Modelling the transmission dynamics of two-strain Dengue in the presence awareness and vector control☆

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ABSTRACT

In this paper, a mathematical model describing the transmission of two-strain Dengue virus between mosquitoes and humans, incorporating vector control and awareness of susceptible humans, is proposed. By using the next generation matrix method, we obtain the threshold values to identify the existence and stability of three equilibria states, that is, a disease-free state, a state where only one serotype is present and another state where both serotypes coexist. Further, explicit conditions determining the persistence of this disease are also obtained. In addition, we investigate the sensitivity analysis of threshold conditions and the optimal control strategy for this disease. Theoretical results and numerical simulations suggest that the measures of enhancing awareness of the infected and susceptible human self-protection should be taken and the mosquito control measure is necessary in order to prevent the transmission of Dengue virus from mosquitoes to humans.

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1. Introduction

Dengue fever is a vector-borne viral disease transmitted to humans through the bite of an infective female mosquito (for example, Aedes aegypti and Aedes albopictus, which are known as the principal vector of Dengue (Esteva and Vargas, 1999, 2003)). In recent decades, Dengue fever has been made an international public health concern because of its high morbidity and mortality, which happens in most tropical, subtropical and temperate countries. The symptoms of this disease are characterized by high fever, frontal headache, pain behind the eyes, joint pains, nausea, vomiting and other symptoms (Derouich and Boutayeb, 2006). Dengue virus is generally observed clearly in children and older adults, and people usually recover from Dengue fever in three to seven days (Derouich and Boutayeb, 2006). One recent estimate indicates 390 million Dengue infections per year (95% credible interval 284–528 million), of which 96 million (67–136 million) manifest clinically (with any severity of disease) (Bhatt et al., 2013).

With more than one-third of the world's population living in areas at risk for infection of Dengue virus, how to prevent and control the spread of this disease has been one of the hot topic from many points of view, including medical scientists and mathematics (Centers for Disease Control and Prevention). So far, many mathematical models have been proposed to study the dynamic behaviors of Dengue transmission. For example, Esteva and Vargas (1999) proposed an SIR model for the transmission of Dengue fever with variable human population size, and found three threshold parameters which govern the existence of the endemic proportion equilibrium, the increase of the human population size, and the behaviours of the total number of human infective. And in Amaku et al. (2013), considered the impact of vector-control strategies on the human prevalence of Dengue virus. Garba et al. (2008) proposed a deterministic model for the transmission dynamics of Dengue fever, which allows transmission by exposed humans and mosquitoes, and obtained the existence and local asymptotical stability of the disease-free equilibrium for the basic reproduction number is less than unity. Besides, authors also discussed the phenomenon of backward bifurcation. Other examples also can be found in Blayneh et al. (2009); Cai and Li (2010); Cai et al. (2017); Esteva and Vargas (1998, 2000); Rodrigues et al. (2010) and the research in this area is still going on.

It is well known that there are five distinct serotypes of Dengue virus (DEN1, DEN2, DEN3, DEN4 and DEN5) according clinical data collected from the past many years (https://en.wikipedia.org/wiki/Dengue.fever). So, an individual reside in an endemic area can be there are five Dengue viruses infectious during his lifetime, one with each serotype. Epidemiological studies (Stech and Williams, 2008) support the recovery people re-infected with a different serotype face an increased risk of developing Dengue hemorrhagic fever and Dengue shock syndrome. A person recovery from infection by one of the five serotypes will provide lifelong homologous immunity, but this immunity confers only temporary cross-immunity againsts subsequent infection by the four other serotypes. Once infected, a mosquito remains infected for life because of its short life-span, transmitting the virus to susceptible individuals during probing and feeding. Therefore, taking into account Dengue fever pathogen diversity and the transmission mechanism, several investigators have studied the multi-strain Dengue fever transmission models. Examples can be found in Feng and Velasco-Hernández (1997) where Feng et al. proposed an SIR vector transmitted disease with two pathogen strains to simulate the spread of Dengue virus in mosquitoes and between people, to study both the epidemiological trends of the disease and conditions that permit coexistence in competing serotypes. Sriprom et al. (2007) introduced a mathematical model describing the sequential transmission dynamics of Dengue virus infection in the presence of two serotypes of Dengue virus, and obtained the conditions governing the stabilities of disease-free equilibrium, boundary equilibria and interior equilibrium. More research can be found in Esteva and Vargas (2003); Kooi et al. (2013); Mishra and Gakkhar (2014); Nuraini et al. (2007) and the references therein.

As is known to all, there is no specific treatment for Dengue, although there are a number of vaccines under development, including the tetravalent Dengvaxia which has been approved for use in several countries and recommended for introduction in ares with high endemicity (World Health Organization, 2016). Until the efficacy of this vaccine is properly established, however, Dengue fever control strategies are based on taking appropriate preventive measures. The main measures are mosquitoes reduction mechanisms and personal protection against exposure to mosquitoes. Mosquitoes reduction mechanisms entail the elimination of mosquitoes breeding sites (such as cleaning culverts, roadside ditches etc., disposing of solid waste properly and removing artificial man-made habitats) and adulticiding (killing of adult mosquitoes by spraying insecticides) (Mishra and Gakkhar, 2014; Yang and Ferreira, 2008). On the other hand, personal protection is based on preventing mosquitoes from biting human (by using window screens, long-sleeved clothes, insecticide treated materials, coils and vaporizers).

Motivated by the above discussion, this paper is aimed at describes more effectively control strategies to control and eliminate Dengue virus. For all this, we propose a non-linear multi-strain model to describe the dynamics of primary and secondary infection of Dengue fever, where two control strategies, susceptible human awareness and vector control are introduced to prevent the spread of Dengue virus. The paper is structured as follows. In Section 2, a Dengue transmission model with two serotypes viruses and control strategies is introduced. In Section 3, we calculate the basic reproduction number and analyze the stability of boundary equilibria for this model. The existence of the interior equilibrium and the persistence of this disease are given in Section 4. The sensitivity of threshold conditions, and the existence and uniqueness of the optimal control strategies are derived in Section 5 and Section 6, respectively. In Section 7, by carrying out some numerical simulations, we try to confirm the main theoretical results, to illustrate some key factors to prevent and control

the spread of Dengue fever. Some concluding remarks are present in the last section.

2. Model formulation

In this section, we present a mathematical model to examine the transmission dynamics of Dengue virus between mosquitoes and humans. This multi-strain model considers the presence of two serotypes namely, serotype-1 and serotype-2 where 1 and 2 can be DEN1, DEN2, DEN3, DEN4 or DEN5. The populations involved in the transmission are human and mosquitoes, and $N(t)$ and $M(t)$ denote the total human and mosquitoes population size at time t, respectively. Consider the transmission mechanism of Dengue fever, we divide the population into eight compartments: susceptible humans denoted $S(t)$; primary infective humans with serotype-i denoted $I_i(t)$; recovered from serotype-i (and immune serotype-i, susceptible to serotype-j) humans, $R_i(t)$; secondary infective humans with serotype-j, $Y_j(t)$; recovered from secondary infection of either of the serotypes, and immune to both serotypes, $R(t)$; susceptible mosquitoes denoted $U(t)$; infected mosquitoes with serotype-i, $V_i(t)$, where i, $j = 1, 2$ and $i \neq j$.

Based on the transmission rules of Dengue virus, a two-strains Dengue model with awareness and vector control is given by the following nonlinear differential equations

$$\begin{cases} \frac{dS(t)}{dt} = \omega - S(t)\sum_{i=1}^{2}\alpha_i V_i(t) - \mu S(t) - mS(t), \\ \frac{dI_i(t)}{dt} = \alpha_i S(t)V_i(t) - \gamma_i I_i(t) - \mu I_i(t), \\ \frac{dR_i(t)}{dt} = \gamma_i I_i(t) - \sigma_j \alpha_j V_j(t)R_i(t) - \mu R_i(t), \quad i \neq j, \\ \frac{dY_i(t)}{dt} = \sigma_i \alpha_i V_i(t)R_j(t) - (\gamma_i + d + \mu)Y_i(t), \quad i \neq j, \\ \frac{dR(t)}{dt} = \sum_{i=1}^{2}\gamma_i Y_i(t) - \mu R(t) + mS(t), \\ \frac{dU(t)}{dt} = \omega_1 - U(t)\sum_{i=1}^{2}\beta_i(I_i(t)+Y_i(t)) - cU(t) - \mu_1 U(t), \\ \frac{dV_i(t)}{dt} = \beta_i(I_i(t)+Y_i(t))U(t) - cV_i(t) - \mu_i V_i(t). \end{cases} \quad (1)$$

Here, the susceptibility index to serotype-i σ_i is a positive real number that may mimic either cross-immunity ($0 < \sigma_i < 1$) or increased susceptibility ($\sigma_i > 1$) by Antibody Dependent Enhancement (ADE), where the pre-existing antibodies to previous Dengue infection cannot neutralize but rather enhance the new infection. There is no definite argument about the value of parameters σ_i in medicine and mathematics. In terms of $\sigma_i > 1$, there are many works have been done by some scholars, see Feng and Velasco-Hernández (1997); Kooi et al. (2013, 2014) and references therein. Throughout this paper, we just investigate the case of $0 < \sigma_i < 1$. The meanings and possible values of other parameters of model (1) are given in Table 1.

From the above model, we obtain $N(t) = S(t) + I_1(t) + R_1(t) + Y_2(t) + I_2(t) + R_2(t) + Y_1(t) + R(t)$, $M(t) = U(t) + V_1(t) + V_2(t)$, and

$$\frac{dN(t)}{dt} = \omega - \mu N(t) - d(Y_1(t) + Y_2(t)) \leq \omega - \mu N(t),$$

$$\frac{dM(t)}{dt} = \omega_1 - (c + \mu_1)M(t).$$

It follows that $M(t) \to \omega_1/(c + \mu_1)$, $N(t) \leq \omega/\mu$ as $t \to \infty$. Therefore, we only in the following areas

$$\begin{aligned} \Omega = \{ & (S(t), I_1(t), I_2(t), R_1(t), R_2(t), Y_1(t), Y_2(t), R(t), U(t), \\ & V_1(t), V_2(t)) \in \mathbb{R}_+^{11} \mid 0 < S(t) + I_1(t) + R_1(t) \\ & + Y_2(t) + I_2(t) + R_2(t) + Y_1(t) + R(t) \leq \omega/\mu, 0 < U(t) \\ & + V_1(t) + V_2(t) \leq \omega_1/(c + \mu_1) \} \end{aligned}$$

discuss the dynamic behavior of model (1), where $\mathbb{R}_+^{11} :=$ $\{(x_1, x_2, \cdots, x_{11}) \mid x_i \geq 0, i = 1, 2, \cdots, 11\}$.