The Simulation Model of Dengue Transmission by Gender of Human in Thailand

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Abstract: Dengue disease can be transmitted to human by the biting of infected Aedes aegypti mosquitoes. This disease has 4 serotypes such as DEN-1, DEN-2, DEN-3 and DEN-4. The symptoms of this disease are high fever, headache, body aches, nausea and rash. This paper describes the spread of this disease by formulating the dynamical model between human and mosquito populations. The human are separating into man and woman populations. The standard dynamical modelling method is used to analyze our dynamical model. The numerical solutions are presented. The basic reproduction value of the disease is found. The way for reducing the transmission of this disease is introduced.

Keywords: Dengue, Model, Gender, Standard Dynamical Modelling

1. INTRODUCTION

Dengue fever is a disease that spreads during the rainy season caused by dengue virus. This disease can happen to all age groups. It can cause life-threatening complications. The person infected with dengue fever can be re-infected if the person gets a different type of infection. Dengue virus contacted by female mosquitoes. Mosquitoes suck the blood of patients with dengue virus. The infection will implant itself in the mosquito's stomach and salivary glands, with an incubation period of 8-12 days. When an infected mosquito bites another person, the virus enters the bloodstream of the person being bitten. Dengue patients who have been exposed to any strain of the virus will have specific immunity to that strain. If the person infected with a different strain of the virus from the first time, it can be dengue fever again. In general, the symptoms of the second disease are usually more severe than the first [1]. Each year, it was found that the distribution of all 4 strains rotated. and there are different predominant pathogens in each year causing disease outbreaks all along because people do not have immunity to that strain of virus. Dengue fever is transmitted from person to person with Aedes mosquitoes being the main mosquitos. After being bitten for about 3-8 days, the symptoms of dengue fever will begin such as High fever, red rash, headache, muscle pain body aches. If the condition is severe, abnormal bleeding may occur and shock. The mosquitoes will be tricky during the daytime by sucking human blood as food. This disease is more common in tropical countries. There will be reports of higher outbreaks during the rainy season. It can happen for all sexes and ages, not limited to young children only. The Aedes mosquito that is the carrier of dengue fever is the female Aedes mosquito. It looks like white and black stripes on the abdomen, body, and legs. It is found a lot in houses and gardens. The disease can be active during daytime and reproduce by laying eggs in standing water. It is often found in containers that have stagnant water such as water jars, flower vases, cupboard legs. old tires and other scrap materials, etc [2],[3]. In Thailand since 1973, it has been found that there is a circulating distribution of 4 types of germs: DEN-1, DEN-2, DEN-3 and DEN-4. The situation of dengue disease in 2023 (between January 1 - March 1, 2023). It was found 6,156 patients, 4 deaths. The age group with the highest morbidity rate are 5-14 years old. The female to male ratio was 1:1.10. The areas with the highest morbidity rates were Bangkok, the South, the Central, the North and the Northeast. The monthly number of dengue patients in year 2023 compared to year 2022 found that in January there were 6.6 times more patients than last year [4]. In 2020, Shak et al. constructed epidemic model of dengue disease. They used Caputo and Fabrizio fractional

derivatives [5]. In 2021, Din et al. used a stochastic Markovian dynamics approach to describe the dengue transmission and the threshold of the disease [6]. In 2023, Li-Martín et al. formulated the mathematical model of dengue disease by separating humans into children and adults. They analyzed by using local and global stability [7]. In this paper, we formulate the dynamical model describing the transmission of dengue disease between human and mosquito populations. The human populations are separated by gender. We analyzed our dynamical model by using standard dynamical method. The numerical analysis of our dynamical model is presented.

2. DYNAMICAL MODEL OF DENGUE DISEASE

The spread of dengue disease is considered via the dynamical model. We separate the human population into man and woman populations. Each population is divided into susceptible, infectious, and recovered human populations. The mosquito population is separated into susceptible and infectious populations. The diagrams are rep-resented as in fig1- fig.3. The variables and parameters are defined in table 1.

Table 1. The definitions of variables and parameters in our dynamical model.

Variables/Parameters	Definitions
S_{mh}	Susceptible man population**.**
I_{mh}	Infectious man population**.**
R_{mh}	Recovered man population**.**
S_{wh}	Susceptible woman population**.**
I_{wh}	Infectious woman population**.**
R_{wh}	Recovered woman population**.**
S_v	Susceptible mosquito population**.**
I_v	Infectious mosquito population**.**
B_m	The constant number of man populations
B_w	The constant number of woman populations
N_v	The total number of mosquito population.
b_m	The contact rate of dengue virus from mosquito to man population
b_w	The contact rate of dengue virus from mosquito to woman population
A	The constant recruitment rate of mosquito population.
a	The contact rate of dengue virus from human population to mosquito population.
μ_v	The death rate of mosquito population**.**
ρ	The rate at which the recovered human change to be susceptible human population.
r	Recovery rate of dengue virus patients.
μ_h	The natural death rate of human population.

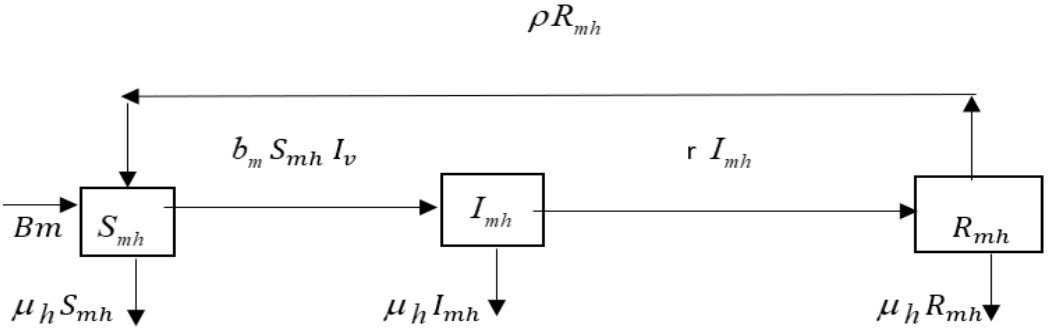


Figure 1. Diagram for man populations

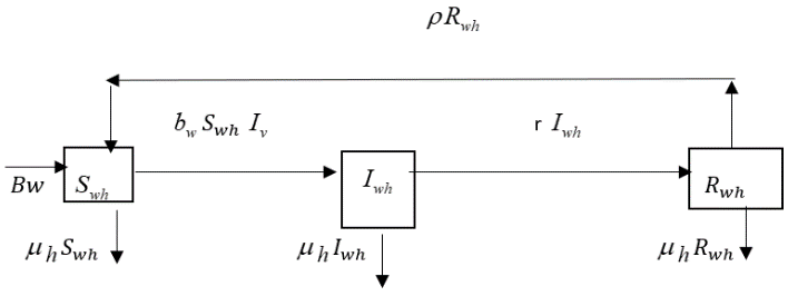


Figure 2. Diagram for woman populations

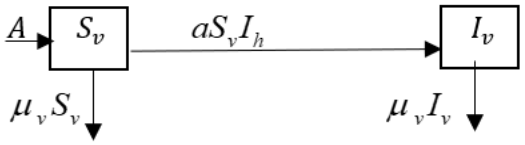


Figure 3. Diagram for mosquito populations

$$\frac{dS_{mh}}{dt} = Bm - b_m S_{mh} I_v - \mu_h S_{mh} + \rho R_{mh}, \quad (1)$$

$$\frac{dI_{mh}}{dt} = b_m S_{mh} I_v - \mu_h I_{mh} - rI_{mh}, \quad (2)$$

$$\frac{dR_{mh}}{dt} = rI_{mh} - \rho R_{mh} - \mu_h R_{mh}, \quad (3)$$

$$\frac{dS_{wh}}{dt} = Bw - b_w S_{wh} I_v - \mu_h S_{wh} + \rho R_{wh}, \quad (4)$$

$$\frac{dI_{wh}}{dt} = b_w S_{wh} I_v - \mu_h I_{wh} - rI_{wh}, \quad (5)$$

$$\frac{dR_{wh}}{dt} = rI_{wh} - \rho R_{wh} - \mu_h R_{wh}, \quad (6)$$

$$\frac{dS_v}{dt} = A - aS_v I_h - \mu_v S_v, \quad (7)$$

$$\frac{dI_v}{dt} = aS_v I_h - \mu_v I_v, \quad (8)$$

$$N_{mh} = S_{mh} + I_{mh} + R_{mh},\ N_{wh} = S_{wh} + I_{wh} + R_{wh},\ N_v = S_v + I_v.$$

Where,

Analytical solutions

The equilibrium states can be found from setting the right hand side of (1) to (8) to zero. Then the equilibrium states are,

The disease free equilibrium state

$$E_0 = \left(\frac{Bm}{\mu_h}, 0, 0, \frac{Bw}{\mu_h}, 0, 0, \frac{A}{\mu_v}, 0 \right) \tag{9}$$

The endemic equilibrium state

$$E_1 = \left(\bar{S}_{mh}, \bar{I}_{mh}, \bar{R}_{mh}, \bar{S}_{wh}, \bar{I}_{wh}, \bar{R}_{wh}, \bar{S}_v, \bar{I}_v \right) \tag{10}$$

Where, $\bar{S}_{mh} = \frac{Bm + \rho \bar{R}_{mh}}{b_m \bar{I}_v + \mu_h}$, $\bar{I}_{mh} = \frac{Bm \bar{I}_v \bar{S}_{mh}}{\mu_h + r}$, $\bar{R}_{mh} = \frac{\bar{I}_{mh} r}{\mu_h + \rho}$, (11)

$$\bar{S}_{wh} = \frac{Bm + \rho \bar{R}_{wh}}{b_m \bar{I}_v + \mu_h}, \quad \bar{I}_{wh} = \frac{Bw \bar{I}_v \bar{S}_{wh}}{\mu_h + r}, \quad \bar{R}_{wh} = \frac{\bar{I}_{wh} r}{\mu_h + \rho}, \tag{12}$$

$$\bar{S}_v = \frac{A}{a(\bar{I}_{mh} + \bar{I}_{wh}) + \mu_v}, \quad \bar{I}_v = \frac{a\left(\bar{I}_{mh} + \bar{I}_{wh}\right) S_v}{\mu_v}. \tag{13}$$

To determine the local stability for each equilibrium state, we know from the sign of the eigenvalues. If all eigenvalues have negative real parts, then that equilibrium state will be local stability.

The eigenvalues can be found from $\det(J - \lambda I) = 0$, where I is the identity matrix and λ are defined as the eigenvalues[8],[9].

The jacobian matrix is defined as

$$J = \begin{pmatrix} -b_m I_v - \mu_h & 0 & \rho & 0 & 0 & 0 & 0 & -b_m S_{mh} \\ b_m I_v & -\mu_h - r & 0 & 0 & 0 & 0 & 0 & b_m S_{mh} \\ 0 & r & -\mu_h - \rho & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -b_w I_v - \mu_h & 0 & \rho & 0 & -b_w S_{wh} \\ 0 & 0 & 0 & b_w I_v & -\mu_h - r & 0 & 0 & b_w S_{wh} \\ 0 & 0 & 0 & 0 & r & -\mu_h - \rho & 0 & 0 \\ 0 & -aS_v & 0 & 0 & -as_v & 0 & -a(I_{mh} + I_{wh}) - \mu_v & 0 \\ 0 & aS_v & 0 & 0 & as_v & 0 & a(I_{mh} + I_{wh}) & -\mu_v \end{pmatrix}$$

For the disease free equilibrium state, we have

$$\lambda_{1,2} = -\mu_h, \lambda_3 = -\mu_v, \lambda_{4,5} = -\mu_h - \rho, \lambda_6 = -\mu_h - r,$$
$$\lambda_{7,8} = \frac{-\mu_h \mu_v (\mu_h + \mu_v + r) \pm \sqrt{\mu_h \mu_v (4aA(b_m Bm + b_w Bw) + \mu_h \mu_v (\mu_h - \mu_v + r)^2)}}{2\mu_h \mu_v}.$$

Thus, the disease free equilibrium state will be local stability for $R_0 < 1$,

where,

$$R_0 = \frac{4aA(b_m Bm + b_w Bw) + \mu_h \mu_v (\mu_h + \mu_v + r)^2}{\mu_h \mu_v (\mu_h + \mu_v + r)^2}. \tag{14}$$

For the endemic equilibrium state, we have

$$\lambda_{1,2} = -\mu_h, \lambda_{3,4} = -\mu_v.$$

The other eigenvalues can be found from

$$\lambda^4 + B_3\lambda^3 + B_2\lambda^2 + B_1\lambda + B_0.$$

where $B_3 = \dfrac{(1+a(I^*_{mh}+I^*_{wh}))(b_wI^*_v+2(2\mu_h+\rho+r))+b_m(I^*_v(1+a(I^*_{mh}+I^*_{wh}))-aS^*_{mh}S^*_v)-ab_wS^*_vS^*_{wh})}{1+a(I^*_{mh}+I^*_{wh})}$,

$$B_2 = \frac{\begin{array}{l}((1+a(I^*_{mh}+I^*_{wh}))(6\mu_h^2+\rho^2+4\rho r+r^2+6\mu_h(\rho+r)+b_wI^*_v(3\mu_h+2(\rho+r)))\\ -abw(3\mu_h+2(\rho+r)))-ab_w(3\mu_h+2\rho+r)S^*_vS^*_{wh}+b_m(I^*_v(1+a(I^*_{mh}+I^*_{wh}))(3\mu_h+2(\rho+r))\\ -a(3\mu_h+2\rho+r)S^*_{mh}S^*_v+b_wI^*_v(I^*_v(1+a(I^*_{mh}+I^*_{wh}))-aS_v(S^*_{mh}+S^*_{wh}))))\end{array}}{1+a(I^*_{mh}+I^*_{wh})},$$

$$B_1 = \frac{\begin{array}{l}(2(1+a(I^*_{mh}+I^*_{wh}))(\mu_h+\rho)(\mu_h+r)(2\mu_h+\rho+r)+b_w(I^*_v(1+a(I^*_{mh}+I^*_{wh}))(3\mu_h^2+\rho^2+3\rho r+r^2+\\ 4\mu_h(\rho+r))-a(\mu_h+\rho)(3\mu_h+\rho+2r)S^*_vS^*_{wh})+b_m(I^*_v(1+a(I^*_{mh}+I^*_{wh}))(3\mu_h^2+\rho+2r)S^*_{mh}S^*_v+\\ b_wI^*_v(2I^*_v(1+a(I^*_{mh}+I^*_{wh}))(\mu_h+\rho+r)-a(2(\mu_h+\rho)+r)S^*_v(S^*_{mh}+S^*_{wh}))))\end{array}}{1+a(I^*_{mh}+I^*_{wh})},$$

$$B_0 = \frac{\begin{array}{l}((1+a(I^*_{mh}+I^*_{wh}))(\mu_h+\rho)(\mu_h+r)+b_wI^*_v(\mu_h+\rho\ \ +r)-ab_w(\mu_h+\rho)S^*_{wh}S^*_v)\\ +b_m((\mu_h+\rho)(\mu_h+r\ \ )(I^*_v(1+a)(I^*_{mh}+I^*_{wh}))(\mu_h+\rho+r)-a(\mu_h+\rho)S^*_v(S^*_{mh}+S^*_{wh}))))\end{array}}{1+a(I^*_{mh}+I^*_{wh})}.$$

After the sign of eigenvalues are checked, the endemic equilibrium state will be local stability when $R_0 > 1$, when R_0 is defined in (14).

Numerical solutions

We simulate the numerical solutions of differential equations by using parameters as in table 2:

Table 2. The values of parameters in our model.

Parameters	Disease free equilibrium state	Endemic equilibrium state	References
B_m	100	1000	assumed
B_w	10	100	assumed
b_m	0.000000055	0.00000055	[4],[10],[11],[12],[13]
b_w	0.00000005	0.0000005	[4],[10],[11],[12],[13]
A	5	100	assumed
a	0.0000095	0.0000095	assumed
μ_v	1/30	1/30	[4],[10],[11],[12],[13]
ρ	1/90	1/90	[4],[10],[11],[12],[13]
r	1/14	1/14	[4],[10],[11],[12],[13]
μ_h	1/(365*65)	1/(365*65)	[4],[10],[11],[12],[13]
R_0	0.9	148.80	

For the disease free equilibrium state:

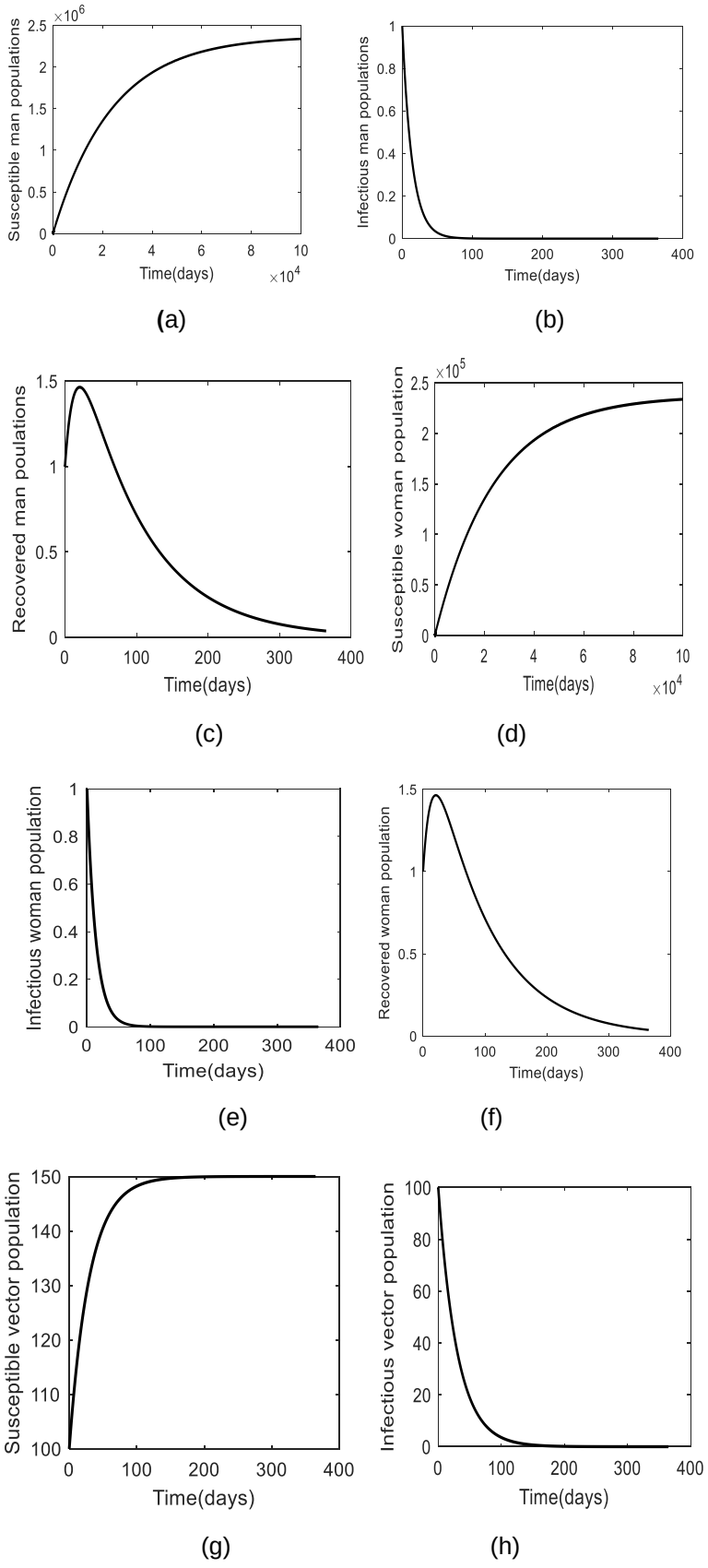


Figure 4. Time series of each population for the disease free equilibrium state.

For the endemic equilibrium state:

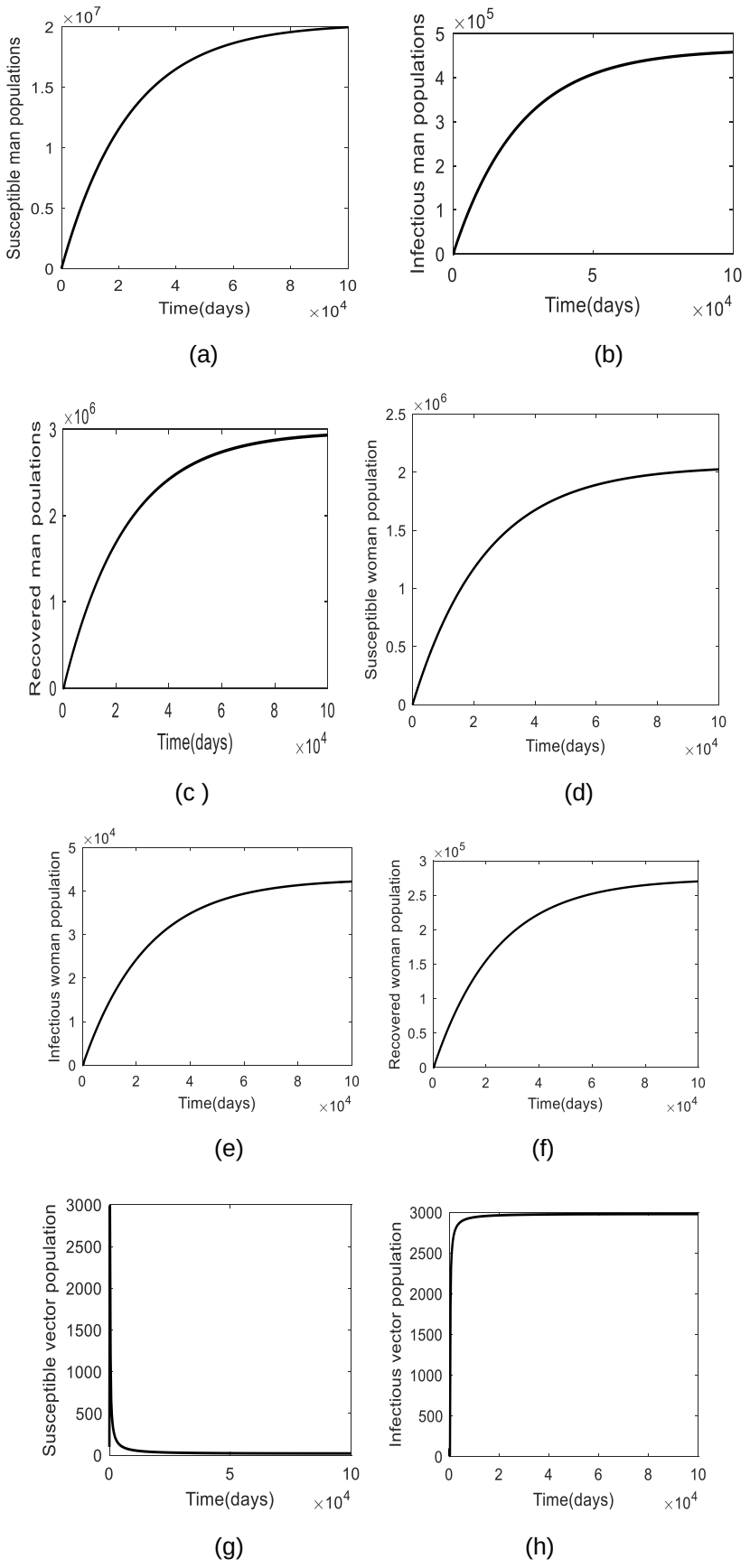
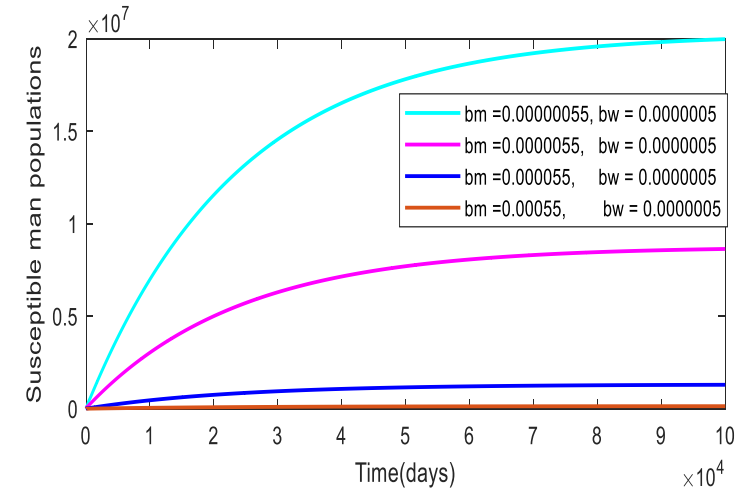
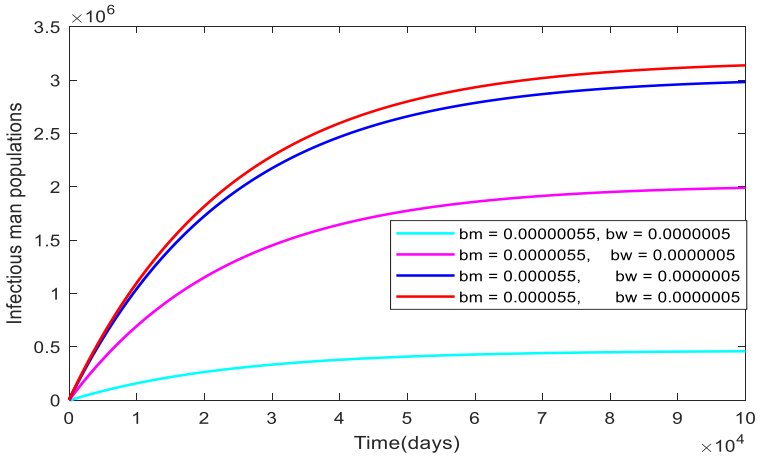


Figure 5. Time series of each population for the endemic equilibrium state.

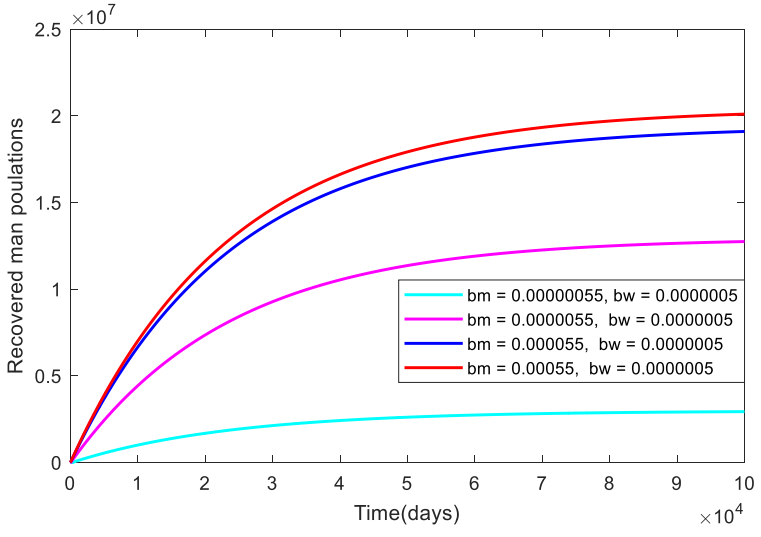
The solutions oscillate to the disease-free state(2,372,500, 0, 0, 237,250, 0, 0,150, 0) for R0 <1. For R0 > 1, the solutions oscillate to the endemic equilibrium state (20,281,900, 465,022, 2,978,130, 2,055,300, 42,839.9, 274,359, 20.5845, 2,979.42) as shown in fig.4 and fig.5.



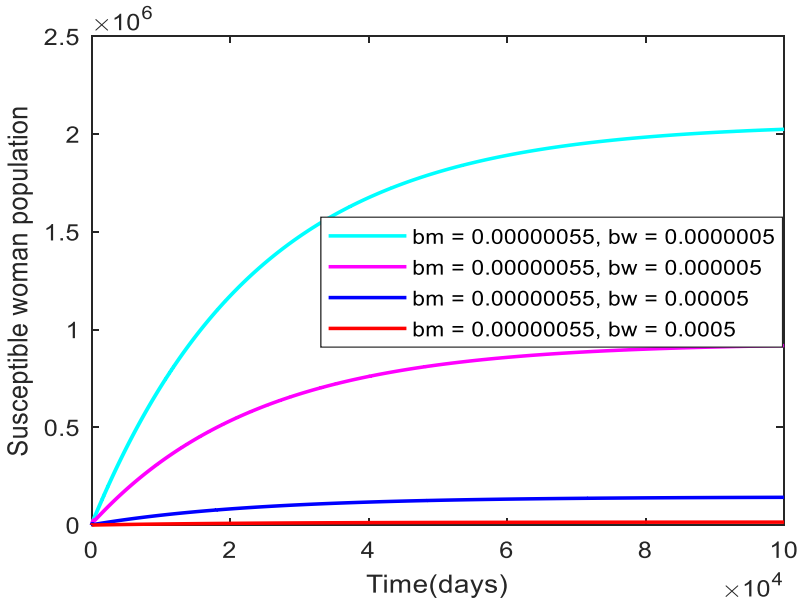
(a)



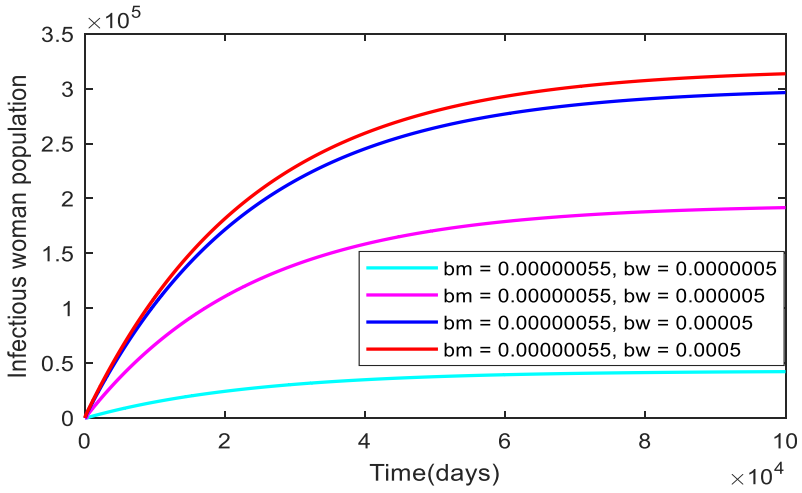
(b)



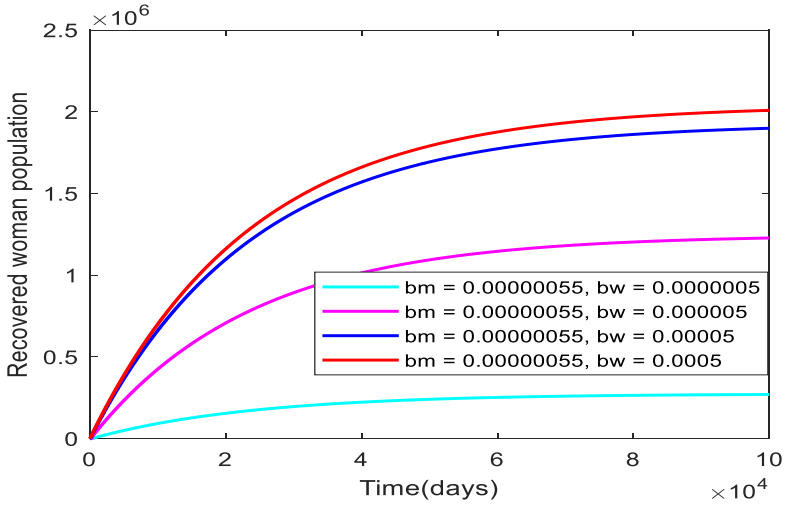
(c)


×10^6
2.5
2
1.5
1
0.5
0
Susceptible woman population
0
2
4
6
8
10
Time(days)
×10^4
bm = 0.00000055, bw = 0.0000005
bm = 0.00000055, bw = 0.000005
bm = 0.00000055, bw = 0.00005
bm = 0.00000055, bw = 0.0005

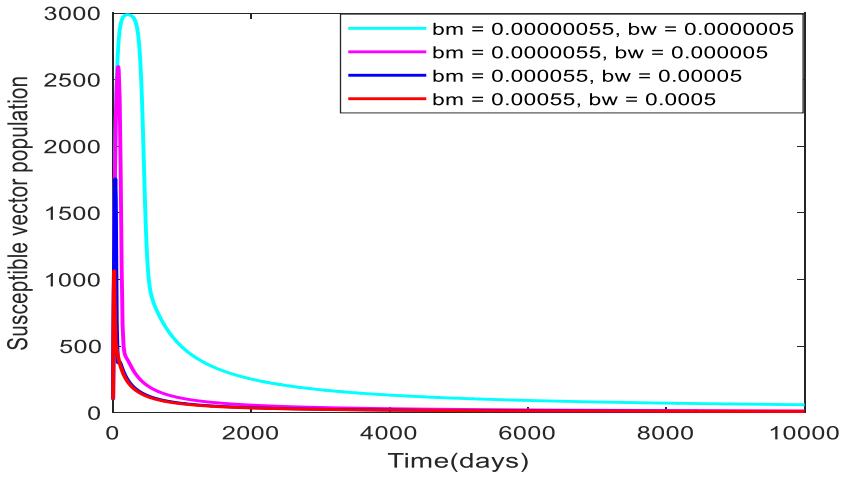
(d)


×10^5
3.5
3
2.5
2
1.5
1
0.5
0
Infectious woman population
0
2
4
6
8
10
Time(days)
×10^4
bm = 0.00000055, bw = 0.0000005
bm = 0.00000055, bw = 0.000005
bm = 0.00000055, bw = 0.00005
bm = 0.00000055, bw = 0.0005

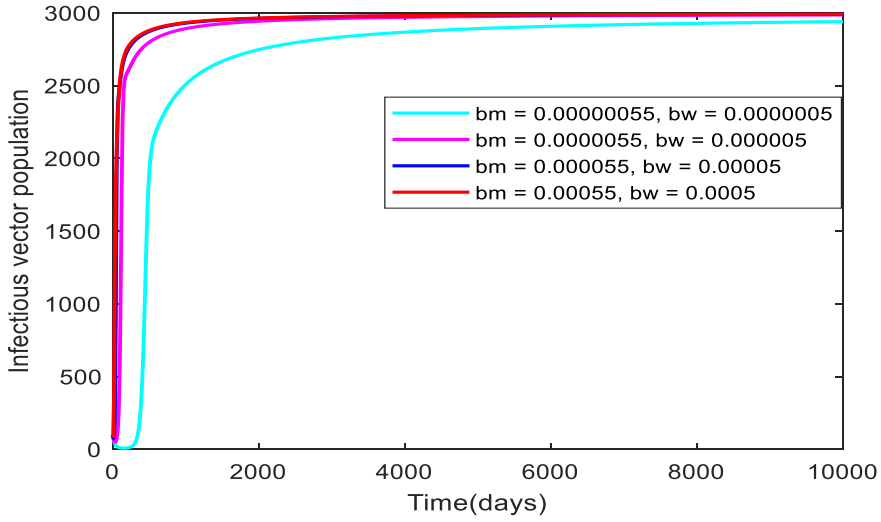
(e)


×10^6
2.5
2
1.5
1
0.5
0
Recovered woman population
0
2
4
6
8
10
Time(days)
×10^4
bm = 0.00000055, bw = 0.0000005
bm = 0.00000055, bw = 0.000005
bm = 0.00000055, bw = 0.00005
bm = 0.00000055, bw = 0.0005

(f)



(g)



(h)

Figure 6. Time series of each population for the different transmission rate of dengue virus.

When the transmission rates of dengue virus are increasing, the infectious and recovered populations are increasing but the susceptible populations are decreasing. The length of the outburst for the infectious populations are decreasing when the transmission rate of dengue virus is increasing as shown in fig.6.

3. DISCUSSION AND CONCLUSION

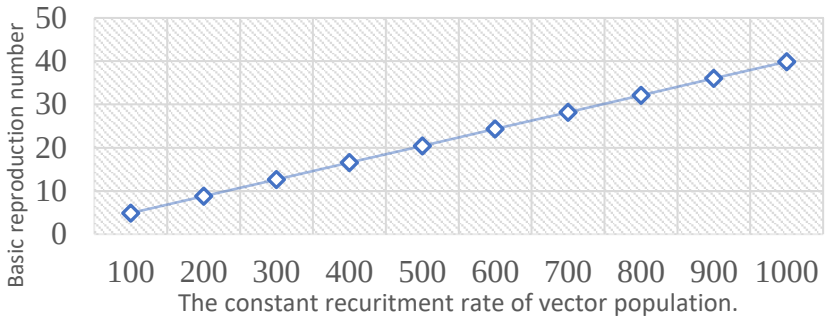
The dynamical model of dengue infection between human and mosquito population is considered. The basic reproduction is defined as

$$R_0 = \frac{4aA(b_m Bm + b_w Bw) + \mu_h \mu_v (\mu_h + \mu_v + r)^2}{\mu_h \mu_v (\mu_h + \mu_v + r)^2}.$$

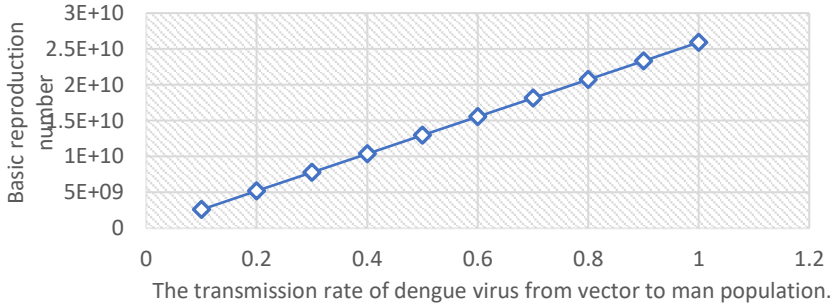
We can see that the contact rate of dengue virus from human to mosquito population, the constant recuritment rate of mosquito population, the contact rate of dengue virus from mosquito to man population, The constant number of man populations, the contact rate of dengue virus from mosquito to woman population, the constant number of man populations are increase, the basic reproduction number of the disease are also increased as in figure 7.


Basic reproduction number
0
1
2
3
4
5
6
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1
The transmission rate of dengue virus from human population to vector population

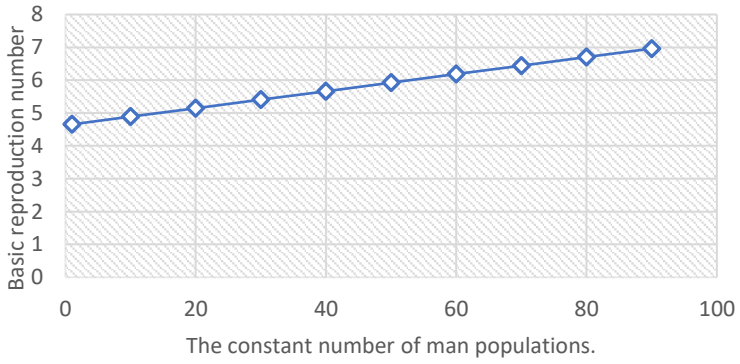
(a)


Basic reproduction number
0
10
20
30
40
50
100
200
300
400
500
600
700
800
900
1000
The constant recuritment rate of vector population.

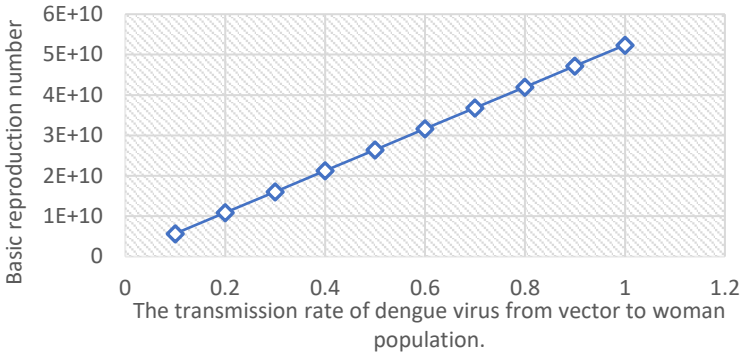
(b)


Basic reproduction number
0
5E+09
1E+10
1.5E+10
2E+10
2.5E+10
3E+10
0
0.2
0.4
0.6
0.8
1
1.2
The transmission rate of dengue virus from vector to man population.

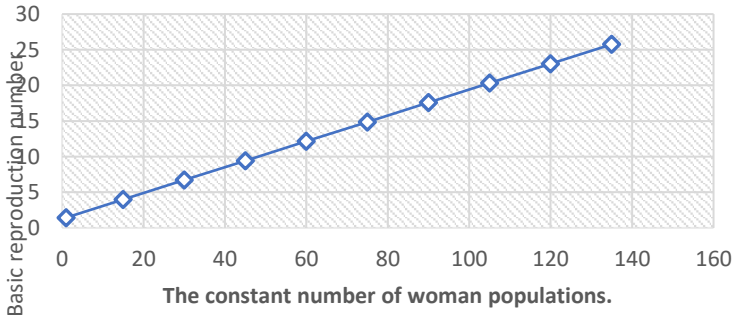
(c)


Basic reproduction number
0
1
2
3
4
5
6
7
8
0
20
40
60
80
100
The constant number of man populations.

(d)



(e)



(f)

Figure 7. The basic reproduction number for the difference contact rate of dengue virus from human to mosquito population, the constant recuritment rate of mosquito population, the contact rate of dengue virus from mosquito to man population, the constant number of man populations, the contact rate of dengue virus from mosquito to woman population, the constant number of man populations

To reduce the transmission of this disease, we should reduce the value of basic reproduction number. For raining season in Thailand, there are frequent rains and waterlogging in many areas. It was born as a breeding ground for mosquitoes. Dengue spreads easily. Many provinces found many patients with dengue disease. In addition, the COVID-19 disease situation continues to spread continuously. The symptoms of both diseases are similar. Therefore, it is difficult to diagnose the disease initially but can be distinguished by dengue disease. There will be high fever and floating for 2-7 days, muscle pain, headache, loss of appetite, nausea, vomiting. Mathematical models are used to explain the spread of many diseases[10-13]. The way for reduce the transmission of this disease is introduced.

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