

Spatial, environmental and entomological risk factors analysis on a rural dengue outbreak in Lundu District in Sarawak, Malaysia

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Abstract. The objective of this study was to elucidate the association of various risk factors with dengue cases reported in Lundu district, Sarawak, by analyzing the interaction between environmental, entomological, socio-demographic factors. Besides conventional entomological, serological and house surveys, this study also used GIS technology to generate geographic and environmental data on *Aedes albopictus* and dengue transmission. Seven villages were chosen based on the high number of dengue cases reported. A total of 551 households were surveyed. An overall description of the socio-demographic background and basic facilities was presented together with entomological and geographical profiles. For serological and ovitrap studies, systematic random sampling was used. Serological tests indicated that 23.7% of the 215 samples had a history of dengue, either recent or previous infections. Two samples (0.9%) were confirmed by IgM ELISA and 49 samples (22.8%) had IgG responses. A total of 32,838 *Aedes albopictus* eggs were collected in 56 days of trapping. Cluster sampling was also done to determine whether any of the risk factors (entomological or geographical) were influenced by geographical location. These clusters were defined as border villages with East Kalimantan and roadside villages along Lundu/Biawas trunk road. The data collected were analyzed using SPSS version 10.01. Descriptive analysis using frequency, means, and median were used. To determine the association between variables and dengue cases reported, and to describe the differences between the two clusters of villages, two-sample *t*-test, and Pearson's Chi-Square were used. Accurate maps were produced with overlay and density function, which facilitates the map visualization and report generating phases. This study also highlights the use of differential Global Positioning System in mapping sites of 1m accuracy. Analysis of the data revealed there are significant differences in clusters of villages attributable to container density, house density, distance of the house from the main road, and number of *Ae. albopictus* eggs from ovitraps set indoor, outdoor and in dumping sites (Person's Chi-Square=6.111, df=1, $p<0.01$). Further analysis using *t*-test showed that house density, container density, indoor mosquitoes egg count, outdoor mosquitoes egg count, and dumping sites mosquitoes egg count were higher at the roadside villages compared to border villages. A number of potential risk factors including those generated from GIS were investigated. None of the factors investigated in this study were associated with the dengue cases reported.

INTRODUCTION

Dengue fever (DF) and dengue haemorrhagic fever (DHF) are the most common arthropod-borne viral diseases. It is estimated that about 50 million cases of dengue infection occur throughout the

world each year and causing 25,000 deaths (WHO, 1999). The World Health Organization (WHO) estimated that more than 2.5 billion people are at risk of dengue infection. In South East Asia, the principal vector of dengue viruses in urban areas is *Aedes aegypti* (= *Stegomyia aegypti*),