

Spatial-temporal diffusion pattern and hotspot detection of dengue in Bandar Baru Bangi, Selangor, Malaysia

*Nuriah Abd Majid, Muhammad Rizal Razman, Sharifah Zarina Syed Zakaria, Nurafiqah Muhamad Nazi, Minhaz Farid Ahmed and Syaidatul Azwani Zulkafli

Institute for Environment and Development (LESTARI), Universiti Kebangsaan Malaysia, Bangi 43600, Selangor Darul Ehsan, Malaysia

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ABSTRACT

In the last few decades, dengue fever has dramatically increased in Malaysia and has caused huge public health concerns. This article examines dengue epidemics spatial and temporal dynamics in Bandar Baru Bangi, Selangor State, Malaysia. The main aim of this study was to study spatial diffusion patterns and to identify the hotspots of dengue reported. The study utilized epidemiological data from the Malaysian Ministry of Health on dengue cases in 2015-2018. These details are analyzed and processed into GIS format. 2015, 2016, 2017, and 2018 dengue outbreak geospatial spread pattern has been investigated and mapped. The hotspot analysis is presented as points on a map and refers to dengue cases locations in the area studied. In 2015-2018, it measured statistics from Getis-Ord Gi for dengue cases. In the region of Bandar Baru in Bangi, with a cluster of high or low values, the associated Z- and p-values are displayed spatially. The chart has varied from -3 (cold spot -99% of confidence) to +3 (hotspots-99% of confidence) to establish the spatial distribution of dengue fever in Bandar Baru Bangi. In this report, persistent hotspot areas indicated that urbanization is one of the key reasons for the impact of dengue and the consequence would lead to reducing the effect within particular areas for the future.

Key words: Dengue, Hotspot, Spatial-temporal, Urban

Introduction

Dengue is a viral disease transmission of mosquitoes which has spread rapidly over recent years to all regions. These mosquitoes also have chikungunya, yellow fever, and Zika. Dengue is common across tropics with local risk variations influenced by rainfall, temperature, relative humidity, and unforeseen conditions (Hazrin *et al.*, 2016). This is an *Aedes aegypti* mosquito-borne viral disease. With over one-third of the world's population living in areas at risk of infection, dengue virus is a significant cause of disease and death in the tropics and

subtropics (Hazrin *et al.*, 2016). Dengue disease ranges from the hemorrhagic fever that is mild to dengue. Most of the dengue vector distribution varies depending on the rainfall (Pathiraja *et al.*, 2018). In Southeast Asia, dengue is a rapidly developing pandemic-prone viral disease. *Aedes aegypti* mosquito is mainly the infection spread to humans through the bites of contaminated female mosquitoes. According to The World Health Organization (2019), other *Aedes* can also serve as vectors, but their contribution to *Aedes aegypti* is secondary. There is also a dengue outbreak in the Philippines, Thailand, Laos, Vietnam, Singapore and, Indonesia,

as well as in Malaysia.

WHO in 2020 reported, most cases of dengue recorded ever worldwide were registered in 2019. Alone in the United States, 3.1 million cases have been registered, with over 25,000 classed as serious. Notwithstanding this unprecedented amount of incidents, dengue-related fatalities were fewer than in the previous year. In Bangladesh (101.000), Malaysia (131.000) Philippines (420.000), Vietnam (320.000), and Asia, a high number of cases were reported. This is higher than the 66,570 cases reported with 111 deaths in the same timeframe in 2018 (World Health Organization, 2019). Increasing dengue cases are causing acute health care and concern among stakeholders and government agencies in Malaysia. There were no specific anti-viral therapies, however, and the vaccine licensed was concerned about the increased risk of hospitalization (Jing and Wang, 2019). The rapid spread is continuing despite significant efforts in research and control methods, resulting in a significant concern in Malaysia. Elements of dengue transmission are involved, including viruses, vectors, and hosts. Several factors such as climatic factors (temperature, precipitation, wind, and relative humidity), human movement and behavior, sociological, cultural, demographic, and ecological factors influence these parameters (virus, vector, and human host) (Gubler, 2011).

Rapid urban growth with comprehensive land-use change processes through the development of new townships and infrastructure, along with population growth needs, has caused the dengue vector breeding ecosystem, *Aedes* mosquitoes in particular (PLAN Malaysia, 2017). The rapid spread of dengue cases in many countries is due to globalization, rapid unplanned urban development, poor water storage, and inadequate sanitation. Climate change also contributes to the spread of dengue virus in Malaysia over the past four decades, such as rising temperatures, increased rainfall, and increased humidity (Noor Nashuha and Samsul Ariffin, 2018). Thus, a comprehensive understanding of temporal and spatial patterns in dengue can help develop disease prevention mitigation strategies and save lives and economic costs for countries at risk of dengue transmission. Previously, in an academic analysis of dengue monitoring, researchers worked together to estimate dengue transmission using predictive statistical analysis and spatial-temporal analysis of mosquito distribution and lo-

cations. The analysis of outbreak transmission using GIS mapping is, therefore, becoming increasingly relevant for disease control and management (Gilruth *et al.*, 2007; Srivastava *et al.*, 2009; Khormi *et al.*, 2011).

GIS has played a significant role in mosquito-borne disease monitoring and control in recent years. This study aims to distinguish dengue cases clustering and determine the pattern for a potential hotspot in an urbanization area. Facilitating maps that are useful for identifying spatially and temporally located areas with a potentially high risk of dengue is critical as management level mitigation and understanding of the vector related disease. In addition to providing an opportunity to improve our knowledge of dengue transmission trends, GIS can also provide an environmentally and socially conscious forum for developing elements of an early warning system for dengue control and prevention (Hazrin *et al.*, 2016).

Materials and Methods

Study Area

This study is located in the town of Bandar Baru Bangi, in the district of Hulu Langat, Selangor State, Malaysia (Figure 1). With coordinates of 2°55'20.6"N and 101°46'50.6"E, Bangi is situated 38 km south of Kuala Lumpur, and one of the towns in Hulu Langat, Selangor's southern district. Located between the towns of Kajang and Putrajaya, it is becoming increasingly popular with for property hunters. Neighbouring townships of Bandar Baru Bangi are Kajang, Putrajaya, Cyberjaya, Nilai, and Seremban are a catchment area of approximately 1.2 million residents (Abd Majid *et al.*, 2018). The climate in Bandar Baru Bangi and its adjacent towns are within the monsoon climate zone that affected by two monsoonal winds, which originate from the northeast between October and February and the southwest from May to September (Olaniyi *et al.*, 2012).

Bandar Baru Bangi is linked directly via Kajang to Kuala Lumpur via a network of roads and highways like PLUS, ELITE, SILK, LEKAS, Kuala Lumpur-Seremban, Cheras-Kajang and the North-South Expressway (NSE) as part of the Greater Klang Valley. It is also linked by the KTM train, and soon by the new Sungai Buloh-Kajang (SBK Line) Mass Rapid Transit (MRT). The growth of infra-

structure, settlement, and road networks increases the density of the population in Bandar Baru Bangi. Despite urbanization, mosquito-borne viral disease in the study area has increased rapidly (Abd Majid *et al.*, 2019).

Data Collection

A full data collection of dengue fever cases recorded from the Ministry of Health of Malaysia between 2015 and 2018 by hospitalized patients in each government and private hospital of Bandar Baru Bangi (Abd Majid *et al.*, 2019). The location coordinates of patients are extracted from the data to locate their distribution spatially using software ArcMap10.5. Metadata for the Bangi district map was provided by PlanMalaysia@Selangor.

Spatiotemporal analysis

Statistical analysis is essential for evaluating dengue spatial distribution and for understanding the factors that may be correlated with the frequency of the cases (ESRI, 2018). The spatial distribution of dengue cases in the Bandar Baru Bangi region has been mapped and analyzed using ArcMap 10.5 spatial statistical tools. The point pattern analysis was used to assess whether there is significant clustering of points in a specific area. The ArcMap 10.5 software tool used in the analysis was the Spatial Autocorrelation and Getis-Ord G_i^* statistics measured in Hot Spot Analysis (ESRI, 2020). This approach offered an intuitive visual presentation of results related to the spread of infections and spatial clusters at various stages of outbreaks in dengue history. The numerical value of Getis-Ord G_i^* was measured using this method, and z-scores and p-values were determined to test the null random distribution hypothesis of the attribute being evaluated (Kajang Municipal Council, 2017). Such findings were used to determine whether the cases of dengue were distributed across the entire study region in a statistically significant manner.

The Getis-Ord local statistic is given as:

$$G_i^* = \frac{\sum_{j=0}^n w_{i,j} x_j - \bar{X} \sum_{j=0}^n w_{i,j}}{\sqrt{\frac{n \sum_{j=0}^n w_{i,j}^2 - (\sum_{j=0}^n w_{i,j})^2}{n-1}}}$$

Where x_j is the attribute value for feature j , $w_{i,j}$ is the spatial weight between feature i and j , n is equal to a total number of features and:

$$\bar{X} = \frac{\sum_{j=1}^n x_j}{n}$$

$$S = \sqrt{\frac{\sum_{j=1}^n x_j^2}{n} - (\bar{X})^2}$$

The G_i^* statistic is a z-score, so no further calculations are required.

Results

Reported patients with positive dengue, hemorrhagic dengue fever, and death caused by dengue infection were tabulated in Table 1. A total of 5853 positive cases of dengue have been recorded across the Bandar Baru Bangi town.

Table 1. Temporal number of dengue fever cases reported in Bandar Baru Bangi from the year 2015 to 2018 (Abd Majid *et al.*, 2019)

Year	2015	2016	2017	2018
Dengue cases reported	1968	1407	1687	791

The Getis-Ord G_i^* hot spot analysis outcome is indicated with three values, which are the Nearest Neighbor (NN), z-scores, and p-value. The scale of spatial clustering of dengue cases ranked from dispersed, which is indicated by negative values and clustered positive values indicate that. From hot spot analysis conducted, significant hot spots and cold spots of dengue cases are classified with G_i^* Bin field that expressed with statistical confidence levels from $+/-3$ bins as 99% confidence level, $+/-2$ bins as 95% confidence level, and $+/-1$ bins as 90% confidence level. The clustering for features in bin 0 is not statistically significant (ESRI, 2020). The z-scores are a statistically significant indicator of whether to reject the null hypothesis or not. The null hypothesis in this study claimed that is no spatial trend in Bandar Baru Bangi among dengue cases.

It is observed that at 99% statistical confidence level, there was a significant increase in cold spots and hot spots from the year 2015 until 2017, but the number dropped drastically in the year 2018 (Table 2). The same situation has been noticed with a statistical confidence level at 95%, but with a reduced number of dengue cases that indicate cold spots and hot spots. However, the number of cold spots and

hot spots at 90% statistical confidence level are varied where there was a slight increase for cold spots in the year 2015 to 2016, but then a sharp drop in the year 2017 and later on the increase substantially in the year 2018. On the other hand, statistically significant hotspots at a 90% confidence level reduced slightly from the year 2015 to 2016 and then rise moderately in the year 2017 and decline again in 2018.

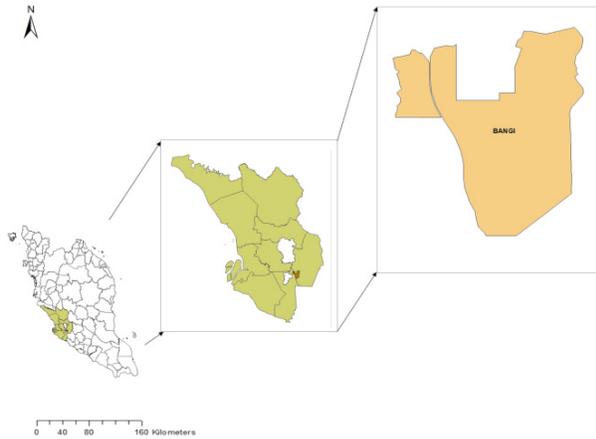


Fig. 1. Location of the study area

The statistically significant hotspots for dengue cases reported in the year 2015 were discovered intensified at the east of Bandar BaruBangsi, centralized at the north and south along the district boundary (Figure 2). The statistically significant negative Z-scores of Getis-Ord G_i^* or the cold spots were observed concentrated in the north and south parts of the district. The Bandar BaruBangsi residential zonation at the north and south of the district name from Section 1 to 7 and Section 15 are related to the higher clustering of hot spots in the same areas, compared to the lower number of cold spots analyzed in the district. Meanwhile, dengue cases where Getis-Ord G_i^* values were significantly different from each other were considered as not significant as they are no hot spots or cold spots.

The statistically significant hotspots for dengue cases reported for the year 2016 were found concentrated in the northeast and south part of the Bandar BaruBangsi (Figure 3). A higher number of statistically significant cold spots were observed concentrated at the west, northeast, and south-eastern parts of the district. Cold spots cluster with 99% statistical confidence level emerged at the west of the district referred to the dispersed spatial clustering in

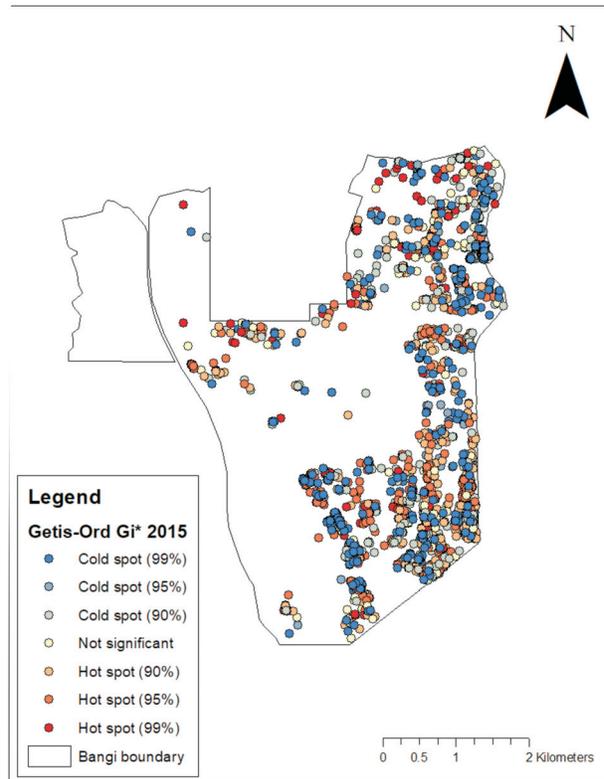


Fig. 2. Hot spot cluster map (2015)

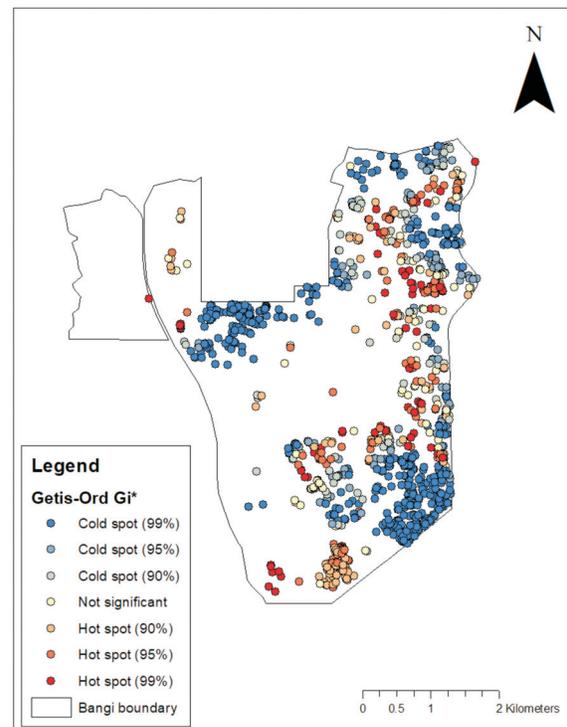


Fig. 3. Hot spot cluster map (2016)

another residential zone in Bandar BaruBangi, namely Section 8 and Section 9.

The statistically significant hotspots for dengue cases reported the year 2017 were found centralized in the northeast of Bandar Baru Bangi (Figure 4). The statistically significant cold spots were observed dispersed at the west and south stretching to the southeast parts of the town. The higher clustering of hot spots centred in residential areas of Section 7 and Section 4 compared to the lower number of cold spots dispersed in Section 8 and 9 at the west, Section 1 to 3, and Section 15 in the south of Bandar Baru Bangi.

The statistically significant hotspots for dengue cases reported the year 2018 were found clustered

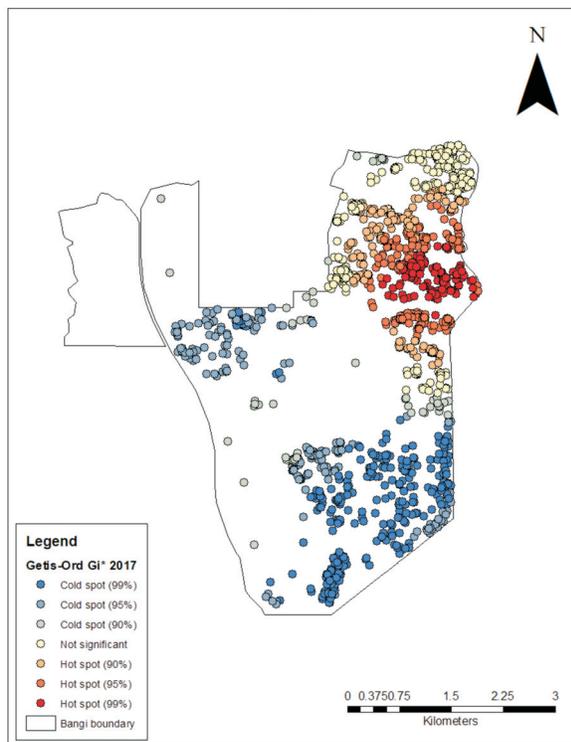


Fig. 4. Hot spot cluster map (2017)

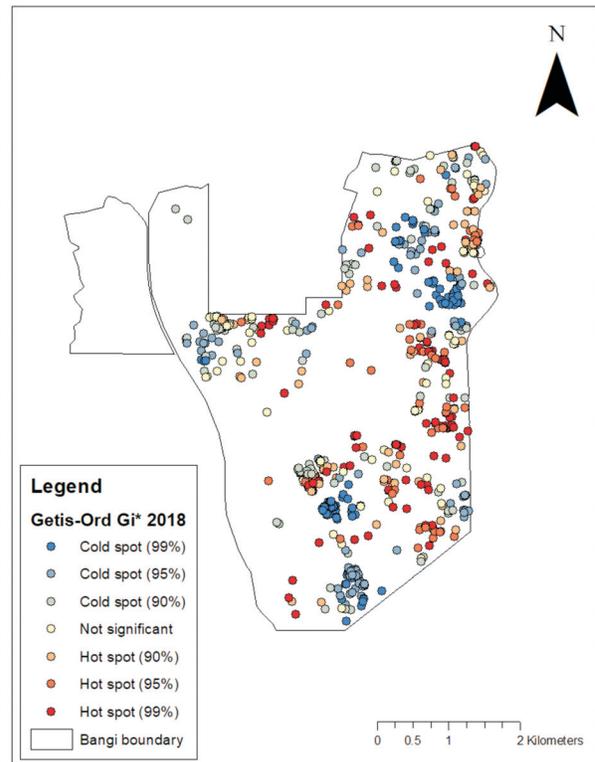


Fig. 5. Hot spot cluster map (2018)

sparingly in most parts of Bandar BaruBangi, covering from northeast, east, south, and west of the district (Figure 5). The statistically significant negative Z-scores of Getis-Ord G_i^* or the cold spots spatial cluster were identified dense at the northeast, south, and some parts at the west of the district. More than half of dengue cases reported in the year 2018 compared to the previous year are related to the small clustering of hot spots and cold spots with different statistical confidence levels analyzed at the same residential areas in the district.

Discussion

Dengue hot spot maps have been used to gain a bet-

Table 2. Getis-Ord G_i^* hotspot analysis

Type of cluster	Gi Bin	Confidence level	Z-score	P-value	Frequency of dengue cases			
					2015	2016	2017	2018
Cold spot	-3	99 %	< -2.58	$p < 0.01$	1	324	560	0
Cold spot	-2	95 %	< -1.96	$p < 0.05$	1	38	23	4
Cold spot	-1	90 %	< -1.65	$p < 0.10$	36	37	8	66
Not significant	0	-	-	-	1858	675	153	591
Hot spot	+1	90 %	> +1.65	$p < 0.10$	71	39	56	30
Hot spot	+2	95 %	> +1.96	$p < 0.05$	0	58	77	46
Hot spot	+3	99 %	> +2.58	$p < 0.01$	1	236	810	54

ter understanding of the spatial trend and pattern of dengue epidemiology. Dengue cases hotspots in the west of Bandar Baru Bangi in 2015 could be derived from the active development and construction of the new business and shopping centre in Section 9 and 8. The number of cold spots remains the same in the south of Bandar Baru Bangi, except there was a significant decrease in 2018. In 2017, the hot spots with the highest dengue cases were clustered and concentrated in the northeastern of Bandar Baru Bangi. During that year, the increase in dengue fever reports helps promote enhanced prevention measures by a top-down system that provides additional fogging entrepreneurs for a larger area, regular monitoring by medical workers from home to home, and much more public work by local authorities to remove Aedes breeding grounds (Higa, 2011; Bandar Baru Bangi, 2017; Persatuan Penduduk Desa Surada, 2017; Team Selangor, 2017; Kementerian Perpaduan Negara, 2018). As a result, a drastic decline of hot spots analyzed for dengue cases in the year 2018 that were observed in the dispersed pattern in the south and east of Bandar Baru Bangi. Constant monitoring on this cluster could be the best case of an epidemic that can be applied as a model to describe the principles of dengue fever spread.

Spatial work in epidemiology is long-standing, but epidemiological studies of GIS were established only in the last decade. GIS is becoming more prominent in disease control with the development of computer technology and spatial analysis methods. Monitoring and preparing for dengue have recently become crucial to the prevention of outbreaks of disease. Therefore, the purpose of this article was to provide useful information on dengue incidences and to map their diffusion patterns and dynamics. Analysis of spatial tools is another platform for the examination and proof of changes in spatial patterns over time. The study found that the location is critical for mosquito breeding. Urban areas provide habitats for the reproduction of Aedes mosquitoes with appropriate weather and precipitation.

Dengue is an infectious disease highly transmissible due to its mosquito vector *Aedes aegypti*, which is well suited to the urban environment (Chew *et al.*, 2016). These rapid economic changes over the last 15 years and the subsequent growing urbanization, along with that demographic composition that the modern transport network of the world makes may both have contributed to a more

systematic danger of dengue in urban areas over time (Abdul Samad and Shaharudin, 2017). Urban growth provides suitable breeding spaces and locations, while the Aedes mosquitoes are supplied with good food sources and vector by a higher population of humans and animals. This is the crucial point as the hotspot area is located in the north and east parts of Bandar Baru Bangi. In addition to the increase in development growth in Bandar Baru Bangi, which attracts population concentration to live in its urbanized area, dengue epidemiology needs to be monitored for its city dwellers to be free of the fear of health issues in this district.

Conclusion

Spatial statistical distribution and pattern analysis play a significant role in understanding dengue case epidemiology in the research area. This is because specific systems derive distribution and spatial patterns. The application of GIS enables the hotspot analysis conducted thoroughly to a particular location. Hotspot analysis in this study using Getis-Ord G_i^* shows that the dengue cases in the years 2015-2018 are clustered and concentrated mainly at the northeastern of Bandar Baru Bangi urban area. This study also suggests that Getis-Ord G_i^* as the appropriate pattern analysis after given that the z-score values were consistently significant. Regularly hotspot because of the crowded place with a number of residents much and not cleaned to take care of surrounding. This will give higher cases of dengue.

Progressive geographic-based mapping and information systems will enable the dengue control efforts and epidemiologic data assimilation to guide the management of the disease and its impact from the local to the national levels. Potential urbanization, globalization, climate, human behavior, and lack of vector control have resulted in dengue being spread globally. Therefore, if rapid population growth and continued urbanization continue as predicted, the rate, frequency, geographical distribution, and severity of dengue epidemics will increase gradually in the future. Since the use of Getis-Ord G_i^* for dengue epidemiology in Malaysia is limited, further analyzes can be carried out to understand the causes of dengue cases in hotspot areas, and countermeasures can be determined for the mitigation of incidence in specific areas. This result will help to develop informed to control strategy bases on hotspot place.

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