

Implementation of geographical information systems for the study of diseases caused by vector-borne arboviruses in Southeast Asia: A review based on the publication record

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Abstract

The spread of mosquito-borne diseases in Southeast Asia has dramatically increased in the latest decades. These infections include dengue, chikungunya and Japanese Encephalitis (JE), high-burden viruses sharing overlapping disease manifestation and vector distribution. The use of Geographical Information Systems (GIS) to monitor the dynamics of disease and vector distribution can assist in disease epidemic prediction and public health interventions, particularly in Southeast Asia where sustained high temperatures drive the epidemic spread of these mosquito-borne viruses. Due to lack of accurate data, the spatial and temporal dynamics of these mosquito-borne viral disease transmission countries are poorly understood, which has limited disease control effort. By following studies carried out on these three viruses across the region in a specific time period revealing general patterns of research activities and characteristics, this review finds the need to improve decision-support by disease mapping and management. The results presented, based on a publication search with respect to diseases due to arboviruses, specif-

ically dengue, chikungunya and Japanese encephalitis, should improve opportunities for future studies on the implementation of GIS in the control of mosquito-borne viral diseases in Southeast Asia.

Introduction

The expansion of mosquito-borne infections has increased dramatically since the 1970s along with an increasing number of clinical cases (Rossi *et al.*, 2018). These diseases include dengue and chikungunya, the viruses that cause them are both transmitted by *Aedes* mosquitoes (Manore *et al.*, 2014). Japanese Encephalitis (JE), caused by a yet another vector-borne virus, has drawn attention from the public health sector worldwide (Erlanger *et al.*, 2009). Although this virus is primarily transmitted by *Culex* rather than *Aedes* mosquitoes, the geographical distribution of these mosquito species overlap, especially in Southeast Asian countries (Leta *et al.*, 2018; Pearce *et al.*, 2018; Lam-Phua *et al.*, 2019). Since this region possesses the highest burden of these emerging and re-emerging diseases, large epidemics overburdening local healthcare systems may occur at any time (van Panhuis *et al.*, 2015). In order to detect rapid changes in the incidence rate of infectious diseases, as well as identifying and characterizing the syndromes, disease surveillance and prompt management of epidemic potential are mandatory (Christaki, 2015). Given their mode of transmission, emerging and re-emerging mosquito-borne diseases may expeditiously overwhelm available healthcare facilities both at regional and global levels, hence the need of immediate preventive and control measures (Heymann and Rodier, 2001; Christaki, 2015). Disease emergence can be forecast by simulation or statistical modelling based on disease incidence, population density and environmental factors (Weiss and McMichael, 2004; Jones *et al.*, 2008; Ajelli *et al.*, 2010; Morse *et al.*, 2012; Lipkin, 2013). Epidemic modelling is also commonly used in the control of vector-borne diseases (Barrios *et al.*, 2012).

The use of spatial data and remote sensing to monitor the dynamics of diseases and vectors can assist in disease prediction and identification of hotspots where emerging pathogens are likely to occur (Ford *et al.*, 2009; Morse *et al.*, 2012). Risk-based approaches based on Geographical Information Systems (GIS) can improve the efficiency of disease surveillance and signal early warning for areas at increased risk for disease transmission (Christaki, 2015). In Southeast Asia where sustained high temper-

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atures drive the epidemic spread of mosquito-borne viruses on a continental scale, applications for GIS in disease control effective epidemic prediction can be utmost beneficial (van Panhuis *et al.*, 2015). Furthermore, the increase in international travel and trade, change in land use, as well as the growth of informal settlements in developing countries play a role in the proliferation of these diseases (Sutherst, 2004). However, the dynamics are poorly understood, which limits efficient control due to lack of accurate and detailed spatiotemporal information and demographic data, political constraints and data management issues (Brian and Lawrence, 2001). The urgent need for control of mosquito-borne viral diseases is further supported by the Asia Pacific Strategy for Emerging Diseases (APSED), an approach aimed at strengthening national and regional capacities to manage and respond to emerging disease threats (WHO, 2018). The current review aims at identification of the implementation of GIS in studies related to high-burden mosquito-borne viral diseases in Southeast Asian countries including dengue, chikungunya and JE. It emphasizes the need to implement decision-support capabilities in disease mapping and management using GIS in countries and aims to improve opportunities for future studies on the use of GIS in the control of mosquito-borne viral diseases.

Materials and Methods

We attempted to cover different types of implementation of GIS in studies related to mosquito-borne viral diseases, particularly dengue, chikungunya and Japanese encephalitis. In the initial step, we surveyed the titles and abstracts of electronic articles through (<http://www.ncbi.nlm.nih.gov/pubmed/>) database with search terms including: geographic information system, GIS, remote sensing, spatial, temporal, spatio-temporal, map, dengue, chikungunya, Japanese encephalitis, *Aedes* and *Culex*. We included research articles published from January 2005 through September 2019 written in English. In the second step, we selectively included studies performed in Southeast Asian countries, including Indonesia, Singapore, Malaysia, Thailand, Myanmar, Laos, Vietnam, Cambodia, Philippines, and Brunei. We excluded grey literatures, unpublished data, review articles, letters to the editor and research articles not related to the use of GIS. Study flow chart is depicted in Figure 1. After the bibliographic search, we identified a total of 644 publications. In the first step, we excluded 581 articles due to topic irrelevance (564), duplicate articles (10) and abstract only (7). Following full-text review of 63 articles, 26 articles were excluded due to topic irrelevance and unfitting article types. Finally, a total of 37 complete articles underwent analysis and were included in this review (Table 1). The analysis focused on the various uses of health GIS including disease seroprevalence mapping, vector distribution mapping, spatial relationships and causal factors in disease distribution, disease risk mapping and transmission models, and decision support for disease intervention.

Discussion

The bibliographic search identified a total of 644 publications. Following title and abstract screening, 14 articles were excluded due to topic irrelevance and unfitting article type. Finally, a total of 37 complete articles underwent full-text review and were included in this review (Table 1).

Disease seroprevalence mapping

The most common application of GIS in the field of public health is the identification of disease case distributions, incidence or prevalence (Musa *et al.*, 2013). We identified two studies related to seroepidemiological disease mapping, as shown in Table 2. A study conducted in four states of Peninsular Malaysia assessed chikungunya IgG seropositivity in both rural and urban communities (Azami *et al.*, 2013). The study demonstrated 5.9% seropositivity in clustered distribution in both areas, with individuals living in rural settings being more at risk. Individuals aged 45-64 years were found to be the age group most prevalent for seropositivity. Another study was conducted in Lao PDR to evaluate serological status of individuals against dengue and JE (Vallee *et al.*, 2009). The results showed that IgG-positivity were most frequently found in adults living in the city centre, whereas IgM-positive individuals were more likely to live in the periphery. The findings of these studies can assist decisions-making on implementation of dengue control and/or when to use of dengue and JE vaccination, as they also provide age-specific seroprevalence and seroconversion data (Carabali *et al.*, 2017). Younger individuals are less likely to have been exposed to either virus, and this population may be considered as the target group for vaccination programs (Flasche *et al.*, 2016). Moreover, increasing seroconversion

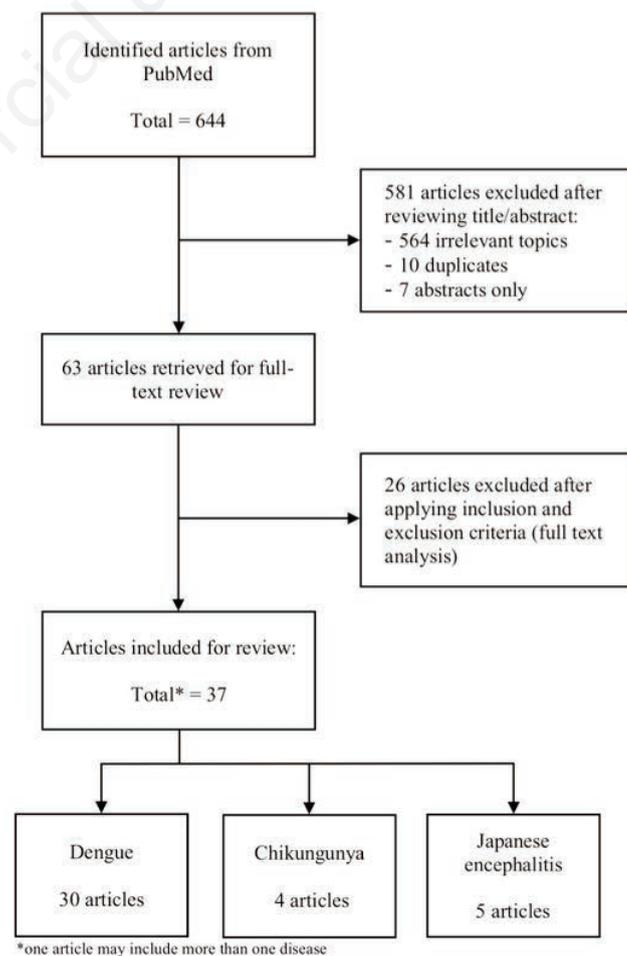


Figure 1. Flowchart of literature selection process.



rate with age is important as it indicates disease transmission in an area (Toan *et al.*, 2015; Villar *et al.*, 2015). These profiles imply that existing vector control measures in study areas are inadequate, and that novel vector control strategies are urgently needed (Sasmono *et al.*, 2018). Only few seroepidemiological studies along with utilisation of GIS have been identified in this review, possibly due to the difficulty and the cost of conducting long-term, cohort-based studies. Therefore, most of the available data regarding disease seroprevalence were derived from passive disease surveillance, leading to significant uncertainties in disease controllability, such as the basic reproductive rate (R_0) that can be used to determine the critical vaccination fraction to eliminate disease transmission and lessen the economic burden (Johansson *et al.*, 2011; Supadmi *et al.*, 2019).

Disease vector distribution mapping

Other than mapping the disease distribution itself, several studies utilised GIS for mapping the vector distribution, which is essential in monitoring expansion of the disease into previously non-endemic areas (Ong *et al.*, 2019). Studies on *Aedes* mosquitoes distribution were mostly reported from Thailand (Chansang and Kittayapong, 2007; Sarfraz *et al.*, 2012; Boonklong and Bhumiratana, 2016), and these studies mainly reported the types of water containers or habitats suitable for mosquito breeding. The ecology and the availability of potential breeding sites differs in urban and rural settings, and one study focused on that showing that the higher the urban-rural gradient, the greater the risk for seasonal and geographical spread of *Aedes* mosquitoes, (Boonklong and Bhumiratana, 2016). Interestingly, another Thai study showed that *Ae. aegypti* and *Ae. albopictus* entomological indices (house index, Breteau index, container index) were found to be influenced by the season and land use (Sarfraz *et al.*, 2012), whereas another study conducted in Malaysia showed the opposite

(Aziz *et al.*, 2014). This might be due to the latter study was based on urban dengue hotspots, while the former study was conducted in villages with different endemicities. In addition, a larval GIS-supported survey of *Ae. aegypti* mosquitoes in Thailand showed a significant clustering of larvae within 10-20 m radius in the study area (Chansang and Kittayapong, 2007). Along with larval indices, dengue entomological indices may represent a fairly close scenario of vector habitat suitability, however the indices were seen to remain weak in predicting dengue cases (Sarfraz *et al.*, 2012). The study details are described further in Table 3. A number of studies utilised geositioned occurrence data of JE cases and its vectors in evaluating the spread of the vectors and their habitats. Several clusters of some *Culex* species were observed in Vietnam, where small clusters were influenced by the presence of cattle, but not by the proximity of rice fields to the house compounds (Hasegawa *et al.*, 2008). This might be due to local practice, in which people washed animal sheds and hence created polluted ground pools that served as potential breeding sites for these mosquitoes. A multinational study was conducted in several Asian countries in predicting the environmental suitability for *Cx. tritaeniorhynchus* distribution, which showed that countries in South Asia and East Asia were the primary locations for the distribution of this mosquito species (Longbottom *et al.*, 2017). The study also predicted some spots of *Cx. tritaeniorhynchus* distribution in Southeast Asian countries. However, due to the sparse availability of data for these countries, it remains unclear if these areas were already inhabited or have yet to be colonised by the species. When GIS and statistical models are combined, spatial distribution of disease vectors can be predicted. Particularly in the presence of a changing environment due to human disruptions or climate change, an impact on mosquito vectors is inevitable, hence longitudinal monitoring of vectors is necessary (Higa, 2011).

Table 1. Number of studies and countries of study origin.

Country	Studied diseases		Japanese encephalitis	Multiple diseases	Total
	Dengue	Chikungunya			
Brunei	-	-	-	-	-
Cambodia	-	-	-	-	-
Indonesia	4	-	-	-	4
Lao PDR	-	-	1**	-	1
Malaysia	6	1	-	-	7
Myanmar	-	-	-	-	-
Philippines	-	-	-	-	-
Singapore	2	-	-	-	2
Thailand	13	2	-	-	15
Vietnam	1	-	1	-	2
Multiple countries*	2	-	3	1***	6
Total	28	3	4	2	37

*Can involve several or all Southeast Asian countries; **Dengue, JE; ***Dengue, Chikungunya.

Table 2. Selected studies on disease seroprevalence mapping.

Author	Publication year	Country	Disease(s) studied	Core findings
Azami <i>et al.</i>	2013	Malaysia	Chikungunya	Anti- IgG seropositivity clustered in both rural and urban communities
Vallee <i>et al.</i>	2009	Lao PDR	Dengue, Japanese encephalitis	Anti-IgG positivity frequently found in the city centre with IgM-positivity more common in the periphery



Spatial relationships and causal factors in disease distribution

In order to understand the disease transmission dynamics and to plan vector control measures, identification of high-risk areas and seasonal variations of disease transmission is essential. A majority of the identified studies dealt with dengue, identifying disease distribution patterns and potential risk factors of transmission (Table 4). Varying results were reported, as different study sites had their own local profiles. A study conducted in remote villages in Sarawak, Malaysia showed the presence of dengue cases in the absence of *Aedes* entomological indices, and consequently also of the principal vector of dengue, with the niche probably filled by *Ae. albopictus*, which is more widely distributed in Sarawak regardless of remoteness of the villages studied (Cheah *et al.*, 2006). Another study performed in Vietnam suggested that the timing and magnitude of annual dengue epidemics were influenced by local biological and ecological drivers, including vector survival, biting behaviour and virus replication within the vector (Cuong *et al.*, 2013).

Clustering of dengue cases was observed in many studies (Vanwambeke *et al.*, 2006; Salje *et al.*, 2012; Yoon *et al.*, 2012; Thomas *et al.*, 2015; Salje *et al.*, 2017) demonstrating focal transmission due to the low flight range of *Aedes* mosquitoes (<100 m) (Bouzid *et al.*, 2016). However, the roles of population growth, human travel and urbanisation have been suggested to drive dengue spatiotemporal clustering and spread in the Asia-Pacific region (Banu *et al.*, 2014). Smaller clusters suggest that most of the cases were transmitted via short-distance human movement (Guzzetta *et al.*, 2018) and that environmental factors might play a role in the development of such focal clusters (Auchincloss *et al.*, 2012). This evidence is strengthened by a multinational study that have demonstrated a higher population density and shorter distances in countries were predominant factors, characterising both dengue and chikungunya outbreaks, reflect a higher probability of vectors and infected individuals moving between neighbouring countries with similar climatic conditions (Rossi *et al.*, 2018). These traits infer that disease control strategies should be focused

not only on peridomestic environment surrounding index cases, but also in other gathering places following human movement (Stoddard *et al.*, 2013).

The complexity of the spread of mosquito-borne viruses is further added by the presence of climate change manifested as either alteration in rainfall patterns, flooding or an increased chance of extreme events. Such changes cause an altered vector ecology and population dynamics leading to geographical expansion of disease vectors and increased threats of disease transmission (Baylis, 2017; Whitehorn and Yacoub, 2019). Spatial variations of dengue cases have been reported in several studies (Jeefoo *et al.*, 2011; Aziz *et al.*, 2012; Astuti *et al.*, 2019; Husnina *et al.*, 2019; Xu *et al.*, 2019), and they show that dengue incidences are strongly associated with rainfall, temperature and humidity. One study also demonstrated that dengue case distribution had a tendency of increased clustering during periods of low rainfall, while heavy rainfall had the opposite effect (Aziz *et al.*, 2012). Although most studies claimed that climatic factors are determinants of dengue, other study reported no significant correlation between climatic factors and dengue incidence (Kesetyaningsih *et al.*, 2018). This might be due to difficulties in statistical analysis (Lai, 2018), as most of the climatic data used in the study performed by Kesetyaningsih *et al.* (2018) were range-type data (minimum-maximum value, mean value and cumulative value). Interestingly, a multinational study identified that the combination of climate, virus and population conditions in Southeast Asia might have initiated the spread of the dengue virus under the influence by particularly high temperatures during a strong El Niño episode (van Panhuis *et al.*, 2015). This inter-annual climate phenomenon may result in fluctuations of draught and flooding which directly increase the epidemics of mosquito-borne viruses, including dengue and chikungunya (Anyamba *et al.*, 2019). Nevertheless, the relationship between climate change and mosquito-borne viruses expansion may not always be linear, for instance, heavy rainfall may also flush away aquatic stages of the vector in breeding places (Seidahmed and Eltahir, 2016; Whitehorn and Yacoub, 2019). The identification of dengue clusters and risk factors associated with disease clustering

Table 3. Studies on disease vector distribution mapping.

Author	Publication year	Country	Disease(s) studied	Core findings
Aziz <i>et al.</i>	2014	Malaysia	<i>Ae. aegypti</i> <i>Ae. albopictus</i>	Mosquito hotspots of various density where land use does not affect mosquito populations
Boonklong <i>et al.</i>	2016	Thailand	<i>Ae. aegypti</i> <i>Ae. albopictus</i>	Seasonal distribution of vectors differing between urban and rural areas according to types of water container
Chansang <i>et al.</i>	2007	Thailand	<i>Ae. aegypti</i> <i>Ae. albopictus</i>	Clustering of larvae within 10-20 m radius of houses
Ong <i>et al.</i>	2019	Singapore	<i>Ae. aegypti</i> <i>Ae. albopictus</i>	Expansion into previously non-dengue areas with increasing <i>Ae. aegypti</i> habitat percentage
Sarfraz <i>et al.</i>	2012	Thailand	<i>Ae. aegypti</i> <i>Ae. albopictus</i>	Settlements around gasoline stations and in vicinity of marsh or rice paddy favourable areas for mosquito vector habitats
Longbottom <i>et al.</i>	2017	Indonesia, Malaysia, Philippines, Thailand, Vietnam	<i>Cx. tritaeniorhynchus</i>	Environmental suitability for <i>Cx. tritaeniorhynchus</i> primarily located across countries in South and East Asia
Hasegawa <i>et al.</i>	2008	Vietnam	<i>Cx. vishnui</i> subgroup <i>Cx. gelidus</i> <i>Cx. quinquefasciatus</i>	Mosquito clusters not observed at scales larger than house compound units; presence of cattle might influence abundance of the vectors



are essential tools to target suitable disease control policies, particularly in designing timely disease surveillance with a focus on intense disease control activities, such as insecticide spraying and active case-finding (Vincenti-Gonzalez *et al.*, 2017; Guzzetta *et al.*, 2018).

As most of this study results demonstrated small disease clusters, the implementation of control interventions at the neighbourhood level may be significantly useful in reducing dengue transmission rather than random interventions.

Table 4. Studies on spatial relationships and causal factors in disease distribution.

Author	Publication year	Country	Studied disease(s)	Major findings
Astuti <i>et al.</i>	2019	Indonesia	Dengue	Incidence in children spatially varied and clustered at the village level; seasonal patterns of dengue incidence strongly associated with rainfall, temperature and humidity
Aziz <i>et al.</i>	2012	Malaysia	Dengue	Spatial distribution more clustered with low mean rainfall, while cases more dispersed during the rainy season
Banu <i>et al.</i>	2014	Indonesia, Lao PDR, Malaysia, Myanmar, Philippines, Singapore, Thailand, Vietnam	Dengue	Clusters of endemicity geographically expanded in Asia-Pacific over 50 years with most likely cluster in Vietnam, Lao PDR and Thailand, possibly due to population growth, travel, urbanisation and lack of effective vector control.
Cheah <i>et al.</i>	2006	Malaysia	Dengue	Risk factors including container density, house density, egg count per positive ovitraps in and around houses not correlated with number of cases
Cuong <i>et al.</i>	2013	Vietnam	Dengue	Annual epidemics occurring later in Ho Chi Minh City than in other provinces with timing and magnitude correlated in nearby districts suggesting influence of local biological and ecological drivers
Husnina <i>et al.</i>	2019	Indonesia	Dengue	Seasonal pattern closely related to minimum temperature and relative humidity with forest cover reduction associated with increasing risk of dengue in only one study area
Jeefoo <i>et al.</i>	2011	Thailand	Dengue	Case distribution clustered in villages with those on the urban fringe reporting higher incidences; outbreak, movement and spread patterns associated with climatic factors but not related to entomologic and epidemiologic factors
Kesetyaningsih <i>et al.</i>	2018	Indonesia	Dengue	Annual incidents in all sub-districts clustered with no environmental factors closely related to dengue incidence
Salje <i>et al.</i>	2012	Thailand	Dengue	Localised transmission within 1-km radius with clustering of particular dengue virus serotypes in the neighbourhood
Salje <i>et al.</i>	2017	Thailand	Dengue	Approximately 60% of case pairs separated <200 m from same virus transmission chain supporting focal transmission at neighbourhood level
Thomas <i>et al.</i>	2015	Thailand	Dengue	Focal spread of dengue virus within radius of 120 m from the index case was associated with the mosquito vector
van Panhuis <i>et al.</i>	2015	Cambodia, Thailand, Lao PDR, Vietnam, Malaysia, Singapore, Philippines	Dengue	Local climate, virus and population conditions may have ignited emergence and spread of dengue virus influenced by high temperatures during strong El Niño episode together with population movement in central Thailand, eastern Mekong and southern Philippines
Vanwambeke <i>et al.</i>	2006	Thailand	Dengue	Weather pattern and dengue infection rate not correlated, whereas land cover playing important role in infection determinant by providing habitats
Yoon <i>et al.</i>	2012	Thailand	Dengue	Spatiotemporal clustering in children with mosquitoes detected within 100-m radius and transmission showing an over-dispersion pattern
Xu <i>et al.</i>	2019	Thailand	Dengue	Distinct seasonality of cases, mostly affected by climatic factors
Rossi <i>et al.</i>	2018	Brunei, Cambodia, Indonesia, Lao PDR, Malaysia, Myanmar, Singapore, Thailand, Vietnam	Dengue, Chikungunya	Higher population density and shorter distances among countries with outbreaks predominant factors characterising both dengue and chikungunya outbreaks in Southeast Asian countries



Disease risk mapping and transmission models

Traditionally, maps were used only when identifying and monitoring associations between location, environment, and disease (Musa *et al.*, 2013). However, the use of mapping with respect to diseases has evolved into transmission models predicting future disease distribution trends. Table 5 describes identified studies related to risk mapping and transmission models supported by georeferenced disease data. Risk mapping can be highly useful in guiding vector control programs, mainly for disease surveillance and epidemic mitigation efforts (Ong *et al.*, 2018). In order to classify certain areas as of low or high risk for disease transmission, several factors need to be identified, *e.g.*, a study on dengue risk prediction mapping conducted in Selangor, Malaysia identified human settle-

ments coverage and non-agricultural areas as risk factors for dengue transmission (Cheong *et al.*, 2014). Similarly, other studies also identified population density and types of land use as risk factors by dengue zone mapping (Nakhapakorn and Tripathi, 2005; Dom *et al.*, 2013; Ong *et al.*, 2018). Another study stratified regions according to vulnerability status of contracting dengue by using the Water-associated Disease Index (WADI) that comprises many elements including climate, land use, population density, type of housing, sanitation quality and sociodemographic factors (Dickin *et al.*, 2013). However, the WADI might not represent all areas in the country equally well since the availability of detailed health data are lacking in some regions. To increase preparedness for potential dengue outbreaks, the public health sector in many

Table 5. Studies in disease risk mapping and transmission models.

Author	Publication year	Country	Studied disease(s)	Major findings
Cheong <i>et al.</i>	2014	Malaysia	Dengue	Prediction map derived from several factors including human settlements and non-agricultural areas, with large share of human settlements associated with higher numbers of dengue cases
Dickin <i>et al.</i>	2013	Malaysia	Dengue	WADI* integrating social and biophysical components classifying study areas into high and low vulnerability with urban environments particularly vulnerable
Dom <i>et al.</i>	2013	Malaysia	Dengue	Areas with different disseminations mainly influenced by land use and population density with urban areas of high and moderate-high risk areas when surrounded by massive developments
Nakhapakorn <i>et al.</i>	2005	Thailand	Dengue	Risk map generated by modelling with climatic factors as independent variables with built-up areas constituting highest risk followed by agricultural areas
Ong <i>et al.</i>	2018	Singapore	Dengue	Risk mapping indicating predicted risk levels in agreement with dengue case densities with numbers of clusters in high-risk areas almost 8 times that of low-risk areas, which represented 50% of residential areas
O'Reilly <i>et al.</i>	2019	Indonesia	Dengue	Predicted spatial concentration of cases with highest risk in urban regions of Java, West Kalimantan and northern Sumatra accounting for 15% of national dengue burden
Chadsuthi <i>et al.</i>	2016	Thailand	Chikungunya	Mathematical modelling showing speed of transmission and incidence in particular areas affected by climatic variations
Chadsuthi <i>et al.</i>	2018	Thailand	Chikungunya	Transmission model using human movement, temperature and rainfall maximum likelihood fit of transmission demonstrating importance of human movement and weather conditions for spread of the virus
Miller <i>et al.</i>	2012	Brunei, Cambodia, Indonesia, Lao PDR, Malaysia, Myanmar, Philippines, Singapore, Thailand, Vietnam	Japanese encephalitis	Ecological niche modelling based on environmental data demonstrating that Vietnam, Cambodia and Thailand have >50% of land area with >25% probability of JE vector presence, which is in line with observed risk of increased numbers of human cases
Samy <i>et al.</i>	2018	Brunei, Cambodia, Indonesia, Lao PDR, Malaysia, Myanmar, Philippines, Singapore, Thailand, Vietnam	Japanese encephalitis	Ecological model predicting an overlapping distribution of vectors and reservoirs in high-risk countries including Myanmar, Lao PDR, Thailand, Vietnam, Malaysia and Indonesia.

*Water-Associated Disease Index.

countries has developed dengue risk maps (Louis *et al.*, 2014). By comparing risk-stratified areas for disease transmission over the years, identification of new or recurring risk areas can assist in prioritising areas for control efforts; hence effective deployment of resources (Ong *et al.*, 2018). Furthermore, risk mapping or risk prediction mapping can potentially be implemented in other areas with similar environmental settings, particularly for diseases transmitted by similar vector species, such as dengue and chikungunya (Cheong *et al.*, 2014). With the advancement of computational science, efforts of disease monitoring and epidemic simulation have been made possible by various types of modelling (Ajelli *et al.*, 2010; Christaki, 2015). Mathematical modelling was used in estimating the burden of dengue in Indonesia (O'Reilly *et al.*, 2019) finding a predicted highest risk of spatial concentration of dengue cases in the urban regions of Java, Kalimantan and Sumatra. The use of a transmission model of chikungunya virus spread in Thailand revealed that climatic variations and human movement affect the speed of virus transmission in particular areas (Chadsuthi *et al.*, 2016; Chadsuthi *et al.*, 2018). Ecological modelling was also used in predicting the risk of JE transmission in multinational studies (Miller *et al.*, 2012; Samy *et al.*, 2018) predicting an overlapping distribution of vectors and reservoirs in high-risk countries including Myanmar, Lao PDR, Thailand, Vietnam, Malaysia and Indonesia. Additionally, more than 25% probability of JE vector presence in over 50% of the land area of Vietnam, Cambodia and Thailand was predicted with an increasing risk of human JE cases in those areas. As mosquito-borne viruses are sensitive to climate fluctuations, modelling disease transmission in a series of unique climatic episodes, including an El Niño event, in Southeast Asia as done by Tipayamongkholgul *et al.* (2009) and Anyamba *et al.* (2019) will be very useful in future epidemic forecasting.

Disease transmission modelling improves our understanding of the role of disease mobility patterns and is an important instrument in assessing both past and current disease epidemics, which are needed for the preparation of future interventions (Christaki, 2015). However, mosquito-borne disease outbreaks are more challenging to predict due to the dynamics of mosquito ecology and human behaviour in different populations (Ford *et al.*, 2009). As mosquito-borne viruses are sensitive to climate change (Ludwig *et al.*, 2019), close monitoring of climatologic parameters is therefore essential to evaluate slight changes that may contribute to disease outbreak.

Decision support for disease intervention

By identifying high-risk areas and accurately modelling the flow of disease transmission, it is possible to target intervention efforts. Three such studies were identified and analysed in this review (Table 6). One of the studies was conducted in Indonesia

and estimated the impact of releasing *Wolbachia*-infected mosquitoes. The results predicted that a nationwide *Wolbachia* campaign could avert up to 86% of dengue cases in areas with high transmission intensity, including urban areas of Java, Kalimantan and Sumatra (O'Reilly *et al.*, 2019). In Thailand, two studies (Kittayapong *et al.*, 2008; Thammapalo *et al.*, 2012) adapted GIS for monitoring disease control interventions. One showed suppression of dengue transmission in treated areas by application of integrated vector control strategies, including source reduction, screening for water jars, application of *Bacillus thuringiensis* subspecies *israelensis* (Bti)-acting as biological pesticide, and insecticide-treated ovitraps (Kittayapong *et al.*, 2008). The other study found that the coverage of space spraying was inadequate (<100 m radius from index case) as evidenced by spreading of dengue infections and increasing number of cases with secondary infection despite timely spraying (Thammapalo *et al.*, 2012). In countries with persistent transmission of mosquito-borne viruses, failure of disease control program should be suspected. A better monitoring and evaluation of disease surveillance and resource allocation for control programs are hence mandatory.

The number of epidemiological studies employing GIS in Southeast Asian countries and elsewhere has increased sharply in the past decade. However, not all of Southeast Asian countries have independently performed and published study national outcomes, *e.g.*, Brunei, Cambodia, Myanmar and Philippines, which have instead been involved in large-scale, multinational studies. Possibly, due to the proportion of national budget available, these countries focused more on case finding and case management than disease surveillance and outbreak mitigation (Caballero-Anthony *et al.*, 2015). Cambodia, Lao PDR, Myanmar, and Vietnam, *i.e.* countries in the Greater Mekong sub-region, might be more concerned in other high-burden, lethal mosquito-borne diseases such as malaria (Cui *et al.*, 2012; Geng *et al.*, 2019), which would explain the lack of research activities regarding mosquito-borne viral diseases. Political constraints and resource allocation may thus also have played a role for the outcomes (Brian and Lawrence, 2001).

In general, most of the identified studies emphasised identification of spatial relationship, risk mapping and transmission model of dengue infection, while publications regarding the use of GIS for research on chikungunya and JE were somewhat limited. Dengue contributes substantially to the economic and disease burden in Southeast Asia; higher than other mosquito-borne viral diseases (Shepard *et al.*, 2013). Nevertheless, these two diseases share similar clinical, epidemiological and diagnostic features with dengue, therefore future studies on chikungunya and JE should be encouraged (O'Reilly *et al.*, 2019). Factors that might contribute to the comparatively small number of published chikungunya- and

Table 6. Studies on decision support for disease intervention.

Author	Publication year	Country	Studied disease(s)	Major findings
O'Reilly <i>et al.</i>	2019	Indonesia	Dengue	Nationwide long-term <i>Wolbachia</i> campaign preventing up to 86% of cases in high-transmission areas
Kittayapong <i>et al.</i>	2008	Thailand	Dengue	Reduction of the number of <i>Ae. aegypti</i> mosquitoes in focal dengue-treated areas by screening for water jars, application of Bti*-bacteria acting as biological pesticide and insecticide-treated ovitraps
Thammapalo <i>et al.</i>	2012	Thailand	Dengue	Increased number of cases with secondary infection despite timely spraying due to inadequate coverage of space spraying

**Bacillus thuringiensis* subspecies *israelensis*.



JE-related studies, could be that the disease burden due to these infections may be perceived to be less than other mosquito-borne diseases. Another reason could be that a majority of Southeast Asian countries have already deployed a national JE immunisation program (Heffelfinger *et al.*, 2017), and that researchers focus on dengue and chikungunya as they assume that the epidemiology of these viruses is similar since they can share vectors.

Conclusions

GIS has shown great promise in location of high-risk areas and populations at risk, identification of areas in need of resources and allocation of effective resources for control. The current review has identified a number of published papers on the use of GIS in dengue, chikungunya, and JE in Southeast Asian countries. Independent studies in all countries should be encouraged, particularly with respect to chikungunya and JE considering the high burden and the overlapping distribution of their mosquito vectors. Only very limited seroprevalence studies and disease intervention monitoring based on GIS were identified. This is important as seropositive populations reflect a long-term burden and ongoing disease transmission in a given area. Monitoring of ongoing interventions using GIS is important as this can assist identifying areas with failed disease control strategies, thus optimising resource allocation in those areas. More focused control strategies are urgently needed yet challenging due to limited data (O'Reilly *et al.*, 2019). There is a need for more integrated research activities with regard to all three diseases covered by this review, addressing knowledge gaps in the implementation of GIS in control strategies, including approaches from seroprevalence studies in determining target population for vaccination program to intervention monitoring.

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