Coexistence of a cross-diffusive dengue fever model in a heterogeneous environment☆

Min Zhu [a,b,*], Zhigui Lin [b], Qunying Zhang [b]

[a] *School of Mathematics and Computer Science, Anhui Normal University, Wuhu 241000, China*
[b] *School of Mathematical Science, Yangzhou University, Yangzhou 225002, China*

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ABSTRACT

A spatio-temporal SIS-SI dengue model with cross-diffusion is formulated as the movements of human and mosquitoes have been intricately linked with the spread of dengue fever. To highlight the impacts of cross-diffusion on the dynamical processes, we focus on the nonnegative steady-state solutions of the dengue model, that is, the coexistence of the corresponding strongly-coupled elliptic system. By means of the relevant eigenvalue problem, we investigate some properties of the basic reproduction number to the model, and further present the existence of coexistence solutions. Our results imply that the virus carried in human and that in mosquitoes can coexist if the basic reproduction number is greater than one and the extent of cross-diffusion is small enough. The final numerical simulations and epidemiological explanations make our analytical findings easier to understand.

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1. Introduction

In modern society, the various infectious diseases have continued to be the major causes of suffering and mortality in developing countries, though the improved sanitation, antibiotics, and vaccination become more and more effective. Especially in recent decades, global warming, environment deterioration, increased international travel and changes in economic patterns will continue to provide opportunities for new and existing infectious diseases, so that some mosquito-borne diseases like dengue fever (DF) have reemerged and are spreading into new regions. The statistics from World Health Organization (WHO) suggests that there are over 50 million people infected and 25,000 deaths due to DF annually, and up to 500 thousand people developing dengue hemorrhagic fever (DHF) or dengue shock syndrome (DSS) [1]. At present, about one third of people in the world are living in the risk zone of dengue fever, particularly in which Africa, America, the Eastern Mediterranean, Southeast Asia and Western Pacific are all high-risk [2].

Dengue fever is an acute infectious disease caused by dengue virus (DENV) and transmitted by mosquitoes, especially Aedes aegypti and Aedes albopictus [3]. The mosquitoes infected by DENV carry the virus for life, and then vertically transmit the virus (adults to eggs), which causes dengue fever to occur constantly. In addition, DENV has four different strains, named as DENV-1, 2, 3 and 4, respectively, so the mechanism how human is infected is relatively complex. It is not entirely clear why secondary infection with a different strain of DENV places people at risk of DHF and DSS [3]. Therefore, in order to prevent and control dengue fever, mathematicians and biologists have established many dengue models [4–10], which have become

useful tools in analyzing the spread and control of dengue fever. More importantly, epidemiology modeling can contribute to suggest crucial date, identify trends and estimate the uncertainty in forecasts for dengue fever and other diseases. For instance, the authors in [7] proposed and analyzed a classic dengue SIR-SI model:

$$
\begin{cases}
S_H'(t) = \mu_h N_H - \dfrac{\beta_H b}{N_H + m} S_H I_V - \mu_H S_H, \\[2mm]
I_H'(t) = \dfrac{\beta_H b}{N_H + m} S_H I_V - (\mu_H + \gamma_H) I_H, \\[2mm]
R_H'(t) = \gamma_H I_H - \mu_H R_H, \\[2mm]
S_V'(t) = A - \dfrac{\beta_V b}{N_H + m} S_V I_H - \mu_V S_V, \\[2mm]
I_V'(t) = \dfrac{\beta_V b}{N_H + m} S_V I_H - \mu_V I_V, \\[2mm]
S_H(0), I_H(0), R_H(0), S_V(0), I_V(0) \ge 0,
\end{cases}
\tag{1.1}
$$

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);
- μ_h, μ_H, γ_H: the birth, death and recovery rate of human, respectively;
- A, μ_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;
- β_H: the contact transmission probability from infectious mosquitoes to susceptible humans;
- β_V: the contact transmission probability from infectious humans to susceptible mosquitoes.

For model (1.1), the global stabilities of its disease-free equilibrium and endemic equilibrium are investigated in [7] with the help of the value of basic reproduction number and the constructions of Lyapunov functions.

Besides, as far as we know infection with one type of DENV usually gives lifelong immunity to that type, but only short-time immunity to the others. However, subsequent infection with a different type increases the risk of severe complications [3], which means that most of recovery persons will become the susceptible once again. Therefore, inspired by the SIS compartment model and (1.1), we formulate the following SIS-SI model to describe the transmission of dengue fever:

$$
\begin{cases}
S_H'(t) = \mu_h N_H - \dfrac{\beta_H b}{N_H + m} S_H I_V + \gamma_H I_H - \mu_H S_H, \\[2mm]
I_H'(t) = \dfrac{\beta_H b}{N_H + m} S_H I_V - \gamma_H I_H - \mu_H I_H, \\[2mm]
S_V'(t) = A - \dfrac{\beta_V b}{N_H + m} S_V I_H - \mu_V S_V, \\[2mm]
I_V'(t) = \dfrac{\beta_V b}{N_H + m} S_V I_H - \mu_V I_V, \\[2mm]
S_H(0) > 0, I_H(0) \ge 0, S_V(0) > 0, I_V(0) \ge 0.
\end{cases}
\tag{1.2}
$$

Naturally, it follows from the first two equations in model (1.2) that

$$(S_H + I_H)'(t) = \mu_h N_H - \mu_H (S_H + I_H),$$

with the initial condition that $(S_H + I_H)(0) = S_H(0) + I_H(0) > 0$. Hence, we can get $\lim_{t \to \infty}(S_H + I_H) = \frac{\mu_h N_H}{\mu_H}$. Performing the same procedure for the last two equations in model (1.2) deduces that $\lim_{t \to \infty}(S_V + I_V) = \frac{A}{\mu_V}$. Thus, the simplified system for model (1.2) is

$$
\begin{cases}
I_H'(t) = \dfrac{\beta_H b}{N_H + m}\left(\dfrac{\mu_h N_H}{\mu_H} - I_H\right) I_V - \gamma_H I_H - \mu_H I_H, \\[3mm]
I_V'(t) = \dfrac{\beta_V b}{N_H + m}\left(\dfrac{A}{\mu_V} - I_V\right) I_H - \mu_V I_V, \\[3mm]
0 \le I_H(0) \le \dfrac{\mu_h N_H}{\mu_H}, \ 0 \le I_V(0) \le \dfrac{A}{\mu_V}.
\end{cases}
\tag{1.3}
$$

It is worth mentioning that dengue fever usually spreads from one area to another because of the diffusions of human and mosquitoes, so that its transmission is affected not only by the characteristics of pathogens (i.e. the microorganisms that can