

## **Finer scale risk analysis of dengue transmission in MOH Akurana in the Kandy district of Sri Lanka**

Dengue is caused by 4 serotypes of the dengue virus, namely, dengue 1, 2, 3 and 4. The disease is transmitted by female mosquitoes of *Aedes aegypti* and *Ae. albopictus* and of the two species, *Ae. aegypti* is the major and epidemic causing vector while *Ae. albopictus* causes epidemics when it presents in high density. Globally, dengue is the fast spreading arboviral disease and over 3.5 billion people, (over 40% of the world's population) in more than 100 countries in the tropical and sub-tropical regions of the world are at risk of dengue transmission. According to the estimates of the World Health Organisation, there may be 50 – 100 million dengue infections worldwide every year and 500 000 people with severe dengue require hospitalization each year, a large proportion of whom are children. About 2.5% of those affected die.

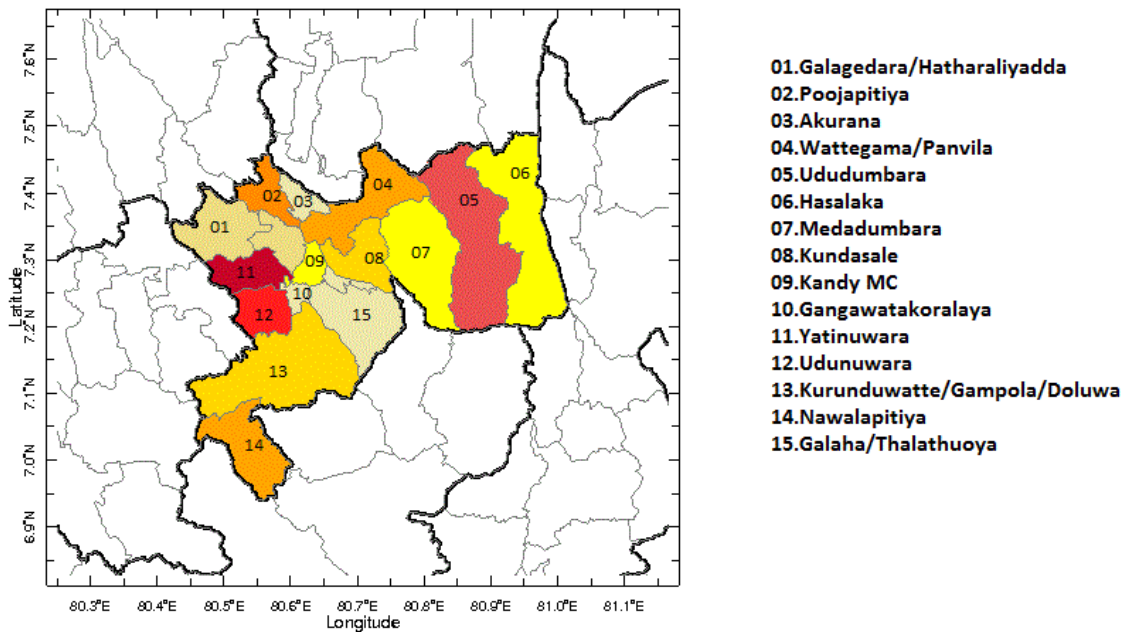
In Sri Lanka, dengue was prevalent since early 1960s, however, the disease became an important public health problem since early 2000s with epidemic at 2 – 3-year intervals. Not only the number of dengue patients (cases), but the spatial distribution of cases was widened over the years. Currently, dengue is endemic in Sri Lanka and patients are reported rural as well as rural areas of the country. The number of reported clinical and serologically positive dengue cases varied from 29,777 to 186,101 from 2010 – 2018 with the major epidemic in 2017 involving the 186,101 cases.

For the transmission of dengue, three factors, namely the virus (viraemic patient, the vector mosquito and a susceptible person needs to be present. In the absence of any of these factors, transmission will not occur. With regard to vector component, distribution and density of dengue vector, *Ae. Aegypti*, depends on the climatic factors specially the precipitation, temperature and relative humidity as they are heterothermic and container breeding species. Thus, study on the impact of climatic factors on the distribution and density of the vector population is of much importance in dengue vector control and thereby the dengue control. However, dengue is a local and focal disease, thus wider scale analysis would not be able to focus the actual transmission spots while finer scale analysis would help to identify actual sites of vector breeding, thus reducing the cost of controlling measures, both human and material costs. The present paper discusses the dengue transmission risk of different GN areas of a subdistrict in the Central Province of Sri Lanka and shows the feasibility of using finer scale mapping for making decisions on vector control.

### **The study area**

The area selected for the study is MOH Akurana, a sub district of the Kandy district in the Central Province of Sri Lanka (Fig 1).

Fig. 1. Map of Sri Lanka showing the Kandy district and MOH Akurana (03)



This MOH is highly receptive and vulnerable for dengue since early 2001. This area shows a heterogeneity in geographical and population distribution. The land area and the population of the area are 31 km<sup>2</sup> (2016) and 63,397 (2012 censuses), respectively with the population density of 2,135 per km<sup>2</sup>

### Data collection

Grama Niladari Level entomological data from 2014 – 2018 were collected from the regional Officer of the Anti-Malaria Campaign in Kandy and MOH Office Akurana, weekly dengue case data was collected from the records maintained at the MOH office Akurana and all data were collected with the permission of Provincial Director of Health Services in the Central province and the RDHS in Kandy. Entomological data included the number of houses surveyed, number of houses positive for *Ae. Aegypti* and *Ae. Albopictus*, number of wet containers and number of wet containers positive for *Ae. Aegypti* and *Ae. Albopictus*. Based on these data, the container index (percentage of wet containers positive for *Ae. Aegypti* and *Ae. Albopictus*), premise/ house index (percentage of houses/premises positive for *Ae. Aegypti* and *Ae. Albopictus*) and breteau index (number of positive containers positive for *Ae. Aegypti* and *Ae. Albopictus* per 100 houses/premises) were calculated.

### Data analysis

Presence and density of *Ae. Aegypti* and *Ae. Albopictus* in different GN areas and dengue cases in different GN areas were to analyse.