Age Structural Model of Zika Virus

J. Lamwong and P. Pongsumpun

Abstract—Zika virus is mosquito-borne flavivirus. It can be transmitted between human by biting of Aedes mosquitoes. It can also transmit chikungunya, yellow fever and dengue disease. Zika virus can spread through mosquito to human, human to mosquito and human to human. In this paper, we account the age structure of zika virus patients. We divide into two groups: human and mosquito. Age structure of human population is separated two groups: juvenile and adult human. Standard dynamical modeling method is used for analyzing the behaviors of solutions. The stability conditions for the disease free and endemic equilibrium states are considered by Routh-Hurwitz criteria. We simulate our model by using numerical method. The numerical simulations are showed to confirm the analytical results.

Index Terms—Basic reproductive number, disease free steady state, endemic steady state, stability, Standard dynamical modeling method, Zika.

I. INTRODUCTION

First discovered case of zika virus was reported in Uganda in 1947. Zika virus is transmitted from person to person by biting of infected Aedes aegypti mosquito, during pregnancy, through sex or through blood transfusion [1]-[3]. Tropical and subtropical regions around the world discovered that the same mosquito also transmit vector-borne diseases such as dengue, chikungunya and yellow fever. In human, the zika virus incubation period for 3 to 14 days before symptoms appear. Typical symptoms of zika virus are headache, muscle and joint pain, mild fever, rash and inflammation of underside of the eyelid is also a common presentation [4]-[5].

The data of people who are infected with this disease indicates that the most of infectious human are adult. The Ministry of Public Health Thailand reported 84 countries of infection with zika virus are shown in Fig.1 [5], [6]. On 12 May 2017, Thailand confirmed 8 new cases of zika virus [7]. In 2017, Lamwong and Pongsumpun [8] studied the transmission cycle between two population groups: human and mosquito. Using standard dynamical modeling method, the threshold parameter is found to separate the different behaviors of two steady states. In 2016, Oleson and Artzrouni [1] created a mathematical model to analyze the zika virus from Rio de Janeiro to Miami during Carnival, they formulated model for mech anisms which drive the transmission of the virus between human and mosquito. Harsha [2] simulated the transmission of zika virus in 11 islands and analyzed the model by method of stochastic agent-based model. Nishiura, Kinoshita, Mizumoto, Yasuda and Nishiura et.al [3] studied zika virus infection as a measurement of transmission potential, reanalyzing past epidemic data from the south pacific and aimed to estimate the basic reproductive number of zika. In this study, the age structure of human is considered to see the different transmission between two groups. The standard dynamical modeling method is used in this study. The conditions for the stability all steady states are given.

II. MATHEMATICAL MODEL

The mathematical model of zika virus is formulated by considering the transmission between two groups: human and mosquito populations. Human population is divided into four groups: susceptible, exposed, infected and recovered classes (SEIR model) and the mosquito is divided into three groups: susceptible, exposed and infected classes (SEI model). The total population of human and mosquito are defined as \( N_H \) and \( N_M \). We defined variables as follows: \( S_1, S_2 \) and \( S_m \) are the number of susceptible juvenile human, susceptible adult human and mosquito population. \( E_1, E_2 \) and \( E_m \) are the number of exposed juvenile human, exposed adult human and mosquito populations. \( I_1, I_e \) and \( I_m \) are the number of infected juvenile human, infected adult human and mosquito populations. \( R_1 \) and \( R_2 \) are the number of recovered juvenile human and adult human populations.

| TABLE I: THE DEFINITION OF PARAMETER FOR OUR MODEL |
|-----------------|-----------------|
| Parameter       | Definition       |
| \( B \)         | Mosquito inflow  |
| \( g \)         | Biting rate of mosquito population |
| \( \beta \)      | Transmission rate of zika from human to mosquito population |
| \( \alpha \)     | The incubation rate of mosquito population |
| \( h \)         | Number of other animal that the mosquito can feed |
The diagram of our model is shown in fig.2. Rate of change for the number in each class is equivalent to the number entering minus the number leaving. The dynamical equations are as follows:

The number of susceptible juvenile human population is increased by new recruitment whereas their reduction through infection from mosquito to juvenile, juvenile move to adult and natural death.

\[
\frac{dS_1}{dt} = CN_1 - \frac{g \beta_1 S_1 I_m}{N_1 + h} - (\alpha_1 + \gamma_1 + \mu_1)S_1 \tag{1}
\]

The number of exposed juvenile human population is increased by infection of susceptible juvenile human population, but reduced through incubation, juvenile move to adult and natural death.

\[
\frac{dE_1}{dt} = \frac{g \beta_1 S_1 I_m}{N_1 + h} - (\alpha_1 + \gamma_1 + \mu_1)E_1 \tag{2}
\]

The number of infected juvenile human population is increased by infection of exposed juvenile human but they diminish by recovery from the disease, juvenile move to adult and natural death.

\[
\frac{dI_1}{dt} = \alpha_1 E_1 - (\epsilon_1 + \gamma_1 + \mu_1)I_1 \tag{3}
\]

The number of susceptible adult human population is increased by juvenile move to adult and decreased due to infection of susceptible adult human and natural death.

\[
\frac{dS_2}{dt} = \gamma S_1 - \frac{g \beta_2 S_2 I_m}{N_1 + h} - \mu_2 S_2 \tag{5}
\]

The number of exposed adult human population is increased by infection of susceptible adult human and juvenile move to adult, but their reduction through incubation and natural death.

\[
\frac{dE_2}{dt} = \frac{g \beta_2 S_2 I_m}{N_1 + h} + \gamma E_1 - (\alpha_2 + \mu_2)E_2 \tag{6}
\]

The number of infected adult human population is increased by incubation and juvenile mover to adult, but Their reductions through recovery and natural death.

\[
\frac{dI_2}{dt} = \alpha_2 E_2 + \gamma I_1 - (\epsilon_2 + \mu_2)I_2 \tag{7}
\]

The number of recovered adult human population is increased by recovery and juvenile move to adult, but their reduction through natural death.

\[
\frac{dR_2}{dt} = \epsilon_2 I_2 + \gamma R_1 - \mu_2 R_2 \tag{8}
\]

The number of infected mosquito population is increased by mosquito inflow but they diminished by infection from juvenile and adult human population and natural death.

\[
\frac{dS_m}{dt} = B - \frac{g \beta_1 S_1 I_m}{N_1 + h} - \frac{g \beta_2 S_2 I_m}{N_1 + h} - \mu_m S_m \tag{9}
\]

The number of exposed mosquito population is increased by infection from juvenile and adult human population whereas their reduction through incubation and natural death.

\[
\frac{dE_m}{dt} = \frac{g \beta_1 S_1 I_m}{N_1 + h} + \frac{g \beta_2 S_2 I_m}{N_1 + h} - (\alpha_m + \mu_m)E_m \tag{10}
\]

The number of infected mosquito population is increased by incubation and decreased due to the natural death.

\[
\frac{dI_m}{dt} = \alpha_m E_m - \mu_m I_m \tag{11}
\]
The total number of human populations is the sum of equations (1)-(8).

\[ N_i(t) = S_i(t) + E_i(t) + I_i(t) + R_i(t) + S_e(t) + E_e(t) + I_e(t) + R_e(t) \]  

(12)

The number of mosquito population is the sum of equations (9)-(11)

\[ N_m(t) = S_m(t) + E_m(t) + I_m(t) \]  

(13)

The variables and parameters of our model are defined in Table I.

III. ANALYTICAL OF MATHEMATICAL MODEL

A. Analytical Solutions

1) The disease free steady state

\[ K_0' = \frac{cN_i}{\gamma + \mu_i}S_i + \frac{c\gamma N_i}{(\gamma + \mu_i)\mu_2}E_i \]

2) The endemic steady state

\[ K_i' = (S_i', E_i', I_i', R_i', S_e', E_e', I_e', R_e', S_m', E_m', I_m') \]

where \[ S_i' = \frac{cN_i(N_i + h)}{\gamma g I_{m}'} + (\gamma + \mu_i)(N_i + h) \]

\[ E_i' = \frac{c\gamma N_i N_i}{g \mu_i (N_i + h)} \]

\[ I_i' = \frac{cN_i \alpha \beta I_{m}'}{(\gamma + \mu_i)(\gamma + \epsilon_i + \mu_i)(g \beta I_{m}'} + (\gamma + \mu_i)(N_i + h)) \]

\[ R_i' = \frac{cgN_i \alpha \beta I_{m}'}{(\gamma + \mu_i)(\gamma + \epsilon_i + \mu_i)(g \beta I_{m}'} + (\gamma + \mu_i)(N_i + h)) \]

\[ S_m' = \frac{cN_i(N_i + h)\gamma'}{(\gamma + \mu_i)(\gamma + \epsilon_i + \mu_i)(g \beta I_{m}'} + (\gamma + \mu_i)(N_i + h)) \]

\[ E_m' = \frac{cgN_i \gamma I_{m}'}{(\gamma + \mu_i)(\gamma + \epsilon_i + \mu_i)(g \beta I_{m}'} + (\gamma + \mu_i)(N_i + h)) \]

\[ I_m' = \frac{cN_i \gamma I_{m}'}{(\gamma + \mu_i)(\gamma + \epsilon_i + \mu_i)(g \beta I_{m}'} + (\gamma + \mu_i)(N_i + h)) \]

\[ R_m' = \frac{cgN_i \gamma I_{m}'}{(\gamma + \mu_i)(\gamma + \epsilon_i + \mu_i)(g \beta I_{m}'} + (\gamma + \mu_i)(N_i + h)) \]

\[ S_{NS}' = \frac{cN_i(N_i + h)\gamma'}{(\gamma + \mu_i)(\gamma + \epsilon_i + \mu_i)(g \beta I_{m}'} + (\gamma + \mu_i)(N_i + h)) \]

\[ E_{NS}' = \frac{cgN_i \gamma I_{m}'}{(\gamma + \mu_i)(\gamma + \epsilon_i + \mu_i)(g \beta I_{m}'} + (\gamma + \mu_i)(N_i + h)) \]

\[ I_{NS}' = \frac{cN_i \gamma I_{m}'}{(\gamma + \mu_i)(\gamma + \epsilon_i + \mu_i)(g \beta I_{m}'} + (\gamma + \mu_i)(N_i + h)) \]

\[ R_{NS}' = \frac{cgN_i \gamma I_{m}'}{(\gamma + \mu_i)(\gamma + \epsilon_i + \mu_i)(g \beta I_{m}'} + (\gamma + \mu_i)(N_i + h)) \]

The eigenvalues are the solution of characteristic matrix at the equilibrium point. The eigenvalues are the solution of characteristic matrix at the equilibrium point. The eigenvalues are the solution of characteristic matrix at the equilibrium point. Therefore, when \( R_0 < 1 \), the disease-free state is local stability and \( R_0 > 1 \), the endemic equilibrium state is local stability.

B. Numerical Solutions

In this paper, we simulate the numerical solution for the transmission of zika virus. The values of the parameter used in this paper are as follows: \( \mu_i = 1/(15 \times 365) \) corresponds to the life cycle 15 years of juvenile human population. \( \mu_e = 1/(70 \times 365) \) corresponds to the life cycle 70 years of adult human population. \( \mu_m = 1/18 \) corresponds to the life cycle 18 day of mosquito population. \( \beta_i = 1/12.5 \) satisfies to the 12.5 days of infecting juvenile human population. \( \beta_m = 1/1111 \) satisfies to the 1111 days of infecting adult human population. \( \beta_e = 1/14.28 \) satisfies to the 14.28 days of infecting mosquito population. \( \alpha_i = \alpha_e = 1/8 \) satisfies to the average incubation 8 days for juvenile and adult human population. \( \alpha_m = 1/10 \) satisfies to the average incubation 10 days of mosquito population. \( \epsilon_i = 1/8 \) satisfies to the average recovered time of 8 days for juvenile human population. \( \epsilon_e = 1/6 \) satisfies to the average recovered time of 6 days for adult human population [1]-[3].
Fig. 3. Numerical solutions of susceptible, exposed, infected juvenile human population, susceptible, exposed, infected adult human population and susceptible, exposed, infected mosquito population on disease-free steady state.
Fig. 4. Numerical solutions of susceptible, exposed, infected juvenile human population, susceptible, exposed, infected adult human population and susceptible, exposed, infected mosquito population on endemic steady state.
IV. CONCLUSIONS

In this study, we analyzed the model of zika virus between human population and mosquito population. The results are found by standard dynamical modeling method. The model has two equilibrium point, disease-free equilibrium point and endemic equilibrium point. The basic reproductive is denote by $R_0$ where

$$R_0 = \frac{(\alpha_1 \gamma_1 \beta_1 + \alpha_2 \gamma_2 \beta_2 + \alpha_3 \gamma_3 \beta_3) \cdot (\gamma_1 + \gamma_2 + \gamma_3 + \mu_1 + \mu_2 + \mu_3)}{(\alpha_1 + \beta_1 + \gamma_1 + \mu_1) \cdot (\alpha_2 + \beta_2 + \gamma_2 + \mu_2) \cdot (\alpha_3 + \beta_3 + \gamma_3 + \mu_3)}$$

Numerical solutions of susceptible, exposed, infected, recovered juvenile human population, susceptible, exposed, infected, recovered adult human population and susceptible, exposed, infected mosquito population for disease-free steady state and endemic steady state are shown in Fig. 3 and Fig. 4, respectively. The solutions converge to $(1.10886,0,0,0,2569.83,0,0,0,108000,0,0)$, where $R_0 = 0.000410695$ for the disease-free steady state. For the endemic steady state, the solutions oscillate to$(48.3,3.823,2.96,2.0001,251.388,37,29.662,1.2718 \times 10^8,4.8 \times 10^8,1.18 \times 10^9,8.36 \times 10^9)$, where $R_0 = 2974.06$. We can see that the behaviors of all populations are depend on the basic reproductive number ($R_0$).

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