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Modeling on the Chikungunya Transmission with Mobility of Migrant Workers

Phithchayapong Chatrakul, Prasit Thongjeam and Surapol Naowarat

Department of Mathematics, Faculty of Science and Technology, Suratthani Rajabhat University, Surat Thani, 84100, Thailand

Address For Correspondence:
Surapol Naowarat, Department of Mathematics, Faculty of Science and Technology, Suratthani Rajabhat University, Surat Thani, 84100, Thailand

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ABSTRACT

Chikungunya is a vector borne disease which is transmitted to human by the bite of an infected Aedes mosquitoes (Aedes albopictus and Aedes aegypti). In this paper, a mathematical model of Chikungunya has been proposed and analyzed. In 2008, the south of Thailand has been occurred a large outbreak of this disease when there are the mobility of population from place to place especially migrant workers. For this model, the human population is divided into two classes; host population and migrant workers population. Thus, migrant workers in rubber plantation have been taken into account in the model. Stability analysis of the model has been carried out. We have derived the threshold condition, basic reproductive number. We found that there has two equilibrium points; disease free equilibrium point and endemic equilibrium point. Local stability of both equilibrium points is discussed and the numerical results are shown for some value of parameters. It concluded that the alternative way to control the spread of Chikungunya fever by reducing the mobility of the migrant workers and host human in the community when the Chikungunya occurs.

INTRODUCTION

Chikungunya fever is an alphavirus that infects humans through the bites from *Ades aegypti mosquitoes and Aedes albopictus* mosquitoes. Symptoms are similar to dengue fever during the acute phase and include rash and higher fever. Outbreaks have occurred in countries in Africa, Asia, Europe, and the Indian and Pacific Oceans (CDC,2016). There is no vaccine to prevent chikungunya virus infection or disease. The way to prevent chikungunya fever is to avoid mosquito bites (WHO,2016). The south of Thailand has been occurred a large outbreak of this disease when there are the mobility of population from place to place especially migrant workers. This paper concentrates on attempts to model and study the effects among these risk groups to inform future treatment and prevention programs.

In the mathematical biology article, several mathematical models have been proposed for analyzing the spread and control of infectious diseases. It’s a valuable tool in the explaining of the phenomena. In particular, mathematical models have been used to understand the dynamics of the chikungunya fever. In 2011, Naowarat et. al. proposed a mathematical model describing the transmission of chikungunya fever. They shown the numerical results and the efficacy of the adulticide for prevention programs. Moulay et. al.(2011) proposed two models involving differential equations for the mosquito population and virus transmission to the human population. They consider a model which takes into account the dynamics of the vector with a non-constant population size and a contact rate that depends on the vector population size. In addition, Yakob and Clements (2013) constructed an ordinary differential equation model to simulate the transmission of infection between

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humans and aedesalbopictus. They demonstrates a strong influence of the rate at which hosts become infectious (inverse of the latent period) to both the peak incidence and total infected population.

In this study, we also propose the transmission model of chikungunya fever in two interacting populations, we consider the total population with size N_{WH}, as we are developed and analyzed a simple SIR (Susceptible - Infected - Recovered) model for chikungunya transmission that incorporates the migrant workers enter in the community. The model consists of a system of differential equations. We assume the human and mosquito population are constant with the same birth rate and death rate. In our model we consider the rate of change of six classes of human population and two classes for mosquito population. The total population is divided into two classes i.e., the total host (N_h) population and the total migrant workers in rubber tree population (N_w). The host population is divided into three subclasses $\bar{S}_H(t)$ $\bar{I}_H(t)$ and $\bar{R}_H(t)$ is the susceptible, infected and recovered host population.

The migrant in rubber tree workers are also divided into three subclasses. $\bar{S}_w(t)$ $\bar{I}_w(t)$ and $\bar{R}_w(t)$ is the susceptible, infected and recovered migrant workers in rubber tree population, respectively. The mosquito population is divided into two subclasses. The total mosquito population denoted by N_m, while the susceptible mosquito and the infected mosquito are represented by $\bar{S}_m(t)$ and $\bar{I}_m(t)$, respectively.

The objective of this study is to determine the effect of the infected migrant workers on the transmission of chikungunya fever. The organization of this paper as follows, in section 2, we formulate the propose model. In section 3, we analyze the model and find equilibrium points and determine the stabilities of each equilibrium points, derive the basic reproductive number. In section 4, we simulate the numerical simulations to support our analytic results. Finally, we conclude our study in section 5.

2. *Model Formulation:*

In this section we formulate a model for the transmission of chikungunya fever. First of all, we assumed that the human population is constant; birth rate equal to death rate. There are two groups of human population that is host population and migrant workers population. The host population is divided into three sub-classes; susceptible host population ($\bar{S}_h$), infected host population($\bar{I}_h$) and recovered host population($\bar{R}_h$). The migrant workers human population is divided into three sub-classes; susceptible migrant workers population($\bar{S}_w$), infected migrant worker population($\bar{I}_w$) and recovered migrant workers population($\bar{R}_w$). The mosquito population is divided into two sub-classes; that is susceptible mosquito population($\bar{S}_m$) and infected mosquito population($\bar{I}_m$). The dynamic of chikungunya model is depicted in Fig.1.

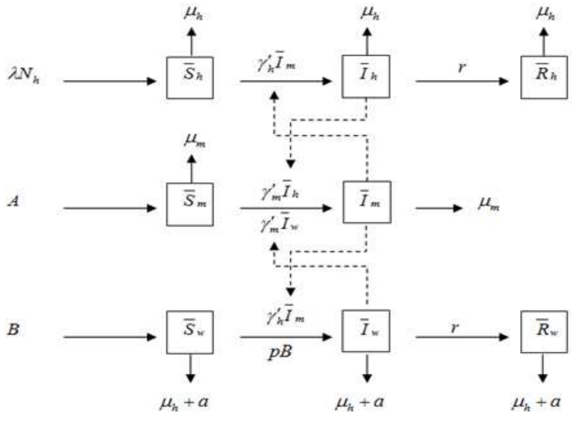


Fig. 1: Diagram for the Chikungunya fever Transmission.

The dynamical model of chikungunya can be expressed by the following differential equations:

$$\frac{d\bar{S}_h}{dt} = \lambda N_h - \gamma'_h \bar{I}_m \bar{S}_h - \mu_h \bar{S}_h \tag{1.a}$$

$$\frac{d\bar{I}_h}{dt} = \gamma'_h \bar{I}_m \bar{S}_h - (r + \mu_h)\bar{I}_h \tag{1.b}$$

$$\frac{d\bar{R}_h}{dt} = r\bar{I}_h - \mu_h \bar{R}_h \tag{1.c}$$

$$\frac{d\bar{S}_w}{dt} = (1-p)B - \gamma'_h \bar{I}_m \bar{S}_w - (\mu_h + a)\bar{S}_w \tag{1.d}$$

$$\frac{d\bar{I}_w}{dt} = pB + \gamma'_h \bar{I}_m \bar{S}_w - (r + \mu_h + a)\bar{I}_w \tag{1.e}$$

$$\frac{d\bar{R}_w}{dt} = r\bar{I}_w - \mu_h \bar{R}_w - a\bar{R}_w \tag{1.f}$$

$$\frac{d\bar{S}_m}{dt} = A - \gamma'_m \bar{I}_h \bar{S}_m - \gamma'_m \bar{I}_w \bar{S}_m - \mu_m \bar{S}_m \tag{1.g}$$

$$\frac{d\bar{I}_m}{dt} = \gamma'_m \bar{I}_h \bar{S}_m + \gamma'_m \bar{I}_w \bar{S}_m - \mu_m \bar{I}_m \tag{1.h}$$

with $\bar{S}_h + \bar{I}_h + \bar{R}_h = N_h$, $\bar{S}_w + \bar{I}_w + \bar{R}_w = N_w$, $\bar{S}_m + \bar{I}_m = N_m$

and $\gamma'_h = \frac{b\beta_h}{N_h + N_w + m}$, $\gamma'_m = \frac{b\beta_m}{N_h + N_w + m}$

where λ is the birth rate of the host population, γ'_h is the unrenormalized rate of transmission of Chikungunya virus from infected mosquito to susceptible human, γ'_m is the unrenormalized rate of transmission of Chikungunya virus from infected human to susceptible mosquito,

μ_h is the natural death rate of host population,

μ_m is the natural death rate of mosquito population,

r is the recovery rate of the host and the migrant population,

p is the percentage of migrant workers in rubber tree who are infectious when they are entering the community,

a is the rate that the migrant workers in rubber tree move out the community which is the reciprocal of time migrant workers in rubber tree staying in the particular community, A is the birth rate of mosquito population,

B is the immigration rate.

We normalized the variables by dividing by total population in each group.

The normalized equations are described as following:

$$\frac{dS_h}{dt} = \mu_h - \gamma_h I_m S_h - \mu_h S_h \tag{2.a}$$

$$\frac{dI_h}{dt} = \gamma_h I_m S_h - (r + \mu_h) I_h \tag{2.b}$$

$$\frac{dS_w}{dt} = (1-p)(a + \mu_h) - \gamma_h I_m S_w - (a + \mu_h) S_w \tag{2.c}$$

$$\frac{dI_w}{dt} = p(a + \mu_h) + \gamma_h I_m S_w - (r + \mu_h + a) I_w \tag{2.d}$$

$$\frac{dI_m}{dt} = \gamma_m I_h (1 - I_m) + \gamma_m N_{wh} I_w (1 - I_m) - \mu_m I_m \tag{2.e}$$

3. *Model Analysis Equilibrium points:*

The model will be analyzed to investigate the equilibrium point and its stability by using standard method. By setting the right hand side of equation (2.a) - (2.e) to zero, we find two possible equilibrium points i.e. the disease free equilibrium point and the endemic equilibrium point.

Disease Free Equilibrium Point (E_0) (case $p = 0$) : In absence of disease, that is $I_h = 0, I_w = 0, I_m = 0$, We obtained, $E_0(S_h, I_h, S_w, I_w, I_m) = (1, 0, 1-p, 0, 0)$

Endemic Equilibrium Point (E_1) (case $0 < p < 1$) : At endemic equilibrium point, we consider in the case of the present of the disease in the community that is $I_h \neq 0, I_w \neq 0, I_m \neq 0$. We obtained, $E_1(S_h^*, I_h^*, S_w^*, I_w^*, I_m^*)$ where

$$S_h^* = \frac{\mu_h}{\mu_h + \gamma_h I_m^*}$$

$$I_h^* = \frac{\mu_h \gamma_h I_m^*}{(r + \mu_h)(\mu_h + \gamma_h I_m^*)}$$

$$S_w^* = \frac{(1-p)(a + \mu_h)}{a + \mu_h + \gamma_h I_m^*} \qquad I_w^* = \frac{p(a + \mu_h)^2 + \gamma_h (a + \mu_h) I_m^*}{(r + a + \mu_h)(a + \mu_h + \gamma_h I_m^*)}$$

$$I_m^* = \frac{\gamma_m I_h^* + \gamma_m N_{wh} I_w^*}{\mu_m + \gamma_m I_h^* + \gamma_m N_{wh} I_w^*}$$

Basic Reproduction Number:

The basic reproductive number (R_0) is defined as the average number of secondary infections caused by an infected individual during the infectious period (Anderson and May,1991). When $R_0 < 1$, each infected individual produces on average less than one new infected individual, so we would expect the disease to die out. On the other hand, if $R_0 > 1$, each individual produces more than one new infected individual, so the disease spread in the population (Diekmann et al., 1990).

To obtain R_0 by using the next generation method and used spectral radius (Van den Driessche and Watmough, 2002). By rewriting equations (2.a)-(2.e) in matrix form;

$$\frac{dX}{dt} = F(X) - V(X)$$

where $X = (S_h, I_h, S_w, I_w, I_m)^T$

$$F(x) = \begin{bmatrix} 0 \\ \gamma_h I_m S_h \\ 0 \\ \gamma_h I_m S_w \\ 0 \end{bmatrix}$$

and
$$V(x) = \begin{bmatrix} -\mu_h + \gamma_h I_m S_h + \mu_h S_h \\ (r+\mu_h) I_h \\ -(1-p)(a+\mu_h) + \gamma_h I_m S_w + (a+\mu_h) S_w \\ -p(a+\mu_h) + (r+\mu_h+a) I_w \\ -r_m I_h - r_m N_{wh} I_w + \gamma_m I_h I_m + \gamma_m N_{wh} I_w I_m + \mu_m I_m \end{bmatrix}.$$

Find the Jacobian matrices of $\mathrm{F}(\mathrm{x})$ and $\mathrm{V}(\mathrm{x})$ evaluated at E_0. Thus, we obtain

$$F = \begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \gamma_h \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \gamma_h \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

and

$$V = \begin{bmatrix} \mu_h & 0 & 0 & 0 & \gamma_h \\ 0 & r+\mu_h & 0 & 0 & 0 \\ 0 & 0 & a+\mu_h & 0 & \gamma_h \\ 0 & 0 & 0 & r+\mu_h+a & 0 \\ 0 & -r_m & 0 & -r_m N_{wh} & \mu_m \end{bmatrix},$$

The Basic reproductive number is defined as the dominant eigenvalue of FV^{-1} that we call as the spectral radius of FV^{-1} denoted by $\rho\left(\mathrm{FV}^{-1}\right)$.

We obtained

$$FV^{-1} = \begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \dfrac{\gamma_h}{\mu_m} \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \dfrac{\gamma_h}{\mu_m} \\ 0 & \dfrac{\gamma_m}{r+\mu_h} & 0 & \dfrac{\gamma_m N_{wh}}{r+\mu_h+a} & 0 \end{bmatrix}$$

Thus, the spectral radius of FV^{-1} denoted by $\rho(FV^{-1})$

$$\rho(FV^{-1}) = \sqrt{\frac{\gamma_h\gamma_m}{\mu_m(r+\mu_h)} + \frac{\gamma_h\gamma_m N_{wh}}{\mu_m(r+\mu_h+a)}}$$ Hence,

$$R_0 = \sqrt{\frac{\gamma_h\gamma_m}{\mu_m(r+\mu_h)} + \frac{\gamma_h\gamma_m N_{wh}}{\mu_m(r+\mu_h+a)}}$$

Local stability of equilibrium points:

1. Local stability of disease free equilibrium:

The local stability of the disease free equilibrium can be analyzed using the Jacobian matrix of the chikungunya model at the disease free equilibrium point. Referring to the results of Van den Driessche and Watmough (2002), the following theorem holds.

Theorem 1:

The disease free equilibrium point for the Chikungunya model is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$.

Proof. The Jacobian matrix of Chikungunya model (Eq. (2.a)-(2.e)) evaluated at the disease-free equilibrium point $E_0(1, 0, 1-p, 0, 0)$, is obtained as

$$J_0 = \begin{bmatrix} -\mu_h & 0 & 0 & 0 & -\gamma_m \\ 0 & -(r+\mu_h) & 0 & 0 & \gamma_h \\ 0 & 0 & -(a+\mu_h) & 0 & -\gamma_h(1-p) \\ 0 & 0 & 0 & -(r+\mu_h+a) & \gamma_h(1-p) \\ 0 & \gamma_m & 0 & \gamma_m N_{wh} & -\mu_m \end{bmatrix}$$

The eigenvalues of the J_0 are obtained by solving $det(J_0 - \lambda I) = 0$. We obtained the characteristic equation:

$$[\lambda + (a+\mu_h)](\lambda+\mu_h)(\lambda^3 + a_1\lambda^2 + a_2\lambda + a_3) = 0 \qquad (3)$$

where

$$a_1 = a + \mu_m + 2r + 2\mu_h$$
$$a_2 = \mu_m(2r + 2\mu_h + a) + (r+\mu_h)(r+\mu_h+a) - \gamma_m\gamma_h - \gamma_m\gamma_h N_{wh}(1-p)$$
$$a_3 = (r+\mu_h)(r+\mu_h+a)\mu_m - \gamma_m\gamma_h(r+\mu_h+a) - \gamma_m\gamma_h N_{wh}(1-p)(r+\mu_h)$$

From the characteristic Eq. (12), we get two of eigenvalue are $\lambda_1 = -(a+\mu_h) < 0$ and $\lambda_2 = -\mu_h < 0$. Next, to determine the other eigenvalues from the characteristic equation $\lambda^3 + a_1\lambda^2 + a_2\lambda + a_3 = 0$. The roots of this equation are negative if it is satisfied with three conditions of Routh-Hurwitz criteria (Allen, 2006). Thus, E_0 is local asymptotically stable for $R_0 < 1$ if $\lambda^3 + a_1\lambda^2 + a_2\lambda + a_3 = 0$ satisfies the following conditions:

1) $a_1 > 0$,
2) $a_3 > 0$.
3) $a_1 a_2 > a_3$.

2. Local stability of endemic equilibrium:

Theorem 2:

The endemic equilibrium point for the Chikungunya model (Eq. (2.a)-(2.e)) is locally asymptotically stable if $R_0 > 1$ and unstable if $R_0 < 1$.

Proof. The Jacobian matrix of the chikungunya model (Eq. (2.a)-(2.e)) evaluated at the endemic equilibrium point $E_1(S_h^*, I_h^*, S_w^*, I_w^*, I_m^*)$, is obtained a

$$J_1 = \begin{bmatrix} -\gamma_h I_m^* - \mu_h & 0 & 0 & 0 & -\gamma_h S_h^* \\ \gamma_h I_m^* & -(r+\mu_h) & 0 & 0 & \gamma_h S_h^* \\ 0 & 0 & -\gamma_h I_m^* - (a+\mu_h) & 0 & -\gamma_h S_w^* \\ 0 & 0 & \gamma_h I_m^* & -(r+\mu_h+a) & \gamma_h S_w^* \\ 0 & \gamma_m(1-I_m^*) & 0 & \gamma_m N_{wh}(1-I_m^*) & -\gamma_m I_h^* - \gamma_m N_{wh} I_w^* - \mu_m \end{bmatrix}.$$

The characteristic equation of Jacobian matrix at E_1, is given by solving $det(J_1 - \lambda I) = 0,$ we obtained :

$$-(\lambda + \mu_h + \gamma_h I_m^*)(\lambda^4 + b_1\lambda^3 + b_2\lambda^2 + b_3\lambda + b_4) = 0 \qquad (4)$$

where

$$b_1 = (\mu_m + \mu_h) + (\gamma_m + \gamma_h)I_m^* + \gamma_m N_{wh} I_w^* + 2(r + a + \mu_h),$$

$$\begin{aligned} b_2 = {} & (\mu_m+\gamma_m I_m^*+\gamma_m N_{wh} I_w^*)(r+2\mu_h+2a+\gamma_h I_m^*)+(a+\mu_h+\gamma_h I_m^*)(r+\mu_h+a) \\ & -\gamma_h S_w^*(\gamma_h N_{wh})(1-I_m^*)+(r+\mu_h)(\mu_m+\gamma_m I_m^*+\gamma_m N_{wh} I_w^*+r+2\mu_h+2a+\gamma_h I_m^*) \\ & -\gamma_h S_h^*\gamma_m(1-I_m^*) \end{aligned}$$

$$\begin{aligned} b_3 = {} & (a+\mu_h+\gamma_h I_m^*)(r+\mu_h+a)(\mu_m+\gamma_m I_m^*+\gamma_m N_{wh} I_w^*)+\gamma_h S_w^*(\gamma_h I_m^*)(\gamma_m N_{wh})(1-I_m^*) \\ & -\gamma_h S_w^*(\gamma_m N_{wh})(1-I_m^*)(a+\mu_h+\gamma_h I_m^*) \\ & +(r+\mu_h)\left[\,(\mu_m+\gamma_m I_m^*+\gamma_m N_{wh} I_w^*)(r+2\mu_h+2a+\gamma_h I_m^*)+(r+2\mu_h+2a+\gamma_h I_m^*),\right. \\ & \left.+(a+\mu_h+\gamma_h I_m^*)(r+\mu_h+a)-\gamma_h S_w^*(\gamma_h N_{wh})(1-I_m^*)\,\right] \\ & -\gamma_h S_h^*\gamma_m(1-I_m^*)(r+2a+2\mu_h+\gamma_h I_m^*) \end{aligned}$$

Obviously, $\lambda_1 = -(\mu_h + \gamma_h I_m^*)$ as the four eigenvalues of $\lambda^4 + b_1\lambda^3 + b_2\lambda^2 + b_3\lambda + b_4 = 0$ have negative real part if they satisfy the Routh-Hurwitz criteria. Thus, E_1 is local asymptotically stable for $R_0 > 1$ if $\lambda^4 + b_1\lambda^3 + b_2\lambda^2 + b_3\lambda + b_4 = 0$ satisfies the following conditions:

1) $b_1 > 0$, 2) $b_3 > 0$, 3) $b_4 > 0$. 4) $b_1 b_2 b_3 > b_3^2 + b_1^2 b_4$.

1. *Numerical Simulations:*

The previous section shows the existence of equilibrium point and their stability conditions. In this study, we solve the system of ordinary differential equations. The numerical results from computer simulation, using parameters values as shown in table1, are obtained as follows Fig. 2 , Fig.3 and Fig. 4

Table 1: Parameter values is used in numerical simulations at Disease Free State.

Parameter	Description	Values
N_{wh}	Total number of host and migrant workers	10,000
γ_h	The unrenormalized rate of transmission of Chikungunya virus from infected mosquito to susceptible human	0.003 year^{-1}
μ_h	Natural death rate of host population	0.0130208 year^{-1}
r	Recovery rate of the host and the migrant population	0.1428 day^{-1}
p	Percentage of migrant workers who infected	0
a	Move out rate of migrant workers	0.09

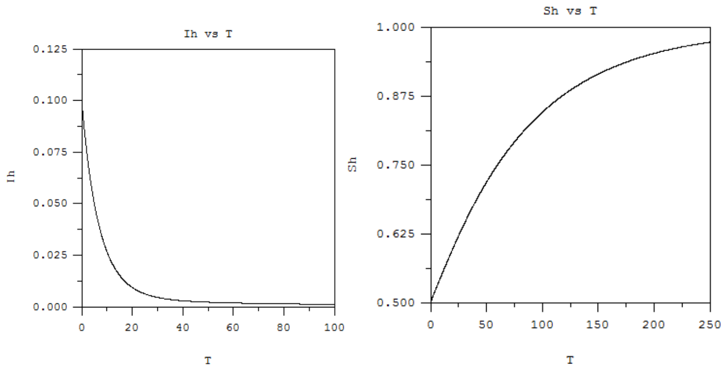
Stability of disease free state:

Using the values of parameters shown in Table 1, we obtained the eigenvalues and the basic reproductive number as follow:

$\lambda_1 = -0.10302083$, $\lambda_2 = -0.01302083$, $\lambda_3 = -0.492877$, $\lambda_4 = -0.155831$ and $\lambda_5 = -0.00293307$

$R_0 = 0.988167 < 1$.

Since all eigenvalues are found to be negative as well as the basic reproductive number is less than one, the disease free equilibrium, $E_0(1, 0, 1, 0, 0)$,will be local asymptotically stable for the above set of parameter values. The results of numerical simulations converge to the disease free equilibrium state as shown in Fig. 2.



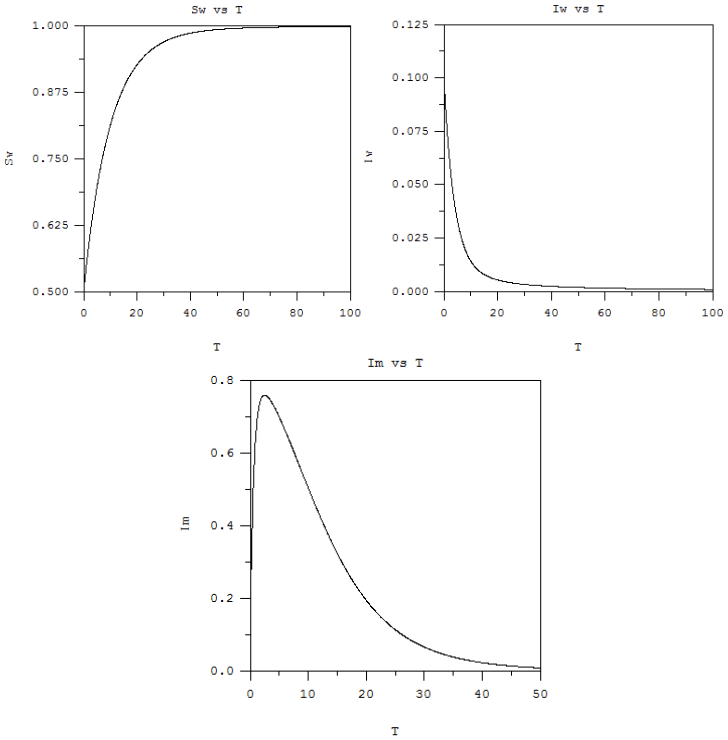


Fig. 2: Time series evolution of the population compartments in the case of the disease free state.

Stability of Endemic state:

Next, when $p = 0.1$ and we change three different values of the move out rate of migrant workers to $a = 0.01, 0.05, 0.07$ and keep others to be those given in Table 1. We obtained the eigenvalues and basic reproductive number as follow:

$a = 0.01$	$a = 0.05$	$a = 0.07$
$R_0 = 1.2031$	$R_0 = 1.0799$	$R_0 = 1.0309$
$\lambda_1 = -0.0153$	$\lambda_1 = -0.0155$	$\lambda_1 = -0.0155$
$\lambda_2 = -0.6255$	$\lambda_2 = -0.8385$	$\lambda_2 = -0.9049$
$\lambda_3 = -0.0089$	$\lambda_3 = -0.0240$	$\lambda_3 = -0.0309$
$\lambda_4 = -0.1531 + 0.2412i$	$\lambda_4 = -0.2171 + 0.2466i$	$\lambda_4 = -0.2446 + 0.2526i$
$\lambda_5 = -0.1531 - 0.2412i$	$\lambda_5 = -0.2171 - 0.2466i$	$\lambda_5 = -0.2446 - 0.2526i$

Since all eigenvalues are found to be negative as well as the basic reproductive number is greater than one, the equilibrium state will be the endemic state,

Case 1 $a = 0.01$

$E_1(0.84, 0.01, 0.81, 0.02, 0.78)$

Case 2 $a = 0.05$

$E_1(0.83, 0.01, 0.86, 0.04, 0.84)$

Case 3 $a = 0.07$

$E_1(0.83, 0.01, 0.87, 0.04, 0.85)$

, which will be local asymptotically stable for the above set of parameter values. The results of numerical simulations oscillate to the endemic equilibrium state as shown in Fig. 3.

Furthermore, we consider the numerical results when the value of the percentage of infected migrant workers in human population are different i.e. $p = 0.1$, $p = 0.5$ and $p = 0.7$ and the move out rate of migrant workers is a = 0.07 while the other parameters fixed like at the endemic state. We obtained the eigenvalues and basic reproductive number as follow:

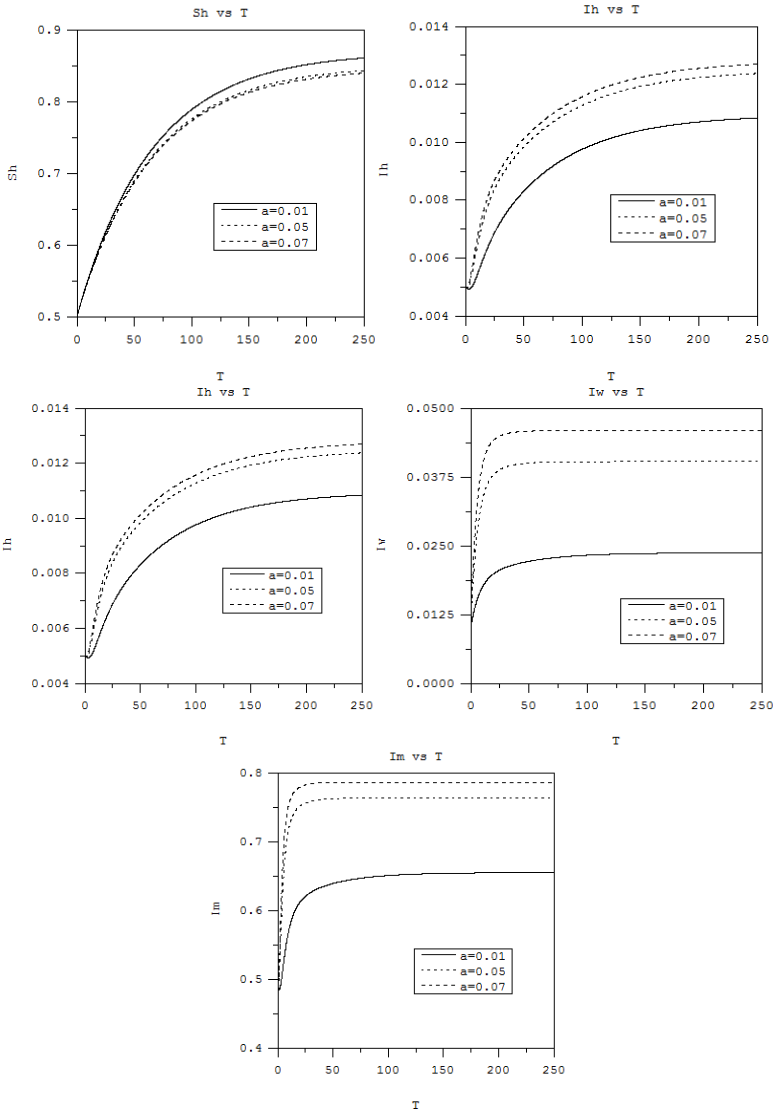


Fig. 3: Time series evolution of the population compartments in the case of the endemic state.

$p = 0.1$	$p = 0.5$	$p = 0.9$
$R_0 = 1.0309$ $\lambda_1 = -0.0155$ $\lambda_2 = -0.9049$ $\lambda_3 = -0.0309$ $\lambda_4 = -0.2446 + 0.2526\,i$ $\lambda_5 = -0.\ 0.2446 - 0.2526\,i$	$R_0 = 1.0309$ $\lambda_1 = -0.0159$ $\lambda_2 = -3.7980$ $\lambda_3 = -0.0516$ $\lambda_4 = -0.2209 + 0.1160\,i$ $\lambda_5 = -0.2209 - 0.1160\,i$	$R_0 = 1.0309$ $\lambda_1 = -0.0159$ $\lambda_2 = -6.6526$ $\lambda_3 = -0.0597$ $\lambda_4 = -0.2116 + 0.0874\,i$ $\lambda_5 = -0.2116 - 0.0874\,i$

Since all eigenvalues are found to be negative as well as the basic reproductive number is greater than one, the equilibrium state will be other cases of the endemic state,

Case 1 $p = 0.1$

$E_1(0.83, 0.01, 0.87, 0.04, 0.85)$

Case 2 $p = 0.5$

$E_1(0.81, 0.01, 0.48, 0.18, 0.96)$

Case 3 $p = 0.9$

$E_1(0.81, 0.01, 0.09, 0.33, 0.97)$

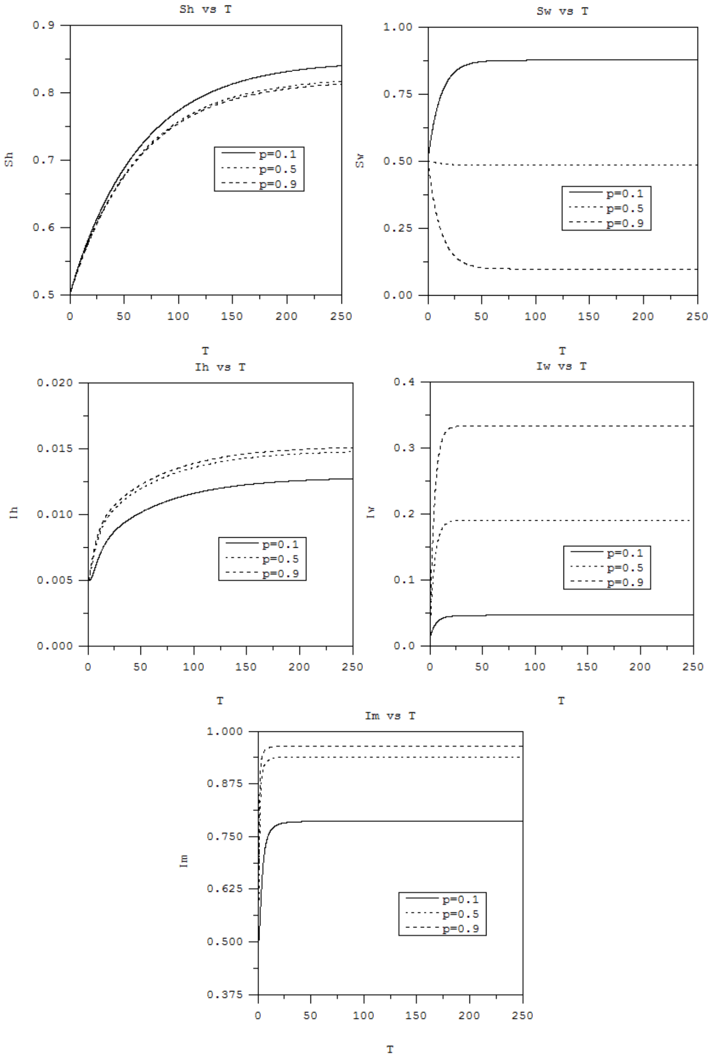


Fig. 4: Time series of the population compartments. The values of parameters are the same as in endemic state with different value of p; $p = 0.1$ $p = 0.5$ $p = 0.9$. The number of infected humans decrease when p increase.

Conclusion:

We formulate the transmission model of chikungunya with mobility of migrant workers and analyzed the analytical results by using standard modeling method. The basic reproductive number is obtained through the use of spectral radius of the next generation matrix. The basic reproductive number is $R_0 = \sqrt{\frac{\gamma_h\gamma_m}{\mu_m(r+\mu_h)} + \frac{\gamma_h\gamma_m N_{wh}}{\mu_m(r+\mu_h+a)}}$. A summary is included here:

The spreading of chikungunya has two states: the disease-free state and the endemic state. The happening of a state depends on a. If $a = 0.09$ provided $R_0 < 1$, then the disease-free state will occur, but if $a = 0.01, 0.05, 0.07$ provided $R_0 > 1$ then the endemic state will occur.

The stability of the model is determined. Routh-Hurwitz criteria is used to prove that each equilibrium point is locally asymptotically stable. In addition, for any initial population, over a long time, the population will converge to the equilibrium points as shown in Fig 2-3.

The higher of the move out rate of migrant workers (a) increase the infected individuals as shown in Fig 3 . Consequently, the immigrants would have the impact in controlling the disease outbreak.

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