# TRANSMISSION MODEL FOR DENGUE DISEASE WITH AND WITHOUT THE EFFECT OF EXTRINSIC INCUBATION PERIOD

Puntani Pongsumpun

Department of Mathematics and Computer Science, Faculty of Science,
King Mongkut's institute of Technology Ladkrabang, Chalongkrung road,
Ladkrabang, Bangkok 10520, Thailand

## ABSTRACT

Dengue disease is transmitted to the human by biting of the infected *Aedes Aegypti*. It can be found in the tropical regions of the world. There are four serotypes of dengue virus, namely DEN-1, DEN-2, DEN-3 and DEN-4. Because the length of the extrinsic incubation period (EIP) of the dengue virus while it is in the mosquito becomes longer as the mean daily temperature is lowered, this should effect the transmission of dengue disease. In this study, we use mathematical models to study the behavior of the transmission of dengue disease. We compare the mathematical model of dengue disease (without the effect of EIP) and the modified mathematical model of dengue disease (with the effect of EIP). We apply standard dynamic analysis to both mathematical models. Numerical results are shown for the two models. We found that dynamic behavior of the endemic state changes while the influence of the seasonal variation of the EIP becomes stronger.

**KEYWORDS**: dengue disease, mathematical model, SIR model, extrinsic incubation period.

## 1. INTRODUCTION

The most arboviral disease which is found in the tropical regions is dengue disease. This disease is classified into three forms; dengue fever (DF), dengue hemorrhagic fever (DHF) and dengue shock syndrome (DSS). DF is a flu-like illness that affects infants, young children and adults, but seldom causes death. DHF is more severe and associated with loss of appetite, vomiting, high fever, headache and abdominal pain. Shock and circulatory failure may occur (DSS). This disease can be transmitted from person to person by biting of the infected *Aedes Aegypti* mosquito. DEN-1, DEN-2, DEN-3 and DEN-4 are four serotypes of dengue virus. Infection by any single type of dengue virus apparently produces permanent immunity to it, but only temporary cross immunity to the others. This disease was reported throughout the nineteenth and early twentieth centuries in the America, southern Europe, North Africa, the eastern Mediterranean, Asia, Australia, and on various islands in the Indian ocean, the south, central Pacific and the Caribbean. DF and DHF have increased in both incidence and distribution over the past 40 years. The first confirmed epidemic of DHF was recorded in the Philippines in 1953-1954. Since then, major outbreaks of DHF with significant mortality have occurred in most countries of the South-East Asia Region, including India, Indonesia, Maldives, Myanmar, Sri Lanka, and Thailand, as well as in Singapore, Cambodia, China, Laos, Malaysia, New Caledonia, Palau, Philippines, Tahiti and Vietnam in the Western Pacific

*Corresponding author. Tel: 662-7373000 ext. 6196. Fax: 662-3264341 ext. 284.
E-mail: kppuntan@kmitl.ac.th, puntani_p@yahoo.com

Region. Over the past 20 years, there was a dramatic increase in the incidence and geographical distribution of DHF, and epidemics now occur each year in some South-East Asian countries. In South-East Asia, 50-100 million people infected with dengue virus are reported each year. The majority of deaths that result from dengue infection are due to DHF and DSS. People who develop DHF have a 5% chance of death but if they go on to develop DSS where the mortality rate can rise as high as 40%. [1].

The ambient temperature of the transmission for dengue virus is above $20^0$ C, and it can not be transmitted at 16 $^0$C. In areas where seasonal changes in temperature are affected, the transmission of dengue virus always decreases with the approach of cold temperatures. For example, the epidemic of dengue virus in Australia ceased as the temperature dropped to 14-15 $^0$C at the beginning of winter. Temperature may also effect the maturation of mosquitoes, higher temperature producing smaller females which are forced to take more blood meals to obtain the protein needed for egg production. The temperature and humidity are thought to influence the extrinsic incubation period of the mosquitoes and is an important variable in causing epidemic transmission [2]. The extrinsic incubation period (EIP) of the mosquito in the low temperature is greater than EIP in the high temperature. If the climate is too cold, the development of virus is slow then the mosquitoes can not survive long enough to become infectious. The mosquitoes never recover from the infection since their infective period ends with their death [3].

In this paper, we compare the behaviors of the transmission of dengue disease by formulating the mathematical models. There is no variation of seasonal in the EIP of the mosquitoes for the first model. The second model, we take into account the seasonal change in the length of the extrinsic incubation period (EIP) of the dengue virus when it is in the mosquito. EIP becomes longer as the mean daily temperature is lowered.

## 2. MATHEMATICAL MODELS

To compare the transmission of dengue disease for the two cases, we formulate the mathematical models by considering the extrinsic incubation period in the mosquito. For the first mathematical model, we assume that every infected mosquito can transmit dengue virus to the human populations (no effect of extrinsic incubation period in mosquitoes). For the second mathematical model, only infectious mosquitoes can transmit dengue virus to the human populations. The effect of extrinsic incubation period in mosquitoes is considered in this model. The human and vector populations are involved in this study. The human populations are separated into three classes, susceptible, infected and recovered human populations. The vector populations are separated into two classes, susceptible and infected vector populations. Susceptible human is the person who both not immune and not infected. Infected human is the person who is transmitted dengue virus from the infected vector. Recovered person is the infected person after the viremia stage until after they recover from dengue virus infection.

Let

$S^h(t)$ be the number of susceptible humans at time t,

$I^h(t)$ be the number of infected humans at time t,

$R^h(t)$ be the number of recovered humans at time t,

$S^v(t)$ be the number of susceptible vector population at time t,

$I^v(t)$ be the number of infected vector population at time t.

The transmission model of dengue disease with no effect of extrinsic incubation period can be described by the following equations [4] :

$$\begin{aligned}
\frac{d}{dt}S^h &= \lambda N_T - \frac{b\beta_h}{N_T} S^h I^v - \mu_h S^h, \\
\frac{d}{dt}I^h &= \frac{b\beta_h}{N_T} S^h I^v - (\mu_h + r) I^h, \\
\frac{d}{dt}R^h &= rI^h - \mu_h R^h, \\
\frac{d}{dt}S^v &= D - \frac{b\beta_v}{N_T} S^v I^h - \mu_v S^v, \\
\frac{d}{dt}I^v &= \frac{b\beta_v}{N_T} S^v I^h - \mu_v I^v
\end{aligned} \qquad (1)$$

with the conditions

$$N_T = S^h + I^h + R^h \qquad \text{and} \qquad N_v = S^v + I^v \qquad (2)$$

where $N_T$ is the total number of human population,

$\lambda$ is the birth rate of the human population,

$b$ is the biting rate of the vector population,

$\beta_h$ is the transmission probability of dengue virus from vector population to human population,

$\beta_v$ is the transmission probability of dengue virus from human population to vector population,

$\mu_h$ is the death rate of the human population,

$r$ is the recovery rate of the human population,

$D$ is the constant recruitment rate of the vector population,

$\mu_v$ is the death rate of the vector population.

The total numbers of populations are assumed that constant for both human and vector populations. So the rates of change for the total human and vector populations are equal to zero. We obtain $\lambda = \mu_h$ for the human population. The total number of vector population is $N_v = D/\mu_v$. We normalize (1) by letting $S = \frac{S^h}{N_T}$, $I = \frac{I^h}{N_T}$, $R = \frac{R^h}{N_T}$, $S_v = \frac{S^v}{N_v}$ and $I_v = \frac{I^v}{N_v}$ then our equations become

$$\frac{dS}{dt} = \lambda - \gamma_h S I_v - \mu_h S,$$

$$\frac{dI}{dt} = \gamma_h S I_v - (\mu_h + r) I \tag{3}$$

and $$\frac{dI_v}{dt} = \gamma_v (1 - I_v) I - \mu_v I_v ,$$

where $$\gamma_v = b\beta_v$$

and $$\gamma_h = b\beta_h n \quad \text{with} \quad n = \frac{(D/\mu_v)}{N_T} \tag{4}$$

with the three conditions

$$S + I + R = 1 \quad \text{and} \quad S_v + I_v = 1 \tag{5}$$

For the second mathematical model, we assume that only infectious mosquitoes can transmit dengue virus to the human populations. Let c is the percentage of infected mosquitoes which are not infectious. So $(1-c)I^v$ is the number of infectious mosquitoes. Then the mathematical model can be described by the following differential equations

$$\begin{aligned}
\frac{d}{dt} S^h &= \lambda N_T - \frac{b\beta_h}{N_T} S^h (1-c) I^v - \mu_h S^h , \\
\frac{d}{dt} I^h &= \frac{b\beta_h}{N_T} S^h (1-c) I^v - (\mu_h + r) I^h , \\
\frac{d}{dt} R^h &= r I^h - \mu_h R^h , \\
\frac{d}{dt} S^v &= D - \frac{b\beta_v}{N_T} S^v I^h - \mu_v S^v , \\
\frac{d}{dt} I^v &= \frac{b\beta_v}{N_T} S^v I^h - \mu_v I^v
\end{aligned} \tag{6}$$

with the conditions

$$N_T = S^h + I^h + R^h \quad \text{and} \quad N_v = S^v + I^v \tag{7}$$

The variation in the extrinsic incubation period (EIP) caused by changes in the temperature. This was the cause of the seasonality in the transmission of dengue disease [2]. In this study, the EIP enters into the model through the dependence of 'c' (the fraction of the infected mosquitoes existing in the EIP) on τ. The fraction is given by

$$\begin{aligned}
c &= \int_0^{\tau} e^{-\mu_v t} dt \\
&= \frac{1 - e^{-\mu_v \tau}}{\mu_v}
\end{aligned}$$

where τ is the length of incubation period (day) of dengue virus in mosquitoes. Substituting this into the probability $\beta_h' = \beta_h (1-c)$ and then expanding the exponential, we obtain

$$\beta_h^{'} = \beta_h \left( 1 - \tau \left( 1 - \frac{\mu_v \tau}{2!} + \frac{\mu_v^2 \tau^2}{3!} + \Lambda \right) \right)$$

As we have already pointed out, the dependence of $\beta_h^{'}$ on T (temperature) appears because the latent period depends on T. Though the dependence looks like a hyperbola, with $\tau$ = 8 days at T = $31^0$C and $\tau$ = 17 days at T = $21^0$C, we have modeled the variation as a sinusoidal variation such that

$$\beta_h^{'} = \beta_h (1 + \varepsilon \sin \varphi t) \tag{8}$$

where ε is a measure of the influence of the seasonality on the transmission process.

Normalizing system models (6), then the differential equations become

$$\frac{dS}{dt} = \lambda - \gamma_h^{'} S I_v - \mu_h S,$$

$$\frac{dI}{dt} = \gamma_h^{'} S I_v - (\mu_h + r) I \tag{9}$$

and $$\frac{dI_v}{dt} = \gamma_v (1 - I_v) I - \mu_v I_v,$$

where $\gamma_v = b\beta_v$

and $\gamma_h^{'} = b\beta_h^{'} n$ with $n = \frac{(D/\mu_v)}{N_T}$ (10)

with the three conditions

$$S + I + R = 1 \quad \text{and} \quad S_v + I_v = 1 \tag{11}$$

## 3. ANALYSIS OF THE MATHEMATICAL MODEL

### 3.1 Analytical results

The equilibrium solutions can be found by setting the right hand side of (3) equal to zero then we have

1) $P^0$ = (1,0,0) is the disease free equilibrium point and
2) $P^1$ = $(S^*, I^*, I_v^*)$ is the endemic disease equilibrium point

where

$$S^* = \frac{L + \beta}{\beta + LA^0}, \tag{12}$$

$$I^* = \frac{A^0 - 1}{\beta + LA^0}, \tag{13}$$

$$\text{and} \qquad I_v^* = \frac{\beta(A^0 - 1)}{A^0(\beta + L)} \tag{14}$$

$$\text{where} \qquad \beta = \frac{b\beta_v}{\mu_v}, \quad L = \frac{\mu_h + r}{\mu_h} \text{ and } A^0 = \frac{b^2\beta_h\beta_v n}{\mu_v(\mu_h + r)}. \tag{15}$$

To determine the local stability of the endemic equilibrium point, we calculate the Jacobian matrix of the right hand side of (3). If all eigenvalues (obtained by diagonalizing the Jacobian matrix) have negative real parts then the equilibrium solution is local stability. Diagonalizing the Jacobian for the *endemic equilibrium point*, the characteristic equation is given by setting $\det(J - \eta I) = 0$

where $J$ is the Jacobian matrix for the endemic equilibrium point,

$\eta$ is the eigenvalue

and $I$ is the identity matrix.

Thus, eigenvalues are obtained by solving

$$\eta^3 + e_0\eta^2 + e_1\eta + e_2 = 0 \tag{16}$$

where

$$e_0 = \mu_h\left(\frac{\beta + LA^0}{L + \beta}\right) + \mu_h L + \mu_v A^0\left(\frac{L + \beta}{\beta + LA^0}\right),$$

$$e_1 = \mu_h^2 L\left(\frac{\beta + LA^0}{L + \beta}\right) + \mu_v\mu_h A^0 + (A^0 - 1)\left(\frac{\mu_v\mu_h\beta L}{\beta + LA^0}\right), \tag{17}$$

$$e_2 = \mu_v\mu_h^2 L(A^0 - 1).$$

Using the Routh-Hurwitz criteria [5] for determine the local stability of the endemic equilibrium point. If the coefficients $e_0$, $e_1$ and $e_2$ satisfy the following inequalities:

$$e_0 > 0, e_1 > 0 \text{ and } e_0 e_1 > e_2 \tag{18}$$

then the equilibrium point is locally stable.

Thus the endemic equilibrium point is locally stable for $A^0 > 1$ where $A^0 = \frac{b^2\beta_h\beta_v n}{\mu_v(\mu_h + r)}$.

The *basic reproductive number* of the disease is given by $A'' = \sqrt{A^0}$, which gives the average number of secondary cases that one case can produce if introduced into a susceptible human. Thus the outbreak of dengue disease in the endemic region can be reduced when the basic reproductive number ( $A''$ ) is greater than one [6].

### 3.2 Numerical results

Numerical solutions are presented for comparing the transmission of dengue disease for the two situations. The program *Turbo Pascal* is used in this study. The values of the parameters used in these 2 situations are $\mu_h$ = 0.0000391 day$^{-1}$ corresponding to a life expectancy of 70 years for human. The mean life of the vector is 14 days, so $\mu_v$ = 0.071 day$^{-1}$. The biting rate of the vector is 1/3 per day. The transmission probability of dengue virus ($\beta_h$, $\beta_v$) are chosen : $\beta_h = 0.5$, $\beta_v = 0.7$. The recovery rate is 1/3 per day. Setting n equals to 10.

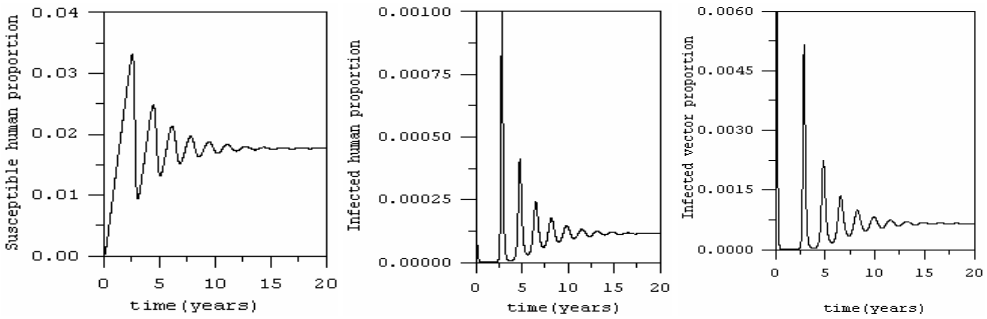


**Figure 1** Numerical solutions of (3) yield the time series solutions of the susceptible human, infected human and infected vector populations. Values of parameters in the model are $\mu_h = 0.0000391$ day$^{-1}$, $\mu_v = 0.071$ day$^{-1}$, b = 1/3 day$^{-1}$, $\beta_h = 0.5$ $\beta_v = 0.7$, n = 10, r = 1/3 day$^{-1}$, $A^0 = 16$, $A'' = 4$. The solutions oscillate to the endemic equilibrium point $S^* = 0.018$, $I^* = 0.00012$ and $I_v^* = 0.00065$, respectively. The period of oscillation is about 3 years.

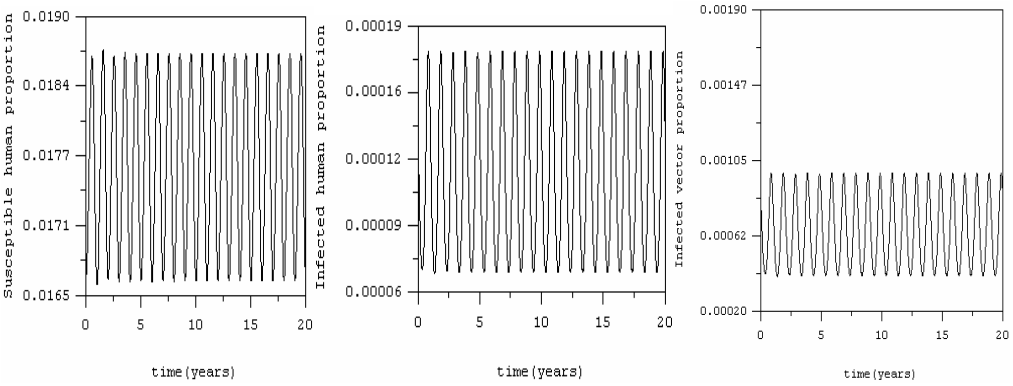


**Figure 2** Numerical solutions of (9) yield the time series solutions of the susceptible human, infected human and infected vector populations. Values of parameters are $\varepsilon = 0.1$ and others parameters are same as in Figure 1.

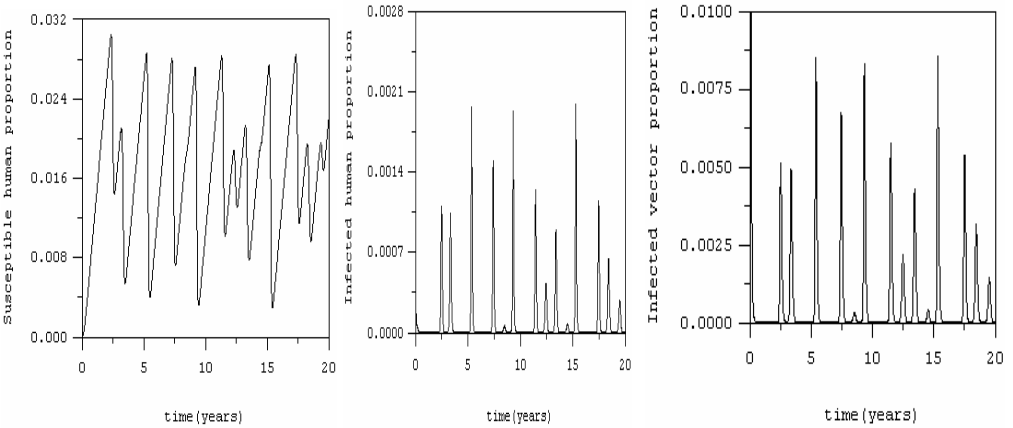


**Figure 3** Numerical solutions of (9) yield the time series solutions of the susceptible human, infected human and infected vector populations. Values of parameters are $\varepsilon = 0.9$ and others parameters are same as in Figure 1.

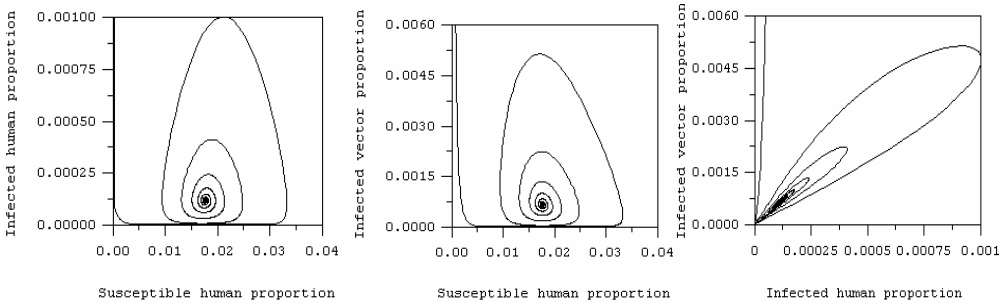


**Figure 4** Numerical solutions of (3), demonstrate the solution trajectory, projected onto $(S,I)$, $(S,I_v)$ and $(I,I_v)$. Values of parameters are same as in Figure 1.

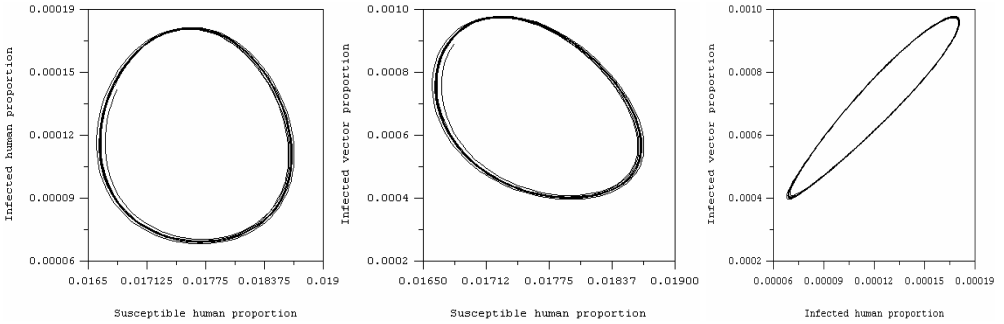


**Figure 5** Numerical solutions of (9), demonstrate the solution trajectory, projected onto $(S,I)$, $(S,I_v)$ and $(I,I_v)$. Values of parameters are same as in Figure 2.

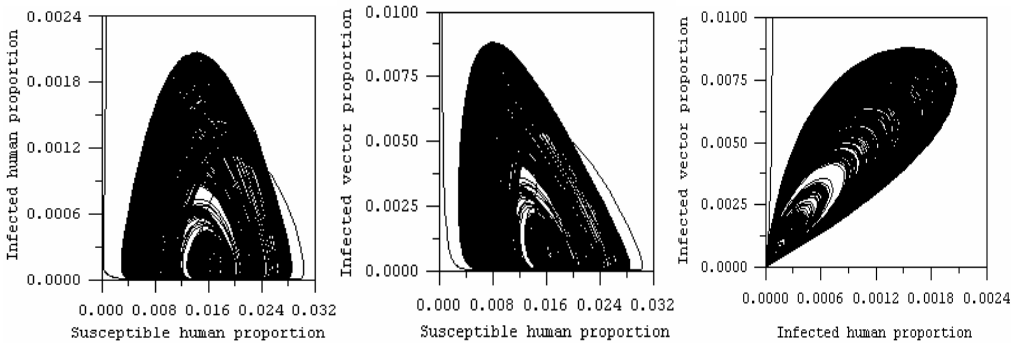


**Figure 6** Numerical solutions of (9), demonstrate the solution trajectory, projected onto $(S,I)$, $(S,I_v)$ and $(I,I_v)$. Values of parameters are same as in Figure 3.

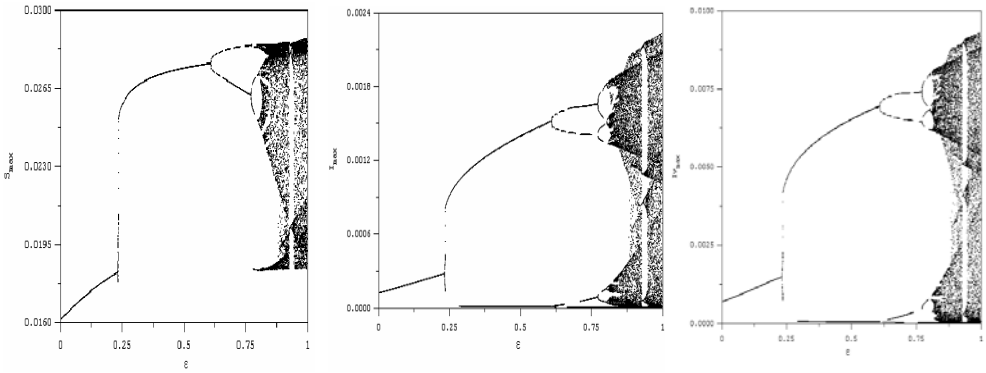

**Figure 7** Bifurcation diagram show the maximum value of susceptible, infected human and infected vector populations for the range of values of the index parameter $\varepsilon$ for (8).

## 4. DISCUSSION AND CONCLUSION

The numerical simulations for the two mathematical models have different behaviors. Figure 1 shows time series solution when there is no seasonal variation of extrinsic incubation period in mosquitoes. Figures 2 and 3 show time series solutions when there is the seasonal variation of extrinsic incubation period in mosquitoes. Figures 4, 5 and 6 show the solution trajectory, the parameters are corresponded to Figures 1, 2 and 3, respectively. The values of parameters for simulation in both models are similar. The values of parameters are satisfied Routh-Hurwitz criterions for the endemic equilibrium point.

For the system model (3), the solutions oscillate to the endemic equilibrium point as we can see from Figure 1. It can be seen from Figure 4 that the stable spiral behavior occurs in this case. From Figures 2 and 5, the solution of the system model (9) oscillate to the 2 points and limit cycle occurs for $\varepsilon = 0.1$. It can be seen from Figures 3 and 6 that the chaotic behavior occurs for $\varepsilon = 0.9$. Thus the complex dynamic behaviors of populations occur while the seasonal variation of the EIP of the mosquitoes is introduced. Bifurcation diagram of each class of the population is showed in Figure 7. It can be seen that the dynamic behavior of the endemic state changes while the influence of the seasonal variation of the EIP becomes stronger.

## REFERENCES


[1] World Health Organization. **1997** *Dengue Haemorrhagic fever : Diagnosis treatment and control*, Geneva.

[2] Kuno, G. **1995** Review of the factors modulating dengue transmission. *Epidemiology Review, 17*, 321-335.

[3] Gubler, D.J. **1998** Dengue and dengue hemorrhagic fever. *Clinical Microbiology Review, 11*, 450-496.

[4] Esteva, L. and Vargas, C. **1998** Analysis of a dengue disease transmission model. *Mathematical Biosciences, 150*, 131-151.

[5] Robert, M. **1973** *Stability and complexity in model ecosystem*, Princeton University Press.

[6] Hethcote, H.W. **2000** The Mathematics of infectious diseases. *Siam Review, 42*, 599-653.