



**POLYMORPHIC ANALYSIS OF FIELD COLLECTED *Aedes albopictus*
FROM SUBANG MURNI, SHAH ALAM USING INTERNAL
TRANSCRIBED SPACER 2 (ITS2) rDNA MARKER**

By

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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.

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ABSTRACT

POLYMORPHISM ANALYSIS OF FIELD COLLECTED *Aedes albopictus* FROM SUBANG MURNI, SHAH ALAM USING INTERNAL TRANSCRIBED SPACER 2 (ITS2) rDNA MARKER

The increase of dengue cases at an alarming rate in Malaysia has been strongly associated with *Ae. aegypti* and *Ae. albopictus* vectors. However, the former is always the subject of interest while the latter is often regarded as the secondary vector despite its worldwide expansion. Studies examining the population genetics structure of *Ae. albopictus* are established, although most of the studies emphasised on the interpopulation genetic diversities using mitochondrial genome markers. Hence, this study was conducted to evaluate the intrapopulation and interpopulation genetic polymorphisms in *Ae. albopictus* from dengue infested area, Subang Murni, Shah Alam, Malaysia using nuclear DNA marker. Ovitrap used to collect *Ae. albopictus* eggs were placed at random in the study area and the eggs were reared to adults in the laboratory. The genomic DNA of five individuals and one pooled sample of *Ae. albopictus* from Subang Murni was obtained and analysed for polymorphism at ITS2 region of ribosomal DNA. 337 bp of PCR products was obtained and sequenced. The sequences were subjected to BLAST and showed high similarities with homologous sequences from NCBI GenBank. Subsequently, the nucleotide sequences were aligned using ClustalX2.1 software. Phylogenetic tree inferred using maximum likelihood method in MEGA5.2 revealed that *Ae. albopictus* population from Subang Murni genetically differs from each other although they were from the same locality. Nevertheless, this population has shown uniform homogeneity when compared with other worldwide populations namely Italy, United States, Japan, China and Greece. This is true except for a particular strain from Subang Murni that was separated in another group together with populations from Italy and Subang Jaya, Malaysia. These findings deduced that there is higher genetic variation within population of the same locality compared to variation at geographical differences. This information may be beneficial to construct the appropriate level of surveillance and control measures needed to prevent the future expansion of this vector and simultaneously reduce the health risks.

Keywords: *Aedes albopictus*, Malaysia, ITS2, genetic polymorphism

CHAPTER 1

INTRODUCTION

1.1 Background of study

The Asian tiger mosquito, *Aedes albopictus* is an invasive and aggressive insect that bites during daytime. It is considered as a threat to the public health due to its ability to transmit arboviruses, primarily dengue virus (DENV) and Chikungunya (CHIKV) virus (Bonizzoni *et al.*, 2013). It is also known that *Ae. albopictus* is a vector capable of transmitting other viruses such as La Crosse virus, Eastern Equine Encephalitis virus, Japanese encephalitis virus and West Nile virus (Medlock *et al.*, 2012). *Ae. albopictus* is indigenous in Southeast Asia. Furthermore, it has established a wide population throughout Europe, Africa, Middle East, North and South America and the Caribbean in the past three decades (Gratz, 2004). The fast spread of *Ae. albopictus* is incredibly alarming due to its status as a competence dengue and chikungunya vector (Benedict *et al.*, 2008).

Ae. albopictus is often regarded as secondary vector and is considered less of a health threat in comparison to its primary counterpart despite its widespread population expansion. This is partly due to the fact that this vector displays a zoophilic feeding behaviour, which makes it less efficient in disease transmission. However, *Ae. albopictus* has been incriminated in several episodes of disease outbreaks, such as in the recent dengue outbreaks in Hawaii, Indian Ocean Islands, Central Africa and Southern China between the years 2001 to 2010. This scenario is similar with the first occurrence of autochthonous dengue transmission in Europe (Bonizzoni *et al.*, 2013). In addition, *Ae. albopictus* was the main culprit behind the Chikungunya virus outbreaks in the South Western Indian Ocean, India, Central Africa and Italy in between the years 2006 to 2007 as suggested by Paupy *et al.* (2009). Therefore, the discriminable role of *Ae. albopictus* as a vector can no longer be neglected. This species is becoming more important in causing