



MODELING AND STABILITY ANALYSIS OF DENGUE SPREADING WITH VECTOR CLASSIFICATION ON AQUATIC AND ADULT STAGES

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Abstract

This paper focuses on the model of dengue fever transmission and stability analysis with vector classification on aquatic and adult stages. The mathematical model is classified into the host (human) and vector (mosquito) population class. The host population splits into three subclasses: susceptible, infected and recovered. The vector population is divided into aquatic, susceptible and infected. Stability analysis is performed for the disease-free equilibrium and endemic equilibrium points. Basic reproduction number is used as a reference for determining the stability of disease-free. The numerical simulation based on Runge-Kutta is used to solve the problem.

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1. Introduction

Dengue is the most rapidly spreading mosquito-borne viral disease in the world [1]. In recent years, more than 55% of the world population live in areas at risk of dengue fever transmission, with over 50 million people infected and 20,000 deaths annually [2]. Dengue hemorrhagic fever (DHF) is one of health problems in the area of Southeast Asia and the Western Pacific. Asian continent obtained the first rank in the patient number of dengue fever annually [1]. Since 1968-2009, World Health Organization (WHO) considered that Indonesia is the country with the highest dengue cases in Southeast Asia. According to the Indonesian health profile in 2014, the number of dengue patients reported as many as 100,347 people with 907 deaths [3].

The mathematical model of vector borne disease has been discussed in many researches such as Okosun et al. [4], Lashari et al. [5] and Kar and Jana [6]. Thome et al. discussed the optimal control of *Aedes Aegypti* mosquitoes by the male sterilization as a biological control and insecticide application [7]. Thome proposed a mathematical model which focused on the vector population only. Furthermore, Rodrigues et al. [8] proposed on the vaccination models and optimal control strategies to dengue. This research proposed two scenarios of vaccination: as a new compartment and a control variable. The mathematical model considered the vector population and human/host populations. Abdelrazec et al. [2] focused the optimal control on the limited space of dengue patients in the hospital. The mathematical model also considered the vector and human populations. The difference with Rodrigues et al. [8] was in the classification of vector population which was classified into the infectious and susceptible larvae. The other researches that concern in dengue issue are available in Feng and Velasco-Hernández [9], Esteva and Vargas [10], Pandey et al. [11], Aldila et al. [12] and Götz et al. [13].

This paper focuses on modeling and stability analysis of dengue spreading with vector classification on aquatic and adult stages. The reconstruction of dynamics system for dengue disease transmission is

discussed in Section 2. Subsequently the stability analysis of dengue disease models will be discussed in Section 3. The numerical simulation results using Runge-Kutta will be explained in Section 4.

2. Mathematical Modeling

The dynamics system is developed based on the host and the vector populations. The host population is composed of three subpopulations: $S_h(t)$ is the susceptible host population at time t , $I_h(t)$ is the infected host population at time t , and $R_h(t)$ is recovered host population and is assumed to be resistant to dengue disease at time t . Furthermore, the vector population is classified into three subpopulations which include $A_v(t)$ for the aquatic vector population comprising eggs, larvae, and pupae at time t , $S_v(t)$ for the susceptible vector population at time t , and $I_v(t)$ for the infected vector population, vector who is infected with dengue virus at time t , thus it can transmit the disease to the host population. The dynamics model is given by the following system of ordinary differential equations:

$$\frac{dS_h}{dt} = b_1 - \alpha_1 I_v S_h - \mu_1 S_h, \quad (1a)$$

$$\frac{dI_h}{dt} = \alpha_1 I_v S_h - \beta_1 I_h - \gamma I_h, \quad (1b)$$

$$\frac{dR_h}{dt} = \beta_1 I_h - \mu_2 R_h, \quad (1c)$$

$$\frac{dA_v}{dt} = b_2 - \eta A_v - \mu_3 A_v, \quad (1d)$$

$$\frac{dS_v}{dt} = \eta A_v - \alpha_2 S_v I_h - \mu_4 S_v, \quad (1e)$$

$$\frac{dI_v}{dt} = \alpha_2 S_v I_h - \mu_5 I_v. \quad (1f)$$

Equation (1a) denotes the dynamics of susceptible host. The susceptible host increased due to the birth rate b_1 and decreased by the natural death rate μ_1 . If the population of susceptible host interacted with the infected vector, then there was an outbreak of dengue virus that caused infection in susceptible host. The decreasing of susceptible host due to the interaction with infected vector would cause the increasing of the infected host by $\alpha_1 I_v S_h$. The dynamics of infected host is presented in equation (1b). The number of infected host decreased because of the death which is expressed by $\gamma_1 I_h$. The death occurring in infected host is assumedly caused by dengue disease. Besides that, the dynamics of infected host may be reduced due to the healing rate, denoted in the form β_1 . Furthermore, equation (1c) describes the dynamics of recovered host. The number of R_h increased because of many infected population who has experienced healing, expressed by $\beta_1 I_h$. In this study, recovered subpopulation is assumed resistant to dengue virus, thus the host's life can only be affected by dengue disease once in a lifetime. Subsequently, the dynamics of aquatic vector in equation (1d) increased due to the birth rate of vector that is expressed in b_2 . If η is the growth rate of the larvae becoming adult vectors, then the number of larvae that becomes adult vector is expressed in the form ηA_v . Susceptible vector is the adult vector group that is susceptible to dengue virus. The interaction between susceptible vector and infected host causes the change rate of susceptible vector decreased. This interaction means that the vector susceptible is infected with dengue virus because S_v bites I_h that caused the dengue virus in the body of infected host transmit into the body of susceptible vector. If the transmission rate of it is denoted by α_2 , then the dynamics of susceptible vector is decreased by $\alpha_2 S_v I_h$, while the dynamics of infected vector increased. The dynamics of susceptible and infected vector are shown in equations (1e)-(1f), respectively. The parameters μ_1 ; μ_2 ; μ_3 ; μ_4 and μ_5 show the rate of natural mortality of subpopulations S_h ; R_h ; A_v ; S_v and I_v , respectively.

3. Stability Analysis

In this section, the stability analysis of dengue transmission model is discussed. This study focuses on the local stability around the equilibrium point.

3.1. Equilibrium point

The equilibrium point of dengue transmissions can be obtained when $\frac{dS_h}{dt} = 0$, $\frac{dI_h}{dt} = 0$, $\frac{dR_h}{dt} = 0$, $\frac{dA_v}{dt} = 0$, $\frac{dS_v}{dt} = 0$, $\frac{dI_v}{dt} = 0$. The stability analysis is proposed for disease-free and endemic cases. Disease-free is a condition that there is no spread of dengue disease in the population, which is $I_h = I_v = 0$. Thus, the disease-free equilibrium point is

$$E_0 = \left\{ \frac{b_1}{\mu_1}, 0, 0, \frac{b_2}{(\eta + \mu_3)}, \frac{\eta b_2}{\mu_4(\eta + \mu_3)}, 0 \right\}.$$

While the endemic equilibrium point indicates that there is an outbreak in the population, which is $I_h \neq 0$ and $I_v \neq 0$ and $E_h^* = (S_h^*, I_h^*, R_h^*, A_v^*, S_v^*, I_v^*)$ obtained by:

$$I_v^* = \frac{b_2 \eta (\alpha_2 \alpha_1 b_1) - (\eta + \mu_3) (\mu_5 \mu_4 \beta_1 \mu_1 + \mu_5 \mu_4 \gamma \mu_1)}{(\mu_5 \alpha_2 \alpha_1 b_1 + \mu_5 \mu_4 \beta_1 \alpha_1 + \mu_5 \mu_4 \gamma \alpha_1) (\eta + \mu_3)},$$

$$S_h^* = \frac{b_1}{(\alpha_1 I_v^* + \mu_1)}, \quad I_h^* = \frac{\alpha_1 I_v^* b_1}{(\beta_1 + \gamma) (\alpha_1 I_v^* + \mu_1)},$$

$$R_h^* = \frac{\beta_1 \alpha_1 I_v^* b_1}{\mu_2 (\beta_1 + \gamma) (\alpha_1 I_v^* + \mu_1)}, \quad S_v^* = \frac{\mu_5 I_v (\beta_1 + \gamma) (\alpha_1 I_v^* + \mu_1)}{\alpha_2 \alpha_1 I_v^* b_1},$$

$$A_v^* = \frac{\mu_5 (\alpha_2 \alpha_1 I_v^* b_1) + \mu_4 (\beta_1 + \gamma) (\alpha_1 I_v^* + \mu_1)}{\eta (\alpha_2 \alpha_1 b_1)}.$$

3.2. Local stability

It is known in advance that the disease-free equilibrium point is defined by E_0 . The eigenvalues of the Jacobian matrix disease-free equilibrium point

$J(E_0)$ is obtained using the equation $|J(E_0) - \lambda I| = 0$, which is

$$k_0\lambda^6 + k_1\lambda^5 + k_2\lambda^4 + k_3\lambda^3 + k_4\lambda^2 + k_5\lambda + k_6 = 0. \quad (2)$$

If the roots of characteristic equation (2) have eigenvalues with negative real part, then the system is stable around the equilibrium point E_0 . Furthermore, the Routh-Hurwitz criterion is used to determine the requirement for the system stability as follows: $k_1 > 0$; $k_1k_2 > k_0k_3$; $l_1k_3 > k_1l_2$; $m_1l_2 > l_1m_2$; $n_1m_2 > m_1n_2$ with

$$l_1 = \frac{k_1k_2 - k_0k_3}{k_1}, \quad l_2 = \frac{k_1k_4 - k_0k_5}{k_1}, \quad m_1 = \frac{l_1k_3 - k_1l_2}{l_1},$$

$$m_2 = \frac{l_1k_5 - k_1l_3}{l_1}, \quad n_1 = \frac{m_1l_2 - l_1m_2}{m_1}, \quad n_2 = \frac{m_1l_3 - l_1m_3}{m_1}.$$

Asymptotic stability of E_0 also be guaranteed by

$$\mathcal{R}_0 = \sqrt{\frac{\alpha_1 b_1 \alpha_2 \eta b_2}{\mu_1 \mu_5 \mu_4 (\eta + \mu_3) (\beta_1 + \gamma)}} < 1.$$

The basic reproduction number \mathcal{R}_0 indicates the number of new infections which are caused by I_v and I_h . As a result, disease-free equilibrium point is asymptotically stable if $\mathcal{R}_0 < 1$. Some parameters such as b_1 , b_2 , α_1 and α_2 can be used to estimate whether new infections will occur in the population.

Furthermore, the stability of the endemic equilibrium point E_h^* is determined by finding the eigenvalues of the Jacobian matrix endemic equilibrium point $J(E_h^*)$. The eigenvalue is obtained using the equation $|J(E_h^*) - \lambda I| = 0$ that is

$$p_0\lambda^6 + p_1\lambda^5 + p_2\lambda^4 + p_3\lambda^3 + p_4\lambda^2 + p_5\lambda + p_6 = 0. \quad (3)$$

For endemic case, the system will be stable around the equilibrium point E_h^* if equation (3) has negative eigenvalues. Similarly, the requirement for the system stability is $p_1 > 0$; $p_1 p_2 > p_0 p_3$; $q_1 p_3 > p_1 q_2$; $r_1 q_2 > q_1 r_2$; $s_1 r_2 > r_1 s_2$ with $q_1 = \frac{p_1 p_2 - p_0 p_3}{p_1}$, $q_2 = \frac{p_1 p_4 - p_0 p_5}{p_1}$, $r_1 = \frac{q_1 p_3 - p_1 q_2}{q_1}$, $r_2 = \frac{q_1 p_5 - p_1 q_3}{q_1}$, $s_1 = \frac{r_1 q_2 - q_1 r_2}{r_1}$, $s_2 = \frac{r_1 q_3 - q_1 r_3}{r_1}$.

4. Numerical Solution

In this section, the dynamics system is solved numerically using Runge-Kutta method. Furthermore, the numerical simulation results are performed with the parameters as shown in Table 1 with initial values are (100, 25, 0, 200, 80, 40).

Table 1. Parameter values

| Parameter | Value | Parameter | Value | Parameter | Value |
|-----------|--------|------------|-------|-----------|---------|
| b_1 | 0,2 | η | 0,25 | γ | 0,00001 |
| b_2 | 0,6 | μ_3 | 0,032 | μ_2 | 0,006 |
| μ_1 | 0,0003 | α_1 | 0,001 | μ_4 | 0,01 |
| β_1 | 0,03 | α_2 | 0,001 | μ_5 | 0,02 |

Figure 1 shows that the number of susceptible hosts decreased significantly since the beginning, while the number of infected hosts increased since the beginning until 20 days. However, between $20 \leq t \leq 200$ days, the number of infected hosts decreased rapidly due to the healing rate β_1 greater than the transmission rate β_1 . This caused the number of recovered increased until $t \leq 90$ days. Furthermore, the susceptible, infected and recovered hosts were stable toward infinity ($t \geq 90$ days). In other words, the system was stable around the equilibrium points which were $E_h^* = (18; 5940; 6; 4786; 32; 3928)$.

Figure 1 shows the dynamics of vector population. The growth rate of aquatic vector A_v decreased continuously since the beginning. This was caused by the birth rate of aquatic vector β_2 which was smaller than the transition rate from aquatic to susceptible vector η . Therefore, the susceptible vector increased since the beginning until $t < 6$ days. Nevertheless, for $6 \leq t \leq 50$ days, the susceptible vector declined continuously due to the high level of interaction between the susceptible vector and infected host. After $t \geq 6$ days, the vector population was stable around the equilibrium point $E_h^* = (2,1277; 32,2792; 10,4561)$ for the aquatic, susceptible and infected subpopulations, respectively.

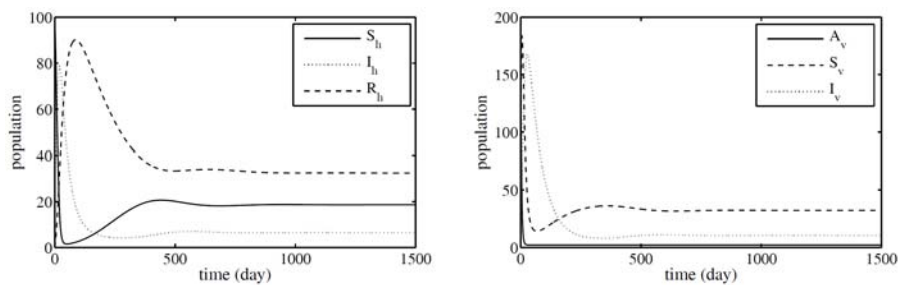


Figure 1. The dynamics of host and vector population.

The dynamics of aquatic and susceptible vector with variation of the parameter η is given in Figure 2. Based on that figure, the bigger transition rate from aquatic vector to susceptible vector η , there is faster decrease in aquatic vector population. This condition caused the susceptible vector increased significantly. Subsequently, Figures 3 and 4 show the change rate of susceptible and infected population for host and vector with various parameters (α_1, α_2) . From this result, the greater (α_1) will cause the susceptible host more rapidly decreased because many populations were infected by dengue disease. At the same time, when the transmission rate α_1 is very high, the number of infected hosts increased significantly at the beginning time. Similarly, if the transmission rate α_2 is higher, then the number of susceptible vectors is more decreased, while the infected vector is more increased.

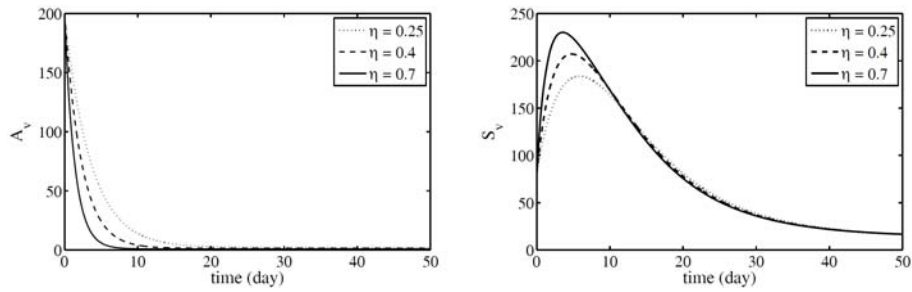


Figure 2. The dynamics of aquatic and susceptible vector with variation of η .

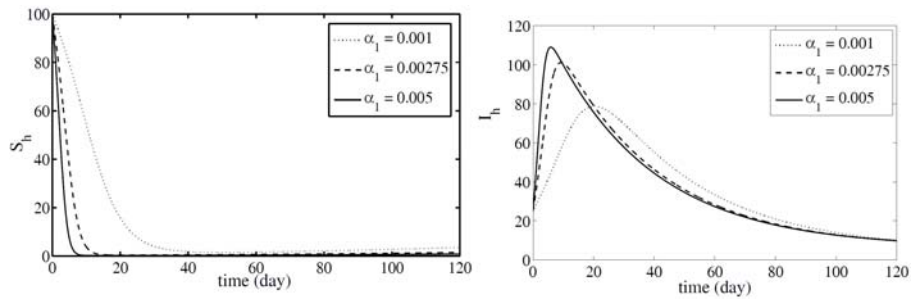


Figure 3. The dynamics of susceptible and infected for host with variation of α_1 .

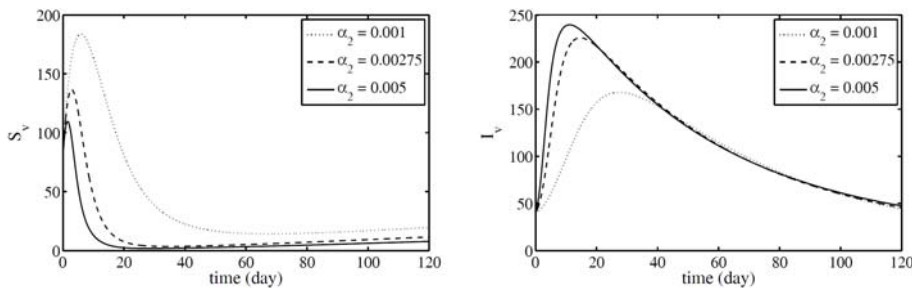


Figure 4. The dynamics of susceptible and infected for vector with variation of α_2 .

Figure 5 shows the illustration of basic reproduction number \mathcal{R}_0 for infected host and vector population. It can be seen that, if $\mathcal{R}_0 > 1$, then the spreading of dengue disease will always exist. However, if $\mathcal{R}_0 < 1$, then

the infection of dengue disease will disappear. In other words, infected population for both of host and vector will be stable at zero.

5. Conclusion

The mathematical model of dengue spreading was classified into the host population and the vector population. The host population was divided into subpopulations that were susceptible S_h , infected I_h and recovered R_h . While the vector population was divided into subpopulations which were aquatic A_v , susceptible S_v and infected I_v . Therefore, the mathematical model consisted of six ordinary differential equations that described the dynamics system of dengue transmission model.

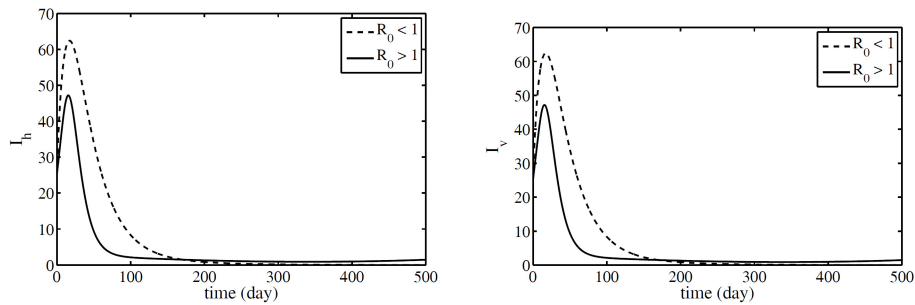


Figure 5. The dynamics of infected host and infected vector with \mathcal{R}_0 .

Furthermore, the model was analyzed for the stability at equilibrium point for disease-free and endemic cases. The stability of the system was determined by Routh-Hurwitz criteria. Moreover, this study also described the asymptotic stability of the equilibrium point using basic reproduction number \mathcal{R}_0 . Basic reproduction number (\mathcal{R}_0) increased if the parameters of host and vector population birth rate (b_1, b_2) and transmission rate (α_1, α_2) increased. If $\mathcal{R}_0 < 1$, then the equilibrium point of disease-free existed and asymptotically stable. It means that the disease would disappear from the population. Whereas, if $\mathcal{R}_0 > 1$, then there was the equilibrium point and the system was asymptotically stable around it for endemic case. It means that every infected population could produce more than one new infected

population. Therefore, the infection of dengue would always spread and exist in the population.

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