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Local Stability Analysis for Age Structural Model of Chikungunya Disease

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ABSTRACT

A mathematical model of Chikungunya disease is used for describing transmission of this disease. Chikungunya disease is caused by Chikungunya virus that is alphavirus. This disease is transmitted by Aedes aegypti and Aedes albopictus. In Thailand, Chikungunya is first found in 1958. The data of infected human with this disease indicates that most of patients are adults particularly agriculture which have much risk of exposure to infection by the mosquitoes. In this paper, we study the age structure of Chikungunya patients by separating human populations into two classes, i.e. juvenile and adult. We apply standard dynamical modeling method for analysis the behaviors of solutions to our model. Conditions of parameters for the disease free and endemic states are determined. The numerical solutions are shown for supporting the theoretical results. The alternative way for controlling this disease is suggested. The basic reproductive number and the condition for reducing the transmission of this disease in each situation are found. However, the season is not considered in this study
KEYWORDS: Basic reproductive number, Chikungunya disease, Local stability, Standard dynamical modeling.

1. INTRODUCTION

Chikungunya is a viral infectious disease. This disease is transmitted to the human by biting of infected *Aedes aegypti* and *Aedes albopictus* mosquitoes. It was first discovered in 1953 on the Makonde Plateau at Tanzania. The name of this disease is derived from the Makonde word of a native in Africa meaning "That which bends up" correspond with the arthritic symptoms of the disease. The transmission occurred when the infectious female mosquitoes transmit the virus to the susceptible human, thus that susceptible human is infected. Symptom of Chikungunya disease appears between 2 and 4 days after the biting of an infected mosquito. The clinical course is characterized by high fever, headache, rash, arthritis affecting multiple joint(like ankles and wrist), myalgia and someone has conjunctivitis (red eyes). Pain joint will disappear in 1-12weeks but someone take many weeks or many years [1, 2, 3]. Symptoms are similar to dengue fever but there is no leakage of plasma out of blood vessel [4]. Until now, this disease has no vaccine; however infected human can be treated with drugs according to symptoms. Chikungunya disease is found in several countries in Asia i.e. Philippines (1954, 1956 and 1968), Thailand (1958 and 2009), India (1964), Sri Lanka (1969), Vietnam (1975) and Indonesia (1973 and 1982) [5]. Mathematical modeling is tool for studying the evolution of vector-borne disease. A deterministic model (consists of a set of differential equations) have a long tradition in the study of infectious diseases. In 2008, Y. Dumont, F. Chiroleu and C. Domerg considered a temporal model for Chikungunya disease by SEIR model and found the stability conditions for the disease and endemic states [2]. In 2010, P. Pongsumpun used standard dynamical modeling method for analyzing the Chikungunya disease by season which effect to the number of mosquitoes in Thailand [1]. In 2011, D. Moulay, M.A. Aziz-Alaoui and M. Cadivel described the mosquito population dynamics and the virus transmission to the human population. They analyzed equilibrium states by Lyapunov functions and found stability of periodic orbits [6]. Recently[7,8], we formulated the mathematical model for describing the transmission of Malaria by considering the age structure of human and season in Thailand. The analyses of our models are given by method of standard dynamical modeling. From the data of Chikungunya patients during 2008 and 2010 in Thailand [9], we can see that there is the different number of patients between juvenile (0-15 years) and adults (more than 15 years) humans as shown in fig. 1.

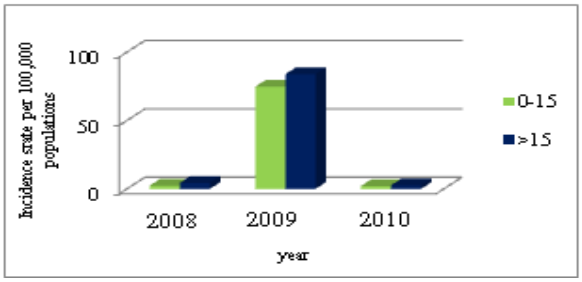

Fig.1 Reported cases of Chikungunya disease per 100,000 populations in Thailand, year 2008-2010 [9].

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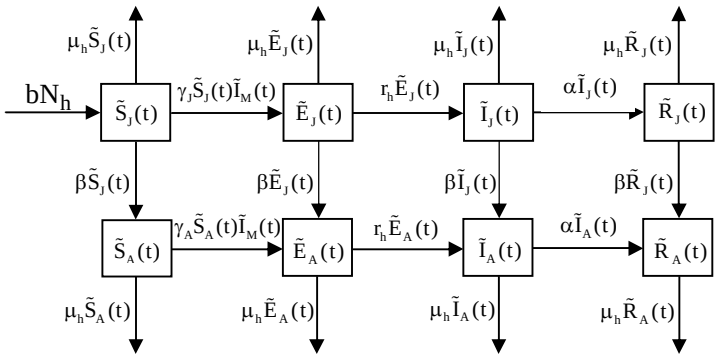
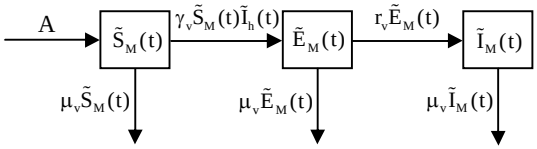
In this paper, we consider transmission of Chikungunya disease by age structure through **S**usceptible-**E**xposed-**I**nfectious-**R**emoved (SEIR) model. SEIR model can be used to describe the dynamical transmission of many infectious diseases. The basic reproductive number is found. The way to reduce the transmission of this disease is suggested. We present the model in section 2. The analytical and numerical results are presented in section 3. Finally, the discussion and conclusion are presented in section 4.

2. Mathematical model

We formulate the mathematical model for Chikungunya virus transmission by considering the dynamical equations for human and mosquitoes. We separate the human population into two groups such that juvenile and adult humans. Each group is divided into four sub-groups such as susceptible, exposed, infectious and recovered. The mosquito is divided into three sub-groups such as susceptible, exposed and infectious. We assume that each population size is constant. The transmission diagrams of human and mosquito populations are given in fig.2.



a). the human population



b). the vector population (mosquito population)

Fig.2 The compartmental diagrams of the model

The dynamical equations for human population are given as follows:

$$\frac{d\tilde{S}_J}{dt} = bN_h - \mu_h\tilde{S}_J - \gamma_J\tilde{S}_J\tilde{I}_M - \beta\tilde{S}_J \quad (1.1)$$

$$\frac{d\tilde{E}_J}{dt} = \gamma_J\tilde{S}_J\tilde{I}_M - \mu_h\tilde{E}_J - r_h\tilde{E}_J - \beta\tilde{E}_J \quad (1.2)$$

$$\frac{d\tilde{I}_J}{dt} = r_h\tilde{E}_J - \mu_h\tilde{I}_J - \alpha\tilde{I}_J - \beta\tilde{I}_J \quad (1.3)$$

$$\frac{d\tilde{R}_J}{dt} = \alpha\tilde{I}_J - \mu_h\tilde{R}_J - \beta\tilde{R}_J \quad (1.4)$$

$$\frac{d\tilde{S}_A}{dt} = \beta\tilde{S}_J - \gamma_A\tilde{S}_A\tilde{I}_M - \mu_h\tilde{S}_A \quad (1.5)$$

$$\frac{d\tilde{E}_A}{dt} = \beta\tilde{E}_J + \gamma_A\tilde{S}_A\tilde{I}_M - r_h\tilde{E}_A - \mu_h\tilde{E}_A \quad (1.6)$$

$$\frac{d\tilde{I}_A}{dt} = \alpha\tilde{I}_J + r_h\tilde{E}_A - \alpha\tilde{I}_A - \mu_h\tilde{I}_A \quad (1.7)$$

$$\frac{d\tilde{R}_A}{dt} = \alpha\tilde{I}_A + \beta\tilde{R}_J - \mu_h\tilde{R}_A \quad (1.8)$$

Let $\tilde{S}_J, \tilde{E}_J, \tilde{I}_J$ and $\tilde{R}_J$ are the number of susceptible, exposed, infectious and recovered juvenile populations at time t and $\tilde{S}_A, \tilde{E}_A, \tilde{I}_A$ and $\tilde{R}_J$ are the number of susceptible, exposed, infectious and recovered adult populations at time t, respectively.

The dynamical equations for mosquito population are given as follows:

$$\frac{d\tilde{S}_M}{dt} = A - \gamma_v\tilde{S}_M\tilde{I}_h - \mu_v\tilde{S}_M \quad (1.9)$$

$$\frac{d\tilde{E}_M}{dt} = \gamma_v\tilde{S}_M\tilde{I}_h - \mu_v\tilde{E}_M - r_v\tilde{E}_M \quad (1.10)$$

$$\frac{d\tilde{I}_M}{dt} = r_v\tilde{E}_M - \mu_v\tilde{I}_M \quad (1.11)$$

Let $\tilde{S}_M, \tilde{E}_M$ and $\tilde{I}_M$ are the number of susceptible, exposed and infectious mosquito populations at time t,respectively.

where $N_h = N_J + N_A, N_J = \tilde{S}_J + \tilde{E}_J + \tilde{I}_J + \tilde{R}_J$, $N_A = \tilde{S}_A + \tilde{E}_A + \tilde{I}_A + \tilde{R}_A$ and $N_M = \tilde{S}_M + \tilde{E}_M + \tilde{I}_M$. (1.12)

The parameters of our model are given as follows:

b is the birth rate of human population,

μ_h is the death rate of human population,

γ_J is the transmission rate of Chikungunya virus from mosquito to juvenile human populations,

γ_A is the transmission rate of Chikungunya virus from mosquito to adult human populations,

β is the transmission rate of Chikungunya virus from juvenile to adult human populations,

r_h is the incubation rate of Chikungunya virus in human population,

α is the recovery rate of human population,

A is the constant recruitment rate of mosquito

γ_v is the transmission rate of this disease from human to mosquito population,

r_v is the incubation rate of Chikungunya virus in mosquito population,

μ_v is the death rate of mosquito population,

$\tilde{I}_h$ is the number of infectious human population,

N_h is the total number of human population,

N_J is the total number of juvenile human population,

N_A is the total number of adult human population,

N_v is the total number of mosquito population.

We assume that the total populations of human and mosquitoes are constant. So the dynamical change of each population is equal to zero. Setting $\frac{dN_h}{dt} = \frac{dN_J}{dt} = \frac{dN_A}{dt} = \frac{dN_v}{dt} = 0$, then we obtained $b=\mu_h$, $\frac{N_h}{N_J} = \frac{\mu_h + \beta}{\mu_h}$, $\frac{N_A}{N_J} = \frac{\beta}{\mu_h}$ and $N_v = \frac{A}{\mu_v}$. We normalized our equations (1.1) - (1.11) by letting $S_J = \tilde{S}_J/N_J, E_J = \tilde{E}_J/N_J$, $I_J = \tilde{I}_J/N_J, R_J = \tilde{R}_J/N_J$, $S_A = \tilde{S}_A/N_A, E_A = \tilde{E}_A/N_A, I_A = \tilde{I}_A/N_A, R_A = \tilde{R}_A/N_A$, $S_M = \tilde{S}_M/N_M, E_M = \tilde{E}_M/N_M$ and $I_M = \tilde{I}_M/N_M$, then the reduced equations become

$$\frac{dS_J}{dt} = (\mu_h + \beta)(1 - S_J) - \gamma_J S_J I_M N_M \quad (2.1)$$

$$\frac{dE_J}{dt} = \gamma_J S_J I_M N_M - (\mu_h + r_h + \beta)E_J \quad (2.2)$$

$$\frac{dI_J}{dt} = r_h E_J - (\mu_h + \alpha + \beta)I_J \quad (2.3)$$

$$\frac{dS_A}{dt} = \mu_h S_J - (\gamma_A I_M N_M + \mu_h)S_A \quad (2.4)$$

$$\frac{dE_A}{dt} = \mu_h E_J + \gamma_A S_A I_M N_M - (r_h + \mu_h)E_A \quad (2.5)$$

$$\frac{dI_A}{dt} = \mu_h I_J + r_h E_A - (\alpha + \mu_h) I_A \quad (2.6)$$

$$\frac{dE_M}{dt} = \gamma_v (1 - E_M - I_M)(I_J N_J + I_A N_A) - (\mu_v + r_v) E_M \quad (2.7)$$

$$\frac{dI_M}{dt} = r_v E_M - \mu_v I_M \quad (2.8)$$

The equations for R_J, R_A and S_M can be obtained from three conditions: $S_J + E_J + I_J + R_J = 1$, $S_A + E_A + I_A + R_A = 1$ and $S_M + E_M + I_M = 1$.

3. ANALYSIS OF THE MATHEMATICAL MODEL

3.1 Equilibrium points

The equilibrium points $(S_J^*, E_J^*, I_J^*, S_A^*, E_A^*, I_A^*, E_M^*, I_M^*)$ are found by setting the right hand side of equations (2.1) - (2.8) equal to zero. So the equilibrium points are as follows:

i). The disease free state: $E_1 = (1,0,0,1,0,0,0,0)$

ii). The endemic disease state: $E_2 = (S_J^*, E_J^*, I_J^*, S_A^*, E_A^*, I_A^*, E_M^*, I_M^*)$ where

$$I_M^* = \frac{-(-n+p) + \sqrt{(-n+p)^2 - 4m(-q+h)}}{2m} \text{ when } m > 0 \text{ and } n > p$$

$$S_J^* = \frac{1}{1+\alpha_1 I_M^*}$$

$$E_J^* = \frac{\alpha_1 I_M^*}{(1+\alpha_1 I_M^*)(1+\alpha_2)}$$

$$I_J^* = \frac{\alpha_1 \alpha_2 I_M^*}{(1+\alpha_2)(1+\alpha_3)(1+\alpha_1 I_M^*)}$$

$$S_A^* = \frac{1}{(1+\alpha_4 I_M^*)(1+\alpha_1 I_M^*)}$$

$$E_A^* = \frac{I_M^*}{(1+\alpha_5)(1+\alpha_1 I_M^*)}\left(\frac{\alpha_1}{1+\alpha_2} + \frac{\alpha_4}{1+\alpha_4 I_M^*}\right)$$

$$I_A^* = \frac{I_M^*}{\alpha_6(1+\alpha_1 I_M^*)}\left(\frac{\alpha_1\alpha_2}{(1+\alpha_2)(1+\alpha_3)} + \frac{\alpha_5}{1+\alpha_5}\left(\frac{\alpha_1}{1+\alpha_2} + \frac{\alpha_4}{1+\alpha_4 I_M^*}\right)\right)$$

$$E_M^* = \frac{\mu_v I_M^*}{r_v} \quad (3)$$

with $\alpha_1 = \frac{\gamma_J N_M}{\mu_h + \beta}, \alpha_2 = \frac{r_h}{\mu_h + \beta}, \alpha_3 = \frac{\alpha}{\mu_h + \beta}, \alpha_4 = \frac{\gamma_A N_M}{\mu_h} \alpha_5 = \frac{r_h}{\mu_h}, \alpha_6 = \frac{\alpha + \mu_h}{\mu_h}, a_1 = \frac{\alpha_1\alpha_2 N_J}{(1+\alpha_2)(1+\alpha_3)},$

$a_2 = \frac{\alpha_1\alpha_2 N_A}{\alpha_6(1+\alpha_2)(1+\alpha_3)}, a_3 = \frac{\alpha_1\alpha_5 N_A}{\alpha_6(\alpha_5+1)(1+\alpha_2)}, a_4 = \frac{\alpha_4\alpha_5 N_A}{\alpha_6(\alpha_5+1)}, a_5 = \frac{f\mu_v}{r_v}, y = a_1 + a_2 + a_3, f = \mu_v + r_v,$

$m = \gamma_v f \alpha_4 y + a_5 r_v \alpha_1 \alpha_4, n = r_v y \alpha_4 \gamma_v, p = f(y + a_4)\gamma_v + a_5 r_v(\alpha_1 + \alpha_4), q = \gamma_v r_v (y + a_4)$ and $h = a_5 r_v$.

I_M^* is positive for $R_0 > 1$, where

$$R_0 = \frac{\gamma_v r_v r_h N_M (\gamma_J N_J + \gamma_A N_A)}{\mu_v(\mu_v + r_v)(\alpha + \mu_h)(\mu_h + r_h)}.$$

3.2 Local Stability

The local stability of each equilibrium point is defined by the signs of all eigenvalues. The eigenvalues (λ) are the solutions of the characteristic equation;

$$\left| J_{E_i} - \lambda I_8 \right| = 0; \; i = 1, 2$$

where J_{E_i} is the Jacobian matrix at the equilibrium point E_i where i = 1, 2

I is the identity matrix dimension 8×8.

If all eigenvalues for each equilibrium point produce the negative real part, then that equilibrium point is locally stability [10,11].

i). Disease free state $E_1 = (1,0,0,1,0,0,0,0)$, the characteristic equation is

$$\left|J_{E_1}-\lambda I_8\right|=0$$

$$\begin{vmatrix} -(\mu_h+\beta)-\lambda & 0 & 0 & 0 & 0 & 0 & 0 & -\gamma_J N_M \\ 0 & -(\mu_h+r_h+\beta)-\lambda & 0 & 0 & 0 & 0 & 0 & \gamma_J N_M \\ 0 & r_h & -(\mu_h+\alpha+\beta)-\lambda & 0 & 0 & 0 & 0 & 0 \\ \mu_h & 0 & 0 & -\mu_h-\lambda & 0 & 0 & 0 & -\gamma_A N_M \\ 0 & \mu_h & 0 & 0 & -(r_h+\mu_h)-\lambda & 0 & 0 & \gamma_A N_M \\ 0 & 0 & \mu_h & 0 & r_h & -(\alpha+\mu_h)-\lambda & 0 & 0 \\ 0 & 0 & \gamma_v N_J & 0 & 0 & \gamma_v N_A & -(\mu_v+r_v)-\lambda & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & r_v & -\mu_v-\lambda \end{vmatrix}=0$$

$$(\mu_h+\lambda)(\mu_h+\beta+\lambda)(\mu_h+\beta+\alpha+\lambda)(\mu_h+\beta+r_h+\lambda)[(\mu_v+\lambda)(\mu_h+\alpha+\lambda)(\mu_h+r_h+\lambda)(\mu_v+r_v+\lambda)$$

$$-\frac{Ar_v r_h \gamma_v N_J}{\mu_v \mu_h}(\gamma_J \mu_h+\gamma_A \beta)]=0 \qquad (4)$$

The eigenvalues are given by

$$\lambda_1=-\mu_h, \lambda_2=-\mu_h-\beta, \lambda_3=-\mu_h-\beta-\alpha, \lambda_4=-\mu_h-\beta-r_h$$

and the remaining 4 eigenvalues are the solutions of

$$(\mu_v+\lambda)(\mu_h+\alpha+\lambda)(\mu_h+r_h+\lambda)(\mu_v+r_v+\lambda)-\frac{Ar_v r_h \gamma_v N_J}{\mu_v \mu_h}(\gamma_J \mu_h+\gamma_A \beta)]=0$$

or
$$\lambda^4+T_4\lambda^3+T_3\lambda^2+T_2\lambda+T_1=0 \qquad (5)$$

where

$$T_1=\mu_v(\mu_h+\alpha)(\mu_h+r_h)(\mu_v+r_v)-\frac{Ar_v r_h \gamma_v N_J}{\mu_v \mu_h}(\gamma_J \mu_h+\gamma_A \beta),$$

$$T_2=\mu_v(\mu_h+\alpha)(\mu_h+r_h+\mu_v+r_v)+(\mu_v+\mu_h+\alpha)(\mu_h+r_h)(\mu_v+r_v),$$

$$T_3=\mu_v(\mu_h+\alpha)+(\mu_v+\mu_h+\alpha)(\mu_h+r_h+\mu_v+r_v)+(\mu_h+r_h)(\mu_v+r_v),$$

$$T_4=2\mu_v+2\mu_h+\alpha+r_h+r_v.$$

We can see that $\lambda_1, \lambda_2, \lambda_3$ and λ_4 have negative real part. We use Routh-Hurwitz criteria [12] for determination the sign of remaining eigenvalues. If it satisfies the following conditions, the eigenvalues will have negative real parts.

$$T_4>0, \qquad (6.1)$$

$$T_2>0, \qquad (6.2)$$

$$T_1>0, \qquad (6.3)$$

$$T_4T_3T_2>T_2^2+T_4^2T_1. \qquad (6.4)$$

From our evaluation, we found that condition (6.1) to (6.4) are satisfied when $R_0<1$;

$$R_0=\frac{\gamma_v r_v r_h N_M(\gamma_J N_J+\gamma_A N_A)}{\mu_v(\mu_v+r_v)(\alpha+\mu_h)(\mu_h+r_h)}.$$

ii). Endemic disease state $E_2=(S_J^*, E_J^*, I_J^*, S_A^*, E_A^*, I_A^*, E_M^*, I_M^*)$, the characteristic equation is

$$\left|J_{E_2}-\lambda I_8\right|=0$$

$$\begin{vmatrix} -(\mu_h+\beta)-\gamma_J I_M N_M-\lambda & 0 & 0 & 0 & 0 & 0 & 0 & -\gamma_J I_M N_M \\ \gamma_J I_M N_M & -(\mu_h+r_h+\beta)-\lambda & 0 & 0 & 0 & 0 & 0 & \gamma_J I_M N_M \\ 0 & r_h & -(\mu_h+\alpha+\beta)-\lambda & 0 & 0 & 0 & 0 & 0 \\ \mu_h & 0 & 0 & -(\gamma_A I_M N_M+\mu_h)-\lambda & 0 & 0 & 0 & -\gamma_A S_A N_M \\ 0 & \mu_h & 0 & \gamma_A I_M N_M & -(r_h+\mu_h)-\lambda & 0 & 0 & \gamma_A S_A N_M \\ 0 & 0 & \mu_h & 0 & r_h & -(\alpha+\mu_h)-\lambda & 0 & 0 \\ 0 & 0 & \gamma_v N_J & 0 & 0 & \gamma_v N_A(1-E_M-I_M) & -\gamma_v(I_J N_J+I_A N_A)-(\mu_v+r_v)-\lambda & \gamma_v(I_J N_J+I_A N_A) \\ 0 & 0 & 0 & 0 & 0 & 0 & \theta_v & -\mu_v-\lambda \end{vmatrix}=0$$

$$(\mu_h+\beta+\alpha+\lambda)(\mu_h+\beta+r_h+\lambda)[(\mu_h+\beta+\frac{\gamma_J A I_M}{d_v}+\lambda)(\mu_h+\frac{\gamma_A A I_M}{\mu_v}+\lambda)(\mu_h+r_h+\lambda)(\mu_h+\alpha+\lambda)(\mu_v+(I_J+I_A\frac{\beta}{\mu_h})\gamma_v N_J$$

$$+r_v+\lambda)(\mu_v+\lambda)+r_v(\mu_h+\alpha+\lambda)(\mu_h+\frac{\gamma_A A I_M}{\mu_v}+\lambda)(\mu_h+r_h+\lambda)(I_J+I_A\frac{\beta}{\mu_h})\gamma_v N_J(\mu_h+\beta+\frac{\gamma_J A I_M}{\mu_v}+\lambda)+r_v\frac{\beta}{\mu_h}(1-E_M-I_M)$$

$$\gamma_v N_J r_h \frac{\gamma_A A I_M}{\mu_v}(\frac{\gamma_A A S_A}{\mu_v}(\mu_h+\beta+\frac{\gamma_J A I_M}{\mu_v}+\lambda)+\mu_h\frac{\gamma_J A S_J}{\mu_v})-r_v\frac{\beta}{\mu_h}(1-E_M-I_M)\gamma_v N_J r_h\frac{\gamma_A A S_A}{\mu_v}(\mu_h+\frac{\gamma_A A I_M}{\mu_v}+\lambda)(\mu_h+\beta$$

$$+\frac{\gamma_J A I_M}{\mu_v}+\lambda)-r_v(1-E_M-I_M)\gamma_v N_J r_h\frac{\gamma_J A S_J}{\mu_v}(\mu_h+\beta+\lambda)]=0 \qquad (7)$$

The eigenvalues are given by $\lambda_1 = -\mu_h - \beta - \alpha, \lambda_2 = -\mu_h - \beta - r_h$ and the remaining 6 eigenvalues are the solutions of

$$(\mu_h + \beta + \frac{\gamma_J AI_M}{d_v} + \lambda)(\mu_h + \frac{\gamma_A AI_M}{\mu_v} + \lambda)(\mu_h + r_h + \lambda)(\mu_h + \alpha + \lambda)(\mu_v + (I_J + I_A \frac{\beta}{\mu_h})\gamma_v N_J + r_v + \lambda)(\mu_v + \lambda) + r_v(\mu_h + \alpha + \lambda)$$
$$(\mu_h + \frac{\gamma_A AI_M}{\mu_v} + \lambda)(\mu_h + r_h + \lambda)(I_J + I_A \frac{\beta}{\mu_h})\gamma_v N_J(\mu_h + \beta + \frac{\gamma_J AI_M}{\mu_v} + \lambda) + r_v \frac{\beta}{\mu_h}(1 - E_M - I_M)\gamma_v N_J r_h \frac{\gamma_A AI_M}{\mu_v}(\frac{\gamma_A AS_A}{\mu_v}$$
$$(\mu_h + \beta + \frac{\gamma_J AI_M}{\mu_v} + \lambda) + \mu_h \frac{\gamma_J AS_J}{\mu_v}) - r_v \frac{\beta}{\mu_h}(1 - E_M - I_M)\gamma_v N_J r_h \frac{\gamma_A AS_A}{\mu_v}(\mu_h + \frac{\gamma_A AI_M}{\mu_v} + \lambda)(\mu_h + \beta + \frac{\gamma_J AI_M}{\mu_v} + \lambda) - r_v(1 - E_M - I_M)$$
$$\gamma_v N_J r_h \frac{\gamma_J AS_J}{\mu_v}(\mu_h + \beta + \lambda)] = 0$$

or
$$\lambda^6 + T_6\lambda^5 + T_5\lambda^4 + T_4\lambda^3 + T_3\lambda^2 + T_2\lambda + T_1 = 0 \quad (8)$$

where

$T_1 = \mu_{vn}\mu_{\theta d}\mu_{vc} + \mu_{JA}\mu_{vn}\mu_{\theta d} + \mu_{Av}\mu_{Iv}\mu_{cd} + \beta\mu_{SJ}\mu_{Iv} + \mu_{Av}\mu_{vn}\mu_{Ev} + \mu_{\theta c}\mu_{Ev} - \mu_{Av}\mu_{Ev}\mu_{Iv}\mu_{cd} - \beta\mu_{Ev}\mu_{SJ}\mu_{Iv} - \mu_{Av}\mu_{vn} - \mu_{\theta c}$,

$T_2 = \mu_{vn}\mu_{\theta d}\mu_{dv} + (\mu_{vn}\mu_{r\theta} + \mu_{2dn}\mu_{\theta d})\mu_{vc} + (\mu_{vn}\mu_{r\theta} + \mu_{2dn}\mu_{\theta d})\mu_{JA} + \mu_{Av}\mu_{Iv} + \mu_{Av}\mu_{Ev}\mu_{2dn} - \mu_{Av}\mu_{Iv}\mu_{Ev} - \mu_{Av}\mu_{2dn} - \mu_{Av}\mu_{2dn} - \mu_{SJ} + \mu_{SJ}\mu_{Ev}$,

$T_3 = \mu_{vn}\mu_{\theta d} + (\mu_{vn}\mu_{r\theta} + \mu_{2dn}\mu_{\theta d})\mu_{dv} + (\mu_{vn} + \mu_{2dn}\mu_{r\theta} + \mu_{\theta d})\mu_{vc} + (\mu_{vn} + \mu_{2dn}\mu_{r\theta} + \mu_{\theta d})\mu_{JA} + \mu_{Av}\mu_{Ev} - \mu_{Av}$,

$T_4 = \mu_{vn}\mu_{r\theta} + \mu_{2dn}\mu_{\theta d} + (\mu_{vn} + \mu_{2dn}\mu_{r\theta} + \mu_{\theta d})\mu_{dv} + (\mu_{2dn} + \mu_{r\theta})\mu_{vc} + \mu_{JA}(\mu_{2dn} + \mu_{r\theta})$,

$T_5 = \mu_{vn} + \mu_{2dn}\mu_{r\theta} + \mu_{\theta d} + (\mu_{2dn} + \mu_{r\theta})\mu_{dv} + \mu_{vc} + \mu_{JA}$,

$T_6 = \mu_{2dn} + \mu_{r\theta} + \mu_{dv}$.

with

$\mu_{2dn} = (2\mu_h + \beta + (\gamma_A + \gamma_J)\frac{AI_M}{\mu_v})$, , $\mu_{r\theta} = 2\mu_h + \alpha + r_h, \mu_{dv} = 2\mu_v + (I_J + I_A \frac{\beta}{\mu_h})\gamma_v N_J + r_v, \mu_{SJ} = r_v\gamma_v N_J r_h \frac{\gamma_J AS_J}{\mu_v}$,

$\mu_{vn} = (\mu_h + \frac{\gamma_A AI_M}{\mu_v})(\mu_h + \beta + \frac{\gamma_J AI_M}{\mu_v}), \mu_{Ev} = E_M + I_M$, $\mu_{\theta d} = (\mu_h + \alpha)(\mu_h + r_h), \mu_{JA} = (I_J + I_A \frac{\beta}{\mu_h})r_v\gamma_v N_J$,

$\mu_{vc} = \mu_v(\mu_v + (I_J + I_A \frac{\beta}{\mu_h})\gamma_v N_J + r_v), \mu_{Iv} = \frac{\gamma_A AI_M}{\mu_v}, \mu_{Av} = r_v\gamma_v N_J r_h \frac{\gamma_A AS_A}{\mu_v}\frac{\beta}{\mu_h}, \mu_{cd} = \mu_h + \beta + \frac{\gamma_J AI_M}{\mu_v}$,

$\mu_{\theta c} = r_v\gamma_v N_J r_h \frac{\gamma_J AS_J}{\mu_v}(\mu_h + \beta)$.

It can be easily seen that λ_1 and λ_2 have negative real parts. We use Routh-Hurwitz criteria to check the sign of remaining eigenvalues. If it satisfies the following conditions, the eigenvalues will have negative real parts.

$\det H_1 = T_6 > 0$ (9.1)

$\det H_2 = T_6T_5 - T_4 > 0$ (9.2)

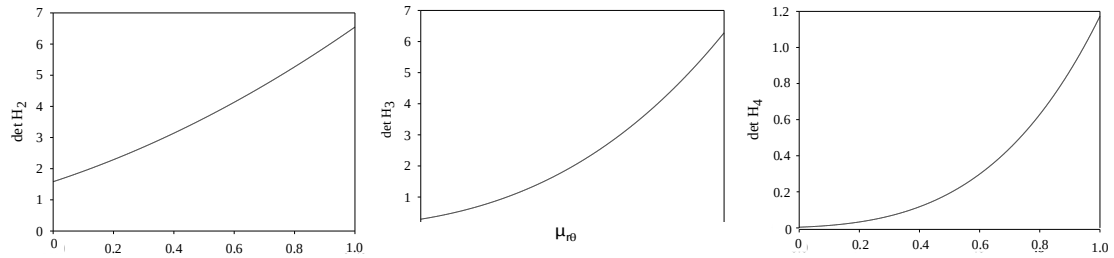
$\det H_3 = -T_4^2 + T_2T_6 + T_4T_5T_6 - T_3T_6^2 > 0$ (9.3)

$\det H_4 = T_3(-T_4^2 + T_2T_6 + T_4T_5T_6 - T_3T_6^2) + T_2(-T_2 + T_4T_5 - T_5^2T_6 + T_3T_6) + T_1T_6(-T_4 + T_5T_6) > 0$ (9.4)

$\det H_5 = T_2T_3(-T_4^2 + T_2T_6 + T_4T_5T_6 - T_3T_6^2) + T_2^2(-T_2 + T_4T_5 - T_5^2T_6 + T_3T_6) + T_1(T_4T_6(-3T_2 + T_3T_6) + T_4^3 + T_6(-T_4^2T_5 + 2T_2T_5T_6 - T_1T_6^2)) > 0$ (9.5)

$\det H_6 = T_1T_2T_3(-T_4^2 + T_2T_6 + T_4T_5T_6 - T_3T_6^2) + T_1T_2^2(-T_2 + T_4T_5 - T_5^2T_6 + T_3T_6) + T_1^2(T_4T_6(-3T_2 + T_3T_6) + T_4^3 + T_6(-T_4^2T_5 + 2T_2T_5T_6 - T_1T_6^2)) > 0$ (9.6)

The inequalities (9.2) to (9.6) are shown in fig.3.



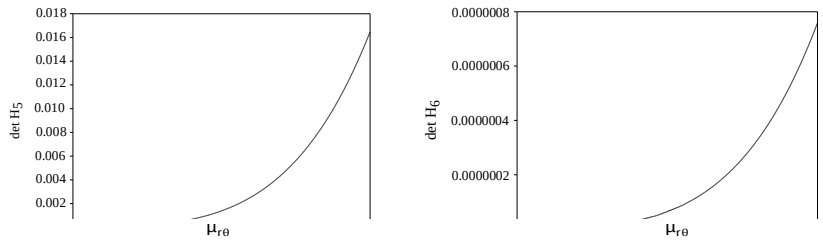
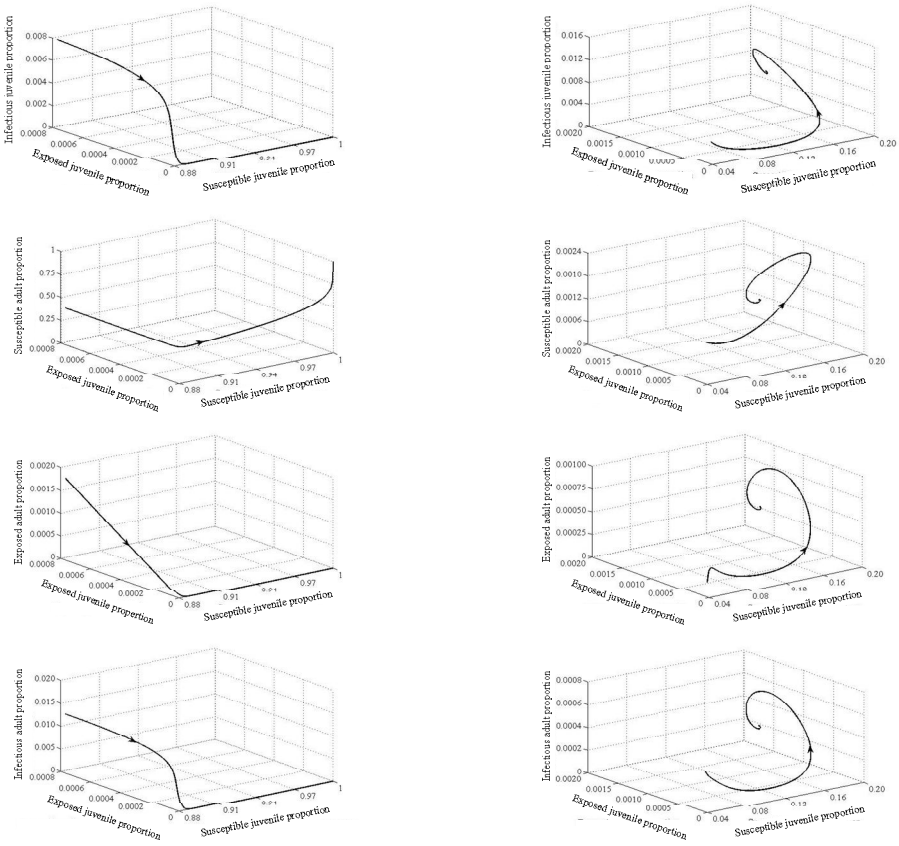


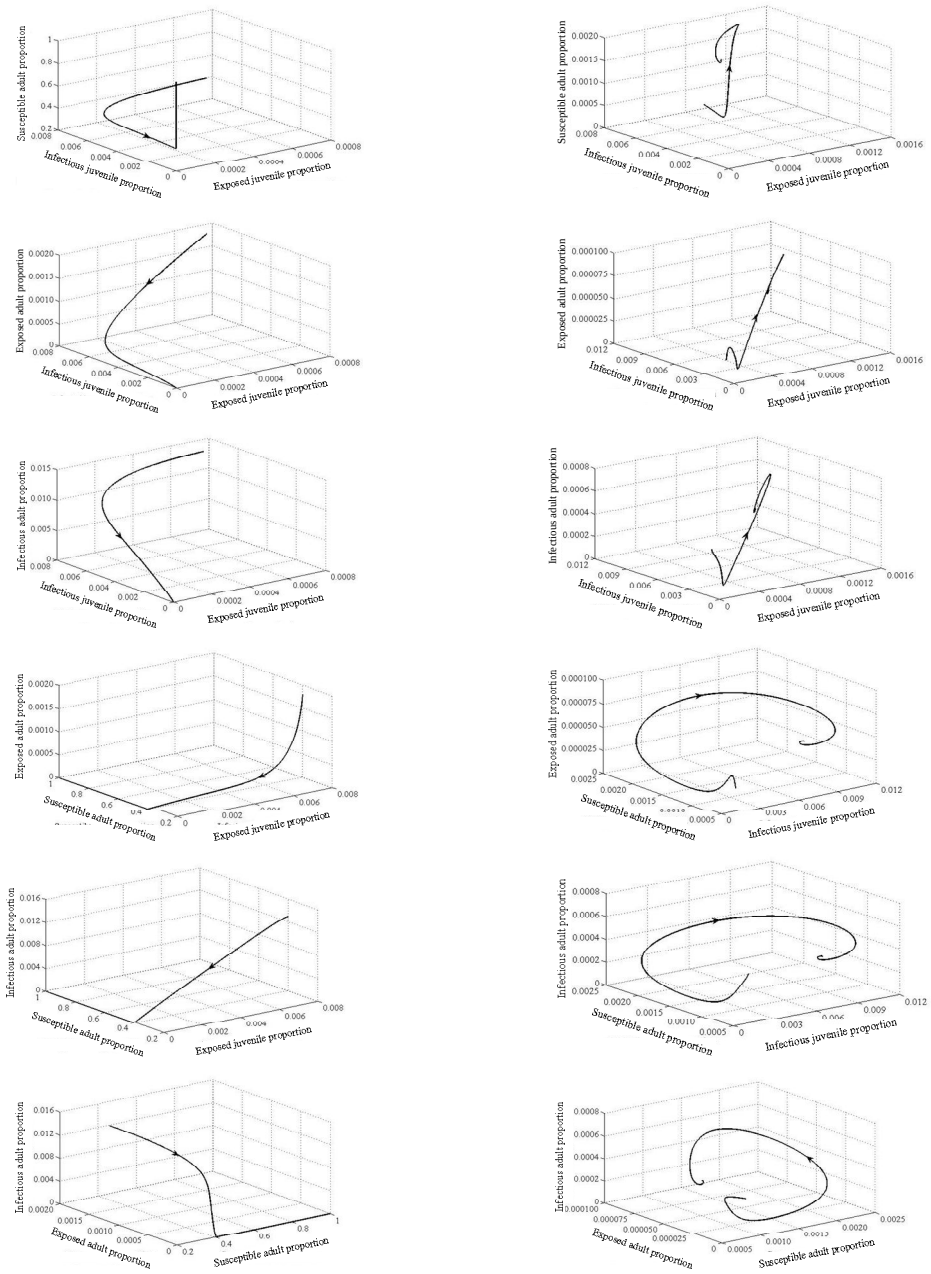
Fig.3 The parameter spaces for the endemic equilibrium point which satisfy the Routh-Hurwitz criteria. The values of the parameters are $N_T = 5,000, N_v = 1,000, \lambda_h = 1/(365\times 65)$ day^{-1}, $\mu_v = 1/(365\times 15)$ day^{-1}, $r_h = 1/6.5$ day^{-1}, $\alpha = 1/45.5$ day^{-1}, $\mu_v = 1/37.5$ day^{-1}, $r_v = 1/4.5$ day^{-1} and $b_v = d_v \times N_v = 1,000/37.5 \approx 27$ day^{-1}

The inequality (9.1) satisfies Routh-Hurwitz criteria because all terms in T_6 have positive values. From fig.3, Routh-Hurwitz criteria (9.2) - (9.6) are satisfied for $R_0 > 1$. Thus, the endemic equilibrium point is locally stable for $R_0 > 1$.

3.3 NUMERICAL RESULTS

In this section, we consider the transmission of this disease on the disease free and endemic regions. The values of the parameters used in this study are $\lambda_h = 1/(365\times 65)$ per day satisfies to a life expectancy of 65 years in human. $\mu_v = 1/37.5$ per day satisfies to the mean life of 37.5 days in mosquitoes. $\beta = 1/(365\times 15)$ per day corresponds to 15 years at which juvenile humans change to be adult humans. $r_h = 1/6.5$ per day satisfies to the average incubation time of 6.5 days in human. $\alpha = 1/45.5$ per day satisfies to the average recovered time of 45.5 days in infectious human population. $r_v = 1/4.5$ per day satisfies to the average incubation time of 4.5 days in mosquitoes [13]. The other parameters are arbitrarily chosen. The numerical solutions trajectories of (2.1) – (2.8) are shown in the fig 4.





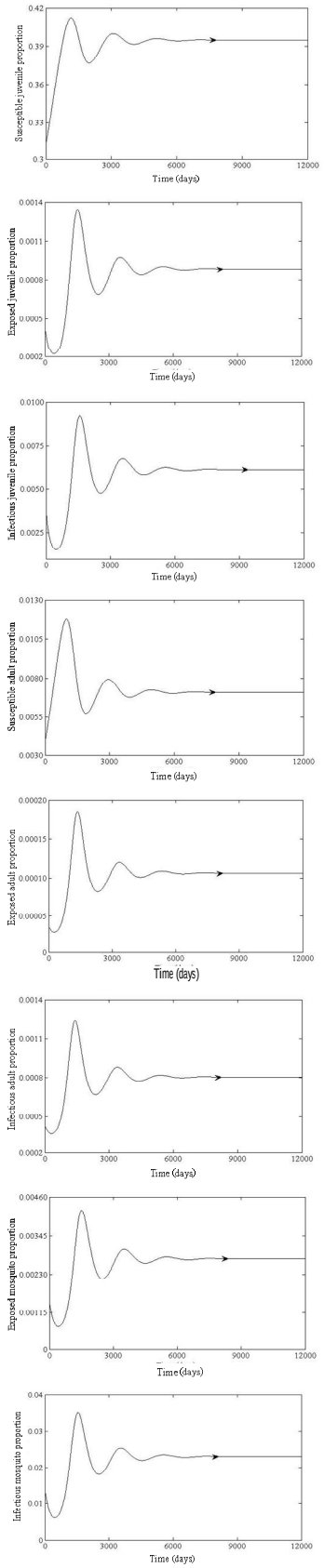
4a). 4b).

Fig.4 Numerical solutions demonstrate trajectories, projected into the 3D-space $(S_J^*, E_J^*, E_A^*), (S_J^*, E_J^*, I_A^*)$, $(S_J^*, E_J^*, I_J^*), (S_J^*, E_J^*, S_A^*), (E_J^*, I_J^*, S_A^*), (E_J^*, I_J^*, E_A^*), (E_J^*, I_J^*, I_A^*), (I_J^*, S_A^*, E_A^*), (I_J^*, S_A^*, I_A^*), (S_A^*, E_A^*, I_A^*)$, respectively. The value of parameters are $N_h = 4,000$, $\mu_h = 0.0000421$ day^{-1}, $\beta = 0.0001826$ day^{-1}, $r_h = 0.1538462$ day^{-1}, $\alpha = 0.0219780$ day^{-1}, $\mu_v = 0.0266667$ day^{-1}, $r_v = 0.2222222$ day^{-1}, $\gamma_J = 0.0000030$, $\gamma_A = 0.0000200$.

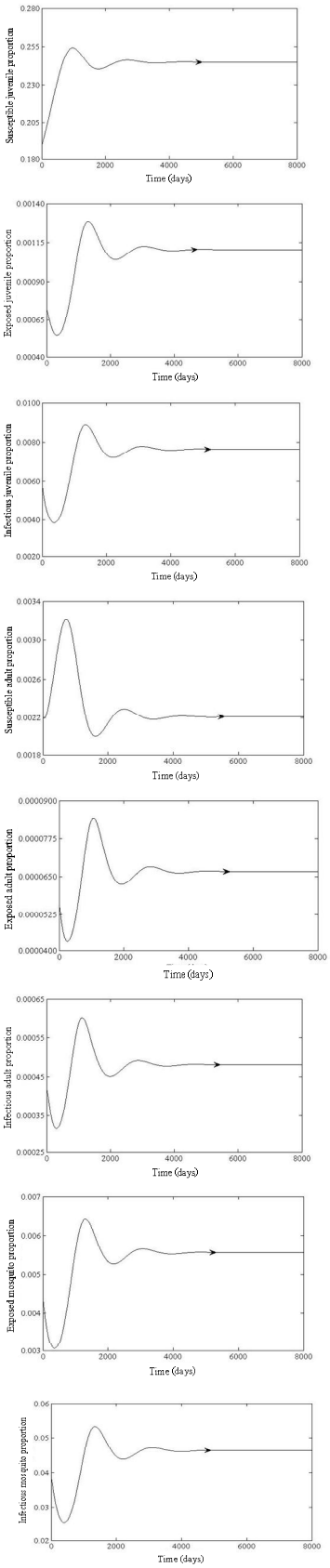
4a). $R_0 < 1$ where $R_0 = 0.0920044$, $N_M = 90$, $\gamma_v = 0.00001$. The fractions of populations $(S_J^*, E_J^*, I_J^*, S_A^*, E_A^*, I_A^*, E_M^*, I_M^*)$ approach to the disease free state $(1,0,0,1,0,0,0,0)$.

4b). $R_0 > 1$ where $R_0 = 194.231$, $N_M = 2,000$, $\gamma_v = 0.00095$. The trajectory of the eight state variable solution $(S_J^*, E_J^*, I_J^*, S_A^*, E_A^*, I_A^*, E_M^*, I_M^*)$ spirals into the endemic disease equilibrium state $E_2 = (0.16732929, 0.00121491, 0.00841828, 0.00094041, 0.00004591, 0.00033684, 0.02237300, 0.18644150)$.

We compare the behaviors of our model when the basic reproductive numbers are difference. The results are shown in fig. 5.


Susceptible juvenile proportion
Time (days)
Exposed juvenile proportion
Time (days)
Infectious juvenile proportion
Time (days)
Susceptible adult proportion
Time (days)
Exposed adult proportion
Time (days)
Infectious adult proportion
Time (days)
Exposed mosquito proportion
Time (days)
Infectious mosquito proportion
Time (days)

5a).


Susceptible juvenile proportion
Time (days)
Exposed juvenile proportion
Time (days)
Infectious juvenile proportion
Time (days)
Susceptible adult proportion
Time (days)
Exposed adult proportion
Time (days)
Infectious adult proportion
Time (days)
Exposed mosquito proportion
Time (days)
Infectious mosquito proportion
Time (days)

5b).

Fig.5 Numerical solutions (2.1) - (2.8) demonstrate behavior of $S_J^*, E_J^*, I_J^*, S_A^*, E_A^*, I_A^*, E_M^*$ and I_M^*, respectively, for $R_0 > 1$with $N_h = 8,000, N_M = 5,000, \mu_h = 0.0000421\ \text{day}^{-1}, \beta = 0.0001826\ \text{day}^{-1}, r_h = 0.1538462\ \text{day}^{-1}$, $\alpha = 0.0219780\ \text{day}^{-1}, \mu_v = 0.0266667\ \text{day}^{-1}, r_v = 0.2222222\ \text{day}^{-1}$.
5a). $R_0 = 51.1135, \gamma_v = 0.00005$. The fractions of populations converge to equilibrium point $E_2 = (0.39476342,$ 0.00088307, 0.00611983, 0.00711127, 0.00010642, 0.00075522,0.00275721, 0.02297677)
5b). $R_0 = 102.2271, \gamma_v = 0.0001$. The fractions of populations converge to equilibrium point $E_2 = (0.24459480,$ 0.00110218, 0.00763713, 0.00220734, 0.00006669, 0.000480560.00555412, 0.04628433)

4. DISCUSSION AND CONCLUSION

In this study, we constructed the mathematical model of Chikungunya and analyzed the results by using standard dynamical modeling method [1]. The basic reproductive number is defined by R_0 where

$$R_0 = \frac{\gamma_v r_v r_h N_M (\gamma_J N_J + \gamma_A N_A)}{\mu_v (\mu_v + r_v)(\alpha + \mu_h)(\mu_h + r_h)} \qquad (10)$$

Fig. 4 shows $(S_J^*, E_J^*, I_J^*, S_A^*, E_A^*, I_A^*, E_M^*, I_M^*)$ moving towards the equilibrium state solutions. We can see that the trajectory solutions approaching to the disease equilibrium state $(1,0,0,1,0,0,0,0)$ when $R_0 < 1$. When $R_0 > 1$, the trajectory solutions spiral into the endemic equilibrium state $E_2 = (0.16732929, 0.00121491, 0.00841828,\ 0.00094041, 0.00004591, 0.00033684, 0.02237300, 0.18644150)$.

Fig. 5 shows time series solutions of susceptible juvenile, exposed juvenile, Infectious juvenile, susceptible adult, exposed adult, Infectious adult, exposed mosquito and Infectious mosquito for the different basic reproductive numbers 5a) $R_0 = 51.1135$ and 5b) $R_0 = 102.2271$. We can see that solutions for $R_0 = 51.1135$ moving towards its equilibrium state slower than $R_0 = 102.2271$.

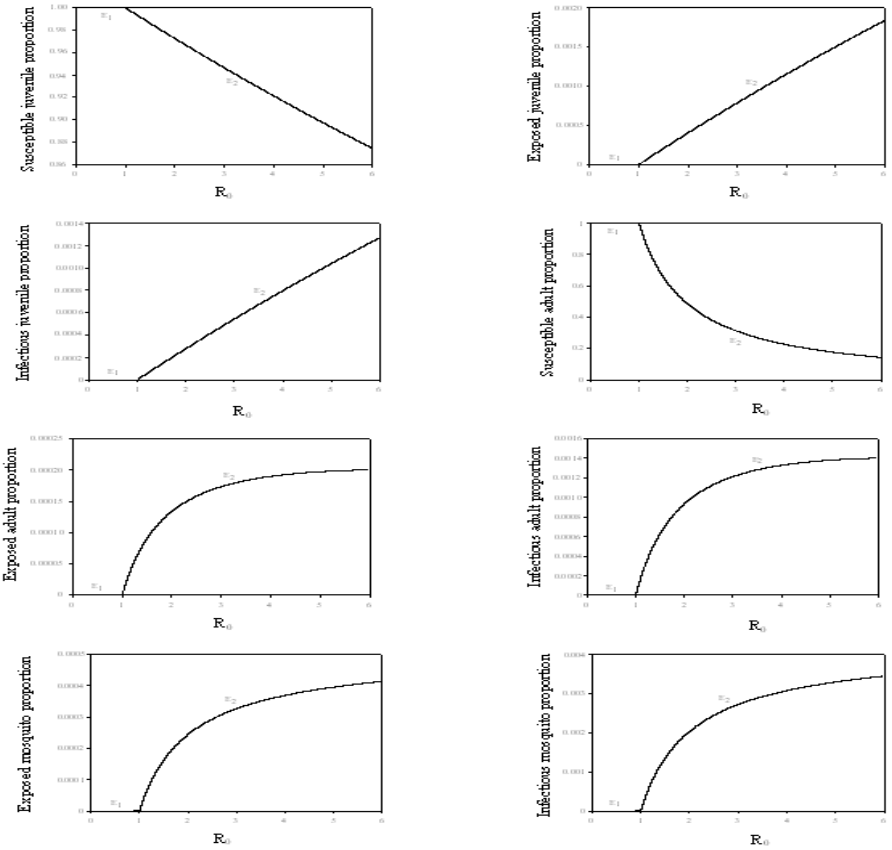


Fig. 6 Bifurcation diagram of the solutions of equations (2.1) to (2.8) for the different values of R_0. ——— denote the stable solutions and - - - - denote the unstable solutions.

The bifurcation diagrams of (2.1) to (2.8) are shown in fig.6. We can see that, when $R_0 < 1$, E_1 will be stable and for $R_0 > 1$, E_2 will be stable. If the basic reproductive number is greater than one, the normalized

susceptible juvenile and susceptible adult proportions are decrease. The normalized exposed of juvenile, adult and mosquito proportions, infectious of juvenile and adult proportions and susceptible mosquito proportions increase. These behaviors occur because there are enough susceptible juvenile and adult to be infected from infectious mosquitoes.

The ultimate goal of any control effort is to reduce (10) below 1, then the number of infectious human proportion will be decreased. This should suggest the alternative way to reduce the outbreak of Chikungunya disease. Therefore, the human population should protect themselves from infected with Chikungunya virus to reduce the biting rate from the vector population. This will cause the basic reproductive number to decrease below one. Consequently, the outbreak of the disease will be reduced.

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