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The impact of human activity on the risk index and spatial spreading of dengue fever☆

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HIGHLIGHTS

- This paper characterizes the gradual expanding process of the contaminated environment.
- We consider the impact of media coverage on dengue fever transmission.
- The free boundary problem adopts the different diffusive patterns for the human and mosquitoes.

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ABSTRACT

To understand how human diffusion and media coverage affect the dynamics of dengue fever epidemiology, we propose a SIR v.s. SI dengue model with a nonlinear contact transmission rate. The free boundaries are also introduced to describe the expanding fronts of the contaminated area caused by the dengue virus. With the help of the basic reproduction number for a relevant problem, we establish the spatio-temporal risk index associated with the diffusive coefficient and media index for our model. Furthermore, some sufficient conditions are obtained to guarantee dengue fever to vanish or to spread, and the asymptotic behavior of the solution for a special system is also discussed when spreading happens. Our results indicate that the degrees of human diffusion and mass media propaganda play an essential role in dengue fever control and prevention. Some numerical simulations, which illustrate the impacts of human activity, are carried out to confirm our analytical findings.
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1. Introduction and model description

More than 2500 kinds of mosquitoes have been found in the world and they transmit many diseases, among which Dengue fever is an acute mosquito-borne disease. According to the statistics from the World Health Organization (WHO), dengue fever infects 50 to 100 million people worldwide a year, leading to 50

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million hospitalizations and approximately 12,500 to 25,000 deaths a year, and about one third of people live in the risky zone of dengue fever globally [1].

Dengue fever is an infectious disease caused by dengue virus (DENV) and transmitted by mosquito, especially Aedes aegypti [2]. This disease was initially found in Cairo, Egypt in 1779, and subsequently proved pandemic in Jakarta, Indonesia and Philadelphia, USA [3], and officially named as dengue fever by the Royal college of Physicians of London, England in 1869 [4]. Dengue fever becomes epidemic mainly in more than 110 countries and regions of the tropics and subtropics between the lines of latitudes 35N and 35S, in which there are some high-risk areas like Africa, America, the Eastern Mediterranean, South-east Asia and the Western Pacific [5]. However, because of the frequent human activities on a global scale [6], the number of regions infected by dengue virus is growing, and the area where dengue fever transmits becomes wider and wider. For instance, dengue fever breaking out in Mediterranean area in 2008 has already involved more than 10 countries in Europe such as France and Croatia [7]. Besides, escalating of Europe's migrant crisis has accelerated the spread of some viruses like dengue fever in recent years. In China, with the increase of urbanization, international movement of people and exchanges among talents, the epidemic region of dengue fever has expanded from the coastal areas like Guangdong and Hainan provinces to the hinterland [8], and especially the largest migration of people in the world once a year—"Transport during the Spring Festival" makes the virus reach wider areas. Therefore, human mobility on a global scale will lead to the gradual "globalization" of this virus.

The high infection rate of dengue fever and high death rate of dengue hemorrhagic fever not only cause some public health problems, but also block the economic growth. Hence, it is very meaningful to focus on and grasp the temporal or spatial propagation of this disease further to formulate some effective control strategies. In this sense, mathematical models play a key role in gaining insights into the pathogenesis of infectious diseases. The first mathematical model of dengue transmission was developed by Fischer and Halstead [9], an SIR v.s. SI epidemiological model was set up by Esteva and Vargas [10], and a number of others [11–13] were based on these two models, all of which aimed to explore the transmission mechanisms of dengue fever. These models, which assume that the crowd is well-mixed and the transmission is instantaneous, are usually spatially-independent. However in reality, humans always move frequently between regions even countries as mentioned in the above, so that the factors about the spatiality and diffusion of population cannot be ignored when we study the spread of infectious diseases [14–21]. In order to make the model more practical, the authors in [18] proposed and analyzed the following dengue model with the crowding effect and spatial variation:

$$\begin{cases} \dfrac{\partial S_H}{\partial t} = d_H \triangle S_H + \mu_b N_H - c(x) S_H N_H - \dfrac{\beta_H(x) b(x)}{N_H + m(x)} S_H I_V - \mu_d S_H, & x \in \Omega, t > 0, \\ \dfrac{\partial I_H}{\partial t} = d_H \triangle I_H + \dfrac{\beta_H(x) b(x)}{N_H + m(x)} S_H I_V - c(x) I_H N_H - (\mu_d + \gamma_H) I_H, & x \in \Omega, t > 0, \\ \dfrac{\partial R_H}{\partial t} = d_H \triangle R_H + \gamma_H I_H - c(x) R_H N_H - \mu_d R_H, & x \in \Omega, t > 0, \\ \dfrac{\partial S_V}{\partial t} = d_V \triangle S_V + A(x) - \dfrac{\beta_V(x) b(x)}{N_H + m(x)} S_V I_H - \mu_V S_V, & x \in \Omega, t > 0, \\ \dfrac{\partial I_V}{\partial t} = d_V \triangle I_V + \dfrac{\beta_V(x) b(x)}{N_H + m(x)} S_V I_H - \mu_V I_V, & x \in \Omega, t > 0, \\ \dfrac{\partial S_H}{\partial \nu} = \dfrac{\partial I_H}{\partial \nu} = \dfrac{\partial R_H}{\partial \nu} = \dfrac{\partial S_V}{\partial \nu} = \dfrac{\partial I_V}{\partial \nu} = 0, & x \in \partial\Omega, t > 0, \end{cases} \tag{1.1}$$

where the variables and parameters are defined as:

· S_H, I_H, R_H: the number of the susceptible, infectious and immune class in the human population, respectively;

· S_V, I_V: the number of the susceptible, infectious class in the mosquito population, respectively;

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