



A Mathematical Model and Sensitivity Analysis of Lassa Fever with Relapse and Reinfection Rate

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Abstract

In this research paper, we depict an unprecedented four-dimensional ordinary differential equation modeling the dynamic transmission of the Lassa fever virus incorporating relapse and reinfection rate. Recent studies showed that the recovered individuals from Lassa fever can again be susceptible; which contradicted the common assumptions made by different researchers on modeling of Lassa fever. So, this article corrects and states the implications of the assumptions on the population density. The numerical simulations unveil the effect of relapse, reinfection, and treatment rate in the affected population. Performing sensitivity analysis suggests all new incorporated parameters can impact the infection dynamics substantially. The stability analysis was carefully estimated where expression for each compartmentalized variable was calculated at both disease-free and persistence (endemic) equilibrium. Also, the basic reproduction number of the novel model was calculated using the Next Generation Matrix. The analytical results justify that the persistence (endemic) and the disease-free equilibrium are locally and globally asymptotically stable using both Routh Hurwitz Criterion and Comparison Theorem.

Keywords: Lassa fever, Reinfection rate, Relapse rate, Treatment rate, Sensitivity analysis.

Introduction

An acute viral hemorrhagic fever and a zoonotic disease termed Lassa fever was firstly observed in 1969 in a small town called Lassa located in Nigeria, Borno state to be precise. This infectious disease is persistent in West African countries and causes about 500,000 cases yearly with approximately 1% mortality. It is observed that the eruption of the severe ailment surfaced in the Central African Republic (CAR), Nigeria, and Liberia among others. It is clinically evident that Lassa fever diseases also exist in Mali, Senegal, and Congo. The

known virus is diagnosed to be transmitted by coming in contact with some liquid or gaseous substances which could be urine and feces of animals (WHO 2019).

Various studies on Lassa fever led to the formulation of different models actualizing the authors' perceptions about the upsurge of Lassa fever to eradicate the threat posed by the infectious diseases. Studies enunciated that the yearly occurrence of biological reproduction can, without a doubt, affect the movement of host-microbe systems (Bolzoni et al. 2006). Then, Okuonghae and Okuonghae (2006) formulated a

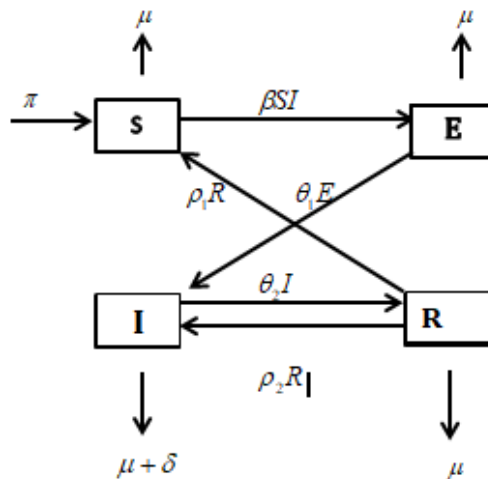
mathematical model portraying the dynamical transmission of Lassa fever. The statuses of their stability analysis for the DFE and persistence equilibrium were analytically examined. According to Ogabi et al. (2012), they built a Susceptible-Infected-Recovered model for the control of Lassa fever out-sending in Edo State specifically in the Northern area, Nigeria. A quantified shift was done by Bawa et al. (2013); where a constructive model for Lassa fever was developed. They partitioned the human size into two (2) which are susceptible, infectious, also the reservoir size into two (2) which are infant and adult as well as representing the virus in the habitat by V. Additionally, Onuorah et al. (2016) built another salient model using the approach termed sex pattern; where their resulting computation of basic reproduction number is 0.129 indicating that the disease would be eventually out of the population. Also, the method employed in Castillo-Chavez et al. (2002) was used to obtain their DFE which justified its global stability. Omale and Edibo (2016) proposed a model which contained control strategies. While Akinpelu and Akinwande (2018) put into consideration, the isolated class of individuals when formulating their mathematical model of Lassa fever. Also, Faniran (2017) presented a mathematical model with a non-drug rate. Then, Mariën et al. (2019) stated in their study that the

implementation of rodent vaccination or incessant control would gradually terminate the virus from the affected population. Loyinmi et al. (2021) constructed a model which captured two species of rodents which are the *Mastomys natalensis* and the *Rattus rattus*.

Having perused different works on Lassa fever disease and its in-out flow transmissions, we noticed that Lassa fever recurrence which result from either relapse of an original infection or exogenetic reinfection with a new strain of Lassa hemorrhagic fever have not been considered from past research studies. So, the model formulated in this paper is novel and quite different from all the previous works; it incorporates the relapse and reinfection rate which eliminates the common assumptions mostly stated by past researchers that “everyone who recovers does not become infected again”. The sensitivity analysis revealed the parameters which have the most prominent effects on the basic reproduction number. Also, the numerical simulations show the adverse effects of the two (2) constraints (relapse and reinfection rate) on the population density.

Materials and Methods

This section provides the schematic diagram and systems of the equation of the proposed model alongside their interpretations:



Considering the schematic diagram above,

$$\frac{dS}{dt} = \pi + \rho_1 R - \beta SI - \mu S \tag{1}$$

$$\frac{dE}{dt} = \beta SI - \theta_1 E - \mu E \tag{2}$$

$$\frac{dI}{dt} = \theta_1 E + \rho_2 R - \theta_2 I - \mu I - \delta I \tag{3}$$

$$\frac{dR}{dt} = \theta_2 I - \rho_1 R - \rho_2 R - \mu R \tag{4}$$

Where the parameters are as follows: π = Recruitment rate, β = Contact rate, μ = Natural death rate, ρ_1 = Relapse rate, θ_1 = Transition from exposed individuals to infectious, θ_2 = Transition from infectious individuals to recovered, δ = Disease induced death rate, ρ_2 = Reinfection rate, S = Susceptible region, E = Exposed region, I = Infected region, R = Recovered region;

Where the total human-size $N(t) = S(t) + E(t) + I(t) + R(t)$

Model assumptions

- 1) Relapse in medicine is a recurrence of disease after it has been apparently cured. So, relapse in Lassa fever connotes the recurrence of the virus after clinical treatment. It is assumed that this recurrence makes the recovered humans become susceptible humans again.
- 2) Reinfection in medicine is a second infection by the causative agent after recovery from or during the course of a primary infection. So, it is assumed that reinfection in Lassa fever is the second infection of the virus which incorporate transcending from the recovered class to the infectious class.

Non- negativity invariant region of the model

The total human-size $N = S + E + I + R$ (5)

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dE}{dt} + \frac{dI}{dt} + \frac{dR}{dt} \tag{6}$$

$$\frac{dN}{dt} = \pi - \mu(S + E + I + R) - \delta I \quad \frac{dN}{dt} = \pi - \mu N - \delta I \tag{7}$$

Theorem 2.1: The resulting solutions provided analytically for the system (1) – (4) is feasible for all $t > 0$

Proof: Let $D = \{S, E, I, R\} \in R^4$ culminates the results of the system (1) – (4) with conditions greater than zero.

Assuming no infection at the primitive stage say $\delta = 0$, then (7) gives

$$\frac{dN}{dt} = \pi - \mu N \tag{8}$$

Then, the resulting solution is

$$N \leq \left(N_0 - \frac{\pi}{\mu} \right) e^{-\mu t} + \frac{\pi}{\mu} \tag{9}$$

N tends to $\frac{\pi}{\mu}$ as $t \rightarrow \infty$ in (9) Hence all feasible solutions of (1)-(4) enter into the region

$$D = \left\{ \begin{array}{l} (S(t), E(t), I(t), R(t)) \in R^4, \text{ : } S(t), E(t), I(t), R(t) \geq 0 \\ S(t) + E(t) + I(t) + R(t) \leq N, N \leq \frac{\pi}{\mu} \end{array} \right\}$$

Non-negativity of solution

Lemma 1: consider the primitive $\{S(0) \geq 0, E(0) \geq 0, I(0) \geq 0, R(0) \geq 0\} \in D$. Then collective solutions $\{S, E, I, R\}$ of the model are non-negative for all $t \rightarrow 0$.

Recall (1)

$$\frac{dS}{dt} = \pi + \rho_1 R - \beta SI - \mu S$$

Removing the positive term $\pi, \rho_1 R$ on R.H.S

$$\frac{dS}{dt} \geq -S(\beta I + \mu)$$

$$S = S_0 e^{-\int (\beta I + \mu) dt}$$

$$\Rightarrow S(t) > 0, \text{ i.e. } S(t) = +ve \text{ for all } t \geq 0$$

Recall (2)

$$\frac{dE}{dt} = \beta SI - (\theta_1 + \mu)E$$

$$\Rightarrow E(t) > 0 \text{ for all } t \geq 0$$

From (3)

$$\frac{dI}{dt} = \theta_1 E + \rho_2 R - (\theta_2 + \mu + \delta)I$$

$$I(t) = I_0 e^{-(\theta_2 + \mu + \delta)t}$$

$$\Rightarrow I(t) > 0 \text{ for all } t \geq 0$$

Recall from (4)

$$\frac{dR}{dt} = \theta_2 I - (\rho_2 + \rho_1 + \mu)R$$

$$\Rightarrow R(t) = R_0 e^{-(\rho_2 + \rho_1 + \mu)t} > 0$$

Then $R(t) > 0$ for all $t \geq 0$

Then,

$$D = \left\{ \begin{array}{l} (S(t), E(t), I(t), R(t)) \in R^4, \text{ : } S(t) > 0, E(t) > 0, I(t) > 0, R(t) > 0 \\ \forall t \geq 0 \text{ and } N \leq \frac{\pi}{\mu} \end{array} \right\}$$

Boundedness of solution

The formulated systems of the equation denote the first-order human ordinary differential equation and its resulting general solution is

$$N \leq \left(N_o - \frac{\pi}{\mu} \right) e^{-\mu t} + \frac{\pi}{\mu} ; N(0) = N_o ; t = 0,$$

Hence, the total human population is bounded $\Rightarrow N_o \leq N(t) \leq \frac{\pi}{\mu}$ (10)

Equilibrium states

Disease free equilibrium (DFE) state

At DFE, $E_0 = \{S^o, E^o, I^o, R^o\}$; and the DFE points is calculated as $E_0 = \left(\frac{\pi}{\mu}, 0, 0, 0 \right)$

The endemic equilibrium state (EES)

Theorem 3: If $R_0 > 1$, the model (1) – (4) show a distinct EES which is denoted as

$$E^* = \{S^*, E^*, I^*, R^*\}$$

At the point of Equilibrium, $\frac{dS}{dt} = \frac{dE}{dt} = \frac{dI}{dt} = \frac{dR}{dt} = 0$

$$E^*(S^*, E^*, I^*, R^*) = \left(\begin{array}{c} \frac{(\theta_1 + \mu)(\theta_2 + \mu + \delta)(\rho_1 + \rho_2 + \mu) - \rho_2 \theta_2}{\beta \pi \theta_1 (\rho_1 + \rho_2 + \mu) - \mu (\theta_1 + \mu) [(\theta_2 + \mu + \delta)(\rho_1 + \rho_2 + \mu) - \rho_2 \theta_2]} \frac{\beta \theta_1 (\rho_1 + \rho_2 + \mu)}{[(\theta_2 + \mu + \delta)(\rho_1 + \rho_2 + \mu) - \rho_2 \theta_2]} \\ \frac{\beta \theta_1 (\rho_1 + \rho_2 + \mu) \{ (\theta_1 + \mu) [(\theta_2 + \mu + \delta)(\rho_1 + \rho_2 + \mu) - \rho_2 \theta_2] - \theta_1 \theta_2 \rho_1 \}}{\beta \pi \theta_1 (\rho_1 + \rho_2 + \mu) - \mu (\theta_1 + \mu) [(\theta_2 + \mu + \delta)(\rho_1 + \rho_2 + \mu) - \rho_2 \theta_2]} \\ \frac{\beta \{ (\theta_1 + \mu) [(\theta_2 + \mu + \delta)(\rho_1 + \rho_2 + \mu) - \rho_2 \theta_2] - \theta_1 \theta_2 \rho_1 \}}{\beta \pi \theta_1 (\rho_1 + \rho_2 + \mu) - \mu (\theta_1 + \mu) [(\theta_2 + \mu + \delta)(\rho_1 + \rho_2 + \mu) - \rho_2 \theta_2]} \\ \frac{\beta \pi \theta_2 (\rho_1 + \rho_2 + \mu) - \mu (\theta_1 + \mu) [(\theta_2 + \mu + \delta)(\rho_1 + \rho_2 + \mu) - \rho_2 \theta_2]}{(\rho_1 + \rho_2 + \mu) \beta \{ (\theta_1 + \mu) [(\theta_2 + \mu + \delta)(\rho_1 + \rho_2 + \mu) - \rho_2 \theta_2] - \theta_1 \theta_2 \rho_1 \}} \end{array} \right) \tag{11}$$

Basic reproduction number

One of the most important thresholds regarding any infectious disease is the basic reproduction number (Diekmann et al. 1990). It helps to determine if a disease can invade a population or not. We, therefore, calculate R_0 using Next Generation Matrix $R_0 = \rho(FV^{-1})$ as demonstrated by Huo and Feng (2013).

Let $x = (E, I, R, S)^T$

Then system (1)–(4) can be written as $\frac{dx}{dt} = F(x) - V(x)$,

Where $F(x) = \begin{pmatrix} \beta SI \\ 0 \\ 0 \\ 0 \end{pmatrix}$, $V(x) = \begin{pmatrix} (\theta_1 + \mu)E \\ -\theta_1 E - \rho_2 R + (\theta_2 + \mu + \delta)I \\ -\theta_2 I + (\rho_1 + \rho_2 + \mu)R \\ -\pi - \rho_1 R + \mu S \end{pmatrix}$ (12)

The Jacobian matrices of $F(x)$ and $V(x)$ at the disease free equilibrium E_0 are respectively

$$DF(E_0) = \begin{pmatrix} F_{3 \times 3} & 0 \\ 0 & 0 \end{pmatrix}, \quad DV(E_0) = \begin{pmatrix} V_{3 \times 3} & 0 \\ 0 & 0 & -\rho_1 & \mu \end{pmatrix}$$

where $F(x) = \begin{pmatrix} 0 & \frac{\beta\pi}{\mu} & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}$, $V(x) = \begin{pmatrix} (\theta_1 + \mu) & 0 & 0 \\ -\theta_1 & (\theta_2 + \mu + \delta) & -\rho_2 \\ 0 & -\theta_2 & (\rho_1 + \rho_2 + \mu) \end{pmatrix}$ (13) Then

$$FV^{-1} = \begin{pmatrix} \frac{\beta\pi\theta_1(\rho_2 + \rho_1 + \mu)}{\mu(\theta_1 + \mu)[(\theta_2 + \mu + \delta)(\rho_2 + \rho_1 + \mu) - \theta_2\rho_2]} & \frac{\beta\pi(\rho_2 + \rho_1 + \mu)}{\mu[(\theta_2 + \mu + \delta)(\rho_2 + \rho_1 + \mu) - \theta_2\rho_2]} & \frac{\beta\pi\rho_2}{\mu[(\theta_2 + \mu + \delta)(\rho_2 + \rho_1 + \mu) - \theta_2\rho_2]} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}$$

The basic reproduction number of the model, denoted by R_0 is thus given by

$$R_0 = \frac{\beta\pi\theta_1(\rho_2 + \rho_1 + \mu)}{\mu(\theta_1 + \mu)[(\theta_2 + \mu + \delta)(\rho_2 + \rho_1 + \mu) - \theta_2\rho_2]} \tag{14}$$

Stability analysis of the model

Local stability analysis of the disease free equilibrium

The local stability of the DFE and EES are resolved using Jacobian Matrices for the model (1) – (4) at the Disease Free Equilibrium point.

$$E^* = \begin{pmatrix} -\mu & 0 & -\frac{\beta\pi}{\mu} & \rho_1 \\ 0 & -(\theta_1 + \mu) & \frac{\beta\pi}{\mu} & 0 \\ 0 & \theta_1 & -(\theta_2 + \mu + \delta) & \rho_2 \\ 0 & 0 & \theta_2 & -(\rho_2 + \rho_1 + \mu) \end{pmatrix}$$

Theorem 1: The DFE point for the system (1) – (4) is locally asymptotically stable for $R_0 < 1$ and unstable otherwise

Proof: The eigenvalues of the Jacobian Matrices J for the model (1) – (4) is evaluated at the DFE and the solutions of the characteristics polynomial equation were justified using the Routh Hurwitz criterion

$|JE_0 - \lambda I| = 0$, $I = 4 \times 4$ unit matrix; and $\lambda_1, \lambda_2, \dots, \lambda_n$ are the eigenvalues

$$|JE_0 - \lambda I| = \begin{vmatrix} -\mu - \lambda & 0 & -\frac{\beta\pi}{\mu} & \rho_1 \\ 0 & -(\theta_1 + \mu) - \lambda & \frac{\beta\pi}{\mu} & 0 \\ 0 & \theta_1 & -(\theta_2 + \mu + \delta) - \lambda & \rho_2 \\ 0 & 0 & \theta_2 & -(\rho_2 + \rho_1 + \mu) - \lambda \end{vmatrix} = 0 \tag{15}$$

Since $\mu + \lambda = 0$, $\lambda_1 = -\mu$

$$\begin{aligned}
 \text{OR} \quad & \left[(\theta_1 + \mu + \lambda)(\theta_2 + \mu + \delta + \lambda)(\rho_2 + \rho_1 + \mu + \lambda) - \rho_2 \theta_2 - \frac{\beta \pi \theta_1 (\rho_2 + \rho_1 + \mu + \lambda)}{\mu} \right] \\
 & = 0 \\
 & \lambda^3 + ((\theta_2 + \mu + \delta) + (\rho_2 + \rho_1 + \mu) + (\theta_1 + \mu)) \lambda^2 + ((\theta_2 + \mu + \delta)(\rho_2 + \rho_1 + \mu) + \\
 & ((\theta_2 + \mu + \delta) + (\rho_2 + \rho_1 + \mu))(\theta_1 + \mu) - \rho_2 \theta_2 - \frac{\beta \pi \theta_1}{\mu}) \lambda + [((\theta_2 + \mu + \delta) \\
 & (\rho_2 + \rho_1 + \mu))(\theta_1 + \mu) - \rho_2 \theta_2 (\theta_1 + \mu) - \frac{\beta \pi \theta_1}{\mu} (\rho_2 + \rho_1 + \mu)] = 0
 \end{aligned} \tag{16}$$

Then, we test for R_0 using Routh Hurwitz Criterion

if $\lambda^3 + a_1 \lambda^2 + a_2 \lambda + a_3 = 0$, provided that $\text{Re } \lambda < 0$,

$a_1 > 0, a_3 > 0; a_1 a_2 - a_3 > 0$.

$\Rightarrow H_1 > 0; H_2 = m_1 m_2 - m_3$; Then, by inspection $H_2 > 0$

Therefore, $R_0 < 1 \forall H_2 > 0$

$$\Rightarrow \beta \pi \theta_1 (\rho_2 + \rho_1 + \mu) < \mu (\theta_1 + \mu) [(\theta_2 + \mu + \delta)(\rho_2 + \rho_1 + \mu) - \rho_2 \theta_2] \tag{18}$$

Thus for $R_0 < 1, H_2 > 0$

Hence the DFE E_0 is locally asymptotically since $R_0 < 1$.

Global stability analysis of the disease free equilibrium

Theorem 2: The DFE $E_0 = \left(\frac{\pi}{\mu}, 0, 0, 0\right)$ of the model (1)-(4) is globally asymptotically stable if

$R_0 < 1$.

Proof: Using comparison theorem for Global stability as implemented by Huo and Feng (2013). The time-rate of change of the existing variables (E, I, R) of the model (1)-(4) can be re-written as

$$\begin{pmatrix} \dot{E} \\ \dot{I} \\ \dot{R} \end{pmatrix} = (F - V) \begin{pmatrix} E \\ I \\ R \end{pmatrix} - \left(1 - \frac{\pi}{\mu} S\right) \begin{pmatrix} 0 & \frac{\beta \pi}{\mu} & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \begin{pmatrix} E \\ I \\ R \end{pmatrix},$$

where F and V are defined in (13). Since $S \leq \frac{\pi}{\mu}$ for all $t \geq 0$ in D, then

$$\begin{pmatrix} \dot{E} \\ \dot{I} \\ \dot{R} \end{pmatrix} \leq (F - V) \begin{pmatrix} E \\ I \\ R \end{pmatrix}, F = \begin{pmatrix} 0 & \beta S & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \& V = \begin{pmatrix} (\theta_1 + \mu) & 0 & 0 \\ -\theta_1 & (\theta_2 + \mu + \delta) & -\rho_2 \\ 0 & -\theta_2 & (\rho_2 + \rho_1 + \mu) \end{pmatrix} \tag{19}$$

$|(F - V) - \lambda I| = 0$; Where $I = 3 \times 3$ identity matrix

$$|(F - V) - \lambda I| = \begin{vmatrix} -(\theta_1 + \mu) - \lambda & \frac{\beta\pi}{\mu} & 0 \\ \theta_1 & -(\theta_2 + \mu + \delta) - \lambda & \rho_2 \\ 0 & \theta_2 & -(\rho_2 + \rho_1 + \mu) - \lambda \end{vmatrix} = 0 \quad (20)$$

Since the eigenvalues $\lambda_1, \lambda_2, \lambda_3$ of the characteristic polynomial all have negative real parts, then model (1)-(4) is stable whenever $R_0 < 1$. So, $(E, I, R) \rightarrow (0, 0, 0)$ as $t \rightarrow \infty$. By comparison theorem in Huo and Feng (2013), it follows that $(E, I, R) \rightarrow (0, 0, 0)$ and $S \rightarrow \frac{\pi}{\mu}$ as $t \rightarrow \infty$. The $(S, E, I, R) \rightarrow E_0$ as $t \rightarrow \infty$. So, E_0 is globally asymptotically stable for $R < 1$.

The parameters used for the model are presented in Table 1.

Table 1: Datum parameters for the model (1)-(4)

S/N	Parameters	Definition of parameters	Clinical values	References
1	π	Recruitment rate	0.15	Akinpelu and Akinwande 2018
2	ρ_1	The transition from recovered to susceptible	0–1	Calibrated
3	ρ_2	Relapse rate	0–1	Calibrated
4	β	Contact rate	0.08	Estimated
5	μ	Natural death rate	0.02	Akinpelu and Akinwande 2018
6	θ_1	The transition from exposed individuals to infectious	0.5	Akinpelu and Akinwande 2018
7	θ_2	The transition from infectious individual to recovered	0–1	Calibrated
8	δ	Disease induced death rate	0.3	Akinpelu and Akinwande 2018

Results and Discussion

Sensitivity analysis

It is expedient to determine the effectiveness of each parameter to the disease invasion. It is mostly used to presume the strength of each parameter incorporated in the analytical model. The normalized forward sensitivity coefficient of a variable related to a parameter is the unit of the relative change in the variable to the relative change in the

parameter. The sensitive index is defined using partial derivatives by

$$\Gamma_f^{R_0} = \frac{\partial R_0}{\partial f} \times \frac{f}{R_0} \quad (21)$$

Where R_0 is sensitively and differentially on the parameter f .

Table 2: Values for numerical solutions of the model

S/N	Parameter	Sign	Result
1	π	Positive	1
2	ρ_1	Negative	0.15998293
3	ρ_2	Positive	0.17598122
4	β	Positive	1
5	μ	Negative	0.02758534
6	θ_1	Positive	0.03846153
7	θ_2	Negative	0.56313993
8	δ	Negative	0.40955631

The sensitivity coefficients of $\Gamma_{\pi}^{R_0}, \Gamma_{\beta}^{R_0}, \Gamma_{\rho_2}^{R_0}, \Gamma_{\theta_1}^{R_0}$ are all positives while the remaining parameters are negatives. Since all coefficients are functions of other parameters, then the sensitivity coefficients will change when other parameter values change. The value of $\Gamma_{\pi}^{R_0} = +1$ simply means that increasing or decreasing R_0 by 20% increases or decreases R_0 by 20%. This

is also true for $\Gamma_{\beta}^{R_0}$. The two have the same effect on the basic reproduction number. The reinfection parameter being a positive value when sensitized, affirmed the huge effect it would have on R_0 in the population dynamic. The same is the transition rate from exposed to infectious individuals. However, the sensitized remaining parameters have a traceable effect on R_0 implying that they all have to be carefully estimated. So, this analysis has shown us the clinical effect of $\pi, \beta, \rho_2, \theta_1$ on the population density. So, it is expedient that these parameters are treated with urgency whenever there is an outbreak of Lassa fever.

Numerical simulations

The numerical solutions of the model (1)–(4) were obtained using the values provided in Table 2. The simulations were conducted using ODE-45 in MATLAB software. The effects are shown in Figures 1–5.

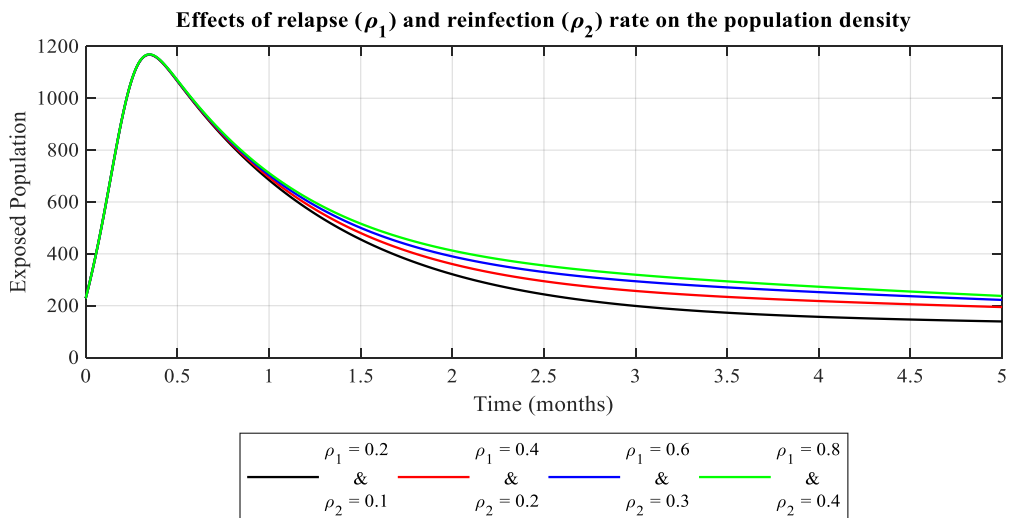


Figure 1: The graph of exposed population with increasing values of relapse and reinfection rate.

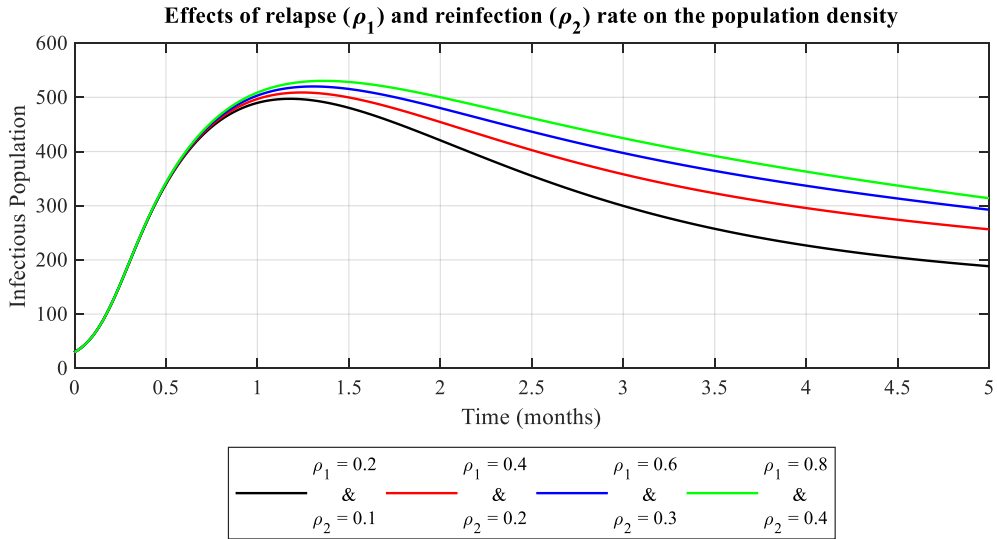


Figure 2: The graph of the infectious population with increasing values of relapse and reinfection rate.

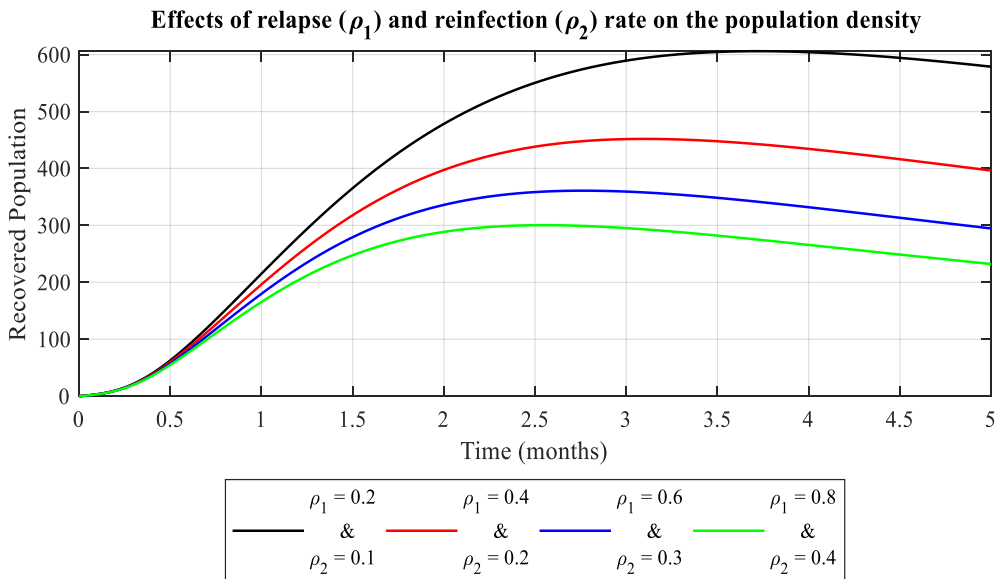


Figure 3: The graph of the recovered population with increasing values of relapse and reinfection rate.

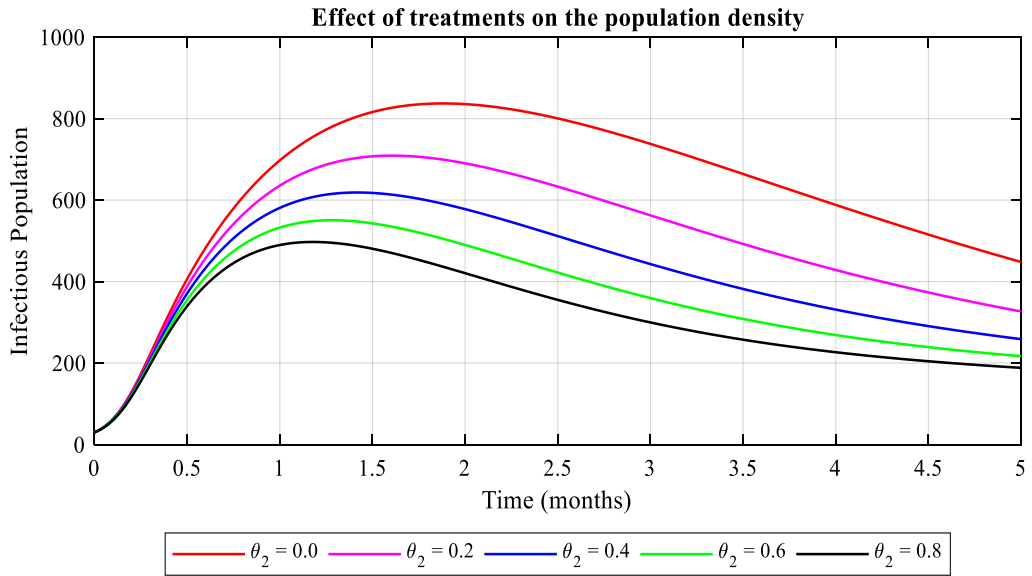


Figure 4: The graph of the infectious population over time when treatment is administered.

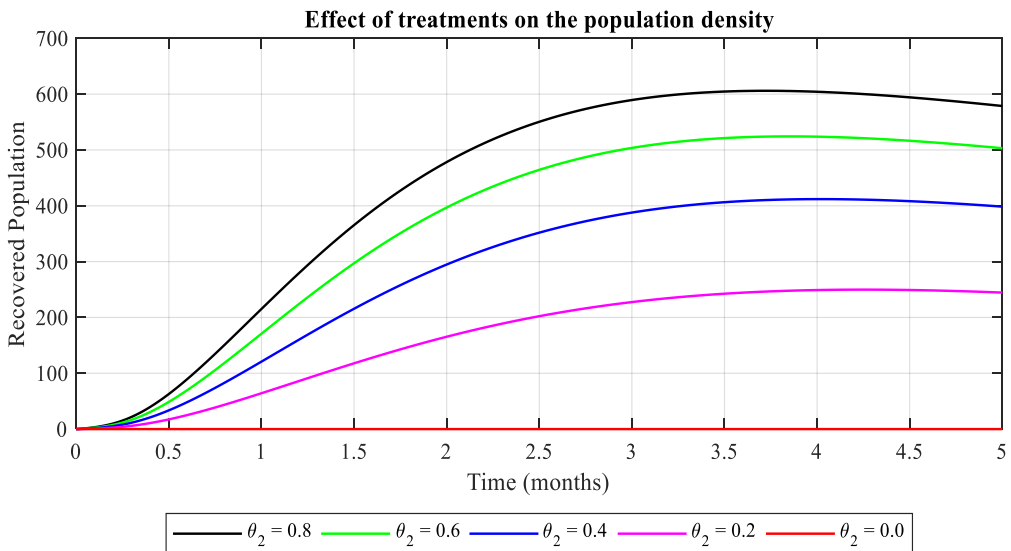


Figure 5: The graph of the recovered population over time when treatment is administered.

Discussion

From the review of various articles on Lassa fever, it is mostly assumed that whoever recovers from the disease cannot be susceptible; which has contradicted the recent outbreak of Lassa fever as documented by NCDC (2019) on the Lassa fever factsheet. So, this assumption is clarified with the above curves in Figures 1, 2, and 3. These

figures show how “relapse and reinfection rate” can affect the dynamical behavior of individuals in the population density. It is observed that numerous reasons could make an individual who has recovered from Lassa fever be susceptible and even become infectious instantaneously. Mostly, it is through ingestion or inhalation of the fluidic substance from Mastomys rodents. The virus

is shed via urine, direct contact with the infectious rodent, touching soiled materials, consumption of contaminated foods, eating of infectious *Mastomys* rodent, lack of protection from open sores and cuts, and so on. So, the above Figures 1, 2 and 3 unveil the implications of neglecting the preventive measures of Lassa fever. It succinctly tells the recovered individuals to nullify the illogical assumption. By so doing, the disease will hastily approach the Disease Free Equilibrium point which is the goal of this research article. It is evident from Figures 1 and 2 that if recovered individuals from the population neglect or carelessly do not take note of the stated preventive measures, the exposed and the infectious individual population will gradually be increasing. Hence, the curves would approach endemic equilibrium. Figure 3 justifies the fact that continuous “relapse and reinfection” in the population would make the recovered class increase instantaneously without any traces of decrement.

Figures 4 and 5 portray the dynamical effect of getting whoever is infectious treated on time. Governments and Health care practitioners are hereby advised to make all that may be required to hasten the treatment of Lassa fever in various medical centers e.g. ribavirin, ICU bed, shelters, etc. With these, the invasion of the disease would be curbed provided that the relapse and reinfection rate is minimal or prevented. It is demonstrated that if the treatment rate θ_2 is drastically increased to 0.8, the infectious curve would hastily be flattened after 5 months. And if everyone takes up the responsibility of exercising all the preventive measures since researchers are yet to license a vaccine for Lassa fever, there would be no record of Lassa fever disease in the affected population after 5 months. This means every infectious individual will recover as shown in Figure 5.

Conclusion

In this research work, a dynamic model was constructed. The non-negativity and boundedness which are the preliminary properties were gotten and were analytically found to be true at all times. A comparative

analysis was simultaneously executed resulting in the deduction of equilibrium points, showing the existence and stability of the equilibriums, and computing the reproduction number. By using the Routh Hurwitz criterion, we established that the reproduction number is less than one. The study of the analytic and qualitative behavior of the model for the dynamics transmission of the virus was critically carried out. Possible threats that can be posed by holding on to the illogical assumption are succinctly shown on the graphs. Also, we demonstrated the effect of getting infectious individuals treated on time. Furthermore, the sensitivity analysis carried out, showed that the reproduction number in the human population is most sensitive to the transmission rate, reinfection rate, transition from exposed to infectious rate, and recruitment rate of the humans. Numerical investigations of the model revealed that the only feasible way of reducing the transmission dynamics of the disease is by taking all preventive measures seriously since the vaccination for Lassa fever is yet to be licensed.

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Conflict of Interest

The authors declare that they have no competing interests

References

- Akinpelu FO and Akinwande R 2018 Mathematical model for Lassa fever and sensitivity analysis. *J. Sci. Eng. Res.* 5(6): 1-9.
- Bawa M, Abdulraham S, Jimoh OR and Adabara NU 2013 Stability analysis of the disease-free equilibrium state of Lassa fever disease. *Int. J. Sci. Technol. Math. Edu.* 9(2): 115-123.

- Bolzoni L, Dobson AP, Gatto M and De Leo GA 2006 The effect of seasonality on the epidemics of wildlife diseases. *Ecol. Lett.* 6(12): 818-828.
- Castillo-Chavez C, Feng Z and Huang W 2002 On the computation of R_0 and its role in global stability. *Mathematical Approaches for Emerging and Re-emerging Infection Diseases: An Introduction* 125: 31-65, *Institute of Mathematics and its Applications*
- Diekmann O, Heesterbeek JAP and Metz JAJ 1990 Definition and computation of the basic reproduction number R_0 in models of infectious diseases in heterogeneous populations. *J. Math. Biol.* 28: 365-382.
- Faniran TS 2017 A mathematical modeling of Lassa fever dynamics with non-drug compliance rate. *J. Math. Trend Technol.* 47(5): 305-318.
- Huo HF and Feng LX 2013 Global stability for an HIV/AIDS epidemic model with different latent stages and treatment. *Appl. Math. Mod.* 37(3): 1480-1489.
- Loyinmi AC, Akinfe TK and Ojo AA 2021 Qualitative analysis and dynamical behavior of a Lassa haemorrhagic fever model with exposed rodents and saturated incidence rate. *Sci. Afr.* 14: e01028
- Mariën J, Borremans B, Kourouma F, Baforday J, Rieger T, Gunther S, Magassouba N, Liers H and Fichet-Calvet E 2019 Evaluation of rodent control to fight Lassa fever based on field data and mathematical modeling. *Emer. Microbes Inf.* 8(1): 640-649.
- Ogabi CO, Olusa TV and Madufor MA 2012 Controlling Lassa fever in northern part of Edo State, Nigeria using SIR model. *New York Sci. J.* 5(12): 190-197.
- Okuonghae D and Okuonghae R 2006 A mathematical model for Lassa fever. *J. Nat. Ass. Math. Phy.* 10: 457-464.
- Omale D and Edibo TE 2016 The mathematical model for Lassa fever transmission with control strategies. *Comp. Info. Sys. Dev. Inf. Allied Res.* 6(4): 25-32.
- Onuorah MO, Ojo MS, Usman DJ and Ademu A 2016 Basic reproductive number for the spread and control of Lassa fever. *Int. J. Math. Trends Technol.* 30(1): 1-7.
- World Health Organization (WHO) 2019 Lassa fever factsheet <https://www.who.int/emergencies/disease-outbreak-news/item/14-february-2019-lassa-fever-nigeria-en>
- Nigerian Center for Disease Control (NCDC) 2019 Lassa fever factsheet <https://lassafever.info/resources/nigeria-centre-disease-control-ncdc-viral-haemorrhagic-fever-factsheet>