outside its origin home-range is the example of the spread of a mosquito vector that is mediated by human activities such as via transportation of dormant eggs in used and waste tires and migration of people (Bonizzoni et al., 2013; Paupy et al., 2009). The rapid invasion of this species poses a great concern to