Stability analysis of SEISEIR-SEI modelling on the dynamics of spread dengue fever with vaccination and insecticide

by Hartati Et Al

Submission date: 18-Jan-2023 11:22AM (UTC+0700)
Submission ID: 1994568499
File name: Hartati_2019_J._Phys.__Conf._Ser._1341_062033.pdf (1.1M)
Word count: 4524
Character count: 22432

Stability analysis of SEISEIR-SEI modelling on the dynamics of spread dengue fever with vaccination and insecticide

Stability analysis of SEISEIR-SEI modelling on the dynamics of spread dengue fever with vaccination and insecticide

H Hartati[1,a], S Toaha[1,b,*] and Kasbawati[1,c]

[1]Department of Mathematics, Hasanuddin University,
Jln. Perintis Kemerdekaan, KM 10, 90245, Makassar, Indonesia

[a] hevrianaanshar@gmail.com, [b]syamsuddint@yahoo.com, [c] kasbawati@gmail.com
[*] corresponding author

Abstract. This article focuses on analysing an SEISEIR-SEI model. This model is a development of SEIR-SEI which studies the spread of dengue fever in human and mosquito. This model considers the exposed compartment for vaccinated, non-vaccinated human and also for mosquito. Fogging strategy is also carried out as an effort to inhibit mosquito breeding. Existence and stability of non-endemic and endemic equilibrium points are investigated and analysed using linearization and eigenvalue methods. From the analyses we found a threshold value for stability of non-endemic equilibrium point. Increasing the rate of mosquito bites can reduce the threshold value and even change non-endemic condition becomes endemic. Vaccination strategy does not change the non-endemic condition, it only speeds up the convergence to the non-endemic condition. Fogging strategy only affects position of the endemic and non-endemic equilibrium points. Reducing the rate of mosquito bites can prevent endemic condition. Several numerical simulations were carried out to confirm the analytical results obtained. From simulations we know that reducing the value of threshold may switch stability of non-endemic equilibrium point from unstable to asymptotically stable.

1. Introduction

Dengue fever is one of the most infectious diseases and become a serious health problem. This disease is caused by the dengue virus which is transmitted by the bites of Aedes Aegypti mosquito [1]. Dengue fever virus (DFV) can be transmitted via transsexual from male mosquitoes to female mosquitoes and also can be transmitted via transovarial from parent mosquitoes to offspring mosquitos [2].

An SEIR epidemic model has been used to investigate and analyse the spread of endemic diseases. In general, the standard model such as SIR and SEIR model for spread of diseases has been developed according to the special conditions and needs. The standard models were developed by adding immunized compartment, migration, and the like [3, 4, 5]. Some strategies on the spread model of endemic diseases virus have been imposed in order to reduce and eliminate the diseases, for examples vaccination, treatments, inject drugs, and control the cost as a consequences of implementing the strategies [6, 7, 8].

In Agusto et al. [9], an SEIR deterministic model for spread of dengue virus was considered and used vaccination and insecticide as control variables to control optimally as a strategy to limit the spread of the diseases. Vaccination and insecticide decreased the rate of infection but increased the cost as consequences of using insecticide. An SIR standard model in [10] was used to analyse the effect of

vaccination as an effort to reduce the rate of spread of the dengue virus. The multi model approach was used to analyse the impact of active finding case in spread of dengue fever. Sensitivity analysis of basic reproduction number was applied to investigate the effect of controlled parameter.

The studies of DFV in [10, 11] were developed by considering an exposed compartment for vaccinated and non-vaccinated humans. The exposed compartment was considered to make the model become more realistic. Vaccination and fogging were also imposed into the model as a strategy to reduce the transmission of dengue fever virus. The resulted model, an SEISEIR-SEI model, was analyzed by showing the existence and stability of non-endemic and endemic equilibrium points. We analyze the stability of non-endemic equilibrium point by following the linearization and eigenvalues methods and also determine a threshold value for non-endemic situation. We need to see the effects of vaccination and insecticide to the stability of the equilibrium points. Numerical simulations are needed to confirm the effect of threshold values.

2. The SEISEIR-SEI model for DFV with vaccination and insecticide

In the dynamics of the spread of infectious diseases, humans are generally divided into four compartments. The population is classified into suspected (S), exposed (E), infected (I), and recovered (R). The SEIR model is usually used to explain the dynamics of disease that has an incubation period. The SIER model is the development of SIS and SIR models. Some of the spreads of diseases were modelled in the form of SIER, for examples model of influenza virus transmission [12], model of rabies virus transmission [13, 14], model of HIV virus transmission [15, 16], and the like model for the spread of other diseases.

In particular [10] studied the SIR model of the spread of dengue fever using vaccines and insecticide as the strategies to reduce the spread of disease. Further, the model that related to dengue fever was developed and became an SEIR-SEI model by incorporating mosquito population dynamics as a vector in the model [17]. The SEIR-SEI model is then developed again by dividing the human population into groups with and without vaccination. We also impose an insecticide into the model as a strategy to reduce the number of mosquitos. The compartments now in the model are rewritten for human without vaccination as suspected (S_H), exposed (E_H), infected (I_H), and recovered (R_H); for human with vaccination as suspected (S_{HV}), exposed (E_{HV}), infected (I_{HV}), and recovered (R_H); for mosquito as suspected (S_V), exposed (E_V), and infected (I_V). The flow of transmission of dengue fever virus with vaccination and fogging (insecticide) on the mosquito as a vector is given in figure 1.

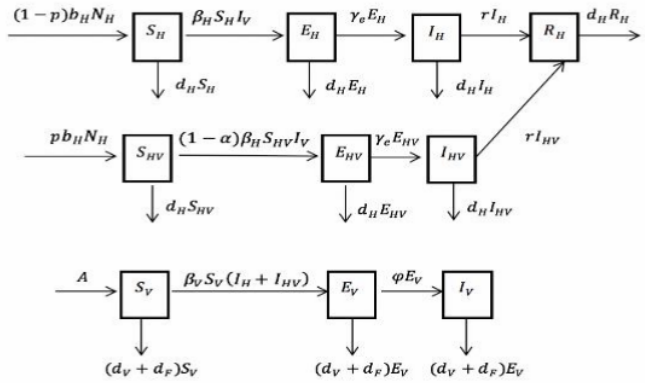

Figure 1. The flow of transmission of dengue fever in the compartments

Parameters used in this model are d_H and d_V which state the mortality rates for human and mosquito. Variables N_H and N_V are the total human and mosquito populations in time t. Paramaters β_H and β_V denote the rate of transmission of the dengue fever virus from mosquito to human and from human to

mosquito. Parameter b_H is the rate of birth for the human. The constant A is the rate of recruitment of mosquito. Parameters γ_e and φ denote the rate from exposed to infected for human and mosquito. Parameter r is the rate of infected to recovered compartment. Parameter d_F is the rate of death for mosquito which is caused by spraying insecticide. Parameter α is the effectiveness of vaccines and p is the fraction of vaccinated newborn. When the vaccination coefficient of $\alpha = 1$, then there will be no mosquitoes infected and transmit virus to the human so that there will be no transmission of dengue fever anymore.

The dynamics of each compartments in human and in mosquitos are stated as a system of autonomous differential equations which contains ten compartments, three compartments for non-vaccinated, three compartments for vaccinated, one compartment for recovered from the disease, and three compartments for mosquito. The dynamics of the compartments is given as

$$\begin{aligned}
\frac{dS_H}{dt} &= (1-p)b_H N_H - \beta_H S_H I_V - d_H S_H \\
\frac{dE_H}{dt} &= \beta_H S_H I_V - \gamma_e E_H - d_H E_H \\
\frac{dI_H}{dt} &= \gamma_e E_H - r I_H - d_H I_H \\
\frac{dS_{HV}}{dt} &= p b_H N_H - (1-\alpha)\beta_H S_{HV} I_V - d_H S_{HV} \\
\frac{dE_{HV}}{dt} &= (1-\alpha)\beta_H S_{HV} I_V - \gamma_e E_{HV} - d_H E_{HV} \\
\frac{dI_{HV}}{dt} &= \gamma_e E_{HV} - r I_{HV} - d_H I_{HV} \\
\frac{dR_H}{dt} &= r(I_H + I_{HV}) - d_H R_H \\
\frac{dS_V}{dt} &= A - \beta_V S_V (I_H + I_{HV}) - (d_V + d_F) S_V \\
\frac{dE_V}{dt} &= \beta_V S_V (I_H + I_{HV}) - \varphi_e E_V - (d_V + d_F) E_V \\
\frac{dI_V}{dt} &= \varphi_e E_V - (d_V + d_F) I_V
\end{aligned} \tag{1}$$

Total number of human population and mosquito population at time t are given as $\boldsymbol{N_H(t) = S_H(t) + E_H(t) + I_H(t) + S_{HV}(t) + E_{HV}(t) + I_{HV}(t) + R_H(t)}$ and $\boldsymbol{N_V(t) = S_V(t) + E_V(t) + I_V(t)}$. In model (1), the total human and mosquito population may be assumed to be constant in time or not constant. It merely depends on the values of parameter, particularly in determining the rates of birth and death of human. After doing normalization and scaling, model (1) is rewritten as

$$\begin{aligned}
\frac{dS_H}{dt} &= (1-p)b_H - \beta_H S_H I_V - d_H S_H \\
\frac{dE_H}{dt} &= \beta_H S_H I_V - \gamma_e E_H - d_H E_H \\
\frac{dI_H}{dt} &= \gamma_e E_H - r I_H - d_H I_H \\
\frac{dS_{HV}}{dt} &= p b_H - (1-\alpha)\beta_H S_{HV} I_V - d_H S_{HV} \\
\frac{dE_{HV}}{dt} &= (1-\alpha)\beta_H S_{HV} I_V - \gamma_e E_{HV} - d_H E_{HV} \\
\frac{dI_{HV}}{dt} &= \gamma_e E_{HV} - r I_{HV} - d_H I_{HV} \\
\frac{dR_H}{dt} &= r(I_H + I_{HV}) - d_H R_H \\
\frac{dN_V}{dt} &= A - (d_V + d_F) N_V \\
\frac{dE_V}{dt} &= \beta_V (N_V - E_V - I_V)(I_H + I_{HV}) - \varphi_e E_V - (d_V + d_F) E_V \\
\frac{dI_V}{dt} &= \varphi_e E_V - (d_V + d_F) I_V
\end{aligned} \tag{2}$$

In model (2), compartment S_V as a variable is eliminated and replaced with variable N_V. The value of equilibrium for compartment S_V is found from the relation $N_V(t) = S_V(t) + E_V(t) + I_V(t)$**.** It is easy to

check that when we assume the mosquito population $N_V(t)$ is constant in time then it will not change forever.

Since the model (2) is non-linear system, we just investigate and analyse the local behaviour of equilibrium points of the model. The linearization and eigenvalues methods will be followed to see the local stabilities. From model (2) we get the Jacobian matrix

$$J = \begin{bmatrix} -a_{11} & 0 & -a_{13} & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ a_{21} & -a_{22} & a_{23} & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & a_{32} & -a_{33} & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & -a_{43} & -a_{44} & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & a_{53} & a_{53} & -a_{55} & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & a_{65} & -a_{66} & 0 & 0 & 0 & 0 \\ 0 & 0 & a_{73} & 0 & 0 & a_{76} & -a_{77} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & -a_{88} & 0 & 0 \\ 0 & 0 & a_{93} & 0 & 0 & a_{96} & 0 & a_{98} & -a_{99} & -a_{910} \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & a_{109} & -a_{1010} \end{bmatrix}, \quad (3)$$

where $a_{11} = I_H\beta_H + d_H$, $a_{13} = a_{23} = \beta_H S_H$, $a_{21} = \beta_H I_H$, $a_{22} = \gamma_e\beta_H$, $a_{33} = a_{66} = r + d_H$, $a_{32} = a_{65} = \gamma_e$, $a_{43} = a_{53} = (1-\alpha)\beta_H S_{HV}$, $a_{44} = (1-\alpha)\beta_H I_H + d_H$, $a_{54} = (1-\alpha)\beta_H I_H$, $a_{55} = \gamma_e + d_H$, $a_{73} = a_{76} = r$, $a_{77} = d_H$, $a_{88} = a_{1010} = d_V + d_F$, $a_{93} = a_{96} = \beta_V(N_V - E_V - I_V)$, $a_{98} = a_{910} = \beta_V(I_H + I_{HV})$, $a_{99} = \beta_V(I_H + I_{HV}) + \varphi + d_V + d_F$, and $a_{109} = \varphi$.

The non-endemic and endemic equilibrium points of model (2) are reached when the rate of all compartments are set to be zero, these are

$\frac{dS_H}{dt} = 0, \frac{dE_H}{dt} = 0, \frac{dI_H}{dt} = 0, \frac{dS_{HV}}{dt} = 0, \frac{dE_{HV}}{dt} = 0, \frac{dI_{HV}}{dt} = 0, \frac{dR_H}{dt} = 0, \frac{dN_V}{dt} = 0, \frac{dE_V}{dt} = 0, \frac{dI_V}{dt} = 0$.

In order to get the equilibrium points, we set model (2) equals zero and solve the following system of equations simultaneously.

$$\begin{aligned} &(1-p)b_H - \beta_H S_H I_V - d_H S_H = 0 \\ &\beta_H S_H I_V - \gamma_e E_H - d_H E_H = 0 \\ &\gamma_e E_H - r I_H - d_H I_H = 0 \\ &pb_H - (1-\alpha)\beta_H S_{HV} I_V - d_H S_{HV} = 0 \\ &(1-\alpha)\beta_H S_{HV} I_V - \gamma_e E_{HV} - d_H E_{HV} = 0 \\ &\gamma_e E_{HV} - r I_{HV} - d_H I_{HV} = 0 \\ &r(I_H + I_{HV}) - d_H R_H = 0 \\ &A - (d_V + d_F)N_V = 0 \\ &\beta_V(I_H + I_{HV})(N_V - E_V - I_V) - \varphi E_V - (d_H + d_F)E_V = 0 \\ &\varphi E_V - (d_H + d_F)I_V = 0 \,. \end{aligned} \quad (4)$$

3. Existence and stability of non-endemic and endemic equilibrium points

The non-endemic equilibrium point in model (2) appears when there are no spreading dengue fever in the populations. This condition is satisfied when $E_H = 0$, $E_{HV} = 0$, and $E_V = 0$. When $E_H = E_{HV} = E_V = 0$, it follows $I_H = I_{HV} = I_V = R_H = 0$. Substituting $E_H = E_{HV} = E_V = I_H = I_{HV} = I_V = R_H = 0$ into equation (4), we get a non-endemic equilibrium point

$$T_0 = (S_H, E_H, I_H, S_{HV}, E_{HV}, I_{HV}, R_H, N_V, E_V, I_V) = \left(\frac{(1-p)b_H}{d_H}, 0, 0, \frac{pb_H}{d_H}, 0, 0, 0, \frac{A}{d_V + d_F}, 0, 0\right). \quad (5)$$

Theorem 1. The non-endemic equilibrium point T_0 of model (2) is locally asymptotically stable when $T_J > 0$ and unstable when $T_J < 0$, where $T_J = -\frac{\gamma_e\beta_H b_H}{d_H}(1-p) + r\gamma_e + \gamma_e d_H + r d_H + d_H^2$.

Proof. Since we just consider local stability of the equilibrium point, we linearize the model around the equilibrium point T_0 via Jacobian matrix method. From model (2) we have Jacobian matrix (3). Evaluating the Jacobian matrix at the non-endemic equilibrium point T_0, we have

$$J(T_0) = \begin{bmatrix} -d_H & 0 & -S_H\beta_H & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & -\gamma_e - d_H & S_H\beta_H & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \gamma_e & -(r+d_H) & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & (\alpha-1)\beta_H S_{HV} & -d_H & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & (1-\alpha)\beta_H S_{HV} & 0 & d_H-\gamma_e & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \gamma_e & d_H-r & 0 & 0 & 0 & 0 \\ 0 & 0 & r & 0 & 0 & r & -d_H & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & d_V-d_F & 0 & 0 \\ 0 & 0 & \beta_V N_V & 0 & 0 & \beta_V N_V & 0 & 0 & d_V+\varphi-d_F & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \varphi & d_V-d_F \end{bmatrix}.$$

From the Jacobian matrix $J(T_0)$ we have characteristic equation $f(\lambda) = det(J(T_0) - \lambda I) = 0$. From which we have

$$f(\lambda) = (\lambda+d_H)^3(\lambda+d_F+d_V)^2(\lambda+d_F+d_V+\varphi)(\lambda+r+d_H)(\gamma_e+\lambda+d_H)(-\gamma_e S_H\beta_H+\gamma_e\lambda+\gamma_e r+\gamma_e d_H+\lambda^2+\lambda r+2\lambda d_H+rd_H+d_H^2).$$

It is easy to see that the eigenvalues $\lambda_1, \lambda_2, \lambda_3, \lambda_4, \lambda_5, \lambda_6, \lambda_7$, and λ_8 are all negative. While the two remaining eigenvalues, λ_9 and λ_{10} are obtained from the quadratic equation $f_1(\lambda) = \lambda^2 + A_1\lambda + A_0 = 0$, where $A_1 = \gamma_e + r + 2d_H$, $A_0 = -\gamma_e\beta_H S_H + \gamma_e r + \gamma_e d_H + rd_H + d_H^2$, and $S_H = \frac{b_H(1-p)}{d_H}$. The roots of $f_1(\lambda)$ have negative real parts when $A_0 > 0$. After substituting the value of $S_H = \frac{b_H(1-p)}{d_H}$ we have $A_0 = T_J = -\frac{\gamma_e\beta_H b_H}{d_H}(1-p) + r\gamma_e + \gamma_e d_H + rd_H + d_H^2$. Therefore, when $T_J > 0$, then the eigenvalues λ_9 and λ_{10} have negative real part. This means that the equilibrium point T_0 is locally asymptotically stable. When $T_J < 0$, then there exists at least one eigenvalue with positive real part. Thus, the theorem is proven.

The value of $T_J = -\frac{\gamma_e\beta_H b_H}{d_H}(1-p) + r\gamma_e + \gamma_e d_H + rd_H + d_H^2$ is a threshold for the eigenvalues λ_9 and λ_{10} to have negative real part. The value of T_J depends on the rate of mosquito bites (β_H) and the rate of vaccine on the babies (p). Now, we analyse the effect of β_H and p to the value of T_J. Then we have

$$\frac{\partial T_J}{\partial \beta_H} = -\frac{\gamma_e b_H(1-p)}{d_H} < 0 \text{ and } \frac{\partial T_J}{\partial p} = \frac{\gamma_e\beta_H b_H}{d_H} > 0.$$

In the case of equilibrium point T_0 is asymptotically stable, then the value of T_J is positive. In this condition, when the value of vaccine on the babies (p) is increased then the value of T_J is also increased and remains positive. But, when the value of the rate of mosquito bites (β_H) is increased then the value of T_J will decrease, it might be positive or might be negative. When the value of T_J becomes negative, then at least one the eigenvalues λ_9 and λ_{10} will have negative real part. Therefore, increasing the value of rate of mosquito bites may lead to the instability of the equilibrium point T_0. There is a switch condition from non-endemic to endemic.

From model (2) we found the endemic equilibrium point, written as

$$T_1 = (S_H^*, E_H^*, I_H^*, S_{HV}^*, E_{HV}^*, I_{HV}^*, R_H^*, N_V^*, E_V^*, I_V^*),$$

where $S_H^* = \frac{a_2a_3}{\gamma_e\beta_H}$, $E_H^* = \frac{a_1\gamma_e\beta_H - a_2a_3d_H}{a_2\beta_H\gamma_e}$, $I_H^* = \frac{a_1\gamma_e\beta_H - a_2a_3d_H}{a_2a_3\beta_H}$, $S_{HV}^* = \frac{a_4a_2a_3\beta_H}{a_1a_5\gamma_e\beta_H - a_2a_3a_5d_H + a_2a_3\beta_Hd_H}$

$E_{HV}^* = \frac{a_5a_4(a_1\gamma_e\beta_H - a_2a_3d_H)}{a_2(a_1a_5\gamma_e\beta_H - a_2a_3a_5d_H + a_2a_3\beta_Hd_H)}$, $I_{HV}^* = \frac{a_5a_4(a_1\gamma_e\beta_H - a_2a_3d_H)\gamma_e}{a_2a_3(a_1a_5\gamma_e\beta_H - a_2a_3a_5d_H + a_2a_3\beta_Hd_H}$,

$R_H^* = \frac{r(a_1\gamma_e\beta_H - a_2a_3d_H)(a_1a_5\gamma_e\beta_H - a_2a_3a_5d_H + a_2a_3\beta_Hd_H + a_5a_4\gamma_e\beta_H)}{a_2a_3\beta_H(a_1a_5\gamma_e\beta_H - a_2a_3a_5d_H + a_2a_3\beta_Hd_H)d_H}$, $N_V^* = \frac{A}{a_7}$, $E_V^* = \frac{C}{D}$, and $I_V^* = \frac{C}{a_7\,D}$.

Besides that we write

$C = A\beta_V\big(a_1{}^2a_5\gamma_e^2\beta_H^2 - 2a_1a_2a_3a_5\gamma_e\beta_Hd_H + a_1a_2a_3\gamma_e\beta_H^2d_H + a_1a_4a_5\gamma_e^2\beta_H^2 + a_2{}^2a_3{}^2\beta_Hd_H{}^2 - a_2a_3a_4a_5\gamma_e\beta_Hd_H\big)$,

$D = (a_1{}^2a_7a_5\gamma_e^2\beta_H^2\beta_V + a_1{}^2a_5\gamma_e^2\varphi\beta_H^2\beta_V + a_1a_2a_3a_5a_6a_7\gamma_e\beta_H^2 - 2a_1a_2a_3a_5a_7\gamma_e\beta_H\beta_Vd_H - 2a_1a_2a_3a_5\gamma_e\varphi\beta_H\beta_Vd_H + a_1a_2a_3a_7\gamma_e\beta_H^2\beta_Vd_H + a_1a_2a_3\gamma_e\varphi\beta_H^2\beta_Vd_H + a_1a_4a_5a_7\,\gamma_e^2\beta_H^2\beta_V + a_1a_4a_5\gamma_e^2\varphi\beta_H^2\beta_V - a_2{}^2a_3{}^2a_5a_6a_7\beta_Hd_H + a_2{}^2a_3{}^2a_5a_7d_H^2\beta_V + a_2{}^2a_3{}^2a_6a_7\beta_H^2d_H - a_2{}^2a_3{}^2a_7d_H^2\beta_V\beta_H - a_2{}^2a_3{}^2\varphi d_H^2\beta_V\beta_H - a_2a_3a_4a_5a_7\gamma_e\beta_H\beta_Vd_H - a_2a_3a_4a_5\gamma_e\beta_H\beta_Vd_H)$,

where $a_1 = (1-p)b_H, a_2 = \gamma_e + d_H, a_3 = r + d_H, a_4 = pb_H, a_5 = (1-\alpha)\beta_H, a_6 = d_F + d_V + \varphi$, and $a_7 = d_F + d_V$.

Evaluating the Jacobian matrix (3) at the equilibrium point T_1 lead us to the characteristic equation $f(\lambda) = det(J(T_1) - \lambda I) = 0$, that is

$f(\lambda) = \frac{1}{a_2{}^2a_3{}^2\beta_H^2(a_1a_5\gamma_e\beta_H + a_2a_3\alpha\beta_Hd_H)}\big((\lambda + d_H)(a_7+\lambda)(a_3+\lambda)(\alpha+\lambda)(a_1a_2a_3\gamma_e\beta_H + a_1a_2\gamma_e\lambda\beta_H + a_1a_3\gamma_e\lambda\beta_H + a_1\gamma_e\lambda^2\beta_H - a_2{}^2a_3{}^2d_H + a_2{}^2a_3\lambda^2 + a_2{}^2a_3{}^2\lambda^2 + a_2a_3\lambda^3)(a_1a_5\gamma_e\beta_H + a_2a_3\lambda\beta_H + a_2a_3\alpha\beta_Hd_H)(a_1{}^2a_5a_7\gamma_e^2\beta_H^2\beta_V + a_1{}^2a_5\gamma_e^2\lambda\beta_H^2\beta_V + a_1{}^2a_5\gamma_e^2\varphi\beta_H^2\beta_V + a_1a_2a_3a_5a_6a_7\gamma_e\beta_H^2 + a_1a_2a_3a_5a_6\gamma_e\lambda\beta_H^2 + a_1a_2a_3a_5a_7\gamma_e\lambda\beta_H^2 - a_1a_2a_3a_5a_7\gamma_e\beta_H\beta_Vd_H + a_1a_2a_3a_5\gamma_e\lambda^2\beta_H^2 - 2a_1a_2a_3a_5a_7\gamma_e\beta_H\beta_Vd_H - \gamma_e\varphi\beta_H\beta_Vd_H + a_1a_2a_3a_7\gamma_e\beta_H^2\beta_Vd_H + a_1a_2a_3\gamma_e\varphi\beta_H^2\beta_Vd_H + a_1a_4a_5a_7\gamma_e^2\beta_H^2\beta_V + a_1a_4a_5\gamma_e^2\lambda\beta_H^2\beta_V + a_1a_4a_5\gamma_e^2\varphi\beta_H^2\beta_V - a_2{}^2a_3{}^2a_5a_6a_7\beta_Hd_H - a_2{}^2a_3{}^2a_5a_6\lambda\beta_Hd_H - a_2{}^2a_3{}^2a_5a_7\lambda\beta_Hd_H + a_2{}^2a_3{}^2a_5a_7\beta_Vd_H^2 - a_2{}^2a_3{}^2a_5\lambda^2\beta_Hd_H + a_2{}^2a_3{}^2a_5\lambda\beta_Vd_H^2 + a_2{}^2a_3{}^2a_5\varphi\beta_Vd_H^2 + a_2{}^2a_3{}^2a_6a_7\beta_H^2d_H + a_2{}^2a_3{}^2a_6\lambda\beta_H^2d_H + a_2{}^2a_3{}^2a_7\lambda\beta_H^2d_H - a_2{}^2a_3{}^2a_7\beta_H\beta_Vd_H^2 + a_2{}^2a_3{}^2\lambda^2\beta_H^2d_H - a_2{}^2a_3{}^2\lambda\beta_H\beta_Vd_H^2 - a_2{}^2a_3{}^2\varphi\beta_H\beta_Vd_H^2 - a_2a_3a_4a_7\gamma_e\beta_H\beta_Vd_H - a_2a_3a_5\gamma_e\lambda\beta_H\beta_Vd_H - 2a_3a_5\gamma_e\varphi\beta_H\beta_Vd_H)\big)$.

From $f(\lambda)$ we know that eigenvalues $\lambda_1, \lambda_2, \lambda_3, \lambda_4, \lambda_5$ are all negative. The eigenvalues $\lambda_6, \lambda_7, \lambda_8$ are the roots of

$$f_3(\lambda) = \lambda^3 + B_2\lambda^2 + B_1\lambda + B_0\,,$$

where $B_2 = \frac{a_1\gamma_e\beta_H + a_2{}^2a_3 + a_2a_3{}^2}{a_2a_3}$, $B_1 = \frac{a_1a_2\gamma_e\beta_H + a_1a_3\gamma_e\beta_H}{a_2a_3}$, and $B_0 = \frac{a_1a_2a_3\gamma_e\beta_H - a_2{}^2a_3{}^2d_H}{a_2a_3}$.

While the eigenvalues λ_9 and λ_{10} are the roots of

$$f_4(\lambda) = \lambda^2 + P_1\lambda + P_0\,,$$

where $P_1 = \frac{R_1}{R_0}$ and $P_0 = \frac{R_2}{R_0}$,

$R_0 = a_2{}^3a_3{}^3\beta_H^2(a_1a_5\gamma_e\beta_H + a_2a_3\alpha\beta_Hd_H)$,

$R_1 = (a_1{}^2a_5\gamma_e^2\beta_H^2\beta_V + a_1a_2a_3a_5a_6\gamma_e\beta_H^2 + a_1a_2a_3a_5a_7\gamma_e\beta_H^2 - 2a_1a_2a_3a_5\gamma_e\beta_H\beta_Vd_H + a_1a_2a_3\beta_H^2\beta_Vd_H + a_1a_4a_5\gamma_e^2\beta_H^2\beta_V - a_2{}^2a_3{}^2a_5a_6\beta_Hd_H - a_2{}^2a_3{}^2a_5a_7\beta_Hd_H + a_2{}^2a_3{}^2a_5a_6\beta_Vd_H^2 + a_2{}^2a_3{}^2a_7\beta_H^2d_H - a_2{}^2a_3{}^2\beta_H\beta_Vd_H^2 - a_2a_3a_4a_5\gamma_e\beta_H\beta_Vd_H)$, and

$R_2 = a_1{}^2a_5a_7\gamma_e^2\beta_H^2\beta_V + a_1{}^2a_5\gamma_e^2\varphi\beta_H^2\beta_V + a_1a_2a_3a_5a_6a_7\gamma_e\beta_H^2 - 2a_1a_2a_3a_5a_7\gamma_e\beta_H\beta_Vd_H - 2a_1a_2a_3a_5\gamma_e\varphi\beta_H\beta_Vd_H + a_1a_2a_3a_7\gamma_e\beta_H^2\beta_Vd_H + a_1a_2a_3a_7\gamma_e\varphi\beta_H^2\beta_Vd_H + a_1a_4a_5a_7\gamma_e^2\beta_H^2\beta_V + a_1a_4a_5\gamma_e^2\varphi\beta_H^2\beta_V - a_2{}^2a_3{}^2a_5a_6a_7\beta_Hd_H + a_2{}^2a_3{}^2a_5a_7\beta_Vd_H^2 + a_2{}^2a_3{}^2a_5\varphi\beta_Vd_H^2 + a_2{}^2a_3{}^2a_6a_7\beta_H^2d_H - a_2{}^2a_3{}^2a_7\beta_H\beta_Vd_H^2 - a_2{}^2a_3{}^2\varphi\beta_H\beta_Vd_H^2 - a_2a_3a_4a_5a_7\gamma_e\beta_H\beta_Vd_H - a_2a_3a_4a_5\gamma_e\varphi\beta_H\beta_Vd_H$.

Following the Routh-Hurwitz stability criteria [18], the equilibrium point T_1 is locally asymptotically stable when the criteria $B_2, B_1, B_0 > 0$, $B_2B_0 - {B_2}^2B_1 > 0$, $P_1, P_0 > 0$ are satisfied.

4. Numerical simulations

4.1. The effect of mosquito bites to the threshold T_J.

Suppose the values of parameter of model (2) are given as $b_H = 0.3$, $\beta_V = 0.3$, $\gamma_e = 0.9$, $r = 0.3$, $\alpha = 0.95$, $A = 0.5$, $\varphi = 0.9$, $d_H = 0.10$, $d_V = 0.54$, and $d_F = 0.25$ in appropriate units. With these parameters we have threshold function $T_J = -\frac{\gamma_e \beta_H b_H}{d_H}(1-p) + r\gamma_e + \gamma_e d_H + r d_H + d_H^2$ is a function of p and β_H, that is $T_J(p, \beta_H) = 0.6200 + (-0.9000 + 0.9000\, p)\beta_H$. Graph of $T_J(p, \beta_H) = 0$ is given in figure 2.

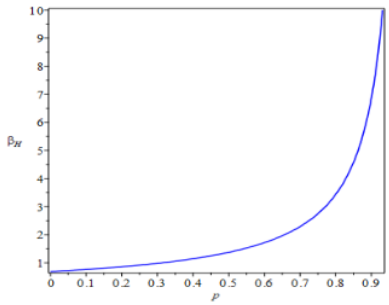

Figure 2. Graph of threshold value of $T_J(p, \beta_H) = 0$.

Figure 2 shows that when the pair value of (p, β_H), lies below the threshold then $T_J(p, \beta_H) > 0$. While when the pair value of (p, β_H) lies above the threshold then $T_J(p, \beta_H) < 0$. When we put a fixed value of p and the value of β_H is increased gradually, we may have condition which is initially the value of $T_J(p, \beta_H) > 0$ and then the value of $T_J(p, \beta_H) < 0$, see table 1. This means that there exists a switch condition from non-endemic to endemic. Put a fixed value of $p = 0.25$ and the value of $\beta_H = 0.875$, 0.90, and 0.93 for simulation.

Table 1. The effect of mosquito bites (β_H) to the value of threshold T_J

Parameter β_H	Threshold T_J	Equilibrium point T_0 and eigenvalues λ_9 and λ_{10}	Equilibrium point T_1 and stability
0.875	0.02937	$\lambda_9 = -0.0183,\ \lambda_{10} = -1.6017, T_0$ stable	T_1 does not exist
0.90	0.01250	$\lambda_9 = -0.0078,\ \lambda_{10} = -1.6122, T_0$ stable	T_1 does not exist
0.93	−0.00775	$\lambda_9 = 0.0047,\ \lambda_{10} = -1.6248, T_0$ not stable	T_1 exists and stable

4.2. Example of endemic condition

In this simulation we show the existence and stability of endemic equilibrium point. We suppose that the values of parameter of model (2) are given as $p = 0.25$, $b_H = 0.3$, $\beta_H = 0.95$, $\beta_V = 0.3$, $\gamma_e = 0.9$, $r = 0.3$, $\alpha = 0.95$, $A = 0.5$, $\varphi = 0.9$, $d_H = 0.10$, $d_V = 0.54$, and $d_F = 0.25$ in appropriate units. We have the threshold value of $T_J = -0.00775$ and the non-endemic equilibrium point is written as

$$T_0 = (0.7500, 0, 0, 0.2500, 0, 0, 0, 0.6329, 0, 0)$$

with eigenvalues $\{-0.1000, -0.1000, -0.1000, -0.7900, -1.6900, -0.6200, -1.0000, -1.000, \mathbf{0.0130}, -0.7900\}$.

The endemic equilibrium point is written as

$$T_1 = (0.72515, 0.02485, 0.03608, 0.24957, 0.00004, 0.00006, 0.01908, 0.63291, 0.00041, 0.00047)$$

with eigenvalues
$\{-0.100, -0.1690, -1.6209, -1.000, -0.0150, -0.6200, -0.08760, -0.7911, -0.1002, -0.7900\}$.

From the value of threshold T_J and the eigenvalues associated with the non-endemic and endemic equilibrium points, we know that the endemic condition exists since all of the eigenvalues associated with the endemic equilibrium point are negative. But, when the value of mosquito bites is decreased gradually, for example, $\beta_H = 0.95, 0.93$, and 0.90, the endemic equilibrium point will not exist and the non-endemic equilibrium point becomes stable, see table 2.

Table 2. The effect of mosquito bites (β_H) to the endemic equilibrium point.

Parameter β_H	Threshold T_J	Equilibrium point T_1 and stability	Equilibrium point T_0 and eigenvalues λ_9 and λ_{10}
0.95	-0.02125	T_1 exists and stable	$\lambda_9 = 0.0130,\ \lambda_{10} = -1.6330, T_0$ not stable
0.93	-0.00775	T_1 exists and stable	$\lambda_9 = 0.0047,\ \lambda_{10} = -1.6248, T_0$ not stable
0.90	0.01250	T_1 does not exist	$\lambda_9 = -0.0078,\ \lambda_{10} = -1.6122, T_0$ stable

5. Results and discussions

The SEISEIR-SEI model (2) has non-endemic and endemic equilibrium points. The non-endemic equilibrium point is locally asymptotically stable when the threshold value of $T_J > 0$ and it is unstable when $T_J < 0$. The threshold value measures whether the real part of all the eigenvalues associated with the non-endemic equilibrium point are negative or not. When the value of $T_J > 0$ then all of the eigenvalues have negative real parts. This means that the non-endemic equilibrium point is locally asymptotically stable. The dengue fever does not spread to human population. We can say that the threshold value of T_J which is obtained from the Jacobian matrix evaluated at the non-endemic equilibrium point seems similar to the basic reproduction number (R_0).

It is found from the analyses that the mosquito bites affect the endemic and non-endemic situations. If the value of mosquito bites (β_H) increases, it will affect the stability of non-endemic equilibrium point. It may switch the non-endemic to endemic situation. Decreasing value of mosquito bites (β_H) may also change the existence of endemic equilibrium point. When the endemic equilibrium point does not exist, the non-endemic equilibrium becomes stable. Vaccination to the baby does not affect the existence and stability of the equilibrium points. It just change the value of each compartments equilibrium but stability of the equilibrium points do not change. Vaccination does not affect the non-endemic and endemic situations.

References

[1] D J Gubler 2002 Epidemic dengue/dengue hemorrhagic fever as a public health, social and economic problem in the 21st century *Trends in Microbiology* **10** 100-103

[2] A Rohani, I Zamree, H L Lee, I Mustafakamalb, M J Norjaizab and D Kamilanc 2007 Detection of transovarial dengue virus from field-caught aedes aegypti and ae. albopictus larvae using C6/36 cell culture and reverse transcriptase-polymerase chain reaction (RT-PCR) techniques *Dengue Bulletin* **31** 47-57

[3] C Sun and Y H Hsieh 2010 Global analysis of an SEIR model with varying population size and vaccination *Applied Mathematical Modelling* **34**(10) 2685-2697

[4] J Li and N Cui 2013 Dynamic Analysis of an SEIR model with distinct incidence for exposed and infectives *Scientific World Journal* 871393. doi: 10.1155/2013/871393

[5] L K Beay, Kasbawati and S Toaha 2017 Effects of human and mosquito migrations on the dynamical behavior of the spread of malaria *AIP Conference Proceedings* 1825, 020006, https://doi.org/ 10.1063/1.4978975

[6] J Wong, M Payne and S Hollenberg 2014 A double-dose hepatitis B vaccination schedule in travelers presenting for late consultation *Journal of Travel Medicine* **21**(4) 260-265
[7] N Scott, M Hellard and E S McBryde 2016 Modeling hepatitis C virus transmission among people who inject drugs: Assumptions, limitations and future challenges *Virulence* **7**(2): 201-208
[8] S C Chen, M Toy, J M Yeh, J Wang and S Resch 2013 Cost-effectiveness of augmenting universal hepatitis B vaccination with immunoglobin treatment *Pediatrics* **131**(4) e1135-e1143. doi:10.1542/peds.2012-1262
[9] F B Agusto and M A Khan 2018 Optimal control strategies for dengue transmission in Pakistan *Mathematical Biosciences* **305** 102-121
[10] P Chanprasopchai, I M Tang and P Pongsumpun 2018 SIR model for dengue disease with effect of dengue vaccination *Comput Math Methods Med*. Article ID 9861572, https://doi.org/10.1155/2018/9861572
[11] I Ghosh, P K Tiwari and J Chattopadhyaya 2019 Effect of active case finding on dengue control: Implications from a mathematical model *J Theor Biol*. **464** 50–62
[12] F Etbaigha, A R Willms and Z Poljak 2018 An SEIR model of influenza a virus infection and reinfection within a farrow-to-finish swine farm *PLoS ONE* **13**(9) e0202493. https://doi.org/10.1371/ journal.pone.0202493
[13] E D Wiraningsih, F Agusto, L Aryati, S Lenhart, S Toaha, Widodo and W Govaerts 2015 Stability analysis of rabies model with vaccination effect and culling in dogs *Applied Mathematical Sciences* **9**(77) 3805-3817
[14] S Ruan 2017 Modeling the transmission dynamics and control of rabies in China *Math Biosci*. **286** 65-93. doi: 10.1016/j.mbs.2017.02.005.
[15] C Sun and Y H Hsieh 2010 Global analysis of an SEIR model with varying population size and vaccination *Applied Mathematical Modelling* **34**(10) 2685-2697
[16] J Li and N Cui 2013 Dynamic Analysis of an SEIR model with distinct incidence for exposed and infectives *Scientific World Journal* 871393. doi: 10.1155/2013/871393
[17] R Isea 2014 Analysis of an SEIR-SEI four-strain epidemic dengue model with primary and secondary infections *Revista Electronica Conosirniento Libre y Licenciarniento (CLIC)* **7** 3-7
[18] J D Murray 2002 *Mathematical biology: An introduction* (New York: Springer)

Stability analysis of SEISEIR-SEI modelling on the dynamics of spread dengue fever with vaccination and insecticide

ORIGINALITY REPORT

4%	4%	5%	6%
SIMILARITY INDEX	INTERNET SOURCES	PUBLICATIONS	STUDENT PAPERS

PRIMARY SOURCES

1	Submitted to Universitas Hasanuddin Student Paper	4%

Exclude quotes	On	Exclude matches	< 2%
Exclude bibliography	Off		