POLYMORPHIC ANALYSIS OF FIELD COLLECTED *Aedes albopictus* FROM SUBANG BESTARI, SHAH ALAM BASED ON INTERNAL TRANSCRIBED SPACER 2 (ITS2) MARKER

By

WAN ZAINAB WAN OTHMAN

Thesis Submitted in Partial Fulfilment of the Requirements for Bachelor of Medical Laboratory Technology (Hons), Faculty of Health Sciences, University Teknologi MARA

2015

DECLARATION

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

Signature : 

Name : Wan Zainab Wan Othman

Matric Number : 2012604168

Date : 10th July 2015

TABLE OF CONTENT

ABSTRACT

POLYMORPHIC ANALYSIS OF FIELD COLLECTED *Aedes albopictus* FROM SUBANG BESTARI, SHAH ALAM BASED ON INTERNAL TRANSCRIBED SPACER 2 (ITS2) MARKER

The dramatic worldwide expansion of *Aedes albopictus* and its vector competence for numerous arboviruses especially dengue viruses (DENV) represent a growing threat to public health security. Being a secondary vector of DENV, the studies of *Aedes albopictus* is less focused unlike *Aedes aegypti*. The prospect of worldwide polymorphism of *Aedes albopictus* prompted the development of rapid, polymerase chain reaction (PCR)-based method and phylogenetic analysis on internal transcribed spacer 2 (ITS2) marker for evaluating the intrapopulation diversity of this species. ITS2 region was amplified from five singles and one pooled specimens of *Aedes albopictus* collected from Subang Bestari, Shah Alam (SB) along with the lab strain (LS) that act as a positive control and phylogenetic analysis was conducted on them. The obtained result revealed a PCR product of 337bp product. Based on phylogenetic analysis, SB and LS samples were in different clusters to each other including pooled samples. However, they showed a strong ancestral relationship to other global population mostly to the Italy population and highly similar to Mayotte population. The ITS2 marker here implemented revealed the distribution of genetic diversity within and between populations and provides clues on the dispersion dynamics of this species. It appears that the diffusion of this species to global may due to the migration aspect and it may survive in subtropical environments. The ITS2 marker is thus an important tool for future phylogeographical studies in Malaysia.

Keywords: *Aedes albopictus*, DENV, Polymerase Chain Reaction (PCR), Internal transcribed spacer 2 (ITS2), Intrapopulation, Phylogenetic

CHAPTER 1
INTRODUCTION

1.1 Background of the study

The Asian tiger mosquito *Aedes* (Stegomyia) *albopictus* (Skuse,1984) is one of the most invasive mosquitoes in the world (Manni *et al.*, 2015). It is an aggressive, daytime biting insect that has be known as a public health threat to globally following its primary role in transmitting several types of arboviruses including dengue virus (DENV) and Chikungunya virus (CHIKV) (Bonizzoni *et al.*, 2013); which are the causative agents for various types of encephalitis, dengue and Yellow fever (Mousson *et al.*, 2005), underlining its importance as a vector.

The origin of *Aedes albopictus* has been reported in the forest of South-East Asia (Mousson *et al.*, 2005). Eversince its first detection, there has been reports of a decline in the prevalence of the indigenous *Aedes* population (Hamady *et al.*, 2013). In the early 1980s, United States was introduced with this predator which has now spread in many parts of Europe. Moreover, *Aedes albopictus* is also now prevalent in Africa (Yang *et al.*, 2013). The spread of this mosquito is due to active adult flight and passive transportation of immature stages such as eggs and larvae in the international trade. Due to the emergence of this species throughout the world, they have established a worldwide geographical distribution.

Since *Aedes albopictus* has become a critical vector for DENV, vector controlling programmes needs to be improved. In Malaysia, dengue cases have been reported in increase from 2013 to 2014. According to Malaysian Health Minister, Datuk Seri Dr S.Subramaniam, the number of cases reported during the first 9 months of 2014 stands at 77,527 and 149 results in deaths. This is in contrast to the data for the same period which is 23,099 cases and 48 fatalities (Herriman, 2014). Due to this report, it