

A Spatial Dengue Risk Map for the Jaffna District of northern Sri Lanka

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Abstract – Dengue, a mosquito-borne disease, is a major public health concern in Sri Lanka including the northern Jaffna district. Epidemiology of dengue is associated with variations in land-use patterns and socio-economic factors. Jaffna district is one of the administrative locations with high incidence of dengue over the last two decades. The objective of the study was to identify potential dengue risk areas based on land-use patterns and socio-economic and demographic factors in Jaffna district at the Medical Officer for Health (MoH) administrative level applying spatial multi-criteria analysis using Geographic Information System Platform. The analysis also incorporated dengue cases and dengue serotypes identified in 2019 in the Jaffna district. The study reveals that the Nallur MoH division is the very high-risk area for dengue transmission. The identified risk map is expected to be useful for health authorities to prioritize control measures to identified risk areas. A detailed study considering land-use pattern, socio-economy, demography and serotypes over the years is warranted to understand the spatio-temporal patterns in dengue transmission in the Jaffna district.

Keywords: Dengue, Geographic information system, Jaffna district, Risk map, Multi-criteria analysis, DENV serotypes, Sri Lanka

1. INTRODUCTION

The global incidence of dengue has been increasing over the past two decades with a concomitant incidence of the disease and an estimated 2.5 billion people are at risk in the tropics, subtropics, and temperate regions of the world (World Health Organization, 2021, 2022). *Aedes aegypti* and *Ae. albopictus* are respectively the primary and secondary vectors of dengue and also the vectors of other important arboviral diseases such as chikungunya, yellow fever, Rift Valley fever and Zika (World Health Organization, 2022; Powel, 2018; Leta *et al.*, 2018).

Dengue is a major public health problem and considered as one of the leading causes of hospitalization and death among children in Sri Lanka. All four serotypes DENV1-IV are reported to be circulating in the country (Tissera *et al.*, 2020; Epidemiology Unit, Sri Lanka). A total of 186,101 dengue cases, the highest

number of dengue cases recorded so far, were recorded in 2017 (Epidemiology Unit, Sri Lanka). However, there was a significant reduction in the number of reported dengue cases during the COVID-19 movement restrictions (Surendran *et al.*, 2022a) but the trend has been reversed since the normalcy was restored in November, 2021 (Surendran *et al.*, 2022b).

Dengue transmission dynamics are complex, involving interactions between virus, vector (mosquito), and human hosts. Dengue virus is transmitted to humans by the bites of vector mosquitoes. The disease has a broad spectrum of clinical presentations, from undifferentiated dengue fever (DF) to dengue haemorrhagic fever (DHF) to life-threatening dengue shock syndrome (DSS), creating significant health, economic and social burdens in endemic areas (Jayadas *et al.*, 2019 & 2021; Sirisena and Noordeen, 2014). As there is no licensed vaccine for dengue, vector control is the major measure

adopted to control disease transmission (Surendran *et al.*, 2021). The primary mosquito vector *Aedes aegypti* is a highly domesticated urban mosquito that preferentially lives in homes, feeding on humans and laying eggs in human-made containers (Gubler, 1997). It is an opportunistic breeder, highly adapted to urban and domestic environments (Rodhain & Rosen, 1997), whereas the secondary vector *Ae. albopictus* is partially anthropophilic and prevalent mainly in rural areas (Surendran *et al.*, 2019; Surendran *et al.*, 2022b). Dengue transmission shows significant variations in land-use patterns, which include changes in land cover, particularly the rapid unplanned expansion of urbanization leads to the development of urban communities with inadequate housing and poor infrastructure, including water, sewage systems, and waste management (Gubler, 1997; Rodhain and Rosen, 1997; Gubler, 2011).

Land use patterns such as built-up areas, farmlands, and water bodies were considered as criteria to create dengue risk maps (Chang *et al.*, 2009). Human-related socio-economic and demographic factors also influence relationship between dengue virus, mosquito vector, and human host. Evidence from the literature indicates a significant involvement of socioeconomic factors in dengue transmission around the world, including housing, population density, and socioeconomic conditions (Soghaier *et al.*, 2015; Udayanga *et al.*, 2018). Therefore, it is necessary to explore the recent trends of potential socio-demographic factors in the Jaffna district to understand the future severity of dengue risk and to undertake preventive control measures.

Geographic Information System-based tools have been developed to identify risk areas and develop an early warning system to predict or forecast disease prevalence. These tools are considered to be effective in implementing dengue control measures (Withanage *et al.*, 2021; Sumanasinghe *et al.*, 2016). Identifying dengue risk areas is expected to help health

authorities to prioritize their resources to such areas and to prevent further transmission (Kannathasan *et al.*, 2003). In this study, we evaluated the potential risk areas based on land-use patterns and socio-economic and demographic factors in MOH divisions in Jaffna district and also analyzed the demographic information about confirmed dengue cases and dengue serotypes in the year 2019. Since Jaffna district is endemic for dengue, identifying risk areas is of importance to prioritize resources to control the transmission dengue. With this background a study was carried out to identify spatial pattern of dengue risk areas of Jaffna district using Geographic Information System.

2. MATERIALS AND METHODS

2.1 Study Area

The study area, Jaffna (Figure 1), is one of the 25 administrative districts of Sri Lanka, which covers an area of 1025 km² and is located in the Northern Province. This district accounts for 3.8% of the country's total area. The district has fifteen administrative divisions and covers 435 Grama Niladhari Divisions. Jaffna district had a total population of 610,640 in 2020. It is one of the most densely populated districts of Sri Lanka, which consists of 14 MOH divisions, the health administrative divisions in Sri Lanka. Land uses and socio-economic and demographic backgrounds significantly vary among these MOH divisions.

2.2 Data acquisition

Secondary and primary data were used in this study. Secondary data on the *samurthi* receiving members, school density, housing type, and population density were acquired from statistical reports based on Grama Niladhari divisions (Statistical Handbook, 2019) and land use maps from the Survey Department of Sri Lanka. Data on reported dengue cases in 2019 in the 14 MoH divisions were also obtained from the Regional Director for Health Services (RDHS) office. Primary

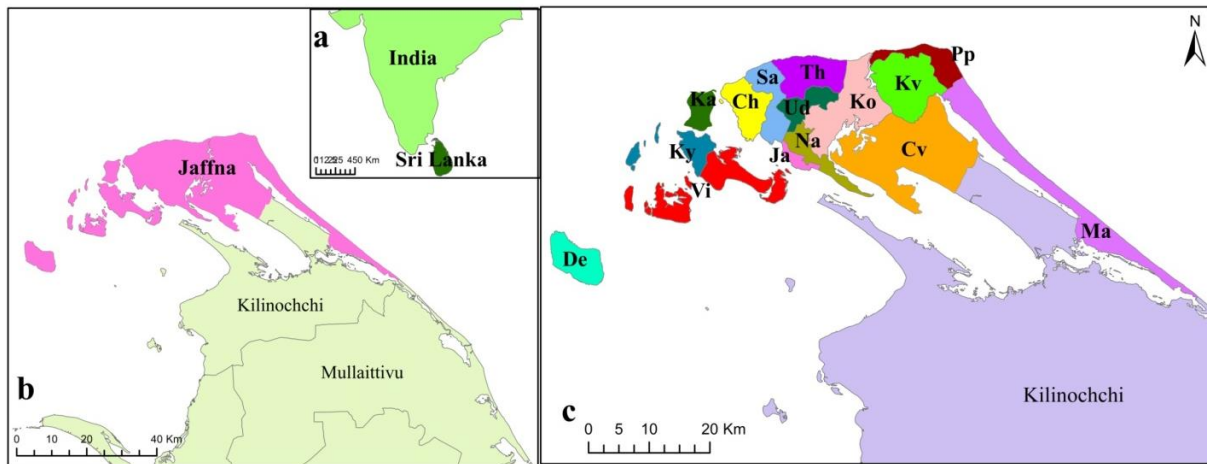


Figure 1: Map of Sri Lanka in relation to India and showing Jaffna district in the northern Sri Lanka and the MoH divisiona of the Jaffna district. (a). Location of Sri Lanka in the Indian ocean in relation to India, (b) Jaffna district in the northern Sri Lanka, (c). MoH divisions of the Jaffna district (De- Delft; Ky- Kayts; Vi- Velanai; Ja- Jaffna; Ch- Chankana; Sa- Sandilipai; Ud- Uduvil, Na- Nallur; Ko- Kopay; Th- Thellipalai; Kv- Karaveddy; Pp- Pointpedro; Ma- Maruthankerny; Cv- Chavakacheri

data for this study was collected through field testing from each land use type. Mainly, a few locations representing different land use patterns were selected as samples and field tests were also carried out to assess the potential for dengue transmission.

2.3 Multi-criteria analysis in GIS

Five criteria, such as land use/cover, population density, socio-economic status, house types and the number of schools, were identified as being relevant to dengue transmission based on previous dengue vector survey, expert knowledge and available literature as reported previously (Kannathasan et al., 2013). The risk was categorized from very high risk to very low risk, where very high risk is related to the high occurrence of dengue and very low risk is related to very few dengue incidences or no dengue incidence (Kannathasan et al., 2013).

Depending on the dengue vector prevalence based on the previous studies and ovitrap-based vector survey, different types of land use patterns in relation to dengue risk were categorized as follows; Built-up areas > Water bodies > Agricultural land > Grass land > Barenland and very high risk was considered to

be in built-up areas, and very low risk was considered to be in barren land (Kanathasan et al., 2013; Surendran et al., 2021). High population density is considered to be one of the favoring factors in dengue transmission. Therefore, the population density above 1700/SqKm considered to be very high risk, and the population densities of 1300-1700/SqKm, 900-1300/SqKm, 500-900/SqKm and <500/SqKm as high risk, moderate risk, low risk and very low risk respectively for the transmission of dengue infection.

Since socio-economic status was associated with the *samurdhi* recipients (a government subsidiary eligible for those monthly income is < 2,500 LKR) considered to be in poor socio-economic status and were considered as high risk groups and the non-recipients as low risk to contact dengue fever. On this basis, the MoH division where 25,000 or more people receive *samurdhi* subsidiary is considered very high risk area, and the MoH area where *samurdhi* recipients were below 5500 was considered very low risk (Table 1).

Considering house types, tents and huts are considered to favour *Aedes* mosquitoes to enter, take bloodmeal (infective bite) and rest, thus

Table.1: Identified demographic risk factors and their risk level related to dengue transmission

Categories	Risk Level	
Land use pattern	Very High	Built up area
	High	Water bodies
	Moderate	Agriculture land
	Low	Grass land
	Very Low	Barren land
Samurthi receiving members	Very High	Above 25000
	High	15500 - 20500
	Moderate	10500 - 15500
	Low	5500 - 10500
	Very Low	500 - 5500
School density	Very High	Above 0.8
	High	0.6 - 0.8
	Moderate	0.4 - 0.6
	Low	0.2 - 0.4
	Very Low	0.0 - 0.2
Population density	Very High	Above 1700/Sq Km
	High	1300 - 1700/ Sq Km
	Moderate	900 - 1300/ Sq Km
	Low	500 - 900/ Sq Km
	Very Low	Below 500/ Sq Km
Houses	Very High	Tents
	High	Huts
	Moderate	Semi-permanent
	Low	Partially Built
	Very Low	Fully Built

these house types were considered as very high risk and high risk respectively for transmitting dengue fever, whereas semi-permanent and partially built houses are considered to be moderate and low risk for dengue transmission and fully built houses as very low risk for dengue transmission (Kannathasan *et al.*, 2013). As dengue is a major infectious disease among children and youngsters (Ariyaratne *et al.*, 2022), the presence of schools was considered a dengue risk factor as a higher number of children and youngsters gather together in one place which could increase the risk of dengue transmission (Table 1).

For the above criteria, a spatial multi-criterion analysis (SMCA) (Malczewski and Rinner, 2015) was used to create the dengue spatial risk map in Geographic Information System Platform.

The combination of multi-criteria evaluation methods and spatial analysis is referred to as SMCA which is a process that combines and transforms geographical data into a decision. This process consists of procedures that involve defining objectives, choosing the criteria to measure the objectives, specifying alternatives, assigning weights to the criteria, and applying the appropriate mathematical algorithm for ranking alternatives. SMCA, hence, is an important way to identify the spatial pattern of Dengue. The SMCA weighting was distributed (Land use pattern 30%, Population density 20%, House type 20%, Economic status 20% and presence of schools 10%) as reported previously (Kanathasan *et al.*, 2013). A standardized and weighted composition map as created to visualize the dengue risk pattern using ArcGIS 10.4 (ESRI, 2010).

Table 2: Detected DENV serotypes among patients admitted to the Jaffna Teaching Hospital and diagnosed for dengue during 2019 (Source: Jeyadas et al., 2019)

MoH Division	DENV serotypes				Total
	DENV-I	DENV-II	DENV-III	DENV-IV	
Velanai		3			3
Nallur	8	10			18
Sandilipay	5	7			12
Chankanai	5	3			8
Uduvil	2	1			3
Kopay	7	9			16
Chavakacheri	1				1
Karaveddy		1			1
Kayts	1				1
Pointpedro	1	2			3
Karainagar	1	1			2
Jaffna	29	11	2	2	44

2.4 Comparison of dengue incidence, localization of DENV serotype, and dengue risk map

The monthly reported dengue cases from January 2019 through December 2019 in the 14 MoH divisions were acquired from the RDHS office and used to correlate the dengue risk map created in GIS based on land use types, socio-economic and demographic patterns. DENV serotyping results for 2019 (Jayadas et al., 2021) were also overlaid on the risk map to validate the created spatial risk pattern.

3. RESULTS

3.1 Spatial dengue risk map

When the land-use pattern was considered in association with the dengue risk, analysis shows that all the MoH areas were considered very high-risk areas which are denoted by the red patches. But Jaffna, Nallur, Chavakacheri, and Thellipalai MoH areas are larger than the other divisions in area-wise (Figure 2A). When population density is considered, Jaffna and Nallur MoH areas were identified as very high-risk areas. MoH areas such as Delft, Velanai and Chavakacheri fell under the very low-risk category (Figure 2B). House type category risk analysis showed that MoH divisions such as Sandilipay, Kopay, and Chavakacheri under high-risk areas and that Jaffna, Kayts,

Maruthankerni, and Velanai under low-risk or very low-risk categories (Figure 2C). The economic status of the people, which is indirectly analyzed via the receipt of *samurdhi* subsidiary, showed that MoH divisions such as Uduvil, Kopay, and Chavakacheri were the very high-risk category divisions while Maruthankerny, Delft, and Velnai are low-risk areas (Figure 2D). Based on the number of schools, Nallur, Jaffna, and Pointpedro MoH divisions were identified as the high-risk category while Chavakacheri and Delft as very low-risk category (Figure 2E). In multi-criteria analysis, the dengue risk map for the Jaffna district shows the Nallur MoH division as a very high-risk area for dengue. Jaffna, Uduvil, Sandilipay, Chankanai, Kopay, and Point Pedro MoH areas are high dengue risk areas. Chavakacheri, Karaveddy, and Thellipalai are moderately risk while Kayts, Karainagar, Maruthankerny, Velanai, and Delft divisions are very low-risk areas for dengue transmission (Figure 3).

3.2 Comparison of dengue incidence, DENV serotype, and risk map

The Nallur MoH area was identified as a very high-risk division but only had 667 dengue cases during 2019, but Jaffna was identified as a risk area, but it recorded the highest number of

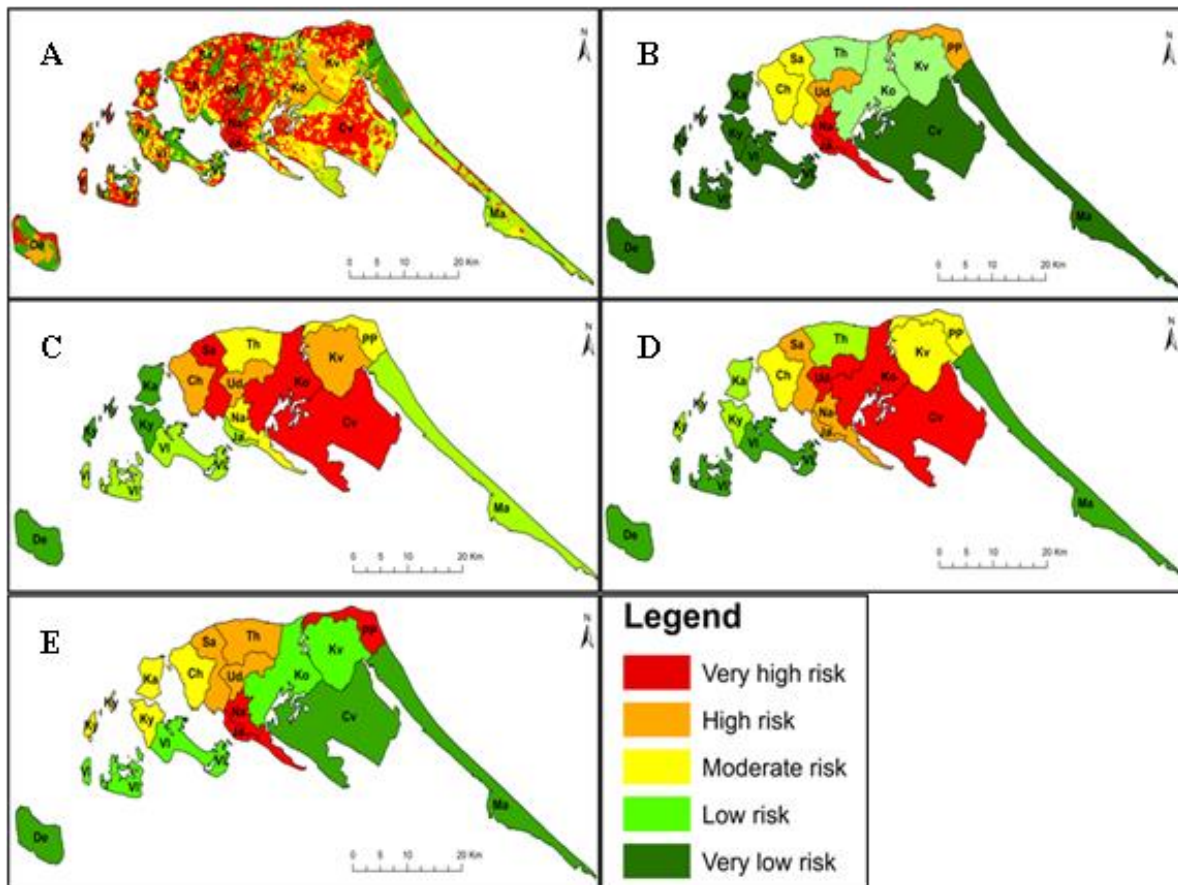


Figure2: Dengue risk pattern based on demography and land use risk categories. **A.** Land use pattern; **B.** Population density; **C.** Household type; **D.** Income based on *Samurdhi*; **E.** Schools)

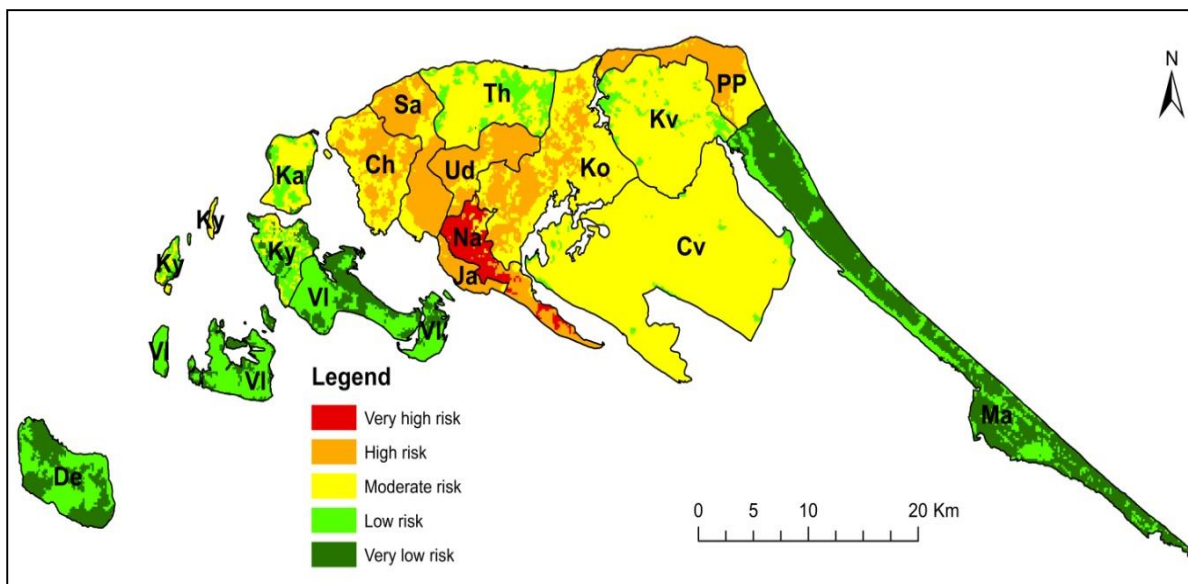


Figure3: GIS-based spatial dengue risk pattern for the Jaffna district based on land use, socio-economics and demographic changes.

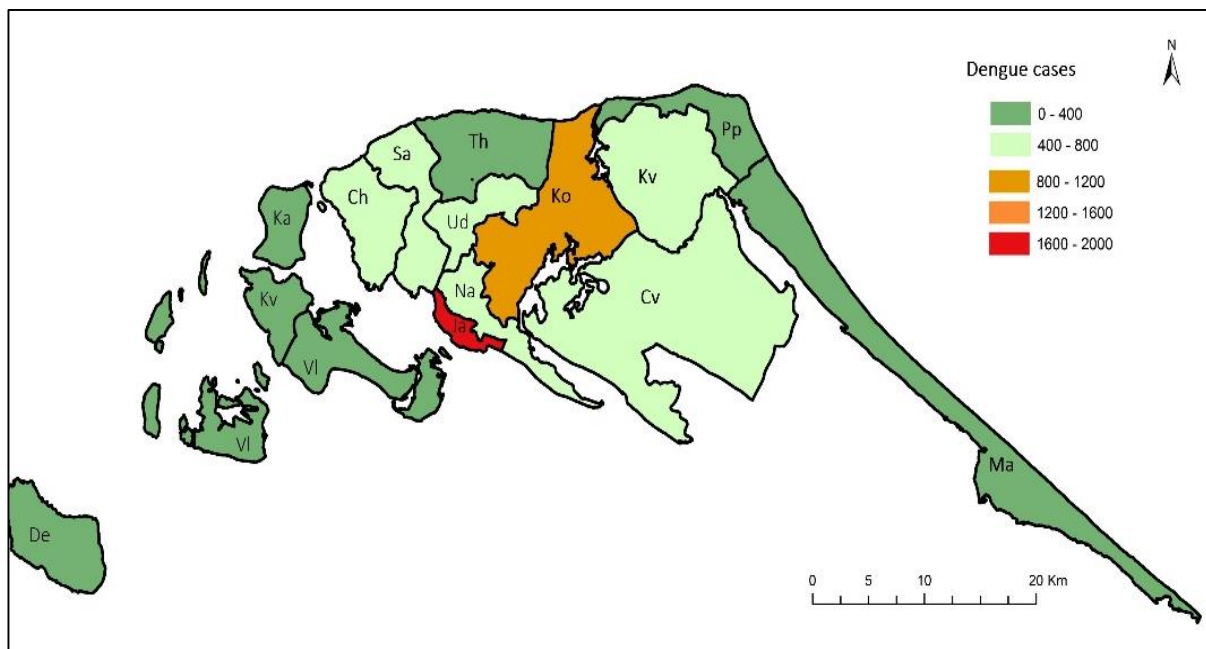


Figure 4: The spatial map showing MoH-wise identified number of dengue cases in the Jaffna district in 2019.

patients (1799) in 2019 (Figure 3 and 4). Kopay MoH area recorded the second highest number of confirmed dengue cases (862) but was identified as high-risk division (Figure 3 and 4).

Other identified high-risk MoH divisions such as Chankkanai, Sandilipay, and Uduvil have recorded 419, 485, and 535 dengue patients respectively. Even though Pointpedro was identified as a high-risk area, only 336 dengue cases were recorded in 2019. Kayts and Velanai MoH divisions were identified as low-risk and very low-risk areas, but in 2019, there were 251, and 141 cases were reported. Other low-risk MoH divisions are Karinagar and Maruthankerny recorded low dengue cases, 73 and 42, respectively (Figure 3 and 4).

In the year 2019, a total of 112 dengue-positive blood samples were screened for DENV serotypes. Serotype DENV-1 was predominant representing 53% followed by DENV-2 (43%) (Table 2, Jayadas et al. 2021), Jaffna and Nallur MoH areas were mainly infected with the DENV2 serotype and Kopay MoH with DENV1. All four serotypes were found

distributed in the Jaffna district in the year 2019 (Figure 5).

4. DISCUSSION

Dengue became a significant health concern in the year 2019 in Jaffna district with 8261 cases reported from all 14 MoH divisions (Epidemiology Unit, 2021). The factors such as dengue virus, *Aedes* vector, and human host play significant roles in the dengue transmission (TuiskunenBäck and Lundkvist, 2013). In the GIS-based spatial dengue risk map, the risk weight was given based on the influence of the vector, virus, and host on dengue transmission (Kanathasanet al. 2013). The created risk-map identified the Nallur MoH area as a very high-risk area, even though Jaffna MoH divisions recorded the highest number of (1799) dengue cases in 2019.

The reason for the difference in the predicted dengue risk map and the MoH-wise actual number of dengue cases could depend on a few other factors apart from land-use patterns, socio-economic status, and spatial and temporal

factors. In this study, we have not included the mobility of the people as a risk factor related to dengue (Kumanan et al., 2019), but mobility could also influence dengue infection. Jaffna MoH region consists the highly populated Jaffna city which is well connected to the rest of the country (Kumanan et al. 2019). An *Aedes* vector survey carried out in 2018 and 2019 in the Jaffna district revealed the presence of both dengue vectors throughout the years (Surendran et al., 2021). Generally, dengue incidence peaks during the southwest monsoon in Sri Lanka. The mobility between the Western province (highly endemic for dengue) and Jaffna city increases dengue cases in Jaffna MoH division significantly and moderately other MoH divisions (Kumanan et al. 2019; Surendran et al. 2021). Climatic factors such as rainfall, relative humidity and temperature were not taken into consideration as these factors do not show significant spatial variation in the district (Surendran et al., 2019). Environmental temperature and relative humidity variations can influence the transmission of dengue in other climate zones, but do not have a significant role in Sri Lanka (Surendran et al., 2022).

Aedes survey revealed that most of the *Aedes* breeding habitats found in the Jaffna district were man-made (Surendran et al., 2021). The *Aedes*-positive containers were mainly plastic containers and disposable cups. Therefore, it is hard to predict the dengue risk with the spatial-temporal risk categories; as a result, there could be variation in the number of dengue cases in the predicted dengue risk areas (Kanathasan et al., 2013; Surendran et al., 2021).

The Jaffna-associated islands namely Kayts and Velanai are identified as low-risk areas even though the two localities recorded a significant number of dengue cases in 2019. The serotype results of these associated islands revealed that DENV1 and DENV2 were the circulating serotypes. As people from these associated islands regularly travel to Jaffna mainland, there is a possibility for them to be exposed to infective bites. In the year 2019, all four dengue

virus serotypes were recorded in the Jaffna district where DENV1 was the dominant serotype. The year and in the Jaffna MoH division recorded all four serotypes, whereas the DENV2 serotype was mainly observed in Nallur, Kopay and Uduvil MoH divisions.

GIS-based dengue risk map is very useful in identifying the dengue risk pattern and expected to be useful for health authorities to prioritize resources to risk areas. Even though small variations are observed in the dengue risk map based on real dengue cases, the prediction map almost considered as the real trend of dengue transmission in the Jaffna district. A detailed study considering serotypes, socio-economy, demography and land-use pattern over the years is warranted to understand the spatio-temporal changes in dengue transmission in the Jaffna district.

5. ACKNOWLEDGEMENTS

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