BAREKENG: Journal of Mathematics and Its Applications
June 2023 Volume 17 Issue 2 Page 0615–0624
P-ISSN: 1978-7227 E-ISSN: 2615-3017
https://doi.org/10.30598/barekengvol17iss2pp0615-0624

DYNAMICAL SYSTEM FOR EBOLA OUTBREAK WITHIN QUARANTINE AND VACCINATION TREATMENTS

Sugian Nurwijaya[1], Ratnah Kurniati MA[2], Sigit Sugiarto[3*]

[1,2,3]*Department of Mathematics Education, Study Program Outside the Main Campus (PSDKU), Pattimura University*
Ir. M. Putuhena Street, Poka, Ambon 97233, Indonesia

*Corresponding author's e-mail: * **sigith.sugiarto@gmail.com***

ABSTRACT

Ebola Virus Disease (EVD) is an infectious disease with a high mortality rate caused by the virus from the family of Filoviridae, the genus of Ebolavirus. Therefore, this research works on the developing model of Ebola disease spread with $S_LS_HVEQIHR$ type. The purpose of this study is to analyze the spread of Ebola disease with the treatments, which are quarantine and vaccination. Then determine the equilibrium point and basic reproduction number (R_0). There are two equilibrium points, the disease-free equilibrium point and the endemic equilibrium point. The analysis results in the model show that if $R_0 < 1$ then the disease free equilibrium point is locally asymptotically stable. If $R_0 > 1$ then the endemic equilibrium point is locally assymptotically stable. Numerical simulations are performed to show the population dynamics when $R_0 < 1$ and $R_0 > 1$.

Article History:

Received: 23rd August 2022
Revised: 5th April 2023
Accepted: 7th April 2023

Keywords:

Dynamical system;
Ebola virus disease;
Equilibrium point;
Stability analysis.

How to cite this article:

S. Nurwijaya, R. K. MA and S. Sugiarto., "DYNAMICAL SYSTEM FOR EBOLA OUTBREAK WITHIN QUARANTINE AND VACCINATION TREATMENTS,"*BAREKENG: J. Math. &App.*, vol. 17, iss. 2, pp. 0615-0624, June, 2023.

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

Research Article •Open Access

1. INTRODUCTION

Ebola Virus Disease (EVD) is a viral infection caused by a virus from the family *Filoviridae*, the genus *Ebolavirus*, that derived from fruit bats, the family *Pteropodidae* [1]. EVD is a deadly infectious disease that was first discovered in the Democratic Republic of Congo (DRC) near the Ebola River in 1976 [2][3]. The last case of EVD reappeared in 2014 on March 23, with deaths reaching 11,315 out of 28,637 cases occurring in 6 countries until January 2016 [4]. EVD is spread through direct contact with infected body fluids in the mouth, nose, eyes or through a break in the skin [5][6]. The virus is not transmitted through the air, by water, or in general, by food [6].

Individuals suffering from EVD do not infect others during the incubation period, which can survive between two days and three weeks. The recovery from EVD relies heavily on the immune response of infected individuals and support for good clinical care. Individuals who have recovered cannot spread the ebola virus. However, Ebola virus can stay in body fluids such as semen and breast milk for some time after recovery [6][7].

For years, researchers have been trying to develop a model for the spread of EVD since Ebola's disease became a deadly infectious disease. The mathematical model of EVD spread aims to analyze the characteristics of the spread of the disease [8][9]. Imran et al. [10] developed a model of the spread of ebola disease with S_LS_HEIHR type by providing treatment in the hospital for infected individuals. The treatment aims to provide recovery to an infected individual or reduce the rate of death caused by EVD.

According to WHO in 2021 [7], the recombinant Vesicular Virus-Ebola Virus Virus vaccine (rVSV–ZEBOV) is effective in reducing the risk of infected populations. So Wintachai and Prathom [11] use the SEIR model equipped with the effectiveness of vaccination to forecast the COVID-19 situation when a vaccine comes out and Muhammad et al. [12] modified the S_LS_HEIHR type of disease model to S_LS_HVEIHR type by adding treatment in the form of vaccine against susceptible individuals to reduce the risk of infection and the S_LS_HEQIHR by adding quarantine treatment to prevent transmission of the disease from infected individuals.

2. RESEARCH METHODS

This research modified the S_LS_HEIHR type of disease model to S_LS_HVEQIHR type by adding treatment in the form of vaccine against susceptible individuals to reduce the risk of infection and adding quarantine treatment to prevent transmission of the disease from infected individuals. The total population at any time instant t, denoted by $N(t)$, is the sum of individual populations in each compartment that includes low risk susceptible individuals $S_L(t)$, high risk susceptible individuals $S_H(t)$, vaccinated individuals $V(t)$, exposed individuals $E(t)$, quarantined individuals $Q(t)$, and infected individuals $I(t)$, Hospitalized individuals $H(t)$, and Recovered individuals $R(t)$, such that, $N(t) = S_L(t) + S_H(t) + V(t) + E(t) + Q(t) + I(t) + H(t) + R(t)$. The flow diagram of Ebola model is shown in **Figure 1**.

Based on the diagram in **Figure 1**, we can obtain a system of ordinary differential equations as follows:

$$\begin{aligned}
\frac{dS_L}{dt} &= \Pi(1-p) - \lambda S_L - \gamma_L S_L - \mu S_L \\
\frac{dS_H}{dt} &= \Pi p - \lambda \psi_H S_H - \gamma_H S_H - \mu S_H \\
\frac{dV}{dt} &= \gamma_L S_L + \gamma_H S_H - \lambda(1-\varepsilon)V - \mu V \\
\frac{dE}{dt} &= \lambda S_L + \lambda \psi_H S_H + \lambda(1-\varepsilon)V - (\xi + \alpha + \mu)E \\
\frac{dQ}{dt} &= \xi E - \tau_Q Q - \mu Q \\
\frac{dI}{dt} &= \alpha E - (\theta_I + \tau + \delta_I + \mu)I \\
\frac{dH}{dt} &= \tau_Q Q + \tau I - (\theta_H + \delta_H + \mu)H
\end{aligned} \tag{1}$$

$$\frac{dR}{dt} = \theta_H H + \theta_I I - \mu R$$

where $\lambda = \frac{\beta(I+\eta H)}{N}$.

According to system of **Equation (1)** we have

$$\frac{dN}{dt} = \Pi - \mu N - \theta_H H - \theta_I I.$$

All parameters are non-negative constants.

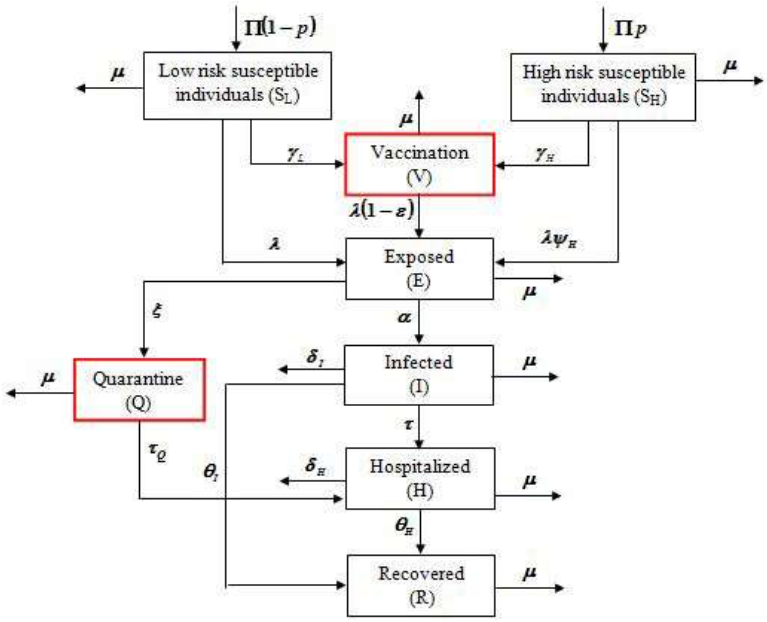

Figure 1. Diagram depicting the dynamics of the Ebola virus

3. RESULTS AND DISCUSSION

In this section, we will determine the equilibrium point, the basic reproduction number, and the stability analysis.

3.1. The Equilibrium Point

The disease-free equilibrium of the system of **Equation (1)** is given by

$$T^0(S_L, S_H, V, E, Q, I, H, R) = (S_L^0, S_H^0, V^0, 0, 0, 0, 0, 0),$$

where

$$S_L^0 = \frac{\Pi(1-p)}{\gamma_L+\mu}, \quad S_H^0 = \frac{\Pi p}{\gamma_H+\mu}, \quad V^0 = \left(\frac{\Pi(1-p)\gamma_L}{\mu(\gamma_L+\mu)} + \frac{\Pi p \gamma_H}{\mu(\gamma_H+\mu)}\right),$$

and the endemic equilibrium of the system (1) is given by

$$T^*(S_L, S_H, V, E, Q, I, H, R) = (S_L^*, S_H^*, V^*, E^*, Q^*, I^*, H^*, R^*)$$

where

$$S_L^* = \frac{\Pi(1-p)}{\gamma_L+\lambda+\mu},$$
$$S_H^* = \frac{\Pi p}{\gamma_H+\lambda\psi_H+\mu},$$
$$V^* = \frac{\gamma_L S_L^* + \gamma_H S_H^*}{\lambda(1-\varepsilon)+\mu},$$
$$E^* = \frac{\lambda S_L^* + \lambda\psi_H S_H^* + \lambda(1-\varepsilon)V^*}{\xi+\alpha+\mu},$$
$$Q^* = \frac{\xi E^*}{\tau_Q+\mu},$$
$$I^* = \frac{\alpha E^*}{\theta_I+\tau+\delta_I+\mu},$$
$$H^* = \frac{\tau_Q Q^* + \tau I^*}{\theta_H+\delta_H+\mu}, \text{ and}$$
$$R^* = \frac{\theta_H H^* + \theta_I I^*}{\mu}.$$

3.2. The Basic Reproduction Number

The basic reproduction number, denoted (R_0) is the expected number of secondary cases produced, in a completely susceptible population, by a typical infective individual. We calculate the basic reproduction number by using the next generation operator approach by van den Driessche and Watmough [13][14]. The next generation matrix at the disease-free equilibrium T^0 is given by:

$$F = \begin{pmatrix} 0 & 0 & \beta\Omega & \beta\eta\Omega \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}$$

where

$$\Omega = \left(\frac{(1-p)\mu}{\gamma_L+\mu} + \frac{\psi_H p\mu}{\gamma_H+\mu} + (1-\varepsilon)\left(\frac{(1-p)\gamma_L}{\gamma_L+\mu} + \frac{p\gamma_H}{\gamma_H+\mu}\right)\right)$$

and

$$V = \begin{pmatrix} k_1 & 0 & 0 & 0 \\ -\xi & k_2 & 0 & 0 \\ -\alpha & 0 & k_3 & 0 \\ 0 & -\tau_Q & -\tau & k_4 \end{pmatrix}$$

where

$$k_1 = \xi + \alpha + \mu, \qquad k_3 = \xi + \alpha + \mu,$$
$$k_2 = \tau_Q + \mu, \qquad k_4 = \theta_H + \delta_H + \mu.$$

The basic reproduction number $R_0$is dominant eigenvalue of $G = FV^{-1}$, thus we get

$$R_0 = \beta\Omega\left(\frac{\alpha k_2 k_4 + \alpha\eta\tau k_2 + \eta\xi\tau_Q k_3}{k_1 k_2 k_3 k_4}\right) = R_0^1 + R_0^2 + R_0^3,$$

where

$$R_0^1 = \beta\Omega\left(\frac{\alpha k_2 k_4}{k_1 k_2 k_3 k_4}\right), \; R_0^2 = \beta\Omega\left(\frac{\alpha\eta\tau k_2}{k_1 k_2 k_3 k_4}\right), \text{ and } R_0^3 = \beta\Omega\left(\frac{\eta\xi\tau_Q k_3}{k_1 k_2 k_3 k_4}\right).$$

3.3. The Stability Analysis

The stability of system of Equation (1) is dependent on the basic reproduction number R_0. The stability analysis of both equilibrium T^0 and T^* will be provided through the following theorems:

Theorem 1. The disease-free equilibrium T^0 for system of Equation (1) is locally asymptotically stable if $R_0 < 1$.

Proof. The Jacobian matrix at T^0 for system of Equation (1) is given by

$$J_{T^0} = \begin{pmatrix} J_{11} & 0 & 0 & 0 & 0 & J_{16} & J_{17} & 0 \\ 0 & J_{22} & 0 & 0 & 0 & J_{26} & J_{27} & 0 \\ J_{31} & J_{32} & J_{33} & 0 & 0 & J_{36} & J_{37} & 0 \\ 0 & 0 & 0 & J_{44} & 0 & J_{46} & J_{47} & 0 \\ 0 & 0 & 0 & J_{54} & J_{55} & 0 & 0 & 0 \\ 0 & 0 & 0 & J_{64} & 0 & J_{66} & 0 & 0 \\ 0 & 0 & 0 & 0 & J_{75} & J_{76} & J_{77} & 0 \\ 0 & 0 & 0 & 0 & 0 & J_{86} & J_{87} & J_{88} \end{pmatrix}$$

where

$$J_{11} = -(\gamma_L + \mu), \qquad J_{46} = \beta\Omega,$$
$$J_{16} = -\frac{\beta}{N} S_L^0, \qquad J_{47} = \beta\eta\Omega,$$
$$J_{17} = -\frac{\beta\eta}{N} S_L^0, \qquad J_{54} = \xi,$$
$$J_{22} = -(\gamma_H + \mu), \qquad J_{55} = -k_2,$$
$$J_{26} = -\frac{\beta}{N}\psi_H S_H^0, \qquad J_{64} = \alpha,$$
$$J_{27} = -\frac{\beta\eta}{N}\psi_H S_H^0, \qquad J_{66} = -k_3,$$
$$J_{31} = \gamma_L, \qquad J_{75} = \tau_Q,$$
$$J_{32} = \gamma_H, \qquad J_{76} = \tau,$$
$$J_{33} = -\mu, \qquad J_{77} = -k_4,$$
$$J_{36} = -\frac{\beta}{N}(1-\varepsilon)V^0, \qquad J_{86} = \theta_I,$$
$$J_{37} = -\frac{\beta\eta}{N}(1-\varepsilon)V^0, \qquad J_{87} = \theta_H,$$
$$J_{44} = -k_1, \qquad J_{88} = -\mu.$$

The eigenvalue was determined for the disease-free equibrium T^0 by using the equation $|J_{T^0} - \lambda I| = 0$, so we get the characteristic equation as follow:

$$(J_{11}-\lambda)(J_{22}-\lambda)(J_{33}-\lambda)(J_{88}-\lambda)(\lambda^4 + a_1\lambda^3 + a_2\lambda^2 + a_3\lambda + a_4) = 0 \tag{2}$$

where

$$a_1 = k_1 + k_2 + k_3 + k_4,$$
$$a_2 = k_1k_2 + k_2k_3 + k_1k_4 + k_2k_4 + k_3k_4 + (1-R_0^1)k_1k_3,$$
$$a_3 = k_1k_2k_3(1-R_0^1) + k_1k_3k_4(1-R_0^2) + k_1k_2k_4(1-R_0^3) + k_2k_3k_4(1-R_0^1),$$
$$a_4 = k_1k_2k_3k_4(1-R_0).$$

According to **Equation (2)**, we obtain eight eigenvalues with four of them are negative:

$$\lambda_1 = J_{11} = -(\gamma_L + \mu), \qquad \lambda_3 = J_{33} = -\mu,$$
$$\lambda_2 = J_{22} = -(\gamma_H + \mu), \qquad \lambda_4 = J_{88} = -\mu.$$

Whereas the others are getting by solving the equation below:

$$(\lambda^4 + a_1\lambda^3 + a_2\lambda^2 + a_3\lambda + a_4) = 0 \tag{3}$$

According to Routh-Hurwitz criterion [15][16], **Equation (3)** on disease-free equilibrium T^0 is stable if the following stability criterion satisfied:

$$a_1 > 0,\ a_2 > 0,\ a_3 > 0,\ a_4 > 0,\ a_1a_2 > a_3, \text{ and } a_1a_2a_3 > (a_3^2 + a_1^2a_4) \tag{4}$$

Based on **Equation (4)**, since all parameters k_1, k_2, k_3, and k_4 are positive, then a_1 is positive. Furthermore, $R_0 < 1$ then the coefficient a_4 will be positive. Further, for coefficient a_2 and a_3 will be positive if $R_0^1 < 1$ and $R_0^2 < 1$ and $R_0^3 < 1$. Since $R_0 < 1$, then $R_0^1 < 1, R_0^2 < 1$, and $R_0^3 < 1$. Afterward to proof $a_1a_2 > a_3$ and $a_1a_2a_3 > (a_3^2 + a_1^2a_4)$, we need the parameter value at condition $R_0 < 1$. So for $R_0 < 1$ the (4) condition is satisfied. Thus, proved that disease-free equilibrium T^0 for system of **Equation (1)** is locally asymptotically stable if $R_0 < 1$.□

Theorem 2. If $R_0 > 1$ then the endemic equilibrium T^* is locally asymptotically stable.

Proof. According to Castillo-Chaves and Song [17], let $\varphi = \beta$ be the bifurcation parameter. According to condition $R_0 = 1$ we have

$$\varphi = \varphi^* = \frac{k_1 k_2 k_3 k_4}{\Omega(\alpha k_2 k_4 + \alpha\eta\tau k_2 + \eta\xi\tau_Q k_3)}.$$

Disease-free equilibrium T^0 has one zero eigenvalue and seven negative eigenvalues if $R_0 = 1$ or $\varphi = \varphi^*$. The zero eigenvalue has right eigenvector $(u_1, u_2, u_3, u_4, u_5, u_6, u_7, u_8)$ and left eigenvector $(v_1, v_2, v_3, v_4, v_5, v_6, v_7, v_8)$. As indicated previously that u_4 is arbitrary positive, then

$$u_5 = \frac{\xi}{k_2} u_4 > 0,$$
$$u_6 = \frac{\alpha}{k_3} u_4 > 0,$$
$$u_7 = \left(\frac{\xi\tau_Q}{k_2 k_4} + \frac{\alpha\tau}{k_3 k_4}\right) u_4 > 0,$$
$$u_8 = \left(\frac{\alpha\theta_I}{\mu k_3} + \frac{\xi\theta_H\tau_Q}{\mu k_2 k_4} + \frac{\alpha\theta_H\tau}{\mu k_3 k_4}\right) u_4 > 0,$$
$$u_1 = -\left(\frac{\alpha\beta\Pi(1-p)}{N(\gamma_L+\mu)^2 k_3} + \frac{\beta\eta\Pi(1-p)}{N(\gamma_L+\mu)^2}\left(\frac{\xi\tau_Q}{k_2 k_4} + \frac{\alpha\tau}{k_3 k_4}\right)\right) u_4 < 0,$$
$$u_2 = -\left(\frac{\alpha\beta\psi_H\Pi p}{N(\gamma_H+\mu)^2 k_3} + \frac{\beta\eta\psi_H\Pi p}{N(\gamma_L+\mu)^2}\left(\frac{\xi\tau_Q}{k_2 k_4} + \frac{\alpha\tau}{k_3 k_4}\right)\right) u_4 < 0,$$
$$u_3 = -\left(\left(\frac{\alpha\beta\Pi(1-p)}{N(\gamma_L+\mu)^2 k_3} + \frac{\beta\eta\Pi(1-p)}{N(\gamma_L+\mu)^2}\left(\frac{\xi\tau_Q}{k_2 k_4} + \frac{\alpha\tau}{k_3 k_4}\right)\right) + \left(\frac{\alpha\beta\psi_H\Pi p}{N(\gamma_H+\mu)^2 k_3} + \frac{\beta\eta\psi_H\Pi p}{N(\gamma_L+\mu)^2}\left(\frac{\xi\tau_Q}{k_2 k_4} + \frac{\alpha\tau}{k_3 k_4}\right)\right) + \right.$$
$$\left(\alpha\beta(1-\varepsilon)\left(\frac{\Pi(1-p)\gamma_L}{N(\gamma_L+\mu)\mu^2 k_3} + \frac{\Pi p\gamma_H}{N(\gamma_H+\mu)\mu^2 k_3}\right)\right) + \left(\beta\eta(1-\varepsilon)\left(\frac{\Pi(1-p)\gamma_L}{N(\gamma_L+\mu)\mu^2} + \frac{\Pi p\gamma_H}{N(\gamma_H+\mu)\mu^2}\right)\left(\frac{\xi\tau_Q}{k_2 k_4} + \frac{\alpha\tau}{k_3 k_4}\right)\right) u_4 < 0.$$

As indicated previously that $v_5$is arbitrary positive, then, $v_1 = v_2 = v_3 = v_8 = 0,$

$$v_7 = \frac{k_2}{\tau_Q} v_5 > 0,\ v_4 = \left(\frac{Nk_2 k_4}{\beta\eta\Omega\tau_Q}\right) v_5 > 0,\ v_6 = \left(\frac{k_2 k_4}{\eta\tau_Q k_3} + \frac{\tau k_2}{\tau_Q k_3}\right) v_5 > 0.$$

Define

$$a = \sum_{k,i,j=1}^{8} v_k u_i u_j \frac{\partial^2 f_k}{\partial x_i \partial x_j}(T^0, \varphi^*),\quad b = \sum_{k,i,j=1}^{8} v_k u_i \frac{\partial^2 f_k}{\partial x_i \partial \varphi}(T^0, \varphi^*). \tag{5}$$

where

$$x_1 = S_L \qquad x_2 = S_H \qquad x_3 = V \qquad x_4 = E$$
$$x_5 = Q \qquad x_6 = I \qquad x_7 = H \qquad x_8 = R$$
$$f_1 = \frac{dx_1}{dt} = \Pi(1-p) - \frac{\varphi(x_6+\eta x_7)}{N} x_1 - \gamma_L x_1 - \mu x_1,$$
$$f_2 = \frac{dx_2}{dt} = \Pi p - \frac{\varphi(x_6+\eta x_7)}{N}\psi_H x_2 - \gamma_H x_2 - \mu x_2,$$
$$f_3 = \frac{dx_3}{dt} = \gamma_L x_1 + \gamma_H x_2 - \frac{\varphi(x_6+\eta x_7)}{N}(1-\varepsilon) x_3 - \mu x_3,$$
$$f_4 = \frac{dx_4}{dt} = \frac{\varphi(x_6+\eta x_7)}{N}\left(x_1 + \psi_H x_2 + (1-\varepsilon) x_3\right) - (\xi + \alpha + \mu) x_4,$$
$$f_5 = \frac{dx_5}{dt} = \xi x_4 - \tau_Q x_5 - \mu x_5,$$
$$f_6 = \frac{dx_6}{dt} = \alpha x_4 - (\theta_I + \tau + \delta_I + \mu) x_6,$$
$$f_7 = \frac{dx_7}{dt} = \tau_Q x_5 + \tau x_6 - (\theta_H + \delta_H + \mu) x_7,$$
$$f_8 = \frac{dx_8}{dt} = \theta_I x_6 + \theta_H x_7 - \mu x_8.$$

According to **Equation (5)**, we obtain

$$a = v_4\left(u_1 u_6 \frac{\varphi^*}{N} + u_1 u_7 \frac{\eta\varphi^*}{N} + u_2 u_6 \frac{\psi_H\varphi^*}{N} + u_2 u_7 \frac{\psi_H\eta\varphi^*}{N} + u_3 u_6 \frac{(1-\varepsilon)\varphi^*}{N} + u_3 u_7 \frac{(1-\varepsilon)\eta\varphi^*}{N}\right) \text{ and}$$
$$b = v_4 u_6 \Omega + v_4 u_7 \eta\Omega.$$

Since $v_4, u_6, u_7 > 0$ and $u_1, u_2, u_3 < 0$, then $a < 0$ and $b > 0$.

Consequently, when φ changes from $\varphi < \varphi^*(R_0 < 1)$ to $\varphi > \varphi^*(R_0 > 1)$, the disease-free equilibrium T^0 stability changes from stable and becomes unstable, while endemic equilibrium T^* coordinates changes from negative becomes positive and thus becomes local asymptotically stable. As a consequence, the endemic equilibrium T^* is locally asymptotically stable if $R_0 > 1$.□

3.4. Numerical Simulations

The numerical simulations were performed to visualize stability properties of the equilibrium points of both T^0 and T^* based on the **Theorem 1** and **Theorem 2**. The initial values used are $S_L(0) = 25$, $S_H(0) = 25$, $V(0) = 10$, $E(0) = 10$, $Q(0) = 10$, $I(0) = 5$, $H(0) = 5$, and $R(0) = 10$. The parameter values used in this simulation are shown in **Table 1**. For the disease free equilibrium we have $R_0 = 0.17786 < 1$ and the disease free equilibrium $T^0(1.571, 0.371, 104.976, 0, 0, 0, 0, 0)$. The population dynamics at condition $R_0 < 1$ is shown in **Figure 2**. For the endemic equilibrium we have $R_0 = 1.93725 > 1$ and the endemic equilibrium $T^*(S_L = 4.078, S_H = 1.145, V = 15.580, E = 15.580, E = 1.418, Q = 1.392, I = 0.150, H = 1.555, R = 20.507)$. The population dynamics at condition $R_0 > 1$ is shown in **Figure 3**.

Figure 2 supports **Theorem 1** and **Figure 3** supports **Theorem 2**. This simulation shows that the system will be stable at around disease-free equilibrium when $R_0 < 1$ and the system will be stable at around endemic equilibrium when $R_0 > 1$.

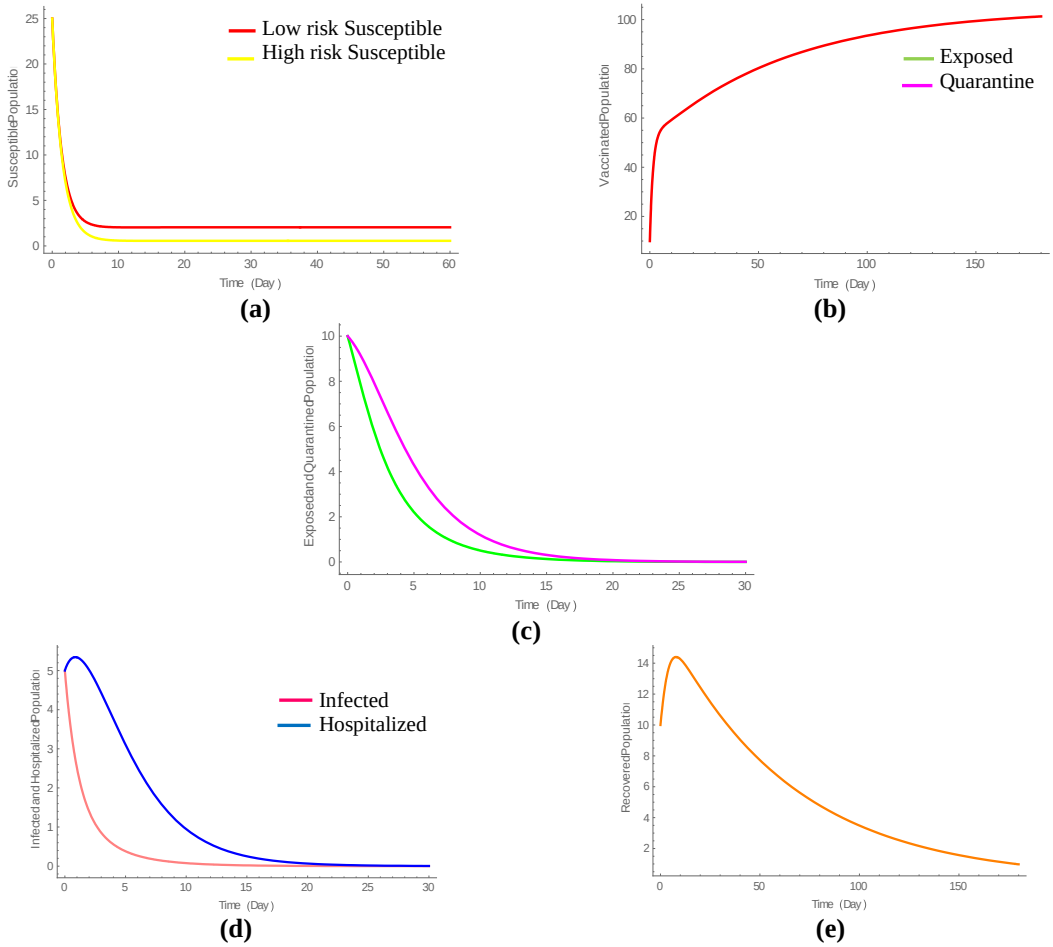

Figure 2. The population dynamics at condition $R_0 < 1$
(a) Low risk and high risk susceptible population, (b) Vaccinated population, (c) Exposed and quarantined population, (d) Infected and hospitalized population, (e) Recovered population

Table 1. Parameter values

Parameter	$R_0 < 1$	$R_0 > 1$
	Value	Value
Π	1.70 in[10]	1.70 in [10]
p	0.20in [10]	0.20in [10]
ψ_H	1.20in [10]	1.20in [10]
β	0.39 in [10]	0.39 in [10]
η	1.50 in [10]	1.50 in [10]
α	0.10in [10]	0.10in [10]
τ	0.16in [10]	0.16in [10]
θ_I	0.10in [10]	0.10in [10]
θ_H	0.20in [10]	0.20in [10]
δ_I	0.67 in [17]	0.67 in[17]
δ_H	0.58 in [17]	0.58 in[17]
μ	0.0159 in [10]	0.0159 in [10]
γ_L	0.65 [assumed]	0.25 [assumed]
γ_H	0.60[assumed]	0.20[assumed]
ε	0.75[assumed]	0.25 [assumed]
ξ	0.35 [assumed]	0.85 [assumed]
τ_Q	0.40 [assumed]	0.85 [assumed]

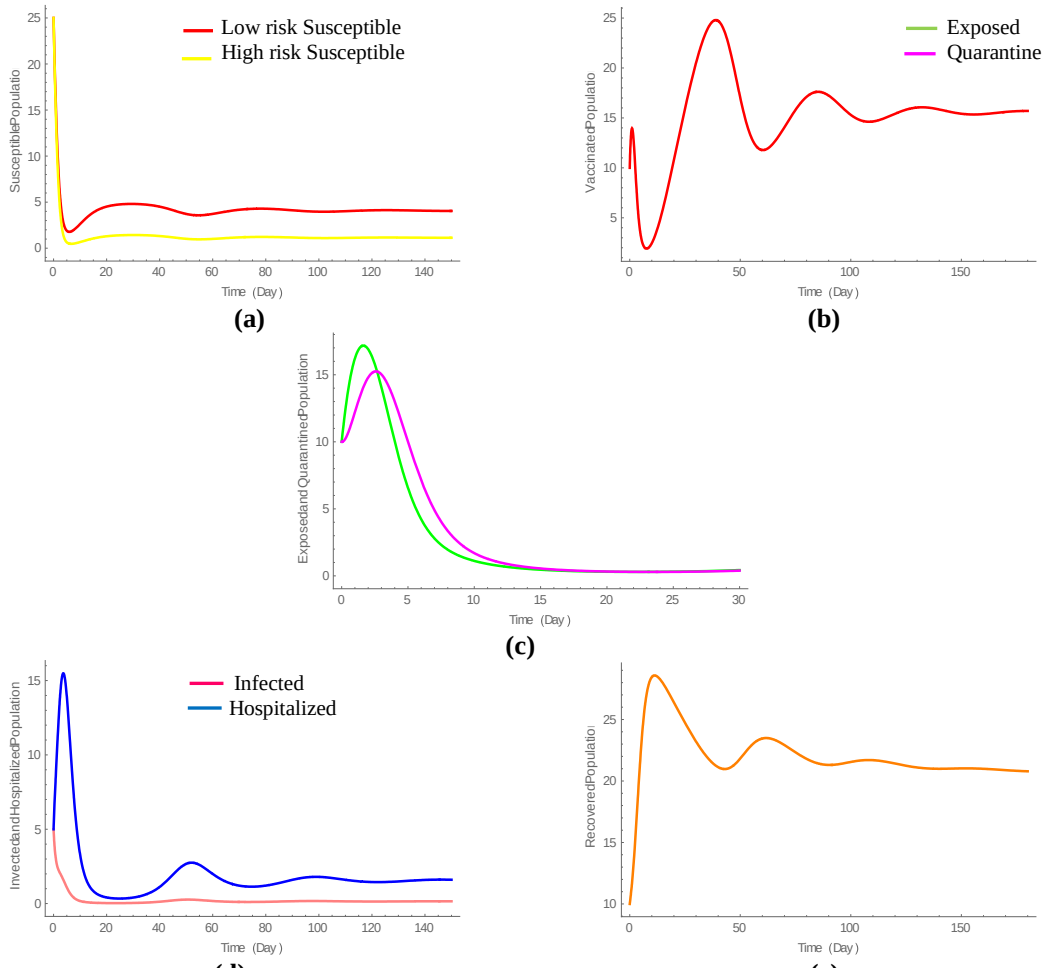

Figure 3. The population dynamics at condition $R_0 > 1$
(a) Low risk and high risk susceptible population, (b) Vaccinated population, (c) Exposed and quarantined population, (d) Infected and hospitalized population, (e) Recovered population

4. CONCLUSION

This study modified mathematical model of Ebola outbreak to consider quarantine and vaccination. The results of the model analysis obtained two equilibrium points, namely, disease-free equilibrium and endemic equilibrium. The basic reproduction number (R_0) was determined. The disease-free equilibrium is locally asymptotically stable on condition $R_0 < 1$, whereas the endemic equilibrium is locally asymptotically stable on condition $R_0 > 1$. The numerical simulation of population dynamics showed similar patterns as expected.

REFERENCES

[1] P. Shears and C. Garavan, "The 2018/19 Ebola epidemic the Democratic Republic of the Congo (DRC): epidemiology, outbreak control, and conflict," *Infect. Prev. Pract.*, vol. 2, no. 1, p. 100038, 2020, doi: 10.1016/j.infpip.2020.100038.

[2] H. Yueh-Min *et al.*, "A Jigsaw-based Cooperative Learning Approach to Improve Learning Outcomes for Mobile Situated Learning," *J. Educ. Technol. Soc.*, vol. 17, no. 1, pp. 128–140, 2014, doi: 10.2307/jeductechsoci.17.1.128.

[3] C. K. Kebenei and P. Okoth, "Ebola Virus Disease, Diagnostics and Therapeutics: Where is the Consensus in Over Three Decades of Clinical Research?," *Sci. African*, vol. 13, p. e00862, 2021, doi: 10.1016/j.sciaf.2021.e00862.

[4] BBC NEWS Africa, "Ebola: Mapping the outbreak," 2016. https://www.bbc.com/news/world-africa-28755033 (accessed Sep. 12, 2021).

[5] J. Sun *et al.*, "Ebola virus outbreak returns to the Democratic Republic of Congo: An urgent rising concern," *Ann. Med. Surg.*, vol. 79, no. May, pp. 3–7, 2022, doi: 10.1016/j.amsu.2022.103958.

[6] Centers for Disease Control, "Ebola (Ebola Virus Disease)," 2021. https://www.cdc.gov/vhf/ebola/transmission/index.html (accessed Sep. 12, 2021).

[7] World Health Organization, "Ebola virus disease," 2021. https://www.who.int/en/news-room/fact-sheets/detail/ebola-virus-disease (accessed Sep. 12, 2021).

[8] P. Diaz, P. Constantine, K. Kalmbach, E. Jones, and S. Pankavich, "A modified SEIR model for the spread of Ebola in Western Africa and metrics for resource allocation," *Appl. Math. Comput.*, vol. 324, pp. 141–155, 2018, doi: 10.1016/j.amc.2017.11.039.

[9] V. Piccirillo, "Nonlinear control of infection spread based on a deterministic SEIR model," *Chaos, Solitons and Fractals*, vol. 149, p. 111051, 2021, doi: 10.1016/j.chaos.2021.111051.

[10] A. Khan, M. Naveed, M. Dur-e-Ahmad, and M. Imran, "Estimating the basic reproductive ratio for the Ebola outbreak in Liberia and Sierra Leone," *Infect. Dis. Poverty*, vol. 4, no. 1, p. 13, 2015, doi: 10.1186/s40249-015-0043-3.

[11] P. Wintachai and K. Prathom, "Stability analysis of SEIR model related to efficiency of vaccines for COVID-19 situation," *Heliyon*, vol. 7, no. 4, p. e06812, 2021, doi: 10.1016/j.heliyon.2021.e06812.

[12] M. D. Ahmad, M. Usman, A. Khan, and M. Imran, "Optimal control analysis of Ebola disease with control strategies of quarantine and vaccination," *Infect. Dis. Poverty*, vol. 5, no. 1, p. 72, 2016, doi: 10.1186/s40249-016-0161-6.

[13] P. Van Den Driessche and J. Watmough, "Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission," *Math. Biosci.*, vol. 180, no. 1–2, pp. 29–48, 2002, doi: 10.1016/S0025-5564(02)00108-6.

[14] A. Alam and S. Sugiarto, "Analisis Sensitivitas Model Matematika Penyebaran Penyakit Antraks pada Ternak dengan Vaksinasi, Karantina dan Pengobatan," *J. Ilm. Mat. Dan Terap.*, vol. 19, no. 2, pp. 180–191, 2022, doi: doi: https://doi.org/10.22487/2540766X.2022.v19.i2.16017.

[15] L. Edelstein-Keshet, *Mathematical Models in Biology*. New York: Random House, 2005.

[16] S. F. Al-Azzawi, "Stability and bifurcation of pan chaotic system by using Routh-Hurwitz and Gardan methods," *Appl. Math. Comput.*, vol. 219, no. 3, pp. 1144–1152, 2012, doi: 10.1016/j.amc.2012.07.022.

[17] C. Castillo-chavez, "Dynamical models of tuberculosis and applications," *CBMS-NSF Reg. Conf. Ser. Appl. Math.*, vol. 1, no. 84, pp. 191–217, 2013.