



## **MATHEMATICAL STUDY OF BITING RATES OF MOSQUITOES IN TRANSMISSION OF DENGUE DISEASE**

\*G. R. Phaijoo, D. B. Gurung

Department of Natural Sciences (Mathematics), School of Science  
Kathmandu University, Kavre, Nepal

\*Corresponding author's email: gangaram@ku.edu.np

*Received 11 December, 2015; Revised 28 December, 2015*

### **ABSTRACT**

Dengue is an infectious disease affecting tropical and subtropical regions worldwide. It is transmitted to person through the biting of infectious aedes mosquitoes. In the paper, SIR model is used to describe the spread of dengue disease due to different biting rates of mosquitoes. The host (human) population is divided into three compartments: susceptible, infected and recovered. The mosquito population is divided into two compartments: susceptible and infected. Associated basic reproduction number is calculated and a sensitivity analysis is performed to determine the relative importance of model parameters to the disease transmission.

**Keywords:** Dengue Fever, SIR Model, Biting Rates, Basic Reproduction Number, Sensitivity Analysis

### **INTRODUCTION**

Dengue is an infectious disease spreading in tropical and subtropical countries. It is a vector borne disease transmitted by the female aedes mosquitoes. Four serotypes of the dengue viruses DEN 1, DEN 2, DEN 3 and DEN 4 cause the dengue fever. Nowadays, dengue fever is endemic in more than hundred countries and it is threatening about 2.5 billion people. During late-monsoon and pre-monsoon the disease occurs in epidemic form as an outcome of increase in breeding places and mosquitoes' population.

In recent years, the number of dengue cases has been increasing dramatically and has become a greater threat than it has been in the past. Although dengue virus infections have been found in our neighbouring country India over a long period of time, there was no documented dengue case in Nepal prior to 2004 [1]. Nowadays, the disease is considered as an emerging disease in Nepal.

To control the dengue disease effectively, one should understand the dynamics of the disease transmission and take all of the corresponding details into account. Kermack and McKendrick contributed on the development of the mathematical theory of epidemics [2]. The authors considered three compartments: Susceptible, Infectious and Removal for the mathematical formulation of the model. Esteva and Vargas used SIR model to study transmission dynamics of the dengue disease [3]. Different mathematical models are proposed to study different aspects of the dengue disease [4 – 9].



### MODEL FORMULATION

To study the transmission process of the dengue fever, host population is divided into three compartments: susceptible, infective and recovered. People who are healthy and may potentially get infected with dengue virus are considered to be in **Susceptible** compartment, people who are infected with dengue and able to transmit the disease are considered to be in **Infective** compartment and people who have recovered from dengue disease are considered to be in **Recovered** compartment.

The population of mosquitoes is divided into two compartments only; mosquitoes that may potentially become infected with dengue virus (**Susceptibles**) and mosquitoes that are infected with dengue (**Infectives**). The recovered class in the mosquito population is not considered as the infection period of the mosquitoes ends with their death.

For the formulation of model equations, the host population divided are denoted by  $h_s$ (susceptible),  $h_i$ (infective) and  $h_r$ (recovered). The mosquito population divided are denoted by  $m_s$ (susceptible) and  $m_i$ (infective).

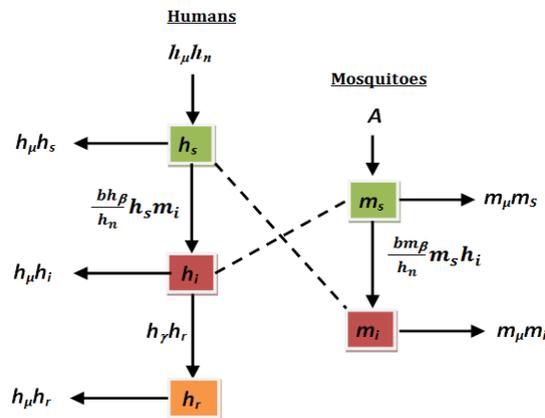


Figure 1: Flow chart of SIR model of dengue disease

The systems of differential equations which describe the dynamics of the dengue disease [3] are:

For human population:

$$\left. \begin{aligned} \frac{dh_s}{dt} &= h_\mu h_n - \frac{h_\beta b}{h_n} h_s m_i - h_\mu h_s, \\ \frac{dh_i}{dt} &= \frac{h_\beta b}{h_n} h_s m_i - (h_\mu + h_\gamma) h_i, \\ \frac{dh_r}{dt} &= h_\gamma h_i - h_\mu h_r \end{aligned} \right\} \quad (1)$$



For mosquito population:

$$\left. \begin{aligned} \frac{dm_s}{dt} &= A - \frac{m_\beta b}{h_n} h_i m_s - m_\mu m_s, \\ \frac{dm_i}{dt} &= \frac{m_\beta b}{h_n} h_i m_s - m_\mu m_i \end{aligned} \right\} \quad (2)$$

Also,

$$\left. \begin{aligned} h_s + h_i + h_r &= h_n, \\ m_s + m_i &= \frac{A}{m_\mu} \end{aligned} \right\} \quad (3)$$

Here,  $h_n$  is the total host population;  $h_s$ ,  $h_i$ ,  $h_r$  respectively are the number of susceptibles, infectives and recovered hosts;  $m_s$ ,  $m_i$  respectively are the number of susceptibles and infectives in the mosquito population,  $h_\mu$ ,  $h_\gamma$  respectively are the birth/death rate and the recovery rate in the host population;  $A$ ,  $m_\mu$  respectively are recruitment rate and the death rate in mosquito population;  $h_\beta$ ,  $m_\beta$  respectively are the transmission probabilities from mosquito to human and human to mosquito; and  $b$  is the biting rate of mosquito.

Setting  $x = \frac{h_s}{h_n}$ ,  $y = \frac{h_i}{h_n}$ ,  $z = \frac{m_i}{A/m_\mu}$  and using the equations (3), above system of equations for human and mosquito population can be reduced to the following three equations;

$$\left. \begin{aligned} \frac{dx}{dt} &= h_\mu(1-x(t)) - \alpha x(t)z(t) \\ \frac{dy}{dt} &= \alpha x(t)z(t) - \beta y(t) \\ \frac{dz}{dt} &= \gamma(1-z(t))y(t) - \delta z(t) \end{aligned} \right\} \quad (4)$$

where,  $\alpha = \frac{bh_\beta A}{h_n m_\mu}$ ,  $\beta = h_\mu + h_\gamma$ ,  $\gamma = bm_\beta$ ,  $\delta = m_\mu$ .

### **DISEASE FREE EQUILIBRIUM POINT**

The disease free equilibrium point of the system (4) is a steady state solution of the system. In disease free situation, the variables  $h_i = 0$ ,  $h_r = 0$ ,  $m_i = 0$ . So, from the system of equations (4)  $y = 0$ ,  $z = 0$  and  $x = 1$ . Hence, the disease free equilibrium point of the system (4) is (1,0,0).

### **BASIC REPRODUCTION NUMBER**

The basic reproduction number, denoted by  $R_0$ , is defined as the average number of secondary infections that occur when one infective is introduced into a completely susceptible host population.



Using the next generation matrix method [9], the basic reproduction number of the present model is obtained as

$$R_0 = \sqrt{\frac{\alpha\gamma}{\beta\delta}} = \sqrt{\frac{Ab^2h_\beta m_\beta}{h_\mu m_\mu^2 (h_\mu + h_\gamma)}} \quad (5)$$

If  $R_0 < 1$ , the infection will die out over a period of time and if  $R_0 > 1$ , the disease will take hold and infection can spread through the population.

### ENDEMIC EQUILIBRIUM POINT

From the system of equations (4), we obtain two equilibrium points

$$(1, 0, 0) \text{ and } \left( \frac{h_\mu\gamma + \beta\delta}{\gamma(h_\mu + \alpha)}, \frac{h_\mu(\alpha\gamma - \beta\delta)}{\beta\gamma(h_\mu + \alpha)}, \frac{h_\mu(\alpha\gamma - \beta\delta)}{\alpha(h_\mu\gamma + \beta\delta)} \right)$$

The first point is disease free equilibrium point. The second equilibrium point if exists is called endemic equilibrium point. The second point exists if  $\alpha\gamma - \beta\delta > 0$ . Also,  $\alpha\gamma - \beta\delta > 0$  if  $R_0 > 1$ . Hence, the endemic equilibrium point exists if  $R_0 > 1$ .

**Table 1:** Parameters and their values

| Parameters | Description   | Values    |
|------------|---|-----------|
| $h_\mu$    | Birth/Death rate of hosts   | 0.0000397 |
| $m_\mu$    | Death rate of mosquitoes  | 0.071429  |
| $h_\gamma$ | Recovery rate   | 0.14286   |
| $b$        | Biting rates  | variable  |
| $h_n$      | Total host population   | 50000     |
| $A$        | Recruitment rate of mosquitoes  | 5000      |
| $h_\beta$  | Transmission probability of dengue virus from the mosquito population to the human population | 0.75      |
| $m_\beta$  | Transmission probability of dengue virus from the human population to the mosquito population | 1         |



**SENSITIVITY ANALYSIS**

Sensitivity Analysis describes the importance of each parameter in the transmission of the disease. We use the analysis to discover the parameter that has high impact on the basic reproduction number  $R_0$ .

**Definition** [10]: The normalized forward sensitivity index of  $R_0$  that depends differentiably on a parameter  $\eta$  is defined as

$$\psi_{\eta}^{R_0} = \frac{\partial R_0}{\partial \eta} \cdot \frac{\eta}{R_0} \tag{6}$$

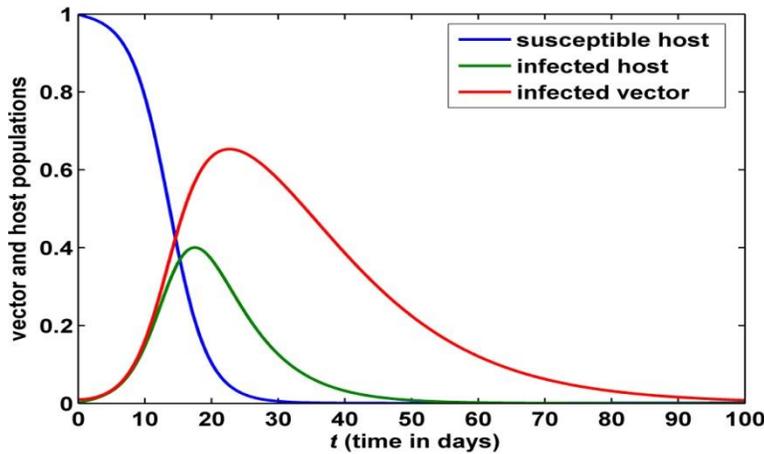
**Table 2:** Sensitivity indices of  $R_0$  evaluated at baseline parameter values

| Parameters ( $\eta$ ) | Baseline values | Sensitivity indices ( $\psi_{\eta}^{R_0}$ ) |
|-----------------------|-----------------|---|
| $b$                   | 0.25            | + 1   |
| $A$                   | 5000            | + 0.5                                       |
| $h_{\gamma}$          | 0.14286         | - 0.49                                      |

Using the definition, the sensitivity indices found are listed in Table 2. Here,  $\psi_b^{R_0} = + 1$  means that increasing (or decreasing) the biting rate  $b$  by 10% increases (or decreases) always  $R_0$  by 10%,  $\psi_A^{R_0} = + 0.5$  means that increasing (or decreasing)  $A$  by 10% increases (or decreases) always  $R_0$  by 5%,  $\psi_{h_{\gamma}}^{R_0} = - 0.49$  means that increasing (or decreasing)  $h_{\gamma}$  by 10% decreases (or increases) always  $R_0$  by 4.9%. Table 2 reflects that biting rate of mosquito  $b$  is the most positive sensitive parameter to the basic reproduction number among the parameters  $b, A$  and  $h_{\gamma}$ . The present paper discusses the numerical results on the impact of the biting rates in the transmission of the disease.

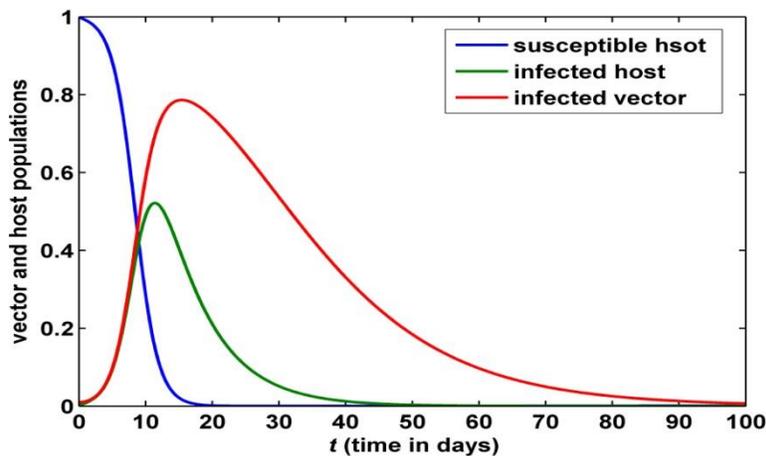
**NUMERICAL RESULTS AND DISCUSSION**

The parameter values for the simulation are considered as shown in Table 1. Figure 2 and Figure 3 describe the behaviour of the solutions showing the dynamics of susceptible host, infected host and infected vector population for the biting rates  $b = 0.45$  and  $b = 0.68$  respectively.



**Figure 2:** Dynamics of susceptible host, infected host and infected mosquito population.

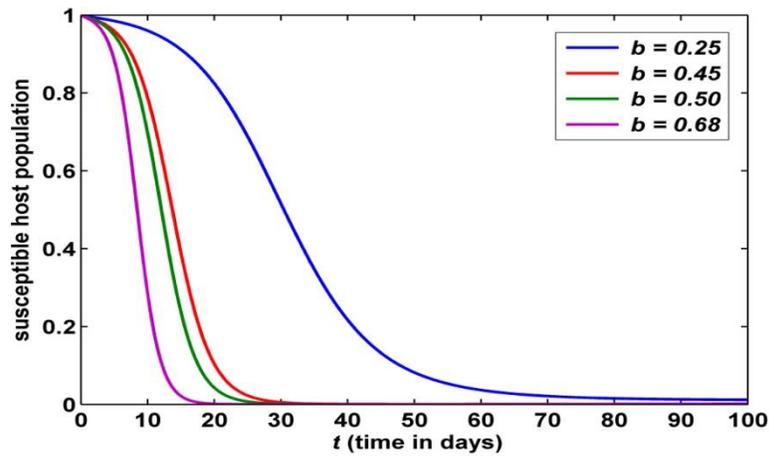
From Figure 2, it is noted that the number of susceptible humans decreases significantly to its least value in about 30 days. The number of virus infected human increases during the period of about 22 days and approaches its maximum level due to interaction with the infected mosquitoes and then the infected host population size starts decreasing due to death and recovery from the disease. The virus infected mosquitoes take about 17 days to reach its peak value.



**Figure 3:** Dynamics of susceptible host, infected host and infected mosquito population.

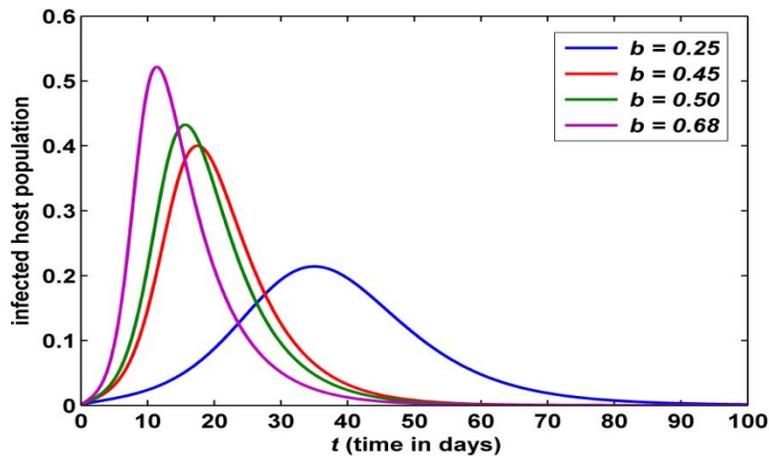
From Figure 3, it is observed that the number of susceptible humans decreases significantly to its least value in about 18 days. The number of virus infected humans increases during the period of about 12 days and approaches its maximum level while the virus infected mosquitoes take about 15 days to reach its peak value.

From Figure 2 and Figure 3, it is observed that the change in population sizes of the susceptible host, infected host and infected mosquito take place more rapidly for the greater values of biting rate.



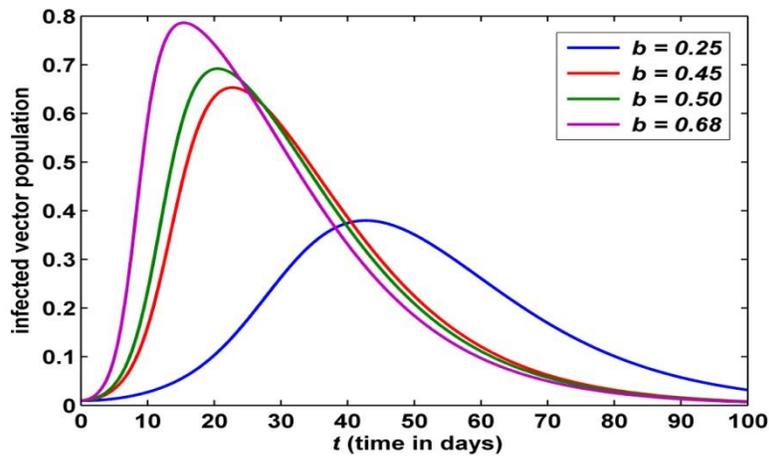
**Figure 4:** Dynamics of susceptible host population with different biting rates.

Figure 4 describes the dynamics of susceptible hosts with different biting rates. It is seen that the susceptible host population takes about 90 days for  $b = 0.25$ ; about 30 days for  $b = 0.45$ ; about 25 days for  $b = 0.50$  and about 18 days for  $b = 0.68$  to reach its least value. Hence, for the increased values of biting rates, the susceptible host population decreases more rapidly.



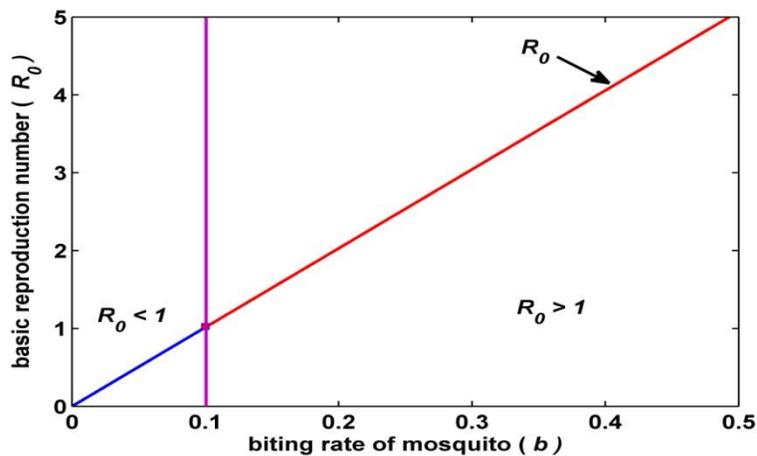
**Figure 5:** Dynamics of infected host population with different biting rates.

From Figure 5, it is observed that the infected host population takes about 35 days to reach its peak value for  $b = 0.25$ ; about 18 days for  $b = 0.45$ ; about 16 days for  $b = 0.50$  and about 13 days for  $b = 0.68$ . Thus, the number of infected hosts increases quickly with the increase in biting rates.



**Figure 6:** Dynamics of infected mosquito population with different biting rates.

From Figure 6, it is seen that the dynamics of infected mosquito population is very similar to the dynamics of infected host population. For different biting rates both the populations change in the same way (Figure 5 and Figure 6). The results show that we can reduce infectives in both host and vector population by controlling the biting rates of mosquitoes.



**Figure 7:** Basic reproduction number with different values of biting rates.

With the increasing values of biting rates of mosquitoes, the value of basic reproduction number increases (Figure 7). For  $b < 0.1$ ,  $R_0 < 1$  and for  $b > 0.1$ ,  $R_0 > 1$ . The results show that for the biting rates less than 0.1, the disease dies out and the disease becomes endemic for the biting rate greater than 0.1 over the time. Thus, biting rates of mosquitoes contribute in increasing the disease transmission.



### CONCLUDING REMARKS

The sensitivity analysis is made to identify the most important parameter that has great impact in the transmission of the disease among the parameters: recruitment rate, biting rate of mosquitoes and recovery rate of host populations. It is observed that the biting rate of mosquitoes is the most positive sensitive parameter.

The study of impact of biting rates in the transmission of the dengue disease shows that the increase in biting rates help in increasing the transmission of the disease. A small change in biting rates leads to greater change in the number of infectives in both human and mosquito population. So, the present study suggests that the strategies that reduce the biting rates of mosquitoes can help in controlling the transmission of the disease.

### REFERENCES

- [1] Poudel A, Shah Y, Khatri B, Joshi D R & Pandey B D, The burden of dengue infections in some vulnerable regions of Nepal, *Nepal Med Coll. J.*, 14 (2012) 114.
- [2] Kermack W O & McKendrick A G, A contribution to the mathematical theory of epidemics, *Proceedings of the Royal Society of London*, 115 (1927) 700.
- [3] Esteva L & Vargas C, Analysis of a dengue disease transmission model, *Mathematical Biosciences*, 150 (1998) 131.
- [4] Soewono E & Supriatna A K, A two dimensional model for the transmission of dengue fever, *Bull. Malaysian Math. Sc. Soc. (Second Series)*, 24 (2001) 49.
- [5] Pongsumpun P, Mathematical model of dengue disease with the incubation period of virus, *World Academy of Sc. Engg and Tech.*, 44 (2008) 328.
- [6] Pinho S T R, Ferreira C P, Esteva L, Barreto F R , Morato e Silva V C & Texeira M G L, Modeling the dynamics of dengue real epidemics, *Phil. Trans. R. Soc. A*, 368 (2010) 5679.
- [7] Side S & Noorani S M, A SIR model for spread of dengue fever disease, *World Journal of Modelling and Simulation*, 9 (2013) 96.
- [8] Phaijoo G R & Gurung D B, Mathematical model of dengue fever with and without awareness in host population, *International Journal of Advanced Engineering Research and Applications (IJAERA)*, 1 (2015) 239.
- [9] van den Driessche P & Watmough J, Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission, *Mathematical Biosciences*, 180 (2002) 29.
- [10] Chitnis N, Hyman J M & Cushing J M, Determining important parameters in the spread of malaria through the sensitivity analysis of a mathematical model, *Bulletin of Mathematical Biology*, 70 (2008) 1272.