Mathematical model of zika virus dynamics with vector control and sensitivity analysis

Sudhanshu Kumar Biswas [a], Uttam Ghosh [b, *], Susmita Sarkar [b]

[a] Department of Mathematics, Sripat Singh College, Murshidabad, West Bengal, India
[b] Department of Applied Mathematics, University of Calcutta, Kolkata, India

A B S T R A C T

In this paper, we have developed and analyzed a deterministic Zika model considering both vector and sexual transmission route with the effect of human awareness and vector control in the absence of disease induce death. To formulate the model, we assume that the Zika virus is being first transmitted to human by mosquito bite, and then it is being transmitted to his or her sexual partner. The system contains at most three equilibrium points among them one is the disease free and other two are endemic equilibrium points, exists under certain conditions. The theoretical analysis shows that the diseases-free equilibrium is locally and globally asymptotically stable if the basic reproduction number is less than one. Theatrically we have established that endemic equilibrium point which is locally asymptotically stable if the basic reproduction number is greater than one. The system exhibits backward bifurcation when the transmission probability per biting of susceptible mosquito with infected humans crosses the critical value. We estimate the model parameters and validate the model by fitting the model with the reported Zika infected human data from 1 to 36 week of 2016 Zika outbreak in Colombia. Furthermore, using the normalised forward sensitivity index method we have established that the model parameter mosquito biting rate, recruitment rate of mosquito, transmission probability per biting of Susceptible (infected) humans with infected (susceptible) mosquito, rate of awareness in host population, recovery rates of infected human are most sensitive parameters of the considered Zika model. Lastly, some conclusions are given to control the spreading of the Zika disease.

1. Introduction

Recently, Zika virus infection has become a dangerous threat for the human society (Cauchemez, 2016; Mlakar, 2016). It is a vector borne disease, spreads through the mosquito borne flavi-virus. In the beginning, the infection transmitted to the human body by the bites of infected *Aedes aegypti* female mosquitoes, which also transmit the dengue, chikungunya, yellow fever, Japanese Encepalitie's virus (European Centre for Disease Control and Prevention (CDC), 2015; World Health Organisation(WHO), 2016) widely in the tropical and subtropical regions. Symptoms of Zika infection are normally mild,

including fever, headaches, rash, conjunctivitis and joint pain due to flavi-virus. Zika infection increases the chances of microcephaly (permanent disabilities) Guillain-Barre syndrome and other neurological disorder in newborn babies from infected mothers (Cauchemez, 2016; Mlakar, 2016).

This virus was first identified from rhesus monkeys in 1947 in the Zika forest of Uganda (Dick, Kitchen, & Haddow, 1952; Sikka, Chattu, & Popli, 2016) and from humans in Nigeria in 1954 (Dick et al., 1952; Macnamara, 1954; Shapshak, 2015, pp. 477–500) but it was not spread in epidemic form among the human population until 2007 (European Centre for Disease Control and Prevention (CDC), 2015; Duffy, 2009). The first Zika outbreak among human occurred in Yap Island, Micronesia in 2007 (European Centre for Disease Control and Prevention (CDC), 2015; Duffy, 2009; Manore and Hyman, 2016). Afterward, this disease highly spread among human in a different country. First Zika virus, epidemic occurred in French Polynesia in the year 2013–2014 (Hancock, Marfel, & Bel, 2014). After 2015, it is spreading rapidly worldwide. The country Brazil, Southern and Central American as well as in Caribbean, countries are highly affected by Zika. World Health Organisation declared Zika as "public health emergency of the international 2016. According to Pan American Health Organisation (PAHO) and WHO, 583451 suspected and 223477 confirmed cumulative Zika cases were reported up to 04 January 2018 by countries and territories in the Americas among which the respective cases for Brazil are 231725 and 137288 respectively.

Recent studies showed that Zika virus can be transmitted not only by vector only, it also spread by sexual interaction which was reported in (Foy, 2011; Dallas County Health Human Services (DCHHS), 2016; Centres for Disease Control and Prevention (CDC), 2016; The Toronto Star, 2016; Musso, 2015). A remarkable observation was given by the authors in (Musso, 2015) reported that though Zika virus was disappeared from the blood of an infected person even then it was present in his semen, which point out the possibility of sexual transmission of the Zika virus.

Though Zika infection is a threat for public health, but at present no vaccination is available to protect from Zika infection and no particular treatment, medicine or fast diagnostic test is available to treat or diagnose this infection. Thus human awareness through health programs and control of mosquitoes through insecticides is the two effective ways to prevent its infection transmission among the host population.

In the last few years, a number of mathematical models have been reported (Agusto et al., 2017a, 2017b; Bearcroft, 1956; Bonyah, Khan, Okosun, & Islam, 2017; Imran, Usman, Dur-e-Ahmad, & Khan, 2017; Kucharski et al., 2016; Perkins, Siraj, Ruktanonchai, Kraemer, & Tatem, 2016; Shah, Patel, & Yeolekar, 2017) to study the Zika virus transmission dynamics. In those models, the investigators have incorporated the following factors, (i) both vector and sexual transmission (Agusto et al., 2017a, 2017b; Shah et al., 2017), (ii) both vector and sexual transmission route with bilinear incidence rate and they established the backward bifurcation and the global stability of DFE for the same model, but in a single model backward bifurcation and the global stability of DFE are contradictory to each other. (iii) the vertical transmission and vector transmission (Agusto et al., 2017a, 2017b; Imran et al., 2017) and (iv) optimal control on spraying insecticides, other prevention, and treatment (Bonyah et al., 2017; Pontryagin, Boltyanskii, Gamkrelidze, & Mishchenko, 1986; Shah et al., 2017). The impact of awareness on dengue dynamics has been studied by Gakkhar and Chavda (Gakkhar & Chavda, 2013).

In order to study the impact of human awareness and vector control, we construct a Zika model including both vector and sexual transmission route, we also include the human awareness (Mishra & Gakkhar, 2014) and vector control. In this work, we have established the wellposedness, positivity and boundedness, the local and global stability of the DFE and the existence and local stability of endemic equilibrium (EE). Finally, we have validated and estimated the model parameters of the considered model comparing the model predictions with the reported zika infected data of a particular area. To explore the model robustness to parameter values used we investigate the sensitivity analysis using the normalised forward sensitivity index. We also studied numerically the impact of sexual transmission on the epidemic growth rate as well as on the basic reproduction number. To the best of our knowledge effect of vector transmission, sexual transmission, vector control, and human awareness has not yet been considered in a single Zika model. So in this paper, we are considering all these four important facts to propose a Zika model and intend to study its dynamical behaviour.

The rest of the paper is organized as follows: The formulation and basic properties of the model have been described in section-2. An investigation of the stability and bifurcation of the model has been reported in section-3. Parameter estimation and model validation done by simulating the model with reported real data done in section-4. Sensitivity analysis of the model is presented in section-5 and section-6 deals with the effect of sexual transmission on basic reproduction number and epidemic growth rate numerically. Finally, all the results have been concluded in the section-7.

2. Model formulation

Let the total human population $N_h(t)$ is classified into four compartments comprised of susceptible human $S_h(t)$, exposed human $E_h(t)$, infected human $I_h(t)$ and recovered human $R_h(t)$. Here we have considered that a human individual who recovered from infection of Zika virus gain lifelong immunity from it. Sine only female mosquito spreads the zika infection so the total female mosquito population $N_v(t)$ is divided into three compartments viz. susceptible mosquitoes $S_v(t)$, exposed mosquitoes $E_v(t)$ and infected mosquitoes $I_v(t)$. Again recovery of mosquito from Zika infection is not taken into consideration due to its short life span.

To formulate the model the following factors are taken into consideration:

(i) Constant recruitment rate for both susceptible human and vector population.
(ii) Natural death rate for both human and vector population.
(iii) Horizontal transmission of infection from infected vectors to susceptible human when infected vectors bite susceptible human.
(iv) Sexual transmission of infection to susceptible human when a susceptible human interact sexually with an infected human.
(v) Horizontal transmission of infection from infected human to susceptible vectors when susceptible vectors bite infected human.
(vi) Two steps of human awareness has considered. At a constant rate susceptible human can take following awareness steps to protect them from zika (a) using mosquito-nets, and mosquito repellents (b) avoiding sexual interaction or using a condom at the period of zika out break.
(vii) Vector control: spray of insecticide and removal of the stagnant water can control vector.

Let, π be the constant recruitment rate of susceptible human and μ be the natural death rate of the human population. Suppose, susceptible individuals acquire infection due to effective contact with an infected vector at rate $\lambda_1 = \frac{b_2 \alpha_1 I_v}{N_h}$, $\lambda_2 = \frac{c \alpha_2 I_h}{N_h}$ be the infection due to sexual interaction with the infected individuals and susceptible human become aware at a constant rate a and enter into recovered class R_h. So the total infection strength of human is $\lambda_h = \lambda_1 + \lambda_2$. Here we assume that the susceptible mosquitoes acquire infection at a rate $\lambda_v S_v$ from infected human where $\lambda_v = \frac{b_2 \alpha_3 I_h}{N_h}$.

Under the above assumptions, the flow diagram for both human population and vector population of the proposed zika model is given in the following flow diagram (see Fig. 1).

According to the assumptions and from the flow diagram, the dynamics of the Zika virus can be represented by the following system of non linear differential equations:

$$
\left.
\begin{aligned}
\frac{dS_h}{dt} &= \pi - (\lambda_1 + \lambda_2)S_h - (\mu + a)S_h \\
\frac{dE_h}{dt} &= (\lambda_1 + \lambda_2)S_h - (\sigma + \mu)E_h \\
\frac{dI_h}{dt} &= \sigma E_h - (\gamma + \mu)I_h \\
\frac{dR_h}{dt} &= \gamma I_h - \mu R_h + aS_h \\
\frac{dS_v}{dt} &= \pi_1 - \lambda_v S_v - (\mu_1 + b)S_v \\
\frac{dE_v}{dt} &= \lambda_v S_v - (\sigma_1 + \mu_1 + b)E_v \\
\frac{dI_v}{dt} &= \sigma_1 E_v - (\mu_1 + b)I_v
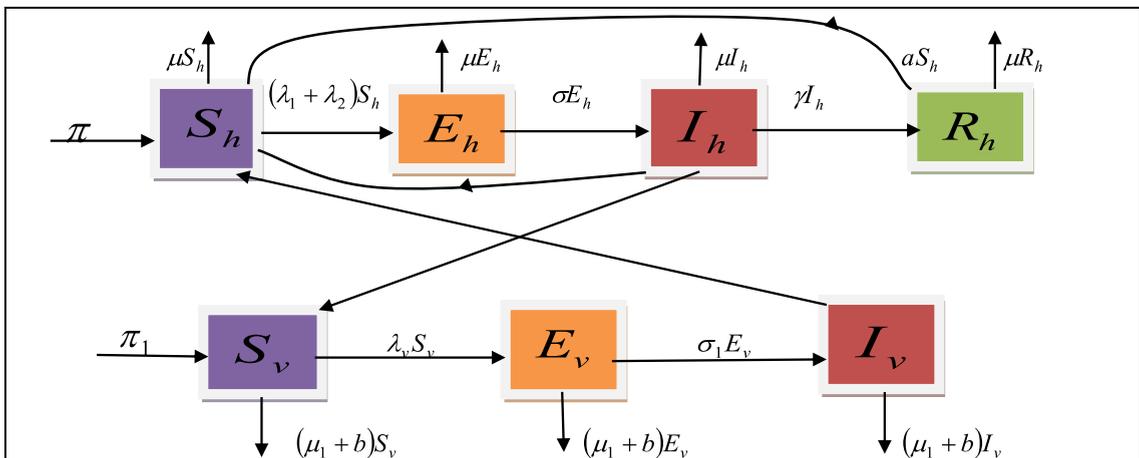\end{aligned}
\right\}
\tag{1}
$$

Fig. 1. Flow diagram of Zika virus in both human and mosquito population.

The state variables and parameters used in the zika transmission model are summarised in Table 1.

2.1. Positivity and boundedness of the solutions

The considered model will be biologically meaningful when all the variables are non-negative for $t \geq 0$. In other words the solution with positive initial conditions will remain positive for all time, which we shall establish in the following Lemma.

Lemma 1. Let $G(t) = (S_h, E_h, I_h, R_h, S_v, E_v, I_v)$ with the initial condition $G(0) \geq 0$. Then the solutions $G(t)$ of the model (1) is non negative for all $t \geq 0$. Also $\lim\limits_{t \to \infty} \sup N_h(t) = \frac{\pi}{\mu}$ and $\lim\limits_{t \to \infty} \sup N_v(t) = \frac{\pi_1}{\mu_1 + b}$ hold.

Proof: Since λ_1 is a function of I_v, N_h and λ_2 is a function of I_h, N_h and for $T = \sup\{t > 0 : G(t) > 0\}$ the first equation of the model (1) can be explicitly written as:

$$\frac{dS_h}{dt} = \pi - \lambda_1(I_v, N_h)S_h(t) - \lambda_2(I_h, N_h)S_h(t) - (\mu + a)S_h(t)$$

Integrating the above equation in the range $[0, T]$ we get,

$$\frac{d}{dt}\left\{ S_h(t) \left[\exp\left(\int_0^T [\lambda_1(I_v(\eta), N_h(\eta)) + \lambda_2(I_h(\eta), N_h(\eta))]d\eta \right) + (\mu + a)T \right] \right\}$$

$$= \pi \exp\left(\int_0^T [\lambda_1(I_v(\eta), N_h(\eta)) + \lambda_2(I_h(\eta), N_h(\eta))]d\eta + (\mu + a)T \right)$$

which gives

$$S_h(T)\exp\left[\left(\int_0^T (\lambda_1(I_v(\eta), N_h(\eta)) + \lambda_2(I_h(\eta), N_h(\eta)))d\eta + (\mu + a)T \right) \right] - S_h(0)$$

$$= \int_0^T \pi \exp\left(\int_0^y [\lambda_1(I_v(\eta), N_h(\eta)) + \lambda_2(I_h(\eta), N_h(\eta))]d\eta + (\mu + a)y \right) dy$$

or

Table 1
Description of state variables and parameters

State variables	Description
N_h	Total human population
S_h	Susceptible human population
E_h	Exposed human population
I_h	Infected human population
R_h	Recovered human population
N_v	Total vector population
S_v	Susceptible vector population
E_v	Exposed vector population
I_v	Infected vector population
Parameters	Description
π, π_1	Recruitment rate of human and mosquito respectively
μ, μ_1	Natural death rate of human and mosquito respectively
b_2	Mosquito biting rate
α_1	Transmission probability per biting of -Susceptible humans with infected mosquito
α_3	Transmission probability per biting of Susceptible mosquito with infected humans.
c	Sexual contact rate between a susceptible human to an infected human
α_2	Transmission probability per sexual contact- among a susceptible and infected human
σ	Progression rate from exposed to infected human
γ	Recovery rate of infected human
a	Rate of awareness in host population
σ_1	Progression rate from exposed to infected mosquito
b	Constant rate of effective mosquito control

$$S_h(T) = S_h(0)\exp\left[-\left(\int_0^T (\lambda_1(I_v(\eta), N_h(\eta)) + \lambda_2(I_h(\eta), N_h(\eta)))d\eta + (\mu + a)T\right)\right]$$

$$+\exp\left[-\left(\int_0^T (\lambda_1(I_v(\eta), N_h(\eta)) + \lambda_2(I_h(\eta), N_h(\eta)))d\eta + (\mu + a)T\right)\right]$$

$$\times \int_0^T \pi \exp\left(\int_0^y [\lambda_1(I_v(\eta), N_h(\eta)) + \lambda_2(I_h(\eta), N_h(\eta))]d\eta + (\mu + a)y\right)dy > 0$$

Similarly it can be shown that $E_h(T), I_h(T), R_h(T), S_v(T), E_v(T)$ and $I_v(T)$ all are positive for all $T > 0$ thus $G > 0$ for all $t > 0$. Hence the first part of the Lemma is proved.

For the next part of the Lemma it should be noted that $0 < S_h(t), E_h(t), I_h(t), R_h(t) \leq N_h(t), 0 < S_v(t), E_v(t), I_v(t) \leq N_v(t)$. Adding first four component equations of the model (1) we have

$$\frac{dN_h}{dt} = \pi - \mu N_h \tag{2}$$

Similarly adding last three equations of the model (1) we have

$$\frac{dN_v}{dt} = \pi_1 - (\mu_1 + b)N_v \tag{3}$$

Integrating and taking limsup and liminf for $t \to \infty$ in the above two equations we get, $\frac{\pi}{\mu} \leq \lim_{t \to \infty} \inf N_h(t) \leq \lim_{t \to \infty} \sup N_h(t) \leq \frac{\pi}{\mu}$ and $\frac{\pi_1}{\mu_1+b} \leq \lim_{t \to \infty} \inf N_v(t) \leq \lim_{t \to \infty} \sup N_v(t) \leq \frac{\pi_1}{\mu_1+b}$, which implies $\lim_{t \to \infty} \sup N_h(t) = \frac{\pi}{\mu}$, and $\lim_{t \to \infty} \sup N_v(t) = \frac{\pi_1}{\mu_1+b}$.

We shall now analyze our proposed zika virus transmission model (1) in the following biologically feasible closed region Ω which is defined below:

$$\Omega = \left\{(S_h, E_h, I_h, R_h, S_v, E_v, I_v) \in \Re_+^7 : S_h + E_h + I_h + R_h \leq \frac{\pi}{\mu}, S_v + E_v + I_v \leq \frac{\pi_1}{\mu_1 + b}\right\}$$

In the next Lemma we shall establish the closed region Ω as a positively invariant set.

Lemma 2. The closed region Ω defined above is a positively invariant set for the model (1) with non-negative initial condition in $\Re^7$.

Proof: Here $N_h = S_h + E_h + I_h + R_h$, so the rate of change of the total human population N_h is obtained from equation (2) in the form.

$\frac{dN_h}{dt} = \pi - \mu N_h$ Similarly total vector population is $N_v = S_v + E_v + I_v$, and hence the rate of change of the total mosquito is obtained from (3), as

$$\frac{dN_v}{dt} = \pi_1 - (\mu_1 + b)N_v$$

Using a standard comparison theorem from Lakshmikantham et al. (1989) it can be shown that
$N_h(t) \leq N_h(0)e^{-\mu t} + \frac{\pi}{\mu}(1 - e^{-\mu t})$ and $N_v(t) \leq N_v(0)e^{-(\mu_1+b)t} + \frac{\pi_1}{\mu_1+b}(1 - e^{-(\mu_1+b)t})$.
This follows $N_h(t) \leq \frac{\pi}{\mu}$ and $N_v(t) \leq \frac{\pi_1}{\mu_1+b}$ if $N_h(0) \leq \frac{\pi}{\mu}$ and $N_v(0) \leq \frac{\pi_1}{\mu_1+b}$ respectively.
Thus the closed region Ω is positively invariant.
Again if $N_h(0) > \frac{\pi}{\mu}$ and $N_v(0) > \frac{\pi_1}{\mu_1+b}$ then the solution contained in Ω or $N_h(t)$ approach to $\frac{\pi}{\mu}$ and $N_v(t)$ approach to $\frac{\pi_1}{\mu_1+b}$ and then the infected classes E_h, I_h, E_v and I_v approach to zero, so Ω is attracting set that is all solutions in $\Re_+^7$ eventually enters in Ω. So, biologically and mathematically the model is well posed in the invariant set Ω (Hethcote, 2000). Hence, it is sufficient to consider the dynamics of the transmission of zika virus model (1) in the invariant set Ω.

3. Steady state analysis

In this section we shall carry out qualitative analysis of the model (1) to investigate existence and stability of the steady states.

3.1. Disease free equilibrium and basic reproduction numbers

The disease free equilibrium (DFE) of the model (1) is obtained by using $E_h = I_h = E_v = I_v = 0$ in the steady state conditions.

Thus the disease free equilibrium point E_0 of the model (1) is given by $E_0(S_h^0, E_h^0, I_h^0, R_h^0, S_v^0, E_v^0, I_v^0) = \left(\frac{\pi}{\mu+a}, 0, 0, \frac{a\pi}{\mu(\mu+a)}, \frac{\pi_1}{\mu_1+b}, 0, 0\right)$.

In order to calculate the basic reproduction number we use the next generation operator method on the model (1). Consider the infected compartments (E_h, I_h, E_v, I_v) at the disease free equilibrium (DFE) and applying Vanden Diressche and Watmaugh (Van den Driessche & Watmough, 2002) technique, the Jacobian matrices F and V (for the new infection terms and the remaining transfer terms respectively) are given by.

$$F = \begin{pmatrix} 0 & \lambda_2^0 S_h^0 & 0 & \lambda_1^0 S_h^0 \\ 0 & 0 & 0 & 0 \\ 0 & \lambda_v^0 S_v^0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}, \quad V = \begin{pmatrix} k_1 & 0 & 0 & 0 \\ -\sigma & k_2 & 0 & 0 \\ 0 & 0 & k_3 & 0 \\ 0 & 0 & -\sigma_1 & k_4 \end{pmatrix}, \quad \text{so that} \quad FV^{-1} = \frac{1}{k_1 k_2 k_3 k_4}\begin{pmatrix} a_1 & a_2 & a_3 & a_4 \\ 0 & 0 & 0 & 0 \\ a_5 & a_6 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}$$

where, $k_1 = \sigma + \mu, k_2 = \gamma + \mu, k_3 = \sigma_1 + \mu_1 + b, k_4 = \mu_1 + b, \lambda_1^0 = \frac{b_2\alpha_1}{N_h^0}, \lambda_2^0 = \frac{c\alpha_2}{N_h^0}, \lambda_v^0 = \frac{b_2\alpha_3}{N_h^0}, a_1 = \lambda_2^0 S_h^0 \sigma k_3 k_4 a_1 = \lambda_2^0 S_h^0 \sigma k_3 k_4,$

$a_2 = \lambda_2^0 S_h^0 k_1 k_3 k_4, a_3 = \lambda_1^0 S_h^0 k_1 k_2 \sigma_1, a_4 = \lambda_1^0 S_h^0 k_1 k_2 k_3, a_5 = \lambda_v^0 S_v^0 \sigma k_3 k_4, a_6 = \lambda_v^0 S_v^0 k_1 k_3 k_4$. Now, the basic reproduction number R_0 is obtained as the spectral radius $\rho(FV^{-1})$ (Van den Driessche & Watmough, 2002) that is the dominant Eigen value of the matrix FV^{-1}.

The characteristic polynomial of the matrix FV^{-1} is $\lambda^2(\lambda^2 - l\lambda - m)$ where $l = a_1/D, m = a_3 a_5/D^2, D = k_1 k_2 k_3 k_4$ and the quadratic polynomial of the above characteristic polynomial is $g(\lambda) = (\lambda^2 - l\lambda - m)$ with $l > 0, m > 0$. So $g(\lambda) = 0$ gives a unique positive root, which provides the basic reproduction number R_0 given below:

$$R_0 = \rho(FV^{-1}) = \frac{1}{2k_1 k_2 k_3 k_4}\left\{\lambda_2^0 S_h^0 \sigma k_3 k_4 + \left((\lambda_2^0 S_h^0 \sigma k_3 k_4)^2 + 4\lambda_1^0 \lambda_v^0 S_h^0 S_v^0 \sigma \sigma_1 k_1 k_2 k_3 k_4\right)^{\frac{1}{2}}\right\}.$$

Again $g(0) = -m < 0$ and $g(1) = 1 - (l + m)$. Define $R_o' = l + m$ that is $R_0' = \frac{\sigma}{k_1 k_2 k_3 k_4}(\lambda_2^0 S_h^0 k_3 k_4 + \lambda_1^0 S_h^0 \sigma_1 \lambda_v^0 S_V^0) = R_{0S}' + R_{0V}'$

where $R_{0S}' = \frac{\lambda_2^0 S_h^0 k_3 k_4 \sigma}{k_1 k_2 k_3 k_4}$ is the contribution from sexual transmission and $R_{0V}' = \frac{\lambda_1^0 S_h^0 \sigma_1 \lambda_v^0 S_v^0 \sigma}{k_1 k_2 k_3 k_4}$ is the contribution from mosquito (vector) transmission. Again from the relation $g(1) = 1 - R_0'$ we have the following three observation:

(i) when $R_0' = 1$ then $g(1) = 0$ thus the positive root of the equation $g(\lambda) = 0$ is one i.e $R_0 = 1$ (ii) when $R_0' < 1$ then $g(1) > 0$ so the positive root of the equation $g(\lambda) = 0$ lies between zero and one as $g(0) < 0$ thus $R_0 < 1$. (iii) when $R_0' > 1$ then $g(1) < 0$ again $g(0) < 0$ so positive root of $g(\lambda) = 0$ greater than one that is $R_0 > 1$. Thus from the above three observation one can conclude that $R_0' = 1(< 1, > 1)$ if and only if $R_0 = 1(< 1, > 1)$. Since two threshold numbers R_0 and R_0' are equivalent so we use only R_0' in the next part of the paper.

3.2.1. Local stability of the disease free equilibrium

Lemma 3. *The disease free equilibrium* (DFE) E_0 *is locally asymptotically stable for* $R_0' < 1$ *and unstable for* $R_0' > 1$ *where* R_0' *is defined in the text.*

Proof. *The variational matrix of the model* (1) *at the disease free equilibrium* $E_0(S_h^0, E_h^0, I_h^0, R_h^0, S_v^0, E_v^0, I_v^0)$ *is given by*

$$J(E_0) = \begin{pmatrix} -(\mu+a) & 0 & -\lambda_2^0 S_h^0 & 0 & 0 & 0 & -\lambda_1^0 S_h^0 \\ 0 & -k_1 & \lambda_2^0 S_h^0 & 0 & 0 & 0 & \lambda_1^0 S_h^0 \\ 0 & \sigma & -k_2 & 0 & 0 & 0 & 0 \\ a & 0 & \gamma & -\mu & 0 & 0 & 0 \\ 0 & 0 & -\lambda_v^0 S_v^0 & 0 & -k_4 & 0 & 0 \\ 0 & 0 & \lambda_v^0 S_v^0 & 0 & 0 & -k_3 & 0 \\ 0 & 0 & 0 & 0 & 0 & \sigma_1 & -k_4 \end{pmatrix}$$

The characteristic roots corresponding to matrix $J(E_0)$ are $-(\mu+a), -\mu, -k_4$ and the remaining four roots are roots of the following equation:

$$x^4 + m_1 x^3 + m_2 x^2 + m_3 x + m_4 = 0$$

where $m_1 = k_1 + k_2 + k_3 + k_4$, $m_2 = k_1 k_2 + k_1 k_3 + k_1 k_4 + k_2 k_3 + k_2 k_4 + k_3 k_4 - \sigma c \alpha_2$,
$m_3 = k_1 k_3 k_4 + k_2 k_3 k_4 + (k_3 + k_4)(k_1 k_2 - \sigma c \alpha_2)$, $m_4 = k_1 k_2 k_3 k_4 (1 - R_0')$

Now by the Routh-Hurtwiz criteria the eigen values of the block matrix B will be negative or have negative real part if $m_i > 0$, for $i = 1, 2, 3, 4$ and $m_1 m_2 m_3 > m_1^2 m_4 + m_3^2$. All these conditions will be satisfied if $R_0' < 1$. Thus by Routh-Hurtwiz criteria the disease free equilibrium (DFE) is locally asymptotically stable if $R_0' < 1$. Thus the disease free equilibrium (DFE) E_0 is locally asymptotically stable for $R_0' < 1$ otherwise it is unstable.

Using the Lemma-3 we can say that zika virus can be eliminated from the population when R_0' can be brought to a value less than unity. It is clear from the expression of R_0 that with the increase of both the rate of awareness (a) in host population and the rate of effective mosquito control (b) R_0 decreases. Thus the factors a and b help us to keep the value of R_0' below unity and increase the range of stability of the disease free equilibrium. Thus we can speak that awareness in host population and vector control helps the society to eliminate zika virus from human population.

3.2.2. Global asymptotic stability of the disease free equilibrium

In this section we have studied the global asymptotic stability of the disease free equilibrium (DFE) to ensure that the elimination of zika virus i.e. elimination of disease is independent of the initial sizes of the subpopulations of the model. For this purpose we consider the feasible region $\Omega_1 = \{X \in \Omega : S_h \leq S_h^0, S_v \leq S_v^0\}$ where $X = (S_h, E_h, I_h, R_h, S_v, E_v, I_v)$ and to establish the invariance of the region we shall establish the following Lemma.

Lemma 4. *The region Ω_1 is a positively invariant for the model* (1).
Proof: *From the first equation of the model* (1) *we have*

$$\frac{dS_h}{dt}(t) = \pi - (\lambda_1 + \lambda_2)S_h(t) - (\mu+a)S_h(t) \leq \pi - (\mu+a)S_h(t) = (\mu+a)\left(\frac{\pi}{\mu+a} - S_h(t)\right)$$

$= (\mu+a)(S_h^0 - S_h(t))$ as $S_h^0 = \frac{\pi}{\mu+a}$ which gives $S_h(t) \leq S_h^0 - [S_h^0 - S_h(0)]e^{-(\mu+a)t}$. Thus if $S_h(0) \leq S_h^0$ for all $t \geq 0$ then $S_h(t) \leq S_h^0$ for all $t \geq 0$.
Again from the fifth equation of the model (1) we have

$$\frac{dS_v}{dt}(t) = \pi_1 - \lambda_v S_v - (\mu_1 + b)S_v(t) \leq \pi_1 - (\mu_1 + b)S_v(t)$$

$$= (\mu_1 + b)\left\{\frac{\pi_1}{\mu_1 + b} - S_v(t)\right\} = (\mu_1 + b)\left(S_v^0 - S_v(t)\right).$$

Which gives $S_v(t) \leq S_v^0 - (S_v^0 - S_v(0))e^{-(\mu_1+b)t}$. Thus if $S_v(0) \leq S_v^0$ for all $t \geq 0$ then $S_v(t) \leq S_v^0$ for all $t \geq 0$.
Summing above two we have the region Ω_1 is positively invariant and attracts all solutions in $\Re^7$ for the model (1). In the next theorem we have studied the global asymptotic stability of E_0.

Theorem 1. *The disease free equilibrium E_0 of the model* (1) *is globally asymptotically stable (GAS) in Ω_1 whenever $R_0' \leq 1$.*
Proof: Let $X_1 = (S_h, R_h, S_v)$ and $X_2 = (E_h, I_h, E_v, I_v)$ and grouping the model (1) *into*

$$\frac{dX_1}{dt} = F(X_1, 0)$$

$$\frac{dX_2}{dt} = G(X_1, X_2)$$

where $F(X_1, 0)$ is obtained from the right hand side of first, fourth and fifth equations of the model (1) with $E_h = I_h = E_v = I_v = 0$ and $G(X_1, X_2)$ is obtained from the right hand side of second, third, sixth and seventh equations of the model (1).

Now considering the reduced model:

$$\left. \begin{array}{l} \dfrac{dS_h}{dt} = \pi - (\mu + a)S_h \\[2mm] \dfrac{dR_h}{dt} = -\mu R_h + aS_h \\[2mm] \dfrac{dS_v}{dt} = \pi_1 - (\mu_1 + b)S_v \end{array} \right\} \tag{5}$$

Let $X_1^0 = (S_h^0, R_h^0, S_v^0) = \left(\frac{\pi}{\mu+a}, \frac{a\pi}{\mu(\mu+a)}, \frac{\pi_1}{\mu_1+b} \right)$ be the equilibrium of the reduced model (5). Now we shall show that X_1^0 is a globally stable equilibrium in Ω_1. To prove this we solve the equations (5) which gives:

$S_h(t) = \frac{\pi}{\mu+a} + \left[S_h(0) - \frac{\pi}{\mu+a} \right] e^{-(\mu+a)t}, S_v(t) = \frac{\pi_1}{\mu_1+b} + \left[S_v(0) - \frac{\pi_1}{\mu_1+b} \right] e^{-(\mu_1+b)}$ and $R_h(t) = \frac{a\pi}{\mu(\mu+a)} - \left(S_h(0) - \frac{\pi}{\mu+a} \right) e^{-(\mu+a)t} +$

$\left(R_h(0) + S_h(0) - \frac{\pi}{\mu+a} - \frac{a\pi}{\mu(\mu+a)} \right) e^{-\mu t}$.

Thus $S_h \to \frac{\pi}{\mu+a}, R_h \to \frac{a\pi}{\mu(\mu+a)}, S_v \to \frac{\pi_1}{\mu_1+b}$ as $t \to \infty$.

This asymptotic nature is independent of initial conditions in Ω_1. Hence the convergence of solutions of (2) is global in Ω_1. Next we require $G(X_1, X_2)$ is to satisfy the following two conditions given in Castill-Chavez et al (Castillo-Chavez, Blower, Van den Driessche, Kirschner, & Yakubu, 2002), namely

1. $G(X_1, \vec{0}) = \vec{0}$ and 2. $\widehat{G}(X_1, X_2) = D_{X_2} G(X_1^0, \vec{0}) X_2 - G(X_1, X_2), \widehat{G}(X_1, X_2) \geq 0$ Where $(X_1^0, \vec{0}) = \left(\frac{\pi}{\mu+a}, 0, 0, \frac{a\pi}{\mu(\mu+a)}, \frac{\pi_1}{\pi_1+b}, 0, 0 \right)$

and $D_{X_2} G(X_1^0, \vec{0}) = \begin{pmatrix} -k_1 & \lambda_2^0 S_h^0 & 0 & \lambda_1^0 S_h^0 \\ \sigma & -k_2 & 0 & 0 \\ 0 & \lambda_v^0 S_v^0 & -k_3 & 0 \\ 0 & 0 & \sigma_1 & -k_4 \end{pmatrix}$ is the Jacobian of $G(X_1, X_2)$ with respect to (E_h, I_h, E_v, I_v) is calculated at $(X_1^0, \vec{0})$.

It is an M-matrix that is off diagonal elements of the matrix are non-negative. The

relation $\widehat{G}(X_1, X_2) = D_{X_2} G(X_1^0, \vec{0}) X_2 - G(X_1, X_2)$ gives $\widehat{G}(X_1, X_2) = \begin{pmatrix} \widehat{G}_1 \\ 0 \\ \widehat{G}_3 \\ 0 \end{pmatrix}$ with $\widehat{G}_1 = c\alpha_2 \frac{S_h^0}{N_h^0} \left(1 - \frac{N_h^0}{S_h^0} \frac{S_h}{N_h} \right) I_h + b_2 \alpha_1 \frac{S_h^0}{N_h^0} \left(1 - \right.$

$\left. \frac{N_h^0}{S_h^0} \frac{S_h}{N_h} \right) I_v. \widehat{G}_3 = b_2 \alpha_3 \frac{S_v^0}{N_v^0} \left(1 - \frac{N_h^0}{S_v^0} \frac{S_v}{N_h} \right) I_h$.

In the region $\Omega_1, S_h \leq S_h^0, S_v \leq S_v^0$ and hence we get $N_h \leq N_h^0$. Thus, if the human population is at equilibrium level then we have

$\left(1 - \frac{N_h^0}{S_h^0} \frac{S_h}{N_h} \right) > 0, \left(1 - \frac{N_h^0}{S_v^0} \frac{S_v}{N_h} \right) > 0$ therefore $\widehat{G}(X_1, X_2) \geq \vec{0}$. So by the theorem in Castilo-Chavez et al (Castillo-Chavez et al., 2002) the disease free equilibrium is globally asymptotically stable as the human population is constant in the absence of disease induced death. The biological significance of the above theorem is that the zika virus can be eliminated from the population if R_0 can be brought down to a value less than or equal to unity what so ever the size of the initial subpopulation in each class.

3.3. Existence and stability of endemic equilibrium point

In this part we shall find conditions for the existence and stability of endemic equilibrium for the model (1). Let $E_1(S^*_h, E^*_h, I^*_h, R^*_h, S^*_v, E^*_v, I^*_v)$ be an arbitrary endemic equilibrium of the model (1) which have been obtained from the steady states of the model, where the components of E_1 are given below:

$$S_h^* = \frac{\pi}{\lambda_h^* + \mu + a}, E_h^* = \frac{\pi \lambda_h^*}{k_1\left(\lambda_h^* + \mu + a\right)}, I_h^* = \frac{\pi \sigma \lambda_h^*}{k_1 k_2\left(\lambda_h^* + \mu + a\right)}, R_h^* = \frac{\pi\left(\gamma \sigma \lambda_h^* + a k_1 k_2\right)}{\mu k_1 k_2\left(\lambda_h^* + \mu + a\right)}$$

$$S_v^* = \frac{\pi_1}{\lambda_v^* + \mu_1 + b}, E_v^* = \frac{\pi_1 \lambda_v^*}{k_3\left(\lambda_v^* + \mu_1 + b\right)}, I_v^* = \frac{\pi_1 \sigma_1 \lambda_v^*}{k_3 k_4\left(\lambda_v^* + \mu_1 + b\right)}$$

with

$$\lambda_v^* = \frac{b_2 \alpha_3 I_h^*}{N_h^*} = \frac{b_2 \alpha_3 \mu \sigma \lambda_h^*}{k_1 k_2\left(\lambda_h^* + \mu + a\right)} \tag{6}$$

$$\lambda_h^* = \frac{b_2 \alpha_1 I_v^*}{N_h^*} + \frac{c \alpha_2 I_h^*}{N_h^*} = \frac{\mu}{\pi}\left[\frac{b_2 \alpha_1 \pi_1 \sigma_1 \lambda_v^*}{k_3 k_4\left(\lambda_v^* + \mu_1 + b\right)} + \frac{c \alpha_2 \pi \sigma \lambda_h^*}{k_1 k_2\left(\lambda_h^* + \mu + a\right)}\right] \tag{7}$$

The expressions of λ_v^*, λ_h^* represent the forces of infection of mosquitoes and human at steady state. Substituting the value of λ_v^* from (6) in (7) and simplifying we get the quadratic equation satisfied by λ_h^* in the form:

$$c_0 \lambda_h^{*2} + c_1 \lambda_h^* + c_2 = 0 \tag{8}$$

where $\quad c_0 = \pi k_1 k_2 k_3 k_4\{b_2 \alpha_3 \mu \sigma + k_1 k_2(\mu_1 + b)\} > 0, c_2 = \pi k_1^2 k_2^2 k_3 k_4 (\mu + a)^2(\mu_1 + b)(1 - R_0')$ The

$c_1 = \pi k_1 k_2 k_3 k_4(\mu + a)[b_2 \alpha_3 \mu \sigma + 2 k_1 k_2(\mu_1 + b)] - \mu \sigma[k_1 k_2 b_2^2 \alpha_1 \alpha_3 \pi_1 \sigma_1 \mu + \{b_2 \alpha_3 \mu \sigma + k_1 k_2(\mu_1 + b)\}c \alpha_2 \pi k_3 k_4]$

endemic equilibrium of the model (1) can be obtained by solving the quadratic equation (8) for λ_h^* and substituting into (1). From the expression of λ_h^* it is clear that c_0 is always positive and c_2 is positive if $R_0' < 1$. Since equation (8) is a second degree equation in λ_h^*, depending on values of λ_h^* the number of endemic equilibrium point will be generated. Thus from the above discussions we can summarize the following theorem:

Theorem 2. *The model* (1) *has*

(a) *An endemic equilibrium if* $c_2 < 0 \Leftrightarrow R_0' > 1$ *or* $c_1 < 0, c_2 = 0$ *that is* $R_0' = 1$.
(b) *A unique coincident endemic equilibrium if* $c_1 < 0$ *and* $c_1^2 - 4 c_0 c_2 = 0$.
(c) *Two endemic equilibria exists if* $c_2 > 0$ *that is* $R_0' < 1$, $c_1 < 0$ *and* $c_1^2 - 4 c_0 c_2 > 0$
(d) *No endemic equilibrium exist other case.*

Theorem 3. *If* $R_0' > 1$ *then the endemic equilibrium of the model* (1) *is locally asymptotically stable.*
Proof: *To prove this theorem we shall use the Krasnoselskii sub linearity trick method* (Esteva & Vargas, 2000; Hethcote & Thieme, 1985). *Here we shall prove that the linearized part of* (1) *around the endemic equilibrium* E_1 *has no solution of the form*

$$\overrightarrow{Y}(t) = \overrightarrow{Y}_0 e^{\omega t} \tag{9}$$

with $\overrightarrow{Y}_0 = (Y_1, Y_2, Y_3, Y_4, Y_5), Y_i, \omega \in C$ *and* $\text{Re}(\omega) \geq 0$ *where C is the set of complex numbers.*
From the system of equations (1) *we consider the following subsystem*:

$$\frac{dE_h}{dt} = \left(\frac{b_2 \alpha_1 I_v}{N_h} + \frac{c \alpha_2 I_h}{N_h}\right)(N_h - E_h - I_h - R_h) - k_1 E_h$$

$$\frac{dI_h}{dt} = \sigma E_h - k_2 I_h$$

$$\frac{dR_h}{dt} = \gamma I_h - \mu R_h + a(N_h - E_h - I_h - R_h) \tag{10}$$

$$\frac{dE_v}{dt} = \frac{b_2 \alpha_3 I_h}{N_h}(N_v - E_v - I_v) - k_3 E_v$$

$$\frac{dI_v}{dt} = \sigma_1 E_v - (\mu_1 + b)I_v$$

Linearizing (10) *around the endemic equilibrium* $E_1(S_h^*, E_h^*, I_h^*, R_h^*, S_v^*, E_v^*, I_v^*)$ *we get*

$$\frac{dE_h}{dt} = -\left(\frac{b_2\alpha_1 I_v^*}{N_h^*} + \frac{c\alpha_2 I_h^*}{N_h^*} + k_1\right)E_h - \left(\frac{b_2\alpha_1 I_v^*}{N_h^*} + \frac{c\alpha_2 I_h^*}{N_h^*} - \frac{c\alpha_2 S_h^*}{N_h^*}\right)I_h - \left(\frac{b_2\alpha_1 I_v^*}{N_h^*} + \frac{c\alpha_2 I_h^*}{N_h^*}\right)R_h + \frac{b_2\alpha_1 S_h^*}{N_h^*}I_v$$

$$\frac{dI_h}{dt} = \sigma E_h - k_2 I_h$$

$$\frac{dR_h}{dt} = -aE_h + (\gamma - a)I_h - (\mu + a)R_h \tag{11}$$

$$\frac{dE_v}{dt} = \frac{b_2\alpha_3 S_v^*}{N_h^*}I_h - \left(\frac{b_2\alpha_3 I_h^*}{N_h^*} + k_3\right)E_v - \frac{b_2\alpha_3 I_h^*}{N_h^*}I_v$$

$$\frac{dI_v}{dt} = \sigma_1 E_v - (\mu_1 + b)I_v$$

The jacobian of the linear system (11) at E_1 is

$$J(E_1) = \begin{pmatrix} -(\lambda_h^* + k_1) & J_2 - \lambda_h^* & -\lambda_h^* & 0 & J_3 \\ \sigma & -k_2 & 0 & 0 & 0 \\ -a & \gamma - a & -(\mu + a) & 0 & 0 \\ 0 & J_4 & 0 & -(\lambda_v^* + k_3) & -\lambda_v^* \\ 0 & 0 & 0 & \sigma_1 & -k_4 \end{pmatrix}$$

where $J_2 = \frac{c\alpha_2 S_h^*}{N_h^*}, J_3 = \frac{b_2\alpha_1 S_h^*}{N_h^*}, J_4 = \frac{b_2\alpha_3 S_v^*}{N_h^*}$.

Substitution of a solution of the form (9) in the linearized model (11) yields the following linear equations:

$$\begin{aligned}
\omega Y_1 &= -(\lambda_h^* + k_1)Y_1 + (J_2 - \lambda_h^*)Y_2 - \lambda_h^* Y_3 + J_3 Y_5 \\
\omega Y_2 &= \sigma Y_1 - k_2 Y_2 \\
\omega Y_3 &= -aY_1 - (a - \gamma)Y_2 - (\mu + a)Y_3 \\
\omega Y_4 &= J_4 Y_2 - (\lambda_v^* + k_3)Y_4 - \lambda_v^* Y_5 \\
\omega Y_5 &= \sigma_1 Y_4 - k_4 Y_5
\end{aligned} \tag{12}$$

Solving for Y_2, Y_3, Y_4 from second, third and fifth equation of (12) and then substituting these results into its first and fourth equations we get the following equivalent system:

$$\left[1 + \frac{1}{k_1}\left\{\omega + \frac{\lambda_h^*(\omega + \mu)}{\omega + \mu + a} + \frac{\lambda_h^*\sigma}{\omega + k_2}\cdot\frac{\omega + \mu + \gamma}{\omega + \mu + a}\right\}\right]Y_1 = \frac{J_2}{k_1}Y_2 + \frac{J_3}{k_1}Y_5, \quad \left(1 + \frac{\omega}{k_2}\right)Y_2 = \frac{\sigma}{k_2}Y_1$$

$$\left(1 + \frac{\omega}{\mu + a}\right)Y_3 = -\frac{k_2 + \sigma + \omega}{(\mu + a)(k_2 + \omega)}aY_1 + \frac{\gamma}{\mu + a}Y_2 \tag{13}$$

$$\left(1 + \frac{\lambda_v^*\sigma_1}{(\omega + k_4)(\lambda_v^* + k_3)} + \frac{\omega}{\lambda_v^* + k_3}\right)Y_4 = \frac{J_4}{\lambda_v^* + k_3}Y_2, \quad \left(1 + \frac{\omega}{k_4}\right)Y_5 = \frac{\sigma_1}{k_4}Y_4$$

Adding the first and third equations of (13) and removing the negative term of the left hand side (Esteva, Gumel, & de Leon, 2009) we get the following system of equations:

$$\left.\begin{aligned}
[1 + G_1(\omega)]Y_1 + [1 + G_3(\omega)]Y_3 &= (M\vec{Y})_1 + (M\vec{Y})_3 \\
[1 + G_2(\omega)]Y_2 &= (M\vec{Y})_2 \\
[1 + G_4(\omega)]Y_4 &= (M\vec{Y})_4 \\
[1 + G_5(\omega)]Y_5 &= (M\vec{Y})_5
\end{aligned}\right\} \tag{14}$$

where, $G_1(\omega) = \frac{1}{k_1}\left[\omega + \frac{\lambda_h^*(\omega + \mu)}{\omega + \mu + a} + \frac{1}{k_2 + \omega}\left\{\frac{\lambda_h^*\sigma(\omega + \mu + \gamma)}{\omega + \mu + a} + \frac{ak_1(k_2 + \sigma + \omega)}{\mu + a}\right\}\right], G_2(\omega) = \frac{\omega}{k_2}, G_3(\omega) = \frac{\omega}{\mu + a}, G_4(\omega) = \frac{1}{\lambda_v^* + k_3}\left(\omega + \frac{\lambda_v^*\sigma_1}{\omega + k_4}\right), G_5(\omega) = \frac{\omega}{k_4},$

and $M = \begin{pmatrix} 0 & m_1 & 0 & 0 & m_2 \\ m_3 & 0 & 0 & 0 & 0 \\ 0 & m_4 & 0 & 0 & 0 \\ 0 & m_5 & 0 & 0 & 0 \\ 0 & 0 & 0 & m_6 & 0 \end{pmatrix}$, where $m_1 = \frac{J_2}{k_1}, m_2 = \frac{J_3}{k_1}, m_3 = \frac{\sigma}{k_2}, m_4 = \frac{\gamma}{\mu+a}, m_5 = \frac{J_4}{\lambda_v^* + k_3}, m_6 = \frac{\sigma_1}{k_4}$.

Here the notation $(M\overrightarrow{Y})_i$ represent the i-th co-ordinate of the vector $(M\overrightarrow{Y})$. It should be noted that the matrix M has non-negative entries and the endemic equilibrium $E_1 = (E_h^*, I_h^*, R_h^*, E_v^*, I_v^*, I_v^*)$ satisfies $E_1 = ME_1$. If Y is a solution of (14) then it is possible to find a minimal positive number r such that

$$|\overline{Y}| \le rE_1 \tag{15}$$

where $|\overline{Y}| = (|Y_1|, |Y_2|, |Y_3|, |Y_4|, |Y_5|)$. Here the number r is also the minimal positive number that satisfies the inequality $|Y_1| + |Y_3| \le r(E_h^* + R_h^*)$. We want to show that $\mathrm{Re}(\omega) < 0$. On the contrary we assume $\mathrm{Re}(\omega) \ge 0$ and we consider the two cases: $\omega = 0$ and $\omega \ne 0$.

In first case $\omega = 0$ the system of equations (12) is homogeneous linear system of equations. It is clear that the coefficient determinant Δ is non zero and consequently the system (12) has the unique solution $\overline{Y} = \overline{0}$ which corresponds to the disease free steady state of the system (1).

Next we consider the second case $\omega \ne 0$. By the assumption $\mathrm{Re}(\omega) \ge 0$, we have $\mathrm{Re}G_i(\omega) \ge 0, (i = 1, 2, 3, 4, 5)$ which implies that $|1 + G_i(\omega)| > 1$ for all i. Let us now define $G(\omega) = \min|1 + G_i(\omega)|, i = 1, 2, 3, 4, 5$. Then $G(\omega) > 1$ or equivalently $\frac{r}{G(\omega)} < r$. The property of minimality of r implying $|\overline{Y}| > \frac{r}{G(\omega)}E_1$. Now taking norms of both sides of the second equation of (14) we get

$$G(\omega)|Y_2| \le M(|Y|)_2 \le r(M|E_1|)_2 \le rI_h^* \tag{16}$$

This inequality implies $|Y_2| \le \frac{r}{G(\omega)}I_h^*$ which contradicts. Hence $\mathrm{Re}(\omega) < 0$. Thus the real parts of all eigenvalues of the characteristic equation of the linear system (1) will be negative. So E_1 is locally asymptotically stable.

3.4. Backward bifurcation

In this section we shall study the possibility of a backward bifurcation in the zika model (1) using centre manifold theorem as discussed by in Castillo-Chavez and Song (Castillo-Chavez & Song, 2004).

Theorem 4. The model (1) undergoes backward bifurcation at $R_0' = 1$ whenever the sign of the coefficient a' is positive where a' is defined in (18).

Proof: We redefine the model (1) by changing the variables:
Let $S_h = x_1, E_h = x_2, I_h = x_3, R_h = x_4, S_v = x_5, E_v = x_6, I_v = x_7$. So that

$$N_h = x_1 + x_2 + x_3 + x_4, N_v = x_5 + x_6 + x_7$$

Applying vector notation $\overrightarrow{x} = (x_1, x_2, x_3, x_4, x_5, x_6, x_7)^T$ the model (1) can be written as $\frac{d\overrightarrow{x}}{dt} = \overrightarrow{f}(\overrightarrow{x})$ where $\overrightarrow{f} = (f_1, f_2, f_3, f_4, f_5, f_6, f_7)^T$ as follows:

$$\begin{aligned}
\frac{dx_1}{dt} &= f_1 = \pi - \left(\frac{b_2\alpha_1 x_7 + c\alpha_2 x_3}{x_1 + x_2 + x_3 + x_4}\right)x_1 - (\mu + a)x_1 \\
\frac{dx_2}{dt} &= f_2 = \left(\frac{b_2\alpha_1 x_7 + c\alpha_2 x_3}{x_1 + x_2 + x_3 + x_4}\right)x_1 - (\sigma + \mu)x_2 \\
\frac{dx_3}{dt} &= f_3 = \sigma x_2 - (\gamma + \mu)x_3 \\
\frac{dx_4}{dt} &= f_4 = \gamma x_3 - \mu x_4 + a x_1 \\
\frac{dx_5}{dt} &= f_5 = \pi_1 - \frac{b_2\alpha_3 x_3 x_5}{x_1 + x_2 + x_3 + x_4} - (\mu_1 + b)x_5 \\
\frac{dx_6}{dt} &= f_6 = \frac{b_2\alpha_3 x_3 x_5}{x_1 + x_2 + x_3 + x_4} - (\sigma_1 + \mu_1 + b)x_6 \\
\frac{dx_7}{dt} &= f_7 = \sigma_1 x_6 - (\mu_1 + b)x_7
\end{aligned} \tag{17}$$

For the above system the disease free equilibrium (DFE) E_0' given by $E_0' = (x_1^0, 0, 0, x_4^0, x_5^0, 0, 0)$ *where* $x_1^0 = \frac{\pi}{\mu+a}, x_4^0 = \frac{a\pi}{\mu(\mu+a)}, x_5^0 = \frac{\pi_1}{\mu_1+b}$

The jacobian matrix of the above system at the disease free equilibrium E_0 is given by

$$
J(E_0) = \begin{pmatrix}
-(\mu+a) & 0 & -\lambda_2^0 x_1^0 & 0 & 0 & 0 & -\lambda_1^0 x_1^0 \\
0 & -k_1 & \lambda_2^0 x_1^0 & 0 & 0 & 0 & \lambda_1^0 x_1^0 \\
0 & \sigma & -k_2 & 0 & 0 & 0 & 0 \\
a & 0 & \gamma & -\mu & 0 & 0 & 0 \\
0 & 0 & -\lambda_v^0 x_5^0 & 0 & -k_4 & 0 & 0 \\
0 & 0 & \lambda_v^0 x_5^0 & 0 & 0 & -k_3 & 0 \\
0 & 0 & 0 & 0 & 0 & \sigma_1 & -k_4
\end{pmatrix}.
$$

Taking α_3 as a bifurcation parameter we found $R_0'(\alpha_3 = \alpha_3^*) = 1$, which gives. The jacobian of the transformed model (17) at the disease free equilibrium at $\alpha_3 = \alpha_3^*$ has a simple zero eigenvalue and all other eigenvalues have negative real part. So the centre manifold theory can be used to study the dynamics of the model (17) near $\alpha_3 = \alpha_3^*$. In particular we will use the theorem given by Castillo-Chavez and Song (Castillo-Chavez & Song, 2004). *The necessary computation for the theorem given bellow:*

The right eigenvector:

The right eigenvector of the jacobian associated with zero eigenvalue at $\alpha_3 = \alpha_3^*$ is given by: $W = (w_1, w_2, w_3, w_4, w_5, w_6, w_7)^T$ *where,* $w_1 = -\left(\frac{c\alpha_2 k_3 k_4 (\mu_1 + b)}{\sigma_1 b_2 \alpha_3^* \pi_1} + \frac{b_2 \alpha_1 \mu}{\pi} \right) \frac{\pi}{(\mu+a)^2}, w_2 = \frac{k_2 k_3 k_4 (\mu_1 + b)\pi}{\sigma \sigma_1 b_2 \alpha_3^* \mu \pi_1}, w_3 = \frac{k_3 k_4 \pi (\mu_1 + b)}{\sigma_1 b_2 \alpha_3^* \mu \pi_1},$

$w_4 = \frac{1}{\mu}(w_3 \gamma + a w_1), w_5 = -\frac{k_3}{\sigma_1}, w_6 = \frac{k_4}{\sigma_1}, w_7 = 1 > 0$

The left eigenvector of the jacobian matrix associated with zero eigenvalue at α_3^* is given by

$V = (0, v_2, v_3, 0, 0, v_6, 1)$ *where* $v_2 = \frac{k_4(\mu+a)}{b_2 \alpha_1 \mu}, v_3 = \frac{k_1 k_4 (\mu+a)}{ab_2 \alpha_1 \mu}$ *,* $v_6 = \frac{\sigma_1}{k_3} > 0$. *The bifurcation coefficients a'and b'are given by*

$$
a' = \sum_{k,i,j=1}^{7} v_k w_i w_j \frac{\partial^2 f_k}{\partial x_i \partial x_j} = v_2 \sum_{i,j=1}^{7} w_i w_j \frac{\partial^2 f_2}{\partial x_i \partial x_j}
$$

where

$$
+ v_3 \sum_{i,j=1}^{7} w_i w_j \frac{\partial^2 f_3}{\partial x_i \partial x_j} + v_6 \sum_{i,j=1}^{7} w_i w_j \frac{\partial^2 f_6}{\partial x_i \partial x_j} + v_7 \sum_{i,j=1}^{7} w_i w_j \frac{\partial^2 f_7}{\partial x_i \partial x_j}
$$

$$
\frac{\partial^2 f_2}{\partial x_3 \partial x_1} = \frac{\partial^2 f_2}{\partial x_1 \partial x_3} = \frac{c\alpha_2 \mu a}{\pi(\mu+a)}, \frac{\partial^2 f_2}{\partial x_7 \partial x_1} = \frac{\partial^2 f_2}{\partial x_1 \partial x_7} = \frac{b_2 \alpha_1 \mu a}{\pi(\mu+a)}, \frac{\partial^2 f_2}{\partial x_7 \partial x_2} = \frac{\partial^2 f_2}{\partial x_2 \partial x_7} = \frac{\partial^2 f_2}{\partial x_7 \partial x_3} = \frac{\partial^2 f_2}{\partial x_3 \partial x_7}
$$

$$
= \frac{\partial^2 f_2}{\partial x_7 \partial x_4} = \frac{\partial^2 f_2}{\partial x_4 \partial x_7} = -\frac{b_2 \alpha_1 \mu^2}{\pi(\mu+a)}, \frac{\partial^2 f_2}{\partial x_3 \partial x_2} = \frac{\partial^2 f_2}{\partial x_2 \partial x_3} = \frac{\partial^2 f_2}{\partial x_4 \partial x_3} = \frac{\partial^2 f_2}{\partial x_3 \partial x_4} = -\frac{c\alpha_2 \mu^2}{\pi(\mu+a)}, \frac{\partial^2 f_2}{\partial x_3^2} = -\frac{2c\alpha_2 \mu^2}{\pi(\mu+a)} \quad \text{and all others de-}
$$

$$
\frac{\partial^2 f_6}{\partial x_3 \partial x_1} = \frac{\partial^2 f_6}{\partial x_1 \partial x_3} = \frac{\partial^2 f_6}{\partial x_3 \partial x_2} = \frac{\partial^2 f_6}{\partial x_2 \partial x_3} = \frac{\partial^2 f_6}{\partial x_4 \partial x_3} = \frac{\partial^2 f_6}{\partial x_3 \partial x_4} = \frac{1}{2}\frac{\partial^2 f_6}{\partial x_3^2} = -\frac{b_2 \alpha_3^* \pi_1 \mu^2}{(\mu+b)\pi^2}, \frac{\partial^2 f_6}{\partial x_5 \partial x_3} = \frac{\partial^2 f_6}{\partial x_3 \partial x_5} = \frac{b_2 \alpha_3^* \mu}{\pi}.
$$

rivatives are zero so that

$$
a' = \frac{2k_4 a r_2}{b_2 \alpha_1 \pi}(rc\alpha_2 + b_2 \alpha_1) + \frac{2\mu\sigma_1 rr_2 \alpha_3^* \pi_1}{(\mu_1 + b)\pi^2 k_3}(b_2\mu + a) - \frac{2k_4}{\pi b_2 \alpha_1} \begin{pmatrix} rr_2 c\alpha_2 a + r_2 b_2 \alpha_1 a + rr_3 c\alpha_2 \mu + r_3 b_2 \alpha_1 \mu + r^2 c\alpha_2 \mu + \\ r^2 c\alpha_2 \gamma + rb_2 \alpha_2 \mu + r\gamma b_2 \alpha_1 \end{pmatrix}
$$

$$
\frac{2\mu\sigma_1 r\alpha_3^*}{(\mu_1 + b)\pi^2 k_3}\left(r_3 b_2 \pi_1 \mu + rb_2 \pi_1 \mu + r\gamma b_2 \pi_1 + \frac{k_3}{\sigma}\pi(\mu_1 + b)b_2 \alpha \right)
$$

(18)

the value of $b' = \sum_{k,i=1}^{7} v_k w_i \frac{\partial^2 f_k}{\partial x_i \partial \alpha_3^*} = v_6 \sum_{i=1}^{7} w_i \frac{\partial^2 f_6}{\partial x_i \partial \alpha_3^*}$ as $\frac{\partial f_k}{\partial \alpha_3^*} = 0, k = 1, 2, 3, 4, 7$ and $v_5 = 0$ and the only non-zero derivative is $\frac{\partial^2 f_6}{\partial x_3 \partial \alpha_3^*} = \frac{b_2 \pi_1 \mu}{\pi(\mu_1 + b)}$. Therefore $b' = \frac{\sigma_1 rb_2 \pi_1 \mu}{k_3 \pi(\mu_1 + b)} > 0$.

Hence the model (1) *undergoes backward bifurcation at* $R'_0 = 1$ *whenever* $a' > 0$.

In backward bifurcation a stable disease free equilibrium (*DFE*) *co-exists with two endemic equilibrium* (*EE*) *among which one is unstable and other one is stable when* $R'_0 < 1$. *The biological significance of the backward bifurcation phenomenon of the zika model* (1) *is that the condition* $R'_0 < 1$ *for elimination of zika from population is the necessary condition but not sufficient, in that case elimination of zika depend on initial sizes of the population that fact is present in* Fig. 2.

4. Model fitting to the Zika infected data in Colombia: Parameter Estimation and Model validation

In this section we have validated the considered Zika model (1) *considering the reported Zika infected human data of* 1 *to* 36 *weeks* 2016 *in Colombia which is given in* Table 2. *The data has been provided by National Institute of Health SIVIGILA, Colombia which also has been used in literature* (Aranda, Gonzalez-Para, & Benincasa, 2019). *We found the best fitted model parameters for the considered model* (1) *with the above said data by using MATLAB minimization software package fmincon. In order to fit the model* (1) *to the weekly reported Zika infected data in Colombia to the year* 2016 *we considered the initial susceptible human as* 19471223 *and the initial number of infected populations as* 2173 *as reported in* (Aranda et al., 2019) *and initial density of the other populations we assume arbitrarily. Similarly, some model parameters are assumed arbitrarily and then using the MATLAB minimization software package the remaining parameters have been estimated and those values summarized in* Table 3.

In Fig. 3 *we have plotted the reported Zika infection data in Colombia from* 1 *to* 36 *week of* 2016 *using blue dots and considering the estimated model parameters we have predicted the density of the infected populations up to* 80 *weeks. It is clear from the prediction of the solution curve that the disease will no longer out break after* 50 *weeks in Colombia, which is supported by the reported real cases in the same region by WHO* (Zika-Epidemiological Repo, 2017). *Our model we predict that there will be* 113 *average weekly cases during* 37 *to* 52 *week of the year* 2016 *which is close to* 130 *reported real cases by WHO* (Zika-Epidemiological Repo, 2017). *According to our model prediction zika will be eradicated from Colombia on or after* 28 *week of* 2017 *which also supported by real data* (Zika-Epidemiological Repo, 2017).

The theoretical finding in Lemma-3, 4 and theorem-1are graphically verified considering the model parameters as given Table 3 (*see* Fig. 4). *For these values of the parameters the value of basic reproduction number is less than unity. Hence the disease free equilibrium point is globally asymptotically stable for these parametric values. In* Fig. 4 *we have presented the time series of* I_h, *and* I_v *for different initial values of the populations. It is clear that if the system starts for different initial points then it will ultimately*
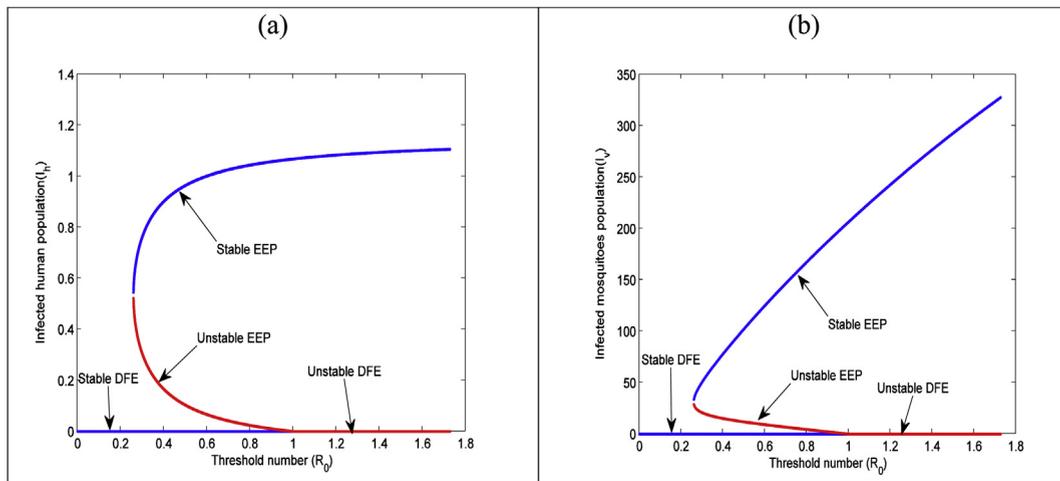

Fig. 2. *Backward bifurcation diagram of the modified zika model* (17) *for:* (*a*) *infected human* (*b*) *infected mosquito population using the parameter values* $\pi = 3.3, \pi_1 = 1000, \mu = 0.8, \mu_1 = 0.35, \alpha_1 = 0.4, \sigma_1 = 2/7$ *and the values of the other parameters presented in* Table 3.

Table 2
The weekly reported data of Zika infection cases in Colombia from 1 to 36 week of 2016 provided by National Institute of Health SIVIGILA, which also used in (Aranda et al., 2019).

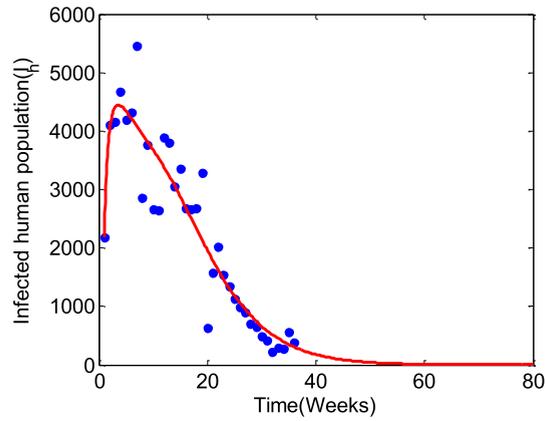| Week	Cases	Week	Cases	Week	Cases	Week	Cases
1	2173	10	2655	19	3281	28	705
2	4105	11	2639	20	638	29	648
3	4166	12	3882	21	1567	30	496
4	4669	13	3808	22	2014	31	416
5	4198	14	3059	23	1539	32	215
6	4316	15	3364	24	1344	33	301
7	5460	16	2671	25	1128	34	271
8	2865	17	2665	26	991	35	568
9	3767	18	2687	27	892	36	383

Fig. 3. *The reported infected populations* (*the blue dots*) *and the best. fitted solution* (*solid red curve*) *the model* (1).

Table 3
Parameter values and their Sensitivity indices of the model (1) with respect to.R_0'.

| Parameter	Values	Source	Sensitivity index
b_2	0.45	Agusto et al. (2017a, 2017b)	1.99928242
μ	0.00019204	Estimated	1.01880565
π_1	100	Assume	0.99964121
α_1	0.04441746	Estimated	0.99964121
α_3	0.04791129	Estimated	0.99964121
σ_1	0.02070591	Estimated	0.50624931
σ	0.35808521	Estimated	$5.36009473 \times 10^{-04}$
α_2	0.03362689	Estimated	$3.58792179 \times 10^{-04}$
c	0.00552894	Estimated	$3.58792179 \times 10^{-04}$
π	0.01747	Kucharski et al. (2016)	-0.99964121
γ	0.07098011	Estimated	-0.99730175
a	0.00000440	Estimated	-0.02239870
μ_1	0.02053120	Estimated	$-1.92341903 \times 10^{-06}$
b	0.00071429	Assume	$-6.69166430 \times 10^{-08}$
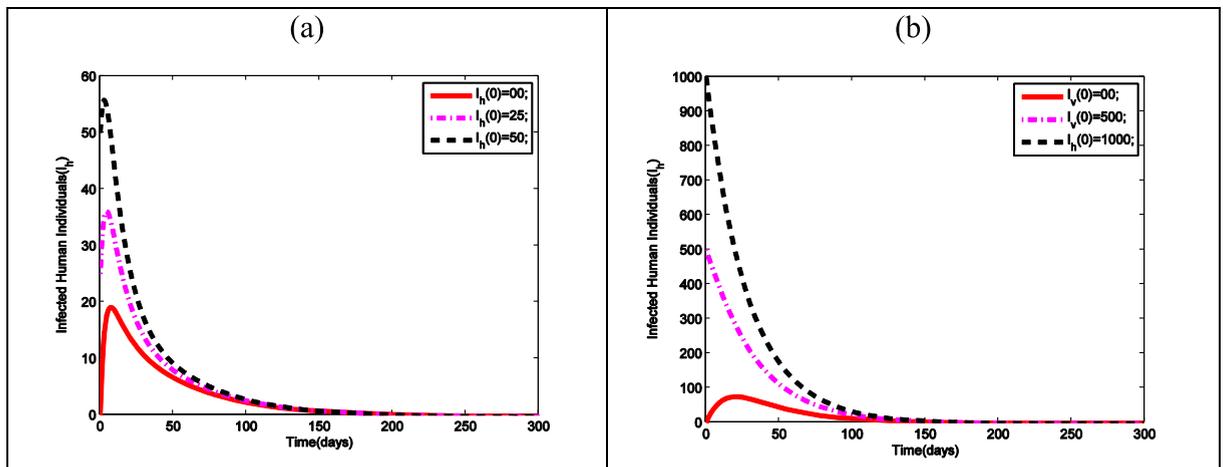
Fig. 4. *Time series for* (*a*) *infected human* I_h *and* (*b*) *infected mosquito* I_v *populations for the parameters given in* Table 3 *with different initial conditions for the model* (1).

converge to $I_h = 0$ and $I_v = 0$ respectively. Thus from the Fig. 4 it clear that system is locally as well globally asymptotically stable if the condition stated in the corresponding lemmas and theorem is satisfied.

Since the system contains fourteen parameters among them some parameters are highly sensitive. A small change of the parameters will affect highly the system. In this next section using sensitivity analysis we shall determine the highly sensitive parameters.

5. Sensitivity analysis

Using sensitivity analysis we shall determine the parameters those have high significant impact on the threshold number R'_0 of the zika model (1). Such analysis tells us the importance of each parameter on disease transmission and this will help the public helth authorities to place of priority for prevention and controlling the spread of the zika virus in the human population. Such information is also important for experimental design, data assimilation and reduction of complex nonlinear model (Powell, Fair, Le Claire, Moore, & Thompson, 2005).

In order to perform such analysis we shall use the normalised forward sensitivity index of a variable with respect to a parameter which is expressed as the ratio of the relative variation in the variable to the relative variation in the parameter. The sensitivity index can be defined using partial derivatives.

Definition 4.1. The normalised forward sensitivity index of R'_0 that depends differentiably on a parameter l is defined by $\gamma_l^{R'_0} = \frac{\partial R'_0}{\partial l} \cdot \frac{l}{R'_0}$ (Chitnis, Hyman, & Cushing, 2008).

Using the explicit expression of R'_0 in the above sensitivity index formula we have derived an expression for the sensitivity of R'_0 with respect to each parameter. Then using the base line values of parameters, given in Table 3 we have estimated the numerical values for the sensitivity index and the results are also summarised in Table 3.

A small variation in a most sensitive parameter will create large quantitative variation. Thus it should be carefully estimated whether a small variation in a least sensitive parameter will not create large variation so it need not require too much effort to estimate such least sensitive parameters.

Table 3 presents the base line value of parameters used for the numerical simulation and it also shows the sensitivity indices of the zika model with respect to R'_0. From Table 3 it is clear that the mosquito biting rate b_2 is the most sensitive parameter with sensitivity index 1.999 which indicates that increase (or decrease) the mosquito biting rate b_2 by 10% will be followed by an immediate increase (or decrease) in R'_0 by 19.99%. Similarly increase (or decrease) of the parameters $\pi_1, \alpha_1, \alpha_3, \sigma_1$ by 10% will be followed by an immediate increase (or decrease) in R'_0 by 9.99%, 9.99%, 9.99%, 5.56% respectively.

Though the recruitment rate of human has the most negative sensitivity index but in the epidemiological context the important parameters which have negative sensitivity indices are γ, a, μ_1, b. The significance of negative sensitivity indices of the above said parameters are increase (or decrease) in the parameters γ, a by 10% will be followed by an immediate decrease (or increase) in R'_0 by 9.97%, 0.224% respectively. In summary, the zika sensitivity analysis identifies the most important parameters driving the transmission mechanism of the zika virus. The results suggest that a control strategy that reduces the mosquito biting rate, recruitment rate of mosquito, transmission probability per biting of susceptible humans by infected mosquito, transmission probability per biting of susceptible mosquito with infected humans, progression rate from exposed to infected mosquito, progression rate from exposed to infected human, transmission probability per sexual contact among a susceptible and infected human and sexual contact rate between a susceptible human to an infected human ($b_2, \pi_1, \alpha_1, \alpha_3, \sigma_1, \sigma,$ α_2, c) respectively and the control strategy that increase rate of recovery rate of infected human, awareness in host population,
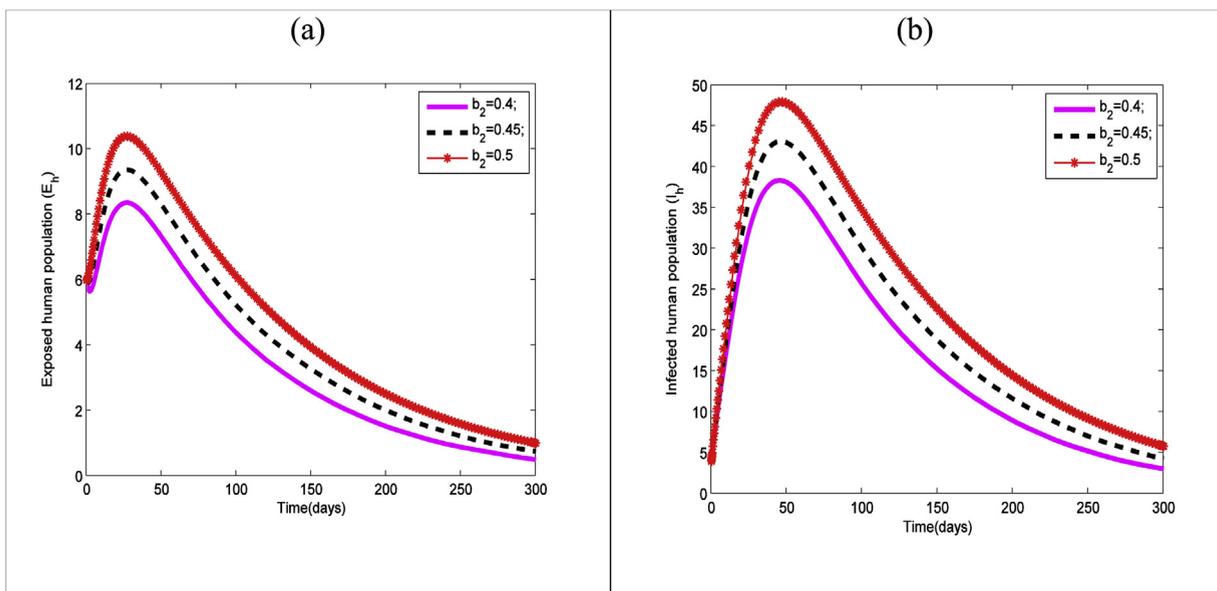

Fig. 5. Time series of the model (1) for the different values of b_2 of (a) Exposed human population (b) infected human population, other parameter values presented in Table 3.

death rate of mosquito and constant rate of effective mosquito control (γ, a, μ_1, b) will effectively resist the spread of zika virus in the human population.

Now, to verify the sensitive parameters we have plotted the solution curve for the number of infected and exposed humans for different values of the model parameters keeping the initial conditions same. To simulate the system numerically we have to use the estimated model parameter as presented in Table 3 with the initial conditions: $S_h(0) = 1000, E_h(0) = 06, I_h(0) = 04$, $R_h(0) = 00, S_v(0) = 4000, E_v(0) = 500, I_v(0) = 100$.

The time series of exposed human and the infectious human are plotted in Fig. 5(a) and (b) respectively for different values of mosquito biting rate (b_2). It is clear from the figures that the number of both class increases due to the increase (decrease) in b_2. Thus the mosquito bite rate plays an important role to spreads the zika virus.

The effect of sexual contact rate (c) between a susceptible human and an infected human on exposed and infectious human population has been presented in Fig. 6(a) and (b) respectively. It is clear from Fig. 6(a and b) that due to increase or decrease of sexual contact rate (c) both the exposed and infectious human population increases or decreases.

The effect of human awareness rate (a) on zika transmission dynamics among human presented in Fig. 7(a and b). From these two figures it is clear that increase of human awareness decreases both exposed and infectious human population and vice-versa.
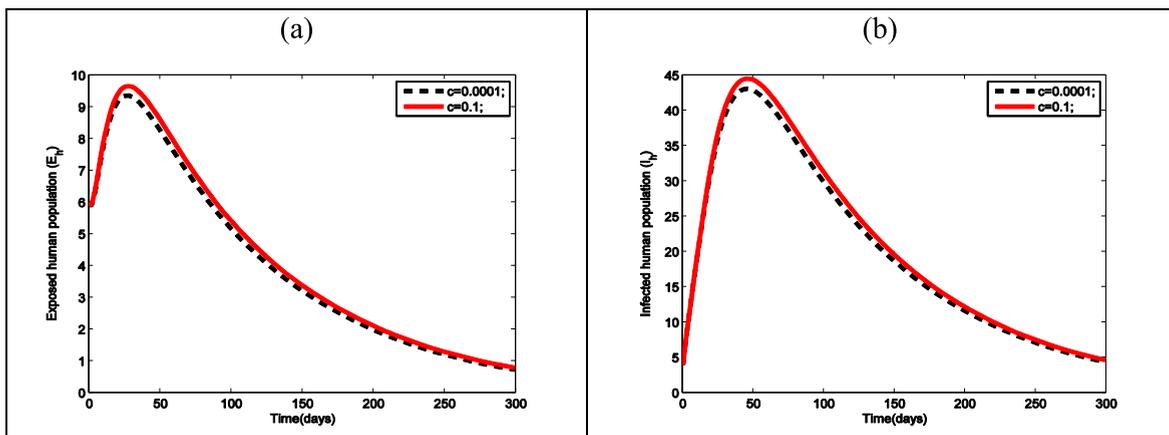

Fig. 6. Time series presenting the effect of Sexual contact rate c between a susceptible human to an infected human on the (a) exposed human and (b) infected human, using the parameter values presented in Table 3.
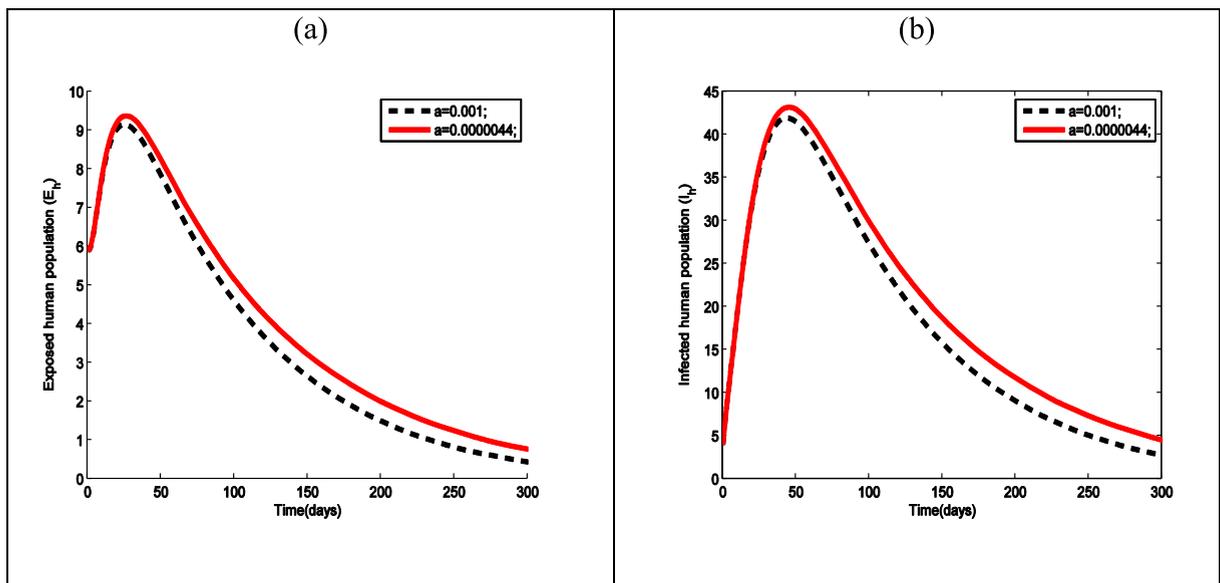

Fig. 7. Time series of Zika model (1) for different values of human awareness a and other parameter values presented in Table 3: (a) exposed human and (b) infected human.

In Fig. 8 we have presented the time series of exposed human and infected human for different values of vector control (b). It is clear from the figure that both the exposed human population and infectious human population decrease as the vector control increase.

Thus from the above series of time series analysis it is clear that the amount of exposed and infected human population decrease when the vector biting rate (b_2), the sexual contact rate (c) among susceptible human to infected human decrease and the human awareness rate (a) the vector control rate (b) increase. Considering above said four facts simultaneously as a precautionary measures we presents the behaviour of the infected human population in Fig. 9. The figure shows that the number of infected human population decreases when the vector biting rate and the sexual contact rate decreases and the human awareness rate and the vector control rate increases simultaneously over a period of time.

6. Effect of sexual transmission on epidemic growth rate and basic reproduction number

In this section we have established the effect of sexual transmission to the epidemic growth rate as well as basic reproduction number. In deterministic epidemic model the disease free equilibrium (DFE) locally stable if the basic reproduction number $R'_0 < 1$ and unstable if $R'_0 > 1$ (Van den Driessche & Watmough, 2002) and for $R'_0 > 1$ disease outbreak occurs. The dominant eigen value of the jacobian matrix at the disease free equilibrium (DFE) is the initial outbreak growth rate (r). In our model the dominant eigenvalue of the jacobian matrix at the DFE is the dominant root of the corresponding characteristic equation (4). It is a four degree equation, so it is not easy to find the explicit expression of the dominant root *i.e.*to find the initial epidemic growth rate of the model. So, we shall establish the effect of sexual transmission on epidemic growth rate and basic reproduction number numerically. In Fig. 10(a) and (b) we have presented the effect of α_2 on the basic reproduction number R_0 and the epidemic growth rate r respectively. Fig. 10(a and b) show that the basic reproduction number and the epidemic growth rate both increase with the increase of the transmission probability per sexual contact between susceptible and infected human.

7. Conclusion

In this work, we have developed and analyzed a deterministic ODE model for Zika virus transmission dynamics that incorporates both mosquito and sexual transmission paths, which also includes vector control and human awareness. The positivity and boundedness of the proposed model are investigated here. We obtained the basic reproduction number by next-generation matrix technique. The steady-state analysis shows that the disease-free equilibrium (DFE) is and globally asymptotically stable if the basic reproduction number R'_0 less than unity. The conditions for the existence of endemic equilibrium of the model are obtained. Using the Krasnoselskii sub linearity trick method we have established that the endemic equilibrium is locally asymptotically stable if the basic reproduction number R'_0 is greater than one. Under some condition the model exhibits the phenomenon of backward bifurcation. The biological significance of this result is that the condition reproduction number less than unity for the elimination of zika virus from the population is the necessary condition but not sufficient. We estimate the model parameters and validate the model by using the reported Zika infection data in Colombia of the year 2016.
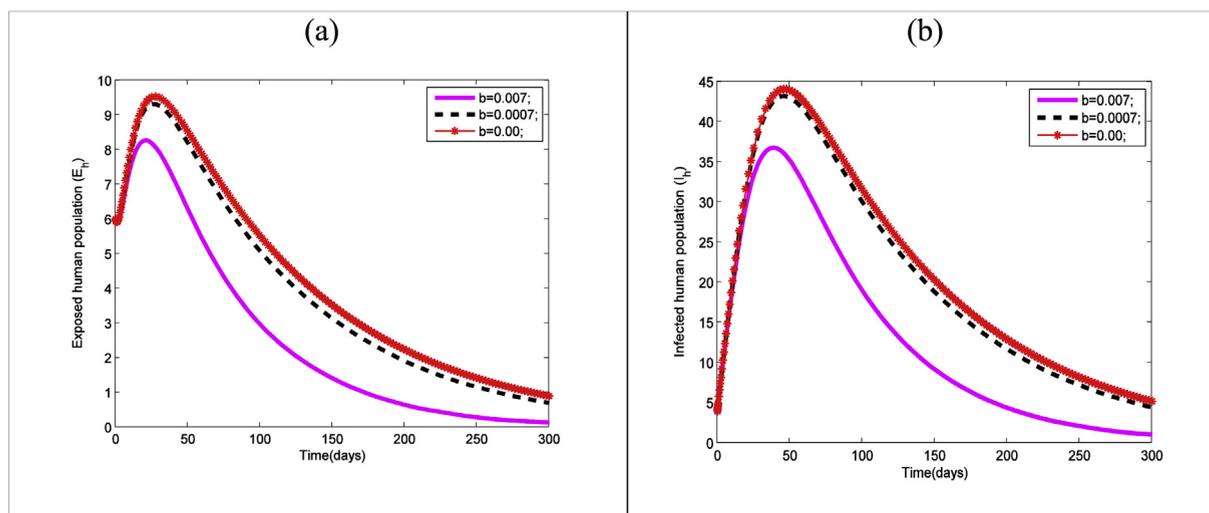

Fig. 8. Time series of the Zika model (1) showing the effect of vector control b on the (a) exposed human and (b) infected human using the parameter values presented in Table 3.
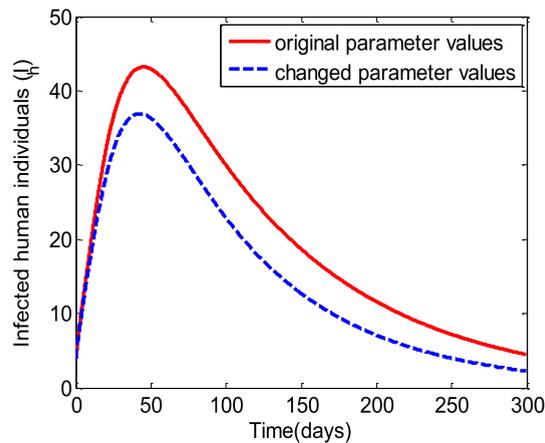
Fig. 9. Time series of the zika model (1) presenting the effect of vector biting rate, sexual contact rate, human awareness and vector control simultaneously on the behaviour of the infected human population. The solid line graphics obtained using the parameter values $b_2 = 0.45, c = 0.00552894, a = 0.0000044, b = 0.00071429$ and the dashed line graphics obtained by using the parameter values $a = 0.0000088, b_2 = 0.4, c = 0.001382235, b = 0.00214287$ the other parameter values presented in Table 3.
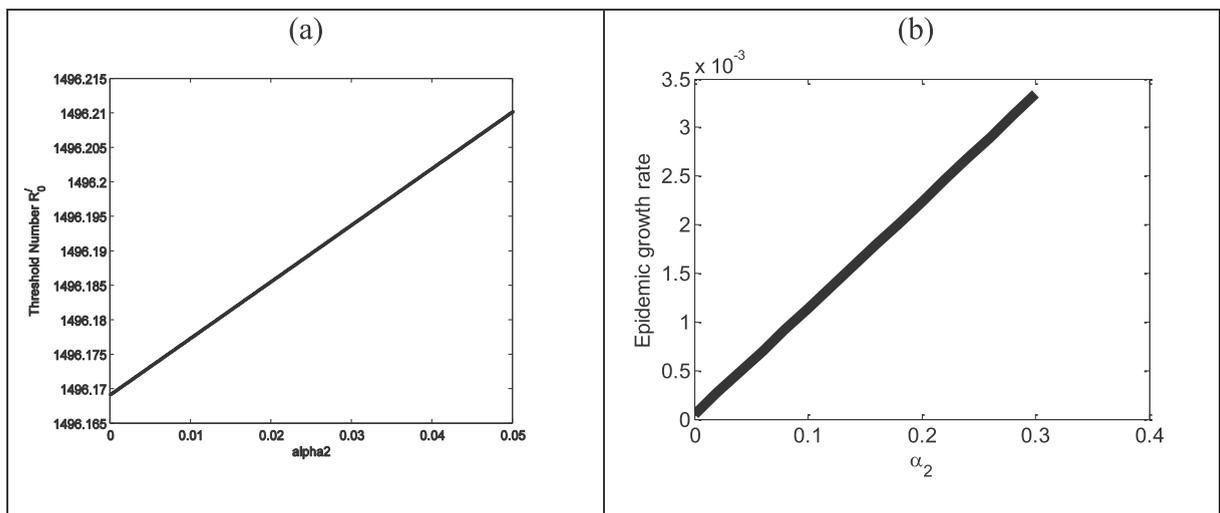

Fig. 10. Presents the effect of α_2 on (a) the basic reproduction number R_0 and on (b) the epidemic growth rate r using the parameter values $\pi = 0.08547, c = 0.4$ and the values of the others parameter presented in Table. 3.

The effect of sexual transmission both on basic reproduction number and epidemic growth rate have been established numerically which shows that with the increase of sexual transmission rate the density of exposed and infected populations both increases. So we can control zika virus by controlling sexual transmission rate. Sensitivity and numerical analyses were done to determine the impact of the parameters on the zika infection. The most effective parameters were found the mosquito biting rate, recruitment rate of mosquito, transmission probability per biting of a susceptible human with an infected mosquito, the rate of the awareness host population and the recovery rate of the infected human population. This model will help the public health planar to frame a policy for controlling Zika. In further, we will extend the model incorporating the optimal control theory.

Declaration of competing interest

The Authors have no conflict of interest regarding the model and methodology.

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