Impact of Yellow Fever with Multiple Control Measures: Mathematical Model

Preety Kalra and Indu Ratti*
Department of Mathematics, School of Chemical Engineering and Physical Sciences, Lovely Professional University, Punjab, India
E-mail: *prof.induratti@yahoo.com

Abstract. Yellow fever is a vector borne disease caused by infected mosquitoes. It is a life threatening disease which is endemic in many parts of the world. Continuous efforts to eradicate and minimize the disease burden are being done using theoretical and statistical models. In this paper, we have considered a mathematical model for transmission of yellow fever for human and mosquito populations. Vaccination and insect repellent are introduced in the model as control measures. Stability analysis for disease free equilibrium is being done. The threshold parameter, that is, reproduction number is calculated which will predict the direction in which disease can be eliminated.

1. Introduction
Infectious diseases have always threatened and invaded human populations. Apart from the loss of human lives, they create a big burden on the economy of the country in the sense of money, medical facilities, equipment for treatment and human efforts. Looking back in history of these diseases, poor sanitation, not taking preventive control measures in time, the level of interaction of human population with the host vector are some of the factors to which blame of an epidemic can be put on. However many of the diseases still exists and spread inspite of taking precautions. By the researcher in [1], yellow fever virus is the prototype member of the genus Flavivirus. This group of viruses is transmitted between vertebrates by arthropod viruses. Mostly found in tropical regions of South America and Africa, it is transmitted to primates by mosquitoes: Aedes spp. in Africa and Sabethes spp. in South America. The species responsible for urban yellow fever is Aedes aegypti. It has been studied by [2] and [3], yellow fever is viral haemorrhagic fever caused by biting of a mosquito Aedes aegypti, a YF vector of the urban cycle of the disease. After incubation period of 3 to 6 days, the disease becomes symptomatic with symptoms like mild fever, jaundice, vomiting, muscle pain and the disease may aggravate to death in some cases. Further it has been observed by Johansson et al. [4] yellow fever also being an old disease was considered to have been controlled in mid 1900s by vaccination but its return is the main cause which is matter of concern. Inwang [5] studied mathematical formulae for resistance potential of mosquitoes to DDT. Mosquito control is studied by many researchers like Esteva et al. [6] and Kesselring et al. [7]. There is no particular antiviral drug for the disease but timely detection and taking precautionary measures may increase the chances of patient’s survival. Mathematical modeling has played an important role in fighting against these diseases. Health care policies and cost effective treatment are blessings of researchers doing epidemiological studies. Zaleta et
al. [8] discussed a sample vaccination model by considering many endemic states. The authors studied factors like policies concerning vaccination, vaccine coverage rate, the waning period. (i.e. the period after which the immunity due to vaccine fails) and effectiveness of vaccine. The calculation was discussed in terms of threshold parameter, Basic Reproduction number \(R_0\) [9]. It is a numerical value which represents the average number of secondary infections caused by infective person upon interaction with susceptible. If \(R_0 < 1\), the disease will die out. If \(R_0 > 1\), the disease will invade the population causing epidemic and many times it may end up in steady endemic state. Zhao et al. [10] modelled yellow fever outbreak in Luanda, Angola. Their model helped to find that vaccination saved 5.1 fold more people from death. The study revealed that \(R_0\) can be changed by changing several factors like use of insecticide, travelling to endemic area and precautionary measures circulated through media. Bodine et al. [11] modelled yellow fever by taking different control measures like vaccination, use of insect repellent, reapplication of repellent after its waning period and human’s tendency to apply insect repellent according to their state as infected or recovered. Though vaccination is an effective measure to control the disease but there are certain limitations for vaccination like restricted access to health care facilities, immuno deficient persons, pregnant women, small children and belief system of person for vaccination. Statistical and theoretical studies have been done by researchers in [12], [13], [14], [15], [16], [17], [18] and [19]. Whether to vaccinate or not should be decided by various factors like travel destination, local weather, exposure of individuals with vectors etc. Studies showing adverse effect of vaccine is also done by researchers like Monath et al. [20] and Ribeiro et al. [21]. The authors suggested that vaccination for yellow fever should be avoided keeping in view its adverse effects Yellow fever vaccine cannot be made mandatory due to its detrimental effects. Similar studies were done by Collins et al. [22], Raimundo et al. [23] and Sage Working group [24]. Codecco et al. [25] studied the effects of pre-emptive vaccination to populations who have uncertainty regarding risk of infection. Through his model, the author suggested that vaccination should be done if risk of epidemic is there otherwise ethical issues regarding vaccine does not make mindset of people ready for the vaccination. Keeping in view all the above factors, there is need to use other control measures like use of insect repellent, bed nets, decreasing interaction between humans and hosts, timings to visit the places where the disease is endemic. In our model, we will be using insect repellent as protective measure along with vaccine as control strategy. To our knowledge, there have been no work in yellow fever compartmental modeling, in which protected class of individuals has been taken. We will perform stability analysis and interpret it in terms of reproduction number. Protected class for human population have been introduced in this model to whom temporary protection is given. The reason for taking this class is that the persons who travel to yellow fever endemic regions are normally non immune. So the common practice to have protection is in the form sprays, application of repellent to avoid contact with mosquitoes etc.

2. Mathematical Model

2.1. Model Formulation

We propose a mathematical model for yellow fever transmission for mosquito and human populations. It is being assumed that the two populations mixes deliberately without any obstruction. The total human population and total mosquito population is denoted by \(N_h(t)\) and \(N_m(t)\). These are divided into different epidemiological compartments of individuals namely susceptible class \(S_h(t)\), protected class \(P_h(t)\), infected class \(I_h(t)\) and temporary immune class \(R_h(t)\) whereas the mosquito population is divided into two classes namely susceptible class \(S_m(t)\) and infected class \(I_m(t)\). The transfer between the compartments is denoted by different epidemiological parameters. The susceptible human population gets infected when they are bitten by infected mosquitoes. The susceptible human population is assumed to be increased
Figure 1. Flow diagram of the system

by constant birth rate $b_h$. We have a proportion $\theta$ ($0 \leq \theta \leq 1$) of susceptible individuals which are taken under preventive measures and are going to the protected class. It is being assumed that protection will reduce the likelihood of infection. The factor associated with it is denoted by $\omega$. Here $\omega = 0$, the protection is effective and if $\omega = 1$, then the protection is not effective. This protection is temporary as it wanes with time. So, the protected humans may return to the susceptible class at a constant rate $\delta_1$. Infected humans acquire temporary immunity to join the immune class at a constant rate $\phi$. The disease does not transmit vertically and the human populations have a constant rate of natural death denoted by $\mu_h$. Also, infected humans die disease induced death at a constant rate $\alpha$.

For mosquitoes, the recruitment is through constant birth rate $b_m$. Susceptible mosquitoes, when bite an infectious individual at a constant rate $a$, gets infected with transmission probability $\beta_2$ and $\beta_1$ is the transmission probability of getting infection from infected mosquito to human. There is no recovered class for mosquitoes as they never recover from the disease once they are infected. In the model, there is no difference between vaccinated and recovered humans as current yellow fever vaccine confers lifelong immunity which is same as recovery from disease.

Under these assumptions, the progress of the disease is described by the following set of
differential equations

\begin{align*}
\dot{S}_h &= b_h N_h - a \beta_1 \frac{S_h I_m}{N_m} - \theta S_h + \delta_1 P_h - \mu_h S_h - \epsilon S_h, \\
\dot{P}_h &= \theta S_h - \omega a \beta_1 \frac{P_h I_m}{N_m} - (\delta_1 + \mu_h) P_h, \\
\dot{I}_h &= \frac{a \beta_1 S_h I_m}{N_m} + \omega a \beta_1 P_h I_m - (\phi + \alpha + \mu_h) I_h, \\
\dot{R}_h &= \phi I_h - \mu_h R_h + \epsilon S_h, \\
\dot{S}_m &= b_m N_m - a \beta_2 S_m \frac{I_h}{N_h} - \mu_m S_m, \\
\dot{I}_m &= a \beta_2 S_m \frac{I_h}{N_h} - \mu_m I_m.
\end{align*}

The total population $N_h$ and $N_m$ can be determined from

\begin{align*}
N_h &= S_h + P_h + I_h + R_h, \\
N_m &= S_m + I_m.
\end{align*}

Also upon adding all the equations (1 – 6) in the model for human and mosquito populations, we get

\begin{align*}
\dot{N}_h &= b_h N_h - \mu_h N_h - \alpha I_h, \\
\dot{N}_m &= b_m N_m - \mu_m N_m.
\end{align*}

It is quite clear from equation (7), that in the absence of the disease ($\alpha = 0$), population $N_h$ grows exponentially if $b_m > \mu_m$. $N_h$ is constant if $b_h = \mu_h$, $N_h$ decreases if $b_h < \mu_h$.

Considering equation (8), $N_m = c_1 e^{(b_m - \mu_m) t}$, which implies that $N_m$ is constant if $b_m = \mu_m$, $N_m$ decreases if $b_m < \mu_m$ and it grows exponentially if $b_m > \mu_m$.

2.2. Description of parameters in the model

Table 1: Description of parameters in the model system

| Parameter | Description                                      | Units            |
|-----------|--------------------------------------------------|------------------|
| $a$       | Mosquito biting rate                             | per vector per day |
| $\beta_1$ | Transmission rate of YF from mosquito to human   | per bite         |
| $\beta_2$ | Transmission rate from human to mosquito         | per bite         |
| $\theta$  | Proportion of susceptible individuals under protection | per population |
| $\delta_1$ | Rate at which individuals move from protected class to susceptible class after protection wanes | per population |

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Table 1 – continued from previous page

| Parameter | Description                     | Units       |
|-----------|---------------------------------|-------------|
| $\mu_h$  | Natural death rate for humans   | day$^{-1}$  |
| $\mu_m$  | Natural death rate for mosquitoes| day$^{-1}$  |
| $\epsilon$ | Effective vaccination rate of susceptible humans | day$^{-1}$  |
| $\phi$   | Constant rate to join temporary immunity class | day$^{-1}$  |
| $b_h$    | Birth rate of humans            | day$^{-1}$  |
| $b_m$    | Birth rate of mosquitoes        | day$^{-1}$  |
| $\alpha$ | Yellow fever induced death rate | day$^{-1}$  |
| $\omega$ | Factor related to infection, $\omega = 0$ : protection is effective, $\omega = 1$ : protection is ineffective | numeric value |

3. Dynamical Behaviour of the Model

3.1. Boundedness of the model

Before analysis of the model, we will explore the basic features. As the model deals with the dynamics of mosquitoes and humans, all parameters in the above model are assumed to be non-negative.

In this section, the boundedness of the model will be discussed in the form of the following theorem with the initial conditions $S_h(0) > 0, P_h(0) > 0, I_h(0) > 0, R_h(0) > 0, S_m(0) > 0$ and $I_m(0) > 0$.

**Theorem 3.1.** With the initial conditions for the model proposed to lie in $\tau$, where

$$\tau = \{(S_h, P_h, I_h, R_h, S_m, I_m) \in R_+^6 : S_h \geq 0, P_h \geq 0, I_h \geq 0, R_h \geq 0, S_m \geq 0, I_m \geq 0\}.$$

then there exists a unique solution for the above system of equations (1 – 6) and the solution remains in $\tau$ for all time $t \geq 0$.

**Proof.** Considering that the right hand side of the equations (1 – 6) in the model are continuous and also it has continuous partial derivatives in the region $\tau$, we can deduce that the model has a unique solution that exists for all time $t \geq 0$. Thereby, it will be sufficient to show that $S_h \geq 0, P_h \geq 0, I_h \geq 0, R_h \geq 0, S_m \geq 0$ and $I_m \geq 0$ for all future time $t$.

Let $t_1 = \sup\{t > 0 : S_h \geq 0, P_h \geq 0, I_h \geq 0, R_h \geq 0, S_m \geq 0, I_m \geq 0\}$.

Considering equation (1) of the model, we have

$$\dot{S}_h = b_h N_h - g_1 S_h I_m - \theta S_h + \delta_1 P_h - \mu_h S_h - \epsilon S_h. \quad (9)$$

The above equation can be rewritten as
\[ \dot{S}_h + [f(t) + (\theta + \epsilon + \mu_h)] S_h = F(t), \]

where \( f(t) = \frac{a \beta_h I_h}{N_h} \) and \( F(t) = b_h N_h + \delta_1 P_h. \)

So, \( \frac{d}{dt}(S_h(t))[\exp(\theta + \epsilon + \mu_h)t + \int_0^t f(\eta)d\eta]] = F(t)\exp[(\theta + \epsilon + \mu_h) + \int_0^t f(\eta)d\eta]. \)

On integrating, the above equation becomes
\[ S_h(t_1)\exp(\theta + \epsilon + \mu_h)t_1 + \int_0^{t_1} f(\eta)d\eta] - S_h(0) = \int_0^{t_1} f(\xi)\exp[(\theta + \epsilon + \mu_h)\xi + \int_0^\xi f(\eta)d\eta]d\xi. \]

Therefore,
\[ S_h(t_1) = S_h(0)\exp[-((\theta + \epsilon + \mu_h)t_1 + \int_0^{t_1} f(\eta)d\eta)] + \exp[-((\theta + \epsilon + \mu_h)t_1 + \int_0^{t_1} f(\eta)d\eta)] \times \int_0^{t_1} F(\xi)\exp(\theta + \epsilon + \mu_h)\xi + \int_0^\xi f(\eta)d\eta]d\xi. \]

Hence, \( S_h \geq 0. \)

Similarly, we can show that \( P_h \geq 0, I_h \geq 0, R_h \geq 0, S_m \geq 0 \) and \( I_m \geq 0. \) Therefore, the proof of the theorem is complete.

Assuming that the two populations of humans and mosquitoes do not change notably during the time interval under consideration, we can consider them to be relatively constant. Hence, without loss of generality, the populations in each compartments can be scaled by total species of the respective population to make the model dimensionless.

This is done by the transformations as \( s_h = \frac{S_h}{N_h}, p_h = \frac{P_h}{N_h}, i_h = \frac{I_h}{N_h}, r_h = \frac{R_h}{N_h}, s_m = \frac{S_m}{N_m}, i_m = \frac{I_m}{N_m}. \)

The system of equations reduces to
\[
\begin{align*}
   \dot{s}_h & = b_h - a \beta_1 s_h i_m - \theta s_h + \delta_1 p_h - \mu_h s_h - \epsilon s_h, \\
   \dot{p}_h & = \theta s_h - \omega a \beta_1 p_h i_m - (\delta_1 + \mu_h) p_h, \\
   \dot{i}_h & = a \beta_1 s_h i_m + \omega a \beta_1 p_h i_m - (\phi + \alpha + \mu_h) i_h, \\
   \dot{r}_h & = \phi i_h - \mu_h r_h + \epsilon s_h, \\
   \dot{s}_m & = b_m - a \beta_2 s_m i_h - \mu_m s_m, \\
   \dot{i}_m & = a \beta_2 s_m i_h - \mu_m i_m.
\end{align*}
\]

3.2. Equilibrium Points of the system

To check the behavior of the system, we need to solve it to find the equilibrium points. We will be equating to zero the right hand side of the equations from (10 – 15). While solving, the system of equations will be solved for four out of six variables and the remaining two can be obtained from \( s_h = 1 - p_h - i_h - r_h \) and \( s_m = 1 - i_m. \)

Now, we want to find equilibrium points in the disease free state, that is, when the disease is not present in the society.
Disease free equilibrium is given by $E_0(s_h', p_h', r_h', s_m, 0)$ where

\[
\begin{align*}
    s_h' &= \frac{Db_h}{(\theta + \mu_h + \epsilon) - \theta \delta_1}, \\
    p_h' &= \frac{b_h \theta}{(\theta + \mu_h + \epsilon) - \theta \delta_1}, \\
    r_h' &= \frac{Db_h \epsilon}{(\theta + \mu_h + \epsilon) - \theta \delta_1}, \\
    s_m' &= \frac{b_m}{\mu_m}.
\end{align*}
\]

Here $s_h' \geq 0, p_h' \geq 0$ and $r_h' \geq 0$ provided $(\theta + \mu_h + \epsilon) - \theta \delta_1 > 0$.

Endemic equilibrium $E^*(-p_h^*, i_h^*, r_h^*, i_m^*)$ is given as

\[
\begin{align*}
    p_h^* &= \frac{ABC}{\omega \alpha a^2 \beta^2} - \frac{a \beta_1 (a^2 \omega \beta_2 + CD)}{\omega \alpha (\theta)}, \\
    i_h^* &= \frac{B a \beta_2}{b m}, \\
    r_h^* &= \frac{\phi B}{\mu H a \beta_2} + \frac{c (a^2 \omega \beta_2 + CD)}{\mu b C}, \\
    i_m^* &= \frac{a \beta_2}{a \beta_2 + b m},
\end{align*}
\]

where $A = \phi + \alpha + \mu_h, B = a \beta_2 + b_m - \mu_m, C = a \beta_2 + b_m$ and $D = \delta_1 + \mu_h$.

### 3.3. Stability Analysis

#### 3.3.1. Local stability of disease-free equilibrium

In this section, firstly we will discuss the threshold parameter $R_0$. It is called basic reproduction number and is defined as the number of secondary infections that occurs when an infected individual is introduced into a completely susceptible population. We have computed $R_0$ by next generation matrix [26] and its value is

$R_0 = \sqrt{\frac{a^2 \beta_1 \beta_2 (\delta_1 + \mu_h + \theta \omega)}{(\phi + \alpha + \mu_h)((\theta + \mu_h + \epsilon)D - \theta \delta_1)}}$.

**Theorem 3.2.** The disease free equilibrium $E_0(s_h, p_h, 0, r_h, s_m, 0)$ is locally asymptotically stable if $R_0 < 1$.

**Proof.** The local stability at the equilibrium point $E_0$ is done by finding out the eigen values. The jacobian matrix for the system is given by

\[
J_0 = \begin{pmatrix}
-\omega a \beta_1 i_m - (\delta_1 + \mu_h) & 0 & -\omega a \beta_1 p_h \\
\omega a \beta_1 i_m & -(\phi + \alpha + \mu_h) & a \beta_1 s_h + \omega a \beta_1 p_h \\
0 & a \beta_2 s_m & -\mu_m
\end{pmatrix}
\]

The jacobian matrix calculated at $E_0(s_h, p_h, 0, r_h, s_m, 0)$ is

\[
J_0 = \begin{pmatrix}
-(\delta_1 + \mu_h) & 0 & -\frac{-\omega a \beta_1 b_h \theta}{(\theta + \mu_h + \epsilon)D - \theta \delta_1} \\
0 & -(\phi + \alpha + \mu_h) & a \beta_2 \frac{b_m}{\mu_m} \\
0 & a \beta_2 \frac{b m}{\mu_m} & -\mu_m
\end{pmatrix}
\]
where $a_{23} = a \beta_1 s_h + \omega a \beta_1 p_h$,
which gives the eigen value $\lambda = -(\delta_1 + \mu_h) < 0$.
The other two eigen values can be obtained from
\[
\lambda^2 + (\phi + \alpha + \mu_h + \mu_m) \lambda - a^2 \beta_1 \beta_2 s_m (s_h + \omega p_h) = 0.
\]
It can be written as
\[
\lambda^2 + A_1 \lambda + A_2 = 0,
\]
where $A_1 = \phi + \alpha + \mu_h + \mu_m > 0$,
and $A_2 = -a^2 \beta_1 \beta_2 s_m (s_h + \omega p_h) = (1 - (R_0)^2) A \frac{b_m}{\mu_m}$,
\[
A_2 > 0 \text{ if } (1 - (R_0)^2) A \frac{b_m}{\mu_m} > 0,
\]
i.e. $R_0 < 1$.

According to Routh-Hurwitz criteria $A_1 > 0$ and $A_2 > 0$ Here above two conditions are satisfied for $R_0 < 1$. Therefore, the disease free equilibrium $E_0$ is locally asymptotically stable for $R_0 < 1$.

### 3.3.2. Local stability of endemic equilibrium

**Theorem 3.3.** The endemic equilibrium is locally stable if the following conditions holds.
$A_1 > 0$, $A_2 > 0$ and $A_1 A_2 - A_3 > 0$, where $A_1$, $A_2$ and $A_3$ are given below.

**Proof.** The local stability of endemic equilibrium is investigated by the eigen value of the system at the point $E^*$ while assuming that $i_h \neq 0$.

Jacobian matrix $J_1$ for the given system is
\[
J_1 = \begin{pmatrix}
-a_{11} & a_{12} & -a_{13} \\
a_{21} & -a_{22} & a_{23} \\
a_{31} & a_{32} & -a_{33}
\end{pmatrix}
\]
where
\[
a_{11} = \omega a \beta_1 i_m + (\delta_1 + \mu_h) \\
a_{12} = 0 \\
a_{13} = \omega a \beta_1 p_h \\
a_{21} = \omega a \beta_1 i_m \\
a_{22} = (\phi + \alpha + \mu_h) \\
a_{23} = a \beta_1 s_h + \omega a \beta_1 p_h \\
a_{31} = 0 \\
a_{32} = a \beta_2 s_m \\
a_{33} = \mu_m.
\]

The characteristic equation for $E^*$ is given by $det(J_1 - \lambda I_3) = 0$,
where $I_3$ is the identity matrix. Now for determining the stability at $E^*$, we will be using Routh-Hurwitz criteria to determine the stability of the characteristic equation
\[ \lambda^3 + A_1 \lambda^2 + A_2 \lambda + A_3 = 0 \]

where the coefficients \( A_i \)'s are given by

\[
A_1 = (a_{11} + a_{22} + a_{33}), \\
A_2 = [a_{11}(a_{22} + a_{33}) + (a_{22}a_{33} - a_{23}a_{32})], \\
A_3 = a_{11}(a_{22}a_{33} - a_{23}a_{32}) + a_{13}a_{21}a_{32}.
\]

According to Routh-Hurwitz criteria, all the eigen values of Jacobian \( J_1 \) have negative eigen values iff the following conditions hold. Therefore, endemic equilibrium will be locally asymptotically stable provided

\[
A_1 > 0, A_2 > 0, A_3 > 0 \\
A_1A_2 - A_3 > 0.
\]

4. Numerical Simulations

Using initial conditions \( S_h(0) = 100, P_h(0) = 20, I_h(0) = 10, R_h(0) = 10, S_m(0) = 120, \)
\( I_m(0) = 20 \) and parameters values: \( b_h = 10, a = 10, \beta_1 = .001, \theta = 0.2, \delta_1 = 0.05, \mu_h = .01, \epsilon = 0.1, \omega = 1, \phi = 0.02, \alpha = 0.01, b_m = 0.1, \mu_m = 0.1, \beta_2 = 0.01. \) To check the sensitivity of model outcomes to the changes in various parameters, the model was simulated for different scenarios. To check the effect of mosquito interaction with humans, the parameters relating to mosquito bite and transmission of YF, values of \( a \) and \( \beta_1 \) were varied. The system changes from disease free state to endemic state when the values \( a = 1, \beta_1 = 0.0001 \) were changed to \( a = 4, \beta_1 = 0.01 \) which reflected in the change of value of \( R_0 \) changing from 0.2749 to 1.0997 while keeping all other parameters fixed. This is shown in Figure 2 and 3. Then the simulations were done with varying values of \( a \) only keeping all other fixed. Depending upon \( a \in [1,12], \) the basic reproduction number \( R_0 \) varies from 0.0869 to 1.0433. It can be interpreted as the insect biting rate increases, the infection increases in human population as shown in Fig 4 and 5. As the yellow fever transmission parameter for humans, \( \beta_1 \) increases, there is increase in infection in human populations as can be seen in Figure 6 and 7. It is apparent from the simulations and verified numerically that as we increase \( \beta_1 \) from 0.001 to .002, the value of \( R_0 \) changes from 0.8694 < 1 to 1.2295 > 1. It is apparent that by reducing \( \beta_1 \), there will be reduction in severity of disease. To examine the effects of temporary immunity attained through insect repellent on the severity of disease, all other parameters were fixed except \( \phi \). It can be interpreted as On increasing the value of \( \phi \), the value of \( R_0 \) decreases. The value of \( R_0 \) decreases from 1.0039 to 0.8694 as we increased the value of \( \phi \) from 0.01 to 0.02. It can be interpreted as that even the small amount of insect repellent has a dampening effect on the progress of disease. This will result in pushing the disease onset in time and hence slower the death rate in case of epidemic. The peak of the curve decreases rapidly as is clear in the Fig 8 and 9. Various vaccination programmes can be materialised to make the susceptible population decrease in time. This can be done by starting vaccination programmes in the time before the activity of the mosquitoes reaches its peak, that is, during colder months. To model this different values of vaccination rates were considered for simulation. Figure 10 and 11 represent the effect of vaccination rate \( \epsilon \) on the infected population \( I_h \). The greater the value of \( \epsilon \), the smaller is the infection in human population.
Figure 2. Simulation results for disease free state when $a = 1, \beta_1 = 0.0001$.

Figure 3. Simulation results for endemic state for $a = 4, \beta_1 = 0.01$.

Figure 4. Simulation results for infective state of humans for $a = 1$.

Figure 5. Simulation results for infective state of humans for $a = 12$.

Figure 6. Simulation results for infective state of humans for $\beta_1 = 0.001$.

Figure 7. Simulation results for infective state of humans for $\beta_1 = 0.002$.

5. Conclusion
We proposed and studied a mathematical model for the transmission of yellow fever in which we have considered two populations namely humans and mosquitoes. We calculated disease free and endemic equilibrium and discussed their local stability. Numerical simulations were done for different scenarios. Our results showed that disease can be controlled by reducing mosquito biting rate and disease transmission parameter. Since, vaccines are not easily available in all
areas which are affected by yellow fever. Therefore, the use of insect repellent to reduce the contact between mosquito and human can reduce the chances of epidemic. It has been shown numerically that preventive measures like application of insect repellent plays an important role along with vaccination. As we increased the value of parameter related to temporary protection through insect repellent, the value of $R_0$ changes from $<1$ to $>1$. The parameter used to check the disease transmission ($R_0$) is shown to be highly sensitive to this preventive measure giving temporary immunity.

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