BAREKENG: Journal of Mathematics and Its Applications
September 2023 Volume 17 Issue 3 Page 1641–1652
P-ISSN: 1978-7227 E-ISSN: 2615-3017
https://doi.org/10.30598/barekengvol17iss3pp1641-1652

SEIR MODEL SIMULATION WITH PART OF INFECTED MOSQUITO EGGS

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ABSTRACT

Dengue hemorrhagic fever (DHF) is an acute febrile disease caused by the dengue virus, which is transmitted by various species of Aedes mosquitoes. The SEIR model is a mathematical model for studying the spread of dengue fever. In this model, it is assumed that some mosquito eggs have been infected because infected mosquitoes can transmit the virus to their eggs. The main vector of this disease is the Aedes albopictus mosquito. Analysis was carried out to assess the stability of the equilibrium point, and numerical simulations were carried out to see changes in population numbers due to changes in parameter values. A disease-free equilibrium (DFE) point, which is stable given the basic reproductive number $\mathfrak{R}_0 < 1$. *An endemic point whose stability is guaranteed if the value* $\mathfrak{R}_0 > 1$. *The numerical simulations show that an increasing mosquito mortality rate decreases the number of exposed, susceptible humans. Furthermore, an increase in the average bite of an infected mosquito will increase the number of exposed, susceptible humans. For the mosquito population, increasing mosquitoes' mortality rate will decrease the number of exposed, susceptible mosquitoes. Finally, an increase in the average bite of an infected mosquito will increase the number of exposed, susceptible mosquitoes.*

Article History:

Received: 29th April 2023
Revised: 10th August 2023
Accepted: 18th August 2023

Keywords:

Dengue hemorrhagic fever;
Aedes albopictus;
SEIR model;
Equilibrium point;
Stability analysis

How to cite this article:

J. U. L. Mangobi., "SEIR MODEL SIMULATION WITH PART OF INFECTED MOSQUITO EGGS," *BAREKENG: J. Math. & App.*, vol. 17, iss. 3, pp. 1641-1652, September, 2023.

Journal homepage: *https://ojs3.unpatti.ac.id/index.php/barekeng/*
Journal e-mail: *barekeng.math@yahoo.com; barekeng.journal@mail.unpatti.ac.id*

Research Article · Open Access

1. INTRODUCTION

Dengue Hemorrhagic Fever (DHF) is an acute febrile illness caused by the dengue virus. This virus has four virus serotypes, namely Dengue I–IV [1]–[3]. Dengue virus is transmitted by various species of Aedes mosquitoes. This mosquito is a very effective vector due to the association of mosquitoes with human life. Also, biting and blood sucking behavior in some people by an adult female mosquito. Thus, it is so easy for this disease to become an epidemic in the human population.

Dengue fever is common in Indonesia. There have been four recorded extraordinary events, namely in 1988, 1998, 2004 and 2006. The WHO estimates that around 2.5 billion people worldwide are at risk of dengue [4]. With these facts, the DHF epidemic control program is a top priority for WHO and the Indonesian Ministry of Health.

Since 1962, the prevention of dengue epidemics has focused on the eradication of mosquitoes carrying the dengue virus. However, we understand that efforts to control the dengue epidemic in Indonesia are still far from satisfactory. Various obstacles such as low amount of government budget for epidemic control, limited infrastructure and lack of data and information are the major causes for our delay in preventing and controlling this epidemic.

Mathematical modeling can help understand and identify the relationship between the spread of DHF and various epidemiological parameters. Among the mathematical models are the Susceptible-Infected-Recovered (SIR) model and the Susceptible-Exposed-Infected-Recovered (SEIR) model. This article discusses the SEIR model which refers to the study by Erickson *et al* [5]–[7].

This model is a modification of the SIR model introduced by Derouich *et al* [8]. The modification is done by adding the Exposed step. This addition was made because the dengue virus requires an intrinsic and extrinsic incubation period before spreading [9]. The main vector in this model is the Aedes albopictus mosquito, due to the large number of dengue cases caused by this mosquito [10]. In addition, Aedes albopictus mosquitoes have greater coverage and are more difficult to control [11], [12]. In the SEIR model, stability analysis and simulation were performed with functional programming using Mathematica 8.0 software (Wolfram Research, Inc, Champaign, IL).

2. RESEARCH METHODS

This research modifies the SEIR model introduced by Erickson *et al* into a new SEIR model by adding the β_e parameter to the birth factor of infected mosquitoes. The new parameter β_e, represents the probability of transmission of the virus from the female mosquito to her eggs. The SEIR model by Erickson et al previously assumed that all mosquito eggs were healthy. According to the research, infected mosquitoes can transmit the virus to their eggs, so a modification of the model is necessary to obtain a better model. This new model assumes that some mosquito eggs are already infected.

The state of the mosquito population has changed due to the assumption that some of their eggs are infected. The number of infected mosquito populations will increase due to the birth of infected mosquitoes. This has an impact on reducing the number of susceptible mosquito populations because some of the mosquito eggs have been infected. Meanwhile, the human population in the model is still the same as in the previous model.

In this model, the human population N_h is divided into four subpopulations, namely susceptible humans S_h, exposed humans E_h, infected humans I_h, and recovered humans R_h, while the mosquito population N_v is divided into three subpopulations, namely susceptible mosquitoes S_v, exposed mosquitoes E_v, and infected mosquitoes I_v. The assumptions used are that the total mosquito population is constant while the total human population is not constant and that the human and mosquito populations are closed populations.

The transmission of the virus from mosquitoes to humans is by bite when the virus is found in the salivary glands of the mosquito. After that, the virus needs 4-6 days, which is an intrinsic incubation period before causing disease. During this incubation period, susceptible humans are considered open to infection by the virus. Thus, these susceptible humans are then grouped into exposed human subpopulations.

Transmission of the virus from humans to mosquitoes can only occur if a susceptible mosquito bites an infected human who is suffering from viremia, which is a medical condition where the dengue virus is in human blood. This condition lasts from 2 days before the fever until 5 days after the fever. Moreover, the

virus requires 8-10 days, which shows an extrinsic incubation period before causing disease. During this incubation period, susceptible mosquitoes are considered to have been exposed to virus infection. The mosquitoes were then grouped into an exposed mosquito subpopulation.

Schematically, the pattern of spread of DHF (dengue virus) assuming that some of the mosquito eggs are infected can be depicted in the following compartment diagram.

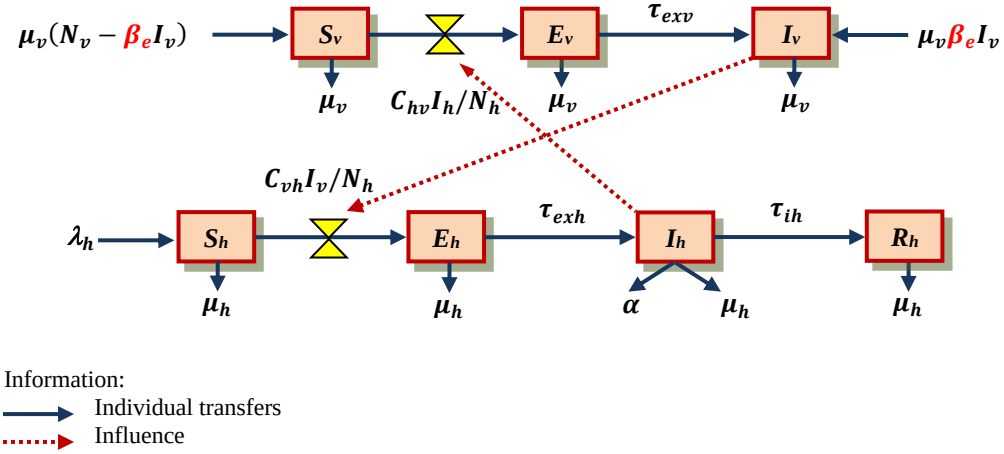


Figure 1. The SEIR model diagram assumes that some of the mosquito eggs are infected

The meaning of the compartment diagram (**Figure 1**) is:

1. The growth rate of vulnerable humans takes into account the factors of birth, death and migration proportion of susceptible humans to exposed humans, writes:

$$\frac{dS_h}{dt} = \lambda_h N_h - \left(\frac{C_{vh} I_v}{N_h} + \mu_h\right) S_h = \lambda N_h - \left(\frac{C_{vh} I_v}{N_h} + \mu_h\right) S_h$$

   where taken $\lambda = \lambda_h$. The proportion of movement of susceptible humans to exposed humans is influenced by the probability of contact between infected mosquitoes and susceptible humans C_{vh}. This probability value is the multiplication of the probability of virus transmission from infected mosquitoes to susceptible humans p_{vh} by the average number of infected mosquito bites b_i. So, $C_{vh} = p_{vh} b_i$.

2. The growth rate of exposed humans takes into account the mortality factor, the proportion of displacement of susceptible humans to exposed humans and the proportion of displacement of exposed humans to infected humans, writes:

$$\frac{dE_h}{dt} = \frac{C_{vh} I_v}{N_h} S_h - (\tau_{exh} + \mu_h) E_h.$$

3. The growth rate of infected people takes into account the mortality factor, both natural deaths and deaths due to DHF, the proportion of people exposed to infected people and the proportion of infected people moving towards recovered people, written:

$$\frac{dI_h}{dt} = \tau_{exh} E_h - (\tau_{ih} + \alpha + \mu_h) I_h.$$

4. The growth rate of recovered humans takes into account the mortality factor and the proportion of infected humans moving to recovered humans, writes:

$$\frac{dR_h}{dt} = \tau_{ih} I_h - \mu_h R_h.$$

5. The growth rate of susceptible mosquitoes takes into account the factors of birth, death and the transfer ratio of susceptible mosquitoes to exposed mosquitoes, writes:

$$\frac{dS_v}{dt} = \mu_v(N_v - \beta_e I_v) - \left(\frac{C_{hv} I_h}{N_h} + \mu_v\right) S_v$$

   The proportion of movement of susceptible mosquitoes to exposed mosquitoes is influenced by the probability of contact between susceptible mosquitoes and infected humans C_{hv}. This probability value

is the multiplication of the probability of virus transmission from infected humans to susceptible mosquitoes p_{hv} by the average bite rate of susceptible mosquitoes b_s. So, $C_{hv} = p_{hv}b_s$.

6. The growth rate of exposed mosquitoes takes into account the mortality factor, the proportion of movement is the proportion of transfer of susceptible mosquitoes to exposed mosquitoes and the proportion of movement of mosquitoes exposed to infected mosquitoes, writes:

$$\frac{dE_v}{dt} = \frac{C_{hv}I_h}{N_h}S_v - (\tau_{exv} + \mu_v)E_v.$$

7. The growth rate of infected mosquitoes takes into account the mortality factor and the proportion of mosquito movement exposed to infected mosquitoes, writes:

$$\frac{dI_v}{dt} = \mu_v\beta_e I_v + \tau_{exv}E_v - \mu_v I_v.$$

Based on the description above, the SEIR model can be stated as follows:

Human population

$$\begin{cases} \frac{dS_h}{dt} = \lambda N_h - \left(\frac{C_{vh}I_v}{N_h} + \mu_h\right)S_h \\ \frac{dE_h}{dt} = \frac{C_{vh}I_v}{N_h}S_h - (\tau_{exh} + \mu_h)E_h \\ \frac{dI_h}{dt} = \tau_{exh}E_h - (\tau_{ih} + \alpha + \mu_h)I_h \\ \frac{dR_h}{dt} = \tau_{ih}I_h - \mu_h R_h \end{cases} \quad (1)$$

Mosquito population

$$\begin{cases} \frac{dS_v}{dt} = \mu_v(N_v - \beta_e I_v) - \left(\frac{C_{hv}I_h}{N_h} + \mu_v\right)S_v \\ \frac{dE_v}{dt} = \frac{C_{hv}I_h}{N_h}S_v - (\tau_{exv} + \mu_v)E_v \\ \frac{dI_v}{dt} = \mu_v\beta_e I_v + \tau_{exv}E_v - \mu_v I_v \end{cases} \quad (2)$$

conditionally

$$S_h + E_h + I_h + R_h = N_h \text{ and } S_v + E_v + I_v = N_v \quad (3)$$

as well as

N_h : total human population
N_v : total mosquito population
λ : human birth rate
μ_v : mosquito mortality rate
β_e : probability of transmission of the virus from the female mosquito to her eggs
μ_h : natural human mortality rate
α : human mortality rate due to DHF
τ_{exh} : proportion of exposed humans moving towards infected humans
τ_{exv} : proportion of mosquitoes exposed compared to infected mosquitoes
τ_{ih} : proportion of infected humans moving towards cured humans
C_{hv} : probability of contact between susceptible mosquitoes and infected humans
C_{vh} : probability of contact between infected mosquitoes and susceptible humans

Moreover, the **Equation (1)** and **Equation (2)** and **Equation (3)** can be simplified for example

$$S^h = \frac{S_h}{N_h}, E^h = \frac{E_h}{N_h}, I^h = \frac{I_h}{N_h}, R^h = \frac{R_h}{N_h}, S^v = \frac{S_v}{N_v}, E^v = \frac{E_v}{N_v} \text{ and } I^v = \frac{I_v}{N_v},$$

and also in this model assuming the value is $C_{hv} = C_{vh} = c$, then the system can to write:

$$\begin{cases} \frac{dS^h}{dt} = \lambda - (ncI^v + \mu_h)S^h \\ \frac{dE^h}{dt} = ncI^v S^h - (\tau_{exh} + \mu_h)E^h \\ \frac{dI^h}{dt} = \tau_{exh}E^h - (\tau_{ih} + \alpha + \mu_h)I^h \\ \frac{dE^v}{dt} = cI^h(1 - E^v - I^v) - (\tau_{exv} + \mu_v)E^v \\ \frac{dI^v}{dt} = \tau_{exv}E^v - \mu_v(1 - \beta_e)I^v \end{cases} \quad (4)$$

with $n = \frac{N_v}{N_h}$ and set conditions

$$S^h + E^h + I^h + R^h = 1 \text{ and } S^v + E^v + I^v = 1 \quad (5)$$

3. RESULTS AND DISCUSSION

3.1 The Equilibrium Point and Stability

In this section, the equilibrium point of the **Equation (4)** is sought in a region that has biological significance, called Ω, with $\Omega = \{(S^h, E^h, I^h, E^v, I^v) \in \mathbb{R}_+^5 | S^h + E^h + I^h \leq 1, E^v + I^v \leq 1\}$. This point is obtained by solving **Equation (4)** when $\frac{dS^h}{dt} = \frac{dE^h}{dt} = \frac{dI^h}{dt} = \frac{dE^v}{dt} = \frac{dI^v}{dt} = 0$. Using Mathematica software, a disease-free equilibrium is obtained

$$T_1(S^h, E^h, I^h, E^v, I^v) = T_1\left(\frac{\lambda}{\mu_h}, 0, 0, 0, 0\right) \quad (6)$$

and endemic equilibrium

$$T_2(S_*^h, E_*^h, I_*^h, E_*^v, I_*^v) \quad (7)$$

with

$S_*^h = \{(\mu_v + \tau_{exv})[c\lambda\tau_{exh} + \mu_v(\mu_h + \tau_{exh})(\alpha + \mu_h + \tau_{ih})]\}/\{c\tau_{exh}[cn\tau_{exv} + \mu_h(\mu_v + \tau_{exv})]\}$

$E_*^h = -[-c^2n\lambda\tau_{exh}\tau_{exv} + \mu_h^3\mu_v(\mu_v + \tau_{exv}) + \alpha\mu_h\mu_v(\mu_h + \tau_{exh})(\mu_v + \tau_{exv}) + \mu_h\mu_v\tau_{exh}(\mu_v + \tau_{exv})\tau_{ih} + \mu_h^2\mu_v(\mu_v + \tau_{exv})(\tau_{exh} + \tau_{ih})]/\{c\tau_{exh}(\mu_h + \tau_{exh})[cn\tau_{exv} + \mu_h(\mu_v + \tau_{exv})]\}$

$I_*^h = (-\mu_h\mu_v(\mu_v + \tau_{exv}) + \{(c^2n\lambda\tau_{exh}\tau_{exv})/[(\mu_h + \tau_{exh})(\alpha + \mu_h + \tau_{ih})]\})/\{c[cn\tau_{exv} + \mu_h(\mu_v + \tau_{exv})]\}$

$E_*^v = \{\mu_v[-\mu_h(\alpha + \mu_h)\mu_v^2(\mu_h + \tau_{exh}) - [-c^2n\lambda\tau_{exh} + \mu_h(\alpha + \mu_h)\mu_v(\mu_h + \tau_{exh})]\tau_{exv} - \mu_h\mu_v(\mu_h + \tau_{exh})(\mu_v + \tau_{exv})\tau_{ih}]\}/\{cn\tau_{exv}(\mu_v + \tau_{exv})[c\lambda\tau_{exh} + \mu_v(\mu_h + \tau_{exh})(\alpha + \mu_h + \tau_{ih})]\}$,

$I_*^v = 1/n((-\mu_h/c) + \{\lambda\tau_{exh}[cn\tau_{exv} + \mu_h(\mu_v + \tau_{exv})]\})/\{(\mu_v + \tau_{exv})[c\lambda\tau_{exh} + \mu_v(\mu_h + \tau_{exh})(\alpha + \mu_h + \tau_{ih})]\}$.

The disease-free equilibrium T_1 will be stable when $\Re_0 = \sqrt{\xi} < 1$ for $0 \leq \xi < 1$, otherwise T_1 is unstable when $\Re_0 = \sqrt{\xi} > 1$. The endemic equilibrium T_2 will be stable when $\Re_0 = \sqrt{\xi} > 1$, while T_2 is unstable when $\Re_0 = \sqrt{\xi} < 1$ for $0 \leq \xi < 1$. The $\Re_0$ symbol in this case is called the basic reproduction number. This number is a measure of the potential spread of the disease in a population.

The basic reproduction number is defined as the expected value of the number of susceptible populations that become infected during the infection period. The basic reproduction number is determined from the nonnegative eigenvalue with the largest modulus in the next generation matrix **[13]–[19]**. This matrix is constructed from sub-populations that cause infection only.

In this study, the basic formula for the reproduction number is given by

$$\Re_0 = \sqrt{\xi} = \frac{c\sqrt{n}\sqrt{\lambda}\sqrt{\tau_{exh}}\sqrt{\tau_{exv}}}{\sqrt{(1 - \beta_e)\mu_h\mu_v(\mu_h + \tau_{exh})(\mu_v + \tau_{exv})(\alpha + \mu_h + \tau_{ih})}}$$

with

$$\xi = \frac{c^2 n\lambda\tau_{exh}\tau_{exv}}{(1-\beta_e)\mu_h\mu_v(\mu_h+\tau_{exh})(\mu_v+\tau_{exv})(\alpha+\mu_h+\tau_{ih})}$$

and the next generation matrix $K = FV^{-1}$ is given by

$$K = \begin{pmatrix} 0 & \frac{cn\lambda\tau_{\text{exv}}}{(1-\beta_e)\mu_h\mu_v(\mu_v+\tau_{\text{exv}})} & 0 & \frac{cn\lambda}{(1-\beta_e)\mu_h\mu_v} \\ \frac{c(\mu_v\tau_{\text{exh}}+\tau_{\text{exh}}\tau_{\text{exv}})}{(\mu_h+\tau_{\text{exh}})(\mu_v+\tau_{\text{exv}})(\alpha+\mu_h+\tau_{\text{ih}})} & 0 & \frac{c}{\alpha+\mu_h+\tau_{\text{ih}}} & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}$$

with

$$F = \begin{pmatrix} 0 & 0 & 0 & \frac{\lambda}{\mu_h} \\ 0 & 0 & c & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix} \text{ dan } V = \begin{pmatrix} \tau_{exh}+\mu_h & 0 & 0 & 0 \\ 0 & \tau_{exv}+\mu_v & 0 & 0 \\ -\tau_{exh} & 0 & \tau_{ih}+\alpha+\mu_h & 0 \\ 0 & -\tau_{exv} & 0 & \mu_v(1-\beta_e) \end{pmatrix}.$$

3.2 Simulation of Population Dynamics of Dengue Virus Transmission

To analyze population dynamics, modifications were made to the mosquito mortality rate μ_v and the average number of bites of infected mosquitoes b_i. These two parameters were chosen because they were considered influential in overcoming the epidemic. The μ_v value was taken at [0.01, 0.09] with a step of 0.01, while the b_i value was taken at [0.25, 0.60] with a step of 0.01**[20]**–**[23]**. Other parameter values can be viewed in **Table 1** below.

Table 1. Definition and Values Of The Parameters of the SEIR Model In Numerical Simulation

Parameter	Notasi	Nilai
The rate of human births per day	λ	$2{,}244 \times 10^{-5}$
The probability of transmission of the virus from infected mosquitoes to humans per day	p_{vh}	4×10^{-1}
The rate of human deaths due to dengue per day	α	3×10^{-3}
The rate of natural human deaths per day	μ_h	$3{,}571 \times 10^{-5}$
Proportion of human movements exposed to infected humans per day	τ_{exh}	10^{-1}
Proportion of mosquitoes exposed to infected mosquitoes per day	τ_{exv}	$1{,}111 \times 10^{-1}$
The proportion of infected humans transferred to recovered humans per day	τ_{ih}	$2{,}5 \times 10^{-1}$
The probability of transmission of the virus from infected mosquitoes to their eggs	β_e	3×10^{-1}

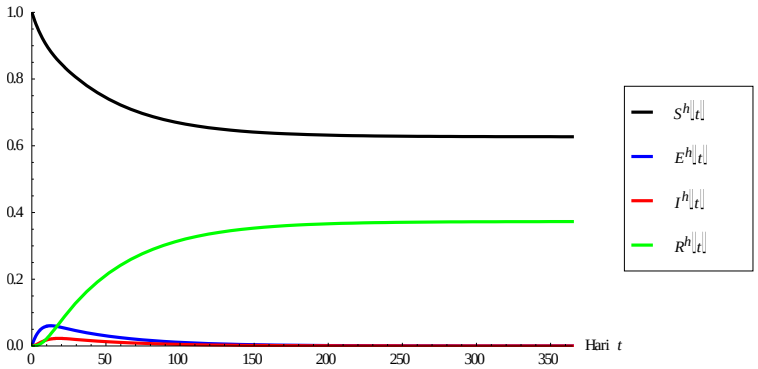
***Data source**:* Erickson *et al* and Derouich *et al*.

Figure 2 below shows the stability of each subpopulation, both in the human population and in the mosquito population, for the conditions $\Re_0 < 1$. Based on the values of the parameters in Table 1 and taking the values μ_v and b_i at predetermined intervals, the image of the population dynamics below is obtained for the values $\mu_v = 0{,}07$ and $b_i = 0{,}3$ with the value $\Re_0 = 0{,}67$.

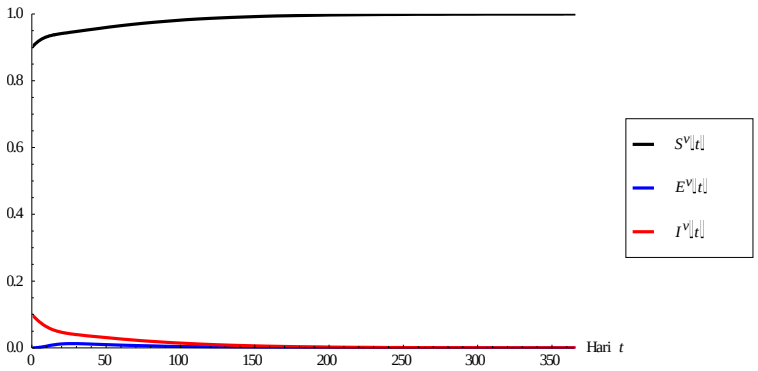
Figure 2a shows that the number of susceptible human subpopulations S^h after being infected with the virus, since the start of the simulation decreased until it stabilized at $S^h = 0{,}593$. In contrast, what happened to the exposed E^h and infected I^h human subpopulations, first increased and then decreased until it stabilized at $E^h = 0$ and $I^h = 0$. In the recovered human subpopulation R^h, since the start of the simulation, it increased until it stabilized at $R^h = 1 - \left(S^h + E^h + I^h\right) = 0{,}407$.

In **Figure 2b**, the number of exposed mosquito subpopulations E^v initially increased and then decreased until it stabilized at $E^v = 0$. Contrary to what happened to the subpopulation of infected mosquitoes I^v, since the start of the simulation, it decreased until it stabilized at $I^v = 0$. In the susceptible mosquito subpopulation S^v, it increased until it stabilized at $S^v = 1 - (E^v + I^v) = 1$.

Thus, we can say that the number of each subpopulation is stable at a disease-free equilibrium $T_1\left(S^h, E^h, I^h, E^v, I^v\right) = T_1(\lambda/\mu_h, 0, 0, 0, 0)$ with $\lambda/\mu_h = 0{,}628$. This suggests that the human subpopulation is exposed and infected and that mosquitoes are exposed and infected towards zero.



(*a*)



(*b*)

Figure 2. Dynamics of the human population (*a*) and the mosquito population (*b*) as a function of time t for the conditions $\mathfrak{R}_0 < 1$

In addition, simulations were carried out on human and mosquito populations by modifying the values of the parameters μ_v and b_i. Taking the values of these two parameters satisfies the condition $\mathfrak{R}_0 < 1$, so they can be simulated for several different conditions as shown in **Table 2**, **Figure 3** and **Figure 4**.

Table 2. Simulation for conditions $\mathfrak{R}_0 < 1$

Model parameters		$\mathfrak{R}_0$	Model parameters		$\mathfrak{R}_0$
$\mu_v = 0{,}03$	$b_i = 0{,}30$	0,97	$\mu_v = 0{,}05$	$b_i = 0{,}25$	0,59
$\mu_v = 0{,}05$	$b_i = 0{,}30$	0,70	$\mu_v = 0{,}05$	$b_i = 0{,}30$	0,70
$\mu_v = 0{,}07$	$b_i = 0{,}30$	0,56	$\mu_v = 0{,}05$	$b_i = 0{,}35$	0,82
$\mu_v = 0{,}09$	$b_i = 0{,}30$	0,47	$\mu_v = 0{,}05$	$b_i = 0{,}40$	0,94

Figure 3 shows the evolution of the number of each subpopulation when the value of the mosquito mortality rate μ_v is modified. In the human population, as shown in **Figures 3(a) – 3(d)**, if the mosquito mortality rate μ_v increases and the values of the other parameters are constant, then the number of susceptible human subpopulations increases while the number of other subpopulations increases. -human populations are decreasing. Indeed, an increase in the mosquito mortality rate leads to a decrease in the number of mosquitoes, including infected mosquitoes. As a result, the ratio of susceptible human movements to exposed humans decreased, so the number of vulnerable humans increased.

In the mosquito population as shown in **Figures 3(e) – 3(g)**, if the mosquito mortality rate μ_v increases and the values of other parameters are constant, then the number of susceptible mosquito subpopulations increases while the number of other mosquito subpopulations decreases. This increase in the mosquito mortality rate leads to a decrease in the number of infected mosquitoes so that the number of infected humans decreases. As a result, the transfer ratio of susceptible mosquitoes to exposed mosquitoes decreases so that the number of susceptible mosquitoes increases.

The increase or decrease in the number of each subpopulation tends to be different for each increase in the mosquito mortality rate, both in the human population and in the mosquito population. The maximum number of exposed human subpopulations occurred on day 15 with a proportion of 12% and a mosquito

mortality rate of 0.03. In the infected human subpopulation, the maximum occurred on day 21 with a proportion of 5% and a mosquito mortality rate of 0.03.

Figure 4 shows the evolution of the number of each subpopulation when the average number of bites of infected mosquitoes b_i is modified. In the human population, as shown in **Figures 4(a) – 4(d)**, if the average number of bites of infected mosquitoes b_i increases and the values of the other parameters are constant, then the number of susceptible human subpopulations decreases. while the number of other human subpopulations increases. An increase in the average number of bites of infected mosquitoes b_i may increase the value of the probability of contact between infected mosquitoes and susceptible humans. As a result, the proportion of vulnerable humans moving towards exposed humans increases.

In the mosquito population shown in **Figures 4(e) – 4(g)**, if the average number of bites of infected mosquitoes b_i increases and the values of other parameters are the same, then the number of susceptible mosquito subpopulations decreases. while the number of other mosquito subpopulations increases. This is due to the increasing value of the contact probability between susceptible mosquitoes and infected humans such that the transfer ratio of susceptible mosquitoes to exposed mosquitoes increases.

The increase or decrease in the number of each subpopulation tends to be different for each increase in the average number of bites of infected mosquitoes, both in the human population and in the mosquito population. The maximum number of exposed human subpopulations occurred on day 13 with a proportion of 14% and the average number of bites of infected mosquitoes was 0.4. In the infected human subpopulation, the maximum occurred on day 18 with a proportion of 5% and a mosquito mortality rate of 0.4.

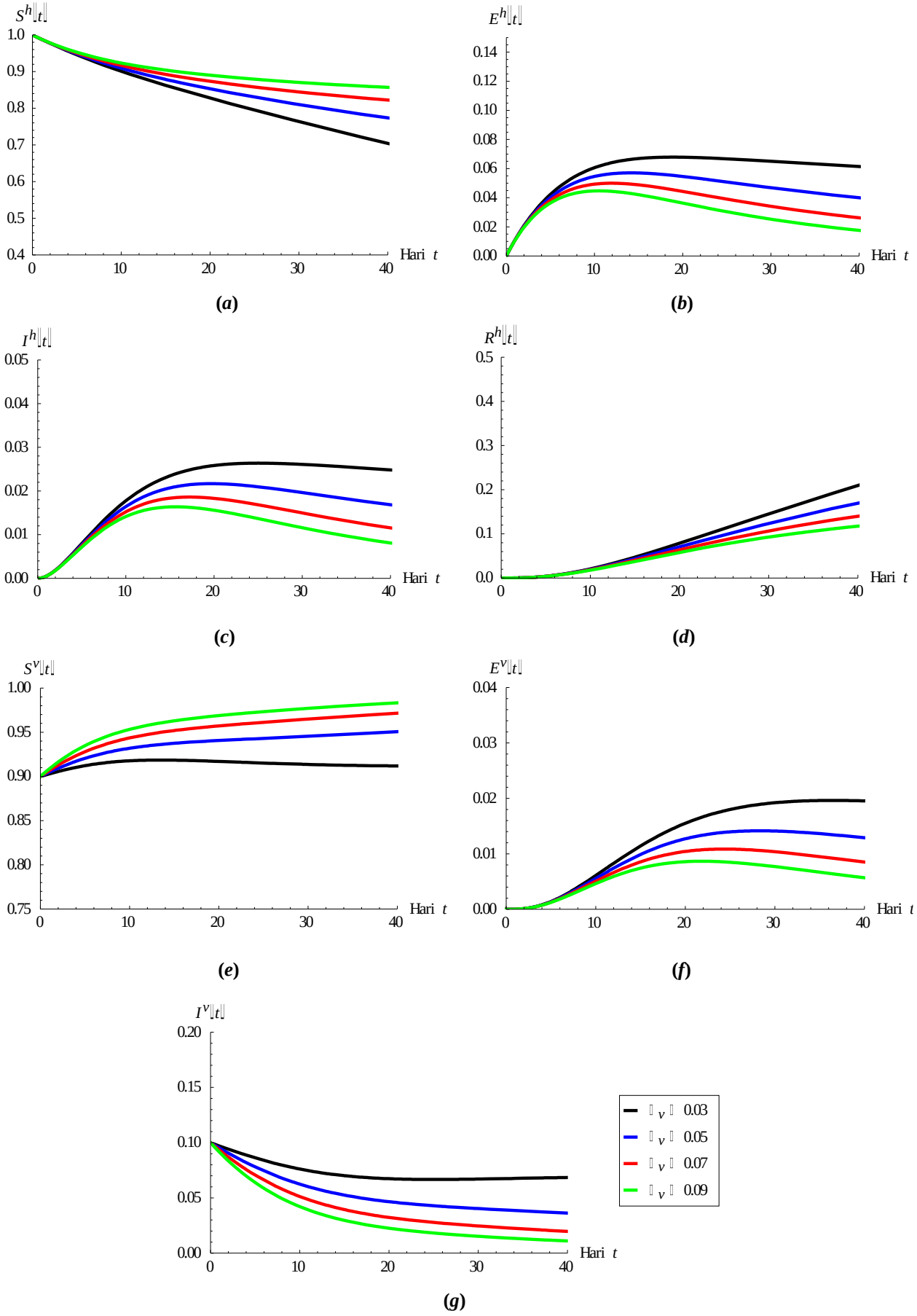


Figure 3. The dynamics of the human population (*a*) susceptible S^h, (*b*) exposed E^h, (*c*) infected I^h, and (*d*) recovered R^h, and the mosquito population (*e*) susceptible S^v, (*f*) exposed E^v, (*g*) infected I^v against time t under condition $\mathfrak{R}_0 < 1$ and the value of the parameter μ_v is modified

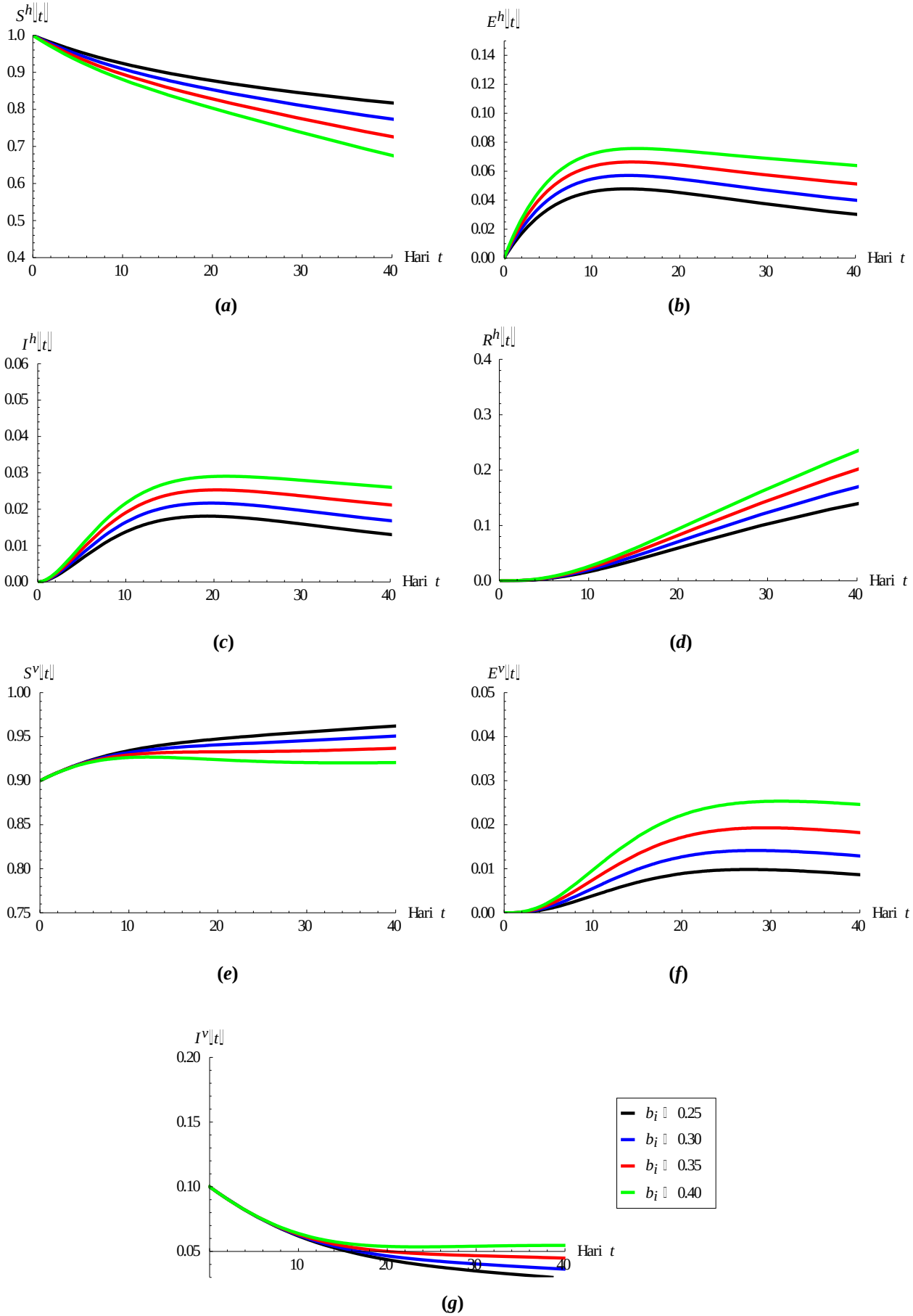


Figure 4. The dynamics of the human population (*a*) susceptible S^h, (*b*) exposed E^h, (*c*) infected I^h, and (*d*) recovered R^h, and the mosquito population (*e*) susceptible S^v, (*f*) exposed E^v, (*g*) infected I^v against time t under condition $\Re_0 < 1$ and the value of the parameter b_i is modified

4. CONCLUSIONS

This research resulted in the following conclusions:

1. In general, the resulting model can indicate the presence of endemics in an area for certain parameter values. This can be seen from the equilibrium point calculation of the SEIR model.
2. This research produces two equilibrium points:
   a. The disease-free equilibrium point $T_1(S^h, E^h, I^h, E^v, I^v) = T_1(\lambda/\mu_h, 0, 0, 0, 0)$ which is always present and is the point that is stable if the value of the basic reproduction number is $\Re_0 < 1$.
   b. The endemic equilibrium point $T_2(S_*^h, E_*^h, I_*^h, E_*^v, I_*^v)$ where S_*^h is the number of susceptible human subpopulations, E_*^h is the number of exposed human subpopulations, I_*^h is the number of infected human subpopulations, E_*^v is the number of exposed mosquito subpopulations, I_*^v is the number of infected mosquito subpopulations. The stability of this endemic fixed point is guaranteed if the value $\Re_0 > 1$.
3. Through observations in numerical simulations, the dynamic results for each subpopulation are affected by the selection of the $\Re_0$ value. In this paper, the value of $\Re_0$ is influenced by several parameter values, but the focus of the simulation is the mosquito mortality rate μ_v and the average number of bites of infected mosquitoes b_i:
   a. In the human population, the greater the mosquito mortality rate, the fewer susceptible humans become exposed, and the greater the average number of infected mosquito bites, the greater the number of susceptible humans who become exposed.
   b. In the mosquito population, the greater the mosquito mortality rate, the fewer susceptible mosquitoes that become exposed, and the greater the average number of infected mosquito bites, the greater the number of susceptible mosquitoes that become exposed.
4. The increase or decrease in the number of each subpopulation tends to be different for each increase in the mosquito mortality rate or for each increase in the average number of bites of infected mosquitoes, both in the human population and the mosquito population.

ACKNOWLEDGMENT

The authors would like to thank to all participants involved in this research.

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