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Effects of Human and Mosquito Migrations on the Dynamical Behavior of the Spread of Malaria

Lazarus Kalvein Beay[1], Kasbawati[1,*], Syamsuddin Toaha[1]

[1]*Department of Mathematics, Hasanuddin University*
Jl. Perintis Kemerdekaan Km. 10 Tamalanrea Makassar Indonesia

[*]Corresponding author: kasbawati@unhas.ac.id

Abstract. Malaria is one of infectious diseases which become the main public health problem especially in Indonesia. Mathematically, the spread of malaria can be modeled to predict the outbreak of the disease. This research studies about mathematical model of the spread of malaria which takes into consideration the migration of human and mosquito populations. By determining basic reproduction number of the model, we analyze effects of migration parameter with respect to the reduction of malaria outbreak. Sensitivity analysis of basic reproduction number shows that mosquito migration has greater effect in reducing the outbreak of malaria compared with human migration. Basic reproduction number of the model is monotonically decreasing as mosquito migration increasing. We then confirm the analytic result by doing numerical simulation. The results show that migrations in human and mosquito populations have big influences in eliminating and eradicating the disease from the system.

INTRODUCTION

Currently there are many kinds of infectious diseases in the world. It can be spread through a variety of media such as air, water, direct contact or by insects including mosquitoes [14]. One of the classic infectious diseases is malaria. It is transmitted through the bite of a female Anopheles mosquitoes [7]. Parasites genus Plasmodium that enter to the human body through the bite will result in malaria-infected [3, 4, 12]. These types of parasite are Plasmodium Vivax, Plasmodium falciparum, Plasmodium ovale, and Plasmodium malaria [3,11]. Based on years of inoculation of sporozoites, plasmodium in humans is usually first detected at 7-14 days. The clinical symptoms such as sweating, pain, and fever will be visible a few days after the bite [2].

Malaria threatens 40% of human life on earth. These diseases affect the social, economic and health problem for countries in the tropics. Although research has been carried out against this disease for hundreds of years, malaria remains a major health problem. In 2008 there were 109 countries declared as endemic malaria [3, 11]. There are also 300 million clinical cases each year that were recorded as the incidence of malaria in the world. In addition, estimated at more than 2 billion people are at risk of malaria infection [2, 12]. The victim died due to malaria worldwide is more than 1 million people each year [7, 2, 12, 12]. The amount is potentially increase significantly related to the incidence of climate change [16].

Understanding the dynamics of disease transmission would help in the handling in the population [14]. Recently designed mathematical model to study the dynamics behavior of infectious diseases, including malaria, has been carried out to quantify the impact of infection disease in humans [1, 2, 3, 5, 6, 13, 9, 10, 11, 14]. The generated models involved many critical factors that directly influence the spread of the disease. In this research, we also study the dynamical behavior of malaria using mathematical model of Agusto et. al. [2]. We extend the model by taking into consideration migration in both human and mosquito populations. Migration is an important feature in the spread of malaria since it becomes one of mobility patterns that can cause infection of malaria [8, 11, 15].

We organize the paper as follow. In Section 2, we present model formulation of malaria by considering migration factors. In Section 3, we derive the steady-state solutions of the model, and we generate the basic reproduction number

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of the model in Section 4. We also present sensitivity analysis of basic reproduction number of the model in Section 4. Some numerical simulations are presented in Section 5 and we derive conclusions in the last section.

SEIRS-SEI MODEL OF MALARIA

In this section, we generate model of malaria using SEIRS model for human population and SEI model for mosquito population. The model follows the line of Agusto, et. al. [2]. In SEIRS model, human population is divided into four compartments, i.e., susceptible (S_h), exposure (E_h), infective (I_h), and recovered (R_h). While in mosquito population, we divide it into three compartments, i.e. susceptible (S_v), exposure of malaria parasite (E_v), and infective (I_v). We assume that total of human population and mosquito population is a constant population such that we have $N_h=S_h+E_h+I_h+R_h$ and $N_v=S_v+E_v+I$v. We assume that human population enters the system and resides in susceptible compartment with a constant rate Λ_h, and leaves the system via natural death with a constant rate μ_h. So does for mosquito population which enters the system with constant rate Λ_v and leaves the system via natural death with constant rate μ_v. Transfer of individual from one compartment to the other compartment occurs based on the following assumptions. Susceptible individuals will get infection when they are bitten by infectious mosquitoes with biting rate ε_h. However there is a probability β that the biting contact will successfully transfer malaria viruses. Therefore we have the rate of susceptible individuals becomes infective individuals $\beta\varepsilon_h\phi I_v$ where ϕ is a contact rate of infected mosquito per human per unit of time. We assume that susceptible individuals which is successfully infected will enters exposed class. Infection process will continue in exposed class during $1/\alpha_h$ time until they move to the infectious class. In the infectious class, we assume that there is a treatment for the infected individuals. Consequently, malaria symptoms will stay in the infected individual body during $1/\tau$ time before they move to the recovery class. There is also spontaneous recovery rate with constant rate b, $0 \leq b < \tau$. Infected individual who cannot survive from the disease will die at a constant rate ψ. During recovery phase, there exists a period where individual will lost their immunity and move to the susceptible class again with constant rate κ.

In the mosquito population, susceptible mosquitoes will move to the exposed class after biting infected human population at a rate $\lambda\varepsilon_v\phi(I_h+\eta R_h)$ with biting rate ε_v and probability λ (whether the susceptible mosquito successfully infected or not). We assume that not only infected human that can transmit malaria symptoms but also recovered human. However there is a fractional $\eta \in [0,1)$, which defines proportion of recovered human that can transmit viruses to the susceptible mosquito. When susceptible mosquitos are successfully infected, they will move to the exposed class. During $1/\alpha_v$ unit of time, they will move to the infectious class that can spread viruses to human body. In this model formulation, we take into consideration migration in human and mosquito populations. We assume that migration will occurs in human and mosquito classes with constant rate σ_h and σ_v, respectively. By using these assumptions we get the following SEIRS-SEI system in terms of ordinary differential equations:

$$\begin{aligned}
\frac{dS_h}{dt} &= \Lambda_h + \kappa R_h - \beta\varepsilon_h\phi I_v S_h - \mu_h S_h - \sigma_h S_h,\\
\frac{dE_h}{dt} &= \beta\varepsilon_h\phi I_v S_h - (\alpha_h + \mu_h)E_h - \sigma_h E_h,\\
\frac{dI_h}{dt} &= \alpha_h E_h - (b+\tau)I_h - (\psi + \mu_h)I_h - \sigma_h I_h,\\
\frac{dR_h}{dt} &= (b+\tau)I_h - (\kappa + \mu_h)R_h - \sigma_h R_h,\\
\frac{dS_v}{dt} &= \Lambda_v - \lambda\varepsilon_v\phi(I_h + \eta R_h)S_v - \mu_v S_v - \sigma_v S_v,\\
\frac{dE_v}{dt} &= \lambda\varepsilon_v\phi(I_h + \eta R_h)S_v - (\alpha_v + \mu_v)E_v - \sigma_v E_v,\\
\frac{dI_v}{dt} &= \alpha_v E_v - \mu_v I_v - \sigma_v I_v.
\end{aligned} \tag{1}$$

Initial conditions that impose the model (1) are $S_h(0) = S_{h0}, E_h(0) = E_{h0}, I_h(0) = I_{h0}, R_h(0) = R_{h0}, S_v(0) = S_{v0}, E_v(0) = E_{v0}, I_v(0) = I_{v0}$.

STEADY STATE SOLUTIONS

By setting model (1) equals to zero we get the first steady state solution,

$$\Sigma_0 = \left(S_{h_0}, E_{h_0}, I_{h_0}, R_{h_0}, S_{v_0}, E_{v_0}, I_{v_0}\right) = \left(\frac{\Lambda_h}{\mu_h+\sigma_h}, 0,0,0, \frac{\Lambda_v}{\mu_v+\sigma_v}, 0,0\right). \tag{2}$$

This solution is called disease free-equilibrium due to the extinct of infected population in human and mosquito populations at steady state conditions. The second steady state solution is

$$\Sigma_1 = \left(S_{h_1}, E_{h_1}, I_{h_1}, R_{h_1}, S_{v_1}, E_{v_1}, I_{v_1}\right) = \left(S_{h_1}, E_{h_1}, I_{h_1}, R_{h_1}, \frac{\Lambda_v}{(\theta_v + c_5)}, \frac{\theta_v \Lambda_v}{c_4(\theta_v + c_5)}, \frac{\Lambda_v \theta_v\, \alpha_v}{c_4 c_5 (\theta_v + c_5)}\right), \tag{3}$$

with

$$S_{h_1} = \frac{c_1\, c_2\, c_3\, \Lambda_h}{c_1\, c_2\, c_3\, (\theta_h + \mu_h + \sigma_h) - \kappa\, \alpha_h\, \theta_h\, (b+\tau)},$$
$$E_{h_1} = \frac{c_2\, c_3\, \theta_h\, \Lambda_h}{c_1\, c_2\, c_3\, (\theta_h + \mu_h + \sigma_h) - \kappa\, \alpha_h\, \theta_h\, (b+\tau)},$$
$$I_{h_1} = \frac{c_3\, \alpha_h\, \theta_h\, \Lambda_h}{c_1\, c_2\, c_3\, (\theta_h + \mu_h + \sigma_h) - \kappa\, \alpha_h\, \theta_h\, (b+\tau)},$$
$$R_{h_1} = \frac{\alpha_h\, \theta_h\, \Lambda_h\, (b+\tau)}{c_1\, c_2\, c_3\, (\theta_h + \mu_h + \sigma_h) - \kappa\, \alpha_h\, \theta_h\, (b+\tau)},$$
$$\theta_h = \beta \varepsilon_h \phi I_v,$$
$$\theta_v = \lambda \varepsilon_v \phi (I_h + \eta R_h),$$
$$c_1 = \alpha_h + \mu_h + \sigma_h,$$
$$c_2 = b + \tau + \psi + \mu_h + \sigma_h,$$
$$c_3 = \kappa + \mu_h + \sigma_h,$$
$$c_4 = \alpha_v + \mu_v + \sigma_v,$$
$$c_5 = \mu_v + \sigma_v.$$

This solution is an endemic equilibrium solution where the infected populations exist in the system. It will be positive if it fulfils the following condition

$$\frac{c_1 c_2 c_3 (\theta_h + \mu_h + \sigma_h)}{\kappa \alpha_h \theta_h (b+\tau)} > 1. \tag{4}$$

BASIC REPRODUCTION NUMBER

Basic reproduction number (R_0) is one of important features in epidemic modeling. Basic reproduction number of model (1) is generated by deriving the next generation matrix of the model. Suppose $\mathcal{F}_i(\boldsymbol{x})$ is a function that contains the rate of new infections at compartment *i* and $\mathcal{V}_i(\boldsymbol{x})$ is a function that contains the rate of transfer of individuals between the compartment *i*, with $\boldsymbol{x} = (E_h, I_h, R_h, E_v, I_v)$. From system (1) we have

$$\boldsymbol{\mathcal{F}}(\boldsymbol{x}) = \begin{pmatrix} \beta \varepsilon_h \phi I_v S_h \\ 0 \\ 0 \\ \lambda \varepsilon_v \phi (I_h + \eta R_h) S_v \\ 0 \end{pmatrix}, \tag{5}$$

$$\boldsymbol{\mathcal{V}}(\boldsymbol{x}) = \begin{pmatrix} (\alpha_h + \mu_h + \sigma_h) E_h \\ -\alpha_h E_h + (b + \tau + \psi + \mu_h + \sigma_h) I_h \\ -(b+\tau) I_h + (\kappa + \mu_h + \sigma_h) R_h \\ (\alpha_v + \mu_v + \sigma_v) E_v \\ \alpha_v E_v - (\mu_v + \sigma_v) I_v \end{pmatrix}. \tag{6}$$

Differentiating equation (5) and (6) at $\boldsymbol{x}$ and evaluating at Σ_0 gives the following matrix F and V,

$$F = \left(\frac{\partial \mathcal{F}_i}{\partial x_j}(\Sigma_0)\right) = \begin{pmatrix} 0 & 0 & 0 & 0 & \beta \varepsilon_h \phi S_{h_0} \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & \lambda \varepsilon_v \phi S_{v_0} & \lambda \varepsilon_v \phi \eta S_{v_0} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{pmatrix}, \tag{7}$$

$$V = \left(\frac{\partial \mathcal{V}_i}{\partial x_j}(\Sigma_0)\right) = \begin{pmatrix} c_1 & 0 & 0 & 0 & 0 \\ -\alpha_h & c_2 & 0 & 0 & 0 \\ 0 & (b+\tau) & c_3 & 0 & 0 \\ 0 & 0 & 0 & c_4 & 0 \\ 0 & 0 & 0 & -\alpha_v & c_5 \end{pmatrix}. \tag{8}$$

Inverse of matrix V is

$$V^{-1} = \begin{pmatrix} \frac{1}{c_1} & 0 & 0 & 0 & 0 \\ \frac{\alpha_h}{c_1 c_2} & \frac{1}{c_2} & 0 & 0 & 0 \\ \frac{(b+\tau)\alpha_h}{c_1 c_2 c_3} & \frac{(b+\tau)\alpha_h}{c_2 c_3} & \frac{1}{c_3} & 0 & 0 \\ 0 & 0 & 0 & \frac{1}{c_4} & 0 \\ 0 & 0 & 0 & \frac{\alpha_v}{c_4 c_5} & \frac{1}{c_5} \end{pmatrix}. \tag{9}$$

Using matrix F and V^{-1} we get the next generation matrix,

$$FV^{-1} = \begin{pmatrix} 0 & 0 & 0 & \frac{\beta\varepsilon_h\phi S_{h_0}\alpha_v}{c_4 c_5} & \frac{\beta\varepsilon_h\phi S_{h_0}}{c_5} \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ \frac{\lambda\varepsilon_v\phi S_{v_0}\alpha_h(c_3+(b+\tau)\eta)}{c_1 c_2 c_3} & \frac{\lambda\varepsilon_v\phi S_{v_0}(c_3+(b+\tau)\eta)}{c_2 c_3} & \frac{\lambda\varepsilon_v\phi S_{v_0}\eta}{c_3} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{pmatrix}. \tag{10}$$

Characteristic equation of matrix FV^{-1} is defined as

$$\det\left(FV^{-1} - \lambda I\right) = 0,$$

or

$$\lambda^5 - \left(\left(\frac{\lambda\varepsilon_v\phi S_{v_0}\alpha_h(c_3+(b+\tau)\eta)}{c_1 c_2 c_3}\right)\left(\frac{\beta\varepsilon_h\phi\alpha_v S_{h_0}}{c_4 c_5}\right)\right)\lambda^3 = 0.$$

By factorizing the characteristic equation we get eigenvalues $\lambda_1 = \lambda_2 = \lambda_3 = 0$, and

$$\lambda_{4,5} = \pm\sqrt{\frac{\alpha_h\alpha_v\lambda\beta(c_3+(b+\tau)\eta)\phi^2\varepsilon_h\varepsilon_v S_{h_0}S_{v_0}}{c_1 c_2 c_3 c_4 c_5}}.$$

Since R_0 is defined as the spectral radius of matrix FV^{-1}, we get

$$R_0 = \sqrt{\frac{\alpha_h\alpha_v\lambda\beta(c_3+(b+\tau)\eta)\phi^2\varepsilon_h\varepsilon_v S_{h_0}S_{v_0}}{c_1 c_2 c_3 c_4 c_5}}. \tag{11}$$

To quantify effects of migrations to the spread of disease, we investigate sensitivity of R_0 with respect to the migration parameters. Effects of human migration is quantified by differentiating R_0 with respect to σ_h. By differentiating R_0 with respect to σ_h, we get the following result

$$\frac{\partial R_0}{\partial \sigma_h} = \frac{1}{2}R_0(1-\omega), \tag{12}$$

with

$$\omega = \frac{1}{(\mu_h+\sigma_h)} + \frac{1}{(\alpha_h+\mu_h+\sigma_h)} + \frac{1}{(b+\tau+\psi+\mu_h+\sigma_h)} + \frac{1}{(\kappa+\mu_h+\sigma_h)}.$$

Equation (12) shows that if $1-\omega < 0$ then $\frac{\partial \mathrm{R}_0}{\partial \sigma_h} < 0$. It means that R_0 monotonically decreases on the σ_h. The greater number of human migration, the smaller value of R_0. While if $1-\omega > 0$ then $\frac{\partial \mathrm{R}_0}{\partial \sigma_h} > 0$. This condition leads to the increasing of value of R_0. For mosquito migration, we have the following analysis. By differentiating R_0 with respect to σ_v, we get

$$\frac{\partial R_0}{\partial \sigma_v} = -\frac{1}{2R_0}\left(R_0^2\varpi\right) = -\frac{1}{2}(R_0\varpi), \tag{13}$$

with

$$\varpi = \frac{2}{(\mu_v+\sigma_v)} + \frac{1}{(\alpha_v+\mu_v+\sigma_v)}.$$

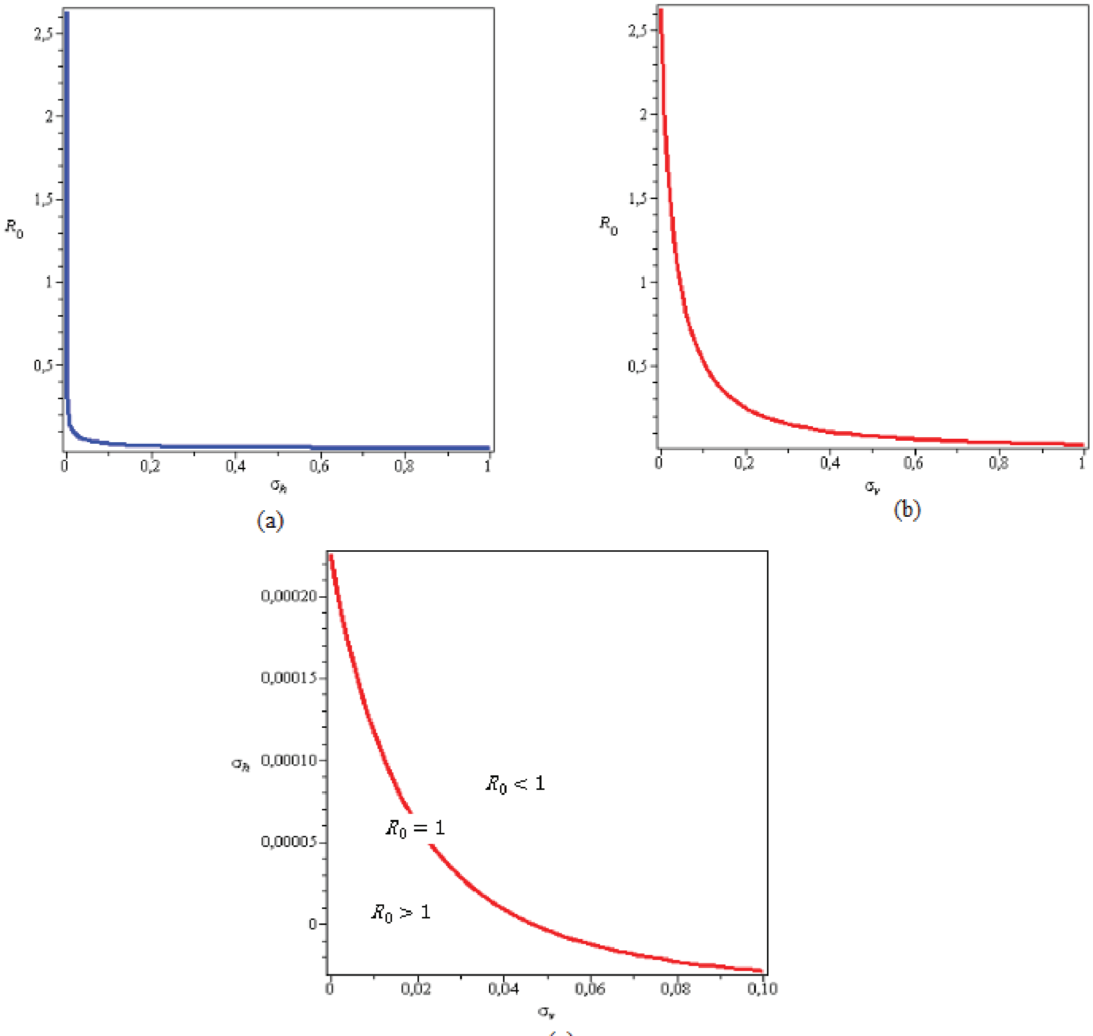
From equation (13), we can see that $\frac{\partial R_0}{\partial \sigma_v} < 0$. It means that the greater mosquito migration, the smaller R_0 will be.

NUMERICAL RESULTS

In this section we present numerical simulation to show effects of migration on human population and mosquito population. This simulation will also confirm our sensitivity analysis in the previous section. Table 1 gives the values of parameter used in this simulation. We assume that initial value of variables are $S_h(0) = 700$, $E_h(0) = 100$, $I_h(0) = 0$, $R_h(0) = 0$, $S_v(0) = 5000$, $E_v(0) = 500$, $I_v(0) = 30$.

Figure 1-(a) shows the values of R_0 when σ_h is varied from $0 \leq \sigma_h \leq 1$. When $\sigma_h = 0$, we get R_0=2.60 which is greater than one. It means that when there is no migration in human population endemic condition will exist in the system. When the rate of human migration is increased with σ_h = 0.2, we get R_0=0.0129 which is less than one. This condition leads the system free from endemic at steady state condition. The smaller value of R_0 the greater number of human that should be migrated. Figure 2 and 3, respectively, show the dynamical behavior of human and mosquito populations in all classes when human migration is varied.

Furthermore when we vary parameter of mosquito migration from $0 \leq \sigma_v \leq 1$, we get the results which are presented in Figure 1-(b). When $\sigma_v = 0$, we have $R_0 = 2.6037$ which is greater than one. This condition leads to the stability of endemic equilibrium in human and mosquito population. When mosquitos are migrated with the rate constant $\sigma_v = 0.2$, we have $R_0 = 0.2493$. The greater mosquitos which are migrated, the smaller value of R_0. These results indicate that the existence of migration in both human and mosquito populations can be one of controls in reducing the spread of malaria. The range of control parameters numerically is given in Figure 1-(c). Practically, migration in mosquito population occurs when its habitat is perturbed by changing their food patter. Dietary changes in the mosquito population are leading to migratory flight [9].



(a)

(b)

(c)

FIGURE 1. Graphs of R_0 when: (a) σ_h is varied; (b) σ_v is varied; (c) σ_h and σ_v are varied ($R_0 = 1$).

TABLE 1. Parameter values on the malaria model.

Parameter	Values	Reference	Parameter	Values	Reference
ε_h	0.5	[2]	Λ_v	0.071	[2]
ε_v	0.3	[2]	ψ	0.0001	[13]
β	0.83	[13]	ϕ	0.6	[2]
λ	0.09	[2]	b	0.005	[2]
μ_h	0.00004	[13]	η	0.001	[2]
μ_v	0.04	[2]	τ	0.5	[2]
κ	1/(2x365)	[2]	σ_h	0 – 1.0	Assumed
α_h	1/17	[2]	σ_v	0 – 1.0	Assumed
α_v	1/18	[2]	Λ_v	0.071	[2]
Λ_h	0.00099	[13]	ψ	0.0001	[13]

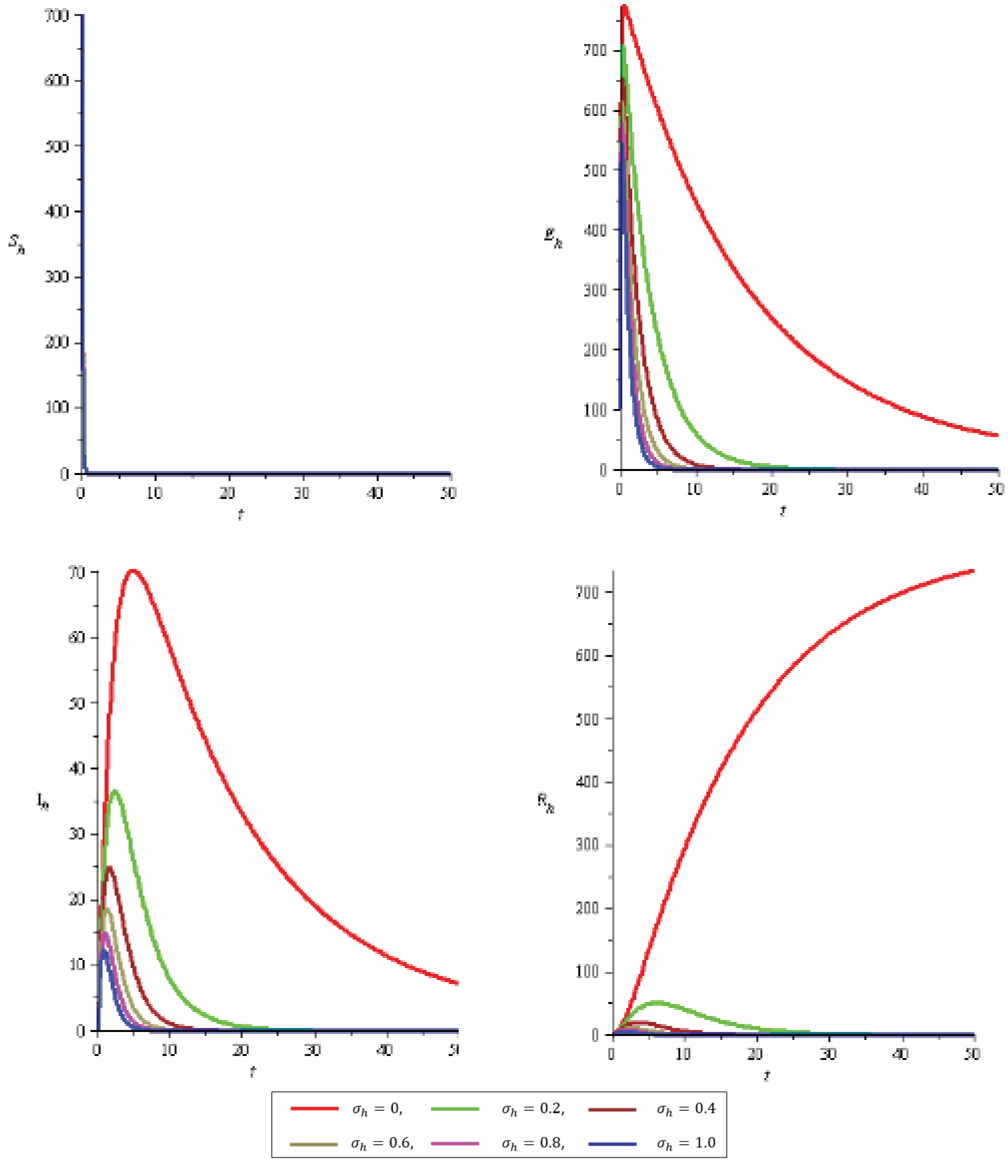


FIGURE 2. Dynamical behavior of human population when human migration is varied.

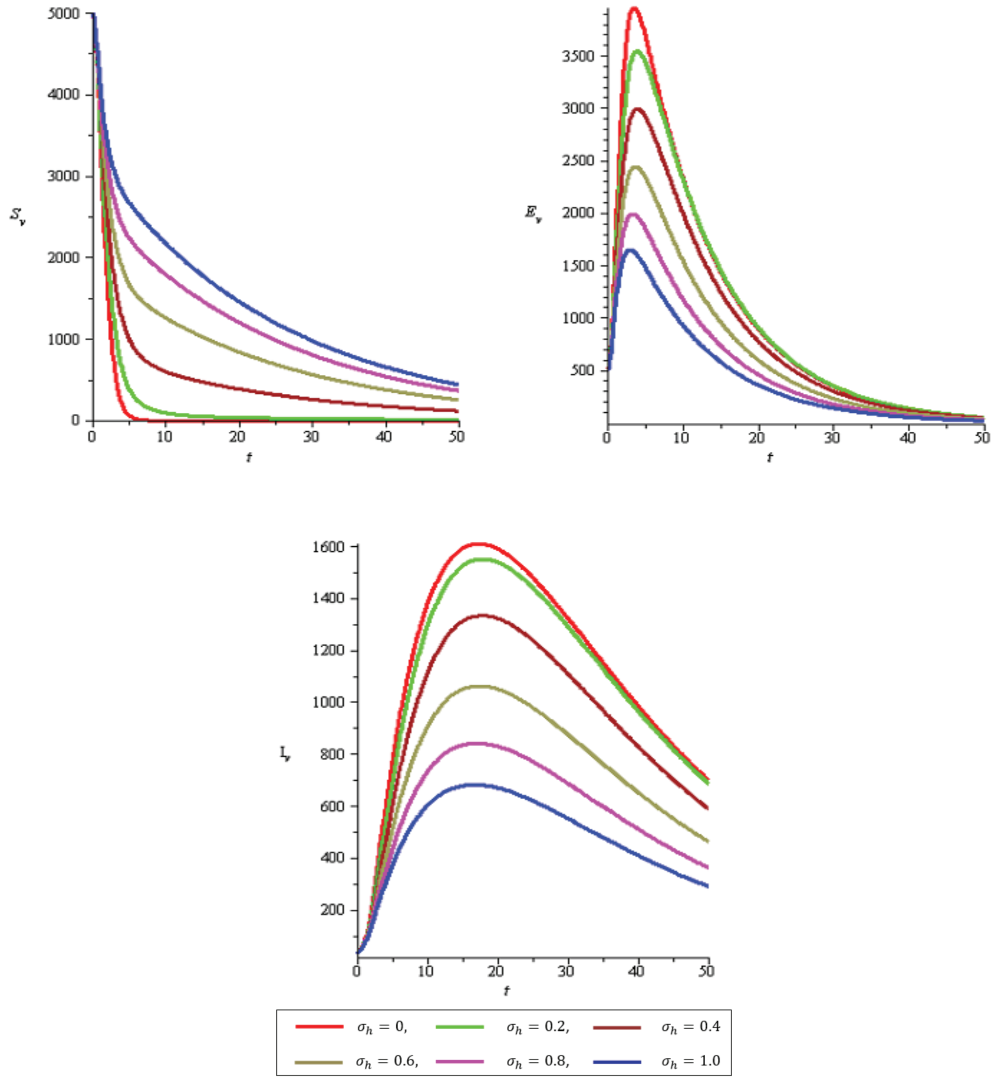


FIGURE 3. Dynamical behavior of mosquito population when human migration is varied.

CONCLUSIONS

In this paper we derived mathematical model of malaria by taking into consideration migration factors in human and mosquito populations. Analytically we found that basic reproduction number of the model was monotonically decreasing with respect to the migration parameters. It indicated that the greater migration in both populations the smaller probability of outbreak will occur in the system. Numerically we found that migration in mosquito population has the greatest effect in reducing the outbreak of malaria. Therefore minimizing the residence time of mosquitoes in the system became one of controls in reducing the growth of malaria infections.

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