



Available online at <http://scik.org>

J. Math. Comput. Sci. 11 (2021), No. 6, 7665-7698

<https://doi.org/10.28919/jmcs/6274>

ISSN: 1927-5307

## TRANSMISSION DYNAMICS OF ZIKA VIRUS IN PRESENCE OF VERTICAL TRANSMISSION AND SOME PREVENTIVE MEASURES

SUDHANSHU KUMAR BISWAS<sup>1</sup>, UTTAM GHOSH<sup>2,\*</sup>, SUSMITA SARKAR<sup>2</sup>

<sup>1</sup>Department of Mathematics, Sripat Singh College, Jiaganj, Murshidabad, W.B., India

<sup>2</sup>Department of Applied Mathematics, University of Calcutta, Kolkata, India

Copyright © 2021 the author(s). This is an open access article distributed under the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

**Abstract.** Zika virus (ZIKV) infection is a vector-borne human disease which enhances the chance of various types of neurological complications in affected individual. In this work we have studied a mathematical model of ZIKV by incorporating vector, direct (sexual) and vertical transmission paths of the virus. In our model also we have considered different kind of preventive measures like as: protection of susceptible individuals from mosquito bites, isolation of infected individuals from mosquito, protection of susceptible individuals from sexual interaction with infected individuals, and mosquitoes control effort. We have found the analytical expression of basic reproduction number and studied the stability of the disease free equilibrium point. Existence of endemic equilibrium point and its stability are also studied. The proposed model exhibits a backward bifurcation when the virus transmission probability from infected human to mosquito crosses the crucial value. We have fitted the model to real data and estimated the key model parameters and their 95% confidence interval which depict the ZIKV outbreak in French Polynesia in 2013-14. We also have estimated the basic reproduction number using first nine epidemic weeks (EW) data and the estimated value is 2.87 with lower and upper values are 2.47 and 3.32 respectively. The effective reproduction number of the outbreak also has been studied and which decreases gradually from 5.404 to 0.2499 during the period 11<sup>th</sup> October, 2013 and 28<sup>th</sup> March, 2014. According to our sensitivity analysis, the basic reproduction number is the most sensitive with controllable parameters, biting rate, mosquito recruitment

---

\*Corresponding author

E-mail address: [uttam\\_math@yahoo.co.in](mailto:uttam_math@yahoo.co.in)

Received June 12, 2021

rate, mosquito death rate and recovery rate from infection. Finally, numerically we have studied the impact of different parameters on the basic reproduction number and on the number of infected human population.

**Keywords:** Zika virus; stability analysis; backward bifurcation; effective reproduction number; sensitivity analysis.

**2010 AMS Subject Classification:** 37N25, 49J15, 92D30.

## 1. INTRODUCTION

The ZIKV is the pathogen of zika disease. It is a mosquito carried Flavivirus and very similar to DENV (dengue virus) and symptoms of both infections are also very similar. The ZIKV infected *Aedes aegypti* female mosquitoes transmit the virus among the susceptible human population through biting and the virus also transmit from human to mosquito when the susceptible mosquito bites an infected human. The virus may transmit among the susceptible sexual partners from an infected partner through sexual interaction [1, 2, 3, 4, 5, 6, 7]. It was established through the lab base experiments [5, 8, 9, 10] and they showed the existence of ZIKV in semen for a long time period even after it disappears from blood.

Though the initial symptoms of the infection are mild like as headaches, fever, conjunctivitis and joint pain, maculopapular rash etc., but it has long time affect on some permanent disability in human life. It may be cause of microcephaly in newborn infants when the pregnant mother becomes infected by this virus [11, 12]. It also causes of some permanent disabilities such as Guillain-Barre Syndrome [13, 14] and some other neurological complications among infected adult individuals.

The ZIKV infection outbreak was first documented in Yap Island of Micronesia in April 2007 [19, 20, 21] after the first isolation of the virus from a monkey in Uganda in 1947 [15, 16] and some confirmed human infection cases were reported from Africa and South-east Asia until 2007 [15, 17, 18, 44]. First severe outbreak was occurred in French Polynesia and south Pacific in 2013-2014 with an estimated 28000 people were infected. It was a mild infection and was limited to Africa and Pacific Asia up to a date but the disease was spread rapidly in many other parts of the world from 2013-2014 onward. In April 2015, zika outbreak were began from Brazil and then it rapidly spread to many Southern, Central American and Caribbean Countries with more than 140000 suspected and confirmed cases arises and the similar outbreak in

North America was occurred in 2016. For the major outbreak, the WHO declared the zika epidemic as a “ public health emergency of the international concern ” [45] on 1<sup>st</sup> February, 2016. The Emergency Operations Centre of U.S. CDC’s has reached to the highest level of activation on February 3, 2016 [46] to prevent the outbreak. Till date there is no vaccine to protect the infection and no antiviral therapies, medicines are available to treat this infection.

Transmission dynamics of zika virus infection investigation through mathematical modelling which may be useful to provide better understanding, insights into the behaviour of the disease dynamics and its controlling. Several mathematical models have been studied to explore the spreading dynamics and control strategies of zika virus infection after its outbreak among different countries [22, 23, 24, 25, 42, 43, 49].

Kucharski et al. [22] considered an ordinary differential equation model to investigate the transmission dynamics of ZIKV in French Polynesia in 2013-2014 but they neglect sexual transmission path in their model. Gao et al. [23] formulated a Zika model incorporating sexual transmission to study the effect of zika spreading through mathematical modelling but they did not consider the vertical transmission path of the virus. The authors in[24] studied the zika virus dynamics using a mathematical model, where they considered both vector and sexual transmission route without modelling vertical transmission.

Zika virus can transmit vertically like vertical transmission of dengue in mosquitoes [26, 27, 28, 29, 30]. To estimate the effect of vertical transmission, Augusto et al. [31] proposed a zika model incorporating vertical transmission of zika virus in human. Imran et al. [32] included vertical transmission both for human and mosquitoes, but they did not include the sexual transmission of zika virus in their model. Due to lack of particular vaccine, medicine or antiviral therapy to protect from the infection of the virus, different kind of prevention controls like: mosquito bites prevention using mosquito-net, sexual protection, isolation of infected human from mosquitoes and mosquitoes control through insecticide spray are effective ways for protection of zika infection.

Here, we have developed and studied a novel ODE zika model by introducing vertical transmission of the virus in mosquitoes and incorporating the above said prevention controls in the

model [49]. To formulate the mathematical model for spreading of zika virus we are considering the following factors: (i) both vector (mosquito) and sexual (direct) transmission, (ii) vertical transmission in mosquito only, (iii) three types of constant control such as: (a) protect susceptible human from mosquito bites using skin covering dresses or mosquito-net and use of mosquito-repellent at a constant rate, (b) isolate infected human from mosquito by keeping an infected human under mosquito-net until recover from Zika infection to protect zika virus transmission from the infected human to a susceptible mosquito at a constant rate, (c) protect susceptible human from sexual interaction with infected human at a constant rate to protect ZIKV transmission through sex and (iv) mosquito control effort at a constant rate using insecticide spray.

The paper is organised as follows: the model formulation and two basic properties (positivity and bounded property) have been studied in section-2. The steady state and the backward bifurcation analysis have been done in section-3. In section-4, we have studied the ZIKV outbreak in French Polynesia in 2013-2014 including the model fitting to the data, estimated the model parameters estimation and validate the model with real data. The basic reproduction number of the outbreak and the effective reproduction number have been studied in section-5. In section-6, sensitivity analysis of the basic reproduction number has been done and in section-7 we have presented numerical simulation to show the impact of some important parameters on the basic reproduction number and on the infected human population. Finally, in section-8 some conclusive remarks are given.

## 2. MODEL FORMULATION

In order to formulate the model, the human population  $N_h(t)$  at any instant  $t$  is divided into four classes including susceptible individuals  $S_h(t)$ , exposed individuals  $E_h(t)$ , infected individuals  $I_h(t)$  and recovered individuals  $R_h(t)$ , implying  $N_h(t) = S_h(t) + E_h(t) + I_h(t) + R_h(t)$ . Similarly vector population  $N_v(t)$  at the same time  $t$  is divided into three classes viz. susceptible vectors  $S_v(t)$ , exposed vectors  $E_v(t)$  and infected vectors  $I_v(t)$  implying,  $N_v(t) = S_v(t) + E_v(t) + I_v(t)$ .

The disease transmission rate from infected mosquito to the susceptible human is  $\lambda_{hv} = \frac{b_2 \alpha_1 I_v}{N_h}$

and from the infected human to the susceptible mosquito is  $\lambda_{vh} = \frac{b_2\alpha_3(1-q)I_h}{N_h}$ . where  $q$  is the fraction of infected individuals who are isolated from mosquito by using mosquito-net. A susceptible individual may be infected (at a rate  $\lambda_{hs} = \frac{c\alpha_2(1-p_2)I_h}{N_h}$ ) when he/she interact sexually with infected partner. The vertical transmission in mosquito population plays important role for zika transmission. Here a proportion of newborn mosquitoes enter into the exposed class with the population density  $rb_1E_v + sb_1I_v$  with  $0 \leq r,s \leq 1$ .

To comprise the controlling strategies some prevention control at a constant rate are included in the model. Those are, (a) a constant rate of protection ( $p_1$ ) from mosquito bites are taken by susceptible individual, by using skin covering dresses, mosquito-net or mosquito repellent, (b) a constant rate of protection ( $p_2$ ) from sexual interaction are taken by susceptible human with infected human, by using sexual preventive measures or avoiding sexual interaction in outbreak period to protect sexual transmission of the virus to his/her susceptible sexual partner, (c) a constant rate of isolation ( $q$ ) are given to infected human from mosquitoes by keeping an infected human under mosquito-net to protect zika transmission from an infected human to a susceptible human through mosquitoes (d) employed a constant rate of mosquito control ( $b$ ) by using insecticide spray. The recovered human individuals from Zika infection as assumed to gain lifelong immunity but due to short life span of mosquitoes the Zika infected mosquitoes never recover from it. The used symbols mentioned above are presented in table-1 and the schematic diagram of the virus transmission is presented in Fig.-1.

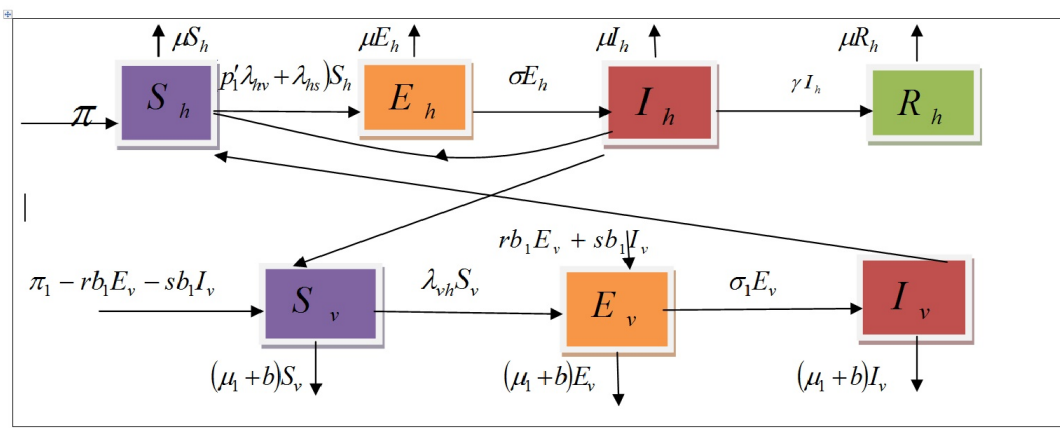


FIGURE 1. Schematic diagram of ZIKV transmission in human-mosquito population

Our assumption and the schematic diagram of ZIKV transmission lead to the following system of non linear ordinary differential equations.

$$(1) \quad \begin{cases} \frac{dS_h}{dt} = \pi - \left( \frac{(1-p_1)b_2\alpha_1 I_v}{N_h} + \frac{c\alpha_2(1-p_2)I_h}{N_h} \right) S_h - \mu S_h \\ \frac{dE_h}{dt} = \left( \frac{(1-p_1)b_2\alpha_1 I_v}{N_h} + \frac{c\alpha_2(1-p_2)I_h}{N_h} \right) S_h - (\sigma + \mu) E_h \\ \frac{dI_h}{dt} = \sigma E_h - (\gamma + \mu) I_h \\ \frac{dR_h}{dt} = \gamma I_h - \mu R_h \\ \frac{dS_v}{dt} = (\pi_1 - rb_1 E_v - sb_1 I_v) - \frac{b_2\alpha_3(1-q)I_h}{N_h} S_v - (\mu_1 + b) S_v \\ \frac{dE_v}{dt} = rb_1 E_v + sb_1 I_v + \frac{b_2\alpha_3(1-q)I_h}{N_h} S_v - (\sigma_1 + \mu_1 + b) E_v \\ \frac{dI_v}{dt} = \sigma_1 E_v - (\mu_1 + b) I_v \end{cases}$$

The description of the state variables and parameters have used in the model are presented in table-1.

TABLE 1. Description of model parameters

Parameters	Description
$\pi, \pi_1$ :	Recruitment rate of host and vector respectively.
$\mu, \mu_1$ :	Normal death rate of host and vector respectively .
$b_2$ :	Vector biting rate.
$\alpha_1$ :	Transmission probability from infected vector to host.
$\alpha_3$ :	Transmission probability from infected host to vector.
$c$ :	Host to host sexual contact rate.
$\alpha_2$ :	Transmission probability per sexual contact.
$\sigma, \sigma_1$ :	Rate of progression from exposed to infected host and vector respectively .
$\gamma$ :	Recovery rate .
$b$ :	Effective vector control rate.
$r, s$ :	Fraction of offspring of vector get infection by birth in exposed and infected classes respectively.
$b_1$ :	Birth rate of vector.
$p_1$ :	Rate of protection from vector bites taken by susceptible host.
$p_2$ :	Rate of protection from sexual contact taken by infected host.
$q$ :	Rate of isolation of infected host from vector.

**2.1. Basic Properties.** In this section we shall explore two basic properties, the positivity and boundedness of the model solution. In lemma-1, we shall prove that all the state variables are non-negative for  $t \geq 0$ .

**Lemma.1:** Let the initial condition  $F(0) \geq 0$  with  $F(t) = (S_h, E_h, I_h, R_h, S_v, E_v, I_v)$ , then the solutions  $F(t)$  of the model (1) are non-negative for all  $t \geq 0$ .

*Proof.* Let  $t_1 = \sup \{t > 0, F(t) > 0\}$ , then using integrating factor method on the first component equation of the model (1) gives

$$\begin{aligned} \frac{d}{dt} \left[ S_h(t) \exp \left\{ \int_0^t [p'_1 \lambda_{hv}(I_v(\xi), N_h(\xi)) + \lambda_{hs}(I_h(\xi), N_h(\xi))] d\xi + \mu t \right\} \right] \\ = \pi \exp \left\{ \int_0^t [p'_1 \lambda_{hv}(I_v(\xi), N_h(\xi)) + \lambda_{hs}(I_h(\xi), N_h(\xi))] d\xi + \mu t \right\} \end{aligned}$$

On integration over  $[0, t_1]$  provides

$$\begin{aligned} S_h(t_1) \exp \left\{ \int_0^{t_1} [p'_1 \lambda_{hv}(I_v(\xi), N_h(\xi)) + \lambda_{hs}(I_h(\xi), N_h(\xi))] d\xi + \mu t_1 \right\} - S_h(0) \\ = \int_0^{t_1} \pi \exp \left\{ \int_0^y [p'_1 \lambda_{hv}(I_v(\xi), N_h(\xi)) + \lambda_{hs}(I_h(\xi), N_h(\xi))] d\xi + \mu y \right\} dy \\ \text{or } S_h(t_1) = \left\{ S_h(0) + \int_0^{t_1} \pi \exp \left\{ \int_0^y [p'_1 \lambda_{hv}(I_v(\xi), N_h(\xi)) + \lambda_{hs}(I_h(\xi), N_h(\xi))] d\xi + \mu y \right\} dy \right\} \\ \cdot \exp \left[ - \left\{ \int_0^{t_1} [p'_1 \lambda_{hv}(I_v(\xi), N_h(\xi)) + \lambda_{hs}(I_h(\xi), N_h(\xi))] d\xi + \mu t_1 \right\} \right] > 0 \end{aligned}$$

Using the same technique we can prove that all other components of  $F > 0$  for all  $t$ . So the lemma is established. □

Thus the closed region

$$\Omega = \left\{ (S_h, E_h, I_h, R_h, S_v, E_v, I_v) \in R_+^7 : 0 \leq S_h + E_h + I_h + R_h \leq \frac{\pi}{\mu}, 0 \leq S_v + E_v + I_v \leq \frac{\pi_1}{\mu_1 + b} \right\}$$

is biologically feasible for the model (1).

In the following lemma we shall establish that  $\Omega$  is positively invariant set.

**Lemma.2:** The region  $\Omega$  is positively invariant set for the system (1) for non-negative initial conditions in  $R^7$ .

*Proof.* From the first four component equation of (1) we have:

$$(2) \quad \frac{dN_h}{dt} = \frac{dS_h}{dt} + \frac{dE_h}{dt} + \frac{dI_h}{dt} + \frac{dR_h}{dt} = \pi - \mu N_h$$

and from the last three component equation of (1) we have:

$$(3) \quad \frac{dN_v}{dt} = \frac{dS_v}{dt} + \frac{dE_v}{dt} + \frac{dI_v}{dt} = \pi_1 - (\mu_1 + b)N_v$$

employing comparison theorem from [33] and using initial condition one can be prove that

$$N_h(t) \leq N_h(0)e^{-\mu t} + \frac{\pi}{\mu}(1 - e^{-\mu t}), N_v(t) \leq N_v(0)e^{-(\mu_1+b)t} + \frac{\pi_1}{(\mu_1+b)}(1 - e^{-(\mu_1+b)t})$$

In particular  $N_h(t) \leq \frac{\pi}{\mu}$  if  $N_h(0) \leq \frac{\pi}{\mu}$  and  $N_v(t) \leq \frac{\pi_1}{\mu_1+b}$  if  $N_v(0) \leq \frac{\pi_1}{\mu_1+b}$

So  $\Omega$  is positively invariant set. So it is sufficient to regard as the zika transmission dynamics generated by the model (1) in  $\Omega$ . Hence in  $\Omega$  the model is mathematically and biologically well posed [34]. Thus each solution of the model (1) with initial condition in  $\Omega$  remains in  $\Omega$  for all  $t > 0$ .  $\square$

### 3. STEADY STATE ANALYSIS

Here we have studied existence and stability of equilibrium points of the model (1).

#### 3.1. Basic Reproduction Number and Local Stability of Disease Free Equilibrium.

In this part we shall derive the expression of the basic reproduction number employing the next generation matrix method [35] and investigate the local stability of the disease free equilibrium (DFE). The model (1) always has a DFE point  $E_0$  which is

$$E_0 (S_h^0, E_h^0, I_h^0, R_h^0, S_v^0, E_v^0, I_v^0) = \left( \frac{\pi}{\mu}, 0, 0, 0, \frac{\pi_1}{\mu_1+b}, 0, 0 \right).$$

The new Zika infection term  $F$  and the remaining transfer term  $V$  are as follows:

$$F = \begin{pmatrix} 0 & \lambda_{hs}^0 S_h^0 & 0 & \lambda_{hv}^0 S_h^0 \\ 0 & 0 & 0 & 0 \\ 0 & \lambda_{vh}^0 S_v^0 & rb_1 & sb_1 \\ 0 & 0 & 0 & 0 \end{pmatrix}, V = \begin{pmatrix} k_1 & 0 & 0 & 0 \\ -\sigma & k_2 & 0 & 0 \\ 0 & 0 & k_3 & 0 \\ 0 & 0 & -\sigma_1 & k_4 \end{pmatrix} \text{ and } FV^{-1} = \begin{pmatrix} a_1 & a_2 & a_3 & a_4 \\ 0 & 0 & 0 & 0 \\ a_5 & a_6 & a_7 & a_8 \\ 0 & 0 & 0 & 0 \end{pmatrix},$$



with  $k_1 = \sigma + \mu, k_2 = \gamma + \mu, k_3 = \sigma_1 + \mu_1 + b, k_4 = \mu_1 + b, a_1 = \frac{\sigma c \alpha_2 p'_2}{k_1 k_2}, a_2 = \frac{c \alpha_2 p'_2}{k_2}, a_3 = \frac{\sigma_1 b_2 \alpha_1 p'_1}{k_3 k_4}, a_4 = \frac{b_2 \alpha_1 p'_1}{k_4}, a_5 = \frac{\sigma b_2 \alpha_3 \mu \pi_1 q'}{\pi k_1 k_2 k_4}, a_6 = \frac{b_2 \alpha_3 \mu \pi_1 q'}{\pi k_2 k_4}, a_7 = \frac{k_4 r b_1 + \sigma_1 s b_1}{k_3 k_4}, a_8 = \frac{s b_1}{k_4}$ .

The characteristic equation of  $FV^{-1}$  is given by  $\lambda^2 g(\lambda) = 0$  where  $g(\lambda) = \lambda^2 - l\lambda - m$  with  $l = a_1 + a_7, m = a_3 a_5 - a_1 a_7$ . The basic reproduction number  $R_0$  is the spectral radius  $\rho(FV^{-1})$  [35] that is the greatest positive root of the equation  $g(\lambda) = 0$  which given by:

$$R_0 = \rho(FV^{-1}) = \frac{1}{2} \left\{ a_1 + a_7 + \left( (a_1 - a_7)^2 + 4a_3 a_5 \right)^{\frac{1}{2}} \right\}.$$

Now we define

$$(4) \quad R'_0 = l + m = \frac{b_2^2 \alpha_1 \alpha_3 p'_1 q' \mu \pi_1 \sigma \sigma_1 + c \alpha_2 p'_2 \sigma \pi k_4 (k_3 k_4 - k_4 r b_1 - s b_1 \sigma_1)}{\pi k_1 k_2 k_4 (k_3 k_4 - k_4 r b_1 - s b_1 \sigma_1)}$$

and hence  $g(1) = 1 - R'_0$ . In the next part we shall establish relation between two threshold numbers  $R_0$  and  $R'_0$  as we shall use it to study the behaviour of the model. To relate them we have considered the following cases:

(i) If  $R_0 = 1$  that is 1 is a root of the equation  $g(\lambda) = 0$  satisfying  $g(1) = 0$  then  $R'_0 = 1$  this means  $R_0 = 1$  implies  $R'_0 = 1$ .

(ii)  $R_0 > 1$  implies

$$R_0 = \frac{1}{2} \left\{ a_1 + a_7 + \left( (a_1 - a_7)^2 + 4a_3 a_5 \right)^{\frac{1}{2}} \right\} > 1$$

or  $(a_1 + a_7)^2 + 4(a_3 a_5 - a_1 a_7) > 4 + (a_1 + a_7)^2 - 4(a_1 + a_7)$   
 or  $a_1 + a_7 + a_3 a_5 - a_1 a_7 > 1$  i.e.  $R'_0 > 1$

(iii) Similarly when  $R_0 < 1$  we can show that  $R'_0 < 1$ .

From above three cases we have  $R'_0 = 1 (< 1, > 1)$  when  $R_0 = 1 (< 1, > 1)$ . The converse of this relation can be established easily. So we can conclude that  $R'_0 = 1 (< 1, > 1)$  iff  $R_0 = 1 (< 1, > 1)$ . Hence applying Theorem 2 of [35] we can establish the following lemma.

**Lemma. 3.** The DFE  $E_0$  of the model (1), is locally asymptotically stable if  $R_0 < 1$  and unstable if  $R_0 > 1$ .

The basic reproduction number  $R_0$  gives the average number of zika infected human individual generated by one infectious individual introduced into fully susceptible human population.

From the Lemma 3 we can say that zika virus can be eliminated from the human population if the basic reproduction number  $R_0$  can be brought to (and maintained at) a value less than unity.

**3.2. Global stability of the DFE.** In order to ensure that the eradication of ZIKV infection from the community does not depend on the initial numbers of the subpopulations, we have to study the global stability of DFE which have done in the theorem-1.

**Theorem. 1.** The DFE  $E_0$  of (1) is globally asymptotically stable (GAS) in the feasible region  $\Omega$  whenever  $R_0 < 1$  i.e ZIKV is then eradicated. On the other hand it is uniformly persistent whenever  $R_0 > 1$  in which case at least an endemic equilibrium exists. The virus persists then.

*Proof.* Let the infected compartment be  $\vec{x} = (E_h, I_h, E_v, I_v)$ . Then from the second, third, sixth and seventh component equation of (1) we have

$$\frac{d\vec{x}}{dt} = (F - V) \vec{x} - \vec{f}(S_h, E_h, I_h, R_h, S_v, E_v, I_v),$$

with

$$\vec{f}(S_h, E_h, I_h, R_h, S_v, E_v, I_v) = \begin{pmatrix} \lambda_{hs}^0 (S_h^0 - S_h) I_h + \lambda_{hv}^0 p'_1 (S_h^0 - S_h) I_v \\ 0 \\ \lambda_{vh}^0 (S_v^0 - S_v) I_h \\ 0 \end{pmatrix}.$$

where  $\lambda_{hv}^0 = \frac{b_2 \alpha_1}{N_h^0}$ ,  $\lambda_{hs}^0 = \frac{(1-p_2)c\alpha_2}{N_h^0}$  and  $\lambda_{vh}^0 = \frac{(1-q)b_2\alpha_3}{N_h^0}$ . Now from the first equation of (1) we have  $\frac{dS_h}{dt} = \pi - (p'_1 \lambda_{hv} + \lambda_{hs}) S_h - \mu S_h \leq \pi - \mu S_h$ . Which gives  $\limsup_{t \rightarrow \infty} S_h(t) \leq \frac{\pi}{\mu} = S_h^0$  this consequently implies  $S_h(t) \leq S_h^0$ . Similarly from the fifth equation of (1) we have

$\limsup_{t \rightarrow \infty} S_v(t) \leq \frac{\pi_1}{\mu_1 + b} = S_v^0$  which implies  $S_v(t) \leq S_v^0$ .

Now we note that  $\lambda_{hs}^0 (S_h^0 - S_h) I_h + \lambda_{hv}^0 p'_1 (S_h^0 - S_h) I_v = (\lambda_{hs}^0 I_h + \lambda_{hv}^0 p'_1 I_v) (S_h^0 - S_h) \geq 0$  as  $S_h(t) \leq S_h^0$  and  $\lambda_{vh}^0 (S_v^0 - S_v) I_h \geq 0$  as  $S_v(t) \leq S_v^0$ . Thus  $\vec{f}(S_h, E_h, I_h, R_h, S_v, E_v, I_v) \geq 0$ , after

some simple calculation we have

$$V^{-1}F = \begin{pmatrix} 0 & \frac{c\alpha_2 p'_2}{k_1} & 0 & \frac{b_2 \alpha_1 p'_1}{k_1} \\ 0 & \frac{\sigma c \alpha_2 p'_2}{k_1 k_2} & 0 & \frac{\sigma b_2 \alpha_1 p'_1}{k_1 k_2} \\ 0 & \frac{b_2 \alpha_3 q' \mu \pi_1}{\pi k_3 k_4} & \frac{r b_1}{k_3} & \frac{s b_1}{k_3} \\ 0 & \frac{\sigma_1 b_2 \alpha_3 q' \mu \pi_1}{\pi k_3 k_4^2} & \frac{\sigma_1 r b_1}{k_3 k_4} & \frac{\sigma_1 s b_1}{k_3 k_4} \end{pmatrix},$$

as  $V^{-1}F$  is irreducible, so employing the theorems 2.1 and 2.2 of [37] it follows that  $L = w^T V^{-1}x$  with  $w(> 0)$  is the left eigenvector of  $V^{-1}F$  is a Lyapunov function for system (1). Now  $w^T V^{-1}F = \rho (V^{-1}F) w^T = \rho (FV^{-1}) w^T = R_0 w^T$  where  $\rho$  denotes the spectral radius, thus when  $R_0 < 1$  then

$$\frac{dL}{dt} = w^T V^{-1} \frac{dx}{dt} = w^T V^{-1} ((F - V)x - f(S_h, E_h, I_h, R_h, S_v, E_v, I_v)) \leq w^T V^{-1} (F - V)x = (R_0 - 1) w^T x \leq 0,$$

Thus using  $L$  as a Lyapunov function and applying LaSalle's invariance principle [47], implies that  $E_0$  is the largest invariant subset of the feasible region when  $\frac{dL}{dt} = 0$ . It shows that  $E_0$  is the globally asymptotically stable in the feasible region when  $R_0 < 1$ .

On the other hand for  $R_0 > 1$  using  $L$  and an applying theorem 2.2 of [37] we can confirm the uniformly persistence of ZIKV i.e existence at least one endemic equilibrium of the model (1). Hence the theorem is proved.  $\square$

To justify this result numerically we presents the time series for the infected host and vector in Fig.-2, values of the parameters taken from table-2. The figures present the global asymptotic stability of the DFE  $E_0$  for  $R_0 < 1$  in accordance with theorem 1.

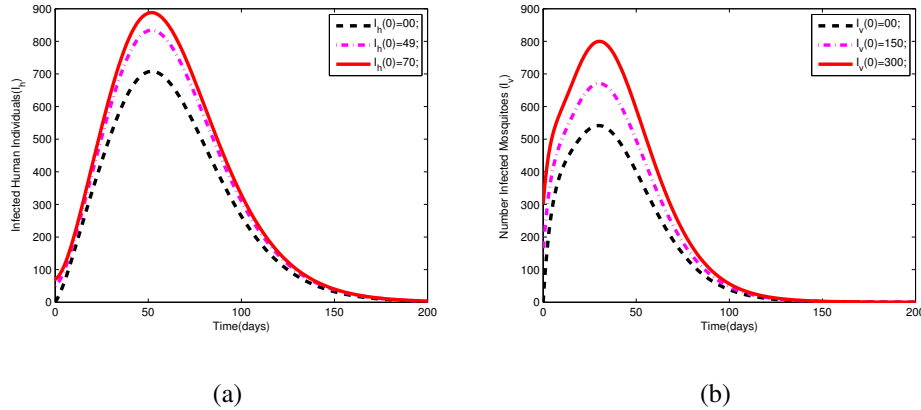


FIGURE 2. Time series of (a) infected host  $I_h$  and (b) infected vector  $I_v$  population, the values of the parameters taken from table-2 with initial conditions  $S_h(0) = 259500, E_h(0) = 70, R_h(0) = 00, S_v(0) = 2499910, E_v(0) = 700$ .

**3.3. Existence and stability of endemic equilibrium point.** Here we shall study the existence and stability of the endemic equilibrium of the system (1)

Let  $E_1 (S_h^*, E_h^*, I_h^*, R_h^*, S_v^*, E_v^*, I_v^*)$  be an endemic equilibrium point of the model (1) where  $S_h^* = \frac{\pi}{\lambda_h^* + \mu}, E_h^* = \frac{\pi \lambda_h^*}{k_1(\lambda_h^* + \mu)}, I_h^* = \frac{\pi \sigma \lambda_h^*}{k_1 k_2 (\lambda_h^* + \mu)}, R_h^* = \frac{\pi \sigma \gamma \lambda_h^*}{k_1 k_2 \mu (\lambda_h^* + \mu)}, \lambda_h^* = p'_1 \lambda_{hv}^* + \lambda_{hs}^*, S_v^* = \frac{(k_3 k_4 - k_4 r b_1 - s b_1 \sigma_1) \pi_1}{k_4 (k_3 k_4 - k_4 r b_1 - s b_1 \sigma_1) + k_3 k_4 \lambda_{vh}^*}, E_v^* = \frac{k_4 \pi_1 \lambda_{vh}^*}{k_4 (k_3 k_4 - k_4 r b_1 - s b_1 \sigma_1) + k_3 k_4 \lambda_{vh}^*}$  and  $I_v^* = \frac{\pi_1 \sigma_1 \lambda_{vh}^*}{k_4 (k_3 k_4 - k_4 r b_1 - s b_1 \sigma_1) + k_3 k_4 \lambda_{vh}^*}$  with,

$$(5) \quad \lambda_{vh}^* = \frac{b_2 \alpha_3 q' \mu \sigma \lambda_h^*}{k_1 k_2 (\lambda_h^* + \mu)}$$

$$(6) \quad \lambda_h^* = \frac{\pi}{\mu} \left[ \frac{b_2 \alpha_1 p'_1 \pi_1 \sigma_1 \lambda_{vh}^*}{k_4 (k_3 k_4 - k_4 r b_1 - s b_1 \sigma_1) + k_3 k_4 \lambda_{vh}^*} + \frac{c \alpha_2 P'_2 \pi \sigma \lambda_h^*}{k_1 k_2 (\lambda_h^* + \mu)} \right]$$

Here  $\lambda_{vh}^*$  and  $\lambda_h^*$  are respectively the forces of infection of vector and host at steady state. Using (5) in (6), we have the following quadratic equation in  $\lambda_h^*$ :

$$(7) \quad a_0 \lambda_h^{*2} + a_1 \lambda_h^* + a_2 = 0$$

with  $a_0 = \pi k_1 k_2 k_4 \{k_3 b_2 \alpha_3 q' \mu \sigma + k_1 k_2 (k_3 k_4 - k_4 r b_1 - s b_1 \sigma_1)\} > 0,$   
 $a_1 = \pi k_1 k_2 k_3 k_4 \mu \{k_3 b_2 \alpha_3 q' \mu \sigma + 2 k_1 k_2 (k_3 k_4 - k_4 r b_1 - s b_1 \sigma_1)\}$   
 $- \mu \sigma [k_1 k_2 b_2^2 \alpha_1 \alpha_3 \pi_1 \mu \sigma_1 + \{b_2 \alpha_3 \mu \sigma + k_1 k_2 (\mu_1 + b)\} c \alpha_2 \pi k_3 k_4],$

$a_2 = \pi k_1^2 k_2^2 k_3 k_4^2 \mu^2 (\mu_1 + b) (1 - R'_0)$ . The real positive root of the equation (7) provide the endemic equilibrium of the model (1). Here  $a_0$  is positive and  $a_2$  is positive for  $R'_0 < 1$ . So the number of real positive roots of the equation (7) depends on the sign of  $a_1$  and on the discriminant of the equation(7). Based on the above discussions we can summarize in the following theorem in connection of the existence and number of endemic equilibrium of the model:

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

- (a) one endemic equilibrium for  $a_2 < 0 \Leftrightarrow R'_0 > 1$ .
- (b) coincident endemic equilibrium for (i)  $a_1 < 0, a_2 = 0$  that is  $R'_0 = 1$  or (ii)  $a_1 < 0$  and  $a_1^2 - 4a_0a_2 = 0$ .
- (c) two endemic equilibrium for  $a_2 > 0$  that is  $R'_0 < 1, a_1 < 0$ , and  $a_1^2 - 4a_0a_2 > 0$ .
- (d) no endemic equilibrium for  $a_1 > 0$  and  $a_2 > 0$  that is  $R'_0 < 1$ .

**Theorem. 3.** The endemic equilibrium of the model (1) is locally asymptotically stable whenever  $R'_0 > 1$ .

**Proof of the theorem-3 are given in Appendix-I.**

**3.4. Study of backward bifurcation.** Here we shall investigate the backward bifurcation by applying centre manifold theorem [40] in the model (1).

**Theorem. 4** The model (1) exhibits a backward bifurcation at  $R'_0 = 1$  when the sign of the bifurcation coefficient  $\phi$  given in (9) is positive.

*Proof.* To prove this theorem we redefine the system (1) by using following change of variables: Let  $S_h = x_1, E_h = x_2, I_h = x_3, R_h = x_4, S_v = x_5, E_v = x_6, I_v = x_7$ . Hence  $N_h = x_1 + x_2 + x_3 + x_4$  and  $N_v = x_5 + x_6 + x_7$  Using vector notation  $\vec{x} = (x_1, x_2, x_3, x_4, x_5, x_6, x_7)^T$  the system (1) changes to the following form:

$$\frac{d\vec{x}}{dt} = \vec{f}(\vec{x}) \text{ where } \vec{f} = (f_1, f_2, f_3, f_4, f_5, f_6, f_7)^T$$

explicitly:

$$(8) \quad \left\{ \begin{array}{l} f_1 = \frac{dx_1}{dt} = \pi - \left( \frac{b_2 \alpha_1 p'_1 x_7 + c \alpha_2 p'_2 x_3}{x_1 + x_2 + x_3 + x_4} \right) x_1 - \mu x_1 \\ f_2 = \frac{dx_2}{dt} = \left( \frac{b_2 \alpha_1 p'_1 x_7 + c \alpha_2 p'_2 x_3}{x_1 + x_2 + x_3 + x_4} \right) x_1 - (\sigma + \mu) x_2 \\ f_3 = \frac{dx_3}{dt} = \sigma x_2 - (\gamma + \mu) x_3 \\ f_4 = \frac{dx_4}{dt} = \gamma x_3 - \mu x_4 \\ f_5 = \frac{dx_5}{dt} = \pi_1 - r b_1 x_6 - s b_1 x_7 - \frac{b_2 \alpha_3 q' x_3 x_5}{x_1 + x_2 + x_3 + x_4} - (\mu_1 + b) x_6 \\ f_6 = \frac{dx_6}{dt} = r b_1 x_6 + s b_1 x_7 + \frac{b_2 \alpha_3 q' x_3 x_5}{x_1 + x_2 + x_3 + x_4} - (\sigma_1 + \mu_1 + b) x_6 \\ f_7 = \frac{dx_7}{dt} = \sigma_1 x_6 - (\mu_1 + b) x_7 \end{array} \right.$$

The DFE ( $E_0$ ) of the system (8) is given by  $E_0(x_1^0, 0, 0, 0, x_5^0, 0, 0)$  with  $x_1^0 = \frac{\pi}{\mu}$ ,  $x_5^0 = \frac{\pi_1}{\mu_1 + b}$ . The variational matrix of the system (8) at the DFE is given below

$$J^*(E_0) = \begin{pmatrix} -\mu & 0 & -c \alpha_2 p'_2 & 0 & 0 & 0 & -b_2 \alpha_1 p'_1 \\ 0 & -k_1 & c \alpha_2 p'_2 & 0 & 0 & 0 & b_2 \alpha_1 p'_1 \\ 0 & \sigma & -k'_2 & 0 & 0 & 0 & 0 \\ 0 & 0 & \gamma & -\mu & 0 & 0 & 0 \\ 0 & 0 & -\frac{b_2 \alpha_3 q' \pi_1 \mu}{\pi k_4} & 0 & -k_4 & -r b_1 & -s b_1 \\ 0 & 0 & \frac{b_2 \alpha_3 q' \pi_1 \mu}{\pi k_4} & 0 & 0 & r b_1 - k_3 & s b_1 \\ 0 & 0 & 0 & 0 & 0 & \sigma_1 & -k_4 \end{pmatrix},$$

To investigate the backward bifurcation we consider transmission probability from infected human to mosquito  $\alpha_3$  as a bifurcation parameter. Suppose at  $\alpha_3 = \alpha_3^*$  the relation  $R'_0(\alpha_3^*) = 1$  holds and  $J(E_0)$  has one zero eigenvalue and others are negative or have negative real parts for this critical value. Hence the dynamics of the system (8) near  $\alpha_3 = \alpha_3^*$  can be studied using the centre manifold theorem [40].

The right eigenvector of the variational matrix corresponding to zero eigenvalue is obtained by:  
 $W = (q_1, q_2, q_3, q_4, q_5, q_6, 1)^T$  with  $q_1 = -\frac{1}{\mu}(c \alpha_2 p'_2 q_3 + b_2 \alpha_1 p'_1)$ ,  $q_2 = \frac{k'_2 q_3}{\sigma}$ ,  $q_3 =$

$$\frac{1}{A\sigma_1} (k_4(k_3 - rb_1) - sb_1\sigma_1),$$

$$q_4 = \frac{\gamma q_3}{\mu}, q_6 = \frac{k_4}{\sigma_1}, q_5 = -\frac{1}{k_4} (Aq_3 + rb_1q_6 + sb_1), A = \frac{b_2\alpha_3q'\pi_1\mu}{\pi k_4}$$

and the left eigenvector of the variational matrix corresponding to zero eigenvalue is obtained by:  $V = (v_1, v_2, v_3, v_4, v_5, v_6, 1)$  with  $v_1 = 0, v_2 = \frac{k_4 - sb_1s_6}{b_2\alpha_1p'_1}, v_3 = \frac{k_1s_2}{\sigma}, v_4 = 0, v_5 = 0, v_6 = \frac{\sigma_1}{k_3 - rb_1}$ . Now, we compute the bifurcation coefficients  $\phi$  and  $\psi$  where

$$\phi = \sum_{k,i,j=1}^7 v_k w_i w_j \frac{\partial^2 f_k}{\partial x_i \partial x_j} = v_2 \sum_{i,j=1}^7 w_i w_j \frac{\partial^2 f_2}{\partial x_i \partial x_j} + v_3 \sum_{i,j=1}^7 w_i w_j \frac{\partial^2 f_3}{\partial x_i \partial x_j} + v_6 \sum_{i,j=1}^7 w_i w_j \frac{\partial^2 f_6}{\partial x_i \partial x_j} + v_7 \sum_{i,j=1}^7 w_i w_j \frac{\partial^2 f_7}{\partial x_i \partial x_j}$$

$$(9) \quad \phi = \frac{2b_2\alpha_3q'\pi_1\mu^2\sigma_1q_3v_7w_7^2}{\pi^2k_4(k_3 - rb_1)} \left\{ Lq_5 - q_1 - 2q_2 - 2q_3 - 2q_4 - q_3q_4 - \frac{c\alpha_2p'_2q_3}{b_2\alpha_1p'_1}(q_2 + q_3) \right\}$$

and the other coefficient,

$$\psi = \sum_{k,i=1}^7 v_k w_i \frac{\partial^2 f_k}{\partial x_i \partial \alpha_3^*} = v_6 \sum_{i=1}^7 \frac{\partial^2 f_6}{\partial x_i \partial \alpha_3^*} = \frac{\sigma_1 rb_2 \pi_1 \mu}{k_3 \pi (\mu_1 + b)} v_7 w_7 > 0,$$

So the system (1) exhibits backward bifurcation at  $R'_0 = 1$  for  $\phi > 0$ . The phenomenon of backward bifurcation both for infected human and mosquito represents in figure-3.

In the case of backward bifurcation a stable DFE co-exists with a stable endemic equilibrium when the reproduction number  $R'_0$  is less than unity. In the case of backward bifurcation the condition  $R'_0 < 1$  for elimination of the virus from population is a necessary but not sufficient condition, in that case elimination of the virus depend on initial numbers of the sub-population.

□

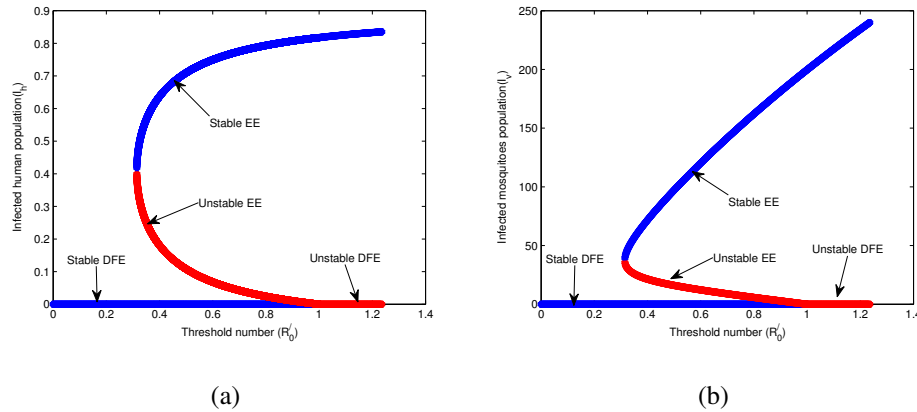


FIGURE 3. Backward bifurcation plot for the model (1): (a) infected host (b) infected vector population the used values of the parameters are  $\pi = 3.5, \mu = 1.25, \mu_1 = 0.35, b_2 = 0.4, \sigma = 0.7, \gamma = 1/9, b = 1/20, p_1 = 0.05, p_2 = 0.05, q = 0.01, r = 0.01, b_1 = 0.2, \alpha_1 = 0.4, \alpha_2 = 0.06, \alpha_3 = 0.35, \sigma_1 = 2/7, s = 0.05, c = 2/365, \pi_1 = 1000$

#### 4. DATA FITTING AND PARAMETER ESTIMATION IN FRENCH POLYNESIA

Here we have fitted the model to the weekly reported data and estimated key model parameters. we have used the data of French Polynesia reported from the whole territory during the period 11<sup>th</sup> October of 2013 to 28<sup>th</sup> March 2014 [48]. The model predicted weekly infected cases is  $I_h(t)$  obtained from the solution of third component equation of (1). We have been used the solutions to find the best-fit model parameters using a non-linear least squares regression technique which minimizes the sum of the squared residuals given as:

$$R(\Phi) = \sum_{j=1}^n [I_{ht_j}(\Phi) - \bar{I}_{ht_j}]^2$$

Where  $\Phi = \{b_2, c, \alpha_1, \alpha_2, \alpha_3, \sigma, \gamma, \mu_1, \sigma_1\}$ , set of nine key parameters, those are to be estimated and  $I_{ht_j}, \bar{I}_{ht_j}$  are numbers of weekly zika infected individuals according to model prediction and reported data respectively. Here  $n$  denotes the total number of data survey weeks. All computations have been done by employing MATLAB minimization software package fmincon (see Fig-4a). To fit this model to the reported Zika cases we assume that initially the total population, approximately 259500 [50] are susceptible. As our fitting process starts from 41<sup>th</sup> week



of 2013 and on which week the reported case was 49, so we consider initial number of infected human is 49 and we consider initial exposed, and recovered human are 70 and 00 respectively and the initial number of susceptible, exposed, infected number of vector populations arbitrarily chosen as 2499910, 700, 300 respectively. In this fitting process some model parameters have taken from some published literature [31, 49] and the most influential nine model parameters  $b_2, c, \alpha_1, \alpha_2, \alpha_3, \sigma, \gamma, \mu_1, \sigma_1$  are estimated by using the MATLAB minimization software package along with their 95% confidence interval (C.I) and all the computations are summarised in table-3.

The best fitted model solution along with reported cases are presented in figure-4(a) where the blue solid line represents the model predicted weekly number of infected cases and red dots denotes the reported cases [48]. The distribution of the corresponding residuals presents in figure-4(b). Since the residuals are small and randomly distributed so the fitness of real data with the model is good. In order to compare the model prediction with real data we present a bar diagram (see figure-4(c)) comparing the week wise number of model predicted cases (blue bar) and reported infected cases (red bar) from 41<sup>th</sup> week of 2013 to 14<sup>th</sup> week of 2014 in French Polynesia.

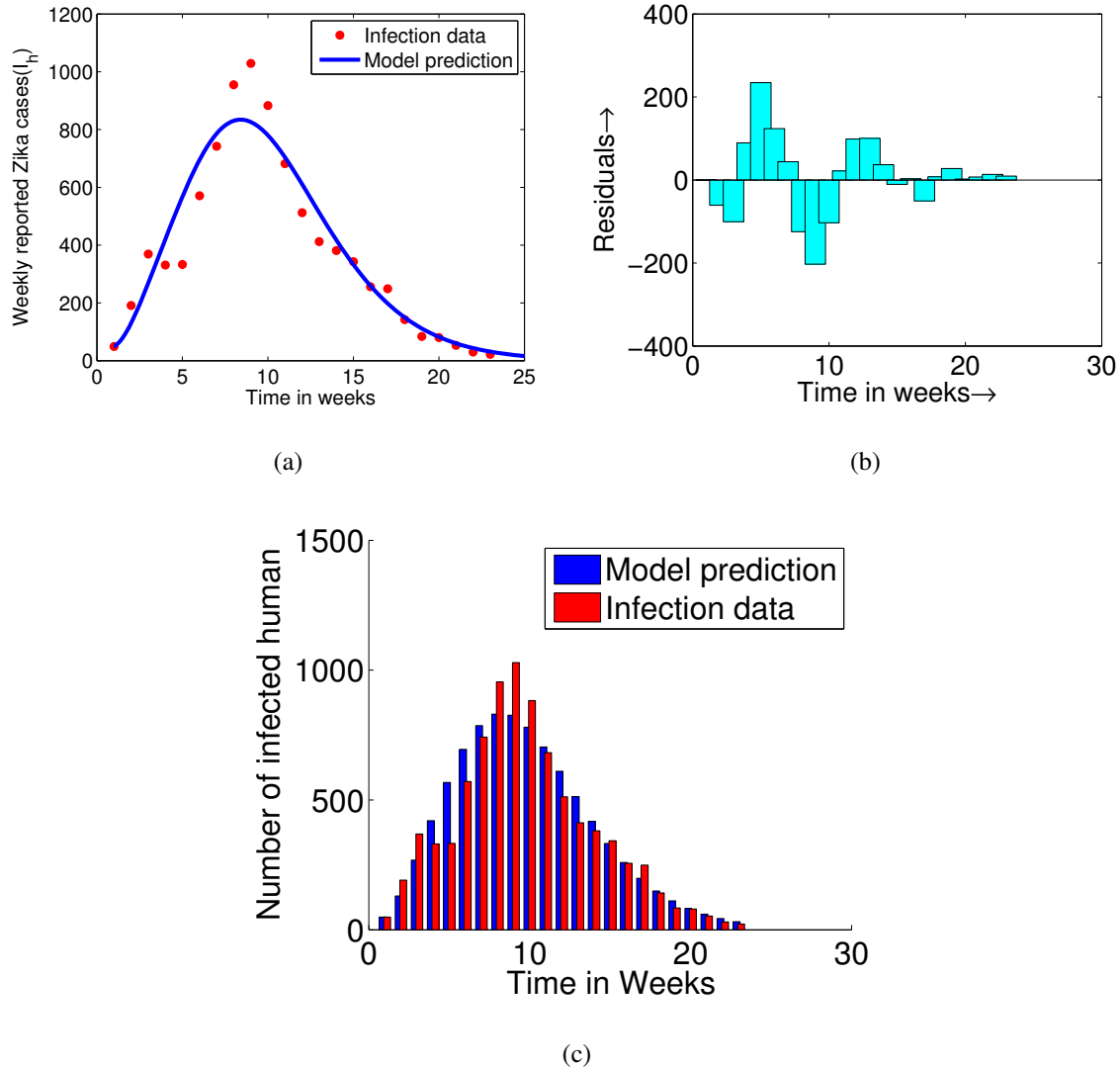


FIGURE 4. The best fitted solution (blue curve) of the model with the weekly reported human cases (the red dots) from 41<sup>th</sup> week, 2013 to 11<sup>th</sup> week, 2014 in French Polynesia. (b)The corresponding distribution of the residuals of the data fit in figure-(a). (c) Bar diagram: blue bar denote model predicted weekly cases and red bar denote the reported weekly cases.

## 5. INITIAL BASIC REPRODUCTION NUMBERS AND THE EFFECTIVE REPRODUCTION NUMBER OF THE OUTBREAK

In this section we shall study the initial basic reproduction number and the effective reproduction number  $R(t)$  for the Zika outbreak in French Polynesia in 2013-2014. First one is estimated in section-5.1 and second one is estimated in section-5.2.

### 5.1. Estimation of the basic reproduction number from reported data. .

There are various ways to estimate the basic reproduction number  $R_0$  for vector-borne diseases using reported disease outbreak data. In this part we have estimated the basic reproduction number  $R_0$  from initial growth phase of the zika outbreak in French Polynesia in 2013-2014. Let us assume that at the early stage of the outbreaks the cumulative number of cases  $q(t)$  varies as  $exp(\Lambda t)$  i.e.  $q(t) \propto exp(\Lambda t)$ , where  $\Lambda$  is the force of infection. In the same way the number of exposed and infected host and vector population vary similarly. So we have,

$$(10) \quad \begin{cases} E_h(t) = E_{h0}exp(\Lambda t) \\ I_h(t) = I_{h0}exp(\Lambda t) \\ E_v(t) = E_{v0}exp(\Lambda t) \\ I_v = I_{v0}exp(\Lambda t) \end{cases}$$

where  $E_{h0}, I_{h0}, E_{v0}$  and  $I_{v0}$  are constants. Further we assume that the number of non-susceptible be negligible then

$$(11) \quad \begin{cases} S_h(t) = N_h \\ S_v(t) = N_v \end{cases}$$

Now substituting (10) and (11) in second, third, sixth and seventh component equations of the model equation (1) we have

$$(12) \quad \begin{cases} (\Lambda + k_1)E_{h0} = (1 - p_1)b_2\alpha_1I_{v0} + (1 - p_2)c\alpha_2I_{h0} \\ (\Lambda + k_2)I_{h0} = \sigma E_{h0} \\ (\Lambda + k_3)E_{v0} = rb_1E_{v0} + sb_1I_{v0} + \frac{(1 - q)b_2\alpha_3\pi_1\mu}{\pi k_4}I_{h0} \\ (\Lambda + k_4)I_{v0} = \sigma_1E_{v0} \end{cases}$$

Using (12) in the expression of  $R_0$  we have determined the relation between the basic reproduction number  $R_0$  and the force of infection  $\Lambda$  as follows:

$$(13) \quad R_0 = \frac{1}{k_1k_2k_3k_4} [(\Lambda + k_1)(\Lambda + k_2) \{(\Lambda + k_3)(\Lambda + k_4) - rb_1\Lambda - k_4rb_1 - sb_1\sigma_1\} - B]$$

with  $B = (1 - p_2)c\alpha_2\sigma \{ \Lambda^2 + (k_3 + k_4)\Lambda - rb_1\Lambda \} + k_1k_2(k_4rb_1 + \sigma_1sb_1)$ . We have to estimate the force of infection  $\Lambda$  to compute the basic reproduction number  $R_0$  from the relation (13). Here we consider the first nine weeks cases as in this period the weekly new cases directly varies as cumulative number of cases  $q(t)$  i.e. weekly number of new cases proportional to  $\Lambda q(t)$ , so we can compute  $\Lambda$  by plotting the weekly number of new cases verses the cumulative number of cases  $q(t)$ , the phase of exponential growth of the cumulative number of cases is evidenced by a linear growth of the curve and the slope of that curve is the force of infection. This linear growth of the curve is estimated by a least square linear fit [51] in figure-5(b) by using reported data of zika outbreaks in French Polynesia in 2013-2014. The time series of reported new zika infected human cases in French Polynesia in 2013-2014 presented in figure-5(a). The slope of the line presented in figure-5(b) i.e the force of infection  $\Lambda = 0.21409791 \pm 0.03426873 \text{week}^{-1}$ . Now using this estimated value of  $\Lambda$  and other estimated parameters from table-2 in (13), we have estimated the basic reproduction number, which is  $R_0 = 2.86985$  with lower and upper values of  $R_0$  are 2.46573 and 3.32158 respectively.

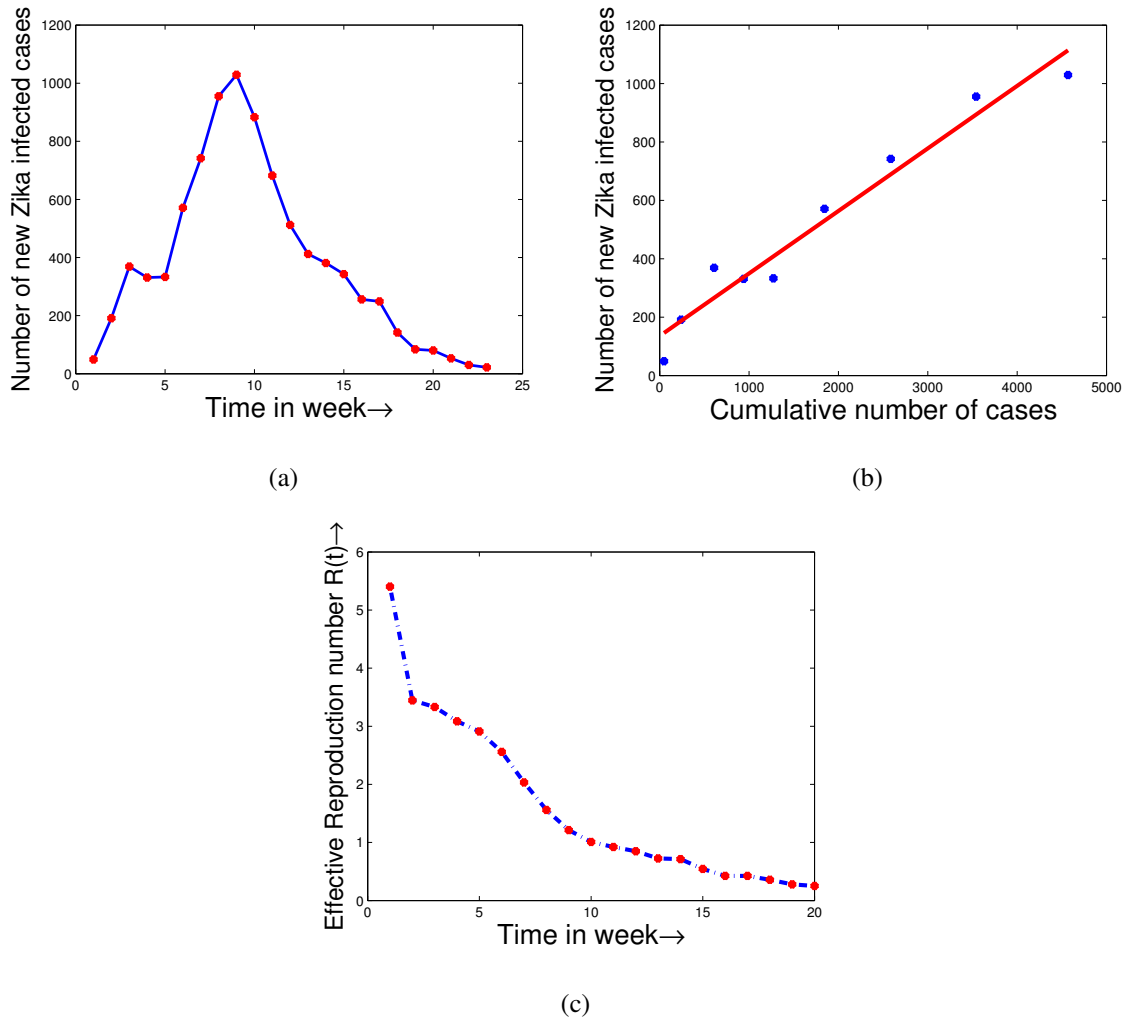


FIGURE 5. (a) The time series of reported new zika infected cases during 41<sup>th</sup> week, 2013 to 11<sup>th</sup> week, 2014 from French Polynesia. (b) The weekly number of infected cases versus the cumulative number of cases reported during the period 41<sup>th</sup> to 49<sup>th</sup> week of 2013 from French Polynesia as in this period new cases grow exponentially with cumulative number of cases and the least-squares linear fit. The linear phase of the fit gives  $\Lambda = 0.21409791 \pm 0.03426873 \text{week}^{-1}$ . (c) The effective reproduction number  $R(t)$  versus time  $t$  in weeks of the Zika outbreak in French Polynesia during 11<sup>th</sup> October, 2013 to 28<sup>th</sup> March, 2014. Used parameters taken from table-2.

**5.2. Effective reproduction number of the outbreak.** Here we shall study the effective reproduction number  $R(t)$ . It is defined as the average number of secondary infections

producing from a primary infected case at the time  $t$  week. The number  $R(t)$  provides an indication of the severity of the outbreak. It helps us by giving information about the necessary measures to control the outbreak. The estimation of  $R(t)$  done from the weekly new infection curve of the Zika infected cases by using the following equation derived from the renewal equation from birth process.

$$(14) \quad R(t) = \frac{b(t)}{\int_{\tau=0}^{\infty} b(t-\tau)g(\tau)d\tau}$$

where  $b(t)$  denote the number of new cases at  $t^{\text{th}}$  week and  $g(t)$  is the generation interval distribution for the Zika disease. In the model (1) considered exposed and infective stages both for human and mosquito populations. The constant rates of leaving the exposed and infected classes for human and mosquito are  $k_1 = \sigma + \mu, k_2 = \gamma + \mu, k_3 = \sigma_1 + \mu_1 + b$  and  $k_4 = \mu_1 + b$ . Therefore the generation interval distribution function  $g(t)$  will be the combination of the four exponential functions  $k_1e^{-k_1t}, k_2e^{-k_2t}, k_3e^{-k_3t}$  and  $k_4e^{-k_4t}$  in the form given by:

$$(15) \quad g(t) = \sum_{i=1}^4 \frac{k_1 k_2 k_3 k_4 e^{-k_i t}}{\prod_{j=1, j \neq i}^4 (k_j - k_i)}$$

with  $t \geq 0$  and mean of the distribution  $T = \frac{1}{k_1} + \frac{1}{k_2} + \frac{1}{k_3} + \frac{1}{k_4}$ . The relation is valid for the force of infection  $\Lambda > \min\{-k_1, -k_2, -k_3, -k_4\}$ .

Using the weekly Zika incidence data, estimated model parameters and substituting  $g(t)$  from (15) in equation (14) we estimate  $R(t)$  and presents in figure-5. The figure presents the time evolution of the effective reproduction number  $R(t)$  of the Zika outbreak in French Polynesia from 11th October, 2013 to 28th March, 2014. It is clear from the figure that the value of  $R(t)$  decrease gradually from 5.404 to 0.2499. It implies that the disease decrease gradually during that period.

## 6. SENSITIVITY ANALYSIS

In this section we have done sensitivity analysis to determine the parameters which have significant impact on the basic reproduction number  $R'_0$ . The analysis provides us the importance

of model parameters on zika virus transmission, which also provides guidance to control zika outbreak. Here we have studied the normalised forward sensitivity index of the basic reproduction number  $R'_0$  w.r.t different parameter which is defined as the ratio of the relative variation in the threshold number  $R'_0$  to the relative variation in the parameter.

**Definition 6.1:** [41] The normalized forward sensitivity index of  $R'_0$  which depends differentially on a parameter  $p$  is defined by  $\gamma_p^{R'_0} = \frac{\partial R'_0}{\partial p} \frac{p}{R'_0}$ .

Using the definition 6.1 in the analytical expression of  $R'_0$  we have found an expression for the sensitivity of  $R'_0$  w.r.t each model parameter. To estimate the numerical values of the sensitivity indices we have used the estimated parameter values from the second column of table-2 and the computed sensitivity indices are presented in fourth column of table-2.

TABLE 2. Parameter values and their sensitivity indices with respect to  $R'_0$

Parameters	Values	95% C.I.	Source	Sensitivity Indices
$b_2$	0.55104	0.5509-0.5668	Estimated	1.9493
$\pi_1$	142	-	Assumed	0.9746
$\alpha_1$	0.16197	0.1595-0.1642	Estimated	0.9746
$\alpha_3$	0.17725	0.1745-0.1797	Estimated	0.9746
$\mu$	$1/(70 \times 365)$	-	[31]	0.9738
$\sigma_1$	0.13283	0.1315-1343	Estimated	0.3312
$\alpha_2$	0.21201	0.2095-0.2148	Estimated	0.0238
$c$	0.04514	0.0445-0.0457	Estimated	0.0238
$b_1$	0.54286	-	Assumed	0.0014
$s$	0.001	-	Assumed	0.00091025
$r$	0.001	-	Assumed	0.00047057
$\sigma$	0.12616	0.1243-0.1275	Estimated	$1.7402 \times 10^{-16}$
$\mu_1$	0.06795	0.0667-0.0687	Estimated	-2.2590
$\gamma$	0.07104	0.0697-0.0714	Estimated	-0.9979
$\pi$	0.01747	-	[49]	-0.9746
$p_1$	0.1	-	Assumed	-0.1083
$p_2$	0.1035	-	Assumed	-0.0027
$q$	0.000104	-	Assumed	-0.00010137
$b$	0.00072	-	Assumed	$-2.492 \times 10^{-05}$

According to our findings the most positive sensitive parameters are mosquito biting rate ( $b_2$ ), mosquito recruitment rate ( $\pi_1$ ), transmission probability from infected mosquito to human ( $\alpha_1$ ), transmission probability from infected human to mosquito ( $\alpha_3$ ), human death rate ( $\mu$ ). The most negative sensitive parameters are mosquito death rate ( $\mu_1$ ), infection recovery rate ( $\gamma$ ), human recruitment rate ( $\pi$ ). We have to estimate the above said parameters carefully and we have give importance to control the outbreak.

## 7. NUMERICAL SIMULATION

In order to justify numerically the results obtained from the sensitivity analysis we presents the graphical presentation of the basic reproduction number  $R'_0$  with respect to different model parameters. Here we use the parameter values from the table-2 or stated along with the initial conditions  $S_h(0) = 259500, E_h(0) = 70, I_h(0) = 49, R_h(0) = 00, S_v(0) = 2499910, E_v(0) = 700, I_v(0) = 300$ .

In figure-6(a-d) we have presented graphically the basic reproduction number  $R'_0$  with respect to the parameters:  $b_2, \alpha_1, \alpha_3$  and  $\pi_1$  respectively.

Figure-6(a) shows that basic reproduction number  $R'_0$  increases non-linearly with mosquito biting rate  $b_2$  whereas in all other figures 6(b-d) the number  $R'_0$  increases linearly. Moreover figures 6(a-d) shows that increase from zero value when each of the parameters  $b_2, \alpha_1, \alpha_3, \pi_1$  varies from zero respectively. So the transmission of the virus can be prevented by decreasing the mosquito biting ( $b_2$ ) or the recruitment rate of mosquitoes ( $\pi_1$ ) which can be done by precaution.

In figure-7(a-d) we are given graphical presentation of the basic reproduction number with respect to the parameters  $\mu_1, \gamma, q$  and  $p_1$  respectively.

Figures 7 (a-d) show that the basic reproduction number reduces with the increase of each of the parameters  $\mu_1, \gamma, q$  or  $p_1$  respectively. Moreover these figures also show that  $R'_0$  reduces non-linearly with  $\mu_1$  and  $\gamma$  but linearly with  $q$  and  $p_1$ . This means the Zika epidemic can be rapidly controllable if mosquito death rate and infection recovery rate can be increased. On the other hand isolation of infected human and prevention of susceptible human from mosquito



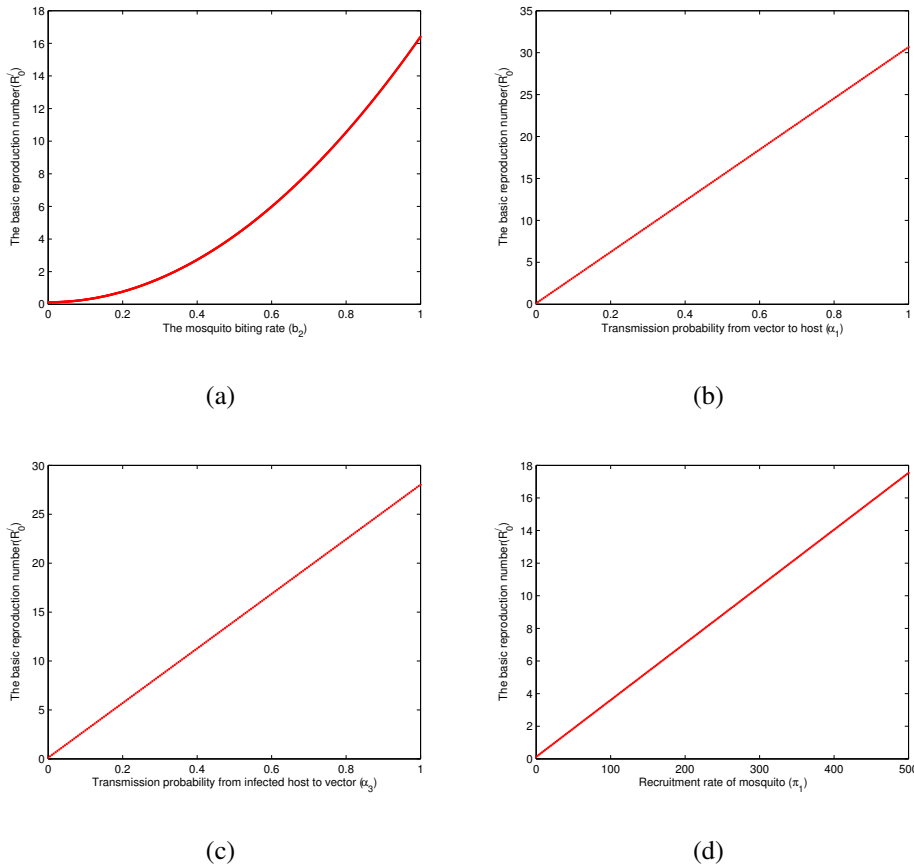


FIGURE 6. Plot of the basic reproduction number  $R'_0$  with respect to (a)  $b_2$  (mosquito biting rate) (b)  $\alpha_1$  (transmission probability from infected mosquito to human for per bite) (c)  $\alpha_3$  (transmission probability from infected human to mosquito for per bite) (d)  $\pi_1$  (recruitment rate of mosquitoes).

slow down epidemic progression but slowly compared to the first two cases. So the transmission of zika virus can be prevented by increasing the death rate mosquitoes ( $\mu_1$ ) or by increasing the prevention control rate  $q$  or  $p_1$  which can be done by taking proper precaution.

Now, in order to find the impact of most sensitive parameters on the infected human population  $I_h(t)$  we have studied the time series for different parameter values. Impact each of the parameter  $b_2, \alpha_1, \alpha_3, c$  and  $\alpha_2$  on  $I_h(t)$  are presented in figure-8(a-e) respectively.

Time series in figures 8(a-e) show that number of infected human  $I_h(t)$  grows first and then decay after reaching a maximum value. The number of infected human  $I_h(t)$  is higher for

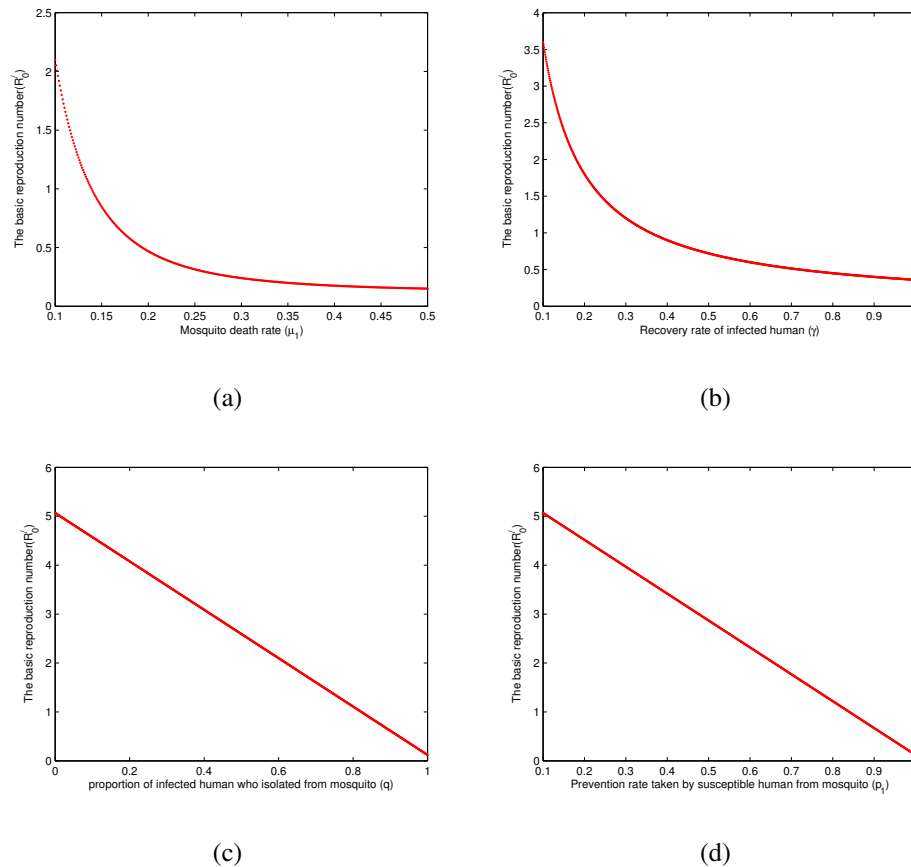


FIGURE 7. Plot of the basic reproduction number  $R'_0$  with respect to (a)  $\mu_1$  (natural death rate of mosquitoes) (b)  $\gamma$  (recovery rate) (c)  $q$  (isolation rate of infected human from mosquito) (d)  $p_1$  (protection rate from mosquito bites taken by susceptible human)

higher values of mosquito biting rate ( $b_2$ ), transmission probability from infected mosquito to susceptible human ( $\alpha_1$ ), from infected human to susceptible mosquito ( $\alpha_3$ ), sexual contact rate ( $c$ ), probability of Zika transmission from infected human to susceptible human ( $\alpha_2$ ) by sexual interaction. But the change in magnitude of  $I_h(t)$  is more prominent in first three cases of human-vector interaction compared to sexual contact. This means the primary cause of Zika epidemic is transmission through mosquito. So to control the disease primary effort should be vector control and secondly the sexual interaction with infected human should also be avoided. That is the spread of Zika virus can be reduced by reducing each of the parameters  $b_2$ ,  $\alpha_1$ ,  $\alpha_3$ ,  $c$  or  $\alpha_2$ .

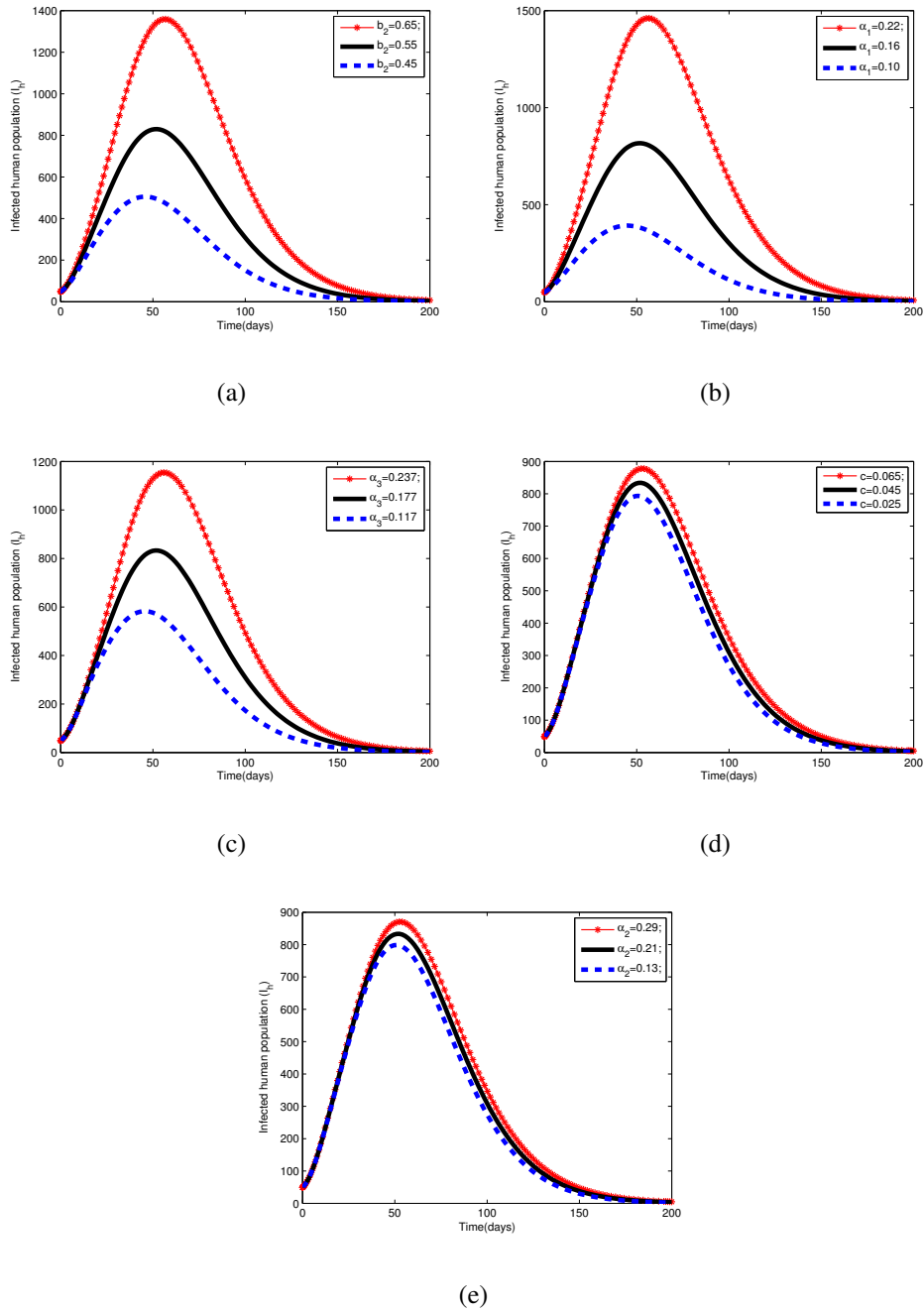


FIGURE 8. The time series of infected human population  $I_h(t)$  for different values of the parameter (a)  $b_2$ ; (b)  $\alpha_1$ ; (c)  $\alpha_3$  ; (d)  $c$  ; (e)  $\alpha_2$  ; (those parameters have positive sensitivity index)

The time series figure-9(a-e) presents the effect of parameters  $\mu_1, \gamma, q, p_1$  and  $p_2$  on  $I_h(t)$  respectively.

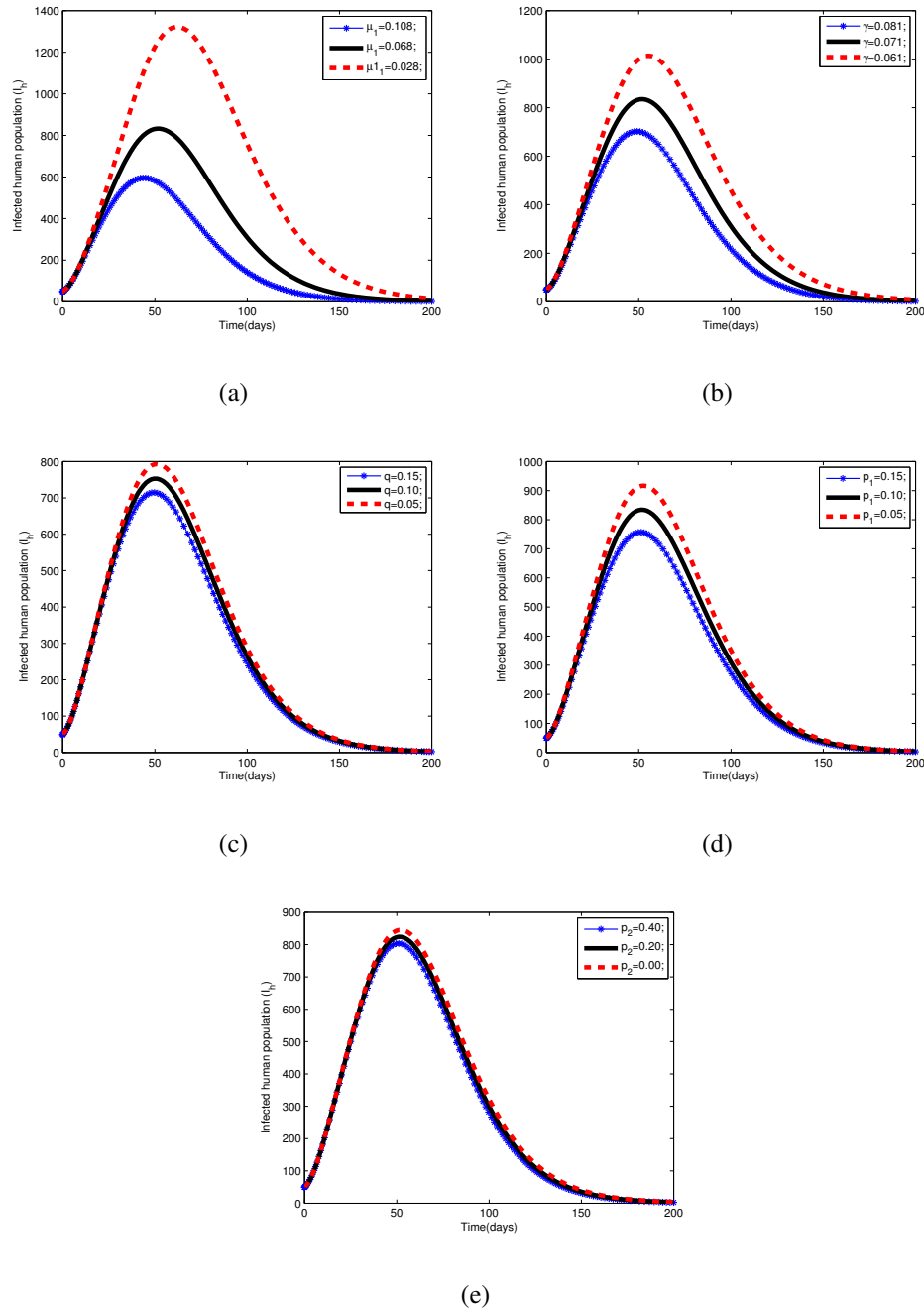


FIGURE 9. The time series of infected human population  $I_h(t)$  for different values of the parameter (a)  $\mu_1$ ; (b)  $\gamma$ ; (c)  $q$ ; (d)  $p_1$ ; (e)  $p_2$ ; (those parameters have negative sensitivity index).

It is clear from the Figures 9(a-e) that the most sensitive parameters are: the mosquito death rate ( $\mu_1$ ), recovery rate of infected human ( $\gamma$ ), isolation rate of infected human from mosquito ( $q$ ), protection rate from mosquito bites taken by susceptible human ( $p_1$ ), and protection rate

from sexual contact taken by infected human ( $p_2$ ) respectively. That is the spread of Zika virus can be reduced by increasing the said parameters  $\mu_1, \gamma, q, p_1$  or  $p_2$ .

## 8. CONCLUSIONS

In this paper we have studied the ZIKV disease dynamics and different kind of disease prevention control by developing a new ODE compartmental zika model. The model is new as: (a) it incorporates three virus transmission path including vector transmission, direct or sexual transmission and vertical transmission path of the virus simultaneously (b) it also incorporates four disease prevention control including protection from mosquito bites, protection from sexual contact, isolation of infected human from mosquito and vector control.

We have studied the basic properties including positivity and boundedness of the model and found the explicit expression of basic reproduction number by next generation matrix method. The model has unique disease free equilibrium (DFE) and it is locally and globally asymptotically stable if the basic reproduction number  $R'_0$  less than unity. The existence and stability of endemic equilibrium also has been studied. The model exhibits backward bifurcation where the stable DFE co-exist with a stable endemic equilibrium when the basic reproduction number  $R'_0$  is less than unity and the virus transmission probability from human to mosquito crosses the critical value.

The key model parameters ( $b_2, c, \alpha_1, \alpha_2, \alpha_3, \sigma, \gamma, \mu_1, \sigma_1$ ) have been estimated by fitting real data reported from French Polynesia in 2013-14 Zika outbreak. By finding the analytical expression of  $R_0$  in terms of the force of infection  $\Lambda$  and other parameters the basic reproduction number (for the first nine week) of the outbreak has been computed and its value is 2.87 with lower and upper values are 2.46 and 3.32 respectively. The effective reproduction of the outbreak also have studied and which decrease gradually from 5.404 to 0.2499 (fig-5c). The sensitivity analysis carried out with respect to the basic reproduction number to identify influential parameters. The influential parameters those have positive sensitivity indices are the mosquito biting rate, recruitment rate of mosquitoes, virus transmission probability from infected mosquito to human and the transmission probability from infected human to mosquito. On the other hand significant parameters those have negative sensitivity indices are the death

rate of mosquitoes, recovery rate, rate of isolation of infected human from mosquito ( $q$ ) and rate of prevention of susceptible human from mosquito bites ( $p_1$ ).

We have verified the effect of most positive and negative sensitive parameters on basic reproduction number numerically. Using time series of infected human we have shown that with the increase each of: the mosquitoes biting rate, recruitment rate of mosquitoes, virus transmission probability from infected mosquitoes to human and transmission probability from infected human to mosquitoes, the number of infected population is increased. On the other hand with the increase of: the death rate of mosquitoes, recovery rate of infected humans, isolation rate of infected human from mosquito ( $q$ ) and protection rate from mosquito bites taken by susceptible human ( $p_1$ ) the number of infected population is decreased.

The control strategy to minimize the transmission of the virus we have to decrease the mosquito biting rate and sexual contact with infected individuals. The prevention rate taken by infected and susceptible human should also be increased which includes vector control.

Our findings predict that, reduction of mosquito biting rate, mosquito recruitment rate; mosquito lifespan and sexual contact rate are four main prevention measures to protect Zika prevalence. Thus to control the disease we have to control the above said most sensitive parameters. This model study will be helpful for health planar to making zika control strategies.

## CONFLICT OF INTERESTS

The author(s) declare that there is no conflict of interests.

## REFERENCES

- [1] B. D. Foy. Probable Non-Vector-Borne Transmission of Zika Virus, Colorado, USA. *Emerg. Infect. Dis.* 17 (2011), 880-882.
- [2] Dallas County Health Human Services (DCHHS), DCHHS Reports First Zika Virus Case in Dallas county Acquired through Sexual Transmission. 2 February 2016.
- [3] Centres for Disease Control and Prevention (CDC), update : Interim Guidelines for Prevention of Sexual Transmission of Zika Virus-United States, 2016, 23 February 2016.
- [4] The Toronto Star, Canada's first case of sexually-transmitted Zika virus confirmed in Ontario, April 25, 2016.

- [5] J. T. Brooks, A. Friedman, R. E. Kachur, M. LaFlam, P. J. Peters, D. J. Jamieson; Update: interim guidance for prevention of sexual transmission of zika virus-United States, July 2016. *MMWR Morb. Mortal Wkly. Rep.* 65(29) (2016), 745.
- [6] E. E. Petersen, D. Meaney-Delman, R. Neblett-Fanfair, F. Havers, T. Oduyebo, S. L. Hills, I. B. Rabe, A. Lambert, J. Abercrombie, S. W. Martin et al; Update: interim guidance for preconception counselling and prevention of sexual transmission of zika virus for persons with possible zika virus exposure-United States, September 2016. *MMWR Morb. Mortal Wkly. Rep.* 65(39) (2016), 1077.
- [7] A. Davidson, S. Slavinski, K. Komoto, J. Rakeman, D. Weiss. Suspected female-to-male sexual transmission of zika virus-New York City, 2016, *MMWR Morb. Mortal Wkly. Rep.* 65(28) (2016), 716.
- [8] B. Atkinson, P. Hearn, B. Afrough, S. Lumley, D. Carter, E. Aarons, A. J. Simpson, T. J. Brooks, R. Hewson: Detection of zika virus in semen. *Emerg Infect. Dis.* 22 (2016), 940.
- [9] N. Nicastri, C. Castilletti, G. Liuzzi, M. Iannetta, M. R. Capobianchi, G. Ippolito, Persistent detection of Zika virus RNA in semen for six months after symptom onset in traveller returning from Haiti to Italy, February 2016. *Eurosurveillance* 21(32) (2016), 30314.
- [10] D. Musso. Potential sexual transmission of Zika virus. *Emerg. Infect. Dis.* 21(2) (2015), 359-361.
- [11] E. L. McGrath, S. L. Rossi, J. Gao, S. G. Widen, A. C. Grant, T. J. Dunn, S. R. Azar, C. M. Roundy, Y. Xiong, D. J. Prusak, et al. Differential responses of human fetal brain neural stem cells to Zika virus infection. *Stem Cell Rep.* 8(3) (2017), 715-727.
- [12] S. A. Rasmussen, D. J. Jamieson, M. A. Honein, L. R. Petersen: Zika virus and birth defects reviewing the evidence for causality. *New Engl. Med.* 374(20) (2016), 1981-1987.
- [13] B. Parra, J. Lizaarazo, J. A. Jimenez-Arango, A. F. Zea-Vera, G. Gonzalez-Manrique, J. Vargas, J. A. Angarita, G. Zuniga, R. Lopez-Gonzalez, C. L. Beltran et al: Guillain-Barre syndrome associated with Zika virus infection in Colombia, *New Engl. J. Med.* 375(16) (2016), 1513-1523.
- [14] N. Brouter, F. Krauer, M. Riesen, A. Khalakdina, M. Almiron, S. Aldighieri, M. Espinal, M. Low, C. Dye: Zika virus as a cause of neurologic disorders. *New Engl. J. Med.* 374(16) (2016), 1506-1509.
- [15] G. W. Dick, S. F. Kitchen, and A. J. Haddow: Zika Virus (I). Isolations and Serological Specificity. *Trans. R. Soc. Trop. Med. Hyg.* 46 (1952), 509-520.
- [16] V. Sikka, V. K. Chattu, R. K. Popli: The emergence of zika virus as global health security threat: A new and a consensus statement of the INDUSEM Joint Working Group (JWG), *J. Glob. Dis.* 8(1) (2016), 3-15.
- [17] F. N. Macnamara, Zika virus: a report on three cases of human infection during an epidemic of jaundice in Nigeria. *Trans. R. Soc. Trop. Med. Hyg.* 48(2) (1954), 139-145.
- [18] P. Shapshak, J. T. Sinnott, C. Somboonwit, J. H. Kuhn, eds., *Global virology I: identifying and investigating viral diseases*, Springer, New York, 2015.

- [19] European Centre for Disease Control and Prevention (CDC), Zika Virus Infection, Factsheet for Health Professionals. (2015).
- [20] M. R. Duffy, Zika virus outbreak on Yap Island, Federated States of Micronesia. *New Engl. J. Med.* 360 (2009), 2536-2543.
- [21] C. Manore and M. Hyman, Mathematical models for fighting Zika virus, *SIAM News*, Retrieved May 2, 2016,(2016).
- [22] A. J. Kucharski, S. Funk, R. M. Eggo, H. Mallet, W. J. Edmunds, E. J. Nilles, Transmission dynamics of Zika virus in Island population: a modelling analysis of the 2013-2014 French Polynesia outbreak, *bioRxiv preprint*.(2016).
- [23] D. Gao, Y. Lou, D. He, T. C.Porco, Y. Kuang, G. Chowell, S. Ruan, Prevention and control of zika as amosquito-borne and sexually transmitted disease: a mathematical modelling analysis. *Sci. Rep.* 6 (2016), 28070.
- [24] F. B. Agosto, S. Bewick, and W. F. Fagan,,: Mathematical model for Zika virus dynamics with Sexual transmission route, *Ecol. Complex.* 29 (2017), 61-81. .
- [25] O. Maxian, A. Neufeld, E. J.Talis, L. M. Childs, J. C. Blackwood: Zika virus dynamics: When does sexual transmission matter? *Epidemics*, 21 (2017), 48-55.
- [26] B. Hull, E. Tikasingh, M. De Souza, R. Martinez: Natural transovarial transmission of dengue 4 virus in *Aedes aegypti* in Trinidad. *Amer. J. Trop. Med. Hyg.* 33 (1984), 1248-1250.
- [27] C. Y. Kow, L. L. Koon, P. F. Yin, Ditection of dengue viruses in field caught male *Aedes aegypti* and *Aedes albopictus* (Diptera: Culicidae) in Singapore by typespecific PCR. *J. Med. Entomol.* 38 (2001), 475-479.
- [28] F. M. Pherez, Factors affecting the emergence and prevalence of vector borne infections(VBI) and the role of vertical transmission (VT), *J. Vector Borne Dis.* 44 (2007), 157-163.
- [29] L. Esteva, C. Vargas, Influence of vertical and mechanical transmission on the dynamics of dengue disease. *Math. Biosci.* 167 (2000), 51-64.
- [30] B. Adams, M. Boots, How important is vertical transmission in mosquitoes for the persistence of dengue? Insight from a mathematical model. *Epidemics*, 2 (2010), 1-10.
- [31] F. B. Agosto, S. Bewick, and W. F. Fagan, Mathematical model of Zika virus with vertical transmission. *Infect. Dis. Model.* 2 (2017), 244-267.
- [32] M. Imran, M. Usman, M. Dur-e-Ahmad, A. Khan, Transmission Dynamics of Zika Fever: A SEIR Based Model, *Differ. Equ. Dyn. Syst.* 29 (2021), 463-486.
- [33] V. Lakshmikantham, S. Leela, and A. A.Martynyuk, *Stability Analysis of Nonlinear System.* Marcel Dekker. Inc., New York and Basel (1989).
- [34] H. W. Hethcote, The mathematics of infectious diseases. *SIAM Rev.* 42(4) (2000). 599-653.



- [35] P. Van den Driessche, J. Watmough, Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission. *Math. Biosci.* 180 (2002), 29-48.
- [36] J. Tumwiine, J. Y. T. Mugisha, and L. S. Luboobi: On oscillatory pattern of malaria dynamics in a population with temporary immunity, *Comput. Math. Meth. Med.* 8(3) (2007), 191-203.
- [37] Z. Shuai, P. Vanden Driessche, Global stability of infectious disease models using Lyapunov functions. *SIAM J. Appl. Math.* 73(4) (2013), 1513-1532.
- [38] H. W. Hethcote, H. R. Thieme: Stability of the endemic equilibrium in epidemic models with subpopulations, *Math. Biosci.* 75 (1985), 205-227.
- [39] L. Esteva, A. B. Gumel, and C. V. de Leon: Qualitative study of transmission dynamics of drug-resistant malaria. *Math. Computer Model.* 50 (2009), 611-630.
- [40] C. Castillo-Chavez, B. Song: Dynamical model of tuberculosis and their applications. *Math. Biosci. Eng.* 1(2) (2004), 361-404.
- [41] N. Chitnis, J. M. Hyman, and J. M. Cushing, : Determining important parameters in the spread of malaria through the sensitivity analysis of a mathematical model, *Bull. Math. Biol.* 70(5) (2008), 1272-1296.
- [42] E. Bonyah, M. A. Khan, K. O. Okosun, and S. Islam. A theoretical Model for Zika virus transmission. *PLOS ONE* 12(10), e0185540 (2017).
- [43] T. A. Perkins, A. S. Siraj, C. W. Ruktanonchai, M. U. G. Kraemer, A. J. Tatem, Model-based projection of Zika virus infections in childbearing women in the Americas, *bioRxiv preprint* (2016).
- [44] W. G. C. Bearcroft, Zika virus infection experimentally induced in human volunteer, *Trans. R. Soc. Trop. Med. Hyg.* 50(5) (1956), 442-448.
- [45] World Health Organisation (WHO), WHO statement on the first meeting of International Health Regulations(2005) Emergency Committee on Zika virus and observed increase in neurological disorders and neonatal malformations, February 1, 2016. <http://www.who.int/>. (Accessed on February 26, 2016).
- [46] Centre for Disease Control and prevention (CDC), CDC Emergency Operations Centre moves to highest of activation for Zika response, February 3, 2016. <http://www.cdc.gov/>.
- [47] J. P. LaSalle, The stability of dynamical systems. *Regional Conference Series in Applied Math.* no 25, SIAM, Philadelphia, 1976.
- [48] Centre d'hygiene et de salubrite publique. Surveillance de la dengue et du Zika en Polynesie francaise. March 28, 2014. [http://www.hygiene-publique.gov.pf/IMG/pdf/bulletin\\_dengue28-03-2014.pdf](http://www.hygiene-publique.gov.pf/IMG/pdf/bulletin_dengue28-03-2014.pdf).
- [49] S. K. Biswas, U. Ghosh, S. Sarkar, Mathematical model of zika virus dynamics with vector control and sensitivity analysis. *Infect. Dis. Model.* 5 (2020), 23-41.
- [50] M. Aubry, Seroprevalence of arboviruses among blood donors in French Polynesia, 2011-2013. *Int. J. Infect. Dis.* 41 (2015), 11-12.

- [51] C. Favier. Early determination of the reproductive number of vector-borne diseases: the case of dengue in Brazil. *Trop. Med. Int. Health* 11 (2006), 332-340.