



## Original articles

A time-periodic dengue fever model in a heterogeneous environment<sup>☆</sup>Min Zhu<sup>\*</sup>, Yong Xu*School of Mathematics and Computer Science, Anhui Normal University, Wuhu 241000, China*

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**Abstract**

The transmission of dengue fever characterizes seasonality and periodicity, in particular, the infection of dengue fever is more serious during the warmer seasons. In this paper, we formulate and study an SIS–SI dengue model associated with the spatial heterogeneity and temporal periodicity. With the help of the spectral radius of next infection operator and eigenvalue problem, we introduce the basic reproduction number  $R_0$  of the dengue model. Furthermore, the existence and nonexistence of the positive  $T$ -periodic solution are obtained, respectively. The asymptotical stability of  $T$ -periodic solution is also investigated. Our analyses reveal that the combination of spatial heterogeneity and temporal periodicity would enhance the persistence of dengue virus in the case of  $R_0 > 1$ . Some theoretical results are illustrated by the final numerical simulations and epidemiological explanations.

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**Keywords:** Dengue fever model; Time periodicity; Spatial heterogeneity; Asymptotic behavior; The basic reproduction number

**1. Introduction and main results**

Dengue Fever (DF), Dengue Hemorrhagic Fever (DHF) and Dengue Shock Syndrome (DSS) are growing public health problems in tropical and subtropical areas. Dengue fever is caused by any of the four serotypes of dengue virus (DENV-1 to -4), and transmitted to human by biting of the infected female mosquitoes as the primary vector [23]. Most people with dengue fever recover without any ongoing problems, whose fatality rate is 1%–5% and less than 1% with adequate treatment. However, those who develop DHF or DSS may have a fatality rate of up to 26%. Each year between 50 and 528 million people are infected and approximately 10,000–20,000 die [8]. It is estimated that more than one-third of the global population is living in endemic infection areas [6].

As no particularly safe and effective vaccine for DF exists at present, a useful method of controlling, preventing and even predicting dengue fever is to understand the changes of mosquito behavior way that can influence the spread

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of DF, and then eliminate the mosquitoes through natural means. Therefore, the complex behavior and dynamics of dengue epidemiology have motivated researchers to model and analyze this disease since 1970s [13]. More recently, there have been a variety of dengue models with different factors, for instance, with seasonality and import [2], limited public health resources [1], crowding effect [16], the inclusion of temporal cross-immunity [12] and so on. Take the model in [10,24] as an example, the following classic dengue SIR–SI model is proposed:

$$\begin{cases} S'_H(t) = \mu_h N_H - \frac{\beta_H b}{N_H + m} S_H I_V - \mu_H S_H, \\ I'_H(t) = \frac{\beta_H b}{N_H + m} S_H I_V - (\mu_H + \gamma_H) I_H, \\ R'_H(t) = \gamma_H I_H - \mu_H R_H, \\ S'_V(t) = A - \frac{\beta_V b}{N_H + m} S_V I_H - \mu_V S_V, \\ I'_V(t) = \frac{\beta_V b}{N_H + m} S_V I_H - \mu_V I_V, \\ S_H(0), I_H(0), R_H(0), S_V(0), I_V(0) \geq 0, \end{cases} \quad (1.1)$$

where the variables and parameters are defined as follows:

- $S_H, I_H, R_H$ : the density of the susceptible, infectious and immune class in the human population at time  $t$ , respectively,  $N_H$  is the total number of human population;
- $S_V, I_V$ : the density of the susceptible, infectious class in the mosquito population, respectively;
- $m$ : the density of alternative hosts available as blood source (such as pets);
- $\mu_h, \mu_H, \gamma_H$ : the birth, death and recovery rate of human, respectively;
- $A, \mu_V$ : the recruitment and the per capita mortality rate of mosquitoes, respectively;
- $b$ : the biting rate of mosquitoes, namely, the average number of bites per mosquito per day;
- $\beta_H$ : the contact transmission probability from infectious mosquitoes to susceptible humans;
- $\beta_V$ : the contact transmission probability from infectious humans to susceptible mosquitoes.

For model (1.1), the authors in [10] not only established the global stability of the endemic equilibrium by the theory of competitive systems and stability of periodic orbits, but also discussed the control measures of the mosquito population in terms of the threshold condition. Later, the authors in [24] investigated the global stabilities of its disease free equilibrium and endemic equilibrium by means of the construction of Lyapunov functions and the following basic reproduction number (which is defined as the average number of secondary infections produced when one infected individual is introduced into a host population where everyone is susceptible [14]),

$$R_0 = \sqrt{\frac{\frac{\beta_H b}{N_H + m} \frac{\mu_h N_H}{\mu_H} \cdot \frac{\beta_V b}{N_H + m} \frac{A}{\mu_V}}{\mu_V (\mu_H + \gamma_H)}}. \quad (1.2)$$

In reality, however, dengue infection with one serotype is confirmed to produce lifelong immunity to that type, but only short-time protection against the other three. The risk of severe disease from secondary infection will increase if someone previously exposed to serotype DENV-1 contracts serotype DENV-2 or -3, or if someone previously exposed to DENV-3 acquires DENV-2 [8]. That way, most of recovery persons will become the susceptible once again. Hence, considering the SIS epidemic compartment structure, we propose the following dengue model, which divide human population into susceptible class and infectious class:

$$\begin{cases} S'_H(t) = \mu_h N_H - \frac{\beta_H b}{N_H + m} S_H I_V + \gamma_H I_H - \mu_H S_H, \\ I'_H(t) = \frac{\beta_H b}{N_H + m} S_H I_V - \gamma_H I_H - \mu_H I_H, \\ S'_V(t) = A - \frac{\beta_V b}{N_H + m} S_V I_H - \mu_V S_V, \\ I'_V(t) = \frac{\beta_V b}{N_H + m} S_V I_H - \mu_V I_V, \\ S_H(0) > 0, I_H(0) \geq 0, S_V(0) > 0, I_V(0) \geq 0. \end{cases} \quad (1.3)$$

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