Ecological Modelling 221 (2010) 2899–2908

Contents lists available at ScienceDirect

Ecological Modelling

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

A dengue model with a dynamic *Aedes albopictus* vector population

Richard A. Erickson[a,b,*], Steven M. Presley[a,b], Linda J.S. Allen[b,c], Kevin R. Long[c], Stephen B. Cox[a,b,*]

[a] Department of Environmental Toxicology, Texas Tech University, Box 41163, Lubbock, TX, USA
[b] The Institute of Environmental and Human Health, Texas Tech University, Box 41163, Lubbock, TX, USA
[c] Department of Mathematics and Statistics, Texas Tech University, Box 41042, Lubbock, TX, USA

ARTICLE INFO

Article history:
Received 2 April 2010
Received in revised form 9 August 2010
Accepted 23 August 2010
Available online 24 September 2010

Keywords:
Disease model
Epidemiology
Medical entomology
Reemerging disease
SEIR/SEI model
Vector ecology

ABSTRACT

Dengue is the most commonly transmitted arthropod-borne virus in the world with 50–100 million cases annually. Within the United States, dengue is a reemerging infectious disease of concern and near the U.S.–Mexico border, up to 75% of the population of some Texas communities have had exposure to dengue. Understanding dengue disease dynamics is critical to predicting and understanding the disease. These dynamics depend upon diverse factors such as socioeconomic conditions, the local environment, and vector biology. Here, we study dengue by examining the role of temperature in driving vector dynamics. To do this, we created a Susceptible, Exposed, Infectious, Recovered host and Susceptible, Exposed, Infectious vector (SEIR/SEI) model. The SEIR/SEI model was then used in conjunction with an *Aedes albopictus* population model to create a vector-based disease model. The vector-based diseased model was then forced by temperature.

Approved for public release; distribution is unlimited.

1. Introduction

Currently, dengue threatens up to 40% of the world's population and there may be 50–100 million infections annually (World Health Organization, 2002). Dengue is also the most commonly transmitted arthropod-borne virus in the world and is viewed by some as the most important arthropod-borne viral threat to public health (Guha-Sapir and Schimmer, 2005; Ludlam et al., 2006). This disease has been known since ancient times and has occurred within the continental United States since colonial times. It was eradicated from the New World because of extensive, post-World War II mosquito control programs. However, when these programs ended, dengue reemerged and has continued to expanded its range until the present (Gubler, 1998).

Other than possibly Hawaii, which had a large dengue outbreak during the early 2000s, Texas is the U.S. state most impacted by dengue. This is because dengue is spilling over to the United States from Mexico. During the first 11 months of 2008, there were 25,604 suspected cases of dengue in the state of Tamaulipas, which is a Mexican state adjacent to Texas (Clark, 2008). Dengue is present within Texas and in some counties along the U.S.–Mexico border, up to 78% of the population has had prior exposure to dengue based upon serological evidence (95% confidence interval 74–83%; Ramos et al., 2008). In the long term, the range and number of dengue cases within the continental United States will likely increase as climate change creates more favorable conditions for the dengue virus (Hales et al., 2002).

The term dengue covers two different manifestations of the disease: classic dengue fever and dengue hemorrhagic fever/dengue shock syndrome. These manifestations are caused by four different viral serotypes, Dengue I–IV (Gubler, 1998). The most common form of dengue, classic dengue fever or breakbone fever, is often asymptotic or similar to the flu but can sometimes have painful headaches, muscle pains, and joint pains. More severe cases can progress to dengue hemorrhagic fever and dengue shock syndrome (Kalayanarooj et al., 1997). Both of these diseases can have mortality rates as high as 20% (Gubler, 1998).

In urban areas and the New World, dengue only has one primary vector, *Aedes aegypti*, and one secondary vector, *Ae. albopictus*. However, in dengue's native range, it is vectored by several *Ae.* spp. (Gubler, 1998). Both *Ae. albopictus* and *Ae. aegypti* were introduced to the New World. *Aedes aegypti*, commonly known as the Yellow Fever mosquito, is native to Africa and was introduced by the colonial slave trade (Lounibos, 2002). *Aedes albopictus* is commonly known as the Asian Tiger mosquito. This species is native to Asia and was introduced to, and subsequently transported within, the United States by the used tire trade in 1980s (Hawley et al., 1987; Gratz, 2004).

Historically, *Ae. aegypti* has been viewed as the primary vector for dengue because it is a more competent vector than *Ae. albopic*-

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* Corresponding authors at: Department of Environmental Toxicology, Texas Tech University, Box 41163, Lubbock, TX, USA. Tel.: +1 806 885 4567; fax: +1 806 885 4577.
E-mail addresses: richard.erickson@ttu.edu, raerickson@gmail.com (R.A. Erickson), stephen.cox@ttu.edu (S.B. Cox).

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doi:10.1016/j.ecolmodel.2010.08.036

Table 1
Dengue outbreaks caused by *Ae. albopictus* when *Ae. aegypti* was not present or *Ae. albopictus* was confirmed to be a dengue vector. The table is a summary of data presented by Gratz (2004).

Year(s)	Outbreak location
1852, 1856, and 1903	Hawaii
1942–1944	Nagasaki, Japan
July 1943	Honolulu, Hawaii
1952	India
1954	Manila, Philippines
1960	Bangkok, Thailand
1970s	Malaysia
1973–1974	Burma
1976-1977	Seychelles
1978	Inland regions of China
1990s to 2000s	India
2003	Brazil

tus and is more commonly found in urban areas (Gubler, 1998). However, *Ae. albopictus* has been confirmed as the primary dengue vector for several outbreaks by either the absence of *Ae. aegypti* or the prevalence of dengue found in *Ae. albopictus* compared to *Ae. aegypti* (Table 1; Gratz, 2004). Additionally, the risks posed by *Ae. albopictus* compared to those posed by *Ae. aegypti* should not be underestimated for several reasons. For example, compared to *Ae. aegypti*, *Ae. albopictus* has a larger range, is more difficult to control, and is considered more of a biting pest within the United States (Estrada-Franco and Craig, 1995). Also, even though the two species have different niches, *Ae. albopictus* often outcompetes *Ae. aegypti* at many locations within the United States when their ranges overlap (Lounibos et al., 2001).

Because of dengue's large global impact, many mathematical models exist that describe its disease dynamics. Some are spatial (e.g., Morrison et al., 1998; Cummings et al., 2004; Favier et al., 2005; Kolivras, 2006; Tran and Raffy, 2006; Almeida et al., 2007; Brunkard et al., 2007). Others are non-spatial Susceptible, Infectious, Recovered (SIR) or Susceptible, Exposed, Infectious, Recovered (SEIR) host models (e.g., Feng and Velasco-Hernandez, 1997; Esteva and Vargas, 1999; Esteva and Matias, 2001; Derouich et al., 2003; Derouich and Boutayeb, 2006). There are models that examine force of infection (e.g., Marques et al., 1994; Esteva and Matias, 2001; Favier et al., 2006; Chowell et al., 2007). Others models describe transmission and circulation cycles (e.g., Ferguson et al., 1999; Coutiho et al., 2006; Wearing and Rohani, 2006; Nago and Koelle, 2007; Thammapalo et al., 2008). There are also models that study the global impact of dengue (e.g., Patz et al., 1998; Jetten and Focks, 1997; Epstein, 1998; Hales et al., 2002).

However, few dengue models explicitly consider vector population dynamics. Instead, many models only relate environmental factors to the disease distribution with a statistical or pattern model. Other models include vector populations, but assume constant population sizes. This may be appropriate for the tropics, but would not be appropriate for temperate regions with seasonal temperatures. A notable exception to this trend is the Dengue Simulation Model (DENSiM) that incorporates a Container Inhabiting Mosquito Simulation Model (CIMSiM; Focks et al., 1993a,b, 1995). Both DENSiM and CIMSiM were designed and parameterized for *Ae. aegpyti*. Additionally, both DENSiM and CIMSiM are parameter intensive. For example, CIMSiM required over a months worth of field observations to validate the model in Australia (Williams et al., 2008).

To better understand the risk and dynamics of dengue transmitted by *Ae. albopictus*, we adapted an existing dengue disease model (Derouich et al., 2003; Derouich and Boutayeb, 2006) and incorporated it into a previously described *Ae. albopictus* population model (Erickson et al., 2010). Our population model was validated against mosquito data from Lubbock, TX. We also examined possible outbreaks of dengue in Lubbock, TX. We chose Lubbock because of the availability of data from a long-term mosquito monitoring program, and its relative proximity to the Texas–Mexico border. Even though dengue is currently not found in Lubbock, TX, an outbreak could occur if it was introduced. For example, during the 1700s, Philadelphia and other northern port cities had summer outbreaks of dengue because ships brought dengue infected mosquitoes (Gubler, 1998). Last, climate change could increase the range of the dengue virus to include Lubbock.

2. Methods

To create our dengue disease model, we modified an existing SIR/SI model by incorporating an "Exposed" stage into both the vector and host equations (Model 1). The new SEIR/SEI model was then modified by incorporating the *Ae. albopictus* model that is presented within Erickson et al. (2010). Initially, the model was evaluated with a constant temperature (Model 2). Next, temperature was allowed to vary (Model 3).

2.1. Model 1

An existing SIR host and SI vector model for dengue was adapted by adding an exposed stage (Fig. 1; Derouich et al., 2003; Derouich and Boutayeb, 2006). An exposed stage was added because dengue requires both an extrinsic and intrinsic incubation period before it can be transmitted (Heymann, 2008). The SEIR host and SEI vector model is a system of ordinary differential equations (Eqs. (1)–(7)), where the total vector population is constant $V_s+V_e+V_i=V_t$ and the total human or host population $H_s+H_e+H_i+H_r=H_t$ is subject to disease-related mortality. The vector and human populations are closed to immigration and emigration. The SEIR human model is

$$\frac{dH_s}{dt}=\lambda H_t-H_s\left(\frac{cV_i}{H_t}+\mu_h\right) \tag{1}$$

$$\frac{dH_e}{dt}=H_s\frac{cV_i}{H_n}-H_e(\tau_{exh}+\mu_h) \tag{2}$$

$$\frac{dH_i}{dt}=H_e\tau_{exh}-H_i(\tau_{ih}+\alpha+\mu_h) \tag{3}$$

$$\frac{dH_r}{dt}=H_i\tau_{ih}-\mu_h H_r. \tag{4}$$

and the SEI vector model is

$$\frac{dV_s}{dt}=\mu_a V_t-V_s\left(\frac{cH_i}{H_t}+\mu_a\right) \tag{5}$$

$$\frac{dV_e}{dt}=V_s\frac{cH_i}{H_t}-V_e(\tau_{exv}+\mu_a) \tag{6}$$

$$\frac{dV_i}{dt}=V_e\tau_{exv}-\mu_a V_i. \tag{7}$$

The number of bites per mosquito per time (contact rate) multiplied by the per-bite vector to host transmission probability is C and is equal to the transmission probability from host to vector. The disease-free equilibrium for this system is $H_s=\lambda/\mu_h$, $V_s=V_t$ with all other state variables equal to zero.

Model parameters came from literature sources and government documents (Table 2). The daily total human growth rate was calculated from US Census data from 2000 to 2006 for Lubbock, TX ($\lambda=2.244\times10^{-5}$). The background human mortality was calculated by inverting the approximate US life expectancy ($\mu_h=1/28,000$ days; American FactFinder, http://factfinder.census.gov/). The contact rate was calculated by multiplying the probability of an infectious *Ae. albopictus* biting a human by the probability that the bite transmitted dengue ($c=0.3\times0.4=0.12$; Hawley, 1988; Vazeille