ORIGINAL ARTICLE

Spatio-temporal Analysis of Dengue Cases in Sabah

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ABSTRACT

Introduction: Dengue fever is a significant public health issue worldwide. Geographic Information System is a powerful tool in public health, allowing for the analysis and visualisation of spatial data to understand disease distribution and identify clusters of cases. Therefore, this study aims to determine the spatiotemporal distribution of dengue cases in Sabah. **Methods:** Quantum Geospatial Information System (QGIS) and GeoDa software were used to determine the spatial distribution, pattern, and cluster analysis. **Results:** The spatial distribution of dengue cases shifted, with most cases concentrated on the east coast of Sabah. The distribution of dengue cases in Beluran, Tenom, Kota Marudu, Kudat, Keningau, and Papar changed from 2017 to 2020. The scatter plots of Moran's index values were generated to analyse the spatial clustering of dengue cases in Sabah over four years: 2017 (Moran's index = 0.271), 2018 (Moran's index = 0.333), 2019 (Moran's index = 0.367), and 2020 (Moran's index = 0.294). The statistical significance of clustering was established by observing p-values below the threshold of 0.05 for all four years. Local indicators of spatial association showed the spatial autocorrelation pattern of high-high (hotspot) areas with elevated dengue incidence and low-low (cold-spot) areas with relatively lower dengue rates. **Conclusion:** This study has provided evidence of dengue case distribution patterns, spatial clustering, and hotspot and coldspot areas. Prioritising these clusters can improve planning and resource allocation for more efficient dengue prevention and control.

Keywords: Dengue cases; Spatial distribution; Spatial clustering; Sabah

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INTRODUCTION

Dengue fever is a significant public health concern in many nations worldwide. It is a devastating vector-borne disease in many countries with subtropical and tropical climates. According to the World Health Organization, dengue fever incidences have surged dramatically in recent decades, from 505,430 cases in 2000 to 4.2 million cases in 2019 (1,2). Malaysia's contribution to the increase in dengue fever and outbreaks in the Western Pacific Region is evident through historical outbreaks in 1973 and the recent surge in dengue cases over the past four years (3–6). Due to changing serotypes, dengue trends in Malaysia cycle every 3-5 years, leading to nationwide outbreaks (7).

Integrating space, time, and relevant variables in the spatial analysis of epidemic phenomena forms the foundation of public health (8). Since the 1980s, spatial analysis has been indispensable in examining disease patterns, identifying hotspots, and understanding their correlation with various factors (8,9). Methods such as Average Nearest Neighbour, Moran's I, LISA (Local indicators of spatial association) and hotspot analysis play a vital role in detecting statistically significant clusters in various diseases, including dengue (10,11). These GIS-driven analyses are instrumental for public health experts in homing in on high-risk dengue areas, enabling focused prevention and control efforts.

A research study in Seremban utilised GIS techniques to investigate the spatial distribution of dengue cases. The findings revealed a clustering pattern of dengue cases along the west coast of the district. This spatial analysis yields valuable insights for targeted interventions and resource allocation in dengue prevention and control activities (11). GIS is essential

for prioritising public health interventions, especially in resource-constrained settings. In Colombia, GIS-driven spatio-temporal analysis identified Patha municipality as a high-risk area for dengue transmission, highlighting its vital role in targeted interventions (12).

Moreover, the predictive capability is a significant advantage of employing GIS and spatial analysis in dengue research and intervention. Nonetheless, there is a need for further research in the spatial-temporal analysis of dengue cases to pinpoint high-risk areas in Sabah. Despite comprehensive vector control initiatives, periodic epidemics strain public health resources. Therefore, this research aims to employ GIS to analyse trends, patterns, clusters, and distributions, enabling the identification of high-risk areas in Sabah prone to potential outbreaks. This information will be invaluable for optimising resource allocation and preparations for dengue control and prevention efforts.

MATERIALS AND METHODS

Study area
The study was conducted in Sabah, Malaysia, situated in the northern region of the island of Borneo. Sabah encompasses an area of 73,904 square kilometres inhabited by approximately 3.9 million people. The state is administratively divided into five divisions, encompassing a total of 25 districts (Figure 1).
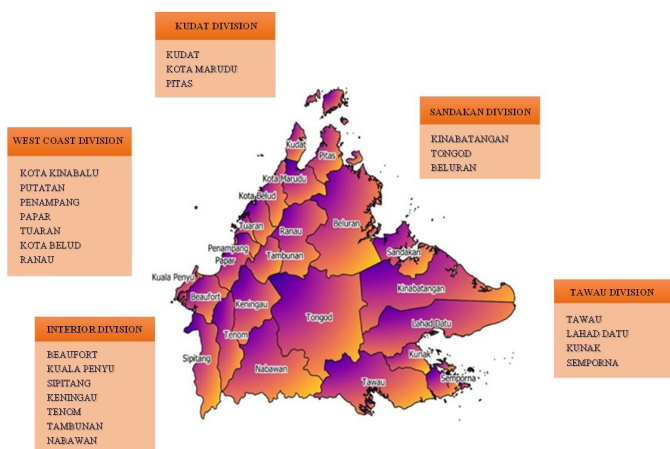

Figure 1 : Geographical Map of Sabah, Malaysia, depicting 25 Districts Divided into Five Administrative Divisions.

Data Collection Method
As reported to the World Health Organization (WHO), a dataset comprising 15,339 registered cases from the Malaysian National Dengue Registry (e-Dengue) for the years 2017 to 2020 was exported into Microsoft Excel. Spatial analysis was conducted using Quantum Spatial Information System (QGIS) 3.18 and GeoDa 1.18 spatial software.

Data Analysis Method
We used QGIS and GeoDa 1.18 software to project latitude and longitude coordinates onto the Sabah map for spatial analysis. The GIS software used in this study is an open-source program, aided in exploring and modeling spatial patterns. We ensured coordinate accuracy through geocoding based on the World Geocoding system and patients address. Data on districts, case numbers, and epidemic years were converted to Excel CSV format and imported into the GIS software. The Sabah Map shapefile was overlaid in QGIS, enabling the generation of heat maps and choropleth maps illustrating disease distribution across the state. QGIS was used to perform spatial distribution, and equal quantiles were classified based on the number of cases by year, and colour coding was done as preferred.

GeoDa 1.18 spatial software was used to analyse spatial autocorrelation to determine the positive or negative correlation between dengue cases and spatial clustering of cases using Univariate Moran I and the Local Indicator Spatial Association (LISA) Cluster Map. A 10-kilometre grid map was created using QGIS 3.18 software to have a clearer vision of the clustering of cases. Spatial autocorrelation analysis of global (Moran's I Index) and local indexes are expressed in the Local Indicator Spatial Association (LISA) Cluster Map alongside the significance p-value < 0.05 in confirming the existence of cluster patterns. The Moran index is calculated as the average of the products of normalized point values, weighted by the spatial relationship between pairs of points. It can be thought of as an extension of the classical Pearson correlation index to account for neighbouring objects, with the incorporation of spatial weights denoted as W(13). Moran's index is a measure used to determine the presence of spatial autocorrelation. A positive value indicates a clustered pattern, while a negative value suggests a random distribution. Spatial patterns can be interpreted as dispersed, random, or clustered.

Where else, LISA generates color-coded results, distinguishing areas as high-high, low-low, high-low, or low-high. Areas identified as high-high and low-high indicate positive spatial autocorrelation, whereas those classified as low-high, and high-low signify negative spatial autocorrelation (14). The LISA Cluster Map provides a meaningful visualization of spatial clustering, employing colour codes with a significance level set at p-value < 0.05. This analysis revealed noteworthy instances of both spatiotemporal and spatial clustering in our study.

Ethical Consideration
This study used secondary data removed from personal information and patient identification. The study was conducted following approval by the Medical Review & Ethics Committee (MREC), the Ministry of Health, National Research Medical Registry (NMRR-21-396-58572 (IIR) and Universiti Malaysia Sabah (UMS)

(JKEtika 1/21 (14)).

RESULTS

During the period from 2017 to 2020, Sabah has reported a total of 15,539 confirmed cases of dengue. Table I below presents the dengue prevalence in Sabah based on the estimated population for each year. The prevalence of dengue cases in Sabah has increased over the study period. In 2017, the prevalence was reported at 66.3 per 100,000 population, followed by a significant rise to 87.9 per 100,000 population in 2018. The trend continued with a nearly twofold increment in 2019, reaching 140.5 per 100,000 population, before experiencing a slight decrease to 104.5 per 100,000 population in 2020. The data in Table II displays the trend of reported dengue cases in Sabah's 25 districts. In 2017, there were 2,560 dengue cases, 3,423 cases in 2018, 5,478 cases in 2019, and 4078 cases in 2020. Over the four years, the top five districts with the highest number of cases were Kota Kinabalu with 3,258 (21.0 %), Tawau with 2,540 (16.3%), Sandakan with 2,477 (15.9%), Lahad Datu with 1,628 (10.5 %), and Semporna with 1,280 (8.2%).

Spatiotemporal Analysis Findings

Spatial distribution patterns are utilised to identify geographic patterns in the distribution of dengue cases. The number of dengue cases per year is the basis for tallying the cases. Figure 1 illustrates the results of spatial-temporal analysis, revealing a shifting pattern in the distribution of dengue cases across districts. Notably, Kota Kinabalu, Sandakan, and Tawau consistently exhibited a concentration of dengue cases over the four years. However, Lahad Datu displayed a decrease in reported dengue cases in 2020. From 2017 to 2020, a shifting pattern of colour coding is observed in Beluran, Tenom, Kota Marudu, Kudat, Keningau, and Papar. In addition, during 2018 and 2019, there was a shift in the concentration of cases in the interior division, accompanied by a modest decrease in cases in Beluran and Lahad Datu. Overall, Tongod and Tambunan districts consistently recorded a low number of cases throughout the four-year duration of this study (Figure 1).

Univariate Local Moran's I analysis was employed in this study to assess the spatial autocorrelation of
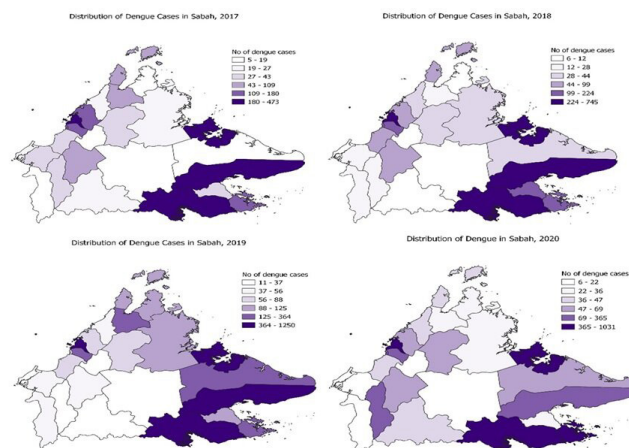

Figure 2 : Spatial Analysis of Dengue Cases: Temporal Trends and Geographic Distribution (2017-2020).
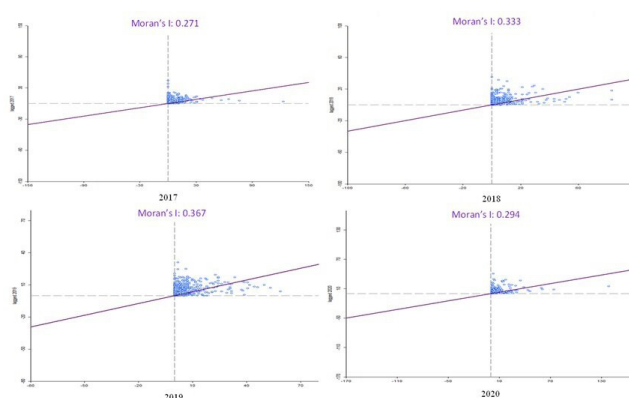

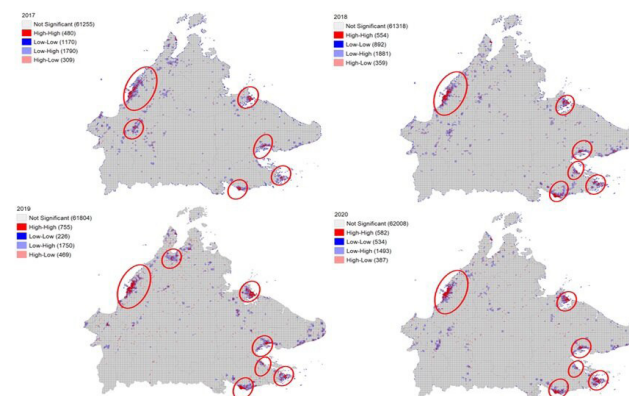**Figure 3 :** Local Moran's Spatial Autocorrelation Analysis (2017-2020).

Figure 4 : Local Indicators of Spatial Association (LISA): Cluster Mapping of Dengue Cases (2017-2020). The circle markings on the map represent areas of high-high (red) spatial clustering.

Table I : Prevalence of Dengue Cases in Sabah, 2017-2020

Year	Dengue Cases	Prevalence (%)	Yearly Estimated Population (million)
2017	2560	66.3	3.86
2018	3423	87.9	3.89
2019	5478	140.5	3.90
2020	4078	104.5	3.90

Table II : Trend of Dengue Cases in Sabah from 2017 to 2020

Variables	Dengue Cases, Year			
	2017 **n, (%)**	**2018** **n, (%)**	**2019** **n, (%)**	**2020** **n, (%)**
Kota Kinabalu	503 (19.6)	733 (21.4)	943 (17.2)	1079 (26.5)
Tawau	381 (14.9)	772 (22.6)	755 (13.8)	632 (15.5)
Sandakan	266 (10.4)	409 (11.9)	1274 (23.3)	528 (12.9)
Lahad Datu	204 (8.0)	334 (9.8)	703 (12.8)	387 (9.5)
Semporna	201 (7.9)	173 (5.1)	382 (7.0)	524 (12.8)
Penampang	115 (4.5)	95 (2.8)	116 (2.1)	127 (3.1)
Tuaran	153 (6.0)	52 (1.5)	72 (1.3)	63 (1.5)
Putatan	131 (5.1)	137 (4.0)	92 (1.7)	78 (1.9)
Kudat	107 (4.2)	94 (2.7)	113 (2.1)	40 (1.0)
Keningau	110 (4.3)	47 (1.4)	51 (0.9)	64 (1.6)
Kota Marudu	47 (1.8)	36 (1.1)	164 (3.0)	50 (1.2)
Papar	47 (1.8)	73 (2.1)	81 (1.5)	45 (1.1)
Kunak	38 (1.5)	234 (6.8)	100 (1.8)	32 (0.8)
Tenom	31 (1.2)	20 (0.6)	24 (0.4)	97 (2.4)
Beluran	19 (0.7)	21 (0.6)	122 (2.2)	34 (0.8)
Ranau	26 (1.0)	38 (1.1)	59 (1.1)	53 (1.3)
Pitas	19 (0.7)	22 (0.6)	96 (1.8)	35 (0.9)
Kinabatangan	14 (0.5)	28 (0.8)	94 (1.7)	37 (0.9)
Kota Belud	20 (0.8)	27 (0.8)	51 (0.9)	40 (1.0)
Beaufort	30 (1.2)	20 (0.6)	47 (0.9)	21 (0.5)
Sipitang	20 (0.8)	21 (0.6)	46 (0.8)	31 (0.8)
Nabawan	25 (1.0)	11 (0.3)	18 (0.3)	44 (1.1)
Kuala Penyu	34 (1.3)	8 (0.2)	37 (0.7)	12 (0.3)
Tambunan	19 (0.7)	10 (0.3)	10 (0.2)	9 (0.2)
Tongod	0 (0.0)	8 (0.2)	28 (0.5)	16 (0.4)
Total	2560	3423	5478	4078

dengue cases each year, utilising the GeoDa software. The analysis was interpreted within the null hypothesis framework, assuming a random case distribution. Figure 3 presents the results of Moran's scatter plot, revealing a clustering pattern with positive spatial autocorrelation for the years 2017 to 2020. The Moran's scatter plots display the corresponding Moran's index values for each year: 2017 (0.271), 2018 (0.333), 2019 (0.367), and 2020 (0.294). The presence of statistically significant clustering is indicated by a p-value of <0.05 across all four years, demonstrating the impact of spatial clustering on the distribution of dengue cases in Sabah. Figure 4 presents the LISA cluster map, which illustrates the significant locations colour-coded based on positive and negative spatial autocorrelation observed in the Local Moran's I scatter plot for the years 2017 to 2020. The map distinguishes between high-high and low-low associations, indicating the clustering of high-risk (hot spots) and low-risk (cold spots) areas, respectively. Both the high-high and low-low categories reflect relationships that suggest the presence of clustering in dengue cases, denoting positive spatial autocorrelation (p < 0.05). Conversely, the low-high and high-low colour-coded locations indicate the presence of spatial outliers, implying negative spatial autocorrelation.

The low-high category in the LISA cluster map refers to localities with fewer reported dengue cases

surrounded by neighbouring localities with many reported dengue cases. Conversely, the high-low category indicates areas with many reported dengue cases surrounded by areas with fewer recorded dengue cases. Among the districts exhibiting significant clustering of dengue cases are Kota Kinabalu, Putatan, Penampang, Sandakan, Lahad Datu, Tawau, Semporna, and Kunak, except for Keningau, which showed high clustering specifically in the year 2017.The districts with localities falling into the low-high and high-low categories are scattered throughout the LISA cluster map. The high-low cases represent localities that are in closer proximity to areas with a igh number of cases.

DISCUSSION

In 2019 and early 2020, there was a significant increase in dengue cases and fatalities reported in other states of Malaysia, particularly Selangor, and in countries within the Western Pacific region (5,15,16). Our study reveals that dengue is a concern throughout the year in Sabah, with varying peaks from year to year. Sabah has an equatorial climate, with dry and rainy seasons that are distinct in the highlands and along the coast (5). From May through December, the west coast receives the most precipitation, while the east coast experiences afternoon showers in June and July (23,24). Studies has found that the spread of dengue is influenced by factors like population growth, rapid urbanization, people moving from rural to urban areas, and challenges in urban infrastructure like waste disposal (17,18). Urbanized areas in coastal southeastern China faced higher dengue risk after extreme wet conditions, while less urbanized regions with very hot weather were also at elevated risk post rainy season, with the only difference being the time lag (19).

However, research conducted in Singapore employed the statistical modelling showed that rainfall flushing reduced dengue outbreak risk. Temporal rainfall patterns and flushing events were linked to this reduction, with the time lag matching mosquito larvae development and infection transmission (20). Future research should explore the impact of hydrological conditions on dengue transmission in endemic areas in Sabah. The eastern coastal areas of Tawau, Lahad Datu, Sandakan, Kunak, Semporna, along with the capital city Kota Kinabalu, have witnessed a notable surge and clustering of reported dengue cases. Sabah's extensive coastline and international borders, linking it with dengue-endemic regions like the Philippines, Thailand, and Indonesia, present a potential risk for the introduction of this vector-borne disease into the state (21–23). Research using a global model to predict imported dengue infections has shown that the risk

of transmission is increased by the close proximity and frequent cross-border movement of individuals, elevating the likelihood of dengue transmission between countries (24).

Clusters with high occurrences are important to identify because they indicate hotspots for dengue outbreaks and significant spatial autocorrelation. Coastal regions are the primary locations of these areas in this study. One notable characteristic of many of the region's coastal areas is Sabah's water village settlements. This area has a widespread issue of waste and litter management. This problem is particularly prominent in the informal settlements of water villages, where the attitudes of some villagers contribute to the problem (25). This situation also similar in Agentina and Vietnam which revealed the incidence of dengue cases are high in slum areas due to improver waste management, poor water supply as well as lack of co-operation by the community living there. Conducting comprehensive assessments and engaging with local stakeholders and water village areas; public health authorities can identify gaps in knowledge and address misconceptions or barriers to effective dengue prevention measure in the informal settlements (26–28). Desired behavior on dengue prevention may not achieved easily however, community based intervention at water village or informal settlements however studies found that understanding social cultural of the community helps in tailored intervention (25). Furthermore, addressing issues related to solid waste management and water supply can significantly impact dengue vectors' breeding sites, reducing the transmission risk (29).

Implementing eco-friendly vector control measures along with community engagement and empowerment has proven to be successful in significantly reducing the density of Aedes mosquitoes, contributing to effective dengue transmission control (29,30). By indirectly influencing the reduction of Aedes mosquitoes' densities, these measures contribute to a decline in the burden of dengue disease (31,32). While our study provides valuable insights, it does have its limitations. Notably, we did not incorporate an average neighborhood analysis, which could have provided further understanding of the spatial patterns of dengue cases. Additionally, we did not delve into the potential impact of rainfall and climate on the distribution of dengue cases. These areas require attention in future research endeavors. It is also recommended to conduct a more detailed investigation into localities classified as low-high outliers to uncover the factors contributing to their consistently low case numbers. Despite these limitations, the clustering findings of this study serve as a valuable guide for interventions in high-risk areas.

CONCLUSION

In conclusion, the geospatial analysis conducted in this study demonstrated a significant spatiotemporal shift in the distribution of dengue cases across the districts over the four-year study period. Additionally, usage of GIS facilitated a comprehensive understanding of the distribution patterns, thereby pinpointing the specific districts that require focused attention especially those districts high number of cases at coastal regions. Therefore, incorporating GIS in epidemiological research proves highly advantageous, allowing for evidence-based decision-making in dengue control and preventive measures. The findings from the cluster analysis hold potential relevance for the state vector control unit, aiding them in formulating targeted strategies especially prioritizing in planning and resource allocation to combat the spread of dengue effectively.

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