



UNIVERSITI TEKNOLOGI MARA

**ASSESSING THE DENGUE VECTOR
BREEDING CHARACTERISTICS IN SIBU
DISTRICT, SARAWAK, MALAYSIA USING
CLUSTER ANALYSIS**

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ABSTRACT

Dengue fever that are caused by dengue virus has currently emerged as one of the major threats to public health in Malaysia. The incriminated vector species for the diseases were caused by *Ae. aegypti* and *Ae. albopictus*. This study was initiated to determine the effect of size of breeding containers that contribute towards the development of *Aedes* immature abundance in urban residential areas in Sibu District, Sarawak, Malaysia. The study areas were divided into high-risk areas and low-risk areas. Therefore, cluster analysis was utilized by using self-organizing map (SOM) to visualize, partitioning and mapping the *Aedes* immature abundance in relation with different size capacity of the containers in the selected areas. In addition, limited studies were conducted to explore and visualize the multi-variable data by using SOM technique toward dengue vector abundance. Accordingly, majority of the studies have proposed the distribution pattern of the dengue vector abundance based on statistical analyses. For statistical analyses such as Chi-Square and Kruskal-Wallis test were also done to evaluate the abundance pattern of potential breeding containers in relation with the prevalence of *Aedes* immature stages. Based from the results, the Chi-Square indicated that there was statistical difference between the number of potential breeding containers and size ($p < 0.05$). The Kruskal-Wallis test indicated that there were no statistically significant associations were found among both of the study areas ($p > 0.05$) for *Ae. aegypti* and *Ae. albopictus* in the number of breeding abundance. The results from the unsupervised clustering techniques indicated that *Ae. albopictus* contributed strongly to the *Aedes* mosquito abundance for both areas identified in Sibu District, Sarawak. The abundance of the *Aedes* immature stages mainly occur in the class of large containers in low-risk areas whereas for high-risk areas, in the class of small containers for both species identified. The findings indicated a need to take action by eliminating the breeding containers which subsequently reducing the distribution of the *Aedes* immature stages for dengue control efforts and preventing dengue fever.

Keywords: *Vector abundance, dengue, Malaysia.*

CHAPTER ONE

INTRODUCTION

1.1 BACKGROUND OF STUDY

Dengue fever has currently emerged dramatically as one of the major public health problems in Malaysia. In Malaysia, the disease is endemic and primarily occurs in urban and suburban areas. Dengue fever (DF) and dengue haemorrhagic fever (DHF) are caused by dengue virus in which consists of four serotypes (DEN 1, DEN 2, DEN 3 and DEN 4) and belonging to genus *Flavivirus* that are transmitted to human by *Aedes* mosquitoes (Gubler, 1997). *Aedes aegypti* and *Aedes albopictus* are two incriminated mosquito species that transmitting the dengue virus (Rudnick, 1965). Walsh *et al.*, (2011) stated that these mosquitoes feed preferably on human blood through the bites of infected female mosquitoes. The widespread distribution of the dengue fever is closely associated to the circulation of the dengue viruses between dengue vector abundance and human-vector contact transmission (Lau *et al.*, 2013).

Vector abundance is defined as any measure of the number of vectors per sample collected in a known and standardized manner during a year at some point (European Centre for Disease Prevention and Control, 2018). In general, the major factors that contribute to dengue vector abundance are based on their breeding characteristics, limited nutrient concentration, density competition and climate and season change. Breeding characteristics such as size of the breeding containers are a major source that highly related to dengue vector abundance. The increase of the dengue vector abundance is influenced by the high availability of potential larval