



Plagiarism Checker X Originality Report

Similarity Found: 10%

Date: Thursday, April 08, 2021

Statistics: 347 words Plagiarized / 3439 Total words

Remarks: Low Plagiarism Detected - Your Document needs Optional Improvement.

ISSN 0854-5154 | eISSN 2442-7349 Dynamical Analysis for A Simple **Model of Zika Virus Transmission** Puji Andayani Universitas Internasional Semen Indonesia, Kompleks PT.Semen Indonesia (Persero) Tbk, Jalan Veteran, Gresik, Indonesia Email: puji.andayani@uisi.ac.id **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 © Institut Teknologi Bandung. All rights reserved.

Received 23 January 2018 Revised 06 May 2019 02 July 2019 Available online 30 September 2019 **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 () and recovery human (). Whereas, for mosquitoes, we divide the population into two subclasses, namely susceptible vector (), and infected vector () [8].

The mathematical model of a system is non-linear 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 (), infected host () and recovered host (). The vector population is divided into three subclasses, suspected (), and infected (). The other work [4] comparing vector-host and SIR model for Please cite this article as: Puji Andayani, Dynamical analysis of zika virus transmission, J. Matem. Sains, 2019, 24, 19-23. DOI Number: 10.5614/jms.2019.24.1.4 20 © Faculty of Mathematics and Natural Sciences ISSN 0854-5154 | eISSN 2442-7349 Institut Teknologi Bandung. All rights reserved. P. Andayani / J. Matem.

Sains, 2017, Vol, page dengue transmission, that divided host populations into susceptible human (?? ??), infected human (?? ??), recovered human (?? ??), and vector populations into the susceptible vector (?? ??), infected vector (?? ??). 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 and . According to the previous assumption, the Zika virus transmission represents the following nonlinear differential equations: $\dot{h} = \lambda h - \beta_1 h^2 - \beta_2 h v - \mu h$, $\dot{h} = \beta_1 h^2 + \beta_2 h v - \mu h - \delta h$, $\dot{v} = \beta_3 h v - \mu v - \delta v$ (1) where $h(t)$, $h(t)$, $h(t)$, $v(t)$, $v(t)$, 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 denote the growth rate of human, β_1 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, μ for the per capita recovery rate of the infective population, δ means the death rate of human, and δ means the death rate of mosquitoes, respectively. Initial conditions of the model (1) are $h(0) = 0$, $h(0) = 0$, $h(0) = 0$, $v(0) = 0$, $v(0) = 0$. (2) Furthermore, the rate of total the human population is $\dot{h}(t) = \lambda h - \beta_1 h^2 - \beta_2 h v$.

(3) With given initial condition (2) it is ensuring that $h(0) = 0$. So, total population $h(t)$ will be positive and bounded for all finite time, . The rate of total dependence of the vector population is $\dot{v}(t) = \beta_3 h v - \mu v - \delta v$. (4) Based on eq.3 and eq.4, then we have $\dot{h} = \lambda h - \beta_1 h^2 - \beta_2 h v$. (5) Accordingly, the region of the system (1) is $O = \{(h, h, h, v, v) | h \geq 0, h \geq 0, h \geq 0, v \geq 0, v \geq 0\}$. (6) Lemma 2.1.

The closed set O is positive invariant and attracting concerning the system (1). Proof. Let (h, h, h, v, v) be the solution of the system (1) with initial value (2). Then we consider the following Lyapunov function $V(h, v) = (\beta_1 h + \beta_2 h + \beta_3 h, \mu v + \delta v)$. (7) The time derivative of (7) is $\dot{V} = (\lambda h - \beta_1 h^2 - \beta_2 h v, \beta_3 h v - \mu v - \delta v)$. (8) From eq.8 we can show that $\dot{V} = \lambda h - \beta_1 h^2 - \beta_2 h v = 0$, for $\lambda = \beta_1 h + \beta_2 h v$, $\mu v - \delta v = 0$, for $\mu = \delta$. (9) It follows (9) that $\dot{V} = 0$ which imply that O is positive invariant.

Then, by comparison theorem (9)(12) can be used to show that $O = (\beta_1, \beta_2) = (\beta_1(0) + \beta_2(0) + \beta_3(0), \mu + \delta)$.

$(0, 0)$. When $R_0 < 1$, then $O = (0, 0) = (h, h)$, so O 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

----- 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

21 © Faculty of Mathematics and Natural Sciences ISSN 0854-5154 | eISSN 2442-7349 Institut Teknologi Bandung. All rights reserved. P. Andayani / J. Matem. Sains, 2017, Vol, page ($h, h, 0, 0$, $h, h, 0, 0$) . The dynamics of the disease is described by the quantity of 0 , as follows $0 = h (h (h + h) + h)$, 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. The characteristic polynomials of the Jacobian (11) as follows, (12) Where, Five eigenvalues are corresponding to equation (18), which are the three of eigenvalues, and have the negative real part. The other eigenvalues can be obtained by solving the following equation, By the fundamental mathematics computation, have negative real parts if and

These conditions are satisfied when 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 where, If substitute to the system (1), then we have the following equations where, By using elementary computation, the solution of is To understand the value of we can see the following

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 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 $\lambda_1 < 0$. Otherwise, when $\lambda_1 > 0$, 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 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 $\lambda_1 < 0$. And globally stable at END when $\lambda_1 > 0$. 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.

ACKNOWLEDGEMENT The authors would like to express our special appreciation and great thanks to Research and Community Service Agency of Universitas Internasional

Semen Indonesia and Direktorat Riset dan Pengabdian Masyarakat (DRPM), Direktorat Jenderal Penguatan Riset dan Pengembangan, the Ministry of Research, Technology, and High Education, Indonesia. Thank you for supporting and funding our research .

REFERENCES [1] A. A. Lashari and G. Zaman, Global dynamics of vector-borne disease with horizontal transmission in host population, *Computers and Mathematics with Applications*, 61 (2011), 745- 754. [2] A. A. Rabaan, A. M. Bazzi, S. H. Al-Ahmed, M. H. Al-Ghaith, J. A.

Al-Tawfiq, Overview of Zika infection, epidemiology, transmission and control measures, *Journal of Infection and Public Health*, 10 (2017), 141-149. [3] A. J. Kucharski, S. Funk, R. M. Eggo, H.P. Mallet, W. J. Edmunds, E. J. Nilles, Transmission dynamics of Zika virus in island populations : a modelling of the 2013-14 French Polynesia outbreak, *PLoS Negl. Tropical Disease*, (2016), doi: 10.1371/journal.pntd.0004726 [4] A. Pandey, A. Mubayi, and J. Medlock, Comparing vector – host and SIR models for dengue transmission, *Mathematical Biosciences*, 246 (2013), 252-259. [5] U.S.

Department of Health & Human Services, Zika Virus, Retrieved September 20, 2016, Center for Disease Control and Prevention, URL: <https://www.cdc.gov/zika/index.html>. [6] D. Kincaid and W. Cheney, *Numerical Analysis : Mathematics of Scientific Computing* 3rd edition, Thomson learning, USA, 2002. [7] I. U. Mysorekar and M. S. Diamond, Modeling zika virus infection in pregnancy, *The new england journal of medicine* (published at nejm.org July 13, 2016). [8] J. Xu and Y. Zhou, Hopf Bifurcation and its stability for a vector-borne disease model with delay and reinfection, *Applied Mathematical Modelling*, 40 (2016), 1685-1702. [9] P. Andayani and W. M.

Kusumawinahyu, Global stability analysis on a predator-prey model with omnivore, *Applied Mathematical Sciences*, 9 (2015), 1771-1782. [10] S. B. Hsu, *Ordinary differential equations with applications*, 2nd edition, Series on Applied Mathematics Vo.21, World Scientific Publishing Co. Pte. Ltd, Singapore, 2013. [11] T. A. Perkins, A. S. Siraj, C. W. Ruktanonchai, M. U. G. Kraemer, and A. J. Tatem, Model-based projections of Zika virus infections in childbearing women in Americas, *Nature Microbiology*, 9 (2016), doi: 10.1038/nmicrobiol.2016.126. [12] V. Lakshmikantham, S. Leela, and A. A.

Martynyuk, *Stability analysis of nonlinear systems*, Marcel Dekker Inc, New York, Basel, 1989.

INTERNET SOURCES:

1% - <https://www.researchgate.net/profile/Puji-Andayani>

1% -

https://www.researchgate.net/publication/282885772_Global_stability_analysis_on_a_predator-prey_model_with_omnivores

<1% - <https://www.sciencedirect.com/science/article/pii/S0010465520300990>

<1% - <https://europepmc.org/article/PMC/PMC7790412>

1% - <https://pubmed.ncbi.nlm.nih.gov/28529970/>

3% -

https://www.researchgate.net/publication/305313704_Modeling_Zika_Virus_Infection_in_Pregnancy

<1% -

https://www.researchgate.net/publication/322008753_Modes_of_Transmission_of_Zika_Virus

2% -

https://www.researchgate.net/publication/220513389_Global_dynamics_of_vector-borne_diseases_with_horizontal_transmission_in_host_population

<1% - <https://iopscience.iop.org/issue/1742-6596/1366/1>

<1% -

<https://journals.plos.org/plosone/article/file?id=10.1371/journal.pone.0185540&type=printable>

1% - <https://jels.ub.ac.id/index.php/jels/article/download/287/281>

<1% -

https://www.researchgate.net/publication/5866203_Importance_of_Bird-to-Bird_Transmission_for_the_Establishment_of_West_Nile_Virus

<1% - <https://www.hindawi.com/journals/jam/2013/592056/>

<1% - <https://www.sciencedirect.com/science/article/pii/S0960077921001466>

<1% -

<https://text-id.123dok.com/document/lq5m493y-analisa-struktur-portal-ruang-tiga-lantai-dengan-metode-kekakuan-dibandingkan-dengan-program-ansys.html>

<1% - <https://core.ac.uk/download/pdf/267896580.pdf>

<1% - <https://downloads.hindawi.com/journals/aaa/2014/219173.xml>

<1% -

https://www.researchgate.net/publication/257829453_Stability_Analysis_of_an_HIVAIDS_Epidemic_Model_with_Screening

<1% - <https://www.sciencedirect.com/topics/mathematics/distinct-eigenvalue>

<1% -

https://www.researchgate.net/publication/310462318_The_transmission_dynamic_and_optimal_control_of_acute_and_chronic_hepatitis_B

<1% - <https://www.sciencedirect.com/science/article/pii/S0025556411000654>

<1% - <https://www.sciencedirect.com/science/article/pii/S0022039610000446>

<1% -

https://www.researchgate.net/publication/228867803_Coupled_dynamics_and_quiescent_states

<1% -

https://www.researchgate.net/publication/26404548_Numerical_stability_analysis_in_respiratory_control_system_models

<1% -

<https://journalofinequalitiesandapplications.springeropen.com/articles/10.1155/2010/598495>

1% -

https://www.researchgate.net/publication/318958809_Mathematical_modelling_of_zika_virus_in_Brazil

1% -

https://www.researchgate.net/publication/259092304_Comparing_vector-host_and_SIR_models_for_dengue_transmission

<1% - <https://ideas.repec.org/e/c/pgl14.html>

1% -

<https://publications.waset.org/9997850/modeling-and-analysis-of-an-sirs-epidemic-model-with-effect-of-awareness-programs-by-media>