Applied Mathematics and Computation 248 (2014) 184–194

Contents lists available at ScienceDirect

Applied Mathematics and Computation

journal homepage: www.elsevier.com/locate/amc

On a reaction–diffusion system modeling the dengue transmission with nonlocal infections and crowding effects

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ARTICLE INFO

Keywords:
Dengue transmission
Crowding effect
Time delays
Threshold dynamics
Persistence
Basic reproduction number

ABSTRACT

In this paper, we intend to understand the influences of the spatial heterogeneity, crowding effect and non-local infection caused by the movements of the latent mosquitoes on the dynamics of dengue transmission. For this purpose, we modify the homogeneous system provided in Esteva and Vargas (1998) to obtain a nonlocal and time-delayed reaction–diffusion system with the Neumann condition on the boundary. Then the basic reproduction number $\mathbf{R}_0$ is defined for the model system, and it can be obtained explicitly when all model parameters are constants. Finally, we show that the global threshold dynamics of the model system can be determined by $\mathbf{R}_0$.

1. Introduction

Dengue disease is transmitted to humans by the bites of Aedes mosquitoes and it is a serious disease in the tropical regions of the world. In order to understand the mechanisms of the spread of the disease, Esteva and Vargas [2] proposed a simplified model for dengue disease where they considered one type of virus and ignored the disease-related death rate. In [6], the authors modified the model proposed in [2] to incorporate the crowding effect in spatially heterogeneous environments. Assume that Ω is a spatial habitat with the smooth boundary $\partial\Omega$ and ν is the outward normal to $\partial\Omega$. Let S_H, I_H, and R_H denote the number of the susceptible, infectious and immune class in the human population; S_V, I_V denote the number of the susceptible, infectious class in the mosquito population. Thus, $N_H := S_H + I_H + R_H$ and $N_V := S_V + I_V$ represent the population sizes of humans and mosquitoes, respectively. The constants μ_b, μ_d, and γ_H stand for the birth, death and recover rate of human species; A and μ_V denote the recruitment and the per capita mortality rate of mosquitoes, respectively. The biting rate b of mosquitoes is the average number of bites per mosquito per day. Mosquitoes bite not only human but also pets. Thus, we assume m is the number of alternative hosts available as blood sources. Let β_H be the transmission probability from infectious mosquitoes to susceptible humans; β_V be the transmission probability from infectious humans to susceptible mosquitoes. Then the dynamics of dengue fever was described by the following system of differential equations [6]:

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http://dx.doi.org/10.1016/j.amc.2014.09.101
0096-3003/

$$\begin{cases} \frac{\partial S_H}{\partial t} = d_H \Delta S_H + \mu_b N_H - c(x) S_H N_H - \frac{\beta_H(x) b(x)}{N_H + m(x)} S_H I_V - \mu_d S_H, \\ \frac{\partial I_H}{\partial t} = d_H \Delta I_H + \frac{\beta_H(x) b(x)}{N_H + m(x)} S_H I_V - c(x) I_H N_H - (\mu_d + \gamma_H) I_H, \\ \frac{\partial R_H}{\partial t} = d_H \Delta R_H + \gamma_H I_H - c(x) R_H N_H - \mu_d R_H, \ x \in \Omega, \ t > 0, \\ \frac{\partial S_V}{\partial t} = d_V \Delta S_V + A(x) - \frac{\beta_V(x) b(x)}{N_H + m(x)} S_V I_H - \mu_V S_V, \\ \frac{\partial I_V}{\partial t} = d_V \Delta I_V + \frac{\beta_V(x) b(x)}{N_H + m(x)} S_V I_H - \mu_V I_V, \\ \frac{\partial S_H}{\partial v} = \frac{\partial I_H}{\partial v} = \frac{\partial R_H}{\partial v} = \frac{\partial S_V}{\partial v} = \frac{\partial I_V}{\partial v} = 0, \ x \in \partial\Omega, \ t > 0. \end{cases} \tag{1}$$

Here, we consider a closed environment in the sense that the fluxes for each of these subpopulations are zero, and hence, we have proposed the Neumann boundary conditions to the Eqs. (1) on the boundary. Furthermore, the crowding effect terms (see, e.g., [5]) in the susceptible class, the infectious class and the immune class in the human population are respectively given by

$$c(x) S_H N_H, \ c(x) I_H N_H \text{ and } c(x) R_H N_H.$$

Assume that the spatial dependent functions $A(x), b(x), c(x), m(x), \beta_H(x), \beta_V(x)$ are positive; Δ is the usual Laplacian operator; $d_H > 0$, $d_V > 0$ denote the diffusion coefficients for humans and mosquitoes, respectively.

It was observed that mosquitoes infected by the dengue disease in one location can move freely in the habitat when this individual becomes infectious. That is, mosquitoes may not stay at the same location in space during the incubation period and the mobility of the individuals in the latent period will result in a delay term with spatial averaging on Ω. We point out that those observations were also discussed in the previous papers [3,8–11,24]. To formulate this process with the latency properly, we introduce the notion of infection age, denoting it by the variable a. The infected mosquito population is divided into two epidemiological categories: latent (E_V) and infectious (I_V) classes. Let $w(x,t,a)$ be the density of the mosquito population with infection age a at time t and location x. We adopt the standard model on describing age structured population with spatial diffusion (see e.g. [12]), we arrive at

$$\frac{\partial w(x,t,a)}{\partial t} + \frac{\partial w(x,t,a)}{\partial a} = d_V \Delta w(x,t,a) - \mu_V w(x,t,a). \tag{2}$$

Let τ be the average incubation period. Then

$$E_V(x,t) = \int_0^\tau w(x,t,a)da, \tag{3}$$

and

$$I_V(x,t) = \int_\tau^\infty w(x,t,a)da. \tag{4}$$

Integrating both sides of (2) from 0 to τ, and from τ to ∞, respectively, we obtain

$$\frac{\partial E_V(x,t)}{\partial t} = d_V \Delta E_V(x,t) - \mu_V E_V(x,t) - w(x,t,\tau) + w(x,t,0), \tag{5}$$

and

$$\frac{\partial I_V(x,t)}{\partial t} = d_V \Delta I_V(x,t) - \mu_V I_V(x,t) - w(x,t,\infty) + w(x,t,\tau). \tag{6}$$

Biologically, we may assume that $w(x,t,\infty) = 0$. Since the recruitment of newly infected mosquitoes ($w(x,t,0)$) is due to the contact of susceptible mosquitoes and infectious humans, it follows that

$$w(x,t,0) = \frac{\beta_V(x) b(x)}{N_H(x,t) + m(x)} S_V(x,t) I_H(x,t). \tag{7}$$

It is easy to see that $N_H := S_H + I_H + R_H$ satisfies the following system equation.

$$\begin{cases} \frac{\partial N_H}{\partial t} = d_H \Delta N_H + (\mu_b - \mu_d) N_H - c(x) N_H^2, & x \in \Omega, \quad t > 0, \\ \frac{\partial N_H}{\partial v} = 0, & x \in \partial\Omega, \quad t > 0. \end{cases} \tag{8}$$

The reaction–diffusion Eq. (8) is a logistic equation and it is known that (8) admits a unique positive steady state $K(x)$ such that (see, e.g. [7, page 506] and [25, Theorem 3.1.5 and the proof of Theorem 3.1.6]):

$$\lim_{t\to\infty} N_H(x,t) = K(x) \text{ uniformly in } x \in \bar{\Omega}, \tag{9}$$

for all solutions with nonnegative and nonzero initial datas provided that $\mu_b > \mu_d$. Biologically, we replace (7) by the following equation