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Mathematical Model for Chikungunya Dynamics

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Abstract

Chikungunya is a re-emerging arboviral disease in Asia and Africa. Aedes spp. Mosquitoes is an identified vector for Chikungunya.Vector borne diseases are the primary cause of death in most of the world countries is hence it becomes pertinent to control these vector borne diseases. In the study, a mathematical model is divided in to six compartments namely Susceptible human, Exposed human, Infected human, Recovered human, Susceptible vector and infected vector. The basic reproduction number and stability analysis are carried out. Local and global stability at equilibrium point for disease free equilibrium and disease exist equilibrium is worked out. The aim of this study is to formulate the dynamical nonlinear mathematical model to describe the transmission of Chikungunya in both human and mosquito populations. Numerical analysis is validated through suitable data.

Keywords: Chikungunya virus, Basic reproduction number, local stability. Global stability.

1. INTRODUCTION

The vector borne disease Chikungunya which is an alphavirus is spread from Aedes mosquitoes and causes fever, rashes and can also lead to high fever and loss of life [1]. The name chikungunya comes from Makonde language of Southern Tanzania and Northern Mozambique which means ‘that which bends’ and true to its name the disease causes joint pain which at times persists for almost a year or sometimes more

than that [8]. The symptom of chikunguniya is joint pain where the small joint pain is most affected [2]. Other symptoms are swelling and muscle stiffness [4]. chikungunya In 2004, in Lamu, Kenya around 13,500 died because of a severe chikungunya epidemic [3]. During this epidemic the disease spread to near adjoining continents and islands of Indian Ocean, parts of Southern Asia and India [4]. Through travelers the disease was spread to parts of Europe and North America. Similarly, in 2005-2006, the French island of Re´union in the Indian Ocean approximately 2,00,000 inhabitants were infected, causing over 200 deaths [10, 5]. WHO sounded alert to the whole world and started monitoring cases and the characteristics of each case [10]. But the number of cases of the disease was so high that the actions of WHO were not enough because of which the hospital staff, doctors helped to corroborate the data. Data from Renault et al. (2007) forms the basis of the current epidemiological study [5].

The literature study of chikungunya infection, the mathematical model studied the transmission in human and virus population [3-5, 23,24]. The Chikungunya disease occurred in an Asian ancestry of America [6, 9]. After that chikungunya quickly spread into central American countries, most of South America, and northern Mexico. Until 2016, in this continent, Chikungunya infected individuals had been reported in 44 countries [7]. The Southern region observed a major outbreak, wherein most of the cases of Chikungunya occurring in 2014. This scenario allowed the coming up of highly competent adese mosquito populations to receive and spread CHIKV. The first case of Chikungunya fever in Mexico was officially reported in Arriaga, Chiapas[1]. The other cases reported in other states include: Campeche, Colima, Chiapas, Guerrero, Michoacán, Morelos, Oaxaca, Tabasco and Veracruz. The state of Jalisco reported one single case [15]. The epidemiological situation described above occurred during the dry season when the densities of Aedes mosquitoes were very low. For 2015, more than 11500 cases were registered throughout the country. The states with the highest number of cases were: Guerrero, Veracruz and Yucatán [3]. In this research we postulate the nonlinear mathematical model for chikunguniya virus with vertical transmission. In recent studies stability analysis of the dynamical models is one of the hot topic in diseases [1,2,6,15-22]. So, in this research the stability analysis of the system is also carries out.

The paper SEIR- CHIKV- model is organized as follow. In section 2, mathematical model by a system of non-linear ordinary differential equations with notations, assumptions of different populations between compartments are described. For this autonomous model accurate estimate of basic reproduction number [11] of the whole system (human – mosquito combined) is calculated at disease free equilibrium and endemic equilibrium points using next generation matrix method. In section 3 model analysis has been discussed. In section 4, Stability Analysis of CHIKV-model has been discussed. In Section 5 numerical simulations and in section 6 conclusions are drawn for autonomous model.

2. MATHEMATICAL MODEL

Mathematical model is derived with following notations.

Table 1: Notations with Model parameters

	Notation
$S_h(t)$	The number of individuals who are susceptible to CHIKV
$E_h(t)$	The number of individuals who are exposed to CHIKV
$I_h(t)$	The number of individuals who are infected to CHIKV
$R_h(t)$	Recovered individuals
$S_h(t)$	The number of mosquitoes who are susceptible to CHIKV
$I_h(t)$	The number of mosquitoes who are infected to CHIKV
$\beta = abm$	Transmission rate
a	mosquito bite rate
b	parasite transmission rate
m	ratio of mosquitoes to human
β_1	The rate at which human infects mosquitoes
γ	Transmission rate from exposed human to infected human
η	Recovery rate
μ	Natural mortality rate
α	Disease induced death
v_1	Vertical transmission rate

The transmission of disease in various compartments is depicts in the following figure 1.

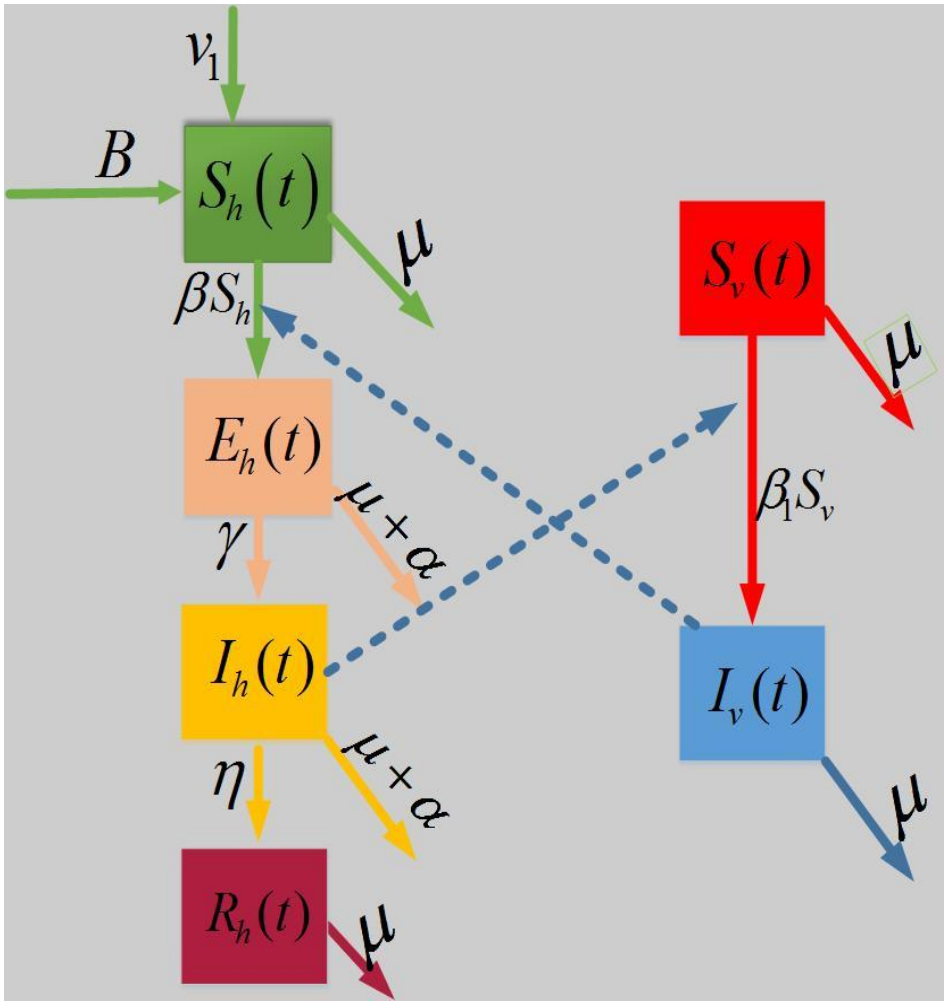

Figure 1: Schematic diagram of Chikungunya transmission

A Non-linear system of differential equations is formulated to study spread of vertical transmission of CHIKV model with control spraying and dropout. The model is sub-divided into entire human population $N_h(t)$ at time t and total vector population $N_v(t)$ at time t. Human population is divided amongst four compartments namely number of susceptible human $S_h(t)$ with CHIKV symptoms, number of exposed CHIKV humans $E_h(t)$, number of infected human $I_h(t)$ and $R_h(t)$, recovered human from chikv-disease. Thus, $N_h(t)=S_h(t)+E_h(t)+I_h(t)+R_h(t)$. Vector population $N_v(t)$ is divided in to two compartments namely number of susceptible vectors $S_v(t)$, number of infected vectors $I_v(t)$. Thus, the total vector population

is $N_v(t) = S_v(t) + I_v(t)$. The nonlinear differential equations are

$$\frac{dS_h}{dt} = B + \nu_1 S_h - \beta S_h I_V - \mu_h S_h$$

$$\frac{dE_h}{dt} = \beta S_h I_V - \gamma_1 E_h - \mu_h E_h$$

$$\frac{dI_h}{dt} = \gamma_1 E_h - \eta I_h - (\mu_h + \alpha) I_h \qquad (1)$$

$$\frac{dR_h}{dt} = \eta I_h - (\mu_h + \alpha) R_h$$

$$\frac{dS_V}{dt} = B_1 - \beta_1 S_V I_h - \mu_V S_V$$

$$\frac{dI_V}{dt} = \beta_1 S_V I_h - \mu_V I_V$$

3. MODEL ANALYSIS

In this section I found the basic properties and CHIKV free equilibrium point and CHIKV exist equilibrium point and also stability analysis of model-1 without optimal controls is carried out.

3.1 Invariant Region of solution of system (1)

Theorem 1

If $S_h(0) = S_{h0} > 0, E_h(0) = E_0 > 0, I_h(0) = I_{h0} > 0, R_h(0) = R_0 > 0, S_v(0) = S_{v0} > 0,$ and $I_v(0) = I_{v0} > 0$ then the $S_h(t), E_h(t), I_h(t), R_h(t), S_v(t), I_v(t)$ of the system are positively invariant for all $t > 0$. Furthermore, $\lim_{t\to\infty} Sup N_h(t) \le \frac{B}{\mu_h}$ and $\lim_{t\to\infty} Sup N_v(t) \le \frac{B_1}{\mu_v}$. In addition, $N_h(0) \le \frac{B}{\mu_h}\left(\text{based on } N_v(0) \le \frac{B_1}{\mu_v}\right)$ then $N_h(t) \le \frac{B}{\mu_h}\left(\text{based on } N_v(t) \le \frac{B_1}{\mu_v}\right)$. The feasible region is $\Omega = \Omega_h \times \Omega_v$, where $\Omega_h = (S_h, E_h, I_h, R_h) \in R_4^+$ and $\Omega_v = (S_v, I_v) \in R_2^+$ is positively invariant.

Proof Let $Z_1 = \sup\{t > 0 : S_h > 0, E_h > 0, I_h > 0, R_h > 0\}$ .by the fact that if $S_h(0) > 0, E_h(0) > 0, I_h(0) > 0, R_h(0) > 0$ then $Z_1 > 0$.

If $t < \infty$, then using the variations for constant formula to the first equation of system (1) is $S_h(Z_1) > S_h(0) e^{\int_0^t (\beta I_V S_h dS_h) + (\mu + \nu_1)t}$.

Clearly, $S_h(Z_1) > 0$, and it can be established in the same way for the other variables. This contradicts the point that Z_1 is the supremum since one of the variables must be equal to Z_1. Thus, $Z_1 = \infty$ which means $S_h, E_h, I_h R_h$ that are positive for all $Z_1 > 0$.

For the second aspect, add first four equations and last two equations of the system-(1) respectively,

$$\frac{dN_h(t)}{dt} = B - v_1 S_h - \mu_h N_h(t)$$

$$\frac{dN_v(t)}{dt} = B_1 - \mu_v N_v(t)$$

Let $0 \le I_h \le N_h(t), B - v_1 S_h - \mu_h N_h(t) \le \frac{dN_h(t)}{dt} < B - \mu_h N_h(t)$ as v_1 is very small.

By applying standard comparison theorem [23], we have

$$N_v(t) = N_v(0) e^{-(\mu_v)t} + \frac{B_1}{\mu_v}\left(1 - e^{-(\mu_v)t}\right).$$

Thus, if

$$N_h(0) \le \frac{B}{\mu_h}\left(\text{based on } N_v(0) \le \frac{B_1}{\mu_v}\right) \text{then } N_h(t) \le \frac{B}{\mu_h}\left(\text{based on } N_v(t) \le \frac{B_1}{\mu_v}\right).$$

Moreover, $\frac{B}{\mu_h} \le \liminf_{t\to\infty} N_h(t) \le \limsup_{t\to\infty} N_h(t) \le \frac{B}{\mu_h}$,

$$\liminf_{t\to\infty} N_v(t) = \frac{B_1}{\mu_v}.$$

Thus, the positivity invariance is to be determined. So, this concludes that it is sufficient to deal with system (1) in the feasible region $\Omega = \Omega_h \times \Omega_v$. So, the model can be assumed as epidemiologically well-posed for mathematical analysis [24].

3.2 Positivity of the solution of system (1)

Theorem 2 If initial conditions of the system (1) are non-negative then the solutions $\left(S_h(t), E_h(t), I_h(t), R_h(t), S_v(t), I_v(t)\right)$ are positive for all $t > 0$.

Proof: Let $Z_1 = \sup\{t > 0 : S_h > 0, E_h > 0, I_h > 0, R_h > 0\}$, for the first equation,

$$\frac{dS_h}{dt} = B - v_1 S_h - \beta S_h I_V - \mu_h S_h = B - \left(\mu_h + \beta I_V + v_1\right) S_h \qquad (2)$$

The integrating factor (I.F.) is $e^{\int_0^t (\beta I_v S_h dS_h) + (\mu + v_1)t}$.

Multiply integrating factor with equation (2) and we have

$$\frac{dS_h(t)}{dt}\left[e^{\int_0^t(\beta I_v S_h dS_h)+(\mu+v_1)t}\right] \geq Be^{\int_0^t(\beta I_v S_h dS_h)+(\mu+v_1)t}.$$

Now, solving the inequality,

$S_h(t)e^{\int_0^t(\beta I_v S_h dS_h)+(\mu-v_1)t} - S_h(0) \geq \int_0^t\left[e^{\int_0^t(\beta I_v S_h dS_h)+(\mu-v_1)t}\right]dk$. Therefore, $S_h(t)$ becomes

$$S_h(t) \geq S_h(0)e^{\int_0^t(\beta I_v S_h dS_h)+(\mu-v_1)t} + e^{-\int_0^t(\beta I_v S_h dS_h)+(\mu-v_1)t} \times \int_0^t\left[e^{\int_0^t(\beta I_v S_h dS_h)+(\mu-v_1)t}\right]dk > 0.$$

Hence, we proved that $S_h(t) > 0$. Similarly, we can be proved for all the other compartments respectively. These complete the proof.

3.3 Equilibrium points

To determine steady state solutions of system (1) by putting right hand side zero, we get the Chikv-free equilibrium point (CFE) $X_0 = \left(\frac{B}{\mu_h}, 0, 0, 0, \frac{B_1}{\mu_v}, 0\right)$ and Endemic Equilibrium point (EEE) $X^* = \left(S_h^*, E_h^*, I_h^*, R_h^*, S_v^*, I_v^*\right)$ in the region

Ω ,where $S_h^* = \frac{B}{\lambda + \mu_h - v_1}$,

$$E_h^* = \frac{B.\beta}{\mu_h(\mu_h+\gamma_1)(\lambda+\mu_h-v_1)}, I_h^* = \frac{B\lambda\gamma_1}{(\mu_h+\gamma_1)(\lambda+\mu_h-v_1)(\eta+\mu_h+\alpha)} \quad (3)$$

$$R_h^* = \frac{B\lambda\gamma_1\eta}{(\mu_h+\gamma_1)(\mu_h+\alpha)(\lambda+\mu_h-v_1)(\eta+\mu_h+\alpha)}$$

$S_h^* = \frac{B_1}{\lambda+\mu_v-v_1}$ and $I_v^* = \frac{B_1}{\lambda_1+\mu_v}$

where $\lambda = \frac{B}{\mu_h}$ and $\lambda_1 = \frac{B_1}{\mu_v}$.

3.4 Basic Reproduction Number

The CHIKV model (1) has a CFE point $X_0 = \left(\frac{B}{\mu_h}, 0, 0, 0, \frac{B_1}{\mu_v}, 0\right)$. The basic reproduction number founded by using the next generation matrix method (8 NBN 2015) as

Let $X' = [E_h \ I_h \ I_V \ s_h]'$, dash denotes derivative.

$$X' = \frac{dX}{dt} = \Im(X) - \upsilon(X)$$

where,

$$\Im = \begin{bmatrix} \beta S_h I_V \\ 0 \\ \beta_1 S_V I_h \\ 0 \end{bmatrix} \quad \text{and} \quad \upsilon = \begin{bmatrix} \gamma_1 E_h + \mu_h E_h \\ -\gamma_1 E_h + \eta I_h + (\mu_h + \alpha) I_h \\ \mu_V I_V \\ -B - v_1 S_h + \beta S_h I_V + \mu_h S_h \end{bmatrix}$$

Let, $F = \dfrac{\partial \Im_i (X_0)}{\partial X_J}$ and $V = \left[\dfrac{\partial \upsilon_i (X_0)}{\partial X_j} \right]$ *for* $i, j = 1, 2, 3$

So,

$$F = \begin{bmatrix} 0 & 0 & \beta S_h & \beta I_v \\ 0 & 0 & 0 & 0 \\ 0 & \beta_1 S_V & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \quad \text{and} \quad V = \begin{bmatrix} \gamma_1 + \mu_h & 0 & 0 & 0 \\ -\gamma_1 & \eta + \mu_h + \alpha & 0 & 0 \\ 0 & 0 & \mu_V & 0 \\ 0 & 0 & \beta S_h & -v_1 + \beta I_V + \mu_h \end{bmatrix}$$

F is transition matrix and V is transmission matrix. Thus,the largest Eigen value of the matrix FV^{-1} that is called basic reproduction number which is equal to the spectral radius of that matrix. So that

$$R_0 = \text{spectral radius of } FV^{-1} = \sqrt{\frac{\beta \beta_1 \gamma_1 \lambda \lambda_1}{\mu_v (\mu_h + \gamma_1)(\eta + \mu_h + \alpha)}} \tag{4}$$

The basic reproduction number or threshold R_0 is computed by simply imposing the non-negativity condition on the infected compartment. In our model, R_0 is a product of the average number susceptible individuals and susceptible mosquitoes per unit time in the presence of infected individuals and infected mosquitoes in the society. It is threshold that suggests whether individuals free from CHIKV disease i.e. $R_0 < 1$, then the society achieves disease free life which makes stability for society and if $R_0 > 1$, the community suffers from CHIKV disease which makes system unstable. In order to reduce the CHIKV disease in the society, a control is needed which is possible through spraying.

4. STABILITY ANALYSIS

In this section, we discussed the local stability and global stability of the system (1).

4.1. Local stability at Chikv-Free Equilibrium (CFE)

Theorem 4: The CHIKV-Free Equilibrium point $X_0 = \left(\frac{B}{\mu_h}, 0, 0, 0, \frac{B_1}{\mu_v}, 0 \right)$ is locally asymptotic stable if $R_0 < 1$. If $R_0 = 1$, X_0 is locally stable and if $R_0 > 1$ then X_0 is unstable.

Proof: The Jacobian matrix of the system (1) at equilibrium point X_0 is

$$J_{xo} := \begin{bmatrix} v_1 - \mu_h & 0 & 0 & 0 & 0 & -\beta\lambda_1 \\ 0 & -\gamma_1 - \mu_h & 0 & 0 & 0 & \beta\lambda_1 \\ 0 & \gamma_1 & -\eta - \mu_h - \alpha & 0 & 0 & 0 \\ 0 & 0 & \eta & -\mu_h - \alpha & 0 & 0 \\ 0 & 0 & -\beta_1\lambda_2 & 0 & -\mu_v & 0 \\ 0 & 0 & \beta_1\lambda_2 & 0 & 0 & -\mu_v \end{bmatrix} \quad (5)$$

It is clear that the Eigen values of the Jacobian matrix are $-\mu_h - \alpha, -\mu_v, -\mu_h + v_1$ and the solution of the characteristic polynomial is

$$p(x) = \lambda^3 + P_2\lambda^2 + P_1\lambda + P_0 = 0$$

Where, $P_2 = \mu_v + \mu_h + \alpha + \gamma_1$ and

$$P_1 = -\mu_h\mu_v - \mu_v\alpha - \mu_v\gamma_1 - \mu_v\gamma_1 - \alpha\gamma_1$$

$$P_0 = \frac{(1 - R_0)(\mu_h + \gamma_1)(\mu_h + \eta + \alpha)}{\beta_1\beta\gamma_1}$$

The solution of $p(x) = 0$ have negative real part if $R_0 < 1$. Thus, the CHIKV free equilibrium point is locally asymptotically stable whenever $R_0 < 1$.Therefore, we say that the Jacobian matrix has all the eigenvalues with negative real part if $R_0 < 1$. Hence X_0 is locally asymptotically stable if $R_0 < 1$. Now, for $R_0 = 1$. $P_1 > 0, P_2 > 0$ and $P_0 = 0$ which shows X_0 is locally stable. If $R_0 > 1$ then, $P_0 < 0$ then X_0 is unstable.

4.2. Local stability at Endemic equilibrium point (EEE) $X^* = \left(S_h^*, E_h^*, I_h^*, R_h^*, S_v^*, I_v^* \right)$

Theorem 5: The Chikv-exist equilibrium point of system (1), is locally asymptotically stable if $R_0 > 1$.

Proof: The Jacobian matrix of system (1) at EEE is determined so that

$$J_{X^*} = \begin{bmatrix} -\beta I_V^* - \mu_h + v_1 & 0 & 0 & 0 & 0 & -\beta S_h^* \\ \beta I_V^* & -\gamma_1 - \mu_h & 0 & 0 & 0 & \beta S_h^* \\ 0 & \gamma_1 & -\eta - \mu_h - \alpha & 0 & 0 & 0 \\ 0 & 0 & \eta & -\mu_h - \alpha & 0 & 0 \\ 0 & 0 & -\beta_1 S_V^* & 0 & -\beta_1 I_h^* - \mu_v & 0 \\ 0 & 0 & \beta_1 S_V^* & 0 & \beta_1 I_h^* & -\mu_v \end{bmatrix} \quad (6)$$

It is clear that the Eigen values of the Jacobian matrix (6) are $-\mu_h - \alpha, -\mu_v$, and other four Eigen values obtain from the characteristic polynomial is as follows:

$$R(x) = \lambda^4 + P_3\lambda^3 + P_4\lambda^2 + P_5\lambda + P_6 = 0$$

Where $P_3 = \beta I_V^* + \beta_1 I_h^* + \alpha + \eta - v_1 + 3\mu_h + \gamma_1 + \mu_v$

$$P_4 = 3\mu_h^2 + \mu_h\left(3\beta_1 I_h^* + 2\beta I_V^* + 3\mu_v + 2\alpha + 2\eta - 2v_1 + \gamma_1\right) + \gamma_1\left(\beta_1 I_h^* + \beta I_V^* + \mu_v + \alpha + \eta - v_1\right)$$
$$+\left(\beta_1 I_h^* + \mu_v\right)\left(\beta I_V^* + \alpha + \eta - v_1\right) + (\alpha + \eta)\left(\beta I_V^* - v_1\right)$$

$$P_5 = \mu_h^3 + \mu_h^2\left(3\beta_1 I_h^* + \beta I_V^* + \mu_v + \alpha + \eta - v_1 + \gamma_1\right) + \mu_h\begin{pmatrix}\gamma_1\left(2\beta_1 I_h^* + \beta I_V^* + 2\mu_v + \alpha + \eta - v_1\right) + + \left(2\beta_1 I_h^* + 2\mu_v\right) \\ \left(\beta I_V^* + \alpha + \eta - v_1\right) + (\alpha + \eta)\left(\beta I_V^* - v_1\right)\end{pmatrix} +$$
$$\begin{pmatrix}\left(I_h^*\left(\beta I_V^* + \alpha + \eta - v_1\right) + \beta S_h^* S_v^*\right)\beta_1 + \mu_v\left(\beta I_V^* + \alpha + \eta - v_1\right) \\ +(\alpha + \eta)\left(\beta I_V^* - v_1\right)\end{pmatrix}\gamma_1 + (\alpha + \eta)\left(\beta_1 I_h^* + \mu_v\right)\left(\beta I_V^* - v_1\right)$$

$$P_6 = \mu_h^3\left(\beta_1 I_h^* + \mu_v\right) + \left(\beta_1 I_h^* + \mu_v\right)\mu_h^2\left(\beta I_V^* + \mu_v + \alpha + \eta - v_1 + \gamma_1\right)$$
$$+\gamma_1\left(\left((\alpha + \eta)\left(\beta I_V^* - v_1\right)I_h^* + \beta S_h^* S_v^* v_1\right)\beta_1 + (\alpha + \eta)\left(\beta I_V^* - v_1\right)\mu_v\right)$$
$$\mu_h\begin{pmatrix}\left(\left(I_h^*\left(\beta I_V^* + \alpha + \eta - v_1\right) + \beta S_h^* S_v^*\right)\beta_1 + \mu_v\left(\beta I_V^* + \alpha + \eta - v_1\right) + (\alpha + \eta)\left(\beta I_V^* - v_1\right)\right)\gamma_1 \\ +(\alpha + \eta)\left(\beta_1 I_h^* + \mu_v\right)\left(\beta I_V^* - v_1\right)\end{pmatrix}$$

Due to the mathematical complication of the computation included in an attempt to prove the Routh-Hurwitz conditions for the stability of Chikv-exist equilibrium , we contemporary the criterion under which endemic is said to be locally asymptotically stable at chikv-exist equilibrium point. If

$P_3 > 0, P_3P_4 - P_5 > 0, (P_3P_2 - P_1) - P_3^2P_6 > 0$ then the polynomial of Chikv-exist equilibrium has roots with negative real parts. Thus theorem (4) shows that the Chikv-free equilibrium whenever it exists, is locally asymptotically stable if $R_0 < 1$ and otherwise unstable

4.2 Global Stability

In this section, we discussed the global stability at chikv-free equilibrium point X_0.

Theorem 5: Suppose $R_0 < 1$, then the chikv-free equilibrium (CFE) X_0 is globally asymptotically stable.

Proof: Here, we have applied the method used in Castillo-Chavez to prove global stability of CFE. We have system (1) as

$$\frac{dS_h}{dt} = B + v_1 S_h - \beta S_h I_V - \mu_h S_h$$

$$\frac{dE_h}{dt} = \beta S_h I_V - \gamma_1 E_h - \mu_h E_h$$

$$\frac{dI_h}{dt} = \gamma_1 E_h - \eta I_h - (\mu_h + \alpha) I_h$$

$$\frac{dR_h}{dt} = \eta I_h - (\mu_h + \alpha) R_h$$

$$\frac{dS_V}{dt} = B_1 - \beta_1 S_V I_h - \mu_V S_V$$

$$\frac{dI_V}{dt} = \beta_1 S_V I_h - \mu_V I_V$$

Let $Y = I_v$ and $Z = (S_h, E_h, I_h, R_h, S_v)$, here $A_0 = (Y_0, Z_0)$, where $Y_0 = (0)$ and $Z_0 = (0,0,0,0,0)$. We have

$$\frac{dY}{dt} = g(Y, Z) = \beta_1 S_V I_h - \mu_V I_V$$

At $Z = Z_0, G(Y, 0)$. Now $\frac{dY}{dt} = G(Y, 0) = -\mu_v I_v$ as $t \to \infty, Y \to Y_0$.

Hence, $Y = Y_0 = (I_{vo} = 0)$ is globally asymptotically stable. From above Equations, we get

$$H^{\sim}(Y,Z) = \begin{bmatrix} \beta S_h I_V \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} \quad \text{and} \quad F_1 = \begin{bmatrix} v_1 - \mu & 0 & 0 & 0 & 0 \\ 0 & -\gamma_1 - \mu_h & 0 & 0 & 0 \\ 0 & \gamma_1 & -\eta - \mu_h - \alpha & 0 & 0 \\ 0 & 0 & \eta & -\mu_h - \alpha & 0 \\ 0 & 0 & 0 & 0 & -\mu_v \end{bmatrix}$$

It is clear that F_1 is an M-matrix. For $S_h \geq 0$ and $I_h > 0$, we have $H^{\sim}(Y,Z) \geq 0$. Hence, Chikv-free equilibrium is globally asymptotically stable if $R_0 < 1$.

5. NUMERICAL SIMULATION

The parametric values are given below in Table 2 in appropriate units.

For given parametric values in table 2, the basic reproduction number (threshold) $R_0 < 1$.

Table 2. Parametric values

Notations	Values	Notations	Values
$S_h(0)$	50	β	0.01
$E_h(0)$	30	β_1	0.5
$I_h(0)$	10	γ	0.04
$R_h(0)$	25	η	0.01
$S_v(0)$	100	μ	0.5
$I_v(0)$	40	α	0.07
μ_v	0.4	v_1	0.02

In figure 2a, the transmission of each individual compartment is shown. It is observed that initially individuals in susceptible compartment decreases while infected

compartment increases but after some treatment at approximately 3 months individual in infected class decreasing and then after they are stabilized. The system becomes stable after 5 months. Figure 2b represents the transmission of mosquitoes in susceptible and infected compartments. In this figure we observe that susceptible mosquitoes gets decreasing while infected mosquitoes increasing initially and after some time they becomes stable.

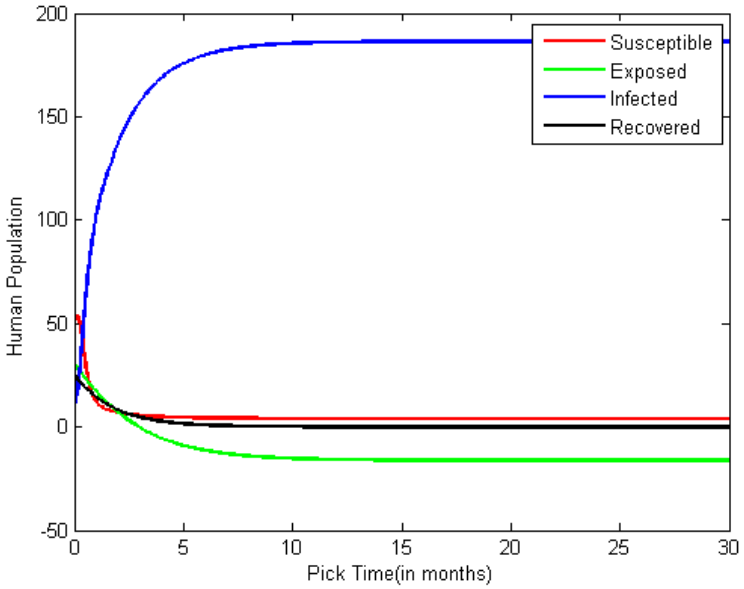

Fig.2a: Transmission in Human Population

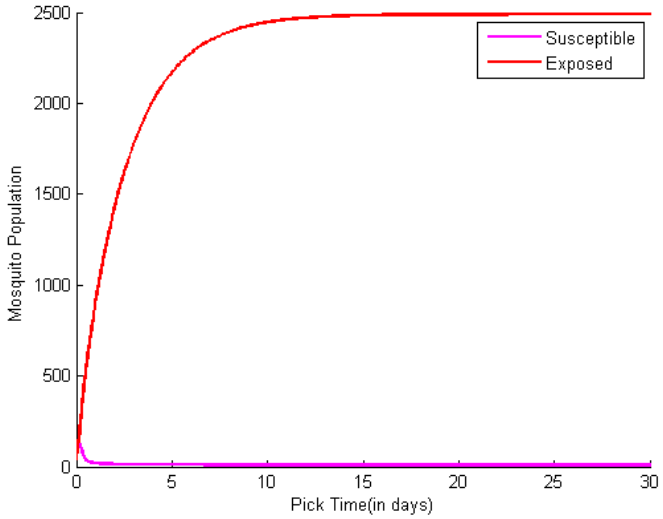

Fig.2b: Transmission in Mosquito Population

6. CONCLUSION

In this paper, the nonlinear mathematical model for chikunguniya virus is studied. Positivity of the system is discussed. The basic reproduction number is calculated using next generation matrix method. The local and global stability for chikv-free equilibrium point and chickv-exist equilibrium point are carried out. Numerical simulation carried out for appropriate values. In future one can apply control to reduce the spread in the society.

REFERENCES

[1] Centro Nacional de Programas Preventivos y Control de Enfermedades, Subsecretar ía de Prevención y Promoción de la Salud, Declaratoria de emergencia epidemiológica EE-2-2014, (2014).

[2] D. Ruiz-Moreno et al., Modeling Dynamic Introduction of Chikungunya Virus in the United States, Plos Neglect. Trop. D., 6 (11)(2012), e1918.

[3] Dirección General de Epidemiología, Boletín Epidemiológico, Semana 01-52, 2015.

[4] F. J. Burt et al, Chikungunya virus: an update on the biology and pathogenesis of this emerging pathogen, The Lancet Infectious Diseases, (2017)

[5] Gerardin P, Guernier V, Perrau J, Fianu A, Le Roux K, et al. (2008)Estimating Chikungunya prevalence in La Reunion Island outbreak by serosurveys: Two methods for two critical times of the epidemic. BMC Infectious Diseases 8: 99.

[6] I. Leparc-Go art et al., Chikungunya in the Americas, The Lancet, 383 (9916) (2014), 514.

[7] L. Fuyura-Kanamori et al., Co-distribution and co-infection of chikungunya and dengue viruses, BMC Infectious Diseases, 16 (1) (2016), 1.

[8] Queyriaux B, Simon F, Grandadam M, Michel R, Tolou H, et al. (2008) Clinical burden of chikungunya virus infection. Lancet Infectious Diseases8:2–3.

[9] R. S. Lanciotti and A. M. Valadere, Transcontinental movement of Asian genotype chikungunya virus, Emerg. Infect. Dis., 20 (8) (2014), 1400.

[10] Renault P, Solet JL, Sissoko D, Balleydier E, Larrieu S, et al. (2007) A Major Epidemic of Chikungunya Virus Infection on Re´union Island, France, 2005–2006. The American Journal of Tropical Medicine and Hygiene 77: 727–731.

[11] Roberts MG, Heesterbeek JAP (2003) A new method for estimating the effort required to control an infectious disease. Proceedings of the Royal Society of London Series B: Biological Sciences 270: 1359–1364.

[12] Robillard PY, Boumahni B, Gerardin P, Michault A, Fourmaintraux A, et al. (2006) Vertical maternal fetal transmission of the chikungunya virus. Ten cases among 84 pregnant women. Presse Medicale 35: 785–788.

[13] Sergon K, Njuguna C, Kalani R, Ofula V, Onyango C, et al. (2008) Seroprevalence of Chikungunya Virus (CHIKV) Infection on Lamu Island,Kenya, October 2004. The American Journal of Tropical Medicine and Hygiene 78: 333–337.

[14] Shah, N. H., Yeolekar, B. M., and Shukla, N. J. (2015). Liquor Habit Transmission Model. Applied Mathematics, 6(8), 1208.

[15] Shah, N. H., Satia, M. H., & Yeolekar, B. M. (2017). Optimum control for spread of pollutants through forest resources. Applied Mathematics, 8(5), 607-620.

[16] Shah, N. H., Satia, M. H., & Yeolekar, B. M. (2018). Stability of 'GO-CLEAN'model through graphs. Journal of Computer and Mathematical Sciences, 9(2), 79-93.

[17] Shah, N. H., Yeolekar, B. M., & Shukla, N. J. (2018). Vertical Transmission of Hepatitis-C Virus (HCV) with Optimal Control on Treatment Expenses. Asian Research Journal of Mathematics, 1-12.

[18] Shah, N. H., Patel, Z. A., & Yeolekar, B. M. (2017). Preventions and controls on congenital transmissions of Zika: mathematical analysis. Applied Mathematics, 8(04), 500.

[19] Shah, N. H., Yeolekar, B. M., & Patel, Z. A. (2017). Epidics of Coruption Using Incidence Function. Economic Computation & Economic Cybernetics Studies & Research, 51(2).

[20] Shah, N. H., Patel, Z. A., & Yeolekar, B. M. (2017). Threshold for vaccination in measles and its vertical transmission. International Journal of Dynamical Systems and Differential Equations, 7(2), 157-168.

[21] Shah, N. H., Satia, M. H., & Yeolekar, B. M. (2019). Global analysis of electronic items with re-manufacturing to control e-waste. International Journal of Environment and Waste Management, 24(3), 259-272.

[22] Shah, N. H., Yeolekar, B. M., & Shukla, N. J. (2018). Vertical Transmission of Hepatitis-C Virus (HCV) with Optimal Control on Treatment Expenses. Asian Research Journal of Mathematics, 1-12.

[23] Sistema Nacional de Vigilancia Epidemiológica, Secretaría de Salud, Dirección General de Epidemiología, Información Epidemiológica de Morbilidad 2005-2014, (2015a).].

[24] Staples JE, Breiman RF, Powers AM (2009) Chikungunya Fever: An Epidemiological Review of a Re-Emerging Infectious Disease. Clinical Infectious Diseases 49: 942–948.