World Applied Sciences Journal 37 (3): 174-185, 2019
ISSN 1818-4952

DOI: 10.5829/idosi.wasj.2019.174.185

Mathematical Model for Controllability of Lassa Fever using Isolation and Treatment Measures

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Abstract: A non–linear deterministic mathematical model is proposed and analysed to study the controllability of lassa fever using isolation and treatment measures. The model is compartmentalised into seven classes with human populations as susceptible, exposed, infected, isolated and treated humans and rodent populations as susceptible and infected. 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 isolated human population. The existence, uniqueness and positivity of the model's solution have been carried out and the results shows that the solution exist and is unique. Again, the disease-free equilibrium state was obtained and analyzed for stability. We obtained an important threshold parameter called the effective reproduction number using the next generation method. If $R_{eff} < 1$ it implies that Lassa fever can be controlled and eradicated within the population in a finite time and if the $R_{eff} > 1$, the disease invades and become endemic in the population. Also, the result of numerical simulation on the key parameters of the model is carried out by examining the impact of isolation rate and treatment rate on the infected human population and the results show that, isolation and treatment are the best possible way to eradicate Lassa fever.

Key words: Controllability · Invariant region Isolation · Lassa fever · Mathematical model · Numerical Simulation · Reproduction Number and Stability

INTRODUCTION

Lassa Fever (LF), technically known as Lassa Hemorrhagic Fever (LHF) is a deadly infectious illness to man caused by a Lassa Virus (LASV) or Lassa Hemorrhagic Fever Virus (LASHFV) from a carrier "multimam-mate rat" (Genus name *Mastomys natalensis)*. This disease was first discovered in the town of Lassa in the North-East Nigeria in 1969 [1, 2]. Lassa fever is known to be endemic in Benin, Guinea, Ghana, Liberia, Mali, Sierra Leone, Togo and Nigeria, and most likely exists in other West African countries [3]. According to WHO risk assessment, 2018 is the largest outbreak of Lassa fever ever reported in Nigeria [4].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 [5]. After few days of infection, followed headache, sore throat, muscle pain, chest pain, nausea, vomiting, diarrhoea, and abdominal pain [6]. This is because the symptoms of the virus are variable and nonspecific and confirmatory laboratory diagnosis is not within the confines of many centres in West Africa [7],[8]. About 80% of people infected with Lassa fever are asymptomatic [9].

However, when 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 [10]. Early supportive care with rehydration and symptomatic treatment of the infected persons improves survival and chances of recovery [11]. The antiviral drug ribavirin seems to be an effective treatment for the Lassa fever virus if given early in the course of clinical illness [12]. Humans become infected with the Lassa fever virus from exposure to urine or faeces of an infected Mastomys rats [13]. This virus may be transmitted between humans through direct contact with the blood, urine, faeces or other bodily secretions of an infected person with Lassa fever [14]. Currently, there is no epidemiological evidence

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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 [11]. Sexual transmission of the Lassa fever virus has also been reported [14]. Inhalation of the tiny particles of infectious material (aerosol) is believed to be the most significant means of exposure [12].

In the reporting Week 27, [11] reported that From 1st January to 8th July 2018, a total of 2115 suspected cases have been reported from 21 states with at least one confirmed case across 71 Local Government Areas (Edo, Ondo, Bauchi, Nasarawa, Ebonyi, Anambra, Benue, Kogi, Imo, Plateau, Lagos, Taraba, Delta, Osun, Rivers, FCT, Gombe, Ekiti, Kaduna, Abia and Adamawa). Of these, 446 were confirmed positive, 10 are probable, 1652 negative (not a case). Since the onset of the 2018 outbreak, there have been 115 deaths in confirmed cases and 10 in probable cases. Case Fatality Rate in confirmed cases is 25.4%. Thirty-nine health care workers have been affected since the onset of the outbreak in seven states-Ebonyi (16), Edo (14), Ondo (4), Kogi (2), Nasarawa (1), Taraba (1) and Abia (1) with ten deaths in all, for Ebonyi (6), Kogi (1), Abia (1), Ondo (1) and Edo (1). However, the most hit states in the outbreak recorded 81% of all confirmed cases, such as Edo (42%), Ondo (24%) and Ebonyi (15%) states. Since 1 January 2018, the number of Lassa fever cases increased from 10 to 70 weekly reported cases [13]. However, since mid-February 2018, there has been a downward trend in the weekly reported number of cases [13]. 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 [3]. Therefore, in this paper, we developed a non–linear deterministic mathematical model to study the controllability of lassa fever using isolation and treatment measures and the description of the model is presented in details.

Formulation of the Model: The model is compartmentalised into seven (7) classes with human populations subdivided into five (5) classes as: susceptible, exposed, infected, isolated, treated humans and rodent populations subdivided into two (2) classes as: susceptible and infected rodents.

Assumptions of the Model:

- We assume that humans susceptible acquired the Infection via interaction with the infected rodent populations at a constant rate.
- We assumed that treatment is only given to isolated human population.
- Recruitment into the susceptible population is either by birth or immigration.
- The total human and rodent populations are given by $N_H = S_H + E_H + I_H + J_H + T_H$ and $N_R = S_R + I_R$ respectively.

The Model Equations: From the above assumptions, flow chart diagram, state variables and parameters, we derived a non-linear differential equations that governed model as follows:

$$\left.\begin{aligned}
\frac{dS_H}{dt} &= \pi_H + \omega T_H - \lambda S_H - \mu_H S_H \\
\frac{dE_H}{dt} &= \lambda S_H - (\mu_H + \alpha)E_H \\
\frac{dI_H}{dt} &= \alpha E_H - (\mu_H + \delta + \phi)I_H \\
\frac{dJ_H}{dt} &= \phi I_H - (\mu_H + \delta + \tau)J_H \\
\frac{dT_H}{dt} &= \tau J_H - (\mu_H + \omega)T_H \\
\frac{dS_R}{dt} &= \pi_R - \beta_1 S_R I_R - \mu_R S_R \\
\frac{dI_R}{dt} &= \beta_1 S_R I_R - \mu_R I_R
\end{aligned}\right\} \quad (1)$$

The total human populations with time are given by:

$$N_H(t) = S_H(t) + E_H(t) + I_H(t) + J_H(t) + T_H(t) \quad (2)$$

and the total rodent populations with time are given by:

$$N_R(t) = S_R(t) + I_R(t) \quad (3)$$

All subject to the following nonnegative initial conditions:

$S_H(0) = S_H^0, E_H(0) = E_H^0, I_H(0) = I_H^0, J_H(0) = J_H^0, T_H(0) = T_H^0, S_R(0) = S_R^0, I_R(0) = I_R^0$

and $N(0) = N_0$, with the force of infection $\lambda = \beta_1 I_R$-$\beta_2 I_H$, where β_1 and β_2 are the effective contact between infected rats and either susceptible humans or susceptible rodents and effective contact between infected human and susceptible human respectively.

The time derivative of (2) is given by:

$$\frac{dN_H}{dt} = \frac{dS_H}{dt} + \frac{dE_H}{dt} + \frac{dI_H}{dt} + \frac{dJ_H}{dt} + \frac{dT_H}{dt} \quad (4)$$

Plugging (1) into (4) gives

$$\frac{dN_H}{dt} = \pi_H - (I_H + J_H)\delta - \mu_H N_H \quad (5)$$

Also,
The time derivative of (3) is given by:

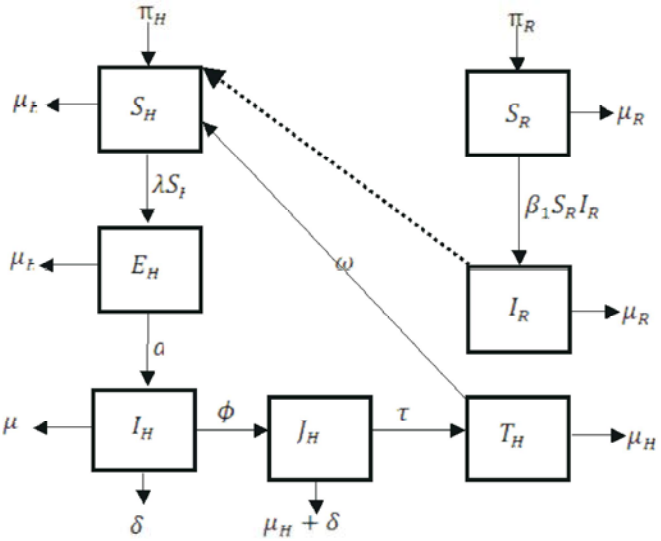

Fig. 1: Flow Chart of the Model

Table 1: State Variables of the Model

Variables	Description
$S_H(t)$	Susceptible human at time t
$E_H(t)$	Exposed human at time t
$I_H(t)$	Infected human at time t
$J_H(t)$	Isolated human at time t
$T_H(t)$	Treated human at time t
$S_R(t)$	Susceptible rodent at time t
$I_R(t)$	Infected rodent at time t

Table 2: State Parameters of the Model

Parameters	Description
π_H	Recruitment rate into the susceptible human
π_R	Recruitment rate into the susceptible rodent
μ_H	Natural death rate in human
μ_R	Natural death rate in rodent
β_2	Effective contact between infected rats and either susceptible human
β_1	Effective contact between infected rats and either susceptible human or susceptible rodent
α	Progression rate to active Lassa fever
ϕ	Isolation rate
τ	Treatment rate
ω	Recovery rate
δ	Human disease induced death
$N_H(t)$	Total population of human with time t
$N_R(t)$	Total population of rodent t
λ	Force of infection

$$\frac{dN_R}{dt} = \frac{dS_R}{dt} + \frac{dI_R}{dt} \quad (6)$$

Substituting (1) into (6) gives

$$\frac{dN_R}{dt} = \pi_R - \mu_R N_R \quad (7)$$

Basic Properties of the Model: In this section, we study some of the basic results of the model system (1) which are critical to the proof of invariant region, existence uniqueness of solution, equilibrium points.

The Invariant Region (Region of Biological Interest): As the system (1) monitors human population, all related state variables and parameters are assumed to be non-negative for all $t \geq 0$. Therefore, the above system is dissipative in the proper subset $\Gamma \subset \mathbb{R}^7_+$. Thus, we state and prove the following results:

Lemma 1: The solutions of the system (1) are feasible for all $t > 0$ if they enter the invariant region $\Gamma = (S_H, E_H, I_H, J_H, T_H, S_R, I_R)$.

Proof 1: Let $\Gamma = (S_H, E_H, I_H, J_H, T_H, S_R, I_R)$ be any solution of the system (1), with non-negative initial conditions. From equation (5), we see that in the absence of Lassa fever ($I_H = J_H = 0$), we obtained;

$$\frac{dN_H}{dt} \leq \pi_H - \mu_H N_H \tag{8}$$

Rearranging (8) gives

$$\frac{dN_H}{dt} + \mu_H N_H \leq \pi_H \tag{9}$$

Solving (9) using the method of integrating factor (IF), we compute the IF as follows:

$$IF = e^{\int \mu_H dt} = e^{\mu_H t} \tag{10}$$

Multiplying both sides of (9) by (10) yields

$$e^{\mu_H t}\frac{dN_H}{dt} + \mu_H N_H e^{\mu_H t} \leq \pi_H e^{\mu_H t}$$

That is,

$$\frac{d}{dt}\left(\mu_H N_H e^{\mu_H t}\right) \leq \pi_H e^{\mu_H t} \tag{11}$$

Integrating both sides of (11) gives

$$N_H(t)e^{\mu_H t} \leq \frac{\pi_H}{\mu_H} e^{\mu_H t} + \psi \tag{12}$$

where ψ is a constant of integration.
This means

$$N_H(t) \leq \frac{\pi_H}{\mu_H} + \psi e^{-\mu_H t} \tag{13}$$

Applying the initial condition in (13): $N_H(0) = N_H^0$, we obtain;

$$N_H^0 - \frac{\pi_H}{\mu_H} \leq \psi \tag{14}$$

Substituting (14) into (13) we have:

$$N_H(t) \leq \frac{\pi_H}{\mu_H} + \left(N_H^0 - \frac{\pi_H}{\mu_H}\right) e^{-\mu_H t} \tag{15}$$

Applying Birkhoff and Rota's theorem on differential inequality of [5] into (15), we have

$$0 \leq N_H(t) \leq \frac{\pi_H}{\mu_H}, \text{ as } t \to \infty \tag{16}$$

The total population approaches $K = \frac{\pi_H}{\mu_H}$, as $t \to \infty$, which is commonly known as the carrying capacity. Therefore, the feasible solutions set of the extended model (1) enters the region below:

$$\left\{\Gamma = \Gamma = (S_H, E_H, I_H, J_H, T_H) \in \mathbb{R}_+^7 : S_H > 0, E_H \geq 0, I_H \geq 0, J_H \geq 0, T_H \geq 0, N_H \leq \frac{\pi_H}{\mu_H}\right\}$$

Thus in this region our model is biologically feasible. Here whenever $N_H > \frac{\pi_H}{\mu_H}$ then $\frac{dN_H}{dt} < 0$ which means the population reduces asymptotically to the carrying capacity and whenever $N_H \leq \frac{\pi_H}{\mu_H}$ every solution with initial conditions in Γ remains in that region for $t, > 0$ so the model is well posed in Γ. Therefore, the region Γ is invariant (i.e. solutions remain positive for all time.) and the model is well posed and biologically meaningful and this ends the proof of the Lemma 1.

Existence and Uniqueness of Solution: We prove the existence and the uniqueness of solution following the approach outlined in the work of [9].

Consider the system of equation below

$$\left.\begin{aligned} X_1' &= f_1(x_1, x_2, \ldots, x_n), X_1(t_0) = X_{10} \\ X_2' &= f_2(x_1, x_2, \ldots, x_n), X_2(t_0) = X_{20} \\ &\vdots \\ X_n' &= f_n(x_1, x_2, \ldots, x_n), X_n(t_0) = X_{n0} \end{aligned}\right\} \tag{17}$$

Rewriting (3.38) in compact form yields

$$X' = f_n(t, x), x(t_0) = x_0 \tag{18}$$

Theorem 1: Let D denote the region $|t - t_0| \leq \alpha, \|x - x_0\| \leq b, x = (x_1, x_2, \ldots, x_n), x_0 = (x_1, x_2, \ldots, x_n)$ and suppose that $f(t, x)$ satisfies the Lipchitz condition

$$\|f(t, x_1) - f(t, y)\| \leq K\|x_1 - y\| \tag{19}$$

Whenever the pairs (t, x_1) and (t, x_2) belong to D, where K is a positive constant. Then, there is a constant $\delta > 0$ such that there exist a continuous vector solution $x(t)$ of the system (18) in the interval $|t - t_0| \leq \alpha$. It is important to note that condition (19) is satisfied by the requirement that $\frac{\partial f_i}{\partial x_j}, i, j = 1, 2, \ldots, n$ be continuous and bounded in D.

We are interested in the region $1 \leq \epsilon \leq \mathcal{H}$ (20)

We look for bounded solution of the form $0 \leq \mathcal{H} \leq \infty$ (21)

We shall prove the following existence theorem:

Theorem 2: Let D denote the region defined in (20) such that (21) and (19) hold. Then there exists a unique solution of model (1) which is bounded in the region D.

Proof: Let the right hand sides of the system of equation (1) be $f_1, f_2, f_3, f_4, f_5, f_6$ *and* f_7
It suffices to show that $\left|\frac{\partial f_i}{\partial x_j}\right|, i, j = 1, 2, \ldots, 7$ be continuous and bounded in D.

Differentiating $f_1, f_2, f_3, f_4, f_5, f_6$ *and* f_7 each partially with respect to $S_H, E_H, I_H, J_H, T_H, S_R$ *and* I_R respectively and taking their norms gives;

$$\left|\frac{\partial f_1}{\partial S_H}\right| = |-(\beta_1 I_R + \beta_2 I_H) - \mu_H| < \infty$$

$$\left|\frac{\partial f_2}{\partial E_H}\right| = |0| < \infty$$

$$\left|\frac{\partial f_3}{\partial I_H}\right| = |-\beta_2 S_H| < \infty$$

$$\left|\frac{\partial f_4}{\partial J_H}\right| = |0| < \infty$$

$$\left|\frac{\partial f_5}{\partial T_H}\right| = |\omega| < \infty$$

$$\left|\frac{\partial f_6}{\partial S_R}\right| = |0| < \infty$$

$$\left|\frac{\partial f_7}{\partial I_R}\right| = |-\beta_1 S_H| < \infty$$

These partial derivatives exist, continuous and are bounded in the same way the other derivatives exist and are bounded. Hence, by Theorem 2, the model system (1) has a unique solution.

Analysis of the Governing Equation: In this section, we consider the Lassa model system (1) with control measures (isolation and treatment), investigate the steady states and their existence and stability in terms of the control reproduction number.

Existence of Disease Free Equilibrium (DFE) (ε_0) of the Model: Here, we compute the model disease free equilibrium state by setting the time-derivatives on the right hand sides of the model system (1) to zero such that

$$\frac{dS_H}{dt} = \frac{dE_H}{dt} = \frac{dI_H}{dt} = \frac{dJ_H}{dt} = \frac{dT_H}{dt} = \frac{dS_R}{dt} = \frac{dI_R}{dt} = 0 \tag{22}$$

So that we now have

$$0 = \pi_H + \omega T_H - (\beta_1 I_R + \beta_2 I_H) S_H - \mu_H S_H \tag{23}$$

$$0 = (\beta_1 I_R + \beta_2 I_H) S_H - (\mu_H + \alpha) E_H \tag{24}$$

$$0 = \alpha E_H - (\mu_H + \delta + \phi) I_H \tag{25}$$

$$0 = \phi I_H - (\mu_H + \delta + \tau) J_H \tag{26}$$

$$0 = \tau J_H - (\mu_H + \omega) T_H \tag{27}$$

$$0 = \pi_R - \beta_1 S_R I_R - \mu_R S_R \tag{28}$$

$$0 = \beta_1 S_R I_R - \mu_R I_R \tag{29}$$

Recall that, the disease free equilibrium state of the model (1) is scenario where there is no disease in the system which implies that

$$E_H = I_H = J_H = T_H = I_R = 0 \tag{30}$$

Plugging (30) into (1) and solving accordingly we obtain

$$\varepsilon_0 = (S_H^0, E_H^0, I_H^0, J_H^0, T_H^0, S_R^0, I_R^0) = \left(\frac{\pi_H}{\mu_H}, 0,0,0,0, \frac{\pi_R}{\mu_R}, 0\right) \tag{31}$$

Effective Reproduction Number (R_{eff}): The basic reproduction number is a key parameter, which govern the behaviour of the model. It can be defined as the expected number of secondary cases produced by a typical infective in a virgin population. That is, population completely susceptible to infection in question [1]. Using the matrix-theory, R_0 is the spectral radius of the next generation matrix for the model. This means R_0 oversees the growth and decline of the successive generation of infective when the epidemic begins [10]. Using the techniques and notation in [8,7], we represent F and V to be matrices for the new infections generated and transmission terms respectively. Thus, the effective reproduction number (R_{eff}) can be computed by:

$$R_{eff} = \rho(FV^{-1}) \tag{32}$$

where $\rho(FV^{-1})$ is the spectral radius of next generation matrix.

We calculate the effective reproduction number (R_{eff}) using the next generation operator method on the system (1) as follows;

The vector F_i of the rates of the new infection in compartment E_H, I_H, J_H, T_H and I_R, is given by

$$F_i = \begin{pmatrix} (\beta_1 I_R + \beta_2 I_H) S_H \\ 0 \\ 0 \\ 0 \\ \beta_1 I_R S_R \end{pmatrix} \tag{33}$$

Also, the remaining transfer terms in compartment E_H,I_H,J_H,T_H and I_R is given by

$$V_i = \begin{pmatrix} (\mu_H + \alpha) E_H \\ (\mu_H + \delta + \phi) I_H - \alpha E_H \\ (\mu_H + \delta + \tau) J_H - \phi I_H \\ (\mu_H + \omega) E_H - \tau J_H \\ \mu_H I_R \end{pmatrix} \tag{34}$$

The matrix of partial derivative of F_i at the disease free equilibrium state at $\varepsilon_0 = (S_H^0, 0, 0, 0, 0, S_R^0, 0)$ is given by

$$F(\varepsilon_0) = \begin{pmatrix} 0 & \frac{\beta_2 \pi_H}{\mu_H} & 0 & 0 & \frac{\beta_1 \pi_H}{\mu_H} \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \frac{\beta_1 \pi_R}{\mu_R} \end{pmatrix} \tag{35}$$

Rewriting (35) yields

$$F(\varepsilon_0) = \begin{pmatrix} 0 & F_{12} & 0 & 0 & F_{15} \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & F_{55} \end{pmatrix} \tag{36}$$

where;

$$\left.\begin{aligned} F_{12} &= \frac{\beta_2 \pi_H}{\mu_H} \\ F_{15} &= \frac{\beta_1 \pi_H}{\mu_H} \\ F_{55} &= \frac{\beta_1 \pi_R}{\mu_R} \end{aligned}\right\}$$

Also, the matrix of the partial derivatives of V_i at the disease free equilibrium state $\varepsilon_0 = (S_H^0, 0, 0, 0, 0, S_R^0, 0)$ is given by

$$V(\varepsilon_0) = \begin{pmatrix} (\mu_H + \alpha) & 0 & 0 & 0 & 0 \\ -\alpha & (\mu_H + \delta + \phi) & 0 & 0 & 0 \\ 0 & -\phi & (\mu_H + \delta + \tau) & 0 & 0 \\ 0 & 0 & -\tau & (\mu_H + \omega) & 0 \\ 0 & 0 & 0 & 0 & \mu_R \end{pmatrix} \tag{37}$$

Equation (38) can also be written as;

$$V(\varepsilon_0) = \begin{pmatrix} V_{11} & 0 & 0 & 0 & 0 \\ -V_{21} & V_{22} & 0 & 0 & 0 \\ 0 & -V_{32} & V_{33} & 0 & 0 \\ 0 & 0 & -V_{43} & V_{44} & 0 \\ 0 & 0 & 0 & 0 & V_{55} \end{pmatrix} \tag{38}$$

where;

$$\left.\begin{aligned} V_{11} &= \mu_H + \alpha & V_{55} &= \mu_R \\ V_{22} &= \mu_H + \delta + \phi & V_{21} &= \alpha \\ V_{33} &= \mu_H + \delta + \tau & V_{32} &= \phi \\ V_{44} &= \mu_H + \omega & V_{43} &= \tau \end{aligned}\right\} \tag{39}$$

Computing the inverse of (39) gives

$$V^{-1} = \begin{pmatrix} \frac{1}{V_{11}} & 0 & 0 & 0 & 0 \\ \frac{V_{21}}{V_{11}V_{22}} & \frac{1}{V_{22}} & 0 & 0 & 0 \\ 0 & \frac{V_{32}}{V_{22}V_{33}} & \frac{1}{V_{11}} & 0 & 0 \\ \frac{V_{21}V_{32}V_{43}}{V_{11}V_{22}V_{33}V_{44}} & \frac{V_{43}}{V_{22}V_{44}} & \frac{V_{43}}{V_{33}V_{44}} & \frac{1}{V_{44}} & 0 \\ 0 & 0 & 0 & 0 & \frac{1}{V_{55}} \end{pmatrix} \quad (40)$$

Rewriting (40) we have;

$$V^{-1} = \begin{pmatrix} A_{11} & 0 & 0 & 0 & 0 \\ A_{21} & A_{22} & 0 & 0 & 0 \\ 0 & A_{32} & A_{33} & 0 & 0 \\ A_{41} & A_{42} & A_{43} & A_{44} & 0 \\ 0 & 0 & 0 & 0 & A_{55} \end{pmatrix} \quad (41)$$

where;

$$\left.\begin{aligned} A_{11} &= \frac{1}{(\mu_H+\alpha)} & A_{33} &= \frac{1}{(\mu_H+\delta+\tau)} \\ A_{21} &= \frac{\alpha}{(\mu_H+\alpha)(\mu_H+\delta+\phi)} & A_{41} &= \frac{\alpha\phi\tau}{(\mu_H+\alpha)(\mu_H+\delta+\phi)(\mu_H+\delta+\tau)(\mu_H+\omega)} \\ A_{22} &= \frac{\phi}{(\mu_H+\delta+\phi)} & A_{42} &= \frac{\tau}{(\mu_H+\delta+\phi)(\mu_H+\omega)} \\ A_{32} &= \frac{\phi}{(\mu_H+\delta+\phi)(\mu_H+\delta+\tau)} & A_{43} &= \frac{\tau}{(\mu_H+\delta+\phi)(\mu_H+\omega)} \\ & & A_{44} &= \frac{1}{(\mu_H+\omega)} \\ & & A_{55} &= \frac{1}{\mu_R} \end{aligned}\right\}$$

To compute FV^{-1}, we use (40) and (41) so that;

$$FV^{-1} = \begin{pmatrix} 0 & F_{12} & 0 & 0 & F_{15} \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & F_{55} \end{pmatrix} \begin{pmatrix} A_{11} & 0 & 0 & 0 & 0 \\ A_{21} & A_{22} & 0 & 0 & 0 \\ 0 & A_{32} & A_{33} & 0 & 0 \\ A_{41} & A_{42} & A_{43} & A_{44} & 0 \\ 0 & 0 & 0 & 0 & A_{55} \end{pmatrix}$$

$$FV^{-1} = \begin{pmatrix} 0 & F_{11}A_{12} & 0 & 0 & F_{11}F_{15} \\ 0 & F_{12}A_{12} & 0 & 0 & F_{12}A_{15} \\ 0 & 0 & 0 & 0 & 0 \\ 0 & F_{41}A_{12} & 0 & 0 & F_{41}A_{15} \\ 0 & 0 & 0 & 0 & F_{55}A_{55} \end{pmatrix} \quad (42)$$

It follows that the effective reproduction number R_{eff} is computed by taking the spectral radius (dominant eigenvalue) of the matrix FV^{-1} using the characteristics equation

$$det\,(FV^{-1} - \lambda_E I) = 0 \tag{43}$$

or

$$\begin{vmatrix} -\lambda & F_{11}A_{12} & 0 & 0 & F_{11}F_{15} \\ 0 & F_{12}A_{12} - \lambda & 0 & 0 & F_{12}A_{15} \\ 0 & 0 & -\lambda & 0 & 0 \\ 0 & F_{41}A_{12} & 0 & -\lambda & F_{41}A_{15} \\ 0 & 0 & 0 & 0 & F_{55}A_{55} - \lambda \end{vmatrix} = 0 \tag{44}$$

Evaluating (44) accordingly gives;

$$\lambda_1 = \lambda_3 = \lambda_4 = 0 \tag{45}$$

and

$$\lambda_2, \lambda_5 = max\left(\frac{\beta_2 \alpha \pi_H}{\mu_H(\mu_H+\alpha)(\mu_H+\delta+\phi)}, \frac{\beta_1 \pi_R}{\mu_R}\right) \tag{46}$$

Therefore, the largest (dominant) eigenvalue also known as the effective reproduction denoted by R_{eff} is given by;

$$\mathcal{R}_{eff} = \frac{\beta_2 \alpha \pi_H}{\mu_H(\mu_H+\alpha)(\mu_H+\delta+\phi)} \tag{47}$$

with $\frac{1}{\mu_H}$, $\frac{1}{(\mu_H+\alpha)}$ and $\frac{1}{(\mu_H+\delta+\phi)}$ which refers to per capital human mortality,

Biological Interpretation: The biological meaning of the parameter components of the effective reproduction number are as follows:

$\left(\frac{\pi_H}{\mu_H}\right)$: The carrying capacity for human population.

$\left(\frac{\alpha}{\mu_H+\alpha}\right)$: The proportion of individuals from the exposed human that becomes infectious.

$\left(\frac{\beta_2}{\mu_H+\delta+\phi}\right)$: The average number of susceptible human infected by a single human infective.

Table 3: Parameters Values for Numerical

Parameters	Values	Sources
π_H	2000	Adewale *et al*., (2016)
π_R	500	Adewale *et al*., (2016)
β_1	0.2	Adewale *et al*., (2016)
$\beta 2$	0.2	Adewale *et al*., (2016)
α	0.003	Adewale *et al*., (2016)
ϕ	0.2	Adewale *et al*., (2016)
r	0.75	Assumed
μ_H	0.02	Adewale *et al*., (2016)
μ_R	0.02	Adewale *et al*., (2016)
δ	0.1	Assumed
ω	0.54	Assumed

Table 4: Parameters Values for Numerical

Variables	Values	Sources
$S_H(t)$	10000	*Akanni et al.*,2018)
$E_H(t)$	3000	*Assumed*
$I_H(t)$	200	*Akanni et al.*, (2018)
$J_H(t)$	1500	*Assumed*
$T_H(t)$	600	*Akanni et al.*, (2018)
$S_H(t)$	200	*Akanni et al.*, (2018)
$I_R(t)$	125	*Akanni et al.*, (2018)

Numerical Simulations: We carryout numerical simulation of the model (1) using the set of reasonable hypothetically estimated parameters and initial values given in Table 3 and 4 whose sources are mainly from [2] as well as assumed values based on the literature of the disease in order to have more realistic simulation results.

The Figures 2 – 4 below are the results obtained from the numerical simulation of the Lassa Fever Virus model with controllability using isolation and treatment measures.

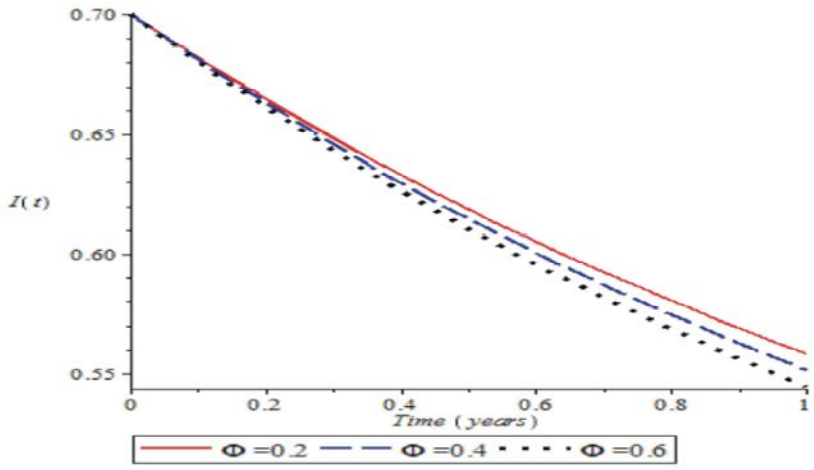

Fig. 2: Simulation results showing the effect of isolation rate ϕ on infected humans.

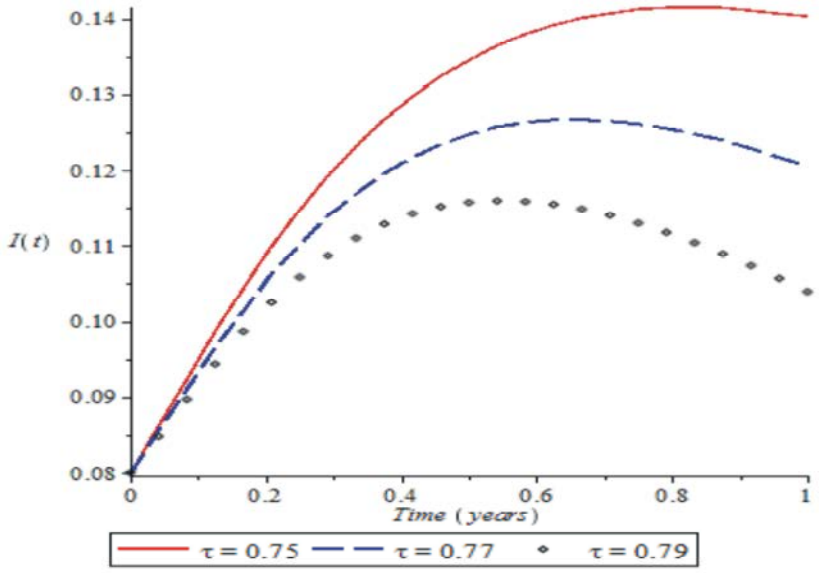

Fig. 3: Simulation results showing the impact of treatment rate τ on infected individuals.

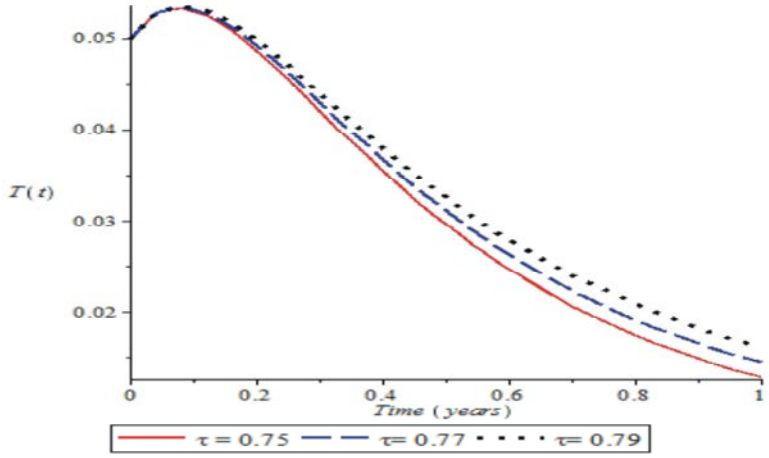

Fig. 4: Simulation results showing the effect of treatment rate τ on treated humans.

RESULTS AND DISCUSSION

The numerical simulations results in Figure (2) presented the impact of isolation rate ϕ on Lassa fever infection. We September 1, 2009observed that, an increase in the isolation rate brings about a declined in the infected humans. This is true because as isolation increases, infected human population on the order hand reduces. This also shows that, isolation of Lassa fever infected humans will go a long way in curtailing the disease outbreak.

In Figure (3), simulation result shows the effect of treatment rate τ on treated humans via isolation. The result depicted indicates that, increasing treatment rate reduces the infected humans' population; this is in line with reality because treatment of the infected persons through isolation brings about reduction in number of person infected with Lassa fever.

The numerical simulation result in Figure (4) highlighted the effect of treatment rate τ on treated humans, which shows that increase in the treatment rate brings about a corresponding increase in the treated humans population, this is true because as treatment is intensified, the number of person with Lassa fever reduces thereby increasing the susceptibility to the disease.

CONCLUSION

A seven (7) non-linear deterministic epidemiological model was formulated to gain a deep understanding into the controllability of lassa fever virus disease using isolation and treatment measures. The basic properties of the model were investigated and analysis shows that there exists a domain Γ where the model is mathematically meaningful and biological well posed. The existence and uniqueness of the model's solution have been carried out and the results shows that the solution exist and is unique. Again, the disease-free equilibrium state was obtained and analyzed. We obtained an important threshold parameter called the effective reproduction number R_{eff} using the next generation method. If $R_{eff} < 1$, it implies that Lassa Fever Virus can be controlled and eradicated within the population in a finite time and if the $R_{eff} > 1$, the disease invade and become endemic in the population. A numerical simulation on the key parameters of the model was carried out by examining the impact of isolation rate and treatment rate on the infected human's population and the results shows that, isolation and treatment are the surest way to eradicate Lassa fever.

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