NUMERICAL STUDY FOR ZIKA VIRUS TRANSMISSION WITH BEDDINGTON-DEANGELIS INCIDENCE RATE

by Universitas Internasional Semen Indonesia

Submission date: 17-Mar-2022 08:13PM (UTC-0500)
Submission ID: 1786746744
File name: Paper_Numerical_Study_of_Zika_FJMS.pdf (920.63K)
Word count: 3080
Character count: 16007

Far East Journal of Mathematical Sciences (FJMS)

http://www.pphmj.com
http://dx.doi.org/10.17654/MS111010145
Volume 111, Number 1, 2019, Pages 145-157 **ISSN: 0972-0871**

NUMERICAL STUDY FOR ZIKA VIRUS TRANSMISSION WITH BEDDINGTON-DEANGELIS INCIDENCE RATE

Puji Andayani[1,*], Lisa Risfana Sari[1], Agus Suryanto[2] and Isnani Darti[2]

[1]Universitas International Semen Indonesia
61122, Gresik, Indonesia

[2]Department of Mathematics
Faculty of Mathematics and Science
Brawijaya University
65145, Malang, Indonesia

Abstract

In this paper, we focus on the behavior of Zika virus transmission with Beddington-DeAngelis incidence rate. The main purpose of this work is to identify the recovery time and predict the endemic condition of Zika virus. The equilibrium points of the system are identified by Jacobian. The basic reproduction number exhibits the natural compartment of disease transmission investigated using next generation matrix (NGM) method. The sensitivity indexes of the parameter are computed to investigate the intervention strategies to prevent the Zika virus transmission. The stability condition of each equilibrium point is shown by numerical simulation. According to numerical solutions, the disease-free and endemic conditions occur for the specific value of the basic reproduction number.

Received: November 8, 2018; Accepted: December 5, 2018

2010 Mathematics Subject Classification: 34D20, 65P40, 37M05.

Keywords and phrases: Zika transmission, Beddington-DeAngelis, next generation matrix, reproduction number, sensitivity analysis.

*Corresponding author

Introduction

Recently, some scientists have studied the transmission of Zika virus, when large epidemics occurred in certain areas. The disease caused by Zika virus has been spread in 2015 around Central America and Africa [1, 15]. In early 2015, the WHO reported that there are 69 countries having infected Zika virus transmission by mosquito bites. There are 13 countries having infected by person-to-person transmission of Zika virus, there are 29 countries having reported congenital syndrome of Zika virus, and 20 countries have reported a GBs case caused by Zika virus [14]. Since an infection in pregnant women appeared, Zika becomes a global concern, because it caused abnormalities as microcephaly, spontaneous abortion, and intrauterine growth restriction. Infection for certain age caused neurological disorder, namely Guillain-Barré syndrome (GBs) [10]. In June 2016, WHO collaborated with UNICEF developing a Zika virus vaccine TPP for use in a future outbreak. WHO also produced more than 20 guidance documents for mothers who needed psychological support [14].

The mathematical model for epidemiology has been widely discussed by several researchers to study the dynamics of the transmission of certain diseases. Formerly, humans commit generation of decisions in strategies to prevent and control their emergence and reemerged the disease. Bonyah and Okosun [3] studied a mathematical model of Zika virus transmission with assuming bilinear incidence rate. However, in the bilinear incidence rate model, there are no inhibiting factors of infection. It is a rare case because humans always try to do preventive actions, for example, 3M, and not having sex with other than partners. Goswami et al. [7] also worked in the mathematical model of Zika virus. They created a model with a saturated incidence rate, by assuming there is an inhibiting factor in the interaction of suspected human and infected human. But the inhibiting factor is only for infected human by decreasing the infection sources. Olaniyi [11] has formulated the mathematical model of Zika virus transmission with three nonlinear models strengthening the infection which are the infected

mosquito, asymptomatic and symptomatic humans. They also computed the sensitivity indexes of the parameters of the system (5) with respect to the basic reproduction number. The sensitivity parameter is used to identify the strategies to prevent and control the Zika virus transmission.

In this paper, we are focused on the mathematical model of Zika virus transmission with saturated incidence rate as using Beddington-DeAngelis functional response. We consider the inhibiting factor of infection with two factors, such as preventative behavior of human and decreasing the infection factor [3, 7, 11], namely keep a house clean, do not make a sex except with partner, or giving quarantine for the pregnant woman.

Mathematical Model

Mathematical model of Zika virus transmission has been analyzed in the previous research. The infection rate of this model is expressed by using bilinear incidence rate. It is assumed that the transmissions rate is corresponding to the number of the population without reasoning the constraints which occur during the transmission process. In fact, the transmissions between populations are influenced by many things, one of them is changes in individual behavior [3]. Considering this, Kaddar [8] and Suryanto [13] developed the SIR model with a saturated incidence rate. Referring to Bonyah and Okosun [3] and Kaddar [8], we constructed a model of the Zika virus transmission with saturated incidence rate. In this work, we use the Beddington-DeAngelis functional response [6], which is

$$p(S_h, I_h) = \frac{1}{1 + \alpha_1 S_h + \alpha_2 I_h}. \quad (1)$$

In the interaction of susceptible human population (S_h) with infected mosquitoes (I_v), the rate of spread is reduced due to preventive actions from humans including doing a clean lifestyle, fogging, and doing $3M$

actions (closing, draining, and burying). The response function used for the interaction of S_h and I_v is as follows:

$$p(S_h, I_v) = \frac{1}{1 + \alpha_3 S_h}. \tag{2}$$

Therefore, a modified model for Zika virus transmission with the rate of saturated transmission is as follows:

$$\begin{cases} \dfrac{dS_h}{dt} = \Lambda_h - \dfrac{\beta_1 S_h I_h}{1 + \alpha_1 S_h + \alpha_2 I_h} - \dfrac{\beta_2 S_h I_v}{1 + \alpha_3 S_h} - \mu_h S_h, \\ \dfrac{dI_h}{dt} = \dfrac{\beta_1 S_h I_h}{1 + \alpha_1 S_h + \alpha_2 I_h} + \dfrac{\beta_2 S_h I_v}{1 + \alpha_3 S_h} - \gamma I_h - \mu_h I_h, \\ \dfrac{dR_h}{dt} = \gamma I_h - \mu_h R_h, \\ \dfrac{dS_v}{dt} = \Lambda_v - \beta_3 S_v I_h - \mu_v S_v, \\ \dfrac{dI_v}{dt} = \beta_3 S_v I_h - \mu_v S_v, \end{cases} \tag{3}$$

where $S_h(t)$, $I_h(t)$, $R_h(t)$, $S_v(t)$ and $I_v(t)$ stand for suspected human, infected human, recovery human, suspected mosquitoes, and infected mosquitoes, respectively. In this study, all of the parameters are positive, where Λ_h denotes the growth rate of human, Λ_v denotes 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 is the per capita recovery rate of the infected population, μ_h means the death rate of humans, I_v means the death rate of mosquitoes, respectively. Further, the total population of the human at the time t is denoted by $N_h(t)$ which is given by $N_h(t) = S_h(t) + I_h(t) + R_h(t)$. The total population of vector (mosquitoes) at the time t is denoted by $N_v(t)$ which is given by $N_v(t) = S_v(t) + I_v(t)$.

Result and Discussion

Equilibrium point

The equilibrium point of the system (3) is found by letting the right-hand side of equation is equal to zero. The system (3) has two equilibrium points, which are disease-free equilibrium (DFE) and endemic equilibrium (END).

Disease-free equilibrium

The disease-free equilibrium of the system (5) is

$$DFE = \left(\frac{\Lambda_h}{\mu_h}, 0, 0, \frac{\Lambda_v}{\mu_v}, 0\right).$$

The disease-free equilibrium always exists.

The basic reproduction number represents the natural compartment for disease transmission model, established by the system of ordinary differential equations [5, 9]. The basic reproduction number is denoted by R_0, which is determined by using the next generation matrix (NGM) method. In this work, the basic reproduction ratio of the system (3) is as follows:

$$F = \begin{pmatrix} \frac{\beta_1 N_h}{\sigma_1} & \frac{\beta_2 N_h}{\sigma_2} \\ \beta_3 N_v & 0 \end{pmatrix}, \quad V = \begin{pmatrix} \gamma + \mu_h & 0 \\ 0 & \mu_v \end{pmatrix},$$

F is the Jacobian of infection matrix with respect to DFE, and V is the Jacobian matrix which decreases the infection. Furthermore, the basic reproduction number is the largest number of eigenvalues of $(F \cdot V^{-1})$:

$$R_0 = \frac{\beta_1 N_h}{2\sigma_1 \delta} + \frac{\sqrt{\mu_v \sigma_2 N_h (4\beta_2 \beta_3 \sigma_1 \delta N_v + \mu_v \beta_1^2 \sigma_2 N_h)}}{2\mu_v \sigma_1 \sigma_2 \delta},$$

where

$$\sigma_1 = 1 + \alpha_1 N_h, \quad \sigma_2 = 1 + \alpha_3 N_h, \quad \delta = \mu_h + \gamma.$$

The local stability of DFE is analyzed by computing the Jacobian of DFE as follows:

$$J(DFE) = \begin{pmatrix} -\mu_h & -J_0 & 0 & 0 & -J_1 \\ 0 & J_0 - \delta & 0 & 0 & J_1 \\ 0 & \gamma & -\mu_h & 0 & 0 \\ 0 & -\beta_3 N_v & 0 & -\mu_v & 0 \\ 0 & \beta_3 N_v & 0 & 0 & -\mu_v \end{pmatrix}.$$

The Jacobian of DFE has five eigenvalues which are $-\mu_h$, $-\mu_h$ and $-\mu_v$. The two others are analyzed by identifying the characteristic polynomial as follows:

$$P(\lambda) = \lambda^2 + a_1\lambda + a_0,$$

where

$$a_1 = \frac{\sigma_1\delta - \beta_1 N_h}{\sigma_1}, \quad a_0 = \frac{\mu_v\sigma_1\sigma_2\delta - N_h(\mu_v\beta_1\sigma_2 + \beta_2\beta_3\sigma_1\delta N_v)}{\sigma_1\sigma_2}.$$

If $R_0 < 1$, then this implies that $a_1 > 0$ and $a_0 > 0$. Further, the polynomial $P(\lambda)$ has two negative real parts of the eigenvalue. Then the disease-free equilibrium is stable. The recovery time for Zika virus will be investigated numerically.

Endemic equilibrium

The endemic equilibrium of the system (5) is

$$END = (S_h^*, I_h^*, R_h^*, S_v^*, I_v^*).$$

The local stability of END is identified by the following Jacobian:

$$J(END) = \begin{pmatrix} -J_2 - \mu_h & -J_3 & 0 & 0 & -J_4 \\ J_2 & J_0J_3 - \delta & 0 & 0 & J_4 \\ 0 & \gamma & -\mu_h & 0 & 0 \\ 0 & -\beta_3 S_v^* & 0 & -\beta_3 I_v^* - \mu_v & 0 \\ 0 & \beta_3 S_v^* & 0 & \beta_3 I_v^* & -\mu_v \end{pmatrix},$$

where

$$J_2 = \frac{\beta_1 I_h^*}{1+\alpha_1 S_h^* + \alpha_2 I_h^*} - \frac{\alpha_1\beta_2 S_h^* I_h^*}{(1+\alpha_1 S_h^* + \alpha_2 I_h^*)^2} + \frac{\beta_2 I_v^*}{1+\alpha_3 S_h^*} - \frac{\alpha_3\beta_3 S_h^* I_v^*}{(1+\alpha_3 S_h^*)^2},$$

$$J_3 = \frac{\beta_1 I_h^*}{1+\alpha_1 S_h^* + \alpha_2 I_h^*} - \frac{\alpha_1\beta_2 S_h^* I_h^*}{(1+\alpha_1 S_h^* + \alpha_2 I_h^*)^2}, \quad J_4 = \frac{\beta_2 S_h^*}{1+\alpha_1 S_h^*}.$$

The stability of endemic equilibrium will be identified numerically.

Numerical result

In this subsection, we illustrate the behavior of the system (5). For the purpose of simulation, we choose some parameter values which satisfy the qualification condition. The following table provides the parameter description and the parameter value which are used in the numerical simulation.

Table 1. The probability of each parameter of the system (5)

Parameter	Probability
Λ_h	$\mu_h N_h$ (person per-day)
μ_h	1/65.365 = 0.00004215 (per-day)
α_1	$0 \le \alpha_1 \le 1$ (person x-day)
α_2	$0 \le \alpha_2 \le 1$ (person x-day)
α_3	$0 \le \alpha_3 \le 1$ (person x-day)
β_1	$0 \le \beta_1 \le 1$ (person x-day)
β_2	$0 < \beta_2 < 1$ (person x-day)
β_3	$0 < \beta_3 < 1$ (person x-day)
γ	1/7 = 0.1428 (per-day)
Λ_v	$\mu_v N_v$ (mosq. per-day)
μ_v	1/14 = 0.0714 (per-day)

Let us consider Table 1 and choose some parameter values which satisfy the condition $R_0 < 1$. Then take some positive initial conditions $S_h(0)$, $I_h(0)$, $R_h(0)$, $S_v(0)$, $I_v(0)$. The following figure confirms that the solution of the system (5) is convergent to disease-free equilibrium point. In this numerical simulation, we use ten variations of parameters which satisfy $R_0 < 1$. From this variation data, we can see that the value of DFE always exists and it is stable when $R_0 < 1$.

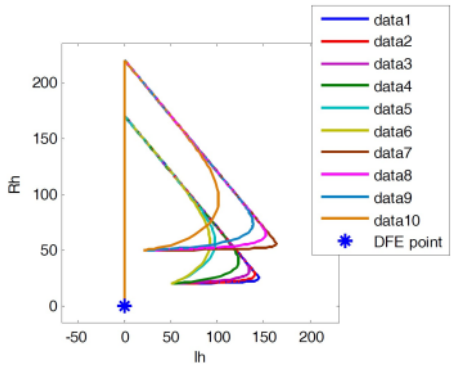

Figure 1. Numerical result of model (5) in R_h - I_h plane when $R_0 < 1$.

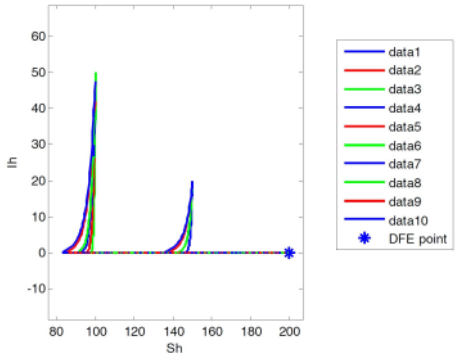

Figure 2. Numerical result of model (5) in S_h - I_h plane when $R_0 < 1$.

The stability condition of disease-free equilibrium means that the infected humans and infected mosquitoes are extinct. Biologically, the

systems are free from Zika virus. The following table describes the condition of disease-free or the infected human is a recovery in a certain time. In this work, we assume that the human density (the amount of population per-km^2) in a province x is N_h [2], and the mosquitoes density is 0.036, while human density is N_v [12]. Then we consider Table 2 and assume that the probability of direct transmission rate is 0.01, the probability of transmission rate between human and infected mosquitoes is 0.01 and the probability of transmission rate between mosquitoes and infected human is 0.01. The parameters of preventive conditions, namely, $\alpha_1 = 0.12$ and $\alpha_3 = 0.1$.

Table 2. Table of recovery time with assumed total population in human province resident in Indonesia

Province	Λ_h	Λ_v	Recovery time (days)
East Java	0.03426795	2.090571	110
Lampung	0.0098631	0.427266	75
West Java	0.055638	0.991310	120
Central Java	0.0434145	0.8782111	115
Bali	0.0302637	1.846286	100
NTB	0.010959	0.668571	80
Maluku	0.0015174	0.092571	70
Papua	0.0004215	0.0774278	70
Indonesia	0.0056481	0.344571	70

Based on Table 2 and the previous assumption, we can see that the Zika virus will be extinct at least in 70 days.

The other case of stability condition is when $R_0 > 1$. This case is hard to analyze analytically, then the numerical simulation is used. Let us consider Table 1 and choose the parameter values of $\Lambda_h = 0.00843$, $\beta_1 = 0.002$, $\beta_2 = 0.002$, $\beta_3 = 0.003$, $\alpha_1 = 0.05$, $\alpha_2 = 0.5$, $\alpha_3 = 0.5$. Then we have the following result.

Table 3. Table of sensitivity index for each parameter of the system (5)

Parameter	Sensitivity index	Interpretation (increasing or decreasing)	Rank
Λ_h	0.259484299	Λ_h by 10%, R_0 by 25%	5
μ_h	–0.259778772	μ_h by 10%, R_0 by 25%	4
α_1	–0.737006130	α_1 by 10%, R_0 by 74%	3
α_2	0	α_2 by 10%, R_0 by 0%	9
α_3	–0.001449337	α_3 by 10%, R_0 by 0.1%	8
β_1	0.995879534	β_1 by 10%, R_0 by 99%	2
β_2	0.0020602326	β_2 by 10%, R_0 by 0.2%	7
β_3	0.0020602326	β_3 by 10%, R_0 by 0.2%	7
$\tilde{a}$	–0.997645294	γ by 10%, R_0 by 99%	1
Λ_v	0.002060232	Λ_v by 10%, R_0 by 0.2%	7
μ_v	–0.00412046	μ_v by 10%, R_0 by 0.4%	6

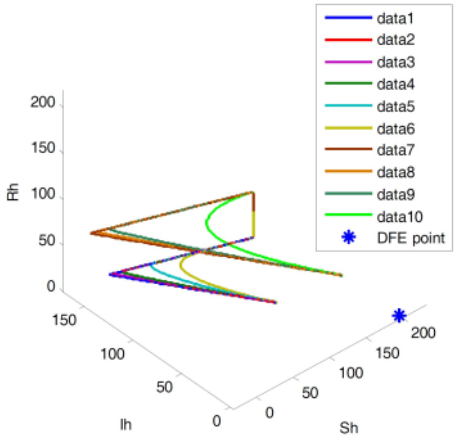

Figure 3. Numerical result of model (5) when $R_0 > 1$.

Based on Figure 3, by choosing ten variations of the parameter, we can see the solution of system (5). It tends to another point besides DFE, which it predicts by endemic equilibrium because no population is zero.

Sensitivity analysis

The sensitivity analysis was performed to determine the relative importance of model parameters of disease transmission. A set of parameter values is used to describe the endemic condition. The sensitivity index is identified with respect to the basic reproduction number. The highest impact of parameter value then becomes a big concern, to decreasing the probability of Zika virus outbreaks.

The advanced normalization sensitivity index of R_0 depends on differentiation on parameters of P defined by equation (5) [4] as follows:

$$I_p^{R_0} = \frac{\partial R_0}{\partial P}\frac{P}{R_0}.$$

Let us use the following parameter values:

$$\mu_v = 0.0714, \quad \mu_h = 0.00004215, \quad \Lambda_h = 0.001, \quad \Lambda_v = 0.002,$$

$$\beta_1 = 0.1, \quad \beta_2 = 0.01, \quad \beta_3 = 0.2, \quad \alpha_1 = 0.12, \quad \alpha_3 = 0.1, \quad \gamma = 0.1428.$$

Based on [4] and the mathematical computation, we have the following result.

According to Table 3, we can conclude that the reproductive number is most sensitive to γ (per capita recovery rate of the infected population) and least sensitive to α_2.

Conclusion

In this work, we studied the transmission of Zika virus by a certain assumption. The equilibrium point of the model is identified such as disease-free condition and epidemic. The basic reproduction number of the model is also determined, then the stability phenomena are investigated. According to analytical computation and numerical simulation, we can see that the disease-free condition always exists and stable if the basic reproduction number is less than one. By considering the DFE condition, the data of

recovery time is also computed to investigate the recovery time of the residents in each area. The area is assumed in certain provinces in Indonesia using the data of residents density in 2015.

The stability of endemic equilibrium means that the epidemic condition is studied numerically under the condition that the basic reproduction number is greater than one. Furthermore, the sensitivity index is also investigated to see which parameter is giving a high impact of Zika virus transmission. Considering the assumptions described in the mathematical model, we have constructed, the role of medical personnel in the recovery process is very large in a case of reduction of Zika virus transmission.

Acknowledgements

The authors express a big appreciation to Direktorat Riset dan Pengabdian Masyarakat (DRPM), Direktorat Jenderal Penguatan Riset dan Pengembangan, the Ministry of Research, Technology, and High Education, Indonesia for the funding support. The authors also would like to give a big thank to Research and Human Responsibility Institute of Universitas International Semen Indonesia for the greatest support.

References

[1] F. Agusto, S. Bewick and W. Fagan, Mathematical model for Zika virus dynamics with sexual transmission route, Ecological Complexity 29 (2017), 61-81.

[2] Badan Pusat Statistik, Kepadatan Penduduk Menurut Provinsi, 2011-2015, 2015. https://www.bps.go.id/.Accessed date: 1 November 2018.

[3] E. Bonyah and K. O. Okosun, Mathematical modeling of Zika virus, Asian Pacific Journal of Tropical Disease 6(9) (2016), 673-679.

[4] N. Chitnis, J. M. Hyman and J. M. Cushing, Determining important parameters in the spread of malaria through the sensitivity analysis of a mathematical model, Bulletin of Mathematical Biology 70(5) (2008), 1272-1296.

[5] P. van den Driessche and J. Watmough, Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission, Math. Biosci. 180 (2002), 29-48.

[6] F. Fitriah, A. Suryanto and N. Hidayat, Numerical study of predator-prey model with Beddington-DeAngelis functional response and prey harvesting, The Journal of Tropical Life Science 5(2) (2015), 105-109.

[7] N. K. Goswami, A. K. Srivastav, M. Ghosh and B. Shanmukha, Mathematical modeling of Zika virus disease with nonlinear incidence and optimal control, IOP Conf. Series: Journal of Physics Conf. Series 1000 (2018), 012114. DOI:10.1088/1742-6596/1000/1/012114.

[8] A. Kaddar, On the dynamics of a delayed SIR epidemic model with a modified saturated incidence rate, Electron. J. Differential Equations (2009), 1-7.

[9] M. Molles, Ecology Concept and Applications, 2nd ed., McGraw-Hill, Mexico City, 2002.

[10] I. U. Mysorekar and M. S. Diamond, Modeling Zika virus infection in pregnancy, New England Journal of Medicine 375(5) (2016), 481-484.

[11] S. Olaniyi, Dynamics of Zika virus model with nonlinear incidence and optimal control strategies, Applied Mathematics and Information Sciences, An International Journal 12(5) (2018), 969-982. http://dx.doi.org/10.18576/amis/120510.

[12] N. Sahrir, H. Ishak and A. Maidin, Environmental characteristic and density mapping of Aegyepti Aedes dengue based on endemicity status of DBD in Kolkata district, JST Kesehatan 6(1) (2016), 70-75.

[13] A. Suryanto, A dynamically consistent numerical method for SIRS epidemic model with non-monotone incidence rate, The 7th IMT-GT International Conference on Mathematics, Statistics and its Applications (ICMSA 2011), 2011.

[14] WHO - World Health Organization, WHO's response to Zika virus its associated complications, WHO Press, Geneva, 2016.

[15] U. S. Department of Health and Human Services, Zika Transmission, from Center for Disease Control and Prevention, 2017. https://www.cdc.gov/zika/transmission/index.html. Accessed Date: Mei 1, 2017.

NUMERICAL STUDY FOR ZIKA VIRUS TRANSMISSION WITH BEDDINGTON-DEANGELIS INCIDENCE RATE

ORIGINALITY REPORT

13%	14%	14%	0%
SIMILARITY INDEX	INTERNET SOURCES	PUBLICATIONS	STUDENT PAPERS

PRIMARY SOURCES

1	discovery.researcher.life Internet Source	8%
2	ppsub.ub.ac.id Internet Source	5%

Exclude quotes	Off	Exclude matches	< 3%
Exclude bibliography	On		

NUMERICAL STUDY FOR ZIKA VIRUS TRANSMISSION WITH BEDDINGTON-DEANGELIS INCIDENCE RATE

GRADEMARK REPORT

FINAL GRADE

/0

GENERAL COMMENTS

Instructor

PAGE 1

PAGE 2

PAGE 3

PAGE 4

PAGE 5

PAGE 6

PAGE 7

PAGE 8

PAGE 9

PAGE 10

PAGE 11

PAGE 12

PAGE 13