Applied Mathematics and Computation 246 (2014) 159–167

Contents lists available at ScienceDirect

Applied Mathematics and Computation

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

The effects of awareness and vector control on two strains dengue dynamics

Arti Mishra *, Sunita Gakkhar

Department of Mathematics, Indian Institute of Technology, Roorkee, Uttarakhand 247667, India

ARTICLE INFO

Keywords:
Epidemic
Basic reproduction number
Awareness
Stability
Vector control

ABSTRACT

The aim of this paper is to study the effects of awareness and mosquito control on dengue epidemic. A non-linear host–vector model has been developed to study the dynamics of primary and secondary infection in the presence of two serotypes of dengue virus. The existence and local stability of equilibrium points have been discussed. The global stability of disease-free equilibrium point has been established. The thresholds for both the serotypes have been computed. The mosquito control and awareness parameters decrease the threshold and thereby enhancing the stability of disease-free state.

1. Introduction

Dengue fever has caught the attention of all over the world and has become the disease of important international health concern. According to the one estimate of WHO report, 2.5 billion of people are living in dengue risk area and 50 to 100 million cases of dengue occur every year [1]. During 1779–1780, the first dengue epidemic was reported from Africa, Asia and North America simultaneously. This shows the presence of mosquitoes and dengue virus for more than 200 years [2]. Dengue fever is a mosquito-borne infectious disease. The mosquitoes live mostly in the tropical and subtropical regions of the world. The *Aedes aegypti* and *Aedes albopictus* female mosquitoes are the prominent carriers of dengue virus of *Flaviviridae* family. When susceptible mosquito bites an infected person, it gets infected. The infected mosquitoes transfer infection on biting susceptible persons. The symptoms of the disease is characterized by high fever, frontal headache, pain behind the eyes, joint pains, nausea, vomiting etc. [3,4].

Dengue virus is having four serotypes denoted by DEN I, DEN II, DEN III and DEN IV. A person living in an endemic area can have as many as four dengue infections during his lifetime, one with each serotype. Infection by any dengue serotype produces lifelong immunity to the recovered individual with respect to the particular, but only temporal cross immunity to the other serotypes. The mosquitoes remain infected through its life time. The spectrum of dengue disease ranges from dengue fever (DF) to more severe dengue hemorrhagic fever (DHF) and dengue shock syndrome (DSS). The people usually recover from DF in three to seven days. Only those who experience secondary infection with an heterologous dengue serotype present DHF/DSS. In general children and older adults usually suffer from dengue fever. Most commonly children under the age of 15 and in some cases senior adults are the victims of DHF/DSS [2,4].

Some investigators have modeled the dynamics of single serotype of dengue virus [5,6]. They have analyzed the model for stability of disease-free and endemic states. Different approaches have been used for the global stability of endemic state. To study the effects of secondary infection, some investigators have incorporated the vector-host dynamics in presence of

* Corresponding author.
E-mail addresses: mishraarti21@gmail.com (A. Mishra), sungkfma@gmail.com (S. Gakkhar).

http://dx.doi.org/10.1016/j.amc.2014.07.115
0096-3003/

multiple dengue strain [7,8]. In particular, Esteva and Vergas [7] have obtained the threshold values and the conditions for the coexistence of two serotypes of dengue virus. Further, Nuraini et al. have modified Esteva and Vergas model for two serotype by including another compartment for severely infected DHF individuals [8]. They are able to predict the severity of DHF. Supriatna et al. [9] have discussed a mathematical model on dengue disease for control by vaccination for single as well as multi-strain model.

In absence of any effective single vaccine which works for all four serotypes of dengue virus [10], the awareness through health programs and mosquitoes control through insecticides are the possible ways to prevent human population from dengue infection [10,11]. The impact of awareness on disease dynamics has been discussed by Gakkhar and Chavda [12]. They have developed a host–vector model in presence of single serotype incorporating human awareness towards disease. The awareness is able to reduce the threshold and enhance the stability of disease-free state. However, the presence of multiple strains of dengue virus in the population may lead to more severe dengue infections like DHF/DSS. To combat the severity of dengue infection in presence of multiple strains, a two pronged strategy comprising of vector control and human awareness about the disease may be employed.

In this paper, a multi-strain dynamic model is proposed for transmission and control of dengue epidemic. Two control strategies namely, vector control and human awareness are being used simultaneously to control the disease. In the next section, formulation of the model is presented. In section three, the positivity and boundedness of the solution has been proved. Further, in section four the basic reproduction number has been obtained. In section five and six, the equilibrium points and their stability have been analyzed. Again, numerical simulation have been carried out to illustrate the analytical findings and further explore the dynamics of the non-linear model. In the last section results have been concluded.

2. The mathematical model

The multi-strain model considers the presence of two serotypes namely, serotype-K and serotype-J where K and J can be from I, II, III or IV. In particular let us consider K = I and J = II. Consider s be the number of susceptible hosts who are susceptible to both serotype-I and serotype-II. Further, i_1, r_1 and i_2, r_2 be the number of primary infected and recovered host population with serotype-I and serotype-II dengue virus respectively. Let i_{21} and i_{12} represent the secondary infected hosts after being recovered from serotype-II and serotype-I respectively. After secondary infection, let r be the number of finally recovered individuals. Let $\bar{n}(t)$ be the total host (human) population at any time t such that $\bar{n}(t) = s(t) + i_1(t) + r_1(t) + i_2(t) + i_{12} + i_{21} + r_2(t) + r(t)$. Natural death is considered in all the classes while the disease-induced death is considered only in secondary infection class. Similarly for mosquitoes (vector), $\bar{m}(t)$ be the total vector population such that $\bar{m}(t) = u(t) + v_1(t) + v_2(t)$. Here u be the susceptible vector population, v_1 and v_2 be the infected vectors with serotype-I and serotype-II respectively. The constant recruitment rates ω and ω_1 are assumed for host and vector population respectively. Mosquitoes are getting infection from primary infection classes only. Due to Disease induced awareness, the secondary infected hosts take extra care/precautions to avoid mosquito bites. Accordingly, mosquitoes are not getting infection from secondary infected hosts. These assumptions led to the following host vector dynamics:

$$\frac{ds}{dt} = \omega - \alpha_1 s v_1 - \alpha_2 s v_2 - \mu s - ms \tag{2.1}$$

$$\frac{di_1}{dt} = \alpha_1 s v_1 - \gamma_1 i_1 - \mu i_1 \tag{2.2}$$

$$\frac{dr_1}{dt} = \gamma_1 i_1 - \beta_1 r_1 v_2 - \mu r_1 \tag{2.3}$$

$$\frac{di_{12}}{dt} = \beta_1 r_1 v_2 - \gamma_1 i_{12} - d_1 i_{12} - \mu i_{12} \tag{2.4}$$

$$\frac{di_2}{dt} = \alpha_2 s v_2 - \gamma_2 i_2 - \mu i_2 \tag{2.5}$$

$$\frac{dr_2}{dt} = \gamma_2 i_2 - \beta_2 r_2 v_1 - \mu r_2 \tag{2.6}$$

$$\frac{di_{21}}{dt} = \beta_2 r_2 v_1 - \gamma_2 i_{21} - d_1 i_{21} - \mu i_{21} \tag{2.7}$$

$$\frac{dr}{dt} = \gamma_1 i_{12} + \gamma_2 i_{21} - \mu r + ms \tag{2.8}$$

$$\frac{du}{dt} = \omega_1 - \sigma_1 i_1 u - \sigma_2 i_2 u - cu - \mu_1 u \tag{2.9}$$

$$\frac{dv_1}{dt} = \sigma_1 i_1 u - \mu_1 v_1 - c v_1 \tag{2.10}$$

$$\frac{dv_2}{dt} = \sigma_2 i_2 u - \mu_1 v_2 - c v_2 \tag{2.11}$$

All model parameters are defined in the Table 1 and are assumed to be positive.