Transmission Model of Chikungunya Fever in the Presence of Two Species of Aedes Mosquitoes

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ABSTRACT

In 2008 there was a large outbreak of Chikungunya fever in the south of Thailand. Chikungunya fever is a febrile disease transmitted to humans by the bite of infected Aedes mosquitoes. The symptoms of this disease are a sudden onset of a fever, chills, headache, nausea, vomiting, joint pain with or without swelling, low back pain and rash. In this study we study the effects of there being two species of Aedes mosquito (Aedes aegypti and Aedes albopictus) present. In this study, we assume that both the human and mosquito populations are constant. A dynamical model of Chikungunya fever is proposed and analyzed. The Routh-Hurwitz criteria are used to determine the stability of the model. The conditions which would lead to either the disease free equilibrium state or the disease endemic equilibrium state to exist is determined. The numerical simulations are done in order to illustrate the behaviors of transmission of disease for different values of parameters. It is shown that the destruction of breeding sites could be an effective method to control this disease.

Keywords: Mathematical Model, Chikungunya Fever, Basic Reproductive Number, Equilibrium Point, Aedes Mosquitoes

1. INTRODUCTION

Chikungunya fever is an emerging, mosquito-borne disease caused by an alphavirus of Togaviridae family, which first was isolated in 1953 in Tanzania (PAHO, 2011). The symptoms of this disease are a high fever, extreme joints pains and an irritating skin rash (Tilston et al., 2009). This disease is self-limiting and some patients suffered from long-lasting arthritis akin (Kucharz and Cebula-Byrsa, 2012). In the major outbreak of this disease in 2005 on the island of Reunion, 244,000 out of a population of 775,000 inhabitants reported that they had experienced these symptoms (Moulay et al., 2011). Chikungunya Virus (CHIKV) is transmitted to humans by the bite of an infected Aedes mosquito, widespread in some tropical regions. The Ae. albopictus mosquito is a highly competent vector for this virus (Poletti et al., 2011). A genetic change at position 226 in the gene for the glycoprotein E1/E2 created a mutated Chikungunya virus strain which had an increased capability for replication in the Ae. albopictus mosquito (Tssetsarkin, 2009).

Mathematical modeling is a useful tool for understanding and describing the transmission of this disease. Pongsumpun (2010) has studied the effects of there being a seasonal variation in the number of mosquitoes on the transmission of this disease. The results showed that length of the outbreak would be shorter if the basic reproduction number would be higher. Poletti et al. (2011) developed a model describing the temporal dynamics of the vector depending on climate factors, coupled to an epidemic transmission model describing the
spread of the epidemic in both humans and mosquitoes. The cumulative number of notified cases predicted by the model was 185 on average, in good agreement with observed data. They found that the basic reproduction number was in the range of 1.8-6. Yakob and Clements (2013) proposed a simple model of the virus transmission between humans and mosquitoes. This model is fitted with data from Reunion epidemic, with basic reproductive number is 4.1. In a latter study, Moulay and Pigne (2013) proposed a metapopulation model to represent both a high-resolution humans and mosquitoes. Numerical results showed the impact of the geographical environment and populations’ mobility on the spread of the disease.

In Asia and the Indian Ocean region the main CHIKV vectors are the *Ae. aegypti* and *Ae. albopictus* mosquitoes. *Ae. albopictus* is particularly resilient and it can survive in both rural and urban area. It has shown a remarkable capacity to adapt to human being and to urbanization, allowing the *Ae. aegypti* mosquito to supersede *Ae. aegypti* mosquito. *Ae. albopictus* has a relatively longer life expectancy about 4 to 8 weeks and a flight radius of 400-600 m. It is aggressive biter and is diurnal. Preechaporn et al. (2007) investigated the seasonal prevalence of *Ae. aegypti* and *Ae. albopictus* in three topographical areas (mangrove, rice paddy and mountainous areas) in both wet and dry seasons in Nakhon Si Thammarat province, Thailand. *Ae. aegypti* larval indices were higher than the *Ae. Albopictus* larval indices in all three topographical areas during both seasons. In this study, we have formulated and analyze the Chikungunya fever model in which both species of the *aedes* mosquitoes are present. In most countries, only one species are present. In Thailand however both species are present.

2. MATERIALS AND METHODS

2.1. Model Formulation

In our model, we assume that human population and mosquito population are constant denoted by $N_h$ and $N_m$ respectively. The dynamics of the disease is depicted in the compartment diagram, Fig. 1.

The human population is divided into the susceptible human ($S_h$), the infected human ($I_h$) and the recover human population ($R_h$) compartment. The mosquito population is divided into four compartments, the susceptible *Ae. aegypti* mosquito ($S_m1$), the infected *Ae. aegypti* mosquito ($I_m1$), the susceptible *Ae. albopictus* mosquito ($S_m2$) and the infected *Ae. albopictus* mosquito ($I_m2$) compartment.

For the mosquito does not exist, since the mosquitoes do not recover after they are infected for over all their life.

The transmission dynamics of the Chikungunya fever are described by the following ordinary differential equations:

\[
\begin{align*}
\frac{dS_h}{dt} &= \lambda_h N_h - (\gamma_{m1} I_m1 + \gamma_{m2} I_m2) S_h - \mu_h S_h \\
\frac{dI_h}{dt} &= (\gamma_{m1} I_m1 + \gamma_{m2} I_m2) S_h - (\mu_h + \mu_m) I_h \\
\frac{dR_h}{dt} &= \mu_h I_h - \mu_h R_h \\
\frac{dS_m1}{dt} &= \alpha_1 - \gamma_{m1} I_m1 S_m1 - \mu_{m1} S_m1 \\
\frac{dI_m1}{dt} &= \gamma_{m1} I_h S_m1 - \mu_{m1} I_m1 \\
\frac{dS_m2}{dt} &= \alpha_2 - \gamma_{m2} I_m2 S_m2 - \mu_{m2} S_m2 \\
\frac{dI_m2}{dt} &= \gamma_{m2} I_h S_m2 - \mu_{m2} I_m2 \\
\end{align*}
\]

The Equation (1c, 1d and 1f) are dropped since it will be assumed that the human and mosquito population are constant. i.e., $R_h = N_h - S_h - I_h$, $S_m1 = N_m1 - I_m1$ and $S_m2 = N_m2 - I_m2$. The number of dependent variables reduced to four, which we pick to be $S_h$, $I_h$, $I_m1$, $I_m2$.

To analyze the model by normalizing the Equation (1a-1g) and defining new variables Equation 2a-2d:

\[
\begin{align*}
\frac{dS_h}{dt} &= \frac{S_h}{N_h} I_h = \frac{I_h}{N_h} R_h = \frac{R_h}{N_h} \\
\frac{dS_m1}{dt} &= \frac{S_m1}{N_m1} I_m1 = \frac{I_m1}{N_m1} = \frac{I_m1}{\alpha_1/(\mu_{m1})} \\
\frac{dS_m2}{dt} &= \frac{S_m2}{N_m2} I_m2 = \frac{I_m2}{N_m2} = \frac{I_m2}{\alpha_2/(\mu_{m2})} \\
\end{align*}
\]

Since the total human and mosquito populations are constant, thus the time rate of change of human population equal to zero, i.e., $\frac{dS_h}{dt} + \frac{dI_h}{dt} + \frac{dR_h}{dt} = 0$.
It means that the birth rate and the death rate of human population are equal, that is \( \lambda_h = \mu_h \). The total number of \( Ae. aegypti \) mosquito and \( Ae. albopictus \) mosquito at equilibrium equal to \( \frac{A_1}{\mu_{m1}} \) and \( \frac{A_2}{\mu_{m2}} \), respectively.

where, \( N_h \) is the total human population:

- \( N_{m1} (N_{m2}) \) is the total \( Ae. aegypti (Ae. albopictus) \) mosquito population
- \( S_h, I_h, R_h \) is the number of susceptible, infected, recovered human population, respectively
- \( S_{m1}, (I_{m1}) \) is the number of susceptible (infected) \( Ae. aegypti \) mosquito population
- \( S_{m2} (I_{m2}) \) is the number of susceptible (infected) \( Ae. albopictus \) mosquito population
- \( \lambda_h (\mu_h) \) is the birth (death) rate of human population
- \( A_1 (A_2) \) is the recruit rate of \( Ae. aegypti (Ae. albopictus) \) mosquito population
- \( \gamma_{m1-h} (\gamma_{m2-h}) \) is the transmission rate of CHIKV from infected \( Ae. aegypti (Ae. albopictus) \) mosquito to human population
- \( r_h \) is the recovery rate of human population
- \( b \) is the biting rate of mosquito population
- \( \beta_{h-m1} (\beta_{h-m2}) \) is the probability that CHIV will be transmitted from infected human population to \( Ae. aegypti (Ae. albopictus) \) mosquito population

\[ \gamma_{h-m1} = \frac{b\beta_{h-m1}}{N_n} \]  \hspace{1cm} (2b)

\[ \gamma_{h-m2} = \frac{b\beta_{h-m2}}{N_n} \]  \hspace{1cm} (2c)

We assume that the transmission rate of CHIV from infected human population to both mosquitoes are equal, \( \gamma_{h-m1} = \gamma_{h-m2} = \gamma_h \) and:

\[ N_n = N_{m1} + N_{m2} \]  \hspace{1cm} (2d)

\( \mu_{m1} (\mu_{m2}) \) is the death rate of \( Ae. aegypti (Ae. albopictus) \) mosquito population.

The reduced model is depicted as following:

\[ \frac{dS_h}{dt} = \mu_h (1 - S_h) - \gamma_{m1-h} (A_1 / \mu_{m1}) I_m S_h \]
\[ - \gamma_{m2-h} (A_2 / \mu_{m2}) I_m S_h \]  \hspace{1cm} (3)
\[ \frac{dI}{dt} = \gamma_{m1-\text{sh}} (A_1 / \mu_{m1}) I_{m1} S_h + \gamma_{m2-\text{sh}} (A_2 / \mu_{m2}) I_{m2} S_h - (r_h + \mu_h) I_h \]  
\( (4) \)

\[ \frac{dI_{m1}}{dt} = \gamma_{h} N_h I_h (1 - I_{m1}) - \mu_{m1} I_{m1} \]  
\( (5) \)

\[ \frac{dI_{m2}}{dt} = \gamma_{h} N_h I_h (1 - I_{m2}) - \mu_{m2} I_{m2} \]  
\( (6) \)

2.2. Analysis of the Model

2.2.1. Equilibrium Points

We first determine the equilibrium points and investigate their stability. It is found that the system has two possible equilibrium points: the disease free equilibrium point and an endemic equilibrium point. Two equilibrium points are found by setting the RHS of Equation 3-6 to zero. Doing this, we obtained.

2.3. Disease Free Equilibrium Point (E₀)

In the absence of disease, that is \( I_h = 0, I_{m1} = 0, I_{m2} = 0 \). Equation 3 reduces to:

\[ \frac{dS_h}{dt} = \mu_h (1 - S_h) \]

The solution of this equation is \( S_h = 1 \). The disease free state becomes \( E_0 = (1, 0, 0, 0) \).

2.4. Endemic Equilibrium Point (E₁)

In the case where the disease is presented, we will have \( I_h \neq 0, I_{m1} \neq 0, I_{m2} \neq 0 \). This gives:

\[ I_{m1}^* = \frac{M_p_1 + M_p_2}{P_1 + P_2} \]  
\( (7) \)

\[ I_{m2}^* = \frac{M_p_1 + M_p_2}{M_p_1 + M_p_2 + M_p \left( P_1 + P_2 \right)} \]  
\( (8) \)

\[ I_h^* = \frac{M_p_1 + M_p_2}{M_p_1 + M_p_2 + M_p \left( P_1 + P_2 \right)} \]  
\( (9) \)

\[ S_h^* = \frac{M_p_1 I_{m1} + M_p_2 I_{m2}}{N_{m1} N_{m2} + N_{m2} M_{m1} + M_{m1} M_{m2}} \]  
\( (10) \)

With:

\[ P_1 = \frac{\gamma_{m1-\text{sh}} A_1}{\mu_{m1}} \]
\[ P_2 = \frac{\gamma_{m2-\text{sh}} A_2}{\mu_{m2}} \]
\[ M_1 = \frac{\mu_{m1-\text{sh}}}{\gamma_{h} N_h} M_{m1} = M_p \left( P_1 + P_2 \right) + M_p \left( P_1 \right) + M_p \left( P_2 \right) \]
\[ M_{m2} = M_p \left( P_1 + P_2 \right) + M_p \left( P_1 \right) + M_p \left( P_2 \right), N_{m1} = P_1 \left( M_p \left( P_1 + P_2 \right) \right) \]

And:

\[ N_{m2} = P_3 \left( M_p \left( P_1 + P_2 \right) \right) \]

The endemic equilibrium point becomes \( E_1 \left( S_h^*, I_{m1}^*, I_{m2}^*, h_h^* \right) \).

2.5. Basic Reproductive Number

The basic reproductive number is obtained by the next generation method. In the notations of Driessche and Watmough (2002), we start with:

\[ \frac{dX}{dt} = f_i (X) \]

where, \( f_i \) is the matrix of new infectious and \( v_i \) is the matrix for the transfers between the compartments in the infective equations. Specifically, we have:

\[ X = \begin{bmatrix} S_h & I_h & I_{m1} & I_{m2} \end{bmatrix} \]
\[ f_i = \begin{bmatrix} 0 & -\gamma_{h} N_h I_h & \gamma_{m1-\text{sh}} (A_1 / \mu_{m1}) S_h & \gamma_{m2-\text{sh}} (A_2 / \mu_{m2}) S_h \end{bmatrix} \]

And:

\[ V_i = \begin{bmatrix} -\mu_h + \gamma_{m1-\text{sh}} (A_1 / \mu_{m1}) S_h + \gamma_{m2-\text{sh}} (A_2 / \mu_{m2}) S_h & \mu_h I_h + \mu_{m1} I_{m1} - \gamma_{h} N_h I_h + \gamma_{h} N_h I_{m1} + \mu_{m1} I_{m1} & -\gamma_{h} N_h I_h + \gamma_{h} N_h I_{m1} + \mu_{m1} I_{m1} + \mu_{m2} I_{m2} \end{bmatrix} \]

where, \( F \) and \( V \) are the Jacobian matrix of \( f \) and \( v \) at \( E_0 \). The basic reproductive number, \( R_0 \), is the threshold for the stability of the disease free equilibrium \( E_0 \). It can be calculated by noting that:

\[ R_0 = \rho \left( V F^{-1} \right) \]

where, \( F^{-1} \) is called the next generation matrix and \( \rho \left( V F^{-1} \right) \) is the spectral radius (dominant eigenvalue) of the matrix \( F^{-1} \). For our model, the Jacobian matrices are:

\[ F(E_0) = \begin{bmatrix} 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \]
And:

\[
V(E_0) = \begin{bmatrix}
\mu_h & 0 & \gamma_{m1 \rightarrow h}(A_1 / \mu_{m1}) & \gamma_{m2 \rightarrow h}(A_2 / \mu_{m2}) \\
0 & r_h + \mu_h & 0 & 0 \\
0 & -\gamma_h N_h & \mu_{m1} & 0 \\
0 & -\gamma_h N_h & 0 & \mu_{m2}
\end{bmatrix}
\]

The inverse of \( V \) is:

\[
V^{-1}(E_0) = \begin{bmatrix}
\frac{1}{\mu_h} - \frac{\gamma_h N_h \gamma_{m1 \rightarrow h}(A_1 / \mu_{m1})}{(r_h + \mu_h) \mu_{m1}} & \frac{\gamma_h N_h \gamma_{m2 \rightarrow h}(A_2 / \mu_{m2})}{(r_h + \mu_h) \mu_{m2}} & 0 & 0 \\
0 & \frac{1}{r_h + \mu_h} & 0 & 0 \\
0 & \frac{\gamma_h N_h}{\mu_{m1}(r_h + \mu_h)} & \frac{1}{\mu_{m1}} & 0 \\
0 & -\frac{\gamma_h N_h}{\mu_{m2}(r_h + \mu_h)} & 0 & \frac{1}{\mu_{m2}}
\end{bmatrix}
\]

This leads to:

\[
FV^{-1}(E_0) = \begin{bmatrix}
0 & 0 & 0 & 0 \\
0 & -\frac{\gamma_h N_h \gamma_{m1 \rightarrow h}(A_1 / \mu_{m1})}{(r_h + \mu_h) \mu_{m1}} & \frac{\gamma_h N_h \gamma_{m2 \rightarrow h}(A_2 / \mu_{m2})}{(r_h + \mu_h) \mu_{m2}} & 0 \\
0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0
\end{bmatrix}
\]

Thus:

\[
\rho(FV^{-1}(E_0)) = \frac{\gamma_h N_h \gamma_{m1 \rightarrow h}(A_1 / \mu_{m1})}{(r_h + \mu_h) \mu_{m1}} + \frac{\gamma_h N_h \gamma_{m2 \rightarrow h}(A_2 / \mu_{m2})}{(r_h + \mu_h) \mu_{m2}}
\]

And so:

\[
R_0 = \gamma_h N_h \gamma_{m1 \rightarrow h}(A_1 / \mu_{m1}) + \gamma_h N_h \gamma_{m2 \rightarrow h}(A_2 / \mu_{m2})
\]

2.6. Local Asymptotical Stability

The local stability of an equilibrium point is determined from the Jacobian matrix of the system of ordinary differential Equation 3-6 evaluated at each equilibrium point. The Jacobian matrix at the disease free state \( E_0 \) is Equation 11:

\[
J_0 = \begin{bmatrix}
-\mu_h & 0 & -\frac{\gamma_{m1 \rightarrow h} A_1}{\mu_{m1}} & -\frac{\gamma_{m2 \rightarrow h} A_2}{\mu_{m2}} \\
0 & -(r_h + \mu_h) & \frac{\gamma_{m1 \rightarrow h} A_1}{\mu_{m1}} & \frac{\gamma_{m2 \rightarrow h} A_2}{\mu_{m2}} \\
0 & \gamma_h N_h & -\mu_{m1} & 0 \\
0 & \gamma_h N_h & 0 & -\mu_{m2}
\end{bmatrix}
\]

The eigenvalues of the \( J_0 \) are obtained by solving \( \det(J_0 - \lambda I) = 0 \). We obtained the characteristic Equation 12:

\[
(\lambda + \mu_h)(\lambda^2 + a_1 \lambda + a_2 \lambda + a_3) = 0
\]

Where:

\[
a_1 = r_h + \mu_h + \mu_{m1} + \mu_{m2},
a_2 = (r_h + \mu_h)(\mu_{m1} + \mu_{m2}) + \mu_{m1}\mu_{m2} - \frac{\gamma_h N_h \gamma_{m1 \rightarrow h} A_1}{\mu_{m1}}
\]

\[
a_3 = (r_h + \mu_h)(\mu_{m1} + \mu_{m2} - \frac{\gamma_h N_h \gamma_{m2 \rightarrow h} A_2}{\mu_{m2}})
\]

One of eigenvalues is \( \lambda_1 = -\mu_h < 0 \). The other three eigenvalues are the solutions of the cubic equation \( \lambda^3 + a_1 \lambda^2 + a_2 \lambda + a_3 = 0 \). The roots of this equation are negative if the coefficients satisfied the three conditions of Routh-Hurwitz criteria (Allen, 2006). \( E_0 \) will be locally asymptotically stable when the coefficients satisfy the conditions \( a_1 > 0 \) Equation 14:
Looking at the coefficients, Equation 13, we see that $a_1$ is always positive and $a_3$ will be positive when Equation 15:

$$\gamma_1 N_i \gamma_{m1} A_{m2} + \gamma_3 N_i \gamma_{m2} A_{m1} < (r_1 + \mu_i) h_{m1} h_{m2}$$

Thus, the disease free equilibrium point will be locally asymptotically stable when $R_0 < 1$.

### 2.6. Disease Endemic Equilibrium Point

To determine the stability of the endemic equilibrium point, $E_1$, we first evaluate the Jacobian matrix at $E_1$ to get Equation 17:

$$J = \begin{bmatrix}
-\mu_i - \frac{\gamma_{s1} h_{m1} A_{s1} h_{m2}}{h_{m1} h_{m2}} & 0 & \frac{\gamma_{s1} h_{m1} A_{s1} h_{m2}}{h_{m1} h_{m2}} & 0 \\
0 & -\mu_i - \frac{\gamma_{s2} h_{m1} A_{s2} h_{m2}}{h_{m1} h_{m2}} & 0 & \frac{\gamma_{s2} h_{m1} A_{s2} h_{m2}}{h_{m1} h_{m2}} \\
0 & 0 & -\mu_i - \gamma_1 h_{m1} & 0 \\
0 & 0 & 0 & -\mu_i - \gamma_3 h_{m1} - \gamma_2 h_{m2}
\end{bmatrix}$$

where, $S_i, I_i, I_i, I_i$ are given by Equation 7-10. The characteristic equation of Jacobian matrix at $E_1$, becomes Equation 18:

$$\lambda^4 + b_4 \lambda^3 + b_3 \lambda^2 + b_2 \lambda + b_1 = 0$$

Where Equation 19:

$$b_1 = \mu_i + \mu_i + r_1 + 2\mu_i + 2\gamma_1 h_{m1} + \frac{\gamma_{s1} h_{m1} A_{s1} h_{m2}}{h_{m1} h_{m2}} + \frac{\gamma_{s2} h_{m1} A_{s2} h_{m2}}{h_{m1} h_{m2}}$$

$$b_2 = (\mu_i + \gamma_1 h_{m1} + \mu_i + r_1 + \gamma_3 h_{m1}) (\mu_i + \gamma_1 h_{m1} + \mu_i + r_1 + \gamma_3 h_{m1}) - (\gamma_1 h_{m1}) (1 - r_1 - \frac{\gamma_{s1} h_{m1} A_{s1} h_{m2}}{h_{m1} h_{m2}})$$

$$b_3 = (r_1 + \gamma_2 h_{m2}) (\mu_i + \gamma_1 h_{m1} + \mu_i + r_1 + \gamma_3 h_{m1}) - (\mu_i + \gamma_1 h_{m1} + \gamma_2 h_{m2}) (r_1 h_{m1} + r_1 h_{m1} - \frac{\gamma_{s2} h_{m1} A_{s2} h_{m2}}{h_{m1} h_{m2}})$$

$$b_4 = - (\mu_i + \gamma_1 h_{m1} + \gamma_2 h_{m2}) (r_1 h_{m1} + r_1 h_{m1} - \gamma_1 h_{m1} - \frac{\gamma_{s1} h_{m1} A_{s1} h_{m2}}{h_{m1} h_{m2}}) - (\mu_i + \gamma_1 h_{m1} + \gamma_2 h_{m2}) (r_1 h_{m1} + r_1 h_{m1} - \gamma_1 h_{m1} - \frac{\gamma_{s2} h_{m1} A_{s2} h_{m2}}{h_{m1} h_{m2}}) - (\mu_i + \gamma_1 h_{m1} + \gamma_2 h_{m2}) (r_1 h_{m1} + r_1 h_{m1} - \gamma_3 h_{m1} - \frac{\gamma_{s3} h_{m1} A_{s3} h_{m2}}{h_{m1} h_{m2}}) - (\mu_i + \gamma_1 h_{m1} + \gamma_2 h_{m2}) (r_1 h_{m1} + r_1 h_{m1} - \gamma_3 h_{m1} - \frac{\gamma_{s3} h_{m1} A_{s3} h_{m2}}{h_{m1} h_{m2}})$$

$$R_0 = R_{01} + R_{02}$$

$$R_{01} = \frac{\gamma_1 N_i \gamma_{m1} A_{m2}}{(r_1 + \mu_i) h_{m1} h_{m2}}$$

$$R_{02} = \frac{\gamma_3 N_i \gamma_{m2} A_{m1}}{(r_1 + \mu_i) h_{m1} h_{m2}}$$
The four eigenvalues of $\lambda^4 + b_1\lambda^3 + b_2\lambda^2 + b_3\lambda + b_4 = 0$ will have negative real part if they satisfy the Routh-Hurwitz criteria. Thus, $E_1$ will be locally asymptotically stable for $R_0>1$ when:

$$\lambda^4 + b_1\lambda^3 + b_2\lambda^2 + b_3\lambda + b_4 = 0$$

Satisfies the following conditions Equation 20:

$$\begin{align*}
& b_1 > 0 \\
& b_2 > 0 \\
& b_3 > 0 \\
& b_1b_2 + b_3 > b_2b_4 \\
& \text{Equation 20}
\end{align*}$$

3. RESULTS

The parameters used in the numerical simulation are given in Table 1.

![Figure 2](image-url) Fig. 2. Time series of (a) susceptible human ($S_h$); (b) infected human ($I_h$), infected $Ae. aegypti$ mosquito ($I_{m1}$), infected $Ae. albopictus$ mosquito ($I_{m2}$) proportions. The values of parameters are in the text and $\lambda_1 = -0.628528$, $\lambda_2 = -0.186016$, $\lambda_3 = -0.0283587$, $\lambda_4 = -0.00457$, $R_0 = 0.000548521<1$. We see that the solutions converge to the disease free equilibrium state as shown.
Fig. 3. Time series of (a) susceptible human, (b) infected human, (c) infected \textit{Ae. aegypti} mosquito and (d) infected \textit{Ae. albopictus} mosquito. The values of parameters are in the text, the solutions converge to the endemic equilibrium state $E_1$ as shown.

Table 1. Parameter values used in numerical simulations at disease free state

<table>
<thead>
<tr>
<th>Parameters</th>
<th>Descriptions</th>
<th>Values</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\mu_h$</td>
<td>Birth (death) rate of human</td>
<td>$1/(65\times365)$ day$^{-1}$</td>
</tr>
<tr>
<td>$N_h$</td>
<td>Total number of human population</td>
<td>20000</td>
</tr>
<tr>
<td>$A_1$</td>
<td>Recruitment rate of \textit{Ae. aegypti} mosquito</td>
<td>90 day$^{-1}$</td>
</tr>
<tr>
<td>$A_2$</td>
<td>Recruitment rate of \textit{Ae. albopictus} mosquito</td>
<td>100 day$^{-1}$</td>
</tr>
<tr>
<td>$\gamma_{m1\rightarrow h}$</td>
<td>Transmission rate of CHIKV from \textit{Ae. aegypti} to human</td>
<td>0.0002 day$^{-1}$</td>
</tr>
<tr>
<td>$\gamma_{m2\rightarrow h}$</td>
<td>Transmission rate of CHIKV from \textit{Ae. albopictus} to human</td>
<td>0.003 day$^{-1}$</td>
</tr>
<tr>
<td>$\gamma_h$</td>
<td>Transmission rate of CHIKV from human to mosquito</td>
<td>0.00001 day$^{-1}$</td>
</tr>
<tr>
<td>$r_h$</td>
<td>Recovery rate of human</td>
<td>1/2 day$^{-1}$</td>
</tr>
<tr>
<td>$\mu_{m1}$</td>
<td>Death rate of \textit{Ae aegypti} mosquito</td>
<td>1/5 day$^{-1}$</td>
</tr>
<tr>
<td>$\mu_{m2}$</td>
<td>Death rate of \textit{Ae albopictus} mosquito</td>
<td>1/7 day$^{-1}$</td>
</tr>
<tr>
<td>$b$</td>
<td>Biting rate of mosquito</td>
<td>1 day$^{-1}$</td>
</tr>
</tbody>
</table>
Fig. 4. (a) Time series of infected human, infected *Ae. aegypti* mosquito and infected *Ae. albopictus* mosquito, proportions. (b) Phase portrait of \((S_h, I_h)\) plan with parameters as given in text, the trajectory approach to the endemic state \(E_1\) as shown.
3.1. Stability of Disease Free State

Using the values of parameters listed in Table 1, we find the eigenvalues and basic reproductive number to be:

\[ \lambda_1 = -0.628528, \lambda_2 = -0.186016, \lambda_3 = -0.0283587, \]
\[ \lambda_4 = -0.00457, R_0 = 0.000548521 < 1 \]

Since all of these eigenvalues are to be negative and the basic reproductive number is less than one, the equilibrium state will be the disease free state, \( E_0 \) as is shown in Fig. 2.

3.2. Stability of Endemic State

We change the value of the recruitment rate of mosquito to \( A_1 = 5,000, A_2 = 10,000 \) and keep the other values of parameters to be those given in Table 1, we find the eigenvalues to be

\[ \lambda_1 = -0.6285525, \lambda_2 = -0.186016, \lambda_3 = -0.0283579, \lambda_4 = -0.004557 \]

and the basic reproductive number to be \( R_0 = 4571.01 > 1 \). Since all of these eigenvalues are to be negative and the basic reproductive number to be greater than one, the equilibrium endemic state will be locally asymptotically stable \( E_1 \) as seen in Fig. 3.

4. DISCUSSION

We formulated the transmission model of Chikungunya fever by taking into account the presence of two species of \( Aedes \) mosquitoes. We found two equilibrium points: Disease free state and endemic disease state. In disease free state, it will be local stability when \( R_0 < 1 \) and the endemic disease state will be local stability when \( R_0 > 1 \). The basic reproductive number is:

\[ R_0 = R_{hi} + R_{he} = \frac{\gamma_1 N_h \gamma_{m1} A_1}{(\tau_h + \mu_i)(\mu_{m1})} + \frac{\gamma_2 N_h \gamma_{m2} A_2}{(\tau_h + \mu_i)(\mu_{m2} \mu_{m1})} \]

It represents the number of secondary case that one case can produce.

5. CONCLUSION

In this study, we have analyzed a transmission model for Chikungunya fever in which two species of mosquitoes are present. This is important to the modeling of this disease in Thailand since both the \( Ae. aegypti \) and \( Ae. albopictus \) mosquitoes are present. In most other countries, only one specie of the \( Aedes \) mosquito is present. Again in Thailand, it was found that both species can inhabit the same breeding sites. By reducing the number of the breeding sites, the reproduction rates of both \( Aedes \) mosquitoes would be reduced. From Fig. 2, changing the recruitment rate \( A_1 \) to 5,000 and \( A_2 \) to 10,000, respectively, we find that the time behaviors of the infected human, the \( Ae. aegypti \) and the \( Ae. albopictus \) mosquitoes decrease sindsodially to the endemic state (Fig. 4a). Figure 4b shows the trajectory of the human population in the \( S_h-I_h \) phase space. The changes seen in the time behaviors shown in Fig. 3 and 4 show that the destruction of the breeding cause equilibrium state to change from being an endemic equilibrium state to a disease free equilibrium state.

6. ACKNOWLEDGEMENT

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7. REFERENCES


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