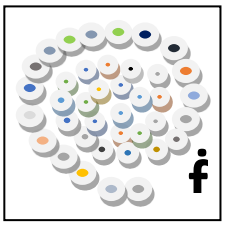

International Journal of Mathematical Analysis and Modelling

(Formerly Journal of the Nigerian Society for Mathematical Biology)

Volume 5, Issue 2 (Sept.), 2022

ISSN (Print): 2682 - 5694
ISSN (Online): 2682 - 5708

International Journal of Mathematical Analysis and Modelling
Volume 5, Issue 2, September 2022, Pages 137 – 170

The transmission dynamics of Lassa fever virus

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Abstract

Lassa fever Virus (LFV) is a rare, acute arena viral hemorrhagic fever caused by Lassa virus, which is often fatal if untreated. In this research work, we developed a model that describes the dynamics of Lassa fever Virus (LFV) disease in human population compartments involved with vital dynamics (birth and death rates), incorporating exposed quarantine individuals of 6 to 21days window period and treatment of infected individuals of 21days $^{(+)}$ of infectious period in the trends of infection progression which are influenced by public health education campaign. A system of Nonlinear differential equations was formulated for the transmission dynamic of Lassa fever virus (LFV). The model has the Basic Reproduction Number (R_o) and effective reproductive number (R_e), the Stability analysis of the model indicated that the local and global disease-free equilibrium (DFE) is stable and indeed when (R_o) < 1 and unstable when (R_o) > 1. Numerical results show that the infected individuals should be quarantined and given health education campaigns before treatment, because both complement each other in reducing the spread of Lassa fever virus as well as increasing the rate of recovery of the infected individuals.

Keywords: Lassa fever virus; transmission dynamics; human population compartments

1 Introduction

In this chapter we reviewed works done by other researchers on mathematical modeling, especially on Lassa fever Virus (LFV). According to (World Health Organization, 2017) Lassa fever Virus (LFV) is an acute, hemorrhagic viral disease that occurs mainly in West African countries and was first discovered in the town of Lassa in the North-East Nigeria in 1969. Though it was first described in the 1950s, but the virus was not identified until 1969, when two missionary nurses died from it in the town of Lassa in Borno, Nigeria (Richmond and Baglole 2003). Lassa fever is a zoonotic disease, i.e., it can be transmitted from an infected animal to a human. Multimammate rats of the genus *Mastomys* is the reservoir host of the virus (Walker *et al*, 2019). It is associated with acute and potentially fatal haemorrhagic illness caused by Lassa virus (Hallam *et al*, 2018). The Lassa fever virus is a zoonotic disease that is primarily transmitted to humans from contact with infected animals; usually a rodent of the genus Mastomys commonly known as multimammate rat (World Health Organization, 2017 &

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2018). The Mastomys rats infected with Lassa fever do not become ill, but can transmit the virus to humans and other primates through the shed of their urine and faeces (World Health Organization, 2017). Lassa fever is known to be endemic in Benin, Ghana, Liberia, Mali, Sierra Leone, and Nigeria, but probably exists in other African countries as well (World Health Organization, 2017 & 2018). The Lassa fever virus usually last for 2-21 days in humans, but because the clinical course of the disease is so variable and nonspecific, clinical diagnosis of the disease in affected patients at early stages has been difficult (World Health Organization, 2017; Sulaiman & Ibrahim, *et al*., 2018), and confirmatory laboratory diagnosis is not within the confines of many centers in West Africa (World Health Organization, 2017; Andrew, *et al.* (2013). About 80% of people infected with Lassa fever are asymptomatic (World Health Organization, 2017). The incubation period of the disease ranges from 6-21 days and the onset of the disease, when it is symptomatic, is usually gradual, starting with fever, general weakness, and malaise (World Health Organization, 2017).

After few days of infection, follows headache, sore throat, muscle pain, chest pain, nausea, vomiting, diarrhea, and abdominal pain (World Health Organization, 2017). In severe cases of the disease, facial swelling, fluid in the lung cavity, bleeding from the mouth, nose, vagina or gastrointestinal tract and low blood pressure may also occur (World Health Organization, 2017). Protein may also be noted in the urine of an infected person (World Health Organization, 2017). However, shock, seizures, tremor, disorientation, and coma may also be seen in the later stages of infection (World Health Organization, 2017). Deafness occurs in 25% of patients who survived the disease (World Health Organization, 2017). In half of the infected cases, hearing returns partially after 1-3 months of recovery, and transient hair loss and gait disturbance may occur during recovery (World Health Organization, 2017). Death usually occurs within the first 14 days of onset in fatal cases (World Health Organization, 2017). It is reported that, 1 out of each 5 infections results in severe disease case, where the virus affects several vital organs such as the liver, spleen and the kidneys (World Health Organization, 2017).

The disease is especially severe in late pregnancies with maternal death and or fetal loss occurring in more than 80% of the cases during third trimester (World Health Organization, 2017). The overall case-fatality rate is 1% and observed case-fatality rate among patients hospitalized with severe cases of the Lassa fever is 15% (World Health Organization, 2017). However, when the presence of the disease is confirmed in a community, prompt isolation of affected patients, good infection prevention and control practices, and rigorous contact tracing can stop outbreaks (World Health Organization, 2017). Early supportive care with rehydration and symptomatic treatment of the infected persons improves survival and chances of recovery (World Health Organization, 2017). The antiviral drug ribavirin seems to be an effective treatment for the Lassa fever virus if given early in the course of clinical illness (World Health Organization, 2018). There is no evidence to support the role of ribavirin as post-exposure prophylactic treatment for the Lassa fever (World Health Organization, 2018). Generally, there is no licensed vaccine for Lassa fever virus (World Health Organization, 2018; Thomas, *et al*., 2005), opined that no experimental vaccine has completely protected non-human primates against Lassa fever.

The Lassa fever virus is usually transmitted to humans via contact with food or household items contaminated with rodents' urine or faeces (World Health Organization, 2017). Humans become infected with the Lassa fever virus from exposure to urine or faeces of an infected Mastomys rats (World Health Organization, 2017). The Lassa virus may also be transmitted among humans through direct contact with the blood, urine, faeces or other bodily secretions of an infected person with Lassa fever (World Health Organization, 2017). Currently, there is no epidemiological evidence supporting airborne spread of the Lassa fever virus among humans, but, person-to-person infections and laboratory transmission can also occur, especially in hospitals lacking adequate infection prevention

and control measures (World Health Organization, 2017). Person-to-person transmission occurs in both community and healthcare settings where the virus may be spread by contaminated medical equipment, such as re-used needles (World Health Organization, 2017). Sexual transmission of the Lassa fever virus has also been reported (World Health Organization, 2017). Infections in humans typically occurs by direct or indirect exposure to animal excrement through the respiratory or gastrointestinal tracts (Okuonghae D. et al, 2006). Inhalation of the tiny particles of infectious material (aerosol) is believed to be the most significant means of exposure (Okuonghae D. et al, 2006). It is possible to acquire the infection through broken skin or mucous membranes that are directly exposed to infectious materials and so, transmission from person-to-person has been established (World Health Organization, 2017; Okuonghae D. et al, 2006). Outbreaks of the Lassa fever virus occurs regularly in West Africa with the most recent one in Nigeria (Vanguard News, 2018). From 1 January 2018 through 18 March 2018, about 1495 suspected cases and 119 deaths have been reported in Nigeria from 20 States of the Federation including Anambra, Bauchi, Benue, Delta, Ebonyi, Edo, Ekiti, FCT Abuja, Gombe, Imo, Kaduna, Kogi, Lagos, Cross River, Nassarawa, Ondo, Osun, Plateau, Rivers and Taraba (World Health Organization, 2018).

During this period, 376 cases were confirmed, 9 were classified probable, 1084 were reported negative and 26 are pending; awaiting laboratory results (World Health Organization, 2018). Among the 376 confirmed and the 9 classified probable cases, 95 deaths were reported giving a case-fatality rate of the confirmed and probable cases to be 24.7% (World Health Organization, 2018). Similar reports about the current ongoing Lassa fever outbreaks and fatality cases in Nigeria can be found in (Ayodemola, 2018; Vanguard News, 2018). Since 1 January 2018, the number of Lassa fever cases increased from 10 to 70 weekly reported cases (World Health Organization, 2018). However, since mid-February 2018, there has been a downward trend in the weekly reported number of cases (World Health Organization, 2018). The Nigeria Center for Disease Control NCDC has built a laboratory in Ebonyi State that has the equipment needed to identify the Lassa fever virus, which is the fourth of its kind to be established by the institution in the country (Vanguard News, 2018).

Mathematical modeling in epidemiology provides an understanding of the mechanisms that influence the spread of diseases, and suggests control strategies. For some diseases, it is found that for a period of time, a part of the infectious class does not show the symptoms (Mohammed, AL-Smadi and Ghaleb, 2014). For modeling such diseases SEIR models are used (Mohammed, AL-Smadi and Ghaleb, 2014). A general SEIR model with vertical transmission for the dynamics of an infectious disease was studied by El-Sheikh and El-Marouf (2003), where a fraction p and q of the offspring from the exposed and the infectious classes, respectively, were assumed to be infected at birth. This study shows that some part of infectious class manifest symptoms. The work of El-Sheikh & El-Marouf (2003) showed that once the disease appears, it eventually persists at the unique endemic equilibrium level. They finally used mathematical tools of differential analysis, persistence theory, Hopf-Andronov-Poincaré bifurcation, and linear system theory to deduce the existence of a family of periodic solutions that bifurcate from a positive interior equilibrium.

A mathematical model for the transmission dynamics of Lassa fever virus can also be found in the work of Faniran (2017). In developing the model, Faniran (2017) neglected the latency/exposure period in the successive trends of infection progression in both humans and the animals. They also neglected human-to-human transmission of the virus in the human host and considered only animal-to-human transmission. This work will add knowledge to this model on human -to -human transmission of Lassa fever virus (LFV). Okuonghae and Okuonghae (2006) formulated a SIS model

coupled to a population of rat species, for the transmission of Lassa fever disease. The equilibrium states of the model were obtained and examined the endemic and epidemic situations. They further calculated the basic reproductive number and gave conditions for disease outbreak. Onuorah et al (2016) developed a Lassa fever model using the sex structure approach. Their model represented the transmission dynamics of the Lassa fever disease using a set of ordinary differential equations. They obtained the disease-free equilibrium. Their computation of basic reproduction number is 0.129 which is less than the one.

Akinpelu and Akinwande (2018) formulated a mathematical model for Lassa fever and Sensitivity analysis. The model was divided into five compartments susceptible (S), latent (L), infected (I), isolated (Is) and recovered (R) classes. The equilibrium states, basic reproduction number were obtained using generation matrix and their stabilities were analyzed using Descartes' rule of sign and comparison test. However, their work lacked global stability which this study has covered. In the work of Nwasuka et al (2019) A mathematical model is formulated and analyzed to study the controllability of Lassa fever incorporating separation of infected individuals and treatment measures. The model assumes that humans susceptible acquired the Infection via interaction with the infected rodent populations at a constant rate and also the model assumes that treatment is only given to separated human population without quarantining of exposed individuals. Therefore, this work covered quarantining of exposed individuals of 6 days to 21 days. Another mathematical model for the transmission dynamics of the Lassa fever infection was developed by Omale and Edibo (2015). In the development of the model, they also neglected the latency/exposure period in the successive trends of infection progression in both humans and the animals and considered re-infection after recovery from the treatment intervention in the humans. They considered linear incidence transmission in the animals and the force of infection in the model did not account for animal-to-human transmission. This work will cover latency/exposure period in the successive trends of infection.

A deterministic mathematical model for transmission dynamics of Lassa fever with quarantine policy was constructed in the work of Tolulope, Akinyemi and Bamidele (2015). In their work, they divided the infectious human population into two; the quarantined and un-quarantined humans and considered both as contributing to human-to-human transmission of the virus in the human host. They subdivided the animal population into adults and infant reservoirs and assumed only the adults contributes in animal-to-human transmission of the Lassa virus. In the model, they assumed humans recover with permanent immunity. This work assumed that human recovery is not with permanent immunity. The work of Onuorah et al (2016) subdivided the human host into males and females and the animal reservoirs into active and inactive reservoirs when developing their model. They incorporated sexual transmission of the virus among sexually active humans as one of the means of transmitting the disease in humans. Sensitivity analysis of parameters in the basic reproduction number of their model revealed that, the reproduction number is most sensitive to parameters representing human birth, condom efficacy and compliance rates. However, their work lacked a qualitative and numerical analysis which this study has covered. In the work of Adewale et al (2016), they developed a mathematical model for the transmission dynamics of the Lassa fever virus with proposed isolation of infectious humans as control strategy on the spread of the disease among humans. Most importantly, they showed that the disease free equilibrium is stable while the endemic equilibrium may or may not be stable depending on the model parameters. This model is important to this study, however, the researchers intend to use a different model which is the S, E, E_q, I, I_T, R model to determine the transmission dynamics of Lassa fever virus (LFV).

The model in James et al (2015) studied the transmission dynamics of Lassa fever virus in animal and humans. The SIR model in their work did not consider the exposed quarantining of

individuals between the 6 to 21 days window period in the transmission dynamics of the virus which this study covered. In Ojo et al (2021), the authors developed and critically analyzed a six compartmental model to study the effect of control variables on the control of Lassa fever in Nigeria. The population is stratified into the human population of susceptible, exposed, infectious, and recovered individuals, and also the rodent population of susceptible and infectious rodents. The model in Mark N. C. *et al* (2015) which is the bases of this work, studied a mathematical model on the dynamics of Lassa fever Virus (LFV) in human population. The model in their work consists of only five (5) compartments. They considered quarantining of infectious treated individuals after window period (i.e. 21 days $^{(+)}$) and neglected exposed quarantine individuals of 6 to 21days of window period of the model which this study covered. A number of gaps have been revealed in the foregoing literature, but it is not clear enough about the extent to which the Lassa fever virus (LFV) disease was analyzed. The study attempted to investigate the transmission dynamics of Lassa fever virus (LFV) whose numerical results show that the infected individuals should be quarantined and given health education campaigns before treatment, because both complement each other in reducing the spread of Lassa fever virus as well as increasing the rate of recovery of the infected individuals.

1.1 Aims and objectives of the study

The aim of this paper is to examines the transmission dynamics of Lassa fever Virus (LFV), and other specific objectives of the study are;

1. Carry out a detailed study of Lassa fever Virus (LFV)
2. Investigate the existence and stability of the equilibrium state of the model.
3. Interpret numerically, the results of the analysis.
4. Use the study in providing useful contribution that will aid in the awareness of the dynamics and possible control measures of the disease.

2 Model formulation

The population (N) is divided into six (6) compartments; susceptible individuals (S), Exposed individuals (E), Exposed quarantine (E_q), infected individuals (I), Infectious Treated (I_T), and Recovered individuals (R), So that, $N(t) = S(t) + E(t) + E_{q,}(t) + I(t) + I_T(t) + R(t)$.

S/N	PARAMETERS	PARAMETERS DESCRIPTION
1	$S(t)$	Number of susceptible at time t
2	$E(t)$	Number of exposed at time t
3	(E_q)	Number of exposed quarantine at time t
4	(I)	Number of infected at time t
5	(I_T)	Number of infected treated at time
6	(R)	Number of recovered at time t
7	$N(t)$	Total population at time t

Table 1: Description of variables

S/N	VARIABLE	VARIABLE DESCRIPTION
1	π	Recruitment rate into susceptible class
2	λ	Rate at which susceptible individuals move to exposed class
3	ϵ	Rate of maturity from exposed to the infected class
4	θ	Rate at which the recovered individuals move to susceptible class
5	τ_1	Rate at which exposed-quarantine individuals move to susceptible class.
6	τ_2	Rate at which exposed-quarantine individuals move to infectious class
7	ν	Rate at which infected individuals move to infectious treated class for treatment.
8	ρ	Rate at which Exposed individuals move to quarantine class
9	f	Rate at which treated infectious individuals recover from the disease
10	μ	Natural death rate
11	β	contact rate between the susceptible and infectious individuals
12	δ_1	Rate at which untreated infected individuals died due to infectious
13	δ_2	Rate at which infected individuals died during treatment
14	κ	proportion from S to I (fast progression)

Table 2: Description of Parameters

2.1 Assumptions of the model

The following assumptions were made during the study:

1. The mixing of individual is homogeneous, meaning that all individuals have equal likelihood of getting infected if they come in adequate contact with infectious individuals and the transmission of infection occurs with a standard incident (βSI)
2. Individuals in each group have homogeneous susceptibility but the susceptibilities of individuals from different groups are distinct and different.
3. We assumed that all recruits are neither infected with Lassa fever virus (LFV).
4. The rate at which recovered individuals become susceptible (θ) is negligible.
5. That some infectious individuals under treatment died as a result of the disease, while some recovered from the disease
6. That some individual died natural death

Model diagram of Lassa fever virus

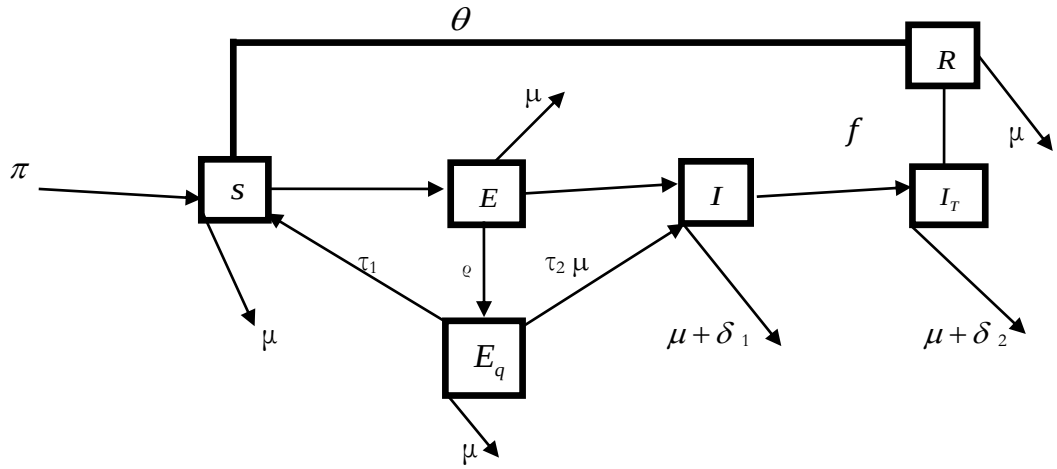

Figure 1. Schematic Diagram

Extended Model Equations

$$\frac{\partial S}{\partial t} = \pi - (\lambda + \mu) + \theta R + \tau_1 E_q$$

$$\frac{\partial E}{\partial t} = \lambda S - (\mu + \in + \rho)E$$

$$\frac{\partial E_q}{\partial t} = \rho E - (\mu + \tau_1 + \tau_2)E_q$$

$$\frac{\partial I}{\partial t} = \in E - (\nu + (\mu + \delta_1))I + \tau_2 E_q$$

$$\frac{\partial I_T}{\partial t} = \nu I - (f + (\mu + \delta_2)I_T$$

$$\frac{\partial R}{\partial t} = fI_T - (\mu + \theta)R \qquad (1)$$

3 Model analysis

In this section, the model equations (1) will be analyzed quantitatively in order to understand the transmission dynamics of Lassa fever virus (LFV). We will therefore, consider the following proof; invariant region, positivity of solution, disease free equilibrium (DFE), endemic equilibrium (EE), basic reproduction number, effective reproduction number, local and global stability analysis of the model.

3.1 Invariant region

In this section, we think of the solutions as having six dimensions, so that at any instance of time (t), we have a vector of solutions with six elements (representing the state variables), real and positive solution. First, we established the positivity of invariant region or set to the above biological model (1) using the total population as $N = S + E + E_q + I + I_T + R$.

Theorem 3.1
The solutions of the system (1) are feasible for all t > 0, if they enter invariant region Ω.

Proof:
Let $\Omega = \left(S, E, E_q, I, I_T, R\right) \in R^6_+$ be any solution of the system (1) with non-negative initial conditions. Using the total population of our model as $N = S + E + E_q + I + I_T + R$.
Hence,

$$\frac{\partial N}{\partial t} = \frac{\partial S}{\partial t} + \frac{\partial E}{\partial t} + \frac{\partial E_q}{\partial t} + \frac{\partial I}{\partial t} + \frac{\partial I_T}{\partial t} + \frac{\partial R}{\partial t}.$$

Considering the force of infection $\lambda = \beta SI$ in our model equation (1), the above equation becomes

$$\frac{\partial N}{\partial t} = \pi - \mu N - dI, \qquad (2)$$

so that,

$$\frac{\partial N}{\partial t} \le \pi - \mu N$$

$$\frac{\partial N}{\partial t} + \mu N \le \pi,$$

where the integrating factor is given as;

$$I.F = \ell^{\int \mu dt}$$
$$I.F = \ell^{\mu t}.$$

Thus, the above differential equation become;

$$\frac{\partial}{\partial t}(N\ell^{\mu t}) \le \pi \ell^{\mu t}$$

$$\partial(N\ell^{\mu t}) \le \pi\ell^{\mu t}dt$$
$$\int\partial(N\ell^{\mu t}) \le \pi\int\ell^{\mu t}dt + C.$$

The above integral becomes

$$N\ell^{\mu t} \le \frac{\pi}{\mu}\ell^{\mu t} + C$$
$$N(t) \le \frac{\pi}{\mu} + C\ell^{-\mu t}, \qquad (3)$$

where C is the constant of integration. Given that at time t = 0, N (t) = N (0), then

$$N(0) \le \frac{\pi}{N} + C$$
$$C = N(0) - \frac{\pi}{\mu}.$$

Hence, equation (4) becomes

$$N(t) \le \left(1-\ell^{-\mu t}\right)\frac{\pi}{\mu} + N(0)\ell^{-\mu t}. \qquad (4)$$

We therefore, apply Birkoff and Rota's theorem on equation (5) as $t\to\infty$, we obtain $N(t) \le \frac{\pi}{\mu}$, hence all the feasible solutions of the model (2) enter the region or set of $\Omega = \left((S,E,E_q,I,I_T,R) \le \frac{\pi}{\mu}\right)$ which is positive invariant, attracting and its sufficient to consider solution in Ω. Thus, in this region or set of our model is biologically feasible whenever $N > \frac{\pi}{\mu}$, then $\frac{\partial N}{\partial t} < 0$ which mean that the population reduces asymptotically to the carrying capacity and whenever $N \le \frac{\pi}{\mu}$ every solution with initial condition in Ω in that region for t >1, so the model is well posed to Ω and biologically meaningful. This ends the proof.

3.2 Positivity of solution

For the system S,E,E_q,I,I_T,R to be biologically meaningful, it is important to prove that all solutions with non-negative initial conditions will remain positive. Here, we will take each differential equations of the dynamical system (2) to illustrates that the corresponding solutions are positive.

Theorem 3.2
Let the initial data be
$\{S(0), E(0), E_q(0), I(0), I_T(0), R(0) \geq 0\} \in R^6_+$. Then, the solution set
$\{S(t), E(t), E_q(t), I(t), I_T(t), R(t)\}$ of the system (1) is positive for all t > 0.

Proof:
From the first equation of the model system (1)

$$\frac{\partial S}{\partial t} = \pi - (\lambda + \mu)S + \theta R + \tau_1 E_q$$

$$\Rightarrow \dot{S} = \pi + \theta R + \tau_1 E_q - (\lambda + \mu)S$$

$$\dot{S} \geq \pi + \theta R + \tau_1 E_q - (\lambda + \mu)S$$

$$\frac{\dot{S}}{S} \geq \pi + \theta R + \tau_1 E_q - (\lambda + \mu)$$

.

After integrating we have,

$$\dot{S}(t) \geq S(0)\left(\ell^{\int -(\lambda+\mu)dt}\right) \geq 0$$

Then, $(\lambda + \mu) \geq 0$
Using the second equation of system (2), we have

$$\frac{\partial E}{\partial t} = \lambda S - (\mu + \in + \rho)E$$

$$\Rightarrow \dot{E} = \lambda S - (\mu + \in + \rho)E$$

$$\frac{\dot{E}}{E} = \lambda S - (\mu + \in + \rho)$$

After integration we get,

$$\dot{E}(t) \geq E(0)\left(\ell^{\int -(\mu+\in+\rho)dt}\right) \geq 0$$

Then, $(\mu + \in + \rho) \geq 0$.

Again from the third equation of system (2), we have

$$\frac{\partial E_q}{\partial t} = \rho E - (\mu + \tau_1 + \tau_2)E_q$$

$$\Rightarrow \dot{E} = \rho E - (\mu + \tau_1 + \tau_2)E_q$$

$$\frac{\dot{E}_q}{E_q} = \rho E - (\mu + \tau_1 + \tau_2)$$

.

After integration we have

$$\dot{E}_q(t) \geq E_q(0)\left(\ell^{\int -(\mu+\tau_1+\tau_2)dt}\right) \geq 0$$

Then, $(\mu+\tau_1+\tau_2) \geq 0$.

From the fourth equation of model (1), we get

$$\frac{\partial I}{\partial t} = \in E + \tau_2 E_q - (\nu + (\mu+\delta_1))I$$

$$\Rightarrow \dot{I} = \in E + \tau_2 E_q - (\nu + (\mu+\delta_1))I$$

$$\frac{\dot{I}}{I} = \in E + \tau_2 E_q - (\nu + (\mu+\delta_1))$$

.

After integrating we have

$$\dot{I}(t) \geq I(0)\left(\ell^{\int -(\nu+(\mu+\delta_1))dt}\right) \geq 0$$

Then,

$(\nu + (\mu+\delta_1) \geq 0$.

From the fifth equation of our model (2)

$$\frac{\partial I_T}{\partial t} = \nu I - (f + (\mu+\delta_2))I_T$$

$$\Rightarrow \dot{I}_T = \nu I - (f + (\mu+\delta_2))I_T$$

$$\frac{\dot{I}_T}{I_T} = \nu I - (f + (\mu+\delta_2))$$

.

After integrating we get

$$\dot{I}_T \geq I_T(0)\left(\ell^{\int -(f+(\mu+\delta_2)dt}\right) \geq 0$$

Then, $(f + (\mu+\delta_2)) \geq 0$.

From the sixth equation of model system (1)

$$\frac{\partial R}{\partial t} = fI_T - (\mu+\theta)R$$

$$\dot{R} = fI_T - (\mu+\theta)R$$

$$\frac{\dot{R}}{R} = fI_T - (\mu + \theta)$$

After integrating we have,

$$\dot{R} \geq R(0)\left(\ell^{\int -(\mu+\theta)dt}\right) \geq 0$$

Then,

$$(\mu + \theta) \geq 0$$

Therefore, all the solutions of the equations (2) are positive for all t > 0 which ends the proof.

3.3 Existence of diseases free equilibrium (DFE) points

Equilibrium state in our model represent the absent of Lassa fever virus in a given susceptible population. Thus, all the infected classes will be set to zero and the entire population will comprise of only susceptible individuals over those who died natural death.

Theorem 3.3
The disease-free equilibrium point of our model exist at the point where

$$\varepsilon_0 = (S, E, E_{q,} I, I_T, R) = (\frac{\pi}{\mu}, 0, 0, 0, 0, 0)$$

Proof:
At equilibrium state the rate of change of each variable is equal to zero, that is;

$$\frac{\partial S}{\partial t} = \frac{\partial E}{\partial t} = \frac{\partial E_q}{\partial t} = \frac{\partial I}{\partial t} = \frac{\partial I_T}{\partial t} = \frac{\partial R}{\partial t} = 0$$

Let, $(S, E, E_{q,} I, I_T, R) = (S^0, E^0, E_q{}^0, I^0, I_T{}^0, R^0)$

Then from the first equation of our model (2)

$$\frac{\partial S}{\partial t} = \pi - (\lambda + \mu)S + \theta R + \tau_1 E_q$$

The rate of change of R, E_q is equal to zero, therefore, taking $R = E_q = 0$

$$\Rightarrow \pi - (\lambda + \mu)S^0 = 0$$

$$S^0 = \frac{\pi}{\mu + \lambda}$$

Taking $\lambda = \beta SI$ as the force of infection we have,

$$S^0 = \frac{\pi}{\mu + \beta SI}$$

Taking the rate of change of (I) to be equal to zero i.e. I = 0, we have

$$S^0 = \frac{\pi}{\mu} \tag{5}$$

Also taking the rate of change of E, E_q, I, I_T, R of our model (2) to be equal to zero i.e. E= E_q = I= I_T = R = 0, then the 2nd to sixth equations of our model become zero (0).

Hence,

$$\varepsilon_0 = \left(S, E, E_q, I, I_T, R\right) = \left(\frac{\pi}{\mu}, 0, 0, 0, 0, 0\right). \tag{6}$$

Therefore, equation (6) represents the state in which there is no infection in the population and it is known as the disease-free equilibrium point (DFE).

3.4 Existence of endemic equilibrium (EE) points

The endemic equilibrium state of the system (1) is the state where the disease cannot be totally eradicated but remains in the population. For the disease to persist in the population, the susceptible class, exposed class, exposed quarantined class, infected class, infected treatment class and Recovered class must not be zero at equilibrium state. In order to obtain the endemic equilibrium state, we solve equation (1) of our model simultaneously taking into account of the fact that

$$(S^*, E^*, E_{q,}{}^* I^*, I_T{}^*, R^*) \neq (0, 0, 0, 0, 0, 0).$$

Theorem 3.4

If $(S^*, E^*, E_{q,}{}^* I,^* I_T{}^*, R^*)$ is equilibrium state, then

$(S^*, E^*, E_{q,}{}^* I^*, I_T{}^*, R^*) \neq (0, 0, 0, 0, 0, 0)$

Proof:

From equation two of our model (1)

$$\frac{\partial E}{\partial t} = \lambda S - (\mu + \in + \rho)E$$

$$\Rightarrow \lambda S^* - (\mu + \in + \rho)E^* = 0$$

$$E^* = \frac{\lambda S^0}{(\mu + \in + \rho)} .$$

We substitute equation (8) into (9) to have thus;

$$E^* = \frac{\lambda \frac{\pi}{\mu}}{(\mu + \in + \rho)}$$

$$E^* = \frac{\lambda \pi}{\mu(\mu + \in + \rho)} \tag{8}$$

We substitute (8) into (3) of our model (2) thus;

$$\frac{\partial E_q}{\partial t} = \rho E - (\mu + \tau_1 + \tau_2)E_q$$
$$\Rightarrow \rho E - (\mu + \tau_1 + \tau_2)E_q = 0$$
$$E_q^* = \frac{\rho E^*}{(\mu + \tau_1 + \tau_2)}$$
$$E_q^* = \frac{\frac{\rho\lambda\pi}{\mu(\mu + \in + \rho}}{(\mu + \tau_1 + \tau_2)}$$
$$E_q^* = \frac{\rho\lambda\pi}{\mu(\mu + \in + \rho)} \times \frac{1}{(\mu + \tau_1 + \tau_2)}$$
$$E_q^* = \frac{\rho\lambda\pi}{\mu(\mu + \in + \rho)(\mu + \tau_1 + \tau_2)}. \quad (9)$$

We substitute (8) and (9) into fourth equation of model (1) to yield

$$\frac{\partial I}{\partial t} = \in E - (\nu + (\mu + \delta_1))I + \tau_2 E_q$$
$$\Rightarrow \in E - (\nu + (\mu + \delta_1))I + \tau_2 E_q = 0$$
$$I^* = \frac{\in E^* + \tau_2 E_q^*}{(\nu + (\mu + \delta_1))}$$
$$I^* = \frac{\in \left(\frac{\lambda\pi}{\mu(\mu + \in + \rho)}\right) + \tau_2 \left(\frac{\rho\lambda\pi}{\mu(\mu + \in + \rho)(\mu + \tau_1 + \tau_2)}\right)}{(\nu + (\mu + \delta_1)}$$
$$I^* = \frac{\in \lambda\pi(\mu + \tau_1 + \tau_2) + \tau_2\rho\lambda\pi}{\mu(\mu + \in + \rho)(\mu + \tau_1 + \tau_2)} \times \frac{1}{(\nu + (\mu + \delta_1))}$$
$$I^* = \frac{\lambda\pi\left[\in (\mu + \tau_1 + \tau_2) + \tau_2\rho\right]}{\mu(\mu + \in + \rho)(\mu + \tau_1 + \tau_2)(\nu + (\mu + \delta_1))}. \quad (10)$$

We substitute (10) into fifth equation of our model (2) to yield

$$\frac{\partial I_T}{\partial t} = \nu I - (f + (\mu + \delta_2)I_T$$
$$\Rightarrow \nu I - (f + (\mu + \delta_2)I_T = 0$$
$$I_T^* = \frac{\nu I^*}{(f + (\mu + \delta_2)}$$
$$I_T^* = \frac{\nu\left(\frac{\lambda\pi\left[\in (\mu + \tau_1 + \tau_2) + \tau_2\rho\right]}{\mu(\mu + \in + \rho)(\mu + \tau_1 + \tau_2)(\nu + (\mu + \delta_1))}\right)}{(f + (\mu + \delta_2)}$$

$$I_T^* = \frac{\nu\lambda\pi\left[\in(\mu+\tau_1+\tau_2)+\tau_2\rho\right]}{\mu(\mu+\in+\rho)(\mu+\tau_1+\tau_2)(\nu+(\mu+\delta_1))(f+(\mu+\delta_2))}. \tag{11}$$

We substitute (11) into sixth equation of our model (2) to have

$$\frac{\partial R}{\partial t} = fI_T - (\mu+\theta)R$$
$$\Rightarrow fI_T - (\mu+\theta)R = 0$$
$$R^* = \frac{fI_T^*}{(\mu+\theta)}$$

$$R^* = \frac{f\left(\frac{\nu\lambda\pi\left[\in(\mu+\tau_1+\tau_2)+\tau_2\rho\right]}{\mu(\mu+\in+\rho)(\mu+\tau_1+\tau_2)(\nu+(\mu+\delta_1))(f+(\mu+\delta_2))}\right)}{(\mu+\theta)}$$
$$R^* = \frac{f\nu\lambda\pi\left[\in(\mu+\tau_1+\tau_2)+\tau_2\rho\right]}{\mu(\mu+\in+\rho)(\mu+\tau_1+\tau_2)(\nu+(\mu+\delta_1))(f+(\mu+\delta_2))(\mu+\theta)}. \tag{12}$$

Finally, we substitute (12) into first of our model (1) to yield

$$\frac{\partial S}{\partial t} = \pi - (\lambda+\mu) + \theta R + \tau_1 E_q$$
$$\pi - (\lambda+\mu)S^* + \theta R^* + \tau_1 E_q^* = 0$$
$$S^* = \frac{\pi + \theta R^* + \tau_1 E_q^*}{(\lambda+\mu)}$$
$$S^* = \frac{\pi + \theta\left(\frac{f\nu\lambda\pi\left[\in(\mu+\tau_1+\tau_2)+\tau_2\rho\right]}{\mu(\mu+\in+\rho)(\mu+\tau_1+\tau_2)(\nu+(\mu+\delta_1))(f+(\mu+\delta_2))(\mu+\theta)}\right) + \tau_1\left(\frac{\rho\lambda\pi}{\mu(\mu+\in+\rho)(\mu+\tau_1+\tau_2)}\right)}{(\lambda+\mu)}$$
$$S^* = \frac{\frac{\pi + \theta f\nu\lambda\pi\left[\in(\mu+\tau_1+\tau_2)+\tau_2\rho\right]}{\mu(\mu+\in+\rho)(\mu+\tau_1+\tau_2)(\nu+(\mu+\delta_1))(f+(\mu+\delta_2))(\mu+\theta)} + \frac{\tau_1\rho\lambda\pi}{\mu(\mu+\in+\rho)(\mu+\tau_1+\tau_2)}}{(\lambda+\mu)}$$
$$S^* = \frac{\pi}{(\lambda+\mu)} + \frac{\theta f\nu\pi\lambda\left[\in(\mu+\tau_1+\tau_2)+\tau_2\rho\right]}{\mu(\mu+\in+\rho)(\nu+\tau_1+\tau_2)(\nu+(\mu+\delta_1))(f+(\mu+\delta_2))(\mu+\theta)} + \frac{\tau_1\rho\lambda\pi}{\mu(\lambda+\mu)(\mu+\in+\rho)(\mu+\tau_1+\tau_2)}$$
$$\pi\mu(\mu+\in+\rho)(\mu+\tau_1+\tau_2)(\nu+(\mu+\delta_1))(\mu+\theta) + \theta f\nu\pi\lambda\in(\mu+\tau_1+\tau_2)$$
$$S^* = \frac{+\tau_2\rho + \tau_1\rho\lambda\pi(\nu+(\mu+\delta_1))(\mu+\theta)}{\mu(\lambda+\mu)(\mu+\in+\rho)(\mu+\tau_1+\tau_2)(\nu+(\mu+\delta_1))(f+(\mu+\delta_2))(\mu+\theta)}$$

$$S^* = \frac{\pi\mu(\mu+\in+\rho)(\mu+\tau_1+\tau_2)(\nu+(\mu+\delta_2))(\mu+\theta)+\theta f\nu\lambda\left[\in(\mu+\tau_1+\tau_2)+\tau_2\rho\right]}{+\tau_1\rho\pi\left[\nu+(\mu+\delta_1)(f+(\mu+\delta_2))(\mu+\theta)\right]}$$
$$\mu(\lambda+\mu)(\mu+\in+\rho)(\mu+\tau_1+\tau_2)(\nu+(\mu+\delta_1))(f+(\mu+\delta_2))(\mu+\theta)$$

$$S^* = \frac{\pi\mu(\mu+\theta)(\mu+\in+\rho)(\mu+\tau_1+\tau_2)(\nu+(\mu+\delta_1))(f+(\mu+\delta_2))+\tau_1\rho\lambda\pi\left[((\nu+(\mu+\delta_1))(f+(\mu+\delta_2))\right]}{+\theta f\nu\pi\lambda\left[\in((\mu+\tau_1+\tau_2)+\tau_2\rho\right]}$$
$$\mu(\lambda+\mu)(\mu+\in+\rho)(\mu+\tau_1+\tau_2)(\nu+(\mu+\delta_1))(f+(\mu+\delta_2))(\mu+\theta)$$

(13)

Hence, equations (8), (9), (10), (11), (12) and (13) represents the state in which there is an infection in the population and it is known as the endemic equilibrium point (EE).

3.5 Basic reproduction number (R_0)

The basic reproduction number denoted by R_0 is an important parameter used to determine how long an infectious disease will prevail or can last in a given population, when $R_0 < 1$. It means an average infected individual produces less than one new secondary case during the infectious period and this implies that with time the disease will die out of the population, thereby giving it a clean health bill. But if $R_0 > 1$, it means the disease will persist in the population. So, for the disease to die out of the population, R_0 must be less than one. Therefore, reproduction number represents the rate of spreading of an infection in a given susceptible population, hence considering model system (1) without control measures, the infectious classes are E, E_q, I, I_T.

To derive the basic reproduction number R_0 of the disease-free equilibrium (DFE), we employ the next generation operator technique described by Diekmann and Heesterbeek (2000), and which was subsequently analyzed by Vanden and Watmough (2002). This method is described as follows; assuming that there are n compartments so that the first m compartments correspond to infected individuals. Let $f_i(x)$ be the rate of appearance of new infectious in compartment i and $V_i^+(x)$ be the rate of transfer of individuals into compartment i by all other means, other than the endemic. Also let $V_i^-(x)$ be the transfer of individuals out of the compartment i. The disease transmission model consists of the system of equation $x_i^{'} = f_i(x) - V_i^+(x)$ where $V_i^+(x) = V_i^-(x) - V_i^+(x)$.

One other important step is to obtain the disease-free equilibrium point x_0, we therefore, compute matrices F and V which are m × m matrices, where m represents the infected classes, define by $F = \left[\frac{\partial F_i}{\partial x_j}(x_0)\right]$ and $V = \left[\frac{\partial V_i}{\partial x_j}(x_0)\right]$ With I ≤ i, j ≤ m, and F is a non-negative and V is a non-singular M matrix, (a matrix with inverse, belong to the class of positive matrices). Since F is non-negative and V is non-singular, then V^{-1} is non-negative and FV^{-1} is also non-negative. We then compute matrix FV^{-1}, defined as the next generation matrix (Diekmann et al., 1990). This is given as $R_0 = \rho(\mathrm{K})$, where $\mathrm{K} = FV^{-1}$, Computing reproduction number, we rewrite equations (1) of our model starting with the Exposed compartment of the population: $E, E_q I, I_T, S, R$ and then followed by the uninfected classes, then the model equations become;

$$\left.\begin{aligned}
\frac{\partial E}{\partial t} &= \lambda S - (\mu + \in + \rho)E \\
\frac{\partial E_q}{\partial t} &= \rho E - (\mu + \tau_1 + \tau_2)E_q \\
\frac{\partial I}{\partial t} &= \in E - (\nu + (\mu + \delta_1))I + \tau_2 E_q \\
\frac{\partial I_T}{\partial t} &= \nu I - (f + (\mu + \delta_2)I_T \\
\frac{\partial S}{\partial t} &= \pi - (\lambda + \mu) + \theta R + \tau_1 E_q \\
\frac{\partial R}{\partial t} &= fI_T - (\mu + \theta)R
\end{aligned}\right\} \qquad (14)$$

Considering our model (14) and only the infectious classes $(E, E_q I, I_T)$ only, we then define f_i and V_i to compute R_0 as follows;

$$f_i = F = \begin{bmatrix} \beta SI \\ 0 \\ 0 \\ 0 \end{bmatrix}.$$

So that

$$\frac{\partial f_i}{\partial x_j}\varepsilon_0 = F = \begin{bmatrix} 0 & 0 & \beta S & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}.$$

Also

$$V_i = V = \begin{bmatrix} (\mu + \in + \rho)E \\ -\rho E + (\mu + \tau_1 + \tau_2)E_q \\ -\in E + \tau_2 E_q + (\nu + (\mu + \delta_1))I \\ -\nu I + (f + (\mu + \delta_1)I_T \end{bmatrix}$$

where,

$K_1 = \mu + \in + \rho$,

$$K_2 = \mu + \tau_1 + \tau_2$$
$$K_3 = \nu + (\mu + \delta_1)$$
$$K_4 = f + (\mu + \delta_2).$$

We take the partial derivative of ν with respect to E, E_q, I, I_T we have

$$\frac{\partial f_i}{\partial x_j}\varepsilon_0 = V = \begin{bmatrix} K_1 & 0 & 0 & 0 \\ -\rho & K_2 & 0 & 0 \\ -\in & -\tau_2 & K_3 & 0 \\ 0 & 0 & -\nu & K_4 \end{bmatrix}.$$

We form the matrix of the co-factor of the determinant

$$V = \begin{bmatrix} K_2K_3 & -\rho K_3 & -\rho\tau_2 + \in K_2 & K_2K_3 \\ 0 & K_1K_3 & K_1\tau_2 & 0 \\ 0 & 0 & K_1K_2 & 0 \\ K_2K_3 & \rho K_3 & -\rho\tau_2 + \in K_2 & K_2K_3 \end{bmatrix}.$$

We take the adjoin of the matrix V to give

$$V^T = \begin{bmatrix} K_2K_3 & 0 & 0 & K_2K_3 \\ \rho K_3 & K_1K_3 & 0 & \rho K_3 \\ \rho\tau_2 + \in K_2 & K_1\tau_2 & K_1K_2 & \rho\tau_2 + \in K_2 \\ K_2K_3 & 0 & 0 & K_2K_3 \end{bmatrix}.$$

We form the inverse of the matrix V

$$V^{-1}\frac{1}{K_1K_2K_3} = \begin{bmatrix} \frac{1}{K_1} & 0 & 0 & \frac{1}{K_1} \\ \frac{\rho}{K_1K_2} & \frac{1}{K_2} & 0 & \frac{\rho}{K_1K_2} \\ \frac{\rho\tau_2 + \in}{K_1K_3} & \frac{\tau_2}{K_2K_3} & \frac{1}{K_3} & \frac{\rho\tau_2 + \in}{K_1K_3} \\ \frac{1}{K_1} & 0 & 0 & \frac{1}{K_1} \end{bmatrix}.$$

Furthermore,

$$\left|FV^{-1}-\lambda I\right|=\begin{bmatrix}\frac{\beta S\rho}{K_1K_2K_3}-\lambda & 0 & 0 & \frac{\beta S}{K_1K_2K_3}\\ 0 & 0-\lambda & 0 & 0\\ 0 & 0 & 0-\lambda & 0\\ 0 & 0 & 0 & 0-\lambda\end{bmatrix}=0 \tag{15}$$

Then, $\lambda^3\left(\frac{\beta S\rho}{K_1K_2K_3}-\lambda\right)=0$.

Therefore, either $\lambda^3=0$ or $\lambda=\frac{\beta S\rho}{K_1K_2K_3}$,

From (15), we obtain four eigenvalues which are by; $\lambda_1=\frac{\beta S\rho}{K_1K_2K_3}$,

$\lambda_2=0$, $\lambda_3=0$ and $\lambda_4=0$

Clearly, λ_1 is the dominant eigenvalue and it becomes the basic reproduction number of our model (2). Therefore, the basic associated reproduction number is

$$(R_0)=\rho(FV^{-1})=\frac{\beta S\rho}{K_1K_2K_3}=1.20>1$$

3.6 Effective reproductive number (R_e)

We incorporate quarantine, health education campaign and treatment as control or intervention strategy to eliminate Lassa fever virus (LFV) disease. When these control measures are deployed to a model, the basic reproduction number of the infectious disease becomes the effective reproduction (R_e), [27]. Considering our model (14) and the infectious classes (E,E_qI,I_T) only, we compute R_e as follows;

$$f_i=F=\begin{bmatrix}\beta(1-\phi)SI\\ 0\\ 0\\ 0\end{bmatrix}.$$

So that,

$$\frac{\partial f_i}{\partial x_j}\varepsilon_0=F=\begin{bmatrix}0 & 0 & \beta(1-\phi)S & 0\\ 0 & 0 & 0 & 0\\ 0 & 0 & 0 & 0\\ 0 & 0 & 0 & 0\end{bmatrix}.$$

Also,

$$V_i = V = \begin{bmatrix} (\mu + \in + \rho)(1-\phi)E \\ -\rho(1+\phi)E + (\mu + \tau_1 + \tau_2)(1+\phi)E_q \\ - \in (1+\phi)E + \tau_2(1+\phi)E_q + (\nu + (\mu + \delta_1)(1+\phi)I \\ -\nu(1+\phi)I + (f + (\mu + \delta_1)(1+\phi)I_T \end{bmatrix},$$

where,

$K_1 = (\mu + \in + \rho)(1+\phi)$

$K_2 = (\mu + \tau_1 + \tau_2)(1+\phi) \quad K_3 = \nu + (\mu + \delta_1)(1+\phi)$

$K_4 = f + (\mu + \delta_2)(1+\phi)$.

We take the partial derivative of ν with respect to E, E_q, I, I_T we have;

$$\frac{\partial f_i}{\partial x_j}\varepsilon_0 = V = \begin{bmatrix} K_1(1+\phi) & 0 & 0 & 0 \\ -\rho(1+\phi) & K_2(1+\phi) & 0 & 0 \\ - \in (1+\phi) & -\tau_2(1+\phi) & K_3(1+\phi) & 0 \\ 0 & 0 & -\nu(1+\phi) & K_4(1+\phi) \end{bmatrix}$$

We form the matrix of the co-factor of the determinant

$$V = \begin{bmatrix} K_2K_3(1+\phi) & -\rho K_3(1+\phi) & -\rho\tau_2(1+\phi) + \in K_2(1+\phi) & K_2K_3(1+\phi) \\ 0 & K_1K_3(1+\phi) & K_1\tau_2(1+\phi) & 0 \\ 0 & 0 & K_1K_2(1+\phi) & 0 \\ K_2K_3(1+\phi) & \rho K_3(1+\phi) & -\rho\tau_2(1+\phi) + \in K_2(1+\phi) & K_2K_3(1+\phi) \end{bmatrix}$$

We take the adjoin of the matrix V to give

$$V^T = \begin{bmatrix} K_2K_3(1+\phi) & 0 & 0 & K_2K_3(1+\phi) \\ \rho K_3(1+\phi) & K_1K_3(1+\phi) & 0 & \rho K_3(1+\phi) \\ \rho\tau_2(1+\phi) + \in K_2(1+\phi) & K_1\tau_2(1+\phi) & K_1K_2(1+\phi) & \rho\tau_2(1+\phi) + \in K_2(1+\phi) \\ K_2K_3(1+\phi) & 0 & 0 & K_2K_3(1+\phi) \end{bmatrix}$$

We form the inverse of the matrix V

$$V^{-1}\frac{1}{K_1K_2K_3(1+\phi)}=\begin{bmatrix} \frac{1}{K_1(1+\phi)} & 0 & 0 & \frac{1}{K_1(1-\phi)} \\ \frac{\rho(1-\phi)}{K_1K_2(1+\phi)} & \frac{1}{K_2(1+\phi)} & 0 & \frac{\rho}{K_1K_2} \\ \frac{\rho\tau_2(1-\phi)+\in(1-\phi)}{K_1K_3(1+\phi)} & \frac{\tau_2(1-\phi)}{K_2K_3(1+\phi)} & \frac{1}{K_3(1+\phi)} & \frac{\rho\tau_2(1-\phi)+\in(1-\phi)}{K_1K_3(1+\phi)} \\ \frac{1}{K_1(1+\phi)} & 0 & 0 & \frac{1}{K_1(1+\phi)} \end{bmatrix}$$

Furthermore,

$$\left|FV^{-1}-\lambda I\right|=\begin{bmatrix} \frac{\beta S\rho(1-\phi)}{K_1K_2K_3(1+\phi)}-\lambda & 0 & 0 & \frac{\beta S(1-\phi)}{K_1K_2K_3(1+\phi)} \\ 0 & 0-\lambda & 0 & 0 \\ 0 & 0 & 0-\lambda & 0 \\ 0 & 0 & 0 & 0-\lambda \end{bmatrix}=0 \qquad (16)$$

Then, $\lambda^3\left(\frac{\beta S\rho(1-\phi)}{K_1K_2K_3(1+\phi)}-\lambda\right)=0$.

Therefore, either $\lambda^3=0$ or $\lambda=\frac{\beta S\rho(1-\phi)}{K_1K_2K_3(1+\phi)}$,

From (16), we obtain four eigenvalues which are by; $\lambda_1=\frac{\beta S\rho(1-\phi)}{K_1K_2K_3(1+\phi)}$,

$\lambda_2=0$, $\lambda_3=0$ and $\lambda_4=0$

Clearly, λ_1 is the dominant eigenvalue and it becomes the effective reproduction number (R_e) of our model (2). Therefore, the basic associated reproduction number is

$$(R_e)=\frac{\beta S\rho(1-\phi)}{K_1K_2K_3(1+\phi)}=0.85<1.$$

Hence, this implies that, since $R_e = 0.85 < 1$, therefore, quarantine, health education campaigns can reduce the spread of Lassa fever virus (LFV) disease. However, when quarantine and health education campaigns are given to all individuals to reduce the spread of Lassa fever virus, it increases the effectiveness of the treatment given to the infected individuals, hence increasing the recovery rate (θ), also reduces the rate of getting infected (β), reducing the rate at which untreated infected individuals died due to infectious (δ_1) and the rate at which infected individuals died during treatment (δ_2) Thus, the effective reproduction number with quarantine and health education campaign $R_e = 0.85 < 1$ and is less than the basic reproduction number

R_0 = 1.20, i.e. ($R_e < R_0$), it implies that Lassa fever virus (LFV) can be controlled in a complete susceptible population (see figure 4.2).

3.7 Local stability analysis of Lassa fever disease free equilibrium (DFE)

Local stability of an equilibrium point means that, if a system is put somewhere near the point, then the system will move itself to the equilibrium point in some time. Epidemiologically, this implies that Lassa fever virus (LFV) will be eliminated from the population whenever R_0 <1 if the initial size of the sub-populations is in the basin of the disease-free equilibrium (DFE), that is a small influx of Lassa fever virus (LFV) infectious individuals into the community will not generate a large Lassa fever virus outbreak, and the disease will die out in time.

Theorem 3.7
Lassa fever Virus free equilibrium of system (2) is locally asymptotically stable if
$R_0 < 1$ and unstable if $R_0 > 1$.

Proof:
To analyze the local stability of the disease-free equilibrium (DFE) and established theorem (3.8.7), we obtain the Jacobean matrix of the Lassa fever model (1) becomes.

$$\left.\begin{aligned} f_1 &= \pi - (\lambda + \mu)S + \theta R + \tau_1 E_q \\ f_2 &= \lambda S - (\mu + \in + \rho)E \\ f_3 &= \rho E - (\mu + \tau_1 + \tau_2)E_q \\ f_4 &= \in E - (\nu + (\mu + \delta_1))I + \tau_2 E_q \\ f_5 &= \nu I - (f + (\mu + \delta_2))I_T \\ f_6 &= fI_T - (\mu + \theta)R \end{aligned}\right\} \qquad (14)$$

The Jacobean matrix of our model (14) is describe as follows

$$J(DFE) = \begin{bmatrix} \frac{\partial f_1}{\partial S} & \frac{\partial f_1}{\partial E} & \frac{\partial f_1}{\partial E_q} & \frac{\partial f_1}{\partial I} & \frac{\partial f_1}{\partial I_T} & \frac{\partial f_1}{\partial E} \\ \frac{\partial f_2}{\partial S} & \frac{\partial f_2}{\partial E} & \frac{\partial f_2}{\partial E_q} & \frac{\partial f_2}{\partial I} & \frac{\partial f_2}{\partial I_T} & \frac{\partial f_2}{\partial R} \\ \frac{\partial f_3}{\partial S} & \frac{\partial f_3}{\partial E} & \frac{\partial f_3}{\partial E_T} & \frac{\partial f_3}{\partial I} & \frac{\partial f_3}{\partial I_T} & \frac{\partial f_3}{\partial R} \\ \frac{\partial f_4}{\partial S} & \frac{\partial f_4}{\partial E} & \frac{\partial f_4}{\partial E_T} & \frac{\partial f_4}{\partial I} & \frac{\partial f_4}{\partial I_T} & \frac{\partial f_4}{\partial R} \\ \frac{\partial f_5}{\partial S} & \frac{\partial f_5}{\partial E} & \frac{\partial f_5}{\partial E_q} & \frac{\partial f_5}{\partial I} & \frac{\partial f_5}{\partial I_T} & \frac{\partial f_5}{\partial R} \\ \frac{\partial f_6}{\partial S} & \frac{\partial f_6}{\partial E} & \frac{\partial f_6}{\partial E_q} & \frac{\partial f_6}{\partial I} & \frac{\partial f_6}{\partial I_T} & \frac{\partial f_6}{\partial R} \end{bmatrix}$$

$$J(DFE)=\begin{bmatrix} -(\beta S+\mu) & 0 & \tau_1 & 0 & 0 & 0 \\ \beta S & -(\mu+\in+\rho) & 0 & 0 & 0 & 0 \\ 0 & \rho & -(\mu+\tau_1+\tau_2) & 0 & 0 & 0 \\ 0 & \in & 0 & -(\nu+(\mu+\delta_1)) & 0 & 0 \\ 0 & 0 & 0 & 0 & -(f+(\mu+\delta_2) & 0 \\ 0 & 0 & 0 & 0 & f & -(\mu+\delta_2) \end{bmatrix}$$

where,

$A_1=-(\beta S+\mu)$
$A_2=-(\mu+\in+\rho)$
$A_3=-(\mu+\tau_1+\tau_2)$
$A_4=-(\nu+(\mu+\delta_1)$
$A_5=-(f+(\mu+\delta_2)$
$A_6=-(\mu+\delta_2)$

$$J(DFE)=\begin{bmatrix} -A_1-\lambda & 0 & \tau_1 & 0 & 0 & 0 \\ \beta S & -A_2-\lambda & 0 & 0 & 0 & 0 \\ 0 & \rho & -A_3-\lambda & 0 & 0 & 0 \\ 0 & \in & 0 & -A_4-\lambda & 0 & 0 \\ 0 & 0 & 0 & 0 & -A_5-\lambda & 0 \\ 0 & 0 & 0 & 0 & f & -A_6-\lambda \end{bmatrix} = 0 \quad (15)$$

where
$\lambda_1=-A_1$
$\lambda_2=-A_2$
$\lambda_3=-A_3$
$\lambda_4=-A_4$
$\lambda_5=-A_5$
$\lambda_6=-A_6$.

The characteristic equation is therefore given by

$(-A_1-\lambda)(-A_2-\lambda)(-A_3-\lambda)(-A_4-\lambda)(-A_5-\lambda)(-A_6-\lambda)=0$, where $\lambda_1,\lambda_2,\lambda_3,\lambda_4,\lambda_5,\lambda_6$ corresponding to $\lambda j,\ j=1,2,...6$ are the eigenvalues. From [15], since all the roots are negative sign that is $\lambda j<0$. We conclude by Routh Hurwitz stability criterion that states that any system can be stable if and only if all the roots of the first column have the same sign. Hence, the model (1) is asymptotically stable.

3.8 Global stability analysis of the disease-free equilibrium (DFE)

By global stability, we mean stability relative to initial states in which the number of each species is positive. It follows that if a perturbation shifts the state of the system from a feasible equilibrium to a feasible state and the system is thereafter left alone, the natural dynamics of the system will drive the state of the system into a neighborhood of the equilibrium. It also means that the system will come to the equilibrium point from any possible starting point (i.e., there is no nearby condition).

Theorem 3.8

The disease free equilibrium is globally asymptotically stable if R_0 <1 and unstable if R_0 >1.

Proof :

Other methods like Lyapunov function can be used to proof global stability, which many authors have used in their various works. We adopt the Comparison theorem to prove the global stability of the disease free equilibrium (GAS), we have to make use of F and M matrices used in calculating the reproduction number (R_0) of our work. The rate of change of the variables of infectious classes of our system (14) (E, E_q, I, I_T, R) can be written as:

$$\frac{\partial x}{\partial t} = (F - V)X - JX, X = (E, E_q, I, I_T, R) \quad \frac{\partial x}{\partial t} = (F - V)X - JX, X = (E, E_q, I, I_T, R).$$

At the disease free equilibrium (DFE), $(S, E, E_q, I, I_T, R) = (\frac{\pi}{\mu}, 0, 0, 0, 0, 0)$,

consequently, equation (14) becomes;

$$(E, E_q, I, I_T, R) = \begin{bmatrix} E \\ E_q \\ I \\ I_T \\ R \end{bmatrix} \leq (F - V) \begin{bmatrix} E \\ E_q \\ I \\ I_T \\ R \end{bmatrix} \tag{16}$$

From [15], all eigenvalues of the matrix $F - V$ have negative real parts. i.e. $|(F - V) - \lambda I| = 0$

$$((F - V) - \lambda I) = \begin{bmatrix} -A_1 - \lambda & 0 & \tau_1 & 0 & 0 & 0 \\ \beta S & -A_2 - \lambda & 0 & 0 & 0 & 0 \\ 0 & \rho & -A_3 - \lambda & 0 & 0 & 0 \\ 0 & \in & 0 & -A_4 - \lambda & 0 & 0 \\ 0 & 0 & 0 & 0 & -A_5 - \lambda & 0 \\ 0 & 0 & 0 & 0 & f & -A_6 - \lambda \end{bmatrix}.$$

The characteristics polynomial of the above matrix was found and can be written as;

$$g(x) = \lambda^6 + F_1\lambda^5 + F_2\lambda^4 + F_3\lambda^3 + F_4\lambda^2 + F_5\lambda + F_6 = 0.$$

Since, $F_1 > 0, F_2 > 0, F_3 > 0, F_4 > 0, F_5 > 0, F_6 > 0$, from our local stability result, where $\rho(FV^{-1}) < 1$ if $R_0 < 1$, which is equivalent to $(F - V)$ having eigenvalues with negative real parts when $R_0 < 1$, it follows that the linearized differential inequality system (16) is stable when $R_0 < 1$.

Consequently, $(E, E_q, I, I_T, R) \to (0,0,0,0,0)$ as $t \to \infty$. Thus, by the comparison theorem, $(E, E_q, I, I_T, R) \to (0,0,0,0,0)$ as $t \to \infty$. Substituting $E = E_q = I = I_T = R = 0$ in (2) $S(t) \to \infty$ as $t \to \infty$. Thus, $(S(t), E(t), E_q(t), I(t), I_T, R(t)) \to (S^0, 0,0,0,0,0)$ as $t \to \infty$ for $R_0 < 1$, thus, our Lassa fever disease free equilibrium is globally asymptotically stable.

4 Numerical simulations of Lassa fever model

In this paper, we give illustration of the analytical results of the work by carrying out numerical simulation of the model using epidemiological parameters given in Table 3. Parameters were obtained from different literature and those unavailable were assumed based on the available information. Some numerical solutions of the model for different initial population sizes is presented using the various values of the parameter and to validate that these solutions are in agreement with qualitative behaviors of the model population: N= $S_0(t) =$ 123600, $E_0(t) =$ 263840, $E_{q0}(t) =$ 185000, $I_0(t) =$ 182700, $I_{T0}(t) =$ 215000, $R_0(t) =$ 290574, the units of values are per day.

Parameters	Parameter description	Approx. values/days	Source
π	Recruitment rate	7342	Assumed
λ	Rate at which susceptible move to exposed class	4.377*10^(-10)	Assumed
$\in$	Rate of maturity from exposed to infected class	10^6	James T. et al, 2015
θ	Recovery rate to susceptible	0.01	James T. et al, 2015
τ_1	Rate of exposed-quarantine to susceptible class	0.42	James T. et al, 2015
τ_2	Rate of exposed-quarantine to infected class	0.05	James T. et al, 2015
ν	Rate of infected class to infectious treated class	0.006	James T. et al, 2015
ρ	Rate of exposed class to exposed-quarantine class	1/24	James T. et al, 2015
f	Rate of infectious-treated to recover class	0.05	James T. et al, 2015
μ	Natural death rate	0.0182	James T. et al, 2015
β	Contact rate between susceptible and infected	0.5	Assumed

δ_1	Lassa fever infected death rate	0.197	James T. et al, 2015
δ_2	Those who died by LFV during treatment	1/30	Assumed
ϕ	Level of re-infection	0.08	Assumed

Table 3: Parameters values of the model

The graph of the basic and effective reproduction numbers are plotted and interpreted as follows:

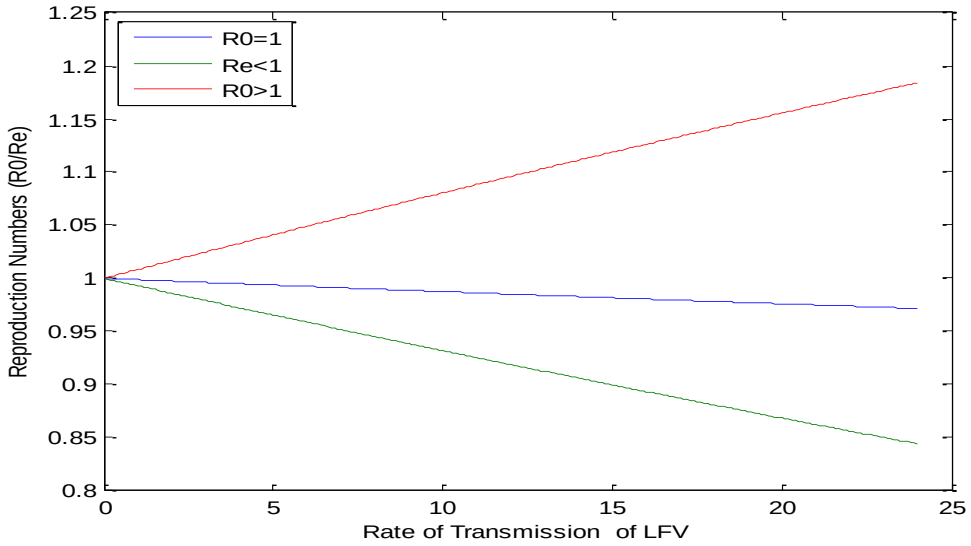

Figure 2: Effect of the rate of contact (β) on the Reproduction Numbers

Figure 2 shows the effect of rate of contact (β) on the basic and effective Reproduction Numbers. Figure 2 gives the following relationship; $R_0 = 1$, means if care is not taken the disease may invade the susceptible population in case of a backward bifurcation. $R_0 > 1$, means even if the infected individuals are treated, effect of the treatment might be very small. Hence, gives little or no recovery to the infected individuals. $R_e < 1$, means quarantine and health education campaign measures reduces the rate of spread of virus and increases the effectiveness of treatment given to infected individuals which also increases the rate of recovery. From the above scenario, it would be observed that when the susceptible are affected with Lassa fever virus, then the basic reproduction number (R_0) increases from $R_0 = 1.00$ to $R_0 = 1.20$ and when they are considered for quarantine and health education campaigns, then the effective reproduction number (R_e) decreases from $R_e = 1.00$ to $R_e = 0.85$. This implies that, when many susceptible individuals are getting infected due to the rate at which the virus is spread, it increases the basic reproduction number (R_0). Also, when few susceptible individuals are getting infected because of the introduction of quarantine and health education campaigns, this decreases the effective reproduction number (R_e).

Simulation of different Epidemiological classes with different parameter values of Lassa fever model

In this section, graphs of different epidemiological classes are plotted to show the transmission dynamics of Lassa fever Virus (LFV) disease.

From figure 3, the diagram shows the change in the dynamics of population with respect to time by varying the rate of spread of LFV model of susceptible population.

Figure 3a, it would be observed that the susceptible population at time (t) = 0 day is p = 20,000 individuals, the population then increases from p = 20,000 individuals to p = 290,000 individuals

at time (t) ≥ 60 days, this is caused by the influx from recruitment rate (π), recovery rate (θ),

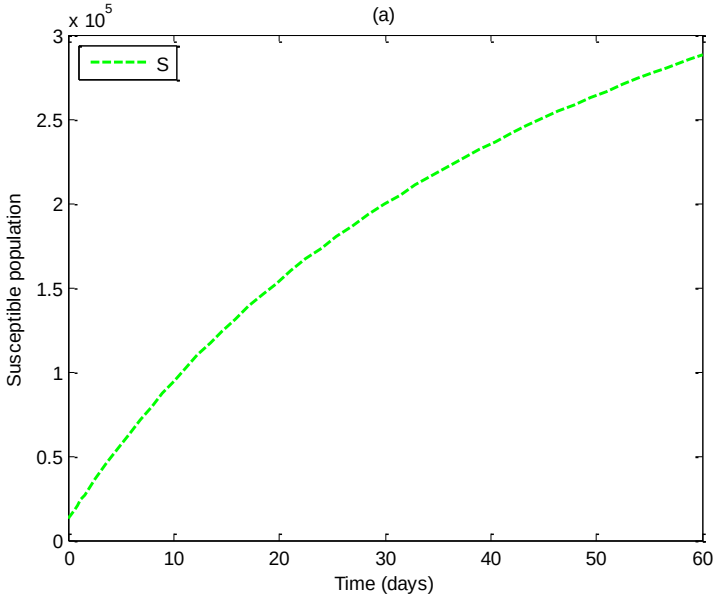

Figure 3a

non-manifested symptom, individual's rate (τ_1), the rate (λ) of movement of those who are exposed and those who died natural death (μ). This is because most individuals are now aware of Lassa fever virus (LFV), its mode of transmission and ways of quarantine and treatment for infected individuals. It is very important to control the recruitment rate into the susceptible population as well as encouraging sufficient behavioral change among them so as to effectively control and eradicate the LFV epidemic from the population/community. Although most of the infected persons under-went treatment and recovered, thereby reducing the spread of the virus to possibly $R_e < 1$.

Finally, it will be observed that the lower the rate of spread of Lassa fever virus among the susceptible population, the slower the rate of progression to exposed population and the higher the rate of spread of LFV, the higher the rate of progression of the disease to exposed population, because time keeps reducing as the rate of spread of the Virus increases. Hence, the transmission rate of LFV infection reduced and thereby reducing the susceptible population.

From the figure above, the diagram shows the change in the dynamics of population with respect

to time by varying the rate of spread of LFV model of exposed population.

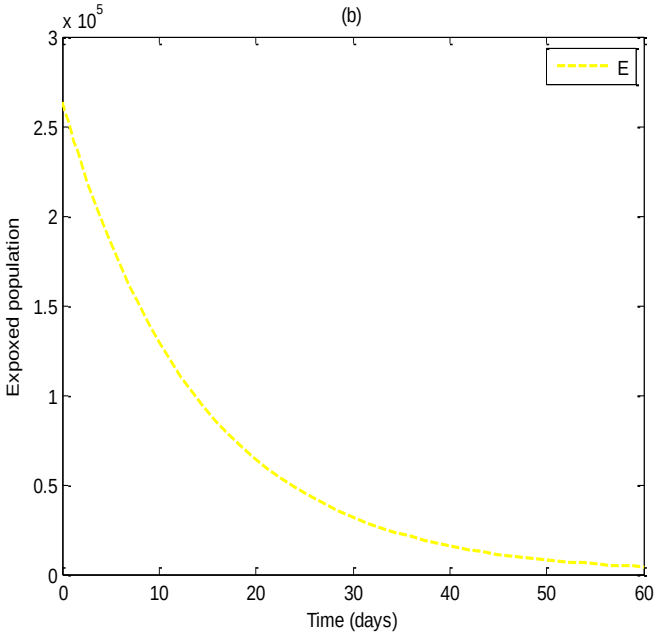

Figure 3b

Figure 3b, it would be also observed that the exposed population at time (t) = 0 day is p = 260,000 individuals, the population then decreases from p = 260,000 individuals to p = 10,000 individuals at time (t) ≤ 60 days, this is caused by the influx of exposed rate (λ) from the susceptible population to exposed population and the going out of infected rate ($\in$) from exposed population to infected population, quarantine rate (ρ) and those who died natural death (μ). This implies that the exposed population decreases as the day increases with the help of quarantine and health education campaigns given to individuals. This is because individual awareness about virus and its methods of prevention has gone a long way to reduce the spread. This is in line with Okuonghae and Okuonghae (2006) who opined that the most effective way to reduce the virus epidemic infection is to carry out quarantine exercise and to educate the people who will go for checkup in order to become aware of their status. We also observed from the graph that if the days are increased further than 60 days, we would be discovered that at time (t) = 70 days to t = 100 day the population of exposed individuals would be asymptotically tending to zero (0) tolerant of the virus.

From the figure above, the diagram shows the change in the dynamics of population with respect to time by varying the rate of spread of LFV model of exposed-quarantine population. Figure 3c, depicts the exposed-quarantine population at time (t) = 0 day and p = 180,000 individuals, the population then continuously decreases from p = 180,000 to p = 10,000 individuals at time (t) ≥ 60 days, this is caused by the influx of quarantine rate (ρ) and going out of non-manifested symptoms individuals rate (τ_1), manifested symptoms individuals rate (τ_2) and those who died natural death (μ). This implies that quarantine, public health education campaigns and treatment as control measures are sufficient for the timely control and eradication of the disease. Hence, these control strategies have significantly reduced the contraction and spread of the virus in the population/community. It can also be observed that if the days are increased further than 60 days, it would be discovered that at time (t) = 70 to t = 100 days the population of exposed-quarantined individuals would be asymptotically tending to zero (0) tolerant of the virus.

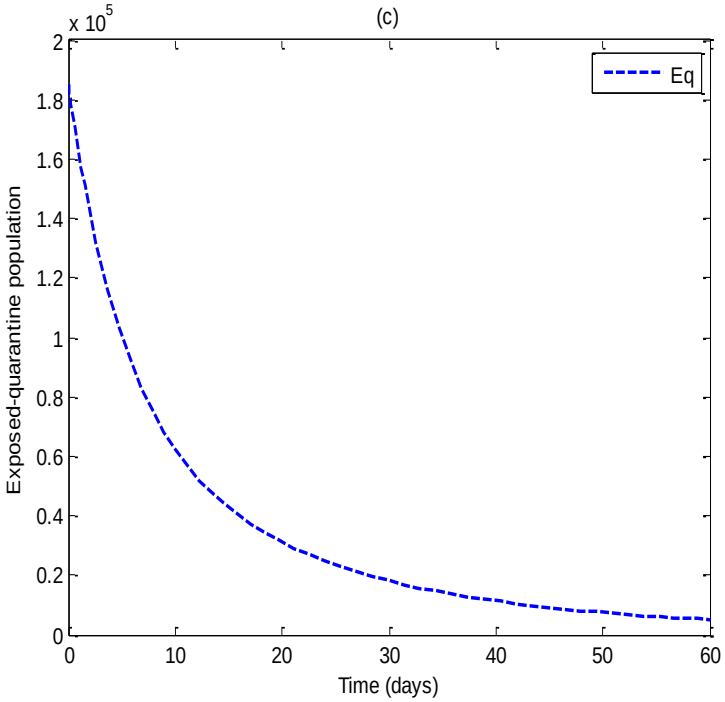

Figure 3c

Figure 3d depicts the population of infected individuals over time, it would be observed that the population of infected is (p) = 180,000 individuals at time (t) = 0 day, the population then decreases constantly from p = 180,000 individuals to p = 10,000 individuals at time (t) ≥ 60 days due to the influx of virus exposed individuals rate ($\in$), manifested symptoms individuals rate (τ_2) after 21 days of quarantined and going out of infectious rate (ν) individuals to undergo treatment, those who died by the virus (δ_1) and those who died natural death (μ). This implies that health education campaigns facilitate good movement of infectious individuals to undergo treatment. This is in line with World Health Organization, (2017) who opined that prompt isolation of

affected patients, good infection prevention, control practices and rigorous contact tracing can stop the virus outbreaks. It is seen that figure 3d is similar to figure 3c respectively.

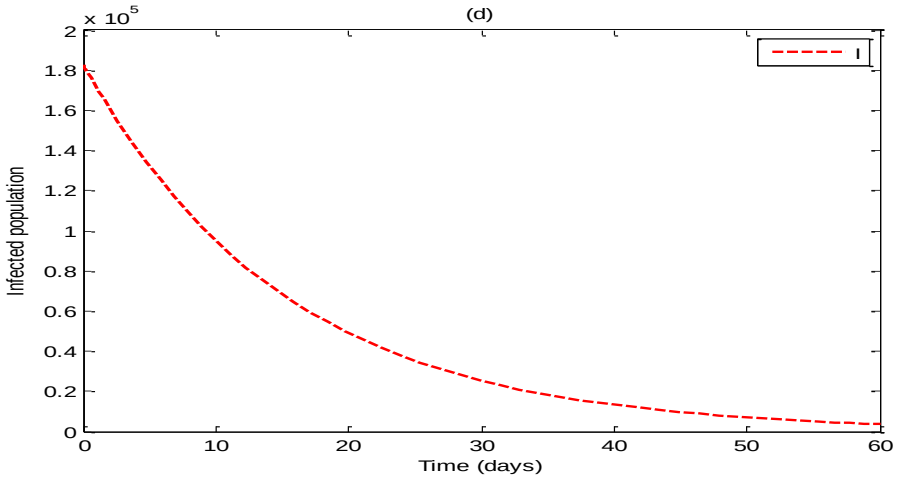

Figure 3d

From the figure above, the diagram shows the change in the dynamics of population with respect to time by varying the rate of spread of LFV model of infected-treated population. Figure 3e, depict the population of infected-treated individuals over time, we observed that the population of infected is (p) = 220,000 individuals at time (t) = 0 day, it would be also observed that the

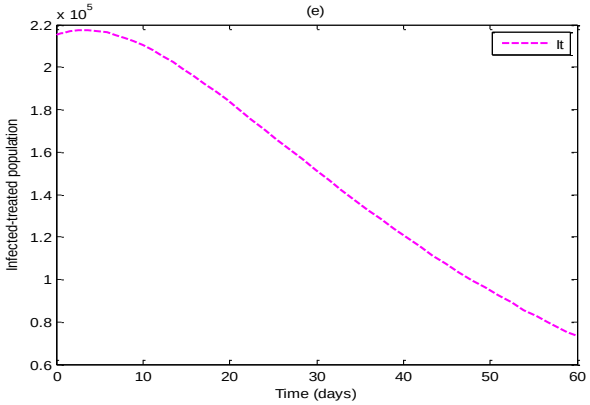

Figure 3e

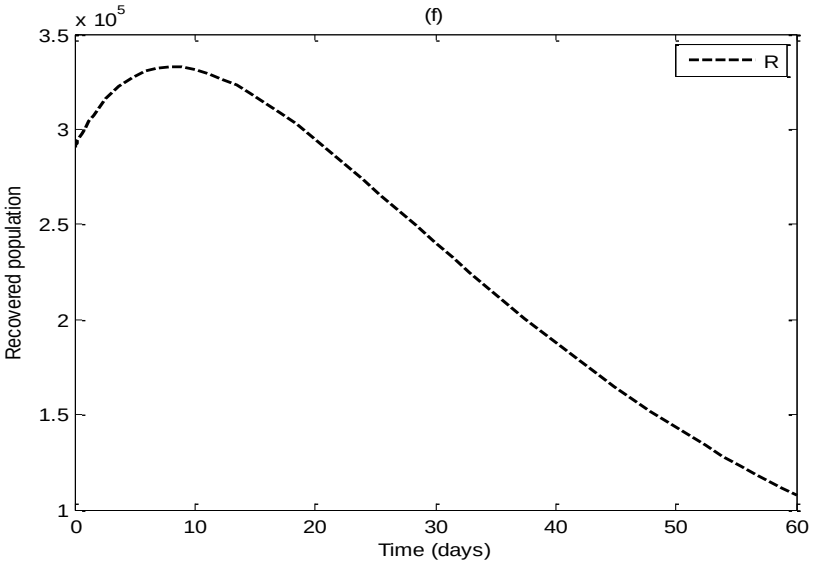

Figure 3f

population then decreases constantly from p = 220,000 individuals to p = 70,000 individuals at time (t) ≥ 60 days due to the influx of infected individuals rate (ν) undergoing treatment, recovery rate (f), the rate (μ) of those who died natural death and the rate (δ_2) of those who died by Lassa fever virus. This implies that quarantine and health education campaigns yielded an effective treatment on infected-treated humans within the possible shorted time of the day. This is in line with World health organization (WHO, 2018) who reported that timely quarantine of exposed and infected individuals should be observed and also a test to know their virus status be carried out. From the figure above, the diagrams show the change in the dynamics of population with respect to time by varying the rate of spread of LFV model of recovered population.

Figure 3f, depicts the population of recovered individuals over time, it will be observed that the population of recovered is (p) = 300,000 individuals at time (t) = 0 day, it then increased gradually to its peak as (p) = 340,000 individuals at time (t) = 10 days and subsequently decreases from p = 340,000 individuals to p = 11,000 individuals at time (t) ≥ 60 days. This is because of the availability of all the control strategies employed to eradicate the virus. Here, many infected persons were given proper awareness about the virus, some were quarantined, treated and recovered to susceptible population while some infected persons died by the virus. Hence, the three control strategies should always be implemented to reduce the spread of the virus.

From the figure above, the diagram shows the change in the dynamics of population with respect to time by varying the rate of spread of LFV model of the total population. Figure 3g, is a summary of all the population of figures 3a to 3f. It will be observed here that the graphs intercept with each other at some points, this really showed the transmission dynamics of Lassa fever virus (LFV). The graph here still contains the same information of figure 3a to 3f. The points of interception of the graph are labelled A, B, C, D, E, F, G, H and interpreted as follows. The point of intercept A: This shows the interception between Susceptible population (S) and Exposed population (E). It is observed here that the number of exposed individuals and susceptible individuals are (p) =

240,000 individuals at time (t) = 32 days. This implies that the exposed individuals are to be quarantined beyond 32 days to avoid more spread of the virus.

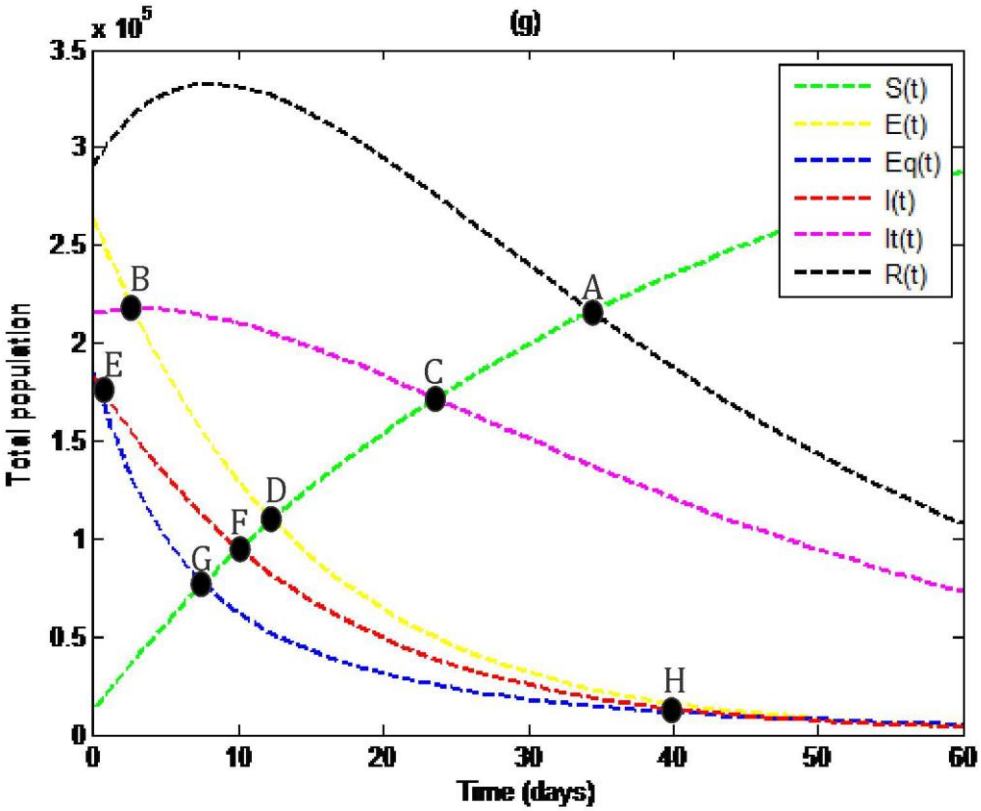

Figure 3g

The point of intercept B: This depicts the interception between exposed population (E) and infected-treated population (I_T). It is observed that the number of exposed individuals who were quarantined before treatment are (p) = 220,000 individuals at time (t) = 3 days. This implies that the combination of quarantine and health education campaigns enhance positive and sufficient behavioral changed on individuals who under-went treatment. This is because there is a good turn-up of individuals who responded for treatment at time (t) = 3 days. The point of intercept C: This shows the interception between susceptible population (S) and infected-treated population (I_T). This depicts that the number of susceptible individuals who contacted the virus and under-went treatment are (P) = 180,000 individuals at time (t) = 24 days. This is because the level of individual awareness of the virus is very high. The point of intercept D: This shows the interception of exposed population (E) and susceptible population (S). This depicts that the number of exposed individuals with the virus from the susceptible population are (P) = 120,000 individuals at time (t) = 12 days. It's implied that this number of exposed individuals were injected with Ribavirin vaccine (antibody) within 12 days of exposure to the virus and the vaccine is only for a short-term protection.

The point of intercept E: This shows the interception between infected population (I) and exposed-quarantine population (E_q). It is observed from the graph that the number of infected individuals who were quarantine due to the virus are (p) = 170,000 individuals at time (t) = 1 day. This is because the infected individuals were controlled at early stage (window period) of the virus

through quarantined. The point of intercept F: This depicts the interception between the susceptible population (S) and infected population (I). It is observed here that the number of susceptible individuals who were infected with the virus are (p) = 100,000 individuals at time (t) = 10 days. This is because some of these susceptible individuals do not practice safety and healthy life style like maintaining a standard community hygiene to control the rat population by regular hand washing, storing foods in rodent proof containers, keeping pet cat at home, avoiding blood and other body fluids when caring for sick people. The point of intercept G: This shows the interception between susceptible population (S) and exposed-quarantined population (E_q). It is observed that some of exposed-quarantined individuals who did not manifest symptoms of the virus during quarantined period, later returned to susceptible population (P) = 90,000 individuals at time (t) = 8 days. This means that the susceptible individuals were not infectious, since they did not manifest symptoms of the virus at time (t) = 8 days.

The point of intercept H: This depict the interception between exposed population (E), infected population (I) and exposed-quarantined population (E_q). It is observed here that the number of the sub-populations are asymptotically tending to stability with (p) = 10,000 individuals at time (t) = 40 days to time (t) ≥ 60 days. This implies that exposed and infected individuals were quarantined, treated and healed, thereby reducing the spread of the virus because health education campaign was given to them.

5 Conclusion

In this work, the transmission dynamics of Lassa fever virus is formulated and rigorously analyzed. The epidemiological and mathematical findings of this work are summarized and concluded below: Based on the results of this work, we conclude that Lassa fever virus (LFV) is a dangerous virus that does not respect individual or a community if not dealt with. Not keeping to Lassa fever virus (LFV) protocol reduces the rate of recovery in infected individuals under treatment as seen in figure 7.2e. Quarantine and health education campaigns reduced the rate of spread of the disease as described in figure 7.2f, therefore infected individuals must be encouraged to take health education to understand very well why they must be quarantined and take their treatment as advised, because these increased their rate of recovery as described in figure 7.2f.
It may be hypothesized that the most effective way to reduce the rate of spread of Lassa fever virus and the prevalent rate is to give people health education in all classes as described in figure 1. Therefore, education programs must reach all communities at all social levels, to increase the awareness about Lassa fever virus (LFV).

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