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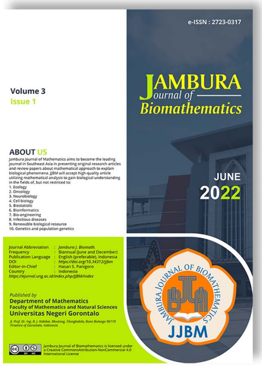
Volume 6, Issue 4, Pages 340–349, December 2025

Received 18 June 2025, Revised 23 September 2025, Accepted 2 December 2025, Published Online 18 December 2025

To Cite this Article : E. Aprianti and S. Sonia,“Stability and Sensitivity Analysis of Parameters in the SEIR-ASEI Model for the Transmission of Dengue Fever”, *Jambura J. Biomath*, vol. 6, no. 4, pp. 340–349, 2025, *https://doi.org/10.37905/jjbm.v6i4.32754*

JOURNAL INFO • JAMBURA JOURNAL OF BIOMATHEMATICS



Homepage : http://ejurnal.ung.ac.id/index.php/JJBM/index
Journal Abbreviation : Jambura J. Biomath.
Frequency : Quarterly (March, June, September and December)
Publication Language : English
DOI : https://doi.org/10.37905/jjbm
Online ISSN : 2723-0317
Editor-in-Chief : Hasan S. Panigoro
Publisher : Department of Mathematics, Universitas Negeri Gorontalo
Country : Indonesia
OAI Address : http://ejurnal.ung.ac.id/index.php/jjbm/oai
Google Scholar ID : XzYgeKQAAAAJ
Email : editorial.jjbm@ung.ac.id

Jambura Journal of Biomathematics, Volume 6, Issue 4, Pages 340–349, December 2025 https://doi.org/10.37905/jjbm.v6i4.32754

Research Article

Stability and Sensitivity Analysis of Parameters in the SEIR-ASEI Model for the Transmission of Dengue Fever

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ARTICLE HISTORY
Received 18 June 2025
Revised 23 September 2025
Accepted 2 December 2025
Published 18 December 2025

KEYWORDS
Aquatic phase
Basic reproduction number
Dengue fever
Sensitivity
Stability

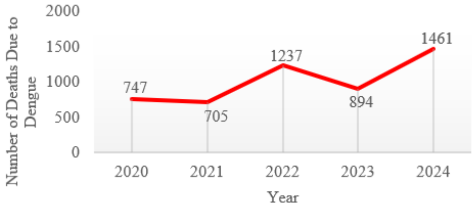
ABSTRACT. *Dengue fever, which is transmitted by female Aedes mosquitoes, is caused by the dengue virus and remains a significant health challenge in tropical countries, including Indonesia. This study developed an SEIR-ASEI type dengue fever transmission model by considering the aquatic phase of mosquitoes and incorporating logistic growth factors in aquatic sub-population. This study aims to analyze the stability of the model using the Vieta Theorem, and the Castillo-Chavez and Song Theorem through a bifurcation approach. The developed model has two equilibrium points, namely, the disease-free equilibrium point and the endemic equilibrium point. The stability of each equilibrium point depends on the value of the basic reproduction number, which is determined through the next-generation matrix. When* $\mathcal{R}_0$ *is less than one, the disease-free equilibrium remains locally asymptotically stable. Conversely, stability of the endemic state is assured when* $\mathcal{R}_0$ *exceeds one. An analysis of parameter sensitivity, using values associated with Aedes aegypti, was conducted to determine the factors that have the most significant impact on disease transmission dynamics. The analysis results showed that adult mosquito mortality was the most sensitive parameter, but parameters in the aquatic phase also influenced changes in the basic reproduction number. Increasing aquatic mortality or reducing mosquito breeding sites could lower the* $\mathcal{R}_0$ *value, potentially reducing transmission rates. Therefore, controlling aquatic mosquitoes is an essential strategy in sustainable dengue prevention and control efforts.*

1. Introduction

Dengue fever is an infectious disease caused by one of four serotypes of dengue virus (DENV 1, DENV 2, DENV 3, and DENV 4). Transmission of the virus to humans occurs through the bite of female *Aedes* mosquitoes (subgenus *Stegomyia*). Among these species, *Aedes aegypti* is the primary vector in spreading outbreaks in tropical and subtropical regions [1]. The classic symptoms of dengue fever are high fever lasting five to seven days and bright red petechiae appearing at the end of the fever [2]. This disease can cause death in a short time and has the potential to cause an epidemic [3].

The data in Figure 1 were obtained from the official website of the Ministry of Health of the Republic of Indonesia, which contains information on the number of cases and deaths due to dengue in Indonesia during the period 2020–2024. Figure 1a shows that the number of dengue cases decreased sharply in 2021, but increased again in 2022. In 2023, there was a slight decrease, but in 2024, the number of cases jumped significantly to 257,271, the highest number during the five-year observation period. Meanwhile, Figure 1b shows that the number of deaths due to dengue fluctuates from year to year. In 2020, there were 747 deaths, then decreased slightly to 705 deaths in 2021. However, in 2022, there was a sharp increase to 1,237 deaths. The number decreased again in 2023 to 894 deaths, before finally surging again in 2024 with 1,461 deaths, which was also the highest death toll in the past five years. In 2024, Indonesia also accounted for 66% of all dengue fever deaths in Asia and has the

(a) Dengue case



(b) Deaths due to dengue

Figure 1. Dengue cases and deaths in Indonesia

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Homepage : http://ejurnal.ung.ac.id/index.php/JJBM/index / E-ISSN : 2723-0317

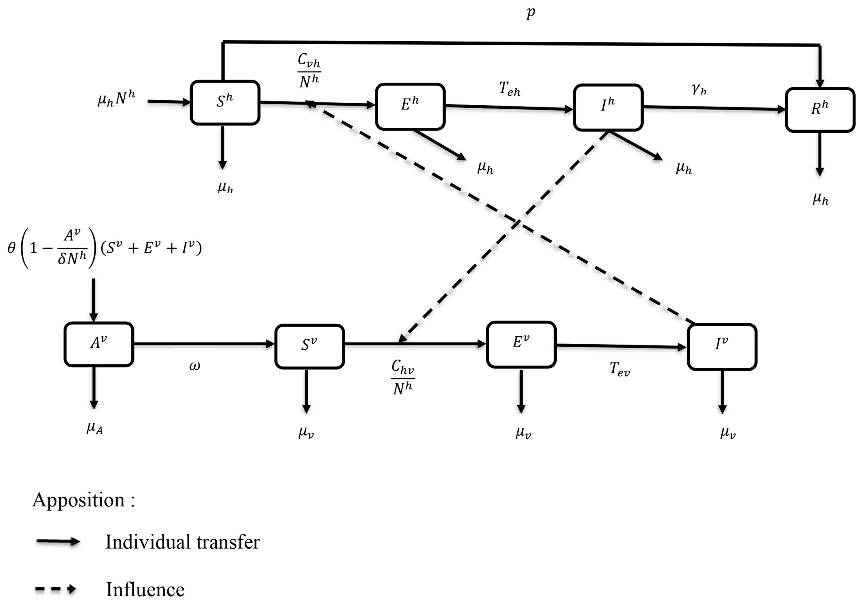


Figure 2. SEIR-ASEI compartment diagram for dengue fever transmission

highest number of cases in the ASEAN region [4]. This pattern indicates that dengue fever remains a serious public health problem in Indonesia. Fluctuations in cases are influenced by various factors, including climate, which contributes to the high incidence of dengue fever [5].

Research on dengue fever has also been conducted in various fields of science, one of which is mathematics through the application of mathematical models. Multiple models that represent the dynamics of disease spread have been developed, including the SIR (susceptible–infectious–recovered) model used to study the spread of dengue fever [6]. However, because the dengue virus requires an incubation period before spreading, around 8-10 days after the dengue virus infects an individual [7], the model can be modified into an SEIR model by adding an exposed sub-population [8]. This model only considers the adult phase of mosquitoes, whereas the mosquito life cycle consists of two main phases, the aquatic phase and the adult phase [9]. The model that explicitly considers the existence of the aquatic phase is the one developed by Inayah *et al.*, as this phase significantly influences the adult mosquito population [10]. However, this model does not account for the environmental carrying capacity of the mosquito population during the aquatic phase.

Therefore, in this study, the authors modified the SEIR–SEI model studied by Bano [8] by adding an aquatic phase and considering the environmental carrying capacity in that phase. The analysis conducted on the modified model included fixed-point stability analysis and sensitivity analysis. Furthermore, numerical simulations were conducted, including bifurcation simulations, population dynamics simulations, and sensitivity simulations to parameters in the aquatic phase by varying their values to identify their influence on the spread of dengue fever.

2. Model Formulation

This model includes two types of population, human and mosquito. The human population is divided into four sub-population, namely S^h as a susceptible human sub-population that is healthy but can be infected through mosquito bites, E^h as a human sub-population that has been exposed to the virus but has not shown symptoms and is not yet infectious, I^h as a human sub-population that is infected and can transmit the virus to mosquitoes, and R^h as a human sub-population that has recovered with the assumption of having permanent immunity. Meanwhile, the mosquito population consists of two phases, namely the aquatic phase and the adult phase (imago). In the aquatic phase, A^v includes the stages of eggs, larvae, and pupa. Furthermore, in the adult phase, there are three sub-population, namely S^v as healthy adult mosquitoes that can be infected, E^v as mosquitoes that have been exposed to the virus but cannot yet transmit it, and I^v as mosquitoes that are infective and capable of transmitting the virus to humans. However, mosquitoes never recover from infection due to their relatively short lifespan [11].

Based on Figure 2, the movement between compartments is depicted by arrows, while the cross-transmission interaction between humans and mosquitoes is shown by dashed arrows. In the human population, each natural birth is assumed to produce a new individual entering the susceptible sub-population (S^h), and the natural birth rate is assumed to be equal to the natural death rate so that the total human population is constant over time $\left(\frac{dN^h}{dt}=0\right)$. Some susceptible individuals acquire immunity through vaccination at a rate of p and move to the recovered sub-population (R^h). Susceptible individuals can be exposed to the virus through the bite of an infected mosquito and subsequently move to the exposed sub-population (E^h) at a rate of C_{vh}, which is the product of the probability of virus transmission from infected mosquitoes to susceptible humans and the average mosquito bite rate. After the incubation period ends, exposed individuals move to the infected sub-population (I^h), where they begin to show symptoms and can transmit the virus to mosquitoes that bite them. Furthermore, infected individuals can recover and move into the recovered sub-population at a rate of γ_h, while natural deaths can occur in each sub-population at a rate of μ_h.

In the aquatic sub-population A^v, the population growth rate follows a logistic growth pattern that describes the dynamics of a population that initially experiences rapid growth, but slows down as the population density increases until it reaches the maximum environmental capacity [12]. The growth rate of the aquatic phase is determined by the reproduction of adult female mosquitoes with an oviposition rate of θ, which is the number of eggs produced by adult mosquitoes per unit time in each sub-population. The growth rate of the aquatic phase is also limited by the environmental carrying capacity of δN^h. The factor $1-\dfrac{A^v}{\delta N^h}$ represents a density-limiting mechanism, so that the larger the aquatic population, the growth rate will decrease due to resource limitations. Furthermore, mosquitoes in the aquatic sub-population will develop into healthy adults at a rate of ω and move to the susceptible sub-population (S^v), while others experience natural death at a rate of μ_A. In the adult phase, susceptible mosquitoes can become infected and subsequently move to the exposed sub-population (E^v) at a rate of C_{hv}, which is the product of the probability of virus transmission from an infected human to a susceptible mosquito and the average mosquito bite rate. After the incubation period ends, the exposed mosquitoes move to the infected sub-population (I^v), where they become infective and capable of transmitting the virus to humans. Natural mortality in mosquitoes can occur in each sub-population at a rate of μ_v.

Based on the explanation above, the system formed is as follows.

$$\begin{aligned}
\frac{dS^h}{dt} &= \mu_h N^h - \left(\mu_h + p + \frac{C_{vh}}{N^h} I^v\right) S^h, \\
\frac{dE^h}{dt} &= \frac{C_{vh}}{N^h} I^v S^h - (T_{eh} + \mu_h) E^h, \\
\frac{dI^h}{dt} &= T_{eh} E^h - (\gamma_h + \mu_h) I^h, \\
\frac{dR^h}{dt} &= p S^h + \gamma_h I^h - \mu_h R^h, \\
\frac{dA^v}{dt} &= \theta \left(1 - \frac{A^v}{\delta N^h}\right) (S^v + E^v + I^v) - (\omega + \mu_A) A^v, \\
\frac{dS^v}{dt} &= \omega A^v - \left(\mu_v + \frac{C_{hv}}{N^h} I^h\right) S^v, \\
\frac{dE^v}{dt} &= \frac{C_{hv}}{N^h} I^h S^v - (T_{ev} + \mu_v) E^v, \\
\frac{dI^v}{dt} &= T_{ev} E^v - \mu_v I^v,
\end{aligned} \tag{1}$$

assuming that all parameters are positive, as defined in Table 1. The total human population is expressed as $N^h = S^h + E^h + I^h + R^h$, and the total mosquito population is expressed as $N^v = S^v + E^v + I^v$.

Before proceeding with further analysis, the model will be simplified by defining non-dimensional variables to reduce the number of parameters and to facilitate the analytical process, as follows:

$$s_h = \frac{S^h}{N^h},\ e_h = \frac{E^h}{N^h},\ i_h = \frac{I^h}{N^h},\ r_h = \frac{R^h}{N^h},\ a_v = \frac{A^v}{N^v},$$
$$s_v = \frac{S^v}{N^v},\ e_v = \frac{E^v}{N^v},\ i_v = \frac{I^v}{N^v},\ n = \frac{N^v}{N^h}.$$

So that $s_h + e_h + i_h + r_h = 1$ and $s_v + e_v + i_v = 1$. If all non-dimensional variables are substituted into system (1), then the system of equations will be as follows:

$$\begin{aligned}
\frac{ds_h}{dt} &= \mu_h - (\mu_h + p + nC_{vh} i_v) s_h, \\
\frac{de_h}{dt} &= nC_{vh} i_v s_h - (T_{eh} + \mu_h) e_h, \\
\frac{di_h}{dt} &= T_{eh} e_h - (\gamma_h + \mu_h) i_h, \\
\frac{dr_h}{dt} &= p s_h + \gamma_h i_h - \mu_h r_h, \\
\frac{da_v}{dt} &= \theta \left(1 - \frac{a_v n}{\delta}\right) - (\omega + \mu_A) a_v, \\
\frac{ds_v}{dt} &= \omega a_v - (\mu_v + C_{hv} i_h) s_v, \\
\frac{de_v}{dt} &= C_{hv} i_h s_v - (T_{ev} + \mu_v) e_v, \\
\frac{di_v}{dt} &= T_{ev} e_v - \mu_v i_v.
\end{aligned}$$

The variable r_h does not affect the other equations, so the system (1) can be written as follows:

$$\begin{aligned}
\frac{ds_h}{dt} &= \mu_h - (\mu_h + p + nC_{vh} i_v) s_h, \\
\frac{de_h}{dt} &= nC_{vh} i_v s_h - (T_{eh} + \mu_h) e_h, \\
\frac{di_h}{dt} &= T_{eh} e_h - (\gamma_h + \mu_h) i_h, \\
\frac{da_v}{dt} &= \theta \left(1 - \frac{a_v n}{\delta}\right) - (\omega + \mu_A) a_v, \\
\frac{ds_v}{dt} &= \omega a_v - (\mu_v + C_{hv} i_h) s_v, \\
\frac{de_v}{dt} &= C_{hv} i_h s_v - (T_{ev} + \mu_v) e_v, \\
\frac{di_v}{dt} &= T_{ev} e_v - \mu_v i_v.
\end{aligned} \tag{2}$$

The reduced system obtained above is completed with the following initial conditions:

$$s_h(0) \geq 0,\ e_h(0) \geq 0,\ i_h(0) \geq 0,\ a_v(0) \geq 0,\ s_v(0) \geq 0,$$
$$e_v(0) \geq 0,\ i_v(0) \geq 0,$$

with

$$\begin{aligned}
s_h(0) + e_h(0) + i_h(0) &\leq 1, \\
a_v(0) &\leq 1, \\
s_v(0) + e_v(0) + i_v(0) &= 1.
\end{aligned}$$

Next, system (2) will be used for analysis.

3. Analytical Results

3.1. Equilibrium Point

The equilibrium condition for system (2) arises by setting the time derivatives to zero and analyzing the resulting system of equations [13]. Thus, two equilibrium points are obtained: the disease-free equilibrium point when no infection circulates in the population, which is stated a

$$S^* = \left(\frac{\mu_h}{p+\mu_h},\ 0,\ 0,\ \frac{\delta\theta}{n\theta+\delta\omega+\delta\mu_A},\ \frac{\delta\theta\omega}{(n\theta+\delta\omega+\delta\mu_A)\mu_v},\ 0,\ 0\right),$$

and the endemic equilibrium, which corresponds to the condition where the disease persists in the population and is denoted by S^{**}. These values are given by

$$\begin{aligned}
s_h^* &= \frac{T_{eh}C_{hv}\mu_h + (T_{eh}+\mu_h)(\gamma_h+\mu_h)\mu_v}{nT_{ev}\delta\theta\omega C_{vh} + (n\theta+\delta\omega+\delta\mu_A)(p+\mu_h)\mu_v(T_{ev}+\mu_v)} \\
&\quad \times \frac{\mu_v(n\theta+\delta\omega+\delta\mu_A)(T_{ev}+\mu_v)}{T_{eh}C_{hv}}, \\
e_h^* &= \frac{1}{nT_{ev}\delta\theta\omega C_{vh} + (n\theta+\delta\omega+\delta\mu_A)(p+\mu_h)\mu_v(T_{ev}+\mu_v)} \\
&\quad \times \left[\frac{nT_{eh}T_{ev}\delta\theta\omega C_{hv}C_{vh}\mu_h}{T_{eh}C_{hv}(T_{eh}+\mu_h)} - \frac{\mu_v^2(\gamma_h+\mu_h)(T_{ev}+\mu_v)}{T_{eh}C_{hv}(T_{eh}+\mu_h)}\right. \\
&\quad \left.\times (n\theta+\delta\omega+\delta\mu_A)(p+\mu_h)(T_{eh}+\mu_h)\right], \\
i_h^* &= \frac{1}{nT_{ev}\delta\theta\omega C_{vh} + (n\theta+\delta\omega+\delta\mu_A)(p+\mu_h)\mu_v(T_{ev}+\mu_v)} \\
&\quad \times \left[\frac{nT_{eh}T_{ev}\delta\theta\omega C_{hv}C_{vh}\mu_h}{c_{hv}(T_{eh}+\mu_h)(\gamma_h+\mu_h)} - \frac{\mu_v^2(\gamma_h+\mu_h)(T_{ev}+\mu_v)}{c_{hv}(T_{eh}+\mu_h)(\gamma_h+\mu_h)}\right. \\
&\quad \left.\times (n\theta+\delta\omega+\delta\mu_A)(p+\mu_h)(T_{eh}+\mu_h)\right], \\
a_\nu^* &= \frac{\delta\theta}{n\theta+\delta\omega+\delta\mu_A}, \\
s_\nu^* &= \frac{nT_{ev}\delta\theta\omega c_{vh} + (n\theta+\delta\omega+\delta\mu_A)(p+\mu_h)\mu_v(T_{ev}+\mu_v)}{T_{eh}C_{hv}\mu_h + (T_{eh}+\mu_h)(\gamma_h+\mu_h)\mu_v} \\
&\quad \times \frac{(T_{eh}+\mu_h)(\gamma_h+\mu_h)}{nT_{ev}C_{vh}(n\theta+\delta\omega+\delta\mu_A)}, \\
e_\nu^* &= \frac{1}{T_{eh}C_{hv}\mu_h + (T_{eh}+\mu_h)(\gamma_h+\mu_h)\mu_v} \\
&\quad \times \left[\frac{nT_{eh}T_{ev}\delta\theta\omega C_{hv}C_{vh}\mu_h}{nT_{ev}C_{vh}(n\theta+\delta\omega+\delta\mu_A)(T_{ev}+\mu_v)}\right. \\
&\quad - \frac{(n\theta+\delta\omega+\delta\mu_A)(p+\mu_h)(T_{eh}+\mu_h)}{nT_{ev}C_{vh}(n\theta+\delta\omega+\delta\mu_A)(T_{ev}+\mu_v)} \\
&\quad \left.\times \mu_v^2(\gamma_h+\mu_h)(T_{ev}+\mu_v)\right], \\
i_\nu^* &= \frac{1}{\mu_v(T_{ev}+\mu_v)(T_{eh}C_{hv}\mu_h + (T_{eh}+\mu_h)(\gamma_h+\mu_h)\mu_v)} \\
&\quad \times \left[\frac{nT_{eh}T_{ev}\delta\theta\omega C_{hv}C_{vh}\mu_h}{nC_{vh}(n\theta+\delta\omega+\delta\mu_A)} - \frac{\mu_v^2(\gamma_h+\mu_h)(T_{ev}+\mu_v)}{nC_{vh}(n\theta+\delta\omega+\delta\mu_A)}\right. \\
&\quad \left.\times (n\theta+\delta\omega+\delta\mu_A)(p+\mu_h)(T_{eh}+\mu_h)\right].
\end{aligned}$$

3.2. *Basic Reproduction Number*

From an epidemiological perspective, the basic reproduction number ($\mathcal{R}_0$) denotes the expected number of new infections generated by one infectious case in a population where everyone is susceptible. This parameter is crucial in evaluating the potential for disease spread and is obtained through the next-generation matrix approach [14].

Based on the system (2), there are four disease compartments, namely e_h, i_h, e_v, and i_v. So the rate of appearance of new infectious individuals and the rate of transfer or removal of non-infectious individuals in compartment i are given as follows:

$$\boldsymbol{F}_i = \begin{pmatrix} nC_{vh}i_v s_h \\ 0 \\ C_{hv}i_h s_v \\ 0 \end{pmatrix},\ \boldsymbol{V}_i = \begin{pmatrix} (T_{eh}+\mu_h)e_h \\ (\gamma_h+\mu_h)i_h - T_{eh}e_h \\ (T_{ev}+\mu_v)e_v \\ \mu_v i_v - T_{ev}e_v \end{pmatrix}.$$

Thus, the new infection rate matrix **F** and the transition matrix **V** are evaluated at the disease-free equilibrium point as follows:

$$\mathbf{F} = \begin{pmatrix} 0 & 0 & 0 & nC_{vh}\left(\dfrac{\mu_h}{p+\mu_h}\right) \\ 0 & 0 & 0 & 0 \\ 0 & C_{hv}\left(\dfrac{\delta\theta\omega}{(n\theta+\delta\omega+\delta\mu_A)\mu_v}\right) & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix},$$

$$\mathbf{V} = \begin{pmatrix} T_{eh}+\mu_h & 0 & 0 & 0 \\ -T_{eh} & \gamma_h+\mu_h & 0 & 0 \\ 0 & 0 & T_{ev}+\mu_v & 0 \\ 0 & 0 & -T_{ev} & \mu_v \end{pmatrix}.$$

Thus, the next-generation matrix is obtained.

$$\boldsymbol{FV}^{-1} = \begin{pmatrix} 0 & 0 & a_{1,3} & a_{1,4} \\ 0 & 0 & 0 & 0 \\ a_{3,1} & a_{3,2} & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix},$$

with

$$\begin{aligned}
a_{1,3} &= \frac{nC_{vh}T_{ev}\mu_h}{(p+\mu_h)\mu_v(T_{ev}+\mu_v)}, \\
a_{1,4} &= \frac{nC_{vh}\mu_h}{(p+\mu_h)\mu_v}, \\
a_{3,1} &= \frac{\delta\theta\omega c_{hv}(T_{eh}T_{ev}\mu_v + T_{eh}\mu_v^2)}{(n\theta+\delta\omega+\delta\mu_A)(T_{eh}+\mu_h)(\gamma_h+\mu_h)\mu_v^2(T_{ev}+\mu_v)}, \\
a_{3,2} &= \frac{\delta\theta\omega c_{hv}}{(n\theta+\delta\omega+\delta\mu_A)(\gamma_h+\mu_h)\mu_v}.
\end{aligned}$$

The largest non-negative eigenvalue of the next-generation matrix is defined as the basic reproduction number, that is,

$$\mathcal{R}_0 = \sqrt{\frac{n\delta\theta\omega C_{hv}C_{vh}T_{eh}T_{ev}\mu_h}{(n\theta+\delta\omega+\delta\mu_A)(p+\mu_h)(T_{eh}+\mu_h)(\gamma_h+\mu_h)\mu_v^2(T_{ev}+\mu_v)}}.$$

3.3. *Stability Analysis of Disease-Free Equilibrium Point*

> **Theorem 1.** *The disease-free equilibrium point S^* in the system (2) is locally asymptotically stable if $\mathcal{R}_0 < 1$ and unstable if $\mathcal{R}_0 >$ 1.*

Proof. The proof of Theorem 1 uses the linearization of the nonlinear system around a disease-free equilibrium point [15]. The

Jacobian matrix obtained is as follows:

$$\boldsymbol{J}=\begin{bmatrix} j_1 & 0 & 0 & 0 & 0 & 0 & j_2\\ 0 & j_3 & 0 & 0 & 0 & 0 & j_4\\ 0 & T_{eh} & j_5 & 0 & 0 & 0 & 0\\ 0 & 0 & 0 & j_6 & 0 & 0 & 0\\ 0 & 0 & j_7 & \omega & -\mu_v & 0 & 0\\ 0 & 0 & j_8 & 0 & 0 & j_9 & 0\\ 0 & 0 & 0 & 0 & 0 & T_{ev} & -\mu_v \end{bmatrix},$$

$$\begin{aligned} j_1 &= -(\mu_h+p),\ j_2=-\frac{nC_{vh}\mu_h}{p+\mu_h},\\ j_3 &= -(T_{eh}+\mu_h),\ j_4=\frac{nC_{vh}\mu_h}{p+\mu_h},\\ j_5 &= -(\gamma_h+\mu_h),\ j_6=-\left(\frac{\theta n}{\delta}+\omega+\mu_A\right),\\ j_7 &= -\frac{C_{hv}\delta\theta\omega}{(n\theta+\delta\omega+\delta\mu_A)\mu_v},\ j_8=\frac{C_{hv}\delta\theta\omega}{(n\theta+\delta\omega+\delta\mu_A)\mu_v},\\ j_9 &= -(T_{ev}+\mu_v). \end{aligned}$$

The eigenvalues (λ) of the Jacobian matrix **J** are obtained by solving $|\lambda\mathbf{I}-\mathbf{J}|=0$ to obtain two negative eigenvalues, namely $\lambda_1=-\mu_v, \lambda_2=-(\mu_h+p), \lambda_3=-\left(\frac{\theta n}{\delta}+\omega+\mu_A\right)$ and the characteristic equation:

$$\lambda^4+a_1\lambda^3+a_2\lambda^2+a_3\lambda+a_4=0 \tag{3}$$

with

$$\begin{aligned} a_1 &= T_{ev}+2\mu_v+\gamma_h+2\mu_h+T_{eh}>0,\\ a_2 &= (\gamma_h+\mu_h)(T_{ev}+\mu_v)+(T_{eh}+\mu_h+\mu_v)(T_{ev}+\mu_v+\gamma_h\\ &\quad +\mu_h)+\mu_v(T_{eh}+\mu_h)>0,\\ a_3 &= (T_{eh}+\mu_h+\mu_v)(\gamma_h+\mu_h)(T_{ev}+\mu_v)+\mu_v(T_{eh}\\ &\quad +\mu_h)(T_{ev}+\mu_v+\gamma_h+\mu_h)>0,\\ a_4 &= \mu_v(T_{eh}+\mu_h)(\gamma_h+\mu_h)(T_{ev}+\mu_v)\left[1-\mathcal{R}_0^2\right]. \end{aligned}$$

The coefficient a_4 in the characteristic equation above can be negative, zero, or positive depending on the value of $\mathcal{R}_0$. If $\mathcal{R}_0<1$, then the coefficient a_4 is positive. If $\mathcal{R}_0=1$, then the coefficient of a_4 is equal to zero. But if $\mathcal{R}_0>1$, then the coefficient of a_4 is negative.

Based on the nature of the roots of the quartic equation for eq. (3), four conditions are obtained which must be met based on Vieta's theorem [16], namely:

$$\begin{aligned} \lambda_4+\lambda_5+\lambda_6+\lambda_7 &= -a_1,\\ \lambda_4\lambda_5+\lambda_4\lambda_6+\lambda_4\lambda_7+\lambda_5\lambda_6+\lambda_5\lambda_7+\lambda_6\lambda_7 &= a_2,\\ \lambda_4\lambda_5\lambda_6+\lambda_4\lambda_5\lambda_7+\lambda_4\lambda_6\lambda_7+\lambda_5\lambda_6\lambda_7 &= -a_3,\\ \lambda_4\lambda_5\lambda_6\lambda_7 &= a_4, \end{aligned}$$

by simplifying and considering the values of a_1, a_2, a_3, and a_4, the above equation becomes:

$$\lambda_4+\lambda_5+\lambda_6+\lambda_7<0, \tag{4}$$

$$\lambda_4\lambda_5+\lambda_4\lambda_6+\lambda_4\lambda_7+\lambda_5\lambda_6+\lambda_5\lambda_7+\lambda_6\lambda_7>0, \tag{5}$$

$$\lambda_4\lambda_5(\lambda_6+\lambda_7)+\lambda_6\lambda_7(\lambda_4+\lambda_5)<0. \tag{6}$$

When $\mathrm{R}_0<1$, then

$$\lambda_4\lambda_5\lambda_6\lambda_7>0. \tag{7}$$

Based on eqs. (4) and (7), four eigenvalues are obtained, with two or four negative to meet the requirements in the equation. Suppose λ_4 and λ_5 are negative, then the stability can be seen from λ_6 and λ_7. Since $\lambda_4<0$ and $\lambda_5<0$ then we obtain $\lambda_4\lambda_5>0$ and $\lambda_4+\lambda_5<0$. If we assume $\lambda_6<0$ and $\lambda_7<0$ then we obtain

$$\lambda_4\lambda_5(\lambda_6+\lambda_7)<0 \quad \text{and} \quad \lambda_6\lambda_7(\lambda_4+\lambda_5)<0,$$

which satisfy eq. (6). If we suppose $\lambda_6>0$ and $\lambda_7>0$, then we obtain

$$\lambda_4\lambda_5(\lambda_6+\lambda_7)>0 \quad \text{and} \quad \lambda_6\lambda_7(\lambda_4+\lambda_5)<0,$$

So, there is not enough evidence to prove that the equation can satisfy eq. (6). So eq. (6) can be satisfied if λ_6 and λ_7 are negative, so the disease-free equilibrium point S^* is locally asymptotically stable if $\mathcal{R}_0<1$.

While when $\mathcal{R}_0>1$, then

$$\lambda_4\lambda_5\lambda_6\lambda_7<0. \tag{8}$$

eq. (8) holds if there is one or three negative eigenvalues. Thus, there is at least one positive eigenvalue. Thus, the disease-free equilibrium point S^* is unstable if $\mathcal{R}_0>1$. □

3.4. *Stability Analysis of Endemic Equilibrium Point*

> **Theorem 2.** *The endemic equilibrium point S^{**} in the system (2) is locally asymptotically stable if $\mathcal{R}_0>1$.*

Proof. The proof of Theorem 2 will use the Castillo-Chaves and Song Theorem with a bifurcation approach [17]. Suppose C_{vh} is chosen as the bifurcation parameter and $x_1=s_h$, $x_2=e_h$, $x_3=i_h$,$x_4=a_v$, $x_5=s_v$, $x_6=e_v$, $x_7=i_v$. So system (2) becomes:

$$\begin{aligned} g_1 &= \mu_h-(\mu_h+p+nC_{vh}x_7)x_1,\\ g_2 &= nC_{vh}x_7x_1-(T_{eh}+\mu_h)x_2,\\ g_3 &= T_{eh}x_2-(\gamma_h+\mu_h)x_3,\\ g_4 &= \theta\left(1-\frac{x_4n}{\delta}\right)-(\omega+\mu_A)x_4,\\ g_5 &= \omega x_4-(\mu_v+C_{hv}x_3)x_5,\\ g_6 &= C_{hv}x_3x_5-(T_{ev}+\mu_v)x_6,\\ g_7 &= T_{ev}x_6-\mu_vx_7 \end{aligned} \tag{9}$$

When $\mathcal{R}_0=1$ then

$$\begin{aligned} C_{vh} &= \frac{\mu_v^2(p+\mu_h)(T_{eh}+\mu_h)(\gamma_h+\mu_h)(T_{ev}+\mu_v)}{n\delta\theta\omega C_{hv}T_{eh}T_{ev}\mu_h}\\ &\quad\times(n\theta+\delta\omega+\delta\mu_A)\\ &= C_{vh}^*. \end{aligned}$$

So the Jacobian matrix of system (9) on S^* with the value $C_{vh}=C_{vh}^*$ will produce three eigenvalues, namely $\lambda_1=-\mu_v$, $\lambda_2=-(\mu_h+p)$, $\lambda_3=-\left(\frac{\theta n}{\delta}+\omega+\mu_A\right)$, $\lambda_4=0$, and the characteristic equation $\lambda^3+a_1\lambda^2+a_2\lambda+a_3=0$ with a_1,a_2,a_3 positive. The other three eigenvalues of the characteristic equation are obtained by solving the equation using Vieta's theorem [16].

Table 1. List of model parameters

Parameter	Definition	Value	Unit	Reference
μ_h	Human birth/death rate	0.0286	1/day	[18] [19]
p	Effectiveness of dengue vaccine	0.00027	1/day	[20]
C_{vh}	The chance of susceptible humans being exposed to the dengue virus from infected mosquitoes	0.35×0.75	1/day	[21][22]
T_{eh}	Inverse of the intrinsic incubation period	1/15	1/day	[23]
γ_h	Recovery rate of infected humans	1/7	1/day	[24]
ω	The rate of change of aquatic mosquitoes into adult mosquitoes	1/11	1/day	[25]
μ_A	Natural mortality rate of mosquitoes in the aquatic stage	0.01	1/day	[26]
θ	Oviposition rate	30	1/day	[26]
δ	Mosquito larvae capacity per human	3	larvae/individual	[21]
μ_v	Mortality rate of adult mosquitoes	1/9.5	1/day	[27]
C_{hv}	The chance of a susceptible mosquito being exposed to the dengue virus from an infected human	0.35×0.4	1/day	[21] [22]
T_{ev}	Inverse of the extrinsic incubation period	1/5.9	1/day	[23]

Based on the properties of the roots of the simplified cubic equation, we obtain

$$\lambda_5 + \lambda_6 + \lambda_7 < 0, \tag{10}$$

$$\lambda_5(\lambda_6 + \lambda_7) + \lambda_6\lambda_7 > 0, \tag{11}$$

$$\lambda_5\lambda_6\lambda_7 < 0. \tag{12}$$

eq. (12) is obtained from three eigenvalues with one or three negative eigenvalues. Suppose λ_5 is negative, then $\lambda_6\lambda_7 > 0$. eq. (11) can be satisfied if $\lambda_6 + \lambda_7 < 0$. So, the result of the two conditions is $\lambda_6 < 0$ and $\lambda_7 < 0$. So, the first assumption of the Castillo-Chaves and Song Theorem is satisfied, namely that one simple zero eigenvalue and the others are negative absolute values.

In addition, the zero eigenvalue is related to the matrix **J**, which has a right eigenvector and a left eigenvector. The right eigenvector corresponding to the zero eigenvalue is obtained as follows.

$$u = \begin{bmatrix} -\dfrac{nC_{vh}\mu_h}{(p+\mu_h)^2}u_7 \\ \dfrac{nC_{vh}\mu_h}{(p+\mu_h)(T_{eh}+\mu_h)}u_7 \\ \dfrac{T_{eh}nC_{vh}\mu_h}{(\gamma_h+\mu_h)(p+\mu_h)(T_{eh}+\mu_h)}u_7 \\ 0 \\ -\dfrac{C_{hv}\,\delta\theta\omega T_{eh}\,nC_{vh}\mu_h}{(n\theta+\delta\omega+\delta\mu_A)\,\mu_v^2\,(\gamma_h+\mu_h)(p+\mu_h)(T_{eh}+\mu_h)}u_7 \\ \dfrac{C_{hv}\delta\omega T_{eh}nC_{vh}\mu_h}{(n\theta+\delta\omega+\delta\mu_A)\mu_v(T_{ev}+\mu_v)(\gamma_h+\mu_h)(p+\mu_h)(T_{eh}+\mu_h)}u_7 \\ u_7 \end{bmatrix}.$$

Since all parameters are positive and assume $u_7 > 0$, then it is obtained that $u_1 < 0, u_2 > 0, u_3 > 0, u_4 = 0, u_5 < 0$ and $u_6 > 0$. The left eigenvector corresponding to the zero eigenvalue is obtained as follows.

$$v = \begin{bmatrix} 0 \\ \dfrac{T_{eh}}{T_{eh}+\mu_h}v_3 \\ v_3 \\ 0 \\ 0 \\ \dfrac{T_{ev}nC_{vh}\mu_hT_{eh}}{\mu_v(T_{ev}+\mu_v)(p+\mu_h)(T_{eh}+\mu_h)}v_3 \\ \dfrac{nC_{vh}\mu_hT_{eh}}{\mu_v(p+\mu_h)(T_{eh}+\mu_h)}v_3 \end{bmatrix}.$$

Since all parameters are positive and assume $v_3 > 0$, it is obtained that $v_1 = v_4 = v_5 = 0, v_2 > 0, v_6 > 0$ and $v_7 > 0$. Furthermore, based on system (9), the second-order partial derivatives are obtained:

$$\begin{aligned}
\frac{\partial^2 g_1(S^*, C^*_{vh})}{\partial x_1 \partial x_6} &= \frac{\partial^2 g_1(S^*, C^*_{vh})}{\partial x_6 \partial x_1} = -nC^*_{vh}, \\
\frac{\partial^2 g_2(S^*, C^*_{vh})}{\partial x_1 \partial x_6} &= \frac{\partial^2 g_2(S^*, C^*_{vh})}{\partial x_6 \partial x_1} = nC^*_{vh}, \\
\frac{\partial^2 g_4(S^*, C^*_{vh})}{\partial x_3 \partial x_4} &= \frac{\partial^2 g_4(S^*, C^*_{vh})}{\partial x_4 \partial x_3} = -C_{hv}, \\
\frac{\partial^2 g_5(S^*, C^*_{vh})}{\partial x_3 \partial x_4} &= \frac{\partial^2 g_5(S^*, C^*_{vh})}{\partial x_4 \partial x_3} = C_{hv}, \\
\frac{\partial^2 g_1(S^*, C^*_{vh})}{\partial x_6 \partial C_{vh}} &= -\left(\frac{n\mu_h}{p+\mu_h}\right), \\
\frac{\partial^2 g_2(S^*, C^*_{vh})}{\partial x_6 \partial C_{vh}} &= \frac{n\mu_h}{p+\mu_h}
\end{aligned}$$

Next, the values of a and b obtained are as follows.

$$\begin{aligned}
a &= \sum_{k,i,j=1}^{6} v_k u_i u_j \frac{\partial^2 g_k(S^*, C^*_{vh})}{\partial x_i \partial x_j} \\
&= 2v_2u_1u_7nC^*_{vh} + 2v_6u_3u_5C_{hv} < 0, \\
b &= \sum_{k,i,j=1}^{6} v_k u_i \frac{\partial^2 g_k(S*, C^*_{vh})}{\partial x_i \partial C_{vh}} \\
&= v_2u_7\left(\frac{n\mu_h}{p+\mu_h}\right) > 0
\end{aligned}$$

The obtained values of a and b correspond to one of the Castillo-Chaves and Song Theorem cases. This shows that when the bifurcation parameter C_{vh} changes from $C_{vh} < C^*_{vh}(\mathcal{R}_0 < 1)$ to $C_{vh} > C^*_{vh}(\mathcal{R}_0 > 1)$, there is a change in the endemic fixed point S^{**}, namely from negative to positive and locally asymptotically stable. ☐

3.5. Parameter Determination

The parameter values used in the sensitivity analysis and numerical simulations were obtained from various sources and assumptions, with a focus on the *Aedes aegypti* mosquito species. These parameters are listed in Table 1.

The human birth rate μ_h is calculated based on the crude birth rate [28], which shows that there are approximately 0.0286 births per 1,000 inhabitants per day in Indonesia in 2023. This estimate refers to the number of live births of 2,871,646 people and the mid-year population of 278,696.2 thousand people.

A systematic review found that female *Aedes aegypti* mosquitoes can bite humans between 0.35 and 0.41 times per day, depending on geographic location and environmental conditions. The time between a person being infected with the dengue virus (through the bite of an infected mosquito) and the appearance of the first clinical symptoms is the intrinsic incubation period (IIP). Meanwhile, the extrinsic incubation period (EIP) is the time required for the dengue virus to develop in the mosquito's body, from when the mosquito takes a blood meal from an infected human until it becomes capable of transmitting the virus to another human [29]. Based on research results from Chan and Johansson in 2012 [23], the estimated average IIP is 5.9 days, with 95% of the IIP estimated to occur between days 3 and 10. The 95% EIP lasts between 5 and 33 days, with an average of 15 days.

The rate of change of mosquitoes from egg to adult is calculated as the inverse of the number of days required to reach that phase [30]. The length of time from egg to adult *Aedes aegypti* mosquito is highly dependent on environmental temperature and food availability. However, in general, the development time of *Aedes aegypti* from egg to adult is around 7-11 days [25]. The mortality rate of mosquitoes can be calculated as the inverse of the mosquito's life expectancy [31]. Based on research by Agustin *et al.* in 2017 [27] regarding the life cycle of *Aedes aegypti* in water hyacinth air-soaked media, adult mosquitoes can live a minimum of 3 days and a maximum of 16 days with an average life span of 9.5 days.

3.6. Sensitivity Analysis

Sensitivity index calculations are performed to determine the degree to which a parameter influences system dynamics [32]. The following shows one of the results of a calculation of the sensitivity index for the parameter δ against the basic reproduction number $\mathcal{R}_0$.

$$\gamma_{\delta}^{\mathcal{R}_0} = \frac{\partial \mathcal{R}_0}{\partial \delta} \times \frac{\delta}{\mathcal{R}_0} = \frac{n\theta}{2(n\theta + \delta(\mu_A + \omega))} \tag{13}$$

If eq. (13) is evaluated using the parameter values in Table 1, the index value obtained is 0.495005. This sensitivity index indicates the magnitude of the relative change in the basic reproduction number resulting from variations in related parameters. The following presents the sensitivity index for each parameter in the model.

Table 2. Sensitivity index

Parameter	Sensitivity Index
μ_v	-1.19156
C_{vh}	0.5
C_{hv}	0.5
ω	0.4955
δ	0.495005
γ_h	-0.416597
μ_h	-0.228832
T_{ev}	0.191558
T_{eh}	0.150105
θ	0.00499505
p	-0.00467613
μ_A	-0.000495005

Based on Table 2, the positive sensitivity indices are $C_{vh}, C_{hv}, \omega, \delta, T_{ev}, T_{eh}$ and θ, meaning that an increase in the value of these parameters increases the value of R_0, and vice versa. Meanwhile, the sensitivity indices with negative values are $\mu_v, \gamma_h, \mu_h, p$ and μ_A, meaning that an increase in the value of these parameters results in a decrease in the value of $\mathcal{R}_0$, and vice versa.

The sensitivity analysis results show that the parameter that most dominantly influences changes in the basic reproduction number ($\mathcal{R}_0$) is the mortality rate of adult mosquitoes (μ_v). This parameter has a negative sensitivity index, indicating that an increase in μ_v will decrease the number of infections, while a decrease in μ_v will increase it. The same is true for the natural mortality rate of aquatic mosquitoes (μ_A), which also has a negative sensitivity index. This means that an increase in μ_A can reduce the population of aquatic mosquitoes, thereby reducing the number of adult mosquitoes and the potential for virus transmission. Interventions that can be implemented to increase mosquito larval mortality include the use of biolarvicides and employing natural predators like larva-eating fish. For adult mosquitoes, this can be achieved through fumigation to kill mosquitoes flying or landing in the surrounding environment.

Several other parameters in the aquatic phase that have a linear effect on the basic reproduction number are the rate of transformation of aquatic mosquitoes into adults (ω) and the capacity of mosquito larvae per person (δ). Reducing either of these parameters, while holding the others constant, will reduce the basic reproduction number and the rate of dengue transmission. This suggests that controlling the aquatic phase is necessary, for example, through the use of insecticides or larvicides with growth-inhibiting effects, which disrupt larval metamorphosis and prevent them from becoming adults. Furthermore, effective environmental management is crucial to reducing larval breeding habitats. These findings align with research by Kleden et al. (2023), which demonstrated that household environmental factors and community behaviors, including the habit of not emptying water reservoirs and a lack of participation in ecological cleanliness activities, significantly increase the risk of dengue fever [33]. Therefore, interventions in the aquatic phase through ecological management and vector control are key strategies for suppressing mosquito populations and reducing the rate of disease transmission.

The sensitivity analysis results show that the vaccination rate (p) and the recovery rate of infected individuals (γ_h) both have negative sensitivity indices to the basic reproduction number ($\mathcal{R}_0$). This negative sensitivity index value indicates that an increase in both parameters contributes to a decrease in the value of $\mathcal{R}_0$, resulting in a lower disease transmission rate. This finding aligns with research conducted by Blante et al. (2024), which shows that an increase in the recovery rate can reduce the value of $\mathcal{R}_0$ in a dengue transmission model [34]. In addition, these results are also consistent with Kamalia and Aldila (2025), who stated that vaccine effectiveness plays a crucial role in suppressing disease spread by reducing the basic reproduction number [35]. Thus, increasing the vaccination rate can directly reduce the potential for transmission, while increasing the recovery rate of individuals accelerates the population's recovery from infection. Furthermore, increasing the recovery rate of the community, due to natural immunity, vaccination, or the effectiveness of treatment, can accelerate the recovery of the general population from a dengue outbreak.

4. Numerical Results

4.1. *Bifurcation Simulation*

The proof of Theorem 2 it is found that there is a bifurcation in system (2), namely a change in the qualitative structure of the system when the bifurcation parameter passes its critical value [36]. To support and compare the results of the theoretical analysis, a numerical simulation was performed using the parameter values listed in Table 1. This simulation aims to describe the relationship between the basic reproduction number ($\mathcal{R}_0$) on the x-axis and the proportion of the human population infected in endemic conditions (i_h^*) on the y-axis.

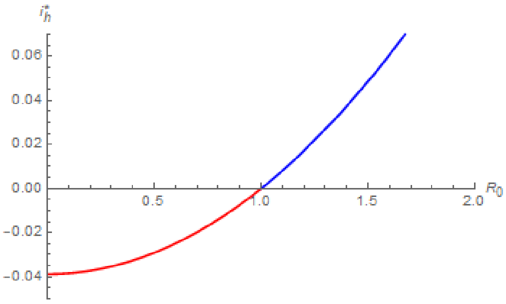
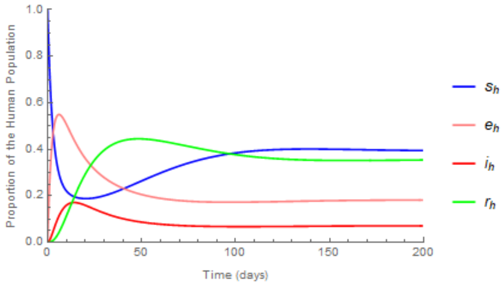
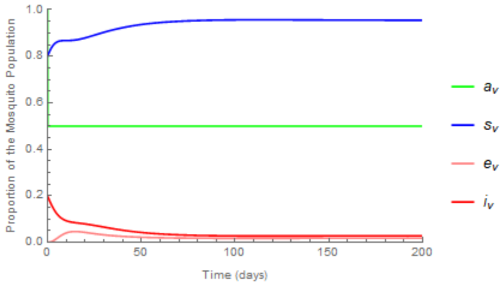


Figure 3. Bifurcation Curve



(a) Human population proportion dynamics



(b) Mosquito population proportion dynamics

Figure 4. Population proportion dynamics of humans and mosquitoes

Figure 3 shows that for $\mathcal{R}_0 < 1$, the i_h^* value is negative and therefore biologically meaningless. However, when $\mathcal{R}_0 > 1$, the i_h^* value becomes positive and increases with increasing $\mathcal{R}_0$, indicating that the disease can persist in the population. These changes indicate the presence of a transcritical bifurcation, where the system transitions from a disease-free state to a stable endemic state when the parameter value passes the critical point $\mathcal{R}_0 = 1$.

4.2. *Population Dynamics Simulation*

In this section, a numerical simulation is performed to illustrate the dynamics of changes in the proportions of each population until a stable condition is reached. The simulation uses the parameter values listed in Table 1, with the basic reproduction number obtained greater than one, namely $\mathcal{R}_0 = 1.67793$. In this simulation, it is assumed that at the initial time ($t = 0$) there are no infected human individuals, while 20% of the mosquito population has been infected with the dengue virus. In addition, the initial value of the proportion of the mosquito population in the aquatic phase is set at $a_v(0) = 1$, which indicates that at the start of the simulation, the mosquito population in the aquatic phase is at its maximum capacity relative to its environment.

Based on Figure 4a, it can be seen that the proportion of the susceptible human population decreased at the beginning of the simulation due to dengue virus infection from infected mosquitoes. This condition caused an increase in the proportion of humans in the exposed and infected phases at the beginning of the simulation. Over time, the proportions of the exposed and infected human populations decreased towards their respective equilibrium points, namely $e_h^* = 0.181098$ and $i_h^* = 0.0704152$. As a result, the proportions of the susceptible and recovered human populations increased again until they reached a stable state at points $s_h^* = 0.393052$ and $r_h^* = 0.355435$. Meanwhile, based on Figure 4b, the proportion of mosquitoes in each sub-population is also approaching a non-zero value, which means towards the respective endemic equilibrium point of $(a_v^*, s_v^*, e_v^*, i_v^*) = (0.499161, 0.954823, 0.0173082, 0.0278691)$. This indicates that although the proportion of infected mosquitoes has decreased, the infection has not entirely disappeared from the population.

Thus, the results of this simulation are consistent with Theorem 2, which states that when the basic reproduction number, $\mathcal{R}_0$, is greater than 1, the system will reach an endemic equilibrium, a condition in which the disease persists in the population for an extended period with a stable infection rate.

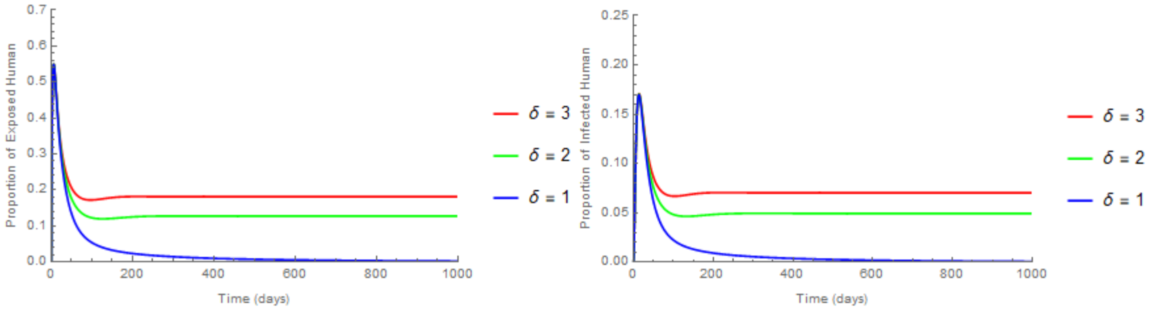
4.3. *Simulation of the Effects of Changing Parameter δ*

In this section, the parameter value δ, representing the capacity of mosquito larvae per human, is varied, with the changes in value shown in Table 3.

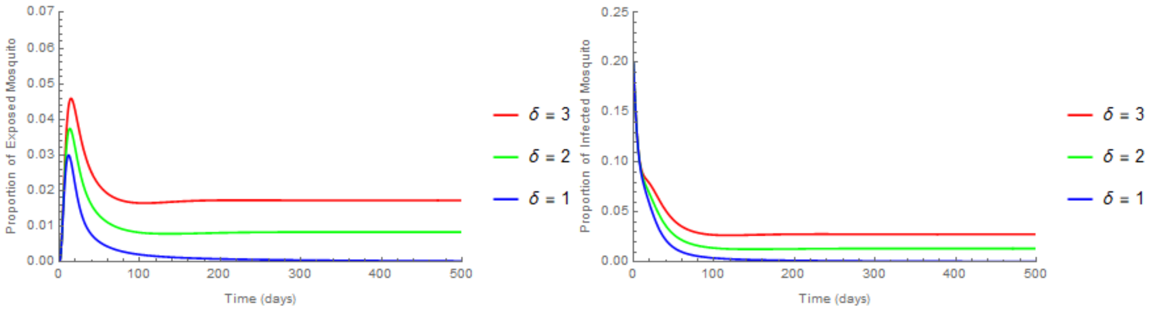
Table 3. Parameter value change δ

Parameter Value δ	Condition $\mathcal{R}_0$
3	1.67793
2	1.37041
1	0.969296

Table 3 shows the effect of changing the parameter value of δ on the basic reproduction number $\mathcal{R}_0$. It can be seen that when $\delta = 3$, $\mathcal{R}_0 > 1$, indicating that the disease can spread and persist in the population. When the value of δ is reduced to 2, the basic



(a) Exposed humans **(b)** Infected humans



(c) Exposed mosquitoes **(d)** Infected mosquitoes

Figure 5. Population proportion dynamics of exposed humans, infected humans, exposed mosquitoes, and infected mosquitoes due to changes in parameter values δ

reproduction number decreases, but still indicates the potential for disease spread. Furthermore, when δ is reduced to 1, the value of $\mathcal{R}_0$ becomes less than one, i.e., $\mathcal{R}_0 < 1$, indicating that the disease cannot persist and will eventually disappear from the population. Next, simulations were performed on exposed and infected sub-population within the human and mosquito populations to further analyze the effect of variations in the parameter value δ on the dynamics of disease spread.

Figure 5 illustrates the impact of changes in the parameter value δ on the dynamics of the proportions of human and mosquito populations in four sub-population: exposed humans, infected humans, exposed mosquitoes, and infected mosquitoes. In all sub-graphs, it can be seen that increasing the value of δ causes an increase in the proportion of exposed and infected individuals, both in the human and mosquito populations. When $\delta = 3$, the proportion of exposed and infected is higher than when $\delta = 2$ and $\delta = 1$. Conversely, at smaller values of δ, the system reaches a stable state with a lower proportion of infections. Even in this model, when the parameter value δ is reduced to 1, meaning that each human only supports about one mosquito larva, the mosquito population reaches a disease-free state on the 300^{th} day. In contrast, the human population reaches a disease-free state on the 600^{th} day. Biologically, these results indicate that the higher the larval capacity per human (the higher δ), the greater the potential for growth the mosquito population, thus increasing the risk of dengue transmission. Therefore, the spread of dengue fever can be suppressed by reducing the capacity of larvae, for example, by effective environmental management to reduce the number of adult mosquitoes.

The simulation results are consistent with the analytical results, i.e., when the value of $\mathcal{R}_0 > 1$, the population will be in an endemic condition. At the same time, when $\mathcal{R}_0 < 1$, the population will be free of disease with no exposed or infected sub-population.

5. Conclusion

This study formulates and analyzes a mathematical model of dengue fever transmission using the SEIR-ASEI model approach. The model includes the SEIR compartment for the human population and the ASEI compartment for the mosquito population, with *Aedes aegypti* as the vector, considering the logistic growth factor in the aquatic sub-population. The analysis results show that the model has two equilibrium points, namely the disease-free and endemic equilibrium, whose local stability depends on the value of the basic reproduction number $\mathcal{R}_0$. Stability analysis shows that the disease-free equilibrium point is locally asymptotically stable when $\mathcal{R}_0 < 1$, indicating that disease elimination is theoretically possible. Conversely, when $\mathcal{R}_0 > 1$, the endemic equilibrium point becomes locally asymptotically stable, indicating continued disease transmission in the population.

The results of the bifurcation simulation also show that changes in the $\mathcal{R}_0$ value trigger the transition from disease-free to endemic conditions. Meanwhile, the results of the sensitivity analysis indicate that the adult mosquito mortality rate (μ_v) is the most influential parameter on the basic reproduction number, with an inverse relationship with $\mathcal{R}_0$. This finding confirms that controlling adult mosquito mortality is an essential strategy. However, interventions in the aquatic phase are also necessary because several parameters in this phase, including the rate of transformation of aquatic mosquitoes into adults (ω) and the capacity of mosquito larvae per human (δ), have a linear effect on the basic reproduction number. Thus, mosquito larval control and environmental management play an essential role in reducing the adult mosquito population and suppressing the $\mathcal{R}_0$ value, thereby reducing the risk of dengue fever spread in an area.

Author Contributions. **Aprianti, E.:** Conceptualization, Methodology, Software, Validation, Formal Analysis, Investigation, Writing - Original Draft, Visualization, and Supervision. **Sonia, S.:** Data Curation, Writing - Review & Editing, and Visualization.

Acknowledgement. The author would like to thank the editor and reviewers for attention and valuable input that helped improve this article. The author also thanks the institution that provided support, facilities, and a conducive academic environment during the research and writing process.

Funding. This research received no external funding and was supported through internal institutional resources.

Conflict of interest. The authors state that there are no conflicts of interest related to this work.

Data availability. No datasets were collected or analyzed in this study.

Abbreviations.

SEIR-ASEI	:	Susceptible–Exposed–Infectious–Recovered (human) model combined with Aquatic–Susceptible–Exposed –Infectious (vector) model
DENV	:	Dengue Virus
IIP	:	Intrinsic Incubation Period
EIP	:	Extrinsic Incubation Period

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