Reaction-Diffusion Generic Model for Mosquito-Borne Diseases

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***Abstract*—Diseases which are transmitted by vector mosquitoes are major health problems in many countries. Although many mathematical models for diseases had been formulated, they are customized. As these diseases are spread by a common vector, similarities in the disease transmission are notable hence it will be beneficial to construct a general model which encompasses the epidemiology aspects and transmission of mosquito-borne diseases. In this paper, a SI (Susceptible-Infectious) generic model for mosquito borne diseases is formulated. The model is made up of partial differential reaction-diffusion equations which incorporate both the human and mosquito populations. Numerical simulation of this model is presented.**

Keywords—diffusion; mosquito-borne diseases; spatial; transmission model; generic

I. INTRODUCTION

Mosquito-borne diseases are infectious diseases that are transmitted from one human to another by mosquitoes. Examples of such diseases are dengue, malaria, yellow fever , West Nile virus and chikugunya. More than one million people die from mosquito-borne diseases each year. In 2010, there were 46171 reported cases of dengue fever (DF) and dengue hemorrhagic fever (DHF), and 134 deaths in Malaysia [1]. Many mathematical models had been constructed according to the epidemiology and factors contributing to the transmission of infectious diseases. To date, theoretical models which study mosquito-borne diseases had been published.

The study using mathematical modeling originated from the works of Ross [2] on malaria. MacDonald did some modification to Ross' model and included the latent period [3]. Since then interests and concern had been pouring in on mathematical modelling to comprehend the transmission and to manage the spread of these diseases. Many compartmental models which consist of ordinary differential equations had been constructed ([2], [3], [4], [5], [6], [7] and [8]). A review on mosquito-borne transmission mathematical models by Reiner et al. [9] mentioned that one of the modelling deficiencies which deserves more attention is spatial heterogeneity. Although not as many as its temporal counterpart, some studies had been done on the spatial spread of diseases through gravity model [10], geographic information system [11], agent-based model [12], cellular automata[13], multi-patch ordinary differential equations ([14] and [15]) and reaction diffusion partial differential equations ([16], [17] and [18]). Initially, a reaction diffusion model was used to study the spread of rabies among wolves [19]. Eventually reaction diffusion models were used to study the transmission of other ailments such as dengue [18], West Nile Virus [21] and malaria ([16] and [20]). In real life, the environment where population stays is different and populations are mobile therefore it is vital to acknowledge these aspects and take into account the spatial component. Considering that environment is spatially continuous and mobility of population is depicted by random diffusion, so giving birth to the use of reaction diffusion partial differential equations for infectious diseases. However, very little is done on this [17].

Disease transmission of mosquito-borne diseases has a mutual ground, that is, humans get infected after bitten by an infectious vector mosquito. Certain clinical aspects of these diseases might differ after humans or mosquitoes get infected, however, the transmission of these diseases remains the same. An infectious human will transfer the disease to a susceptible mosquito when the mosquito bites the human for a blood meal. After which, this mosquito will become infected and go on to infect a susceptible human during another blood meal. This susceptible human will contract the disease and become infectious. Thus, the cycle continues.

Despite the fact that many mathematical models had been formulated since Ross model, majority of these models are disease-specific. They are tailor-made to suit the particular disease. As there are different mosquito-borne diseases, it will be advantageous to create a general model encompassing the common dissemination and factors of such diseases. Integrating spatial and temporal components will enable a greater understanding of the spread of these diseases. A model which can be used to simulate the spread of different mosquito-borne diseases can assist in the creation of an appropriate control measure system. The existence of one system for multiple diseases will be much easier to handle for the vector control unit and health authorities. In addition, this also reduces the usage of multiple models for multiple diseases which can be time and cost consuming.

The aim of this paper is to construct a generic mosquito-borne diseases model which incorporates diffusive movement of humans and mosquitoes. In Section II the formulation of the

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model is presented. Section III shows the numerical analysis of the model. Finally some discussion and conclusion can be found in Section IV.

II. MODEL FORMULATION

After studying mosquito-borne or vector-borne diseases compartmental models, for example [8, 14, 15, 16, 18, 20, 22, 23] there were some notable similarities. Common compartments for host and vector populations were Susceptible and Infectious. The common terms used were birth rate for populations, death rate, force of infection and recovery rate. We would like to propose a generic model for mosquito-borne infectious diseases which combines spatial aspect. Considering the few work on spatial temporal disease modeling [8, 16, 17, 18, 19, 20 and 21] the common terms used for spatial spread were diffusion coefficients and certain location dependent parameters.

Thus, taking all these into account, we are proposing to provide a generic model which incorporates both spatial and temporal factors for both host human and vector mosquito populations which is based on the model in [20]. The human population is divided into Susceptible (S_H) and Infectious (I_H). It is assumed that the density of total human population, $N_H = S_H + I_H$, follows the logistic population growth law thus $\frac{\partial N_H(t,x)}{\partial t} = D_H \frac{\partial^2 N_H(t,x)}{\partial x^2} + B_H N_H(t,x)\left[1 - \frac{N_H(t,x)}{K(x)}\right]$. D_H is the diffusion coefficient for humans, $K(x)$ the carrying capacity and B_H is the natural growth rate. As the equation is subject to Neumann boundary, biologically we can assume that $N_H(t,x) = H(x), \forall t > 0$, thus the total human density stabilizes at $H(x)$ [20]. The mosquito population is also divided into two compartments, namely Susceptible (S_M) and Infectious (I_M). The density of total mosquito population is $N_M = S_M + I_M$.

There are a few differences between the generic model and the model in [20]. The first difference is that, in this model, there is a Susceptible human (S_H) compartment. Infectious humans (I_H) are considered to recover from the disease and become susceptible once more. In addition, it is assumed that the Infectious humans and mosquitoes first contracted the illness before the incubation period at the same location, as some of these mosquito-borne diseases have incubation period where else the model in [20] considered nonlocal cases. As mosquito is the main vector of these diseases, the force of transfer of infection is similar for most mosquito-borne diseases. The rate that Susceptible human (S_H) gets infected at time t and location x is $c\beta \frac{I_M(t,x)}{H(x)}$ while the rate that Susceptible mosquito (S_M) gets infected is $b\beta \frac{I_H(t,x)}{H(x)}$. However in [20] biting rate of mosquitoes, $\beta(x)$ is habitat dependent.

Based on the assumptions and the compartmental model in Figure 1, the model is as follows:

$$\frac{\partial S_H(t,x)}{\partial t} = D_H \frac{\partial^2 S_H(t,x)}{\partial x^2} + \gamma - \frac{c\beta}{H(x)} S_H(t,x) I_M(t,x) + r I_H - d_H S_H(t,x) \quad (1)$$

$$\frac{\partial I_H(t,x)}{\partial t} = D_H \frac{\partial^2 I_H(t,x)}{\partial x^2} + \frac{c\beta}{H(x)} S_H(t-\tau_H,x) I_M(t-\tau_H,x) - (d_H + r) I_H(t,x) \quad (2)$$

$$\frac{\partial S_M(t,x)}{\partial t} = D_M \frac{\partial^2 S_M(t,x)}{\partial x^2} + \Lambda - \frac{b\beta}{H(x)} S_M(t,x) I_H(t,x) - d_M S_M(t,x) \quad (3)$$

$$\frac{\partial I_M(t,x)}{\partial t} = D_M \frac{\partial^2 I_M(t,x)}{\partial x^2} - d_M I_M(t,x) + \frac{b\beta}{H(x)} S_M(t-\tau_M,x) I_H(t-\tau_H,x) \quad (4)$$

The Neumann boundary condition on domain Ω which is the spatial habitat with boundary $\partial\Omega$ where **n** denotes the exterior normal to $\partial\Omega$:

$$\frac{\partial S_H}{\partial \mathrm{n}} = \frac{\partial I_H}{\partial \mathrm{n}} = \frac{\partial S_M}{\partial \mathrm{n}} = \frac{\partial I_M}{\partial \mathrm{n}} = 0, t > 0, x \in \partial\Omega \quad (5)$$

The parameters for the system of partial differential equations above are as below:

D_H : diffusion rate for humans
D_M : diffusion rate for mosquitoes
γ : human recruitment rate
c : transmission probability per bite from $I_M \to S_H$
β : biting rate of mosquitoes on humans
d_H : human death rate
r : recovery rate
Λ : mosquito recruitment rate
b : transmission probability per bite from $I_H \to S_M$
d_M : mosquito death rate
τ_H : incubation period in humans
τ_M : incubation period in mosquitoes

These parameters are assumed to be non-negative.

Using the similar method as in Wang and Zhao [18], the explicit basic reproduction number which we procured is

$$R_0 = \sqrt{\frac{c\beta\gamma}{Hd_M d_H} \times \frac{b\beta\Lambda}{Hd_M(r + d_H)}}. \quad (6)$$

The basic reproduction number is the threshold value whereupon $R_0 > 1$, the disease prevails in the population and when $R_0 < 1$, the disease dies out.