A SEIRS Model Analysis And Simulation For Dengue Fever Transmission

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Abstract: This study aims to obtain a SEIRS model and analysis for dengue fever transmission. The SEIRS model is a modification of the SEIR model; the method used is the lyapunov function method in the global stability analysis of the SEIRS model, simulation models using MATLAB software and the data used is assumption data. The results obtained are the SEIRS model for transmission of dengue fever which is a non-linear differential equation with a seven dimension. The results of the model analysis provide information on the existence theorem, disease-free status and endemic dengue fever. Simulation results can predict the number of dengue fever cases, both for cases of disease-free and endemic dengue fever. Model simulation can be used to predict the number of cases of dengue fever in a region while providing disease status information so that the government can take preventive measures early.

Index Terms: SEIRS model; Model analysis; simulation of SEIRS Model.

1. INTRODUCTION

Dengue fever (DHF) is a disease caused by a virus from the genus Togaviridae, subgenus Flavivirus. This virus infects humans through mosquito bites as a vector. This vector bite will transmit the virus through its saliva, so that healthy people can become infected. In general, this case occurs in tropical and subtropical regions, especially in urban and semi-urban areas because the conditions are suitable for breeding mosquitoes [1]. One of the most worrying aspects of global warming is the possible impact on dengue infectious diseases, which risks infecting 128 countries and 3.9 billion people, more than half of the world's population. Although the mortality rate is only around 2.5%, the disease affects so many people it is a big burden on the health services of the affected countries [1]. Research on mathematical models to detect and predict the number of dengue cases has been carried out [2], [3], [4], [5], [6], [7], [8], [9], [10], [11], [12]. The study built and analyzed the SIR and SEIR models for transmission of dengue fever. The model assumes that patients who have recovered from dengue fever become immune so they will not get infected with dengue fever. Current facts show that many patients who have recovered are infected with dengue. Based on this, this study builds a SEIRS model as a modification of the SEIR model by considering that patients who have recovered can be re-infected with dengue fever. The first part of this paper is to build a SEIRS model; second is to analyze the model by proving the theorem of existence, free-disease and endemic cases of dengue fever. The next part is to analyze the stability of the model and the last part is a simulation of the SEIRS model for cases of free-disease and endemic dengue fever with MATLAB. Simulation results predict the number of dengue fever sufferers in both cases.

2 METHOD

This research is a theoretical and applied study. The model built is the development and modification of the SEIR model [8]. Global analysis of the SEIRS model that contains the existence theorem, free-disease and endemic using the Lyapunov function method [8,10]. Model simulation to predict the number of dengue fever cases uses assumption data for two cases, namely free-disease and endemic using MATLAB Software.

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3 RESULT AND DISCUSSION

3.1 A SEIRS MODEL FOR DENGUE FEVER TRANSMISSION

Changes that occur in each human population in the transmission of DHF for the SEIRS model can be interpreted in the form of Figure 1 below:

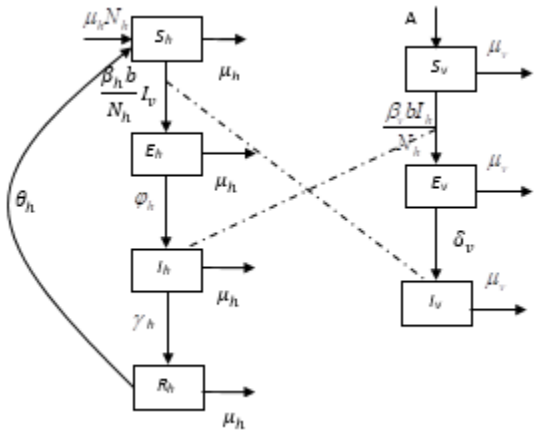

***Fig. 1**. Human Population and Mosquito Scheme for Transmission of DHF SEIRS Model*

The variables and parameters used in the SEIRS model of dengue transmission are defined in the following table 1:

TABLE 1
Variable definitions and model SEIRS parameters

Variable/Parameter	Definition
N_h	Total human population
S_h	Number of Suspected population
E_h	Number of Exposed population
I_h	Number of Infected population
R_{h_Z}	Number of Recovered population

S_v	Number of Suspected vector
E_v	Number of Exposed vector
I_v	Number of Infected vector
β_h	The rate of individuals who have been infected with suspected mosquitoes
b	The average mosquito bite has the potential to be infected
φ_h	The rate of suspected human but has not been infected by the dengue virus
γ_h	The rate of recovered humans from infection with dengue virus
β_v	The rate of mosquitoes that have been infected with exposed individuals
δ_v	The rate of suspected humans but has not been infected by the dengue virus
μ_h	Number of deaths in the human population
μ_v	Number of deaths in the mosquito population

Based on the human and mosquito population scheme in Figure 1, the rate of change in the number of humans that are Suspected, Exposed, Infected and Recovered and the rate of change of vectors that are Suspected, Exposed and Infected DBD against time can be interpreted in equations (1) and (2):

Human Population

$$\begin{aligned}\frac{dS_h}{dt} &= \mu_h N_h - \frac{\beta_h b}{N_h} I_v S_h - \mu_h S_h + \theta_h R_h \\ \frac{dE_h}{dt} &= \frac{\beta_h b}{N_h} I_v S_h - (\mu_h + \varphi_h) E_h \\ \frac{dI_h}{dt} &= \varphi_h E_h - (\mu_h + \gamma_h) I_h \\ \frac{dR_h}{dt} &= \gamma_h I_h - \mu_h R_h - \theta_h R_h\end{aligned} \quad (1)$$

Vector Population

$$\begin{aligned}\frac{dS_v}{dt} &= A - \left(\frac{\beta_v b I_h}{N_h} + \mu_v\right) S_v \\ \frac{dE_v}{dt} &= \frac{\beta_v b I_h}{N_h} S_v - (\mu_v + \delta_v) E_v \\ \frac{dI_v}{dt} &= \delta_v E_v - \mu_v I_v\end{aligned} \quad (2)$$

3.1 Analysis of SEIRS Model for Dengue Fever Transmission

All model variables and parameters are non-negative and can be seen easily in system (1) and system (2), non-negative octants R_+^5 are positive invariants. The following theorem 1 explains the existence of dengue fever transmission.

Theorem 1.

Let $(S_h(t) > 0, I_h(t) > 0, R_h(t) > 0, S_v(t) > 0, I_v(t) > 0)$ is the solution of the equation (1) and (2) with the initial state $(S_{0h}, I_{0h}. R_{0h}, S_{0v}, I_{0v})$ and set in

$$D = \left\{\left(S_h(t), I_h(t), R_h(t), S_v(t), I_h(t)\right) \in R_+^5, L_1 \geq N_h, L_2 \geq \frac{A}{\mu_v}\right\} \quad (3)$$

For the syste of invariants that cover all internal resolutions R_+^5.

Proof

Let an elegant Lyapunov function

$$L(t) = \left(L_1(t), L_2(t)\right) = \left(S_h(t) + E_h(t) + I_h(t) + R_h(t), S_v(t) + E_v(t) + I_v(t)\right) \quad (4)$$

Differential of the function L (t) so that it is obtained:

$$\begin{aligned}\frac{dL}{dt} &= \left(\frac{dL_1}{dt}, \frac{dL_2}{dt}\right) = \left(\frac{dS_h}{dt} + \frac{dE_h}{dt} + \frac{dI_h}{dt} + \frac{dR_h}{dt}, \frac{dS_v}{dt} + \frac{dE_v}{dt} + \frac{dI_v}{dt}\right) \\ &= \left[\left(\mu_h N_h - \left(\frac{b\beta_h I_v}{N_h} + \mu_h\right) S_h + \theta_h R_h\right) + \left(\frac{b\beta_h I_v}{N_h} S_h - (\mu_h + \varphi_h) E_h\right) + (\varphi_h E_h - (\mu_h + \gamma_h) I_h) + (\gamma_h I_h - \mu_h R_h - \theta_h R_h)\right), \left(\left(A - \left(\frac{b\beta_v I_h}{N_h} + \mu_v\right) S_v\right) + \frac{b\beta_v I_h}{N_h} S_v - (\mu_v + \delta_v) E_v + \delta_v E_v - \mu_v I_v\right)] \\ &= (\mu_h N_h - \mu_h S_h - \mu_h E_h - \mu_h I_h - \mu_h R_h, A - \mu_v S_v - \mu_v E_v - \mu_v I_v) \\ &= (\mu_h N_h - (S_h + E_h + I_h + R_h)\mu_h, A - (S_v + E_v + I_v)\mu_v) \\ &= (\mu_h N_h - \mu_h L_1, A - \mu_v L_2)\end{aligned} \quad (5)$$

Then found:

$$\frac{dL_1}{d_t} = \mu_h N_h - \mu_h L_1 \leq 0 \text{ for } L_1 \geq N_h \quad (6)$$

$$\frac{dL_2}{d_t} = A - \mu_v L_2 \leq 0 \text{ for } L_2 \geq \frac{A}{\mu_v} = N_v \quad (7)$$

Based on equations (6) and (7), it is obtained that $\frac{dL}{dt} \leq 0$ which explains that D is a positive invariant set. Conversely, by completing the system of equations (6) and (7) the following results are obtained:

$$0 \leq \left(L_1(t), L_2(t)\right) \leq \left(N_h + L_1(0)e^{-\mu_h t}, \frac{A}{\mu_v} + L_2(0)e^{-(\mu_v t)}\right)$$

With $L_1(0)$ and $L_2(0)$ are initial condition of $L_1(t)$ and $L_2(t)$, then, for $t \to \infty$ found $0 \leq (L_1(t), L_2(t)) \leq \left(N_h, \frac{A}{\mu_v}\right)$

This concludes that D is a set of positive invariants that covers all solutions in R_+^5. This proves theorem 1.

3.2 Global Stability Analysis

The equilibrium points of the SEIRS model of transmission of dengue fever in system (1) are $(S_h^*, E_h^*, I_h^*, R_h^*, S_v^*, E_v^*, I_v^*) = (N_h, 0,0,0, \frac{A}{\mu_v}, 0,0)$. The Jacobian matrix of the system (1) is defined as follows:

$$\mathrm{J} = \begin{bmatrix} -\mu_h & 0 & 0 & \theta_h & 0 & 0 & -b\beta_h \\ 0 & -\mu_h - \varphi_h & 0 & 0 & 0 & 0 & b\beta_h \\ 0 & \varphi_h & -\mu_h - \gamma_h & 0 & 0 & 0 & 0 \\ 0 & 0 & \gamma_h & -\mu_h - \theta_h & 0 & 0 & 0 \\ 0 & 0 & -b\beta_v & 0 & -\mu_v & 0 & 0 \\ 0 & 0 & b\beta_v & 0 & 0 & -\delta_v - \mu_h & 0 \\ 0 & 0 & 0 & 0 & 0 & \delta_v & -\mu_h \end{bmatrix}$$

The Eigen values obtained are:

$$\lambda_1 = -\mu_h \; ; \lambda_2 = -\mu_v; \lambda_3 = -\mu_h - \theta_h \text{ and} \quad (8)$$

$$\lambda_{4,5,6,7} = root\, of(\lambda^4 + (\delta_v + \gamma_h + 4\mu_h + \varphi_h)\lambda^3 + (\delta_v\gamma_h + 3\delta_v\mu_h + \delta_v\varphi_h + 3\gamma_h\mu_h + \gamma_h\varphi_h + 6\mu_h^2 + 3\mu_h\varphi_h)\lambda^2 + (2\delta_v\gamma_h\mu_h + \delta_v\gamma_h\varphi_h + 3\delta_v\mu_h^2 + 2\delta_v\mu_h\varphi_h + 3\gamma_h\mu_h^2 + 2\gamma_h\mu_h\varphi_h + 4\mu_h^3 + 3\mu_h^2\varphi_h)\lambda - b^2\beta_h\beta_v\delta_v\varphi_h + \delta_v\mu_h(\gamma_h\mu_h + \gamma_h\varphi_h + \mu_h^2 + \mu_h\varphi_h) + \gamma_h\mu_h^3 + \gamma_h\mu_h^2\varphi_h + \mu_h^4 + \mu_h^3\varphi_h) \quad (9)$$

From the equation (9), the basic reproduction number R_0 for the system (1) of the SEIRS model can be obtained using the method [13, 14], that is:

$$R_0 = \frac{\mu_v(\delta_v + \mu_v)(\mu_h + \varphi_h)(\mu_h + \gamma_h)}{b^2\beta_h\beta_v(\mu_h + 2\varphi_h)} \quad (10)$$

3.3 Global Stability of Free Disease of Model SEIRS for Dengue Fever Transmission

The system (1) applies free disease equilibrium of $(S_h^*, E_h^*, I_h^*, R_h^*, S_v^*, E_v^*, I_v^*) = (N_h, 0,0,0, A/\mu_v, 0,0)$. Indicating the possibility of the disease to fade out. The following Theorem 2 explains the behavior of the free disease equilibrium globally for

the system (1).

Theorem 2.

If $R_0 \leq 1$, then the free disease equilibrium $(S_h^*, E_h^*, I_h^*, R_h^*, S_v^*, E_v^*, I_v^*) = (N_h, 0,0,0, \frac{A}{\mu_v}, 0,0)$ in global stage is asymptotically stable in D, by assumsing that $\mu_v = \frac{b\beta_h S_h^*}{N_h}$; $\mu_h = \frac{b\beta_v S_v^*}{N_h}$; dan $R_0 \leq 1$

Proof:

An elegant Lyapunov Function constructed for the system is:

$$W(t) = (S_h - S_h^* \ln S_h) + E_h + I_h + R_h + (S_v - S_v^* \ln S_v) \quad (12)$$

The differential of $W(t)$ with respect to time that satisfies the equation (12) is:

$$\begin{aligned}
\dot{W(t)} &= \dot{S_h}\left(1 - \frac{S_h^*}{S_h}\right) + \dot{E_h} + \dot{I_h} + \dot{R_h} + \dot{S_v}\left(1 - \frac{S_v^*}{S_v}\right) + \dot{E_v} + \dot{I_v} \\
&= \left[\left(\mu_h N_h - \left(\frac{b\beta_h I_v}{N_h} + \mu_h\right) S_h + \theta_h R_h\right)\left(1 - \frac{S_h^*}{S_h}\right)\right] + \\
&\quad \left[\frac{b\beta_h I_v}{N_h} S_h - (\mu_h + \varphi_h) E_h\right] + [\varphi_h E_h - (\mu_h + \gamma_h) I_h] + \\
&\quad [\gamma_h I_h - \mu_h R_h - \theta_h R_h] + \left[\left(A - \left(\frac{b\beta_v I_h}{N_h} + \mu_v\right) S_v\right)\left(1 - \frac{S_v^*}{S_v}\right)\right] + \left[\frac{b\beta_v I_h}{N_h} S_v - (\mu_v + \delta_v) E_v\right] + [\delta_v E_v - \mu_v I_v] \\
&= \mu_h N_h \left(1 - \frac{S_h^*}{S_h}\right) + \theta_h R_h \left(1 - \frac{S_h^*}{S_h}\right) - \frac{b\beta_h I_v}{N_h} S_h + \frac{b\beta_h I_v}{N_h} S_h^* - \\
&\quad \mu_h S_h + \mu_h S_h^* + \frac{b\beta_h I_v}{N_h} S_h - \mu_h E_h - \varphi_h E_h + \varphi_h E_h - \\
&\quad \mu_h I_h + \gamma_h I_h + \gamma_h I_h - \mu_h R_h - \theta_h R_h + A\left(1 - \frac{S_v^*}{S_v}\right) - \\
&\quad \frac{b\beta_v I_h}{N_h} S_v + \frac{b\beta_v I_h}{N_h} S_v^* - \mu_v S_v + \mu_v S_v^* + \frac{b\beta_v I_h}{N_h} S_v - \mu_v E_v - \\
&\quad \delta_v E_v - \mu_v I_v \\
&= \mu_h N_h \left(1 - \frac{S_h^*}{S_h}\right) + A\left(1 - \frac{S_v^*}{S_v}\right) + \mu_h S_h^* \left(1 - \frac{S_h}{S_h^*}\right) + \\
&\quad \mu_v S_v^* \left(1 - \frac{S_v}{S_v^*}\right) + \left[\frac{b\beta_h}{N_h} S_h^* - \mu_v\right] I_v + \left[\frac{b\beta_v}{N_h} S_v^* - \mu_h\right] I_h - \\
&\quad \theta_h R_h \left(\frac{S_h^*}{S_h}\right) - \mu_h E_h - \mu_v E_v - \mu_h R_h
\end{aligned} \quad (13)$$

by condition (11) to the equation (13) can be expressed as:

$$\dot{W(t)} = \mu_h N_h \left(1 - \frac{S_h^*}{S_h}\right) + A\left(1 - \frac{S_v^*}{S_v}\right) + \mu_h S_h^* \left(1 - \frac{S_h}{S_h^*}\right) + \mu_v S_v^* \left(1 - \frac{S_v}{S_v^*}\right) - \theta_h R_h \left(\frac{S_h^*}{S_h}\right) - \mu_h E_h - \mu_v E_v - \mu_h R_h \quad (14)$$

For cases $S_h^* = N_h$ and $S_v^* = \frac{A}{\mu_v}$ then equation (14) follow:

$$\begin{aligned}
\dot{W(t)} &= \mu_h N_h \left(2 - \frac{S_h^*}{S_h} - \frac{S_h}{S_h^*}\right) + A\left(2 - \frac{S_v^*}{S_v} - \frac{S_v}{S_v^*}\right) - \theta_h R_h \left(\frac{S_h^*}{S_h}\right) \\
&\quad - \mu_h E_h - \mu_v E_v - \mu_h R_h \\
\dot{W(t)} &= -\mu_h N_h \left(\frac{(S_h - S_h^*)^2}{S_h S_h^*}\right) - A\left(\frac{(S_v - S_v^*)^2}{S_v S_v^*}\right) - \theta_h R_h \left(\frac{S_h^*}{S_h}\right) - \mu_h E_h - \\
&\quad \mu_v E_v - \mu_h R_h
\end{aligned} \quad (15)$$

Equation (15) gives the conclusion that $\dot{W(t)} \leq 0$, This implies if the free-disease equilibrium $S_h^*, E_h^*, I_h^*, R_h^*, S_v^*, E_v^*, I_v^*$ is the global stage asymptotically stable in D. This proves Theorem 2. This theorem shown that, if $R_0 \leq 1$, then an infected individual will not infect others.

3.4. Global Stability of Endemic Equilibrium of Model SEIRS

The SEIRS model of system (1) has an equilibrium point of $P^{**} = (S_h^{**}, E_h^{**}, I_h^{**}, R_h^{**}, S_v^{**}, E_v^{**}, I_v^{**}) \in D$ called endemic equilibrium point, which satisfies:

$S_h^{**} > 0, E_h^{**} > 0, I_h^{**} > 0, R_h^{**} > 0, S_v^{**} > 0, E_v^{**} > 0, I_v^{**} > 0;$

$S_h^{**} = \frac{J_1}{k}; E_h^{**} = \frac{J_2}{k}; I_h^{**} = \frac{J_3}{k}; R_h^{**} = \frac{J_4}{k}; S_v^{**} = \frac{T_1}{l}; E_v^{**} = \frac{T_2}{l};$ and $I_v^{**} = \frac{T_3}{l}$

Where:

$$\begin{aligned}
J_1 &= (\delta_v \mu_h^2 + \delta_v \mu_h \gamma_h + \delta_v \mu_h \varphi_h + \delta_h \gamma_h \varphi_h + \mu_h^2 \mu_v + \mu_h \mu_v \gamma_h \\
&\quad + \mu_h \mu_v \varphi_h + \mu_v \gamma_h \varphi_h)(\mu_h^2 \mu_v + \mu_h b \beta_v \varphi_h \\
&\quad + \mu_h \mu_v \gamma_h + \mu_h \mu_v \theta_h + \mu_h \mu_v \varphi_h + b\beta_v \theta_h \varphi_h \\
&\quad + \mu_v \gamma_h \theta_h + \mu_h \gamma_h \varphi_h + \mu_h \theta_h \varphi_h) \\
J_2 &= (\mu_h + \gamma_h)(\mu_h + \theta_h)(b^2 \beta_v \beta_h \delta_v \varphi_h - \delta_v \mu_h^2 \mu_v - \delta_v \mu_h \mu_v \gamma_h \\
&\quad - \delta_v \mu_h \mu_v \varphi_h - \delta_v \mu_v \gamma_h \varphi_h - \mu_h^2 \mu_v^2 - \mu_h \mu_v^2 \gamma_h \\
&\quad - \mu_h \mu_v^2 \varphi_h - \mu_v^2 \gamma_h \varphi_h) \\
J_3 &= (\mu_h + \theta_h)(b^2 \beta_v \beta_h \delta_v \varphi_h - \delta_v \mu_h^2 \mu_v - \delta_v \mu_h \mu_v \gamma_h - \delta_v \mu_h \mu_v \varphi_h \\
&\quad - \delta_v \mu_v \gamma_h \varphi_h - \mu_h^2 \mu_v^2 - \mu_h \mu_v^2 \gamma_h - \mu_h \mu_v^2 \varphi_h \\
&\quad - \mu_v^2 \gamma_h \varphi_h) \\
J_4 &= \gamma_h(b^2 \beta_v \beta_h \delta_v \varphi_h - \delta_v \mu_h^2 \mu_v - \delta_v \mu_h \mu_v \gamma_h - \delta_v \mu_h \mu_v \varphi_h \\
&\quad - \delta_v \mu_v \gamma_h \varphi_h - \mu_h^2 \mu_v^2 - \mu_h \mu_v^2 \gamma_h - \mu_h \mu_v^2 \varphi_h \\
&\quad - \mu_v^2 \gamma_h \varphi_h) \\
T_1 &= b\beta_h \delta_v \mu_h^2 + b\beta_h \delta_v \mu_h \gamma_h + b\beta_h \delta_v \mu_h \theta_h + b\beta_h \delta_v \gamma_h \theta_h \\
&\quad + b\beta_h \delta_v \mu_h \varphi_h + b\beta_h \delta_v \gamma_h \theta_h + \delta_v \mu_h^3 \\
&\quad + \delta_v \mu_h^2 (\gamma_h + \theta_h + \varphi_h) \\
&\quad + \delta_v \mu_h (\gamma_h \theta_h + \gamma_h \varphi_h + \theta_h \varphi_h) \\
&\quad + \mu_h^2 \mu_v (\mu_h + \gamma_h + \theta_h + \varphi_h) \\
&\quad + \mu_h \mu_v (\gamma_h \theta_h + \gamma_h \varphi_h + \theta_h \varphi_h) + \mu_v \gamma_h \theta_h \varphi_h \\
T_2 &= (\mu_v(\mu_h + \theta_h)(b^2 \beta_h \beta_v \delta_v \varphi_h - \delta_v \mu_h \mu_v (\mu_h + \gamma_h + \varphi_h) \\
&\quad - \mu_h \mu_v^2 (\mu_h + \gamma_h + \varphi_h) - \mu_v^2 \gamma_h \varphi_h) \\
T_3 &= (\mu_h + \theta_h)(b^2 \beta_h \beta_v \delta_v \varphi_h - \delta_v \mu_h \mu_v (\mu_h + \gamma_h + \varphi_h) \\
&\quad - \mu_h \mu_v^2 (\mu_h + \gamma_h + \varphi_h) - \mu_v^2 \gamma_h \varphi_h) \\
k &= b\beta_v(b\beta_h \delta_v \mu_h^2 + b\beta_h \delta_v \mu_h \gamma_h + b\beta_h \delta_v \mu_h \theta_h + b\beta_h \delta_v \mu_h \varphi_h \\
&\quad + b\beta_h \delta_h \theta_h \gamma_h + b\beta_h \delta_h \gamma_h \varphi_h + b\beta_h \delta_h \theta_h \varphi_h \\
&\quad + \delta_v \mu_h^3 + \delta_v \mu_h^2 \gamma_h + \delta_v \mu_h^2 \theta_h + \delta_v \mu_h^2 \varphi_h \\
&\quad + \delta_v \mu_h \theta_h \gamma_h + \delta_v \mu_h \gamma_h \varphi_h + \delta_v \mu_h \theta_h \varphi_h \\
&\quad + \delta_v \gamma_h \theta_h \varphi_h + \mu_h^3 \mu_v + \mu_h^2 \mu_v \gamma_h + \mu_h^2 \mu_v \theta_h \\
&\quad + \mu_h^2 \mu_v \varphi_h + \mu_h \mu_v \gamma_h \theta_h + \mu_h \mu_v \gamma_h \varphi_h + \mu_h \mu_v \theta_h \varphi_h \\
&\quad + \mu_v \theta_h \varphi_h \gamma_h) \varphi_h \\
l &= (\mu_h^2 \mu_v + \mu_h b \beta_v \varphi_h + \mu_h \mu_v (\gamma_h + \theta_h + \varphi_h) + b\beta_v \theta_h \varphi_h + \mu_v \gamma_h \theta_h \\
&\quad + \mu_v \gamma_h \varphi_h + \mu_v \theta_h \varphi_h)\, \delta_v b \beta_h
\end{aligned}$$

Theorem 3 describes the endemic case of the SEIRS model in system (1) for dengue fever transmission.

Theorem 3

If $R_0 > 1$, then the equilibrium status of DF diseases is positively endemic, and the system (1) exists and is in the global stage asymptotically stable in D by assuming that;

$$S_v^{**} = \frac{A}{\mu_v}; S_h^{**} = N_h; \mu_h = \frac{b\beta_v}{mN_h}(\mu_h + \gamma_h + \varphi_h + \theta_h); \mu_v = \frac{mb\beta_h S_v^{**}}{\mu_h + \gamma_h + \varphi_h + \theta_h} \quad (16)$$

Where m= $\frac{\beta_h b}{N_h}$; μ_v is the rate of mosquito's population mortality; N_h is the number of human population which is likely the same as the number of DF suspected, b is the rate of potentially infecting mosquito bites, and $\beta_h b$ is interaction capability between human and mosquitoes as the vector.

Proof.

We constucted the Lyapunov function of the form in equation (17):

$$V(t) = (S_h - S_h^* \ln S_h) + E_h + I_h + R_h + \frac{\mu_h + \gamma_h + \varphi_h + \theta_h}{mS_v^{**}}(S_v - S_v^* \ln S_v) + \frac{\mu_h + \gamma_h + \varphi_h + \theta_h}{mS_v^{**}} E_v + \frac{\mu_h + \gamma_h + \varphi_h + \theta_h}{mS_v^{**}} I_v$$

(17)

The derivative of $V(t)$ with respect to time that satisfies the equation (18) is:

$$\begin{aligned}\dot{V}(t) = {} & \dot{S}_h\left(1-\frac{S_h^{**}}{S_h}\right)+\dot{E}_h+\dot{I}_h+\dot{R}_h+\dot{S}_v\left(1-\frac{S_v^{**}}{S_v}\right)\\ & +\frac{\mu_h+\gamma_h+\varphi_h}{mS_v^{**}}\dot{E}_v+\frac{\mu_h+\gamma_h+\varphi_h}{mS_v^{**}}\dot{I}_v\\ = {} & \left[\left(\mu_h N_h-\left(\frac{b\beta_h I_v}{N_h}+\mu_h\right)S_h+\theta_h R_h\right)\left(1-\frac{S_h^{**}}{S_h}\right)\right]+\\ & \left[\frac{b\beta_h I_v}{N_h}S_h-(\mu_h+\varphi_h)E_h\right]+[\varphi_h E_h-(\mu_h+\gamma_h)I_h]+\\ & [\gamma_h I_h-\mu_h R_h-\theta_h R_h]+\left[\left(A-\left(\frac{b\beta_v I_h}{N_h}+\mu_v\right)S_v\right)\left(1-\right.\right.\\ & \left.\left.\frac{S_v^{**}}{S_v}\right)\left(\frac{\mu_h+\gamma_h+\varphi_h+\theta_h}{mS_v^{**}}\right)\right]+\\ & \left[\frac{b\beta_v I_h}{N_h}S_v-(\mu_v+\delta_v)E_v\right]\left[\frac{\mu_h+\gamma_h+\varphi_h+\theta_h}{mS_v^{**}}\right]+\\ & [\delta_v E_v-\mu_v I_v]\left[\frac{\mu_h+\gamma_h+\varphi_h+\theta_h}{mS_v^{**}}\right]\\ = {} & \mu_h N_h\left(1-\frac{S_h^*}{S_h}\right)+\frac{b\beta_h I_v}{N_h}S_h^{**}-\theta_h R_h\left(\frac{S_h^{**}}{S_h}\right)-\mu_h S_h\left(1-\right.\\ & \left.\frac{S_h}{S_h^{**}}\right)-\mu_h E_h-\mu_h I_h-\mu_h R_h+A\left[\frac{\mu_h+\gamma_h+\varphi_h+\theta_h}{mS_v^{**}}\right]-\\ & A\left[\frac{\mu_h+\gamma_h+\varphi_h+\theta_h}{mS_v}\right]-\frac{b\beta_v I_h}{N_h}\left[\frac{\mu_h+\gamma_h+\varphi_h+\theta_h}{m}\right]\left[\frac{S_v}{S_v^{**}}\right]+\\ & \frac{b\beta_v I_h}{N_h}\left[\frac{\mu_h+\gamma_h+\varphi_h+\theta_h}{m}\right]-\mu_v\left[\frac{\mu_h+\gamma_h+\varphi_h+\theta_h}{m}\right]\left[\frac{S_v}{S_v^{**}}\right]+\\ & \mu_v\left[\frac{\mu_h+\gamma_h+\varphi_h+\theta_h}{m}\right]+\frac{b\beta_v I_h}{N_h}\left[\frac{\mu_h+\gamma_h+\varphi_h+\theta_h}{m}\right]\left[\frac{S_v}{S_v^{**}}\right]-\\ & \mu_v\left[\frac{\mu_h+\gamma_h+\varphi_h+\theta_h}{m}\right]\left[\frac{E_v}{S_v^{**}}\right]-\mu_v\left[\frac{\mu_h+\gamma_h+\varphi_h+\theta_h}{m}\right]\left[\frac{I_v}{S_v^{**}}\right]\\ = {} & -\mu_h N_h\left[2-\frac{S_h^{**}}{S_h}-\frac{S_h}{S_h^{**}}\right]+\frac{b\beta_h I_v}{N_h}S_h^{**}-\theta_h R_h\left(\frac{S_h^{**}}{S_h}\right)-\\ & \mu_h E_h-\mu_h I_h-\mu_h R_h+\frac{\mu_v}{m}(\mu_h+\gamma_h+\varphi_h+\theta_h)\left(\frac{S_v^{**}}{S_v}\right)+\\ & \frac{b\beta_v I_h}{N_h}\left[\frac{\mu_h+\gamma_h+\varphi_h+\theta_h}{m}\right]+\mu_v\left[\frac{\mu_h+\gamma_h+\varphi_h+\theta_h}{m}\right]-\\ & \mu_v\left[\frac{\mu_h+\gamma_h+\varphi_h+\theta_h}{m}\right]\left[\frac{S_v}{S_v^{**}}\right]-\mu_v\left[\frac{\mu_h+\gamma_h+\varphi_h+\theta_h}{m}\right]\left[\frac{E_v}{S_v^{**}}\right]-\\ & \mu_v\left[\frac{\mu_h+\gamma_h+\varphi_h+\theta_h}{m}\right]\left[\frac{I_v}{S_v^{**}}\right]\\ = {} & -\mu_h N_h\left[\frac{(S_h-S_h^{**})^2}{S_h S_h^{**}}\right]-\theta_h R_h\left(\frac{S_h^{**}}{S_h}\right)+\left(\frac{b\beta_h I_v}{N_h}S_h^{**}-\right.\\ & \left.\frac{\mu_v}{S_v^{**}}\left[\frac{\mu_h+\gamma_h+\varphi_h+\theta_h}{m}\right]\right)I_v-\mu_h E_h-\mu_h R_h+\\ & \left(\frac{b\beta_v}{N_h}\left[\frac{\mu_h+\gamma_h+\varphi_h+\theta_h}{m}\right]-\mu_h\right)I_h+\mu_v\left[\frac{\mu_h+\gamma_h+\varphi_h+\theta_h}{m}\right]-\\ & \mu_v\left[\frac{\mu_h+\gamma_h+\varphi_h+\theta_h}{m}\right]\left[\frac{S_v^{**}}{S_v}+\frac{S_v}{S_v^{**}}\right]-\mu_v\left[\frac{\mu_h+\gamma_h+\varphi_h+\theta_h}{m}\right]\left[\frac{E_v}{S_v^{**}}\right]\end{aligned} \quad (18)$$

Substituting equation (16) to equation (18), we can find:

$$\begin{aligned} = {} & -\mu_h N_h\left[\frac{(S_h-S_h^{**})^2}{S_h S_h^{**}}\right]-\theta_h R_h\left(\frac{S_h^{**}}{S_h}\right)-\mu_h E_h-\mu_h R_h+\\ & \mu_v\left[\frac{\mu_h+\gamma_h+\varphi_h+\theta_h}{m}\right]\left[2-\frac{S_v^{**}}{S_v}-\frac{S_v}{S_v^{**}}\right]-\\ & \mu_v\left[\frac{\mu_h+\gamma_h+\varphi_h+\theta_h}{m}\right]\left[\frac{E_v}{S_v^{**}}\right]\\ = {} & -\mu_h N_h\left[\frac{(S_h-S_h^{**})^2}{S_h S_h^{**}}\right]-\mu_v\left[\frac{\mu_h+\gamma_h+\varphi_h+\theta_h}{m}\right]\left[\frac{(S_v-S_v^{**})^2}{S_v S_v^{**}}\right]-\\ & \mu_v\left[\frac{\mu_h+\gamma_h+\varphi_h+\theta_h}{m}\right]\left[\frac{E_v}{S_v^{**}}\right]-\mu_h E_h-\mu_h R_h\end{aligned} \quad (19)$$

The equation (19) shown that $\dot{V}(t)\le 0$ for all $(S_h^{**}, E_h^{**}, I_h^*, R_h^{**}, S_v^{**}, E_v^{**}, I_v^{**})\in D$, and $\dot{V}(t)=0$ for $S_h = S_h^{**}, E_h = E_h^{**}, I_h = I_h^{**}, R_h = R_h^{**}, S_v = S_v^{**}, E_v = E_v^{**}$ and $I_v = I_v^{**}$. Equilibrium P^{**} is a set of positive invariant of the system (1) and (2) that is contained in

$$L=\left\{\left(S_h(t),E_h(t),I_h(t),R_h(t),S_v(t),E_v(t),I_v(t)\right), S_h=S_h^{**}, E_h=\right.$$
$$\left. E_h^{**}, I_h=I_h^{**}, R_h=R_h^{**}, S_v=S_v^{**}, E_v=E_v^{**}, I_v=I_v^{**}\right\}$$

Using asymptotical stability theorem, positive endemic equilibrium P^{**} is in the global stage asymptotically stable in D. This proves Theorem 3.

3.5 Simulation of SEIRS model for dengue fever transmission

SEIRS model simulation using MAPLE with initial condition $S_h(0)$, $E_h(0)$, $I_h(0)$, $R_h(0)$, $S_v(0)$, $E_v(0)$ and $I_v(0)$ in Table 2. Meanwhile, parameter values of the model are classified into parameter for the free disease cases ($R_0 \le 1$), and for the endemic cases ($R_0 > 1$) following in Table 2:

Tabel 2. Nilai awal variabel dan parameter

Variable	Initial Values	Parameter	$(\boldsymbol{R_0 > 1})$	$(\boldsymbol{R_0 \le 1})$
$\boldsymbol{N_h(0)}$	2500	β_h	0.0025	0.001
$\boldsymbol{S_h(0)}$	1300	μ_h	0.2055	0.005
$\boldsymbol{I_h(0)}$	800	b	250	20
$\boldsymbol{R_h(0)}$	400	θ_h	0.03	0.496
$\boldsymbol{N_v(0)}$	2000	γ_h	0.055	0.95
$\boldsymbol{S_v}(0)$	1500	μ_v	0.092	0.0093
$\boldsymbol{I_v}(0)$	500	β_v	0.00204	0.004

Stability Analysis of SEIRS Model for Dengue Fever The stability analysis of the SEIRS model on dengue fever transmission is obtained from equilibrium point values and eigen values λ based on equations (8) and (9), while the type of system stability refers to [15]. Model stability analysis of the SEIRS model for both free disease and endemic dengue fever cases are explained as follows.Free Disease for Dengue Fever Transmission The parameter values of the SEIRS model are used for free-disease cases $(\boldsymbol{R_0 \le 1})$ from the Table 2. Assuming the equation system (1) dan (2) is zero, the equation system (20) is found as follows:

$$\begin{aligned} & 0.13-0.45I_v S_h-0.13S_h\\ & +0.01R_h=0\\ & 0.45I_v S_h-0.33E_h=0\\ & 0.2E_h-0.53I_h=0\\ & 0.4I_h-0.14R_h=0\\ & 0.23-1.5I_h S_v=0\\ & 1.5I_h S_v-0.33E_v=0\\ & 0.1E_v-0.23I_v=0\end{aligned} \quad (20))$$

If the system (20) is resolved, then the SEIRS model equlibrium points for dengue fever transmission are obtained:

$(S_h, E_h, I_h, R_h, S_v, E, I_v) =$
$(0.9916; 0.0034; 0.0012; 0.0037; 0.9917; 0.0058; 0.0025)$.

These points explain that there are 9916 suspected, 34 exposed, 12 infected and 37 recovered populations from 10,000 total human populations. Then there were 9917 suspected, 58 exposed and 25 infected vector out of 10,000 total mosquito populations as vectors.

The Eigen values from the equations (8) and (9) using the parameter values in Table 2 for the SEIRS model for transmission of dengue fever in free-disease cases are:

$$\lambda_1=-0.13, \lambda_2=-0.14, \lambda_3=-0.23, \lambda_4=-0.707,$$
$$\lambda_5=-0.33, \lambda_6=-0.231 \text{ and } \lambda_7=-0.13$$

All eigen values are real and negative, the stability of this equilibrium point is asymptotically stable [15]. Whereas the basic reproductive number based on equation (10) for the free disease case is $R_0 = 0.371$, this means that a sufferer of dengue fever does not transmit it to other individuals.

Endemic Case for Dengue Fever Transmission The parameter values of the SEIRS model are used for endemic cases ($\boldsymbol{R_0 > 1}$) from the Table 2. Assuming the equation system (1) dan (2) is zero, the equation system (21) is found as follows:

$$0.7 - 70I_vS_h - 0.7S_h + 0.001R_h = 0$$
$$70I_vS_h - 1.5E_h = 0$$
$$0.8E_h - 0.71I_h = 0 \quad (21)$$
$$0.01I_h - 0.701R_h = 0$$
$$0.23 - 4I_hS_v = 0$$
$$4I_hS_v - 0.24E_v = 0$$
$$0.24E_v - 0.23I_v = 0$$

If the system equation (21) is resolved, then the SEIRS model fixed points for transmission of dengue fever are obtained:
$(S_h, E_h, I_h, R_h, S_v, E, I_v) =$
$(0.2147; 0.3665; 0.4129; 0.0059; 0.1222; 0.8412; 0.0366)$.
These points explain that there are 2147 suspected, 3665 exposed, 4129 infected and 59 recovered from 10,000 total human populations. Then there were 1222 suspected vector, 8412 exposed and 366 infected out of 10,000 total mosquito populations as vectors.The Eigen values from the equations (8) and (9) using parameter values in Table 2 for the SEIRS model for transmission of endemic dengue fever are: menggunakan nilai-nilai parameter dalam Table 2 untuk model SEIRS pada penularan demam berdarah kasus endemik adalah:

$$\lambda_1 = -0.7, \lambda_2 = -0.7, \lambda_3 = -0.23, \lambda_4 = -1.503,$$
$$\lambda_5 = -1.272, \lambda_6 = -0.737 \text{ and } \lambda_7 = -0.676$$

The Eigen values λ obtained are real but with different sign, thus the stability on this equilibrium point is in stabil asimptotik [15]. The basic reproduction number for the endemic case of dengue fever is $R_0 = 4.232$ which means each of the infected individual will likely infect the other 4 with the Dengue Fever.

3.6 Simulation Result of Model SEIRS for Dengue Fever Transmission

Free Disease for Dengue Fever Transmission The simulation results of the SEIRS model for free-disease cases of dengue fever transmission using MATLAB with initial values and the parameters in Table 2 are presented in Figure 2 and Figure 3 below. The y-axis in Figure 2 shows the prediction of the human population suspect, infected, infected and recovered dengue fever, while the x-axis shows time (in months). The y-axis in Figure 3 shows the prediction of the mosquito population suspected, exposed and infected, while the x-axis shows the time (in months).

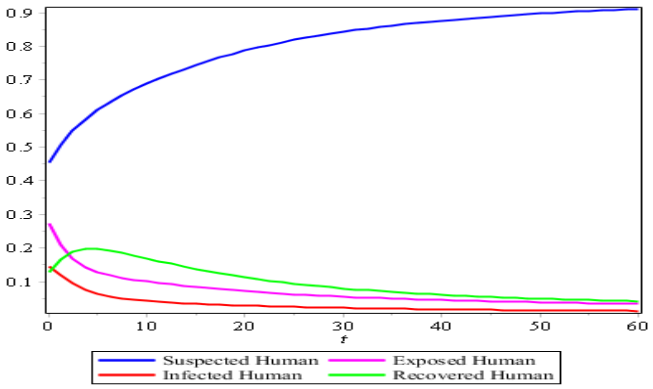

***Fig 2**. Prediction of Suspected, Eksposed, Infected, and Recovered Human for free disease cases*

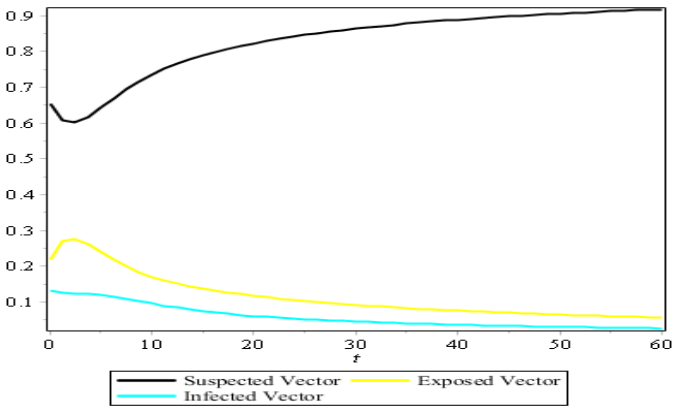

***Fig 3.** Prediction of Suspected, Eksposed, and Infected Mosquito for free disease cases*

According to the Figure 2, the number of cases of dengue fever infection decreased from the 3rd month and continued to decline until it reached a constant in the 13th month, in line with the number of dengue virus carriers that also decreased since the 3rd month as in Figure 3. While the population recovering from dengue fever has increased since the 3rd month and continues to increase. This condition is in accordance with cases of dengue fever which is in the disease-free stage where individuals infected with dengue do not cause other individuals to be infected ($\boldsymbol{R_0 = 0.371 \leq 1}$).
Endemic Case for Dengue Fever Transmission The results of the SEIRS model simulation for endemic cases of dengue fever transmission using MATLAB with initial values and the parameters in Table 2 are presented in Figure 4 and Figure 5 below. The y-axis in Figure 4 shows the prediction of the human population suspected, exposed, infected and recovered of dengue fever, while the x-axis shows time (in months). The y-axis in Figure 5 shows the prediction of the mosquito population suspected, exposed and infected, while the x-axis shows the time (in months)

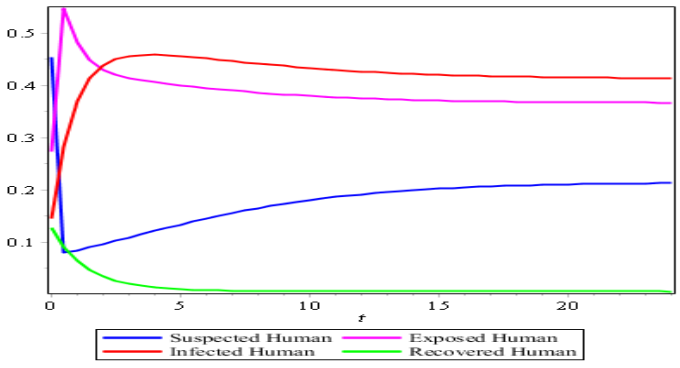

***Fig 4**. Prediction of Suspected, Eksposed, Infected, and Recovered Human for endemic cases*

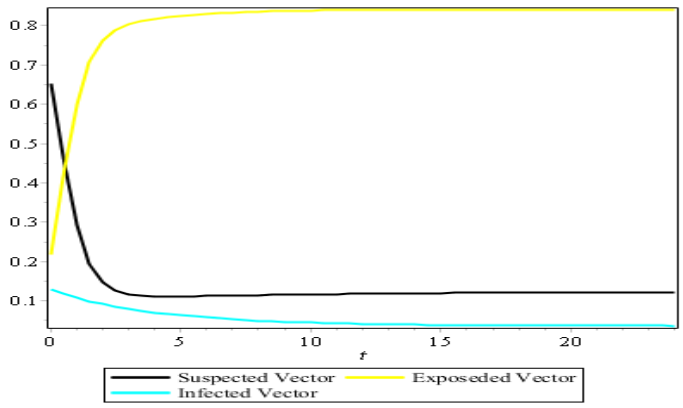

Fig 5. *Prediction of Suspected, Eksposed, and Infected Mosquitoes for endemic cases*

According to the Figure 4, the number of cases of dengue infection has increased very rapidly since the 3rd month and continues to increase until it reaches a constant in the 12th month, this is in line with the number of mosquitoes carrying the dengue fever virus which has also increased very fast since the 3rd month until constant at the 7th month as shown in Figure 5. Whereas the population recovering from dengue fever has decreased since the second month and continues to decline. This condition is in accordance with cases of dengue fever which are in the endemic stage where individuals infected with dengue fever because other individuals to be infected $(\boldsymbol{R_0 = 4.232 > 1})$, which means an individual infected with dengue can cause four other individuals to be infected.

3.7 Discussion

The mathematical model of SIR and SEIR has been done by [2; 3; 4; 6; 8; 9; 10; 11], the model explains the existence, free-disease and endemic cases. Model [3] conducted a simulation using data on the number of dengue fever cases in South Sulawesi in 2014. This study also proved three theorems namely existence, disease-free and endemic cases of dengue fever, but using the SEIRS model. The SEIRS model was built because the current facts show that people who have recovered dengue fever do not become immune so they can get infected again with dengue fever. The SEIRS model simulation is carried out for disease-free and endemic cases using assumption data. The simulation results illustrate the prediction of the number of dengue cases in both cases.

4. CONCLUSION

This study produced a SEIRS model for dengue transmission. The stability analysis of the SEIRS model using the lyapunov function method proves the results of the existence theorem, cases of disease-free and endemic dengue fever. The stability analysis of the SEIRS model also gives a real negative eigenvalue for disease-free and endemic cases, this means that the type of stability of the model is asymptotic stable. The model simulation results using assumption data provide a predictive description of the SEIRS model for free-disease cases$(\boldsymbol{R_0 \leq 1})$, namely the number of infected individuals decreases rapidly because an infected individual doesn't cause other individuals to be infected. Furthermore, endemic cases $(\boldsymbol{R_0 > 1})$ that is, the number of infected individual's increases rapidly because an infected individual causes another individual to become infected with dengue fever.

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