



COMPARATIVE ANALYSIS OF POSSIBLE RISK FACTORS AFFECTING TRANSMISSION OF DENGUE IN THE DISTRICT OF GAMPAHA, SRI LANKA

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INTRODUCTION

Dengue is an arboviral infection transmitted by the bite of infected females of *Aedes* mosquito, namely *Aedes aegypti* (Linnaeus) and *Ae. albopictus* (Skuse) (WHO,2017). More than 70% of disease is spread in the countries of South-East Asia and the Western Pacific covering most of tropical and subtropical regions (Gething et al.,2013). Compared to the other arboviral disease, deaths caused by dengue has increased 30-fold over the last 50 years, putting half of the world's population at risk (Uehera et al.,2017).

In Sri Lanka, dengue has affected most endemic areas. According to Dengue cases reported to the Epidemiology Unit, Sri Lanka, it has reported that the District of Gampaha is holding the second highest number of dengue cases continuously (Epidemiology Unit, 2017). Generally, dengue epidemiology is influenced by a complex interaction of factors that include the degree of urbanization and increased population density, capacity of healthcare systems, effectiveness of vector control services, predominant circulating Dengue Virus (DENV) serotypes and immunity of individual and social behaviour of the population (Chew et al.,2016 and Ehelepola et al.,2012). Limited resources and lack of awareness during the dengue epidemic are the most identified factors that harmfully affected to human in the most of Asia Pacific countries (Goto et al.,2013). However, it is required to identify risk factors associated with the transmission of dengue in the specific region to facilitate dengue control measures.

METHODOLOGY

A dengue high risk (study area) and a low risk (control area) were selected depending on the previously reported dengue cases for past ten years (2012-2017) to the Office of the Regional Epidemiologist, Gampaha. Based on the results, Medical Officer of Health (MOH) of Negombo was selected as the MOH with highest dengue risk. Within Negombo MOH area two Grama Niladhari (GN) Divisions with high dengue risk (study) and low dengue risk (control) areas were selected.

Random sampling method was used as the sampling method for the selection of households. Clusters of households (n=140) in a dengue high risk GN area (Kurana East) was chosen as the study group and cluster of households (n=140) in a dengue low risk GN area (Udayarthoppuwa) was selected as the control group.

The following formula was used to calculate sample size

$$N = \frac{Z^2 P(1 - P)}{d^2}$$

where,

N = sample size

Z = Z statistics for a level for confidence



P = probability prevalence d = expected precision of your prevalence estimates

Primary data were collected at selected households using a pre-tested interviewer-administered questionnaire. Entomological surveillance was conducted inspecting the surrounding of each household for 18 months and counts of adults and larvae were recorded for each month. An entomological survey was conducted using a hand-held mechanical aspirator (for adult mosquitoes) and a standard dipper (for larvae). Data on environmental factors such as cleanliness of the environment, vegetation coverage, type of premises, sources of drinking water and waste disposable system were collected and analyzed. Furthermore, data on socio-economic status were collected.

Ethical Clearance was obtained from Ethical Review Committee of the Faculty of Medicine, University of Kelaniya (Ref: P 101/02/2017). Informed consent was taken from the Heads of each house-holds and all the permission required to conduct field and sample collection processes were obtained from the Provincial Director of Health of Western Province, Regional Director of Health Sciences of Gampaha and all the Public Health Inspectors attached to the district of Gampaha.

House Index was calculated for each surveillance site for larvae (L4) of both *Aedes* species and plotted for further comparisons. Primary data collected from the questionnaire was analyzed using unpaired t-test with 95% confidence interval to find the variables that have shown significant differences in both sites.

RESULTS AND DISCUSSION

According to the entomological surveillance completed for 18 months of period, the counts of adults and larvae varied as follows for both sites.

Adults		High risk	Low risk
	<i>Ae. Albopictus</i>		112
<i>Ae. Aegypti</i>		-	6
Larvae (L4)		High risk	Low risk
	<i>Ae. Albopictus</i>	171	141
<i>Ae. Aegypti</i>	14	6	

Further, entomological indices have been calculated for each dengue species for both sites, and the variation of House-Index (HI) deviates as the plots mentioned in Figures 1 and 2.

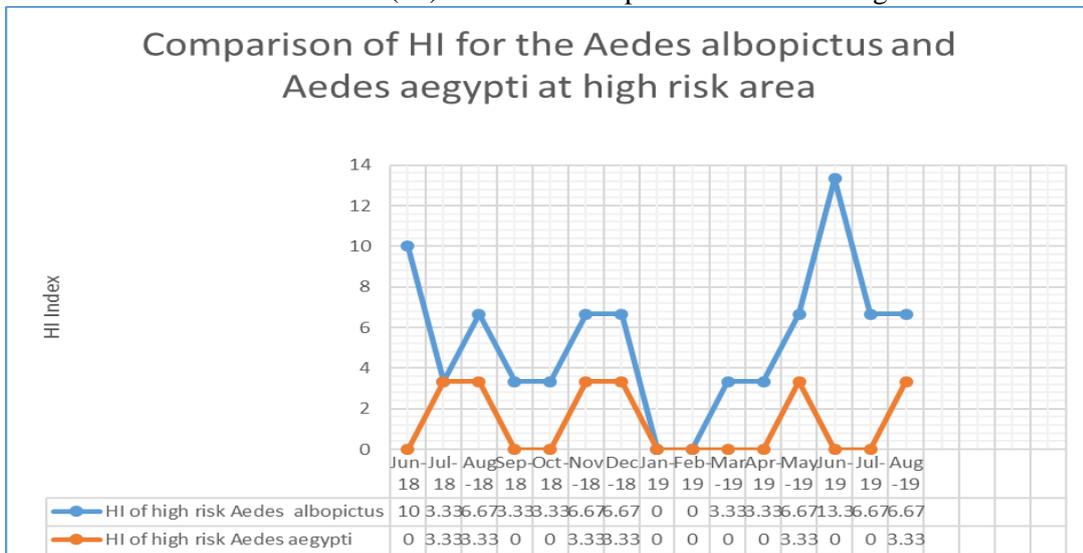




Figure 1: Comparison of HI for the *Ae. albopictus* and *Ae. aegypti* at high-risk area

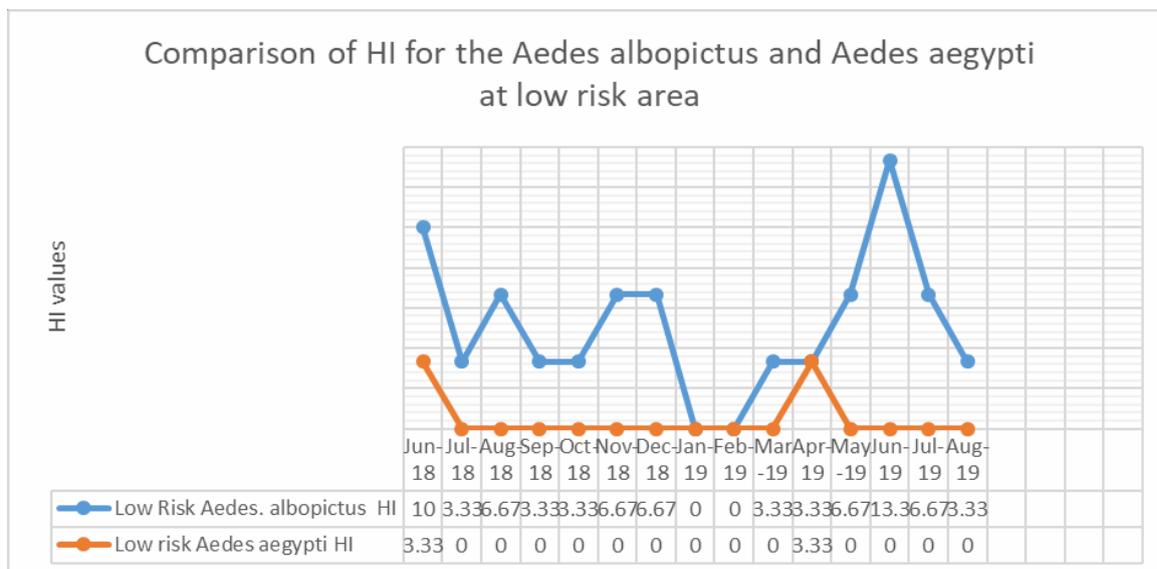


Figure 2: Comparison of HI for the *Ae. albopictus* and *Ae. aegypti* at low-risk area

These plots have clearly shown higher abundance of *Ae. albopictus* compared to the *Ae. aegypti* at both sites. The highest HI values for *Ae. albopictus* in both sites have been reported to the month of June-2019. Primary data collected from the questionnaire were used for unpaired t-test for each variable to find significant difference between the two areas. Summary of the most significant risk factors associated with dengue is shown below.

Variable	High Risk (n=140; Mean)	Low Risk (n=140; Mean)	P value (n=280)/ CI=95%
Source of water	1.43	1.38	0.8779
Waste disposal method	1.23	1.15	0.6655
Monthly income	1.30	1.39	0.5560
Household type	1.18	1.45	0.1312
Educational status	1.50	1.38	0.6870
Presence of previous dengue patients	1.25	1.83	0.0112
Vegetation coverage	1.64	1.18	0.0358
Premise cleanliness	1.10	1.78	0.0377
Presence of potential breeding sites	1.73	1.09	0.0019

As the significance level is 0.05, only the variables of vegetation coverage, premise cleanliness and presence of potential breeding sites have been shown a significant difference at both sites. These factors have potential influence on dengue transmission and have identified as risk factors. Therefore, the presence of previous dengue patients, vegetation coverage, premise cleanliness and presence of potential breeding sites could be considered as the risk factors that have influence Kurana area to stand as the dengue highest GN division with the highest recorded dengue cases.



CONCLUSIONS/RECOMMENDATIONS

According to the entomological surveillance data, it could be concluded that major vector which is responsible for the disease transmission is *Ae. albopictus* compared to the *Ae. aegypti*. From the statistical analysis of primary data, it is clear that presence of high densities of vector species, reporting dengue cases previously, cleanliness of premises, major mosquito prevention method, presence of potential mosquito breeding sites and vegetation coverage may be the most important risk factors affecting transmission of dengue. Therefore, health authorities responsible for dengue control could focus on these risk factors in their vector control campaigns to eradicate dengue from these high risk areas.

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