



# Incorporating the human–*Aedes* mosquito interactions into measuring the spatial risk of urban dengue fever



Tzai-Hung Wen<sup>a,\*</sup>, Min-Hau Lin<sup>b</sup>, Hwa-Jen Teng<sup>c</sup>, Niann-Tai Chang<sup>d</sup>

<sup>a</sup> Department of Geography, National Taiwan University, Taipei, Taiwan

<sup>b</sup> Institute of Health Policy and Management, National Taiwan University, Taipei, Taiwan

<sup>c</sup> Centers for Disease Control (CDC), Ministry of Health and Welfare, Taipei City, Taiwan

<sup>d</sup> Department of Plant Medicine, National Pingtung University of Science and Technology, Pingtung County, Taiwan

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## ABSTRACT

To block human–mosquito interactions by eliminating dengue vectors, *Aedes aegypti* L. and *Aedes albopictus* Skuse have been considered the main strategies for dengue prevention. Spatial targeting of dengue risk areas is the highest priority for implementing control measures. However, the frequency of human–*Aedes* mosquito contacts as human factors for assessing the risk of dengue has not been taken into account by past studies. The objective of this study is to clarify the geographic effects of crowd-gathering places on the frequency of dengue vector for assessing the spatial risk of exposure to dengue in Kaohsiung City, Taiwan. A geographic information system (GIS) was used to integrate crowd-gathering places and ovitrap locations for investigating potential human–mosquito contacts. A negative binomial regression was used to estimate the spatial risk of dengue by integrating vector mosquitoes from the ovitrap survey, urban environmental risk factors and human crowd-gathering places as the surrogate of human activities. We also compared the estimated spatial risk of exposure to dengue with traditional approaches. Our results indicated that the spatial distribution of the residential populations is not consistent with the locations of social activities. Additionally, people closer to crowd-gathering places have a higher frequency of contact with *Ae. aegypti* than with *Ae. albopictus* larvae. The dengue risk is caused by the human–*Aedes aegypti* contacts concentrated around city centers, while the risk caused by the human–*Aedes albopictus* contacts is distributed around the city boundary. Our study concluded that only relying on infected human cases or the abundance of vector mosquitoes is not enough for assessing the spatial risk of dengue. This reliance could ignore the areas with frequent vector existence and; therefore, result in the underestimated risk of dengue transmission. This study demonstrates the methodological framework for estimating the potential dengue risk and identifies the crowd-gathering places that facilitate dengue transmission.

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## Introduction

Dengue and dengue hemorrhagic fever are considered severe global health threats. Billions of people live at risk from dengue, and millions are already infected. This situation has resulted in enormous losses of healthy life years (Hotez, Bottazzi, Franco-Paredes, Ault, & Periago, 2008; Shepard, Undurraga, & Halasa, 2013; Shepard et al., 2014; World Health Organization Dengue and severe

dengue). Due to the high population density and urban environmental characteristics, urbanization is highly associated with the spread of dengue fever in tropical areas (Li et al., 2014; Mulligan, Elliott, & Schuster-Wallace, 2012; Rotela et al., 2007; Vazquez-Prokopec, Kitron, Montgomery, Horne, & Ritchie, 2010; Wu et al., 2009). Currently, there are no available vaccines or antiviral drugs for prevention of dengue infection (Wan et al., 2013). The main strategy to block dengue transmission has been avoiding human–mosquito contacts (World Health Organization, 2009). Spatial targeting of dengue risk areas is a high priority for implementing control measures. Previous studies have focused on spatial mapping of the potential risk of dengue using three main approaches. First, the physical and social environments, which are conducive to

\* Corresponding author. Department of Geography, College of Science, National Taiwan University, No. 1, Sec. 4, Roosevelt Road, Taipei 10617, Taiwan.  
Tel.: +886 2 3366 5847.

E-mail address: [wenthung@ntu.edu.tw](mailto:wenthung@ntu.edu.tw) (T.-H. Wen).

the growth of the dengue vector, are considered high-risk areas. Some studies were conducted in risk areas where meteorological and ecological conditions are suitable for dengue mosquitoes (Hassan, Shohaimi, & Hashim, 2012; Wu, Guo, Lung, Lin, & Su, 2007). Such areas include high-density urban areas and areas with high water-contained receptacles (Caprara et al., 2009; Schmidt et al., 2011; Seng et al., 2008). It was illustrated that these environmental conditions have significant influences on the occurrence of dengue epidemics. The second approach monitored the vector density determined from an entomological survey of dengue (Chadee, Williams, & Kitron, 2005; Moreno-Sanchez, Hayden, Janes, & Anderson, 2006; Sanchez et al., 2006). Based on the principle that more dengue infections are a result of more vector mosquitoes, some studies have identified the high-risk areas with high dengue transmission by mapping and analyzing the spatial distribution of mosquitoes. Third, some studies indicated the reported or confirmed dengue cases as the outcome of human–mosquito contacts and identified them as the indicators, rather than mosquito density or ecological conditions for mapping high-risk epidemic areas (Bhoomiboonchoo et al., 2014; Guzmán et al., 2000; Hsueh, Lee, & Beltz, 2012; Morrison, Getis, Santiago, Rigau-Perez, & Reiter, 1998; Porter et al., 2005; Wen, Lin, Lin, King, & Su, 2006).

The three approaches mentioned above were established for predicting dengue risk areas, but there is still insufficient information to effectively capture human–mosquito contact. First, dengue transmission contains silent infection (Chen et al., 1996; Teixeira et al., 2002). The distribution of dengue cases could not comprehensively reflect the risk of dengue transmission. Moreover, taking the amount of vector mosquitoes or the physical environment (that is suitable for the growth of vectors) as indicators of risk ignores the effects of human behaviors on dengue transmission. Human behavior is an important factor for quantifying human–mosquito contacts. Therefore, the exposure to the risk of dengue is the result of complex interactions between the vector and the human population. Population density is often used in epidemiological studies as the main factor for capturing the concept of at-risk populations. However, the data source of the indicator is either from census or demographic surveys, most of which are based on fixed locations of residence and are not enough to adequately reflect human behaviors geographically. The effects of populated humans at working and leisure activities as human factors are ignored when the population density is used as a surrogate for measuring the spatial risk of dengue transmission.

Population movement is an inevitable component in society, and people travel from their homes to working places, and for leisure activities. Recently, changes in urban conditions and the reduction of transportation costs have led to more people living in rural areas and commuting to work. Additionally, social activities are also important reasons for population mobility. The risk of human exposure to the disease could vary geographically (Hagenlocher, Delmelle, Casas, & Kienberger, 2013; Li et al., 2014; Machado-Machado, 2012; Spiegel et al., 2005). Recent epidemiological studies have incorporated the effects of population mobility, including the locations of daily activities, in assessing the spatial exposure risk for disease transmission (Perchoux, Chaix, Cummins, & Kestens, 2013). Setton et al. (2010) discovered that the estimation of air pollution exposure risk would cause a bias if it only considered an individual's residence and ignored the locations of daily activities (Setton et al., 2010). By tracking GPS trajectories, Vazquez-Prokopec et al. (2009) analyzed mobility patterns for differentiating the locations where effective mosquito–human contacts from virus exposure may have occurred (Vazquez-Prokopec et al., 2009). However, using GPS for tracking individual mobility may involve privacy issues. On the other hand, some studies have assessed the

demographic behaviors and identified environmental risk factors of dengue transmission. Wen, Lin, and Fang (2012) noticed that some crowd-gathering places (e.g., markets, schools and parks) and the commuting behavior played important roles in dengue diffusion (Wen et al., 2012).

Mapping the distribution of dengue cases only incorporates the risk of residences and neglects the spatial relationships between dengue transmission and the locations of daily activities. Previous studies on environmental health have suggested that the location of residence was only one of the exposures of environmental pollution when mapping the spatial distribution of environmental risk. The locations of daily and social activities might be considered a possible exposure to environmental hazards and vector mosquitoes when assessing the spatial risks of hazards or disease transmission (Dons et al., 2011; Setton et al., 2010; Steinle, Reis, & Sabel, 2013).

Moreover, human activities influence the vector ecology (Juliano, 2009; Spiegel et al., 2005). Humans and mosquitoes coexisted in a mutual space that could create an environment for the breeding of mosquitoes. Such spaces include human-made containers (Dickin, Schuster-Wallace, & Elliott, 2014; Heymann, 2005; Li et al., 2014) and food sources (Strickman & Kittayapong, 2003). These positive effects may facilitate the spread of dengue. However, humans tend to look on mosquitoes as annoying insects and try to eliminate them (Spiegel et al., 2005). Those types of human–mosquito interactions might result in the opposite effects on dengue transmission. Thus, the effect of being close to crowd-gathering places to enhance the potential risk of dengue infection remains unclear. Therefore, the objective of this study is to clarify the spatial effects of crowd-gathering places for assessing the spatial risk of exposure to dengue. We propose an innovative analytical framework of assessing the spatial risk of dengue fever by integrating vector mosquitoes from the ovitrap survey, urban environmental risk factors and human social activity places as the surrogate for human social behaviors.

The structure of this paper is as follows: in the next section, we describe the study area, data collection and methodological framework for modeling the dengue risk, including kernel density mapping and statistical models. In results section, we demonstrate the effects of distance from place of social activities on dengue risk. We also compared the predicted spatial risk of exposure to dengue using different approaches, including vector-based and dengue case-based risk estimation. The final section states our conclusions.

## Materials and methods

### Study area

Taiwan, an island state situated in south-eastern Asia, experiences dengue outbreak every year. Dengue is the most severe vector-borne disease of the country. Specifically, several dengue outbreaks had emerged in Kaohsiung City, which is the major metropolis in southern Taiwan (Chang, Huang, & Shu, 2012; King et al., 2000). Every year since 2006, more than one hundred imported cases and more than five hundred indigenous cases are identified (Chang et al., 2012). Indigenous case epidemics mainly start in the summer and end around January or February of the following year. Previous studies have found that imported cases might play a role in epidemics (Shang et al., 2010). Kaohsiung City, the dengue epidemic focus of Taiwan, is located in a tropical zone with distinct wet and dry seasons (Fig. 1). The mean temperature is 25.1 °C (77.2 °F), and the wet season is generally from May to September. There are more than 2.77 million residents in Kaohsiung City, and the population density is approximately 940 persons per square kilometer (Kaohsiung City Government, 2014).

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