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The Analysis of SEIRS-SEI Epidemic Models on Malaria with Regard to Human Recovery Rate

Resmawan[1*], Paian Sianturi[2], Endar Hasafah Nugrahani[2]
[1]Mathematics Department, State University of Gorontalo, [2]Mathematics Department, Bogor Agricultural University
[*]Corresponding author, email: resmawan@ung.ac.id

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Abstract - This article discusses SEIRS-SEI epidemic models on malaria with regard to human recovery rate. SEIRS-SEI in this model is an abbreviation of the population class used in the model, i.e Susceptible, Exposed, Infected, and Recovered populations in humans and Susceptible, Exposed, and Infected populations in mosquito. These epidemic models belong to mathematical models which clarify a phenomenon of epidemic transmission of malaria by observing the human recovery rate after being infected and susceptible. Human population falls into four classes, namely susceptible humans, exposed humans, infected humans, and recovered humans. Meanwhile, mosquito population serving as vectors of the disease is divided into three classes, including susceptible mosquitoes, exposed mosquitoes, and infected mosquitoes. Such models are termed SEIRS-SEI epidemic models. Analytical discussion covers model formation, existence and stability of equilibrium points, as well as numerical simulation to find out the influence of human recovery rate on population dynamics of both species. The results show that the fixed point without disease (x_{dfe}) is stable in condition $\mathcal{R}_0 < 1$and unstable in condition $\mathcal{R}_0 > 1$. The simulation results show that the given treatment has an influence on the dynamics of the human population and mosquitoes. If the human recovery rate from the infected state becomes susceptible to increased, then the number of infected populations of both species will decrease. As a result, the disease will not spread and within a certain time will disappear from the population.

Keywords: Epidemic models, SEIRS-SEI, Malaria, Human recovery

Introduction

Malaria is a disease caused by infection with parasites belonging to genus Plasmodium. In epidemiology, malaria affects both men and women in all age groups. Plasmodium parasites are transmitted through the bite of a female Anopheles mosquito (Anopheles spp.), the primary vector causing malaria.

Some efforts have been made to encounter the impacts of malaria transmission. One of them includes the application of Mathematics in the mathematical branch of epidemiology. It is a branch of mathematics that studies about disease spread and control (Capazzo, 2008). Mathematical modeling in epidemiology has produced a wide variety of mathematical models to explore infectious disease problems. Mathematical modeling for malaria was first performed by Ross in 1911 and was known as the Ross Model. This basic model was then extended by MacDonald in 1957 and was called the Ross-MacDonald model (Ngwa and Shu, 2000). Several similar studies regarding a change in population size are(Ngwa and Shu, 2000) and (Chitnis, 2005).

This article will examine SEIRS-SEI epidemic models on malaria developed from previous models. The study of the models was carried out by specifically taking human recovery rate into account. The term 'human' here refers to an infected person subsequently recovered without immunity and finally susceptible to disease. Analytical discussion includes model formation, existence and stability of equilibrium points, as well as numerical simulation to find out the influence of human recovery rate on population dynamics of both species.

Materials and Methods

Mathematical model

The pattern of malaria transmission is schematically illustrated in the following compartment diagram:

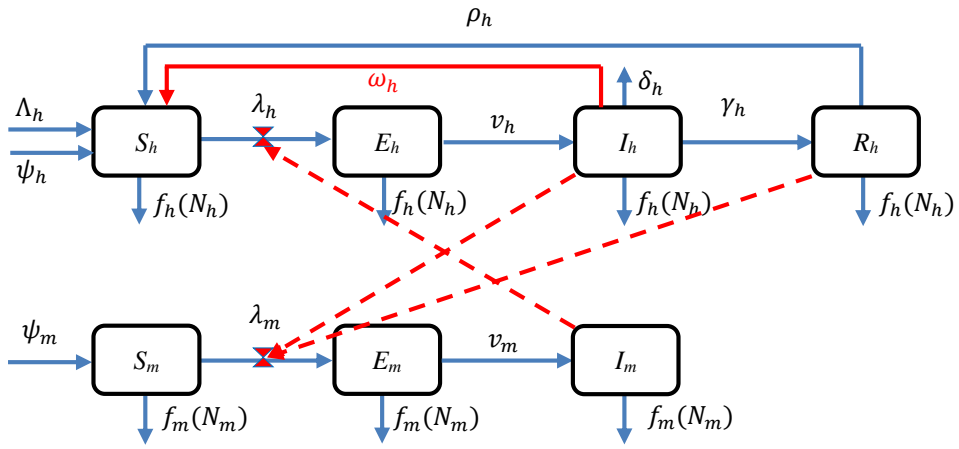

Figure 1. The scheme of malaria transmission based on SEIRS-SEI modification model

Therefore, the system dynamics can be formulated in the following equations:

$$\begin{cases} \dfrac{dS_h}{dt} = \Lambda_h + \psi_h N_h + \omega_h I_h + \rho_h R_h - (\lambda_h + f_h(N_h))S_h \\ \dfrac{dE_h}{dt} = \lambda_h S_h - (v_h + f_h(N_h))E_h \\ \dfrac{dI_h}{dt} = v_h E_h - (\gamma_h + f_h(N_h) + \delta_h + \omega_h)I_h \\ \dfrac{dR_h}{dt} = \gamma_h I_h - (\rho_h + f_h(N_h))R_h \\ \dfrac{dS_m}{dt} = \psi_m N_m - (\lambda_m + f_m(N_m))S_m \\ \dfrac{dE_m}{dt} = \lambda_m S_m - (v_m + f_m(N_m))E_m \\ \dfrac{dI_m}{dt} = v_m E_m - f_m(N_m)I_m \end{cases} \quad (1)$$

where natural death rate follows the function

$$f_h(N_h) = \mu_{1h} + \mu_{2h}N_h \text{and} f_m(N_m) = \mu_{1m} + \mu_{2m}N_m$$

and infection rate follows the equation

$$\lambda_h = b_h(N_h, N_m)\beta_{hm}\frac{I_m}{N_m} \text{and} \lambda_m = b_m(N_h, N_m)\left(\beta_{mh}\frac{I_h}{N_h} + \tilde{\beta}_{mh}\frac{R_h}{N_h}\right).$$

The rate of human and mosquito population change follows the equation obtained from the system (1), expressed as

$$\begin{cases} \dfrac{dN_h}{dt} = \Lambda_h + \psi_h N_h - f_h(N_h)N_h - \delta_h I_h \\ \dfrac{dN_m}{dt} = \psi_m N_m - f_m(N_m)N_m. \end{cases} \quad (2)$$

Description of parameters is presented in Table 1.

Table 1. Parameters of SEIRS-SEI Models

Variable	Description	Units
Λ_h	Human migration rate	human × unit of time^{-1}
ψ_h	Per capita human birth rate.	unit of time^{-1}

ψ_m	Per capita mosquito birth rate.	unit of time^{-1}
σ_h	The average number of mosquito bites on humans per unit of time	unit of time^{-1}
σ_m	The maximum proportion of bites made by a single mosquito on humans per unit of time	unit of time^{-1}
β_{hm}	The probability of infected mosquito-to-susceptible human-transmission	without unit
β_{mh}	The probability of infected human-to-susceptible mosquito-transmission	without unit
$\tilde{\beta}_{mh}$	The probability of recovered human-to-susceptible mosquito-transmission	without unit
v_h	Per capita exposed-to-infected human transmission rate	unit of time^{-1}
v_m	Per capita exposed-to-infected mosquito transmission rate	unit of time^{-1}
γ_h	Per capita infected-to-recovered human effective immunity formation rate	unit of time^{-1}
ω_h	Per capita infected-to-susceptible human recovery rate	unit of time^{-1}
δ_h	Human mortality rate due to malaria infection	unit of time^{-1}
ρ_h	Constant rate of loss of immunity after humans get recovered.	unit of time^{-1}
μ_{1h}	Human mortality rate which does not depend on population density	unit of time^{-1}
μ_{2h}	Human mortality rate which depends on population density	unit of time^{-1}
μ_{1m}	Mosquito mortality rate which does not depend on population density	human^{-1} × unit of time^{-1}
μ_{2m}	Mosquito mortality rate which depends on population density	unit of time^{-1}
		mosquito^{-1} × unit of time^{-1}

Source: Chitnis, 2005 and Chitnis *et al.,* 2006

In addition, the proportion of mosquito bites causing infection is termed infection rate with the following formulation:

$$\lambda_h = \frac{\sigma_m \sigma_h \beta_{hm} I_m}{\sigma_m N_m + \sigma_h N_h} \text{and} \lambda_m = \frac{\sigma_m \sigma_h N_h}{\sigma_m N_m + \sigma_h N_h}\left(\beta_{mh}\frac{I_h}{N_h} + \tilde{\beta}_{mh}\frac{R_h}{N_h}\right).$$

For ease of the analysis in the model (1) – (2), nondimensionalizationwas applied by involving the comparison of the number of each classes and the total number of the species population.
For instance:

$$e_h = \frac{E_h}{N_h}, i_h = \frac{I_h}{N_h}, r_h = \frac{R_h}{N_h}, e_m = \frac{E_m}{N_m}, i_m = \frac{I_m}{N_m}, s_h = \frac{S_h}{N_h}, s_m = \frac{S_m}{N_m} \quad (3)$$

With

$$s_h + e_h + i_h + r_h = 1 \text{ and} s_m + e_m + i_m = 1$$

By bringing down the equation (3), we obtain:

$$\frac{de_h}{dt} = \frac{1}{N_h}\left[\frac{dE_h}{dt} - e_h\frac{dN_h}{dt}\right] \text{and} \frac{de_m}{dt} = \frac{1}{N_m}\left[\frac{dE_m}{dt} - e_m\frac{dN_m}{dt}\right].$$

The variable description is demonstrated in Table 2.

Table 2. Variables of SEIRS-SEI Models

Variable	Description
e_h	The proportion of exposed humans in *t* time
i_h	The proportion of infected humans in *t* time
r_h	The proportion of recovered humans in *t* time
N_h	Total human population in *t* time
e_m	The proportion of exposed mosquitoes in *t* time

i_m	The proportion of infected mosquitoes in *t* time
N_m	Total mosquito population in *t* time

Source: Chitnis, 2005

Under the similar method to other variables, a new seven-dimensional system of equations consisting of two dimensions for the variable of the number of population and five dimensions for each classes of the population with disease, including e_h, i_h, r_h,N_h, e_m, i_m, and N_m is obtained.

$$\begin{cases} \dfrac{de_h}{dt} = \left(\dfrac{\sigma_m\sigma_h N_m\beta_{hm}i_m}{\sigma_m N_m + \sigma_h N_h}\right)(1 - e_h - i_h - r_h) - \left(v_h + \psi_h + \dfrac{\Lambda_h}{N_h}\right)e_h + \delta_h i_h e_h \\ \dfrac{di_h}{dt} = v_h e_h - \left(\gamma_h + \delta_h + \boldsymbol{\omega_h} + \psi_h + \dfrac{\Lambda_h}{N_h}\right)i_h + \delta_h i_h^2 \\ \dfrac{dr_h}{dt} = \gamma_h i_h - \left(\rho_h + \psi_h + \dfrac{\Lambda_h}{N_h}\right)r_h + \delta_h i_h r_h \\ \dfrac{dN_h}{dt} = \Lambda_h + \psi_h N_h - (\mu_{1h} + \mu_{2h}N_h)N_h - \delta_h i_h N_h \\ \dfrac{de_m}{dt} = \left(\dfrac{\sigma_m\sigma_h N_h}{\sigma_m N_m + \sigma_h N_h}\right)(\beta_{mh}i_h + \tilde{\beta}_{mh}r_h)(1 - e_m - i_m) - (v_m + \psi_m)e_m \\ \dfrac{di_m}{dt} = v_m e_m - \psi_m i_m \\ \dfrac{dN_m}{dt} = \psi_m N_m - (\mu_{1m} + \mu_{2m}N_m)N_m \end{cases} \quad (4)$$

Results and discussion

Stability analysis

Equilibrium points

Equilibrium points can be obtained from a solution to the system (4) that is a condition which satisfies:

$$\frac{de_h}{dt} = \frac{di_h}{dt} = \frac{dr_h}{dt} = \frac{dN_h}{dt} = \frac{de_m}{dt} = \frac{di_m}{dt} = \frac{dN_m}{dt} = 0.$$

The aforementioned system has two kinds of equilibrium, including disease-free equilibrium, x_{dfe}, and endemic equilibrium, x_{ee}. By using functional-based software, disease-free equilibrium is obtained as follows:

$$\boldsymbol{x}_{dfe}(e_h, i_h, r_h, N_h, e_m, i_m, N_m) = (0, 0, 0, N_h^*, 0, 0, N_m^*)$$

with

$$N_h^* = \frac{(\psi_h - \mu_{1h}) + \sqrt{(\psi_h - \mu_{1h})^2 + 4\mu_{2h}\Lambda_h}}{2\mu_{2h}} \text{ and } N_m^* = \frac{(\psi_m - \mu_{1m})}{\mu_{2m}}$$

and the endemic equilibrium:

$$x_{ee}(e_h, i_h, r_h, N_h, e_m, i_m, N_m) = (e_h^{**}, i_h^{**}, r_h^{**}, N_h^{**}, e_m^{**}, i_m^{**}, N_m^{**})$$

with

$$e_h^{**} = -\frac{\sigma_h\sigma_m\beta_{hm}i_m^{**}N_h^{**}N_m^{**}(i_h^{**} + r_h^{**} - 1)}{N_h^{**}\left(\sigma_h N_h^{**}(\psi_h + v_h - \delta_h i_h^{**}) + \sigma_m N_m^{**}(\psi_h + v_h - \delta_h i_h^{**} + \sigma_h\beta_{hm}i_m^{**})\right) + (\sigma_h N_h^{**} + \sigma_m N_m^{**})\Lambda_h}$$

$$i_h^{**(1)} = \frac{\Lambda_h + (\psi_h + \gamma_h + \delta_h + \omega_h)N_h^{**}}{2\delta_h N_h^{**}} - \frac{\sqrt{(\Lambda_h + (\psi_h + \gamma_h + \delta_h + \omega_h)N_h^{**})^2 - 4v_h\delta_h e_h^{**}N_h^{**2}}}{2\delta_h N_h^{**}}$$

$$i_h^{**(2)} = \frac{\Lambda_h + (\psi_h + \gamma_h + \delta_h + \omega_h)N_h^{**}}{2\delta_h N_h^{**}} + \frac{\sqrt{(\Lambda_h + (\psi_h + \gamma_h + \delta_h + \omega_h)N_h^{**})^2 - 4v_h\delta_h e_h^{**} N_h^{**2}}}{2\delta_h N_h^{**}}$$

$$r_h^{**} = \frac{\gamma_h i_h^{**} N_h^{**}}{(\psi_h + \rho_h - i_h^{**}\delta_h)N_h^{**} + \Lambda_h}$$

$$N_h^{**(1)} = \frac{\psi_h - \mu_{1h} - \delta_h i_h^{**} + \sqrt{(\mu_{1h} - \psi_h + \delta_h i_h^{**})^2 + 4\mu_{2h}\Lambda_h}}{2\mu_{2h}}$$

$$N_h^{**(2)} = -\frac{\mu_{1h} - \psi_h + \delta_h i_h^{**} + \sqrt{(\mu_{1h} - \psi_h + \delta_h i_h^{**})^2 + 4\mu_{2h}\Lambda_h}}{2\mu_{2h}}$$

$$e_m^{**} = -\frac{\sigma_h\sigma_m N_h^{**}(B_{mh}r_h^{**} + \beta_{mh}i_h^{**})(i_m^{**} - 1)}{\sigma_m N_m^{**}(\psi_m + v_m) + \sigma_h N_h^{**}(\psi_m + v_m + \sigma_m B_{mh}r_h^{**} + \sigma_m\beta_{mh}i_h^{**})}$$

$$i_m^{**} = \frac{v_m e_m^{**}}{\psi_m}$$

$$N_m^{**} = \frac{(\psi_m - \mu_{1m})}{\mu_{2m}}.$$

Basic reproduction number

Basic reproduction number which is notated as $\mathcal{R}_0$ is the expected number of infections per unit of time. The infections occur in a susceptible population resulted from an infected individual.

The basic reproduction number is obtained from the largest real positive eigenvalue of a matrix through the next-generation matrix approach (Diekmann *et al.,* 1990; van den Driessche and Wathmough, 2008; Resmawan, 2017). The fact results in the formulation of basic reproduction number:

$$\mathcal{R}_0 = \sqrt{K_{mh}K_{hm}}. \quad (5)$$

where

$$K_{hm} = \alpha_{hm}.b_m^*.\beta_{hm}.\theta_{hm} \text{and} K_{mh} = \alpha_{mh}.b_h^*\left(\beta_{mh}.\theta_{mh} + \tilde{\beta}_{mh}.\tilde{\theta}_{mh}.\zeta_{mh}\right)$$

with

$$\alpha_{hm} = \frac{v_m}{v_m + \mu_{1m} + \mu_{2m}N_m^*}\alpha_{mh} = \frac{v_h}{v_h + \mu_{1h} + \mu_{2h}N_h^*}$$

$$\theta_{hm} = \frac{1}{\mu_{1m} + \mu_{2m}N_m^*}\theta_{mh} = \frac{1}{\gamma_h + \delta_h + \omega_h + \mu_{1h} + \mu_{2h}N_h^*}$$

$$\tilde{\theta}_{mh} = \frac{1}{\rho_h + \mu_{1h} + \mu_{2h}N_h^*}\zeta_{mh} = \frac{\gamma_h}{\gamma_h + \delta_h + \omega_h + \mu_{1h} + \mu_{2h}N_h^*}$$

The description is written in table 3.

Table 3 Parameters of basic reproduction number

Formula	Description
α_{hm}	The probability that mosquitoes survive from exposed to infected state
α_{mh}	The probability that humans will survive from exposed to infected state.
$b_m^* = b_m(N_h^*, N_m^*)$	The number of contacts between a mosquito and a person per unit of time
$b_h^* = b_h(N_h^*, N_m^*)$	The number of contacts between a person and a mosquito per unit of time

β_{hm}	The probability of infected mosquito-to-susceptible human-transmission
β_{mh}	The probability of infected human-to-susceptible mosquito-transmission
$\tilde{\beta}_{mh}$	The probability of recovered human-to-susceptible mosquito transmission
θ_{hm}	The average lifespans of infected mosquitoes
θ_{mh}	The average period of infection on humans
$\tilde{\theta}_{mh}$	The average period of recovery on humans
ζ_{mh}	The probability that humans will survive from infected to recovered state

In reference to the formulation of the basic reproduction number (5), the following statements are concluded:

1. If $\mathcal{R}_0 < 1$, the number of infected individuals will decline in every generation, and therefore the disease will not spread.
2. If $\mathcal{R}_0 > 1$, the number of infected individuals will increase in every generation, and therefore the disease will spread.

The jacobian matrix

System (4), for instance, is defined as the following function:

$$\dot{\boldsymbol{x}} = f(\boldsymbol{x}), \boldsymbol{x} \in \mathbb{R}^7 \qquad (6)$$

where $\boldsymbol{x} \in \mathbb{R}^7$ includes variables existing in system (4). By performing linearity in system (6) surrounding $\boldsymbol{x}_{dfe}$, the Jacobian matrix for a disease-free equilibrium is obtained.

$$\boldsymbol{J}_{x_{dfe}} = \begin{pmatrix} J_{11} & 0 & 0 & 0 & 0 & J_{16} & 0 \\ J_{21} & J_{22} & 0 & 0 & 0 & 0 & 0 \\ 0 & J_{32} & J_{33} & 0 & 0 & 0 & 0 \\ 0 & J_{42} & 0 & J_{44} & 0 & 0 & 0 \\ 0 & J_{52} & J_{53} & 0 & J_{55} & 0 & 0 \\ 0 & 0 & 0 & 0 & J_{65} & J_{66} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & J_{77} \end{pmatrix}$$

where

$$J_{11} = -v_h - \psi_h - \frac{2\Lambda_h\mu_{2h}}{-\mu_{1h} + \sqrt{4\Lambda_h\mu_{2h} + (\mu_{1h} - \psi_h)^2} + \psi_h}$$

$$J_{16} = -\frac{2\beta_{hm}\mu_{2h}\sigma_h\sigma_m(\mu_{1m} - \psi_m)}{-\mu_{2h}\sigma_m\left(\mu_{1h} + \psi_h + \sqrt{{\mu_{1h}}^2 + 4\Lambda_h\mu_{2h} - 2\mu_{1h}\psi_h + {\psi_h}^2}\right) + \mu_{2h}\sigma_m(2\psi_m - 2\mu_{1m})}$$

$$J_{21} = v_h$$

$$J_{22} = -\gamma_h - \delta_h - \psi_h - \frac{2\Lambda_h\mu_{2h}}{-\mu_{1h} + \sqrt{4\Lambda_h\mu_{2h} + (\mu_{1h} - \psi_h)^2} + \psi_h} - \omega_h$$

$$J_{32} = \gamma_h$$

$$J_{33} = -\rho_h - \psi_h - \frac{2\Lambda_h\mu_{2h}}{-\mu_{1h} + \sqrt{4\Lambda_h\mu_{2h} + (\mu_{1h} - \psi_h)^2} + \psi_h}$$

$$J_{42} = -\frac{\delta_h(-\mu_{1h} + \psi_h + \sqrt{(\mu_{1h} - \psi_h)^2 + 4\mu_{2h}\Lambda_h})}{2\mu_{2h}}$$

$$J_{44} = -\sqrt{(\mu_{1h} - \psi_h)^2 + 4\mu_{2h}\Lambda_h}$$

$$J_{52} = \frac{\sigma_h\sigma_m\beta_{mh}\mu_{2m}(\psi_h - \mu_{1h} + \sqrt{(\mu_{1h} - \psi_h)^2 + 4\mu_{2h}\Lambda_h})}{2(\psi_m - \mu_{1m})\mu_{2h}\sigma_m + \mu_{2m}\sigma_h(\psi_h - \mu_{1h} + \sqrt{(\mu_{1h} - \psi_h)^2 + 4\mu_{2h}\Lambda_h})}$$

$$J_{53} = \frac{\sigma_h \sigma_m B_{mh} \mu_{2m} (\psi_h - \mu_{1h} + \sqrt{(\mu_{1h} - \psi_h)^2 + 4\mu_{2h}\Lambda_h})}{2(\psi_m - \mu_{1m})\mu_{2h}\sigma_m + \mu_{2m}\sigma_h(\psi_h - \mu_{1h} + \sqrt{(\mu_{1h} - \psi_h)^2 + 4\mu_{2h}\Lambda_h})}$$

$$J_{55} = -(v_m + \psi_m)$$

$$J_{65} = v_m;\ J_{66} = -\psi_m;\ J_{77} = \mu_{1m} - \psi_m$$

Eigenvalues

Equilibrium $\boldsymbol{x}_{dfe}$ is stable if and only if each eigenvalue of matrix $\boldsymbol{J}_{\boldsymbol{x}_{dfe}}$ has negative value, and is unstable if and only if there exists at least one eigenvalue of matrix $\boldsymbol{J}_{\boldsymbol{x}_{dfe}}$ with non-negative values (Tu, 1994).

From the above matrix $\boldsymbol{J}_{\boldsymbol{x}_{dfe}}$, seven eigenvalues are obtained. Two of them are indicated below:

$$\eta_1 = -\sqrt{(\mu_{1h} - \psi_h)^2 + 4\mu_{2h}\Lambda_h}$$

$$\eta_2 = \mu_{1m} - \psi_m$$

Meanwhile, the other five are obtained from roots of the characteristic equation:

$$A_5\eta^5 + A_4\eta^4 + A_3\eta^3 + A_2\eta^2 + A_1\eta + A_0 = 0. \qquad (7)$$

In order to evaluate signs of the five eigenvalues in equation (7), Routh-Horwitz stability criteria and Descartes' rule of signs were applied (Chitnis, 2005).

1. Routh-Horwitz stability criteria were used to show that all of the eigenvalues have negative real part if $\mathcal{R}_0 < 1$ and all $A_i$are positive.
2. Descartes' rule of signs was applied to demonstrate that there is a non-negative eigenvalue when $\mathcal{R}_0 > 1$ and a sign change of A_i appears.

Based on system (4) and the formulation of the basic reproduction number (5), it is clear that if $\mathcal{R}_0 < 1$, all of the eigenvalues have negative real part, and therefore the disease-free equilibrium ($\boldsymbol{x}_{dfe}$) is considered stable, while if $\mathcal{R}_0 > 1$, there exists a non-negative eigenvalue, and accordingly the disease-free equilibrium is regarded unstable.

Simulation

A simulation was performed to signify the effectiveness of parameters of human recovery rate (ω_h)towards disease transmission rate. In this case, the increase or decrease in the value of parameter ω_h which can alter the value of basic reproduction number ($\mathcal{R}_0$) will be demonstrated. There are five observed values of ω_h taken from $[1.0 \times 10^{-3},\ 2.6 \times 10^{-3}]$ with step 0.4×10^{-3}. The values of other parameters can be seen in Table 4.

Table 4. Values of parameters for the simulation

Parameter	Value	Parameter	Value
Λ_h	0.041	v_m	0.083
ψ_h	5.5×10^{-5}	γ_h	0.0035
ψ_m	0.13	δ_h	1.8×10^{-5}
β_{mh}	0.24	ρ_h	2.7×10^{-3}
β_{hm}	0.022	μ_{1h}	8.8×10^{-6}
$\tilde{\beta}_{mh}$	0.024	μ_{2h}	2×10^{-7}
σ_h	4.3	μ_{1m}	0.033
σ_m	0.33	μ_{2m}	4×10^{-5}
v_h	0.1		

Figure 2 and Figure 3 illustrate the change in the number of each classes of mosquito and human population after the increase in ω_h value by using such prior values as $S_h = 500, E_h = 50, I_h = 10, R_h = 0, S_m = 4850, E_m = 100, I_m = 50$ with total population $N_h = 560$ and $N_m = 5000$.

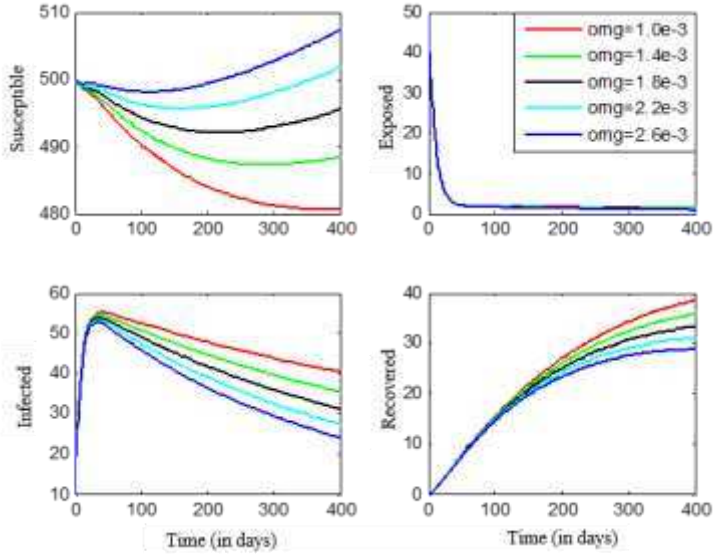

Figure **2**.Human population dynamics after the increase in human recovery rate (ω_h) parameter value

Figure 2 shows the dynamics of the human population after being treated. The figure of top-left, top-right, bottom-left, and bottom-right illustrate thepopulation dynamics in susceptible human, exposed human, infected human, and recovered human classes.If human recovery rate is increased and the values of the other parameters appear to remain constant, the number of susceptible human classes will show an increase (figure of top-left), while the number of the other human classes will decline. This happens since an increase in the human recovery rate leads to a decrease in the number of theinfected human classes, and therefore indirectly causes infected mosquito classes to decrease. The proportion of susceptible human-to-exposed human transformation is, therefore, declining and the number of susceptible humans is increasing.

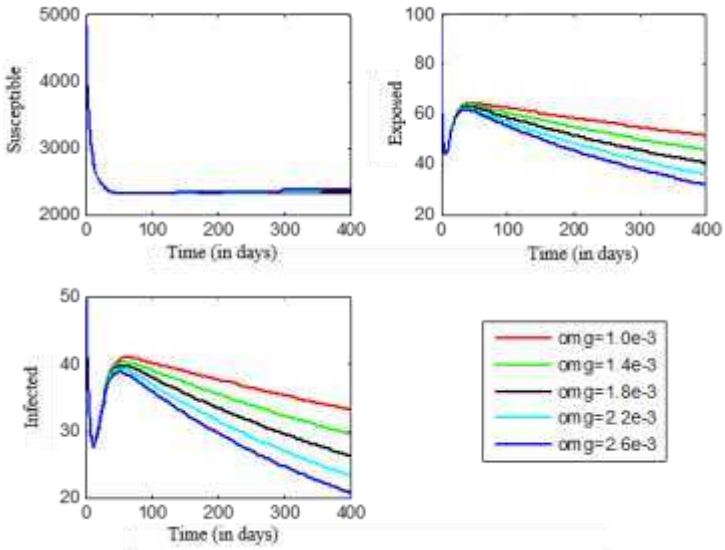

Figure **3**.Mosquito population dynamics after the increase in human recovery rate (ω_h) parameter value

Figure 3 shows the dynamics of the mosquito population after being treated. The figure of top-left, top-right, bottom-left illustrate the population dynamics of susceptible mosquito, exposed mosquito, and infected mosquito classes. If human recovery rate from infected to susceptible classes is increased and the values of the other parameters remain constant, the number of susceptible mosquito classes is increasing, while the number of other mosquito classes is decreasing. The increase in human recovery rate from infected to susceptible classes contributes to the decrease in the number of infected mosquitoes, and accordingly the number of infected humans shows a decrease. As a result, the proportion of susceptible to exposed state-transformation is decreasing and the number of susceptible mosquitoes is increasing.

Either the increase or the decrease in the number of each classes tends to be dissimilar for every increase in human recovery rate in both human and mosquito population. The maximum number of infected human classes and of infected mosquito classes on the 50th day was 55 or approximately 9.8% of the total human population, and 43, or approximately 0.8% of the total mosquito population, respectively, with human recovery rate of 1.0×10^{-3}

Conclusion

By employing the model, two equilibrium points are obtained; disease-free equilibrium and endemic equilibrium. A simulation was carried out to observe the behavior of systems around the equilibrium points. It demonstrates that the given treatment exerts an influence on both mosquito and human population dynamics indicated by the basic reproduction number. Generally, if human recovery rate from infected to susceptible state is increased, the number of infected population of both species will decline. As a result, the disease will not spread and rapidly disappear from the population.

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