MATHEMATICAL MODEL FOR THE TRANSMISSION DYNAMICS OF MARBURG VIRUS DISEASES WITH CONTACT TRACING AND EFFECTIVE QUARANTINE

Washachi, D. Jacob, Orapine, Hycienth O.*, Baidu A.A., Amoka, John Adeiza
Department of Mathematics, Nigerian Army University Biu, Borno State, Nigeria
* Corresponding Author: hycienthorapine@naub.edu.ng

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Abstract:

This paper presents a deterministic mathematical model for the contact tracking and efficient quarantine in the Marburg virus transmission dynamics with animal host. The next generation matrix was applied to get the basic reproduction number for the MARV model, and the Jacobean and Castillo-Chavez method were used to determine the system's local and global stability respectively. Our study's findings demonstrate that the disease-free point is locally asymptotically stable under certain condition $R_0 < 1$ and unstable at $R_0 > 1$. The Marburg Virus model is also globally asymptotically stable. In order to conduct numerical simulations, MATLAB R2019b was used. According to the results of the numerical simulations, enhanced contact tracking and efficient quarantine strategies can reduce or stop the spread of the MARV virus. To reduce the number of fatalities caused by infectious cases, treatment therapy must be used. If no treatment therapy is used, no infected person will survive the MVD.

Key words: Marburg Virus, contact tracking, Quarantine, Local Stability, Global Stability

Introduction

Marburg Virus Disease (MVD) is characterized by an acute hemorrhagic fever caused by the Marburg virus, MARV, one of the most deadly human pathogens (Brauburger *et al*., 2012). The Marburg virus is zoonotic (that is animal-borne) and is sporadically spread to humans and other primates. It is naturally present in Egyptian fruit bats (Rousettus aegyptiacus) (Towner *et al.,* 2009, Brauburger *et al*., 2012, Qian *et al*., 2022).

In August 1967, laboratory workers in Marburg, Frankfurt, and Belgrade, Yugoslavia (now Serbia), contracted a yet unidentified viral disease. This was the beginning of the Marburg virus (MARV). Seven of the 31 patients (25 with main and six with secondary infections) had severe illness that led to death (Slenczka and Klenk, 2007, Brauburger *et al.,* 2012). African green monkeys (Chlorocebus aethiops), which were brought from Uganda and transported to all three locations, were found to be the cause of the virus. Ironically, the main infections happened when the monkeys' kidney cells were removed from them in order to develop poliomyelitis vaccine strains (Siegert *et al.,* 1968, Brauburger *et al*., 2012). The pathogen was named Marburg virus after the city with the most cases and represented the first isolation of a filovirus. The Marburg virus is classified as genus Marburg marburgvirus, and family Filoviridae together with its now well-known cousin, Ebola virus (EBOV), which later first emerged in Africa not until 1976 (Slenczka and Klenk, 2007 and WHO, 1978).

All index cases of Marburg virus outbreaks since then, except perhaps laboratory infections, have occurred in Africa, with some outbreaks being mainly driven by human-to-human transmissions and others being driven by recurrent viral spillover in animals (Johnson *et al.,* 1996; CDC, 2008; Towner *et al.,* 2009; Adjemian, 2011; Pigott, *et al.,* 2015).

The biggest and deadliest of these outbreaks occurred in the Angolan province of Uige in 2004–2005, where 252 cases of Marburg hemorrhagic fever (MHF) now Marburg Virus Diseases (MVD) were documented, resulting in 227 fatalities (Towner, *et al.*,2006). The Angolan MARV epidemic was one of the deadliest filovirus outbreaks ever recorded in Africa, compare with or surpassing the severity of outbreaks brought on by its cousin, the Ebola virus, (EBOV), with a case fatality rate of almost 90%. The MDV case counts observed throughout each of these outbreaks in Africa are meticulously documented by Qian *et al.* (2022). The majority of MARV cases outside of Africa were unintentionally imported cases in Europe and the United States that likewise had a deadly outcome (CDC, 2008, Timen, *et al.,* 2009).

Marburg Virus Disease (MDV) is now without a particular therapy. The ideal method of therapy is giving fluids and taking preventative steps to achieve containment, such as isolating the patient and disinfecting clothes (SRI, 2012; CDC, 2021). It is uncertain how the Marburg virus typically transmits from its animal host to humans; however, for the two cases in tourists visiting Uganda in 2008, unprotected contact with infected bat feces or aerosols are the most likely routes of infection. It is established however, that MARV is transmitted in different ways (1) when people come into contact with the bodily fluids of a person or animal who is already infected. (2) Objects contaminated with body fluids from a person who is sick with or has died from Marburg virus disease (such as clothes, bedding, needles, and medical equipment), (Towner, *et al*.,2006; SRI, 2012; CDC, 2021).

After an incubation period of 2–21 days exposure with MARV, symptoms such as fever, chills, headaches, and myalgia suddenly appear. A maculopapular rash may appear around the fifth day following the start of symptoms. It's possible to have nausea, vomiting, chest discomfort, a sore throat, stomach pain, and diarrhea. Jaundice, pancreatic inflammation, extreme weight loss, shock, liver failure, extensive bleeding, and multi-organ malfunction are just a few of the symptoms that get progressively worse. The majority of the victims die within two weeks of exposure due to a combination of shock, excessive bleeding, and

dehydration. MARV case mortality rates in findings related Marburg hemorrhagic fever outbreaks have typically varied from 23 to 83%, a smaller percentage of persons, however, exhibit stronger and faster immune responses to the virus and survive (Towner, *et al.*, 2006; Pigott, *et al.*, 2015; CDC, 2021).

In recent years, a single MARV case was found in Guinea in West Africa in August 2021, followed by an epidemic of the virus five weeks later. Ghana in the same vein confirmed the deadliest MARV outbreak in July, 2022, (WHO, 2022). This puts Ghana and the surrounding nations at risk of the Marburg virus disease and threat for public health as well as another lockdown following the global COVID-19 Pandemic.

In this paper, we model the spread of the Marburg virus using the compartmental model extended from the work of Tiraga *et al.*, (2021) to help curtain this menace at this its early state in West Africa.

Mathematical Formulation

In this paper, we divided the human population into five compartments: $S(t)$ represents the number of susceptible individuals at time t, $E(t)$ represents the number of exposed individual at time t; the exposed category refers to incubation period where all of the individuals have been infected but are not yet infectious (Tiraga *et al.*, 2021). The Quarantine compartment $Q(t)$, are people who are being observed if they would show symptoms of the disease; those who do not show symptom go back to the susceptible class. $I(t)$ Represents the number of infectious individuals at time t and $R(t)$ represents the number of recovered (or removed) individuals at time t. The Egyptian fruit bats (animal host) is divided into three (3) compartments: susceptible population $S_b(t)$, the exposed animal host $E_b(t)$, the infectious animal host $I_b(t)$.

where Λ is recruitment rate, β is contact rate, ω is the transition rate from exposed to infectious, δ is induced death rate, γ is the recovery rate and μ is the natural death rate.

The recruitment into susceptible population $(S-compartment)$ due to birth or migration at the constant rate Λ and reduced by natural death μS and because the Marburg Virus Disease (MVD) is transmitted by human-to-human and bat-to-human contact, the $S-$compartment will further reduced by $\left(\frac{\beta I}{N}+\frac{\beta_b I_b}{N_b}\right)S$ with the incidence rate for the $I-$compartment and I_b-compartment, given by $\left(\frac{\beta I}{N}+\frac{\beta_b I_b}{N_b}\right)$ where $\beta>0$ and $\beta_b>0$ are contact rates for human and bat respectively. Now as the susceptible human population come in contact with infectious humans or interact with the infectious bats either by direct contact with the bats or bats' excreta or eating fruits contaminated by the bats, they proceed to the exposed compartment E. At this phase of incubation, the exposed humans becomes infectious (for those who show clear signs and symptoms) and enter infected compartment I, at a rate ω while those exposed humans who are asymptomatic are isolated by contact tracing for a close watch into Quarantine compartment Q, at a rate τ. After a close watch and laboratory diagnosis of the quarantine population, those that are without the MARV return to the susceptible population at a rate φ, while those who become infectious are promoted to the infected compartment I. The infected individuals I remain infected and infectious for sometimes before recovering by treatment or reduced by natural death μI and casualty δI. Those who recovered from the MVD by a way of treatment enter to the recovered compartment R at a rate γ and the population of the recovered is normally reduced by μR. The recruitment into the susceptible compartment of bats (the animal host of the MARV) is by natural birth Λ_b and reduced by $\frac{\beta_b I_b}{N_b}S$ with an incident rate for I_b-compartment given by $\frac{\beta_b I_b}{N_b}$. When susceptible bat interact with infectious bats they proceed to the exposed bat compartment E_b, and to this end become infected and enter the infected bat compartment I_b , and remain infectious but no apparent disease in the Egyptian fruit bats. The natural dynamics of Marburg Virus Disease (MVD) is well represented in model transmission diagram in Fig. 1, with the description of the variables and parameters given in Table 1.

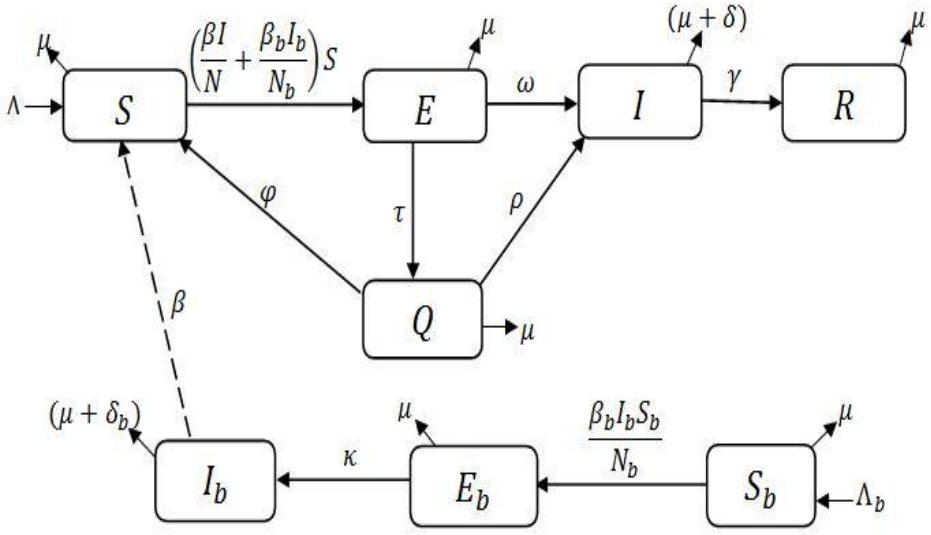

Fig. 1: Model Diagram for the Marburg Virus Diseases

Model Equations

Based on the model diagram in Fig. 1, we have the following equations.

$$\left.\begin{aligned}
\frac{dS}{dt} &= \Lambda + \varphi Q - \left(\mu + \frac{\beta I}{N} + \frac{\beta_b I_b}{N_b}\right) S \\
\frac{dE}{dt} &= \left(\frac{\beta I}{N} + \frac{\beta_b I_b}{N_b}\right) S - (\mu + \omega + \tau) E \\
\frac{dQ}{dt} &= \tau E - (\mu + \rho + \varphi) Q \\
\frac{dI}{dt} &= \omega E + \rho Q - (\mu + \delta + \gamma) I \\
\frac{dR}{dt} &= \gamma I - \mu R \\
\frac{dS_b}{dt} &= \Lambda_b - \left(\mu + \frac{\beta_b I_b}{N_b}\right) S_b \\
\frac{dE_b}{dt} &= \frac{\beta_b I_b}{N_b} S_b - (\mu + \kappa) E_b \\
\frac{dI_b}{dt} &= \kappa E_b - (\mu + \delta_b) I_b
\end{aligned}\right\} \quad (1)$$

With the initial conditions;

$$\left.\begin{aligned}
S(t_0) = S_0, E(t_0) = E_0, Q(t_0) = Q_0 \\
I(t_0) = I_0, \qquad R(t_0) = R_0 \\
S_b(t_0) = S_{b0}\,, E_b(t_0) = E_{b0}, I_b(t_0) = I_{b0}
\end{aligned}\right\}$$

Table 1: Variables/Parameters Description

Variable/ Parameter	Description
$S(t)$	Susceptible human population at time t
$E(t)$	Exposed human population at time t
$I(t)$	Infected human population at time t
$R(t)$	Recovered human population at time t
$Q(t)$	Quarantined human population at time t
$S_b(t)$	Susceptible bat population at time t
$E_b(t)$	Exposed bat population at time t
$I_b(t)$	Infected human population at time t
Λ	Recriutment rate for human population
μ	Natural death rate
δ	Disease induced death rate for Human being
δ_b	Disease induced death rate for Bats
β	Probability of MARV transmission by humans
β_b	Probability of MARV transmission by bats
ω	The rate at which exposed humans get infected
τ	The rate at which exposed humans get quarantine
φ	The rate at which exposed humans moved back to susceptible populations
ρ	The rate at which quarantine humans get infected
γ	Recovery rate from the MVD
Λ_b	Recruitement rate of Bats into the Bat susceptible population
κ	The rate at which exposed bats get infected

Analysis of the Model

In this section, we consider the following results which establish that the Marburg Virus Disease MVD governed by the system (1) is epidemiologically and mathematically well-posed in a feasible Domain given $D = D_H U D_B$ where;

$$D_H = \left\{(S(t), E(t), Q(t), I(t), R(T) \in R_+^5 : N_H \le \frac{\Lambda}{\mu}\right\}$$

$$D_b = \left\{(S_b(t), E_b(t), I_b(t)) \in R_+^3 : N_b \le \frac{\Lambda_b}{\mu}\right\}$$

It has been verified that the model is biologically feasible.

Disease Free Equilibrium

When there is no disease in the population, from the System of equations (1) at MDV free we have;

$$E(t) = Q(t) = I(t) = R(t) = E_b(t) = I_b(t) = 0$$

Therefore, the disease free equilibrium for the Marburg Virus Disease model is given by

$$E_0 = \left(\frac{\Lambda}{\mu}, 0, 0, 0, 0, \frac{\Lambda_b}{\mu}, 0, 0\right)$$

Endemic Equilibrium

To calculate the endemic equilibrium point (EEP), we let

$$\frac{dS(t)}{dt} = \frac{dE(t)}{dt} = \frac{dQ(t)}{dt} = \frac{dI(t)}{dt} = \frac{dR(t)}{dt} = \frac{dS_b(t)}{dt} = \frac{dE_b(t)}{dt} = \frac{dI_b(t)}{dt} = 0$$

And we define;

$$m_1 = \mu + \frac{\beta I}{N} + \frac{\beta_b I_b}{N_b}, \qquad m_2 = \frac{\beta I}{N} + \frac{\beta_b I_b}{N_b},$$
$$m_3 = \mu + \omega + \tau, \qquad m_4 = \mu + \rho + \varphi,$$
$$m_5 = \mu + \delta + \gamma, \qquad m_6 = \mu + \frac{\beta_b I_b}{N_b},$$
$$m_7 = \frac{\beta_b I_b}{N_b}, \quad m_8 = \mu + \kappa,$$
$$m_9 = \mu + \delta_b$$

Thus, the system of equations (2.0-2.1) can be solved in terms of $m_1, m_2, \ldots m_9$ to find the EEP, $E_p = (S,\ E,\ Q,\ I,\ R,\ S_b,\ E_b,\ I_b)$ where

$$S = \frac{\Lambda m_3 m_4}{m_1 m_3 m_4 - m_2 \varphi \tau}$$
$$E = \frac{\Lambda m_2 m_4}{m_1 m_3 m_4 - m_2 \varphi \tau}$$
$$Q = \frac{\Lambda \tau m_2}{m_1 m_3 m_4 - m_2 \varphi \tau}$$
$$I = \frac{\Lambda m_2 (\omega m_4 + \rho \tau)}{m_1 m_3 m_4 m_5 - m_2 m_5 \varphi \tau}$$

$$R = \frac{\Lambda\gamma m_2(\omega m_4 + \rho\tau)}{m_1 m_3 m_4 m_5 \mu - m_2 m_5 \mu\varphi\tau}$$

$$S_b = \frac{\Lambda_b}{m_6}$$

$$E_b = \frac{\Lambda_b m_7}{m_8 m_6}$$

$$I_b = \frac{\kappa\Lambda_b m_7}{m_9 m_8 m_6}$$

Basic Reproduction Number

The basic reproduction number, R_0 of MVD model for system of equations (1) is the number of secondary infections produced by an infectious individual introduced during the period of infectiousness into totally susceptible population. We apply the next generation matrix technique by Diekman, Heesterbeck and Metz (1990) to obtain the basic reproduction number for MVD virus disease R_0. It can be calculated as where;

$$F = \begin{pmatrix} 0 & 0 & \beta & 0 & \frac{\beta_b\Lambda}{\Lambda_b} \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \beta_b \\ 0 & 0 & 0 & 0 & 0 \end{pmatrix},$$

$$V = \begin{pmatrix} m_3 & 0 & 0 & 0 & 0 \\ -\tau & m_4 & 0 & 0 & 0 \\ -\omega & -\rho & m_5 & 0 & 0 \\ 0 & 0 & 0 & m_8 & 0 \\ 0 & 0 & 0 & -\kappa & m_9 \end{pmatrix}$$

And

$$FV^{-1} = \begin{pmatrix} \frac{\beta(\rho\tau + \omega m_4)}{m_3 m_4 m_5} & \frac{\beta\rho}{m_4 m_5} & \frac{\beta}{m_5} & \frac{\beta_b\Lambda\kappa}{m_8 m_9 \Lambda_b} & \frac{\beta_b\Lambda}{m_9\Lambda_b} \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \frac{\beta_b\kappa}{m_8 m_9} & \frac{\beta_b}{m_9} \\ 0 & 0 & 0 & 0 & 0 \end{pmatrix}$$

Hence

$$R_0 = \frac{\beta\left(\rho\tau + \omega\left(\mu + \rho + \varphi\right)\right)}{\left(\mu + \omega + \tau\right)\left(\mu + \rho + \varphi\right)\left(\mu + \delta + \gamma\right)}$$

Local Stability

Theorem 1: The disease free equilibrium E_0 point of MVD model is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$. This proposition is achieved by $|J(E_0) - \lambda I| = 0$, using (1) where;

$$\left|J(E_0) - \lambda I\right| = \begin{vmatrix} -\mu-\lambda & 0 & \varphi & -\beta & 0 & 0 & 0 & -\frac{\beta_b\Lambda}{\Lambda_b} \\ 0 & -m_3-\lambda & 0 & \beta & 0 & 0 & 0 & \frac{\beta_b\Lambda}{\Lambda_b} \\ 0 & \tau & -m_4-\lambda & 0 & 0 & 0 & 0 & 0 \\ 0 & \omega & \rho & -m_5-\lambda & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \gamma & -\mu-\lambda & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & -\mu-\lambda & 0 & -\beta_b \\ 0 & 0 & 0 & 0 & 0 & 0 & -m_8-\lambda & \beta_b \\ 0 & 0 & 0 & 0 & 0 & 0 & \kappa & -m_9-\lambda \end{vmatrix} = 0 \quad (2)$$

Solving the equation (2) we have

$$\lambda_1 = \lambda_2 = 0, \quad \lambda_3 = -(\mu + \delta + \gamma), \quad \lambda_4 = -\mu, \quad \lambda_5 = -(\mu + \rho + \varphi), \quad \lambda_6 = -(\mu + \omega + \tau),$$

$$\lambda_7 = -\frac{1}{2}(\mu + \kappa) - \frac{1}{2}(\mu + \delta_b) + \frac{1}{2}\sqrt{(\mu + \kappa)^2 - 2(\mu + \kappa)(\mu + \delta_b) + (\mu + \delta_b)^2 + 4\beta_b\kappa},$$

$$\lambda_8 = -\tfrac{1}{2}(\mu + \kappa) - \tfrac{1}{2}(\mu + \delta_b) - \tfrac{1}{2}\sqrt{(\mu + \kappa)^2 - 2(\mu + \kappa)(\mu + \delta_b) + (\mu + \delta_b)^2 + 4\beta_b\kappa}$$

Thus, since all the values of $\lambda_i \leq 0, i = 1, 2, 3, 4, 6, 7, 8$ when $R_0 < 1$, we conclude that the disease free equilibrium point is locally and asymptotically stable.

Global Stability of the disease free equilibrium point

For Global stability of the Disease Free Equilibrium, the technique use by Castillo-Chavez, Feng and Huang (2002) was employed. The is rewritten as follows

$$\left.\begin{aligned} \frac{dX}{dt} &= K(X, Z) \\ \frac{dZ}{dt} &= G(X, Z), \qquad G(X, 0) = 0 \end{aligned}\right\} \quad (3)$$

Where $X \in \mathbb{R}^3$ and $X = \{S,\ R,\ S_b\}$ denotes the number of uninfected individuals, $Z \in \mathbb{R}^5$ and $Z = \{E, Q, I, E_b, I_b\}$ denotes the number of infected individuals. $E_0 = \left(\frac{\Lambda}{\mu}, 0, 0, 0, 0, \frac{\Lambda_b}{\mu}, 0, 0\right)$ denotes the disease free equilibrium point of this system, where $X^* = \left(\frac{\Lambda}{\mu}, \frac{\Lambda_b}{\mu}\right)$.

Condition (3.0) maybe met to guaranteed global asymptotic stability.

(**H1**):for $\frac{dX}{dt} k(X, 0), X^*$ is globally asymptotic stable.

(**H₂**): for $G(X,Z) = AZ - \hat{G}(X,Z),\ \hat{G}(X,Z) \geq 0\ ,\ \ \forall (X,Z) \in \Gamma$ where $A = D_z G(X^*, 0)$ is an M matrix and Γ is the region where the model has biological meaning.

Theorem 2

If system (2.0-21) satisfies condition (1), then the fixed point $E_0 = \left(\frac{\Lambda}{\mu}, 0, 0, 0, 0, \frac{\Lambda_b}{\mu}, 0, 0\right)$ is a globally asymptotically stable equilibrium of the system (1), provided that $R_0 \leq 1$ and the conditions (H_1) and (H_2) are satisfied.

Proof.

Consider $K(X,0) = \begin{bmatrix} \Lambda - \mu S \\ \Lambda - \mu S_b \end{bmatrix}$ and $G(X,Z) = AZ - \hat{G}(X,Z)$, where;

$$A = \begin{pmatrix} -(\mu+\omega+\tau) & 0 & \frac{\beta S}{N} & 0 & \frac{\beta_b S}{N_b} \\ \tau & -(\mu+\rho+\varphi) & 0 & 0 & 0 \\ \omega & \rho & -(\mu+\omega+\tau) & 0 & 0 \\ 0 & 0 & 0 & -(\mu+\kappa) & \frac{\beta_b S_b}{N_b} \\ 0 & 0 & 0 & \kappa & -(\mu+\delta_b) \end{pmatrix} \tag{4}$$

$$Z = \begin{pmatrix} E \\ Q \\ I \\ E_b \\ I_b \end{pmatrix}, \qquad G(X,Z) = \begin{pmatrix} \frac{\beta S}{N} - \frac{\beta_b I_b S}{N_b} - (\mu+\omega+\tau)E \\ \tau E - (\mu+\rho+\varphi)Q \\ \omega E + \rho Q - (\mu+\rho+\varphi)Q \\ \frac{\beta_b I_b S_b}{N_b} - (\mu+\kappa)E_b \\ \kappa E_b - (\mu+\delta_b)I_b \end{pmatrix} \tag{5}$$

Given that;

$$\hat{G}(X,Z) = AZ - G(X,Z) \tag{6}$$

Now substituting equations (4), (5) into (6) we have;

$$\hat{G}(X,Z) = \begin{pmatrix} -(\mu+\omega+\tau) & 0 & \frac{\beta S}{N} & 0 & \frac{\beta_b S}{N_b} \\ \tau & -(\mu+\rho+\varphi) & 0 & 0 & 0 \\ \omega & \rho & -(\mu+\omega+\tau) & 0 & 0 \\ 0 & 0 & 0 & -(\mu+\kappa) & \frac{\beta_b S_b}{N_b} \\ 0 & 0 & 0 & \kappa & -(\mu+\delta_b) \end{pmatrix} \begin{pmatrix} E \\ Q \\ I \\ E_b \\ I_b \end{pmatrix} - \begin{pmatrix} \frac{\beta S}{N} - \frac{\beta_b I_b S}{N_b} - (\mu+\omega+\tau)E \\ \tau E - (\mu+\rho+\varphi)Q \\ \omega E + \rho Q - (\mu+\rho+\varphi)Q \\ \frac{\beta_b I_b S_b}{N_b} - (\mu+\kappa)E_b \\ \kappa E_b - (\mu+\delta_b)I_b \end{pmatrix} = \begin{pmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix}$$

Since all the conditions are satisfied, $\hat{G}(X,Z) = 0$, the Disease Free Equilibrium E_0 is globally asymptotically stable.

Numerical Simulation

There is a scarcity of available data for MVD outbreak. We perform numerical simulations, using statistics from Tiraga *et al.*, (2021), WHO (2021), Webots (2018) and Brauburger *et al.*, (2012) for parameter estimations. The population of a typical small village in Angola that had a huge Marburg epidemic might be 253. In our simulation, we take into account a population size of $N = 253$ with 2 initial infected people. (Tiraga *et al.*, 2021). We study the dynamics of the spread in the intervals of days as presented in the following figures.

Table 2: Variables/Parameters values used for MVD model simulation.

Parameter	Value	Reference
$S(0)$	253	Towner, *et al.*,(2006), Tiraga *et al.*, (2021)
$E(0)$	2	Estimated
$Q(0)$	0	Estimated
$I(0)$	2	Tiraga *et al.*, (2021)
$R(0)$	0	Estimated
$S_b(0)$	100	Estimated
$E_b(0)$	40	Estimated
$I_b(0)$	40	Estimated
N	267	Estimated
N_b	180	Estimated
Λ	0.4	Tiraga *et al.*, (2021)
Λ_b	0.55	Estimated
μ	0.20	Estimated
δ	0.90	Towner, *et al.*,(2006)
δ_b	0.05	Estimated
β	0.28	Estimated
β_b	0.90	Estimated
ω	0.15	Estimated
τ	0.85	Estimated
φ	0.10	Estimated
ρ	0.90	Estimated
γ	0.30	Estimated
κ	0.19	Estimated

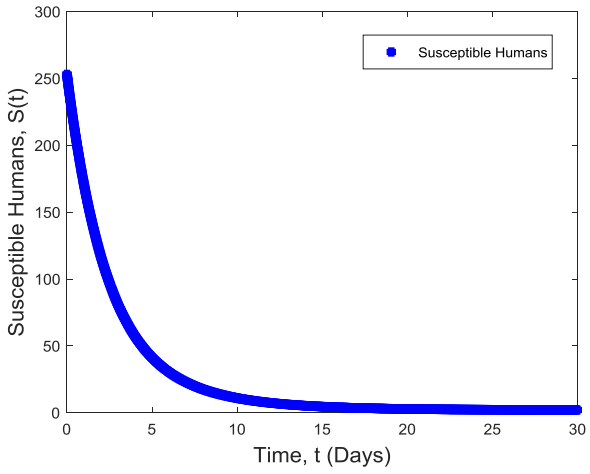

Fig. 2: The dynamics of Susceptible Humans against MARV over a period of 30 days

Figure 2 shows that susceptible population reduced significantly to zero in matter of days because there is no evidence in the literatures that an individual who was once infected with MDV and recovered will still be susceptible to the MARV, hence the result shows permenant inmunity once recovered from the MDV.

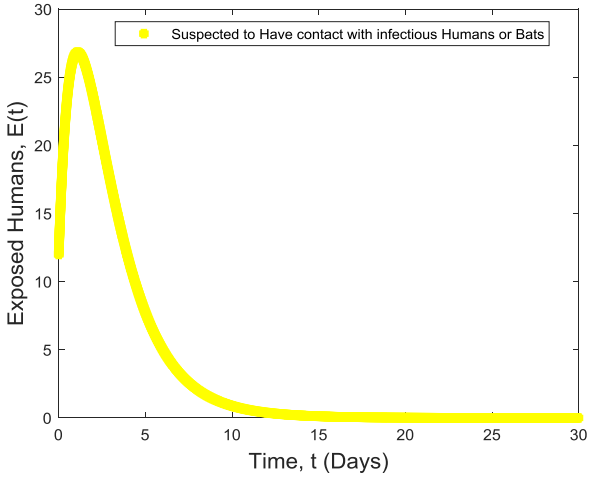

Fig. 3: The dynamics of Exposed Humans to MARV over a period of 30 days

Figure 3 shows that exposed human population will increase rapidly at first but will then reduced drastically because of the introduction of the quarantined compartment which limit the exposed individuals of secondary contact to the susceptible humans, preventing human-to-human transmission.

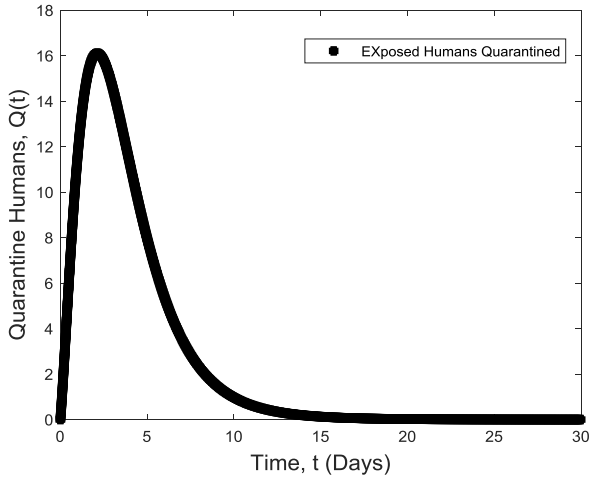

Fig. 4: The dynamics of Quarantined Humans who are exposed to MARV over a period of 30 days.

Figure 4 shows that the number of quarantined human population will increase significantly as the susceptible human class keep having contact with exposed or infectious population. This is because of contact tracing and quarantine is invoke in this dynamical model. On the other hand, as the exposed compartment controlled limiting the secondary infections there will be less pressure on the quarantine compartment.

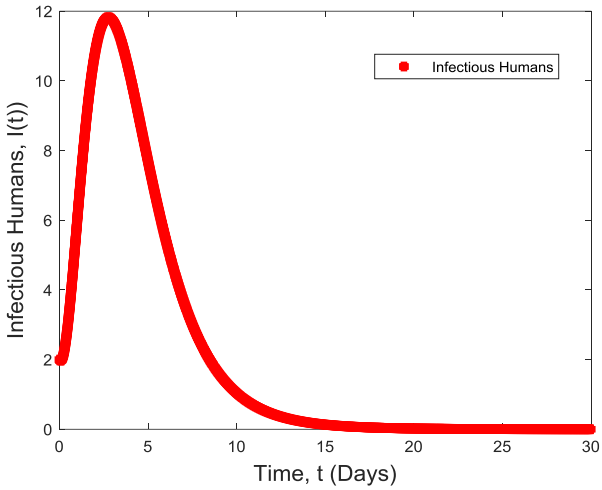

Fig. 5:The dynamics of Infectious Humans with MARV over a period of 30 days

Figure 5 shows that infected and infectious human population will signifcantly increase at first but as the contact tracing is invoke and effective quarantine strategy is deployed together with treatment therapy to manage the already infectious human, MVD and MARV infectious will drastically be reduced to zero among human populations.

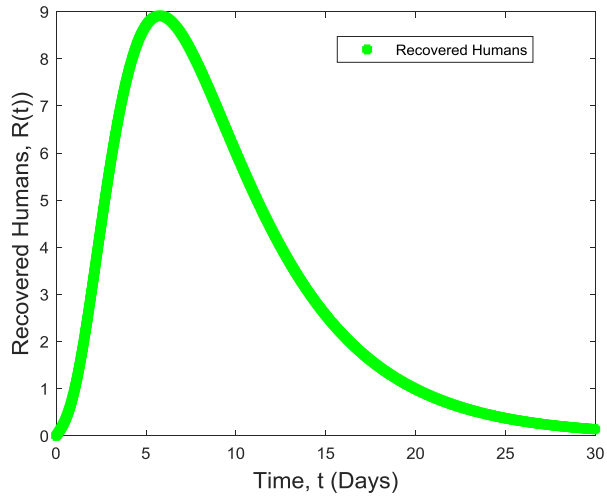

Fig. 6: The dynamics of Treated Humans with MARV over a period of 30 days

Figure 6 shows that the number of recovered humans will increase at lease three in four of infectious individuals will surely recovered from the MDV if the contact tracing, quarantine strategy is deployed and treatment therapy is installed at the early state of the MARV infection of the exposed individuals.

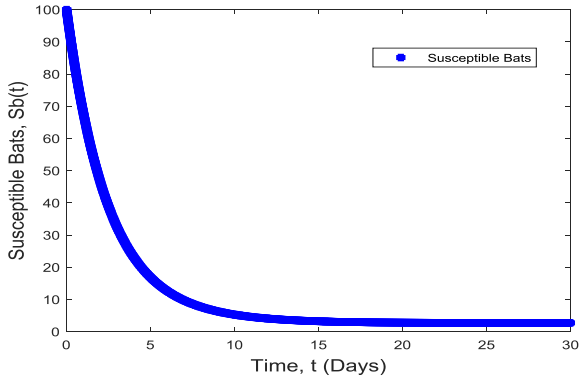

Fig. 7: Showing the dynamics of Susceptible Bats. looking at figure 2 and 7 you will observed that there is no differences between the two susceptible graphs which indicate that if the same approached is employed in the animal host the disease can be eliminated.

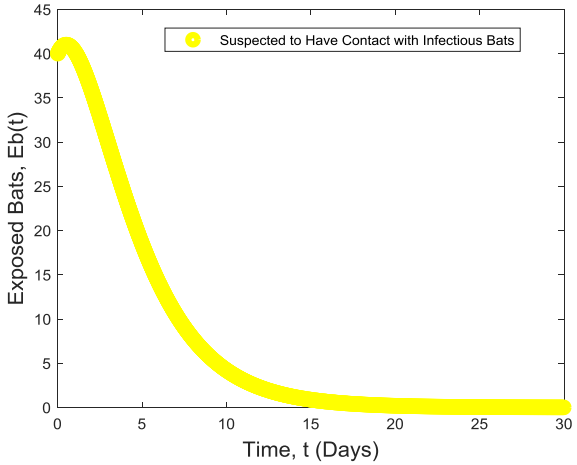

Fig. 8: Showing the dynamics of Exposed Bats

Observing figure 3 and 8 you will oberved that in animal host there is high rate of exposure due to the fact that the number of bat having contact with each is more than that of human hence high rate of exposer, one will also notice that the number of exposed in human reduced drastically in day 10 due to quarantine while that of bats is on day 15.

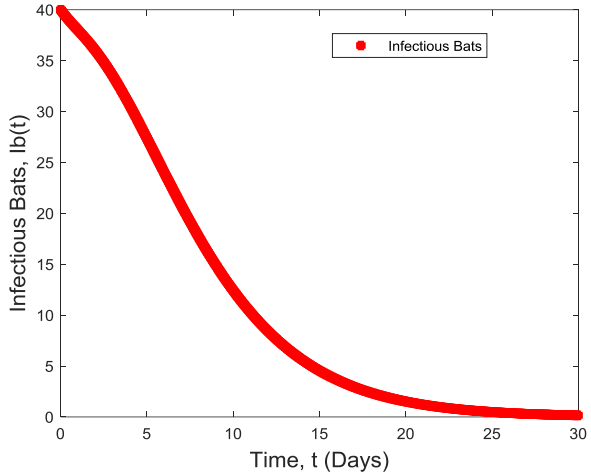

Fig. 9: Showing the dynamics of Infectous Bats Figure

comparing figure 5 and 9 one will observed that with the aid of treatment therapy in less that 12days there is no disease in human population but observing figure 9 is from 22 days that the the infection has reduced within the animal host, may be at this point all the infected animal host might had die from the disease.

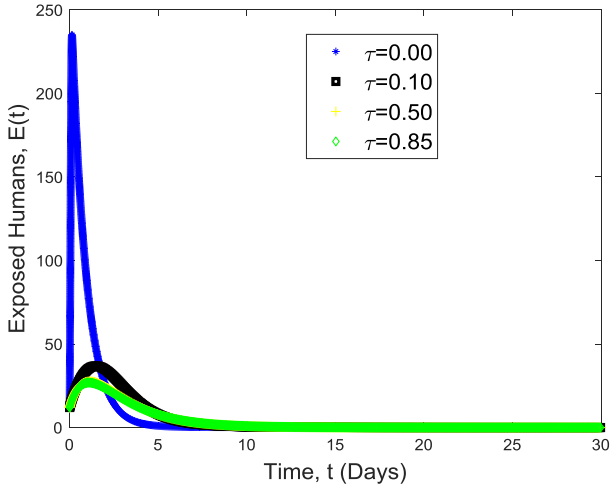

Fig. 10: The effect of Effective Quarantine on Exposed Humans

Figure 10 shows that without introducing contact tracing and quarantine strategy, almost all the susceptiple human population will be exposed to the MARV. It is established here that the more we get the exposed individuals quarantined the less the effect of secondary infection or spread since those exposed or infectious individual will not have contact with the susceptible compartment again to spread the dreaded MARV hence the exposed compartment will be reduced significantly to zero.

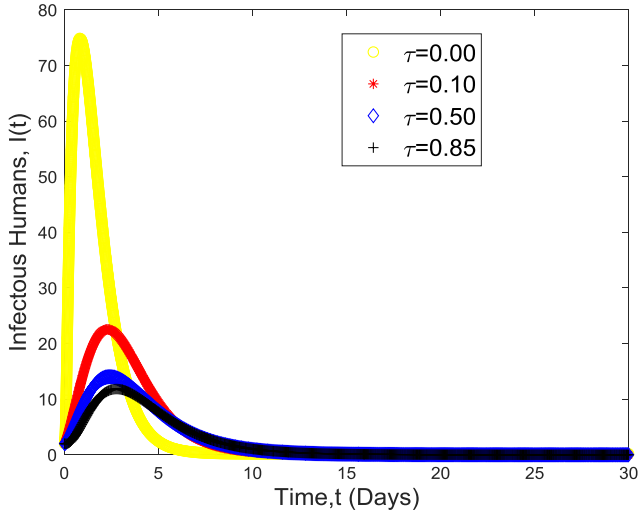

Fig. 11: The effect of Effective Quarantine on Infectious Humans

Figure 11 shows clearly that without effective quarantine ($\tau = 0.00$), MARV infection of Human population will increase rapidly as about 35% of the exposed humans will come out being infected. It is conventional to say here that if the quarantine compartment is removed, the exposed human population will rise rapidly there by increasing the cases of infection in the human population. It is seen in the figure 11 that, however insignificant the quarantine compartment may be, it has great impact on the number of infected cases in the human population.

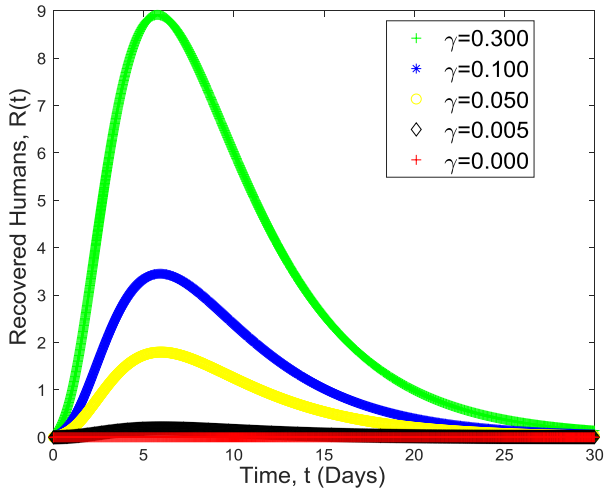

Fig. 12: The effect of Treatment Therapy on Recovered Humans

Figure 12 shows obviously that if no treatment therapy ($\gamma = 0.00$) is installed, no infected and infectious humans will recover from the MDV. The more aggressive the treatment therapy (at least, $\gamma = 0.30$) is deployed to manage infection cases the more lives will be saved. If no effective treatment is mounted, the infected and infectious will die all, even though the disease will be eradicated in among human population because of the active contact tracing and effective quarantine that will guaranteed no further spead of the disease.

Conclusion

In this paper,we studied mathematical model for the transmission dynamics of marburg virus diseases with contact tracing and effective quarantine. The model is divided in to two parts the human compartments and animal host (which is the bats compartments). Analytical studies were carried out and the disease free equilibrium points were obtained. The results showed that the equilibrium point of the model is locally asymptotically stable if $R_0 < 1$ and also globally asymptotically stable using Castilo-Chavez and Feng, (1997) technique. The numerical experiment results carried out indicates that minimizing or eradicating the transmission of MARV can be achieved by increasing contact tracing and quarantine strategy. Treatment therapy must be employed to manage infectious cases in order to minimize death causalities.

While we noted that currently the MVD has no particular treatment therapy, using this model shows that without deploying any treatment therapy at all will result to no infected human surviving the MVD. therefore even as therapy of giving fluids and others (such as isolating the patient and disinfecting clothes) is engaged, there is high need of medical research into production of treatment therapy and vaccination. It is established in this research that taking preventative steps to achieve containment, such as contact tracing and installing quarantine strategy early enough will greatly reduce the spread of transmission and as such bring the infection cases to zero in no time.

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