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Dynamical Analysis for A Simple Model of Zika Virus Transmission

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ABSTRACT

The purpose of this work is to study the stability of a vector-borne model of Zika virus. According to the parameters of the model, there are two equilibrium, namely disease-free equilibrium (DFE) and endemic equilibrium (END). We first provide some sufficient conditions that guarantee the existence of positive equilibriums for the system. The existence of endemic equilibrium and disease-free equilibrium are determined according to the basic reproduction number. Then we show that all solutions of the system are bounded when the initial values are in the first quadrant. Next, we analyze the local stability of the equilibrium by using the standard method of ODE. We also perform some numerical simulations to support the analytical results. The numerical results show that the solutions of the model exhibit the global stable.

Keywords: Zika virus, vector-borne, stability, basic reproduction number

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INTRODUCTION

Zika is one of Vector-borne disease which is infected by mosquitoes, Aedes Aegypti and Aedes Albopictus [5]. On February 1, 2016, Zika virus becomes a Public Health Emergency of International Concern (PHEIC) declared by the World Health Organization(WHO). This declaration recognizes the high potential of Zika to spreads into a whole Americas which endophilic and occupy a very broad range. The concern of the WHO declaration is also derived because of the effect of Zika virus infection on pregnant women to her fetus [11]. It has become a serious problem because Zika virus causes abnormalities genital as microcephaly, spontaneous abortion, and restriction of intrauterine growth [7]. Nearly 5000 cases of microcephaly in the Americas are documented in areas acquaintance Zika virus transmission[11].

In urban areas, the transmission of mosquitoes causes a large-scale epidemic of Zika virus. Sexual transmission is also reported, although the mosquitoes are a major cause of the Zika epidemic virus. So far, all cases of transmission of Zika virus were infected from men to their partner. The virus persistence in the testes and cement has been described and sexual transmission window still unclear, which has increased concern about Zika infection during pregnancy [3] [7].

A mathematical analysis of Zika virus transmission is not much discussed by the researcher. Therefore, in this work we motivated to develop the mathematical model of Zika virus transmission, refers to the model of vector-borne disease [1] and dengue transmission of [4]. In this study, we divide the populations into the population of humans and mosquitoes. The population of human divided into three subclasses, namely susceptible human infected human (I_h) and recovery human (R_h). Whereas, for mosquitoes, we divide the population into two subclasses, namely susceptible vector (S_v), and infected vector (I_v) [8]. The mathematical model of a system is nonlinear ordinary differential equations which refer to the logistic growth model. From the mathematical model, the dynamic analysis worked by determining the equilibrium and analyze its stability [9] [10]. Stability analysis is performed in the form of local analysis. In the last, the results of the analysis have been obtained are illustrated with numerical simulations using Matlab [6] [12].

MATHEMATICAL MODEL

The model of [1] discussed the global dynamics of vector-borne disease with the horizontal transmission. Their model divided the host populations into four subclasses, namely suspected host (S_h), infected host (I_h) and recovered host (R_h). The vector population is divided into three subclasses, suspected (S_v), and infected (I_v). The other work [4] comparing vector-host and SIR model for

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dengue transmission, that divided host populations into susceptible human (H_S), infected human (H_I), recovered human (H_R), and vector populations into the susceptible vector (V_S), infected vector (V_I). In this work, we studied the dynamical analysis of Zika virus transmission. Zika virus spreads by mosquitoes bites. It is similar to dengue and chikungunya [2] [3] [5].

Then we construct a new model of Zika transmission by assuming the following cases:

1. The populations are closed and bounded.
2. The virus also spreads through human sex, blood transfusion, and laboratory exposure.
3. Total time dependent population of human and vectors are $N_h = S_h + I_h + R_h$ and$N_v = S_v + I_v$.

According to the previous assumption, the Zika virus transmission represents the following nonlinear differential equations:

$$\begin{cases} \frac{dS_h}{dt} = \Lambda_h - \beta_1 S_h I_h - \beta_2 S_h I_v - \mu_h S_h, \\ \frac{dI_h}{dt} = \beta_1 S_h I_h + \beta_2 S_h I_v - \gamma I_h - \mu_h I_h, \\ \frac{dR_h}{dt} = \gamma I_h - \mu_h R_h, \\ \frac{dS_v}{dt} = \Lambda_v - \beta_3 S_v I_h - \mu_v S_v, \\ \frac{dS_v}{dt} = \beta_3 S_v I_h - \mu_v I_v \end{cases} \quad (1)$$

where $S_h(t), I_h(t), R_h(t), S_v(t), I_v(t)$, stand for suspected human, infected human, recovery human, suspected vector, and infected vector, respectively. In this study, all of the parameters are positive, where Λ_h denote the growth rate of human, Λ_v denote the growth rate of mosquitoes, β_1 is the rate of direct transmission of the disease, β_2 is the rate of transmission from mosquitoes to human, β_3 is the probability of transmission from human to mosquitoes, γ for the per capita recovery rate of the infective population, μ_h means the death rate of human, and μ_v means the death rate of mosquitoes, respectively.

Initial conditions of the model (1) are

$$S_h(0) \geq 0, I_h(0) \geq 0, R_h(0) \geq 0, S_v(0) \geq 0, I_v(0) \geq 0. \quad (2)$$

Furthermore, the rate of total the human population is

$$\frac{dN_h(t)}{dt} = \Lambda_h - \mu_h N_h(t). \quad (3)$$

With given initial condition (2) it is ensuring that $N_h(0) \geq 0$. So, total population N_h(t) will be positive and bounded for all finite time, t > 0. The rate of total dependence of the vector population is

$$\frac{dN_v(t)}{dt} = \Lambda_v - \mu_v N_v(t). \quad (4)$$

Based on eq.3 and eq.4, then we have

$$\lim_{t\to\infty} N_h \leq \frac{\Lambda_h}{\mu_h} \quad \text{and} \quad \lim_{t\to\infty} N_v \leq \frac{\Lambda_v}{\mu_v}. \quad (5)$$

Accordingly, the region of the system (1) is

$$\Omega = \left\{(S_h, I_h, R_h, S_v, I_v) \in R_+^5, 0 \leq S_h + I_h + R_h \leq \frac{\Lambda_h}{\mu_h}, 0 \leq S_v + I_v \leq \frac{\Lambda_v}{\mu_v}\right\}. \quad (6)$$

Lemma 2.1. The closed set Ω is positive invariant and attracting concerning the system (1).

Proof. Let $(S_h, I_h, R_h, S_v, I_v)$ be the solution of the system (1) with initial value (2). Then we consider the following Lyapunov function

$$L(t) = \big(L_1(t), L_2(t)\big) = (S_h + I_h + R_h, S_v + I_v). \quad (7)$$

The time derivative of (7) is

$$\frac{dL}{dt} = (\Lambda_h - \mu_h L_1, \Lambda_v - \mu_v L_2). \quad (8)$$

From eq.8 we can show that

$$\begin{cases} \frac{dL_1}{dt} = \Lambda_h - \mu_h L_1 \leq 0, & \text{for } L_1 \geq \frac{\Lambda_h}{\mu_h} \\ \frac{dL_2}{dt} = \Lambda_v - \mu_v L_2 \leq 0, & \text{for } L_2 \geq \frac{\Lambda_v}{\mu_v} \end{cases}. \quad (9)$$

It follows (9) that $\frac{dL}{dt} \leq 0$ which imply that Ω is positive invariant. Then, by comparison theorem (9)(12) can be used to show that $0 \leq (L_1, L_2) \leq (L_1(0)e^{\mu_h t} + \frac{\Lambda_h}{\mu_h t}(1 - e^{\mu_h t}), L_2(0)e^{\mu_v t} + \frac{\Lambda_v}{\mu_v t}(1 - e^{\mu_v t}))$. When $t \to \infty$, then $0 \leq (L_1, L_2) \leq \left(\frac{\Lambda_h}{\mu_h}, \frac{\Lambda_v}{\mu_v}\right)$, so Ω is attracting. Thus, proof is complete.

DISEASE-FREE EQUILIBRIUM

The equilibrium of the system (1) is disease-free equilibrium (DFE) and endemic equilibrium (END). The DFE is $E^0 =$

Analisis Dinamik Pada Model Sederhana Penyebaran Virus Zika

ABSTRAK : Tujuan dari penelitian ini adalah untuk mempelajari kestabilan pada model vektor borne penyebaran virus Zika. Berdasarkan parameter pada dua titik kesetimbangan, yaitu titik kesetimbangan bebas penyakit (DFE) dan titik kesetimbangan endemik (END). Pertama, diberikan beberapa kondisi yang menjamin eksistensi titik kesetimbangan positif pada sistem. Eksistensi titik kesetimbangan endemik dan bebas penyakit ditentukan berdasarkan angka reproduksi dasar. Selanjutnya ditunjukkan bahwa semua solusi sistem terbatas saat nilai awal berada di kuadran pertama. Selanjutnya, di analisis kestabilan lokal pada masing-masing titik kesetimbangan dengan menggunakan metode standar ODE. Di akhir juga dilakukan beberapa simulasi numerik untuk mendukung hasil analisis secara matematis. Hasil analisis numerik menunjukkan bahwa solusi dari model tersebut terjadi kestabilan global.

Kata kunci : Virus Zika, vector-borne, kestabilan, angka reproduksi dasar

$\left(\frac{\Lambda_h}{\mu_h}, 0,0, \frac{\Lambda_v}{\mu_v}, 0\right)$. The dynamics of the disease is described by the quantity of R_0, as follows

$$R_0 = \frac{\mu_h N_h(\mu_v N_v \beta_2 \beta_3 + \beta_1 {\mu_v}^2)}{{\mu_v}^2 \mu_h(\mu_h + \gamma)},$$

Lemma 3.1. If $R_0 < 1$, then the disease-free equilibrium (DFE) point of the system (1) is local asymptotically stable, otherwise it is unstable.

Proof. The local stability of the DFE can be verified by linearizing the Jacobian matrix of the system (1) around DFE.

$$\begin{pmatrix} -\mu_h & -\frac{\beta_1\Lambda_h}{\mu_h} & 0 & 0 & -\frac{\beta_2\Lambda_h}{\mu_h} \\ 0 & \frac{\beta_1\Lambda_h}{\mu_h} - \gamma - \mu_h & 0 & 0 & \frac{\beta_2\Lambda_h}{\mu_h} \\ & \gamma & & & \\ 0 & -\frac{\beta_3\Lambda_v}{\mu_v} & -\mu_h & 0 & 0 \\ 0 & & 0 & -\mu_v & 0 \\ 0 & \frac{\beta_3\Lambda_v}{\mu_v} & 0 & 0 & -\mu_v \end{pmatrix}.$$

The characteristic polynomials of the Jacobian (11) as follows,

$$(\lambda + \mu_h)^2(\lambda + \mu_v)(\lambda^2 + a_1\lambda + a_0). \quad (12)$$

Where,

$a_1 = (\mu_h + \gamma) + \mu_v - \beta_1 \mathrm{N}_h,$

$a_0 = \mu_v(\gamma + \mu_h) - \mu_v\beta_1 \mathrm{N}_h - \beta_2\beta_3 \mathrm{N}_v \mathrm{N}_h.$

Five eigenvalues are corresponding to equation (18), which are the three of eigenvalues, $-\mu_h, -\mu_h,$ and $-\mu_v$ have the negative real part. The other eigenvalues can be obtained by solving the following equation,

$$E(\lambda) = \lambda^2 + a_1\lambda + a_0.$$

By the fundamental mathematics computation, $E(\lambda)$ have negative real parts if $a_1 > 0$ and $a_0 > 0$. These conditions are satisfied when $R_0 < 1$. Then, the characteristic polynomial of equation (12) has negative real parts. Then the DFE is locally asymptotically stable.

ENDEMIC EQUILIBRIUM

The endemic equilibrium (END) of the system (1) is $({S_h}^*, {I_h}^*, {R_h}^*, {S_v}^*, {I_v}^*)$ where,

$${S_h}^* = \frac{\mu_v(\Lambda_h + \gamma)(\mu_v + \beta_3 {I_h}^*)}{\beta_1\mu_v(\mu_v + \beta_3 {I_h}^*) + \Lambda_v\beta_2\beta_3},$$

$${R_h}^* = \frac{\gamma {I_h}^*}{\mu_h}, {S_v}^* = \frac{\Lambda_v}{\mu_v + \beta_3 {I_h}^*}, {I_v}^* = \frac{\Lambda_v\beta_3 {I_h}^*}{\mu_v(\mu_v + \beta_3 {I_h}^*)}. \quad (14)$$

If ${I_h}^* \neq 0$ substitute ${S_h}^*, {I_v}^*$ to the system (1), then we have the following equations

$$f({I_h}^*) = c_2({I_h}^*)^2 + c_1{I_h}^* + c_0 \quad (15)$$

where,

$c_2 = \mu_v\beta_1\beta_3(\mu_h + \gamma) > 0,$

$c_1 = (\mu_h + \gamma)({\Lambda_v}^2\beta_2\beta_3 + \mu_h\mu_v\beta_3 + \beta_1{\mu_v}^2),$

$c_0 = {\mu_v}^2\mu_h(\mu_h + \gamma)(1 - R_0).$

By using elementary computation, the solution of is

$$({I_h}^*)_{1,2} = \frac{-c_1 \pm \sqrt{{c_1}^2 - 4c_2c_0}}{2c_2}. \quad (16)$$

To understand the value of ${I_h}^*$, we can see the following lemma.

Lemma 4.1. If $R_0 > 1$, then there only one positive solution of END.

Proof. Let's see the equation (15). If $R_0 > 1$, then we have $c_0 < 0$. According to (16), it is easy to find ${c_1}^2 - 4c_2c_0 > 0$, so that $c_1 < \sqrt{{c_1}^2 - 4c_2c_0}$. By substituting the previous result to the equation (16), it is easy to see that $({I_h}^*)_1 > 0$ and $({I_h}^*)_2 > 0$. So, there is one positive solution of END.

The local stability of the END can be verified by linearizing the Jacobian matrix of the system (1) around END.

$$\begin{pmatrix} -\mu_h - \beta_1{I_h}^* - \beta_2{I_v}^* & \beta_1{S_h}^* & 0 & 0 & \beta_2{S_h}^* \\ \beta_1{I_h}^* + \beta_2{I_v}^* & -\mu_h + \beta_1{S_h}^* - \gamma & 0 & 0 & \beta_2{S_h}^* \\ 0 & \gamma & -\mu_h & 0 & 0 \\ 0 & -\beta_3{S_v}^* & 0 & -\mu_v - \beta_3{I_h}^* & 0 \\ 0 & \beta_3{S_v}^* & 0 & \beta_3{I_h}^* & -\mu_v \end{pmatrix}. \quad (17)$$

The characteristic polynomials of the Jacobian (17) as follows,

$$P_{END}(\lambda) = (\lambda + \mu_v)(\lambda + \mu_h)(\lambda^3 + b_2\lambda^2 + b_1\lambda + b_0). \quad (18)$$

Where,

$b_2 = (\delta + \mu_h + \mu_v) + (\beta_1 + \beta_3){I_h}^* + \beta_2{I_v}^* - \beta_1{S_h}^*,$

$b_1 = \delta^2 + \delta(b_2 - \beta_1{S_h}^*) + (\mu_v + \beta_3{I_h}^*)\big(b_2 - (\mu_v + \delta + \beta_3{I_h}^*)\big) - {S_h}^*(\beta_1\mu_h + \beta_2\beta_3{S_v}^*),$

$b_0 = \delta(\mu_v + \beta_3{I_h}^*)\big(b_2 - (\mu_v + \delta + \beta_3{I_h}^*)\big) - \mu_h{S_h}^*(\beta_1\mu_v + \beta_2\beta_3{S_v}^*).$

According to Jacobian (17) and polynomial (18), we have $b_2 > 0$, $b_0 > 0$, and $b_1b_2 > b_0$. Then the Routh-Hurwitz criterion [13] ensures that END is locally asymptotically stable.

NUMERICAL RESULTS AND DISCUSSION

The mathematical analysis of system (1) has discussed in the previous. Then, in this section, we discuss the numerical result to present the global dynamics of the system (1) when $R_0 < 1$ and $R_0 > 1$. To solve it we are using fourth-order Runge-Kutta methods [6]. First, choose the parameter value as follows $\Lambda_h = 0.3, \Lambda_v = 0.2, \beta_1 = 0.4, \beta_2 =$

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$0.1, \beta_3 = 0.2, \mu_h = 0.2, \mu_v = 0.7$, and $\gamma = 0.6$. Those parameter values satisfy the conditions of $R_0 < 1$. By these parameter values, we can plot any numerical result by using software Matlab.

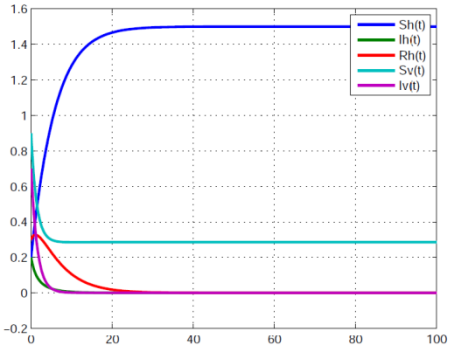

Figure 1: Numerical result of the system (1) when $R_0 < 1$.

Another global stability phenomenon also occurs in case $R_0 > 1$. Choose the parameter value which is satisfy $R_0 > 1$ as follows $\Lambda_h = 0.3$, $\Lambda_v = 0.2, \beta_1 = 0.4, \beta_2 = 0.1, \beta_3 = 0.2, \mu_h = 0.1, \mu_v = 0.17$, and $\gamma = 0.2$. By using software Matlab, we got the following figure.

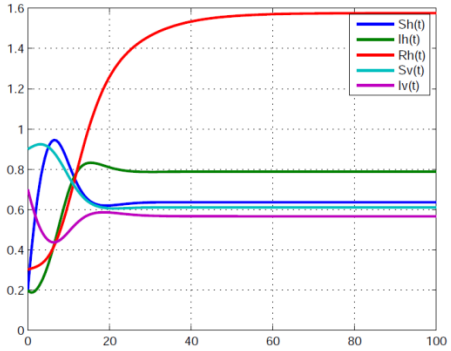

Figure 2: Numerical result of the system (1) when $R_0 > 1$.

Figure 1 shows that by taking initial condition $(0.2; 0.2; 0.3; 0.9; 0.7)$ and the parameter conditions $R_0 < 1$ the solution will tend to DFE. It is mean that the system (1) will free from Zika virus disease, if satisfy the condition $R_0 < 1$. In contrary, endemic condition of system (1) will occurs when satisfying the condition $R_0 > 1$. This phenomenon shows in Figure 2.

Table 1. Probability of each parameter

Parameter	Probability (value)
$\boldsymbol{\Lambda_h}$	$\mu_h N_h$(person per-day)
$\boldsymbol{\mu_h}$	$\frac{1}{lifetime} = \frac{1}{65x365} = 0.0000421$ (per-day)
$\boldsymbol{\beta_1}$	$0 \leq \beta_1 \leq 1$ (person x day)
$\boldsymbol{\beta_2}$	$0 \leq \beta_2 \leq 1$ (mosquitoes x day)
$\boldsymbol{\gamma}$	$0 \leq \gamma \leq 1, \gamma = \frac{1}{recoverytime} = \frac{1}{14} = 0.0714$ (per-day)
$\boldsymbol{\Lambda_v}$	$\mu_v N_v$ (mosquitoes per-day)
$\boldsymbol{\mu_v}$	$\frac{1}{lifetime} = \frac{1}{14} = 0.0714$ (per-day)
$\boldsymbol{\beta_3}$	$0 \leq \beta_3 \leq 1$ (person x day)

Qualitatively, when the total population is increasing either mosquitoes or human populations, hence the transmission of disease will be faster. To reduce the disease transmission of Zika virus explains to the following solutions :

1. Reduce the chances of success virus transmission from humans to mosquitoes and vice versa. This can be done using anti-mosquito repellent or curtains.
2. Reduce the chances of success virus transmission between humans. This can be done by using condom or reduction of the intensity of sexual interaction with humans infected. Better yet, suspended the sexual interaction with infected humans during which the infected has not been recovered.
3. Reduce the mosquito population in the neighborhood and increase the chance of dying mosquitoes, can be done with 3M Program or fumigation (fogging).
4. Increase the chances of recovery of infected humans, as a means of shortening the time of treatment so quickly for healthy people, are infected and immune from the disease.

CONCLUSION

In the previous section, we have studied about Zika virus transmission. In this section, we summarize the following,

1) In Section 2, we construct the Zika virus transmission model by extended the model of [4] and [1]. In this part, we also proved the boundedness of solution, by analysis the positive invariance and attracting the region Ω of the system (1).

2) The model (1) has two equilibrium points. An uninfected equilibrium, what we called Disease Free Equilibrium (DFE), where the Zika virus diseases are not present. Second is endemically infected equilibrium or Endemic Equilibrium (END).

3) In Section 3 and 4, the analytical analysis of Disease Free Equilibrium (DFE) and Endemic Equilibrium (END) is worked, respectively. The existence of equilibrium and linear stabilities are discussed. The linear stability of DFE and END solved by linearized the non-linear equilibrium of system (1) by Jacobian. By compute the Eigenvalue of Jacobian and substituting of each equilibrium, we can conclude that DFE is local asymptotically stable if

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$\boldsymbol{R_0 < 1}$. Otherwise, when $\boldsymbol{R_0 > 1}$, the END is local asymptotically stable.

4) The global stability phenomena of the system (1) identified by numerical results (see Figures 1 and 2) by using fourth-order Runge-Kutta methods. Accordingly, when the combination of parameter satisfies the condition $\boldsymbol{R_0 < 1}$ the trajectories tend to DFE. Otherwise, the trajectories of the system (1) tend to END. So, by numerical analysis, it can be concluded that DFE globally stable under condition $\boldsymbol{R_0 < 1}$. And globally stable at END when $\boldsymbol{R_0 > 1}$.

5) In general, we can avoid Zika virus by using anti-mosquito repellent or curtains, suspended the sexual interaction with infected humans, 3M Program or fumigation (fogging), and treatment so quickly for healthy people are infected and immune from the disease.

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