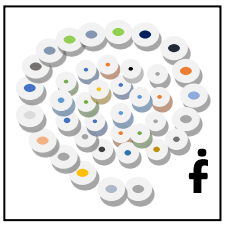

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The transmission dynamics of Lassa fever disease incorporating control measures

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Abstract

In this work, a mathematical model to study the transmission dynamics of Lassa fever with control measures like public health education campaign, isolation and treatment is formulated. The basic properties of the model are examined and the effective reproduction number R_c is computed. Steady states of the model were analyzed for stability, it was found that whenever R_c is < 1, the disease dies out while when R_c is > 1, the disease persists in the population. We found from sensitivity analysis that the most sensitive parameter is the natural death rate of rodents μ_r with a sensitivity index of -2 while the least sensitive parameter is Lassa fever induced death rate with a sensitivity index of -0.0007. We carried out numerical simulation and results sows that isolation, treatment and public health education campaign can reduce the dynamical spread of the disease in the population.

Keywords: Lassa fever; mathematical model; basic reproduction number; disease free equilibrium; stability; sensitivity analysis; endemic equilibrium; bifurcation; multimammate rat; zoonotic disease.

1. Introduction

Lassa fever is an acute viral illness that occurs in West Africa [5]. The illness was discovered in 1969 when two missionary nurses died in Nigeria. The virus is named after a town Lassa in Borno state of Nigeria where the first cases occurred [5, 16]. Lassa fever is a zoonotic disease, meaning that humans become infected from contact with infected animals [20]. The rodent reservoir, or host of Lassa virus is a rodent of genus *Mastomys natalensis*, commonly known as "*multimammate rat*". *Mastomys* rats infected with Lassa virus do not become ill, but can shed the virus in their urine and faeces [20]. Humans become infected with Lassa virus from exposure to urine or faeces of *infected Mastomys rats* [20]. Several cases of disease outbreak have been recorded in 19 states of Nigeria since it was first reported in 1969. The most affected states are Bauchi, Edo, Oyo and Taraba which account for 54% of the confirmed cases [7, 19]. The worst outbreak was recorded in 2012 where 1700 cases including 112 deaths were reported [7, 19].

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A review of earlier works on Lassa fever provides the perspective of this work. In [14], Ogabi *et al* formulated a basic SIR model for the control of Lassa fever in Northern part of Edo State of Nigeria. The disease control was studied based on the basic reproductive number. It was clearly shown in his work that to control the spread of Lassa fever in the endemic areas, the basic reproduction number R_0 must be brought below 1. If it is more than 1, the disease will not die out from the area.

In [12], Mohammed *et al* in their work titled 'sensitivity analysis in a Lassa fever deterministic model' formulated a model with five mutually exclusive compartments related to Lassa fever transmission. The result of their sensitivity analysis showed that the most sensitive parameter is the human immigration, followed by human recovery rate, then person to person contact. This suggests that control strategies should target human immigration, effective drugs for treatment and education to reduced person to person contact.

In [15],Onuorah *et al* developed a Lassa fever model using the sex structure approach. Key to his analysis was the basic reproductive number R_0 . Sensitivity indices of R_0 around the baseline parameter value were computed, which showed that the most sensitive parameter to R_0 is human birth rate, followed by condom efficacy and compliance. In [8], James *et al* proposed a mathematical model for the transmission dynamics of Lassa fever incorporating treatment. The equilibrium states were obtained and analyzed for stability. It was discovered that the zero-equilibrium state is stable when the birth rate of the human population is less than the death rate and same when the birth rate of the *mastomys natalensis* (reservoir) is less than the total death rates.

In [2], Adewale *et al* formulated a model with six compartments to gain insight into the effect of isolation of infected individuals and treatment of infected individuals in the dynamical spread of Lassa fever due to effective contact of human and infected rats. The result shows that the disease dies out whenever the threshold $R_0 < 1$ but spreads when it exceeds unity i.e., $R_0 > 1$.

It is worthy of note that none of the models reviewed incorporated health education campaign as a control strategy, rather, most of the authors advised that health education campaign should be intensified in the affected areas in order to curb the endemic nature of the disease. Furthermore, most of the authors considered treatment of infected individuals without isolation. Our model therefore examines the effect of public health education campaign, isolation and treatment on the spread of Lassa fever disease (LFD) all incorporated at a time. Hence our model is an advanced one that seeks to provide a better study and understanding of the LFD transmission dynamics in a given population.

2. Model formulation

A diagrammatic representation of the model formulation is shown in Figure 1. The total human population $N_h(t)$ is sub-divided into sub-classes as follows: Susceptible humans $S_h(t)$, Exposed humans $E_h(t)$ infectious humans $I_h(t)$, Isolated humans $J_h(t)$, Recovered humans $R_h(t)$, so that $N_h(t) = S_h\ (t) + E_h(t) + I_h(t) + J_h(t) + R_h(t)$, Also, the total population of rats $N_r(t)$ is subdivided into Susceptible $S_r(t)$, and Infected $I_r(t)$, so that; $N_r(t) = S_r\ (t) + I_r(t)$.

The susceptible human population $S_h(t)$, increases by recruitment of individuals into the population by birth or immigration at the level Λ_h, the group also increases as a result of loss of immunity by recovered individuals at a rate Φ. The population decreases by infection following effective contact with infectious rodents and infectious humans at the level β_1 and β_2 respectively. The population also decreases as a result of human natural death at a rate μ_h.

The population of the exposed individuals $E_h(t)$ consists of newly infected individuals following contact with infectious rodents and infectious humans at the rate β_1 and β_2 respectively. The population declines as a result of progression to infectious class at a rate α and human natural death at a rate μ_h.

The population of infectious individuals $I_h(t)$ increases as a result of progression from the exposed class at the rate α. The class decreases as a result of isolation at a rate τ_1, treatment at a rate τ_2, natural death at a rate μ_h and disease induced death at a rate δ. The population of isolated individuals $J_h(t)$ increases as a result of isolation of the infectious individuals at a rate τ_1 .The population decreases due to natural death at the rate μ_h, death due to disease at the rate δ and treatment at the rate τ_3.

We introduce the Recovered compartment $R_h(t)$. The population of the individuals in this group increases as a result of treatment of infectious humans at a rate τ_2 and isolated humans at a rate τ_3. The population decreases as a result of natural death at a rate μ_h and loss of immunity at a rate Φ.

Susceptible rodents (S_r) are generated at a constant recruitment level Λ_r and acquire infection following effective contact with infected rodent at a rate β_1. The rodents suffer death at the rate μ_r. The infected class of the rodents (I_r) has newly infected rodents and reduces by natural death at the rate μ_r.

Variable	Description
$S_h(t)$	Susceptible humans at time t
$E_h(t)$	Exposed humans at time t
$I_h(t)$	Infectious humans at time t
$J_h(t)$	Isolated humans at time t
$R_h(t)$	Recovered humans at time t
$S_r(t)$	Susceptible rats at time t
$I_r(t)$	Infected rats at time t

Table 1: Variables of the model

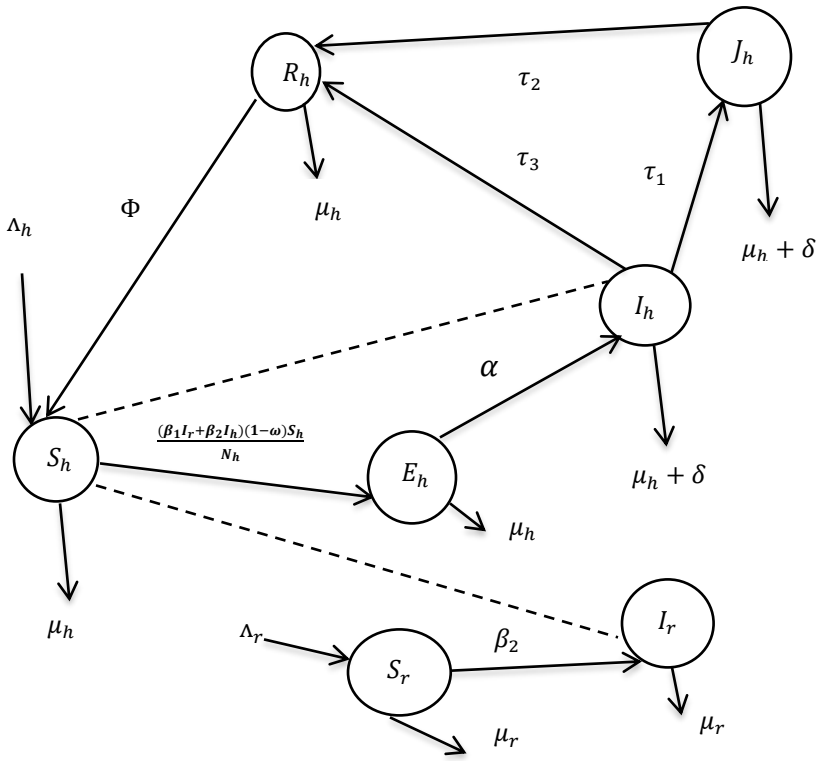

Figure 1: Schematic diagram for the model

2.1. Model equations

$$
\begin{aligned}
\frac{dS_h}{dt} &= \Lambda_h + \Phi R_h - \frac{(\beta_1 I_r + \beta_2 I_h)(1-\omega)S_h}{N_h} - \mu_h S_h \\
\frac{dE_h}{dt} &= \frac{(\beta_1 I_r + \beta_2 I_h)(1-\omega)S_h}{N_h} - (\alpha + \mu_h)E_h \\
\frac{dI_h}{dt} &= \alpha E_h - (\tau_1 + \tau_2 + \mu_h + \delta)I_h \\
\frac{dJ_h}{dt} &= \tau_1 I_h - (\tau_3 + \mu_h + \delta)J_h \\
\frac{dR_h}{dt} &= \tau_3 J_h + \tau_2 I_h - (\mu_h + \Phi)R_h \\
\frac{dS_r}{dt} &= \Lambda_r - \beta_1 S_r I_r - \mu_r S_r \\
\frac{dI_r}{dt} &= \beta_1 S_r I_r - \mu_r I_r,
\end{aligned} \tag{1}
$$

with initial condition

$S_h(0) = S_{h0}$, $E_h(0) = E_{h0}$, $I_h(0) = I_{h0}$, $J_h(0) = J_{h0}$ $R_h(0) = R_{h0}$, $S_r(0) = S_{r0}$, $I_r(0) = I_{r0}$,

$$N_h(t) = S_h(t) + E_h(t) + I_h(t) + J_h(t) + R_h(t), \quad (2)$$

where $N_h(t)$ denotes the total human population at a given time:

$$\frac{dN_h(t)}{dt} = \frac{dS_h}{dt} + \frac{dE_h}{dt} + \frac{dI_h}{dt} + \frac{dJ_h}{dt} + \frac{dR_h}{dt},$$
$$\frac{dN_h(t)}{dt} = \Lambda_h - \mu_h N_h(t) - (I_h + J_h)\delta.$$

$$N_r(t) = S_r(t) + I_r(t). \quad (3)$$

N_r(t) denotes the total population of rats at a given time:

$$\frac{dN_r(t)}{dt} = \frac{dS_r}{dt} + \frac{dI_r}{dt},$$
$$\frac{dN_r(t)}{dt} = \Lambda_r - \mu_r N_r(t).$$

3. Basic properties of the model

3.1. Positivity of solutions

Let the initial data be $\{S_h(0), E_h(0), I_h(0), J_h(0), R_h(0), S_r(0), I_r(0) \geq 0\} \in R_+^7$. Then the solution set $\{S_h(t), E_h(t), I_h(t), J_h(t), R_h(t), S_r(t), I_r(t)\}$ of the system (1.0) to (1.6) is positive for all t >0.

3.2. Feasibility of the model

The closed set $\Omega = \left\{(S_h, E_h, I_h, J_h, R_h, S_r, I_r) \in R_+^7 : N_h \leq \frac{\Lambda_h}{\mu_h}, N_r \leq \frac{\Lambda_r}{\mu_r}\right\}$ is positively Invariant and attracting with respect to the basic model (1).

4. The disease-free equilibrium (DFE)

The disease-free equilibrium (DFE) of a Lassa fever model is the steady state where there is no Lassa fever infection [3]. We denote the DFE by $E_0 = \{S_{h0}, E_{h0}, I_{h0}, J_{h0}, R_{h0}, S_{r0}, I_{r0}\}$. At the disease-free equilibrium,

$$\frac{dS_h}{dt} = \frac{dE_h}{dt} = \frac{dI_h}{dt} = \frac{dJ_h}{dt} = \frac{dT_h}{dt} = \frac{dS_r}{dt} = \frac{dI_r}{dt} = 0.$$

Thus, $E_0 = \{S_{h0}, E_{h0}, I_{h0}, J_{h0}, R_{h0}, S_{r0}, I_{r0}\} = \left\{\frac{\Lambda_h}{\mu_h}, 0,0,0,0, \frac{\Lambda_r}{\mu_r}, 0\right\}$ represents the state of the system (1) in which there is no infection.

5. The basic reproduction number

The basic reproduction number denoted by R_0 is the expected number of secondary Lassa fever infections produced in a completely susceptible population by a typical infective individual. It is one of the most useful threshold parameters in mathematical epidemiology [3].

If $R_0 < 1$, this implies that on average an infected individual produces less than one new infection during the infectious period and the disease dies out. Conversely, if $R_0 > 1$, then each infectious individual produces on average more than one new infection and disease spreads in the population [3]. For a single infected compartment, R_0 is simply the product of the infection rate and the mean duration of the infection. But for complicated models, this simple definition of R_0 is insufficient.

We therefore compute the basic reproduction number R_0 using the next generation method as follows [11]. For the model equations (1), the effective reproduction number (basic reproduction number with controls) is the spectra radius of the next generation matrix i.e., $R_C = \rho(FV^{-1})$.

Our model has four Infective compartments namely the Exposed humans $E_h(t)$, infected humans $I_h(t)$, isolated humans $J_h(t)$ and infected rats $I_r(t)$. It follows that the associated matrices F_i and V_i for new infection in the infected compartments and the remaining transfer terms are given respectively by

$$F_i = \begin{pmatrix} \frac{(\beta_1 I_r + \beta_2 I_h)(1-\omega)S_h}{N_h} \\ 0 \\ 0 \\ \beta_1 S_r I_r \end{pmatrix},$$

$$V_i = \begin{pmatrix} (\alpha + \mu_h)E_h \\ -\alpha E_h + (\tau_1 + \tau_2 + \mu_h + \delta)I_h \\ -\tau_1 I_h + (\tau_3 + \mu_h + \delta)J_h \\ \mu_r I_r \end{pmatrix}.$$

Next, we evaluate F and V which are the Jacobean of F_i and V_i respectively at E_0 such that F is non-negative and V is a non-singular matrix.

Let $K_1 = (1-\omega)$ and $K_2 = \frac{\Lambda_r}{\mu_r}$, then,

$$F = \begin{pmatrix} 0 & \beta_2 K_1 & 0 & \beta_1 K_1 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \beta_1 K_2 \end{pmatrix}.$$

Let $a = (\alpha + \mu_h)$, $b = (\tau_1 + \tau_2 + \mu_h + \delta)$, $c = (\tau_3 + \mu_h + \delta)$, $d = \mu_r$, $e = \alpha$, $f = \tau_1$, then

$$\mathrm{V} = \begin{pmatrix} a & 0 & 0 & 0 \\ -e & b & 0 & 0 \\ 0 & -f & c & 0 \\ 0 & 0 & 0 & d \end{pmatrix},$$

$$FV^{-1} = \begin{pmatrix} \frac{\beta_2 K_1 e}{ab} & \frac{\beta_2 K_1}{b} & 0 & \frac{\beta_1 K_1}{d} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & & 0 \\ 0 & 0 & 0 & \frac{\beta_1 K_2}{d} \end{pmatrix}.$$

We next compute $|FV^{-1} - \lambda I| = 0$ as follows

$$\begin{vmatrix} \frac{\beta_2 K_1 e}{ab} - \lambda & \frac{\beta_2 K_1}{b} & 0 & \frac{\beta_1 K_1}{d} \\ 0 & 0 - \lambda & 0 - \lambda & 0 \\ 0 & 0 & & 0 \\ 0 & 0 & 0 & \frac{\beta_1 K_2}{d} - \lambda \end{vmatrix} = 0 \tag{4}$$

From (4), we obtain the following characteristic equation

$$(\frac{\beta_2 K_1 e}{ab} - \lambda)(0 - \lambda)(0 - \lambda)\Big(\frac{\beta_1 K_2}{d} - \lambda\Big) = 0.$$

The Eigen values of (4) are $\lambda_1 = \frac{\beta_2 K_1 e}{ab}$, $\lambda_2 = \lambda_3 = 0$, $\lambda_4 = \frac{\beta_1 K_2}{d}$.

Let $R_h = \lambda_1 = \frac{\beta_2 K_1 e}{ab}$ and $R_r = \lambda_4 = \frac{\beta_1 K_2}{d}$

Then $R_h = \frac{\alpha\beta_2(1-\omega)}{(\alpha+\mu_h)(\tau_1+\tau_2+\mu_h+\delta)}$, (5)

and $R_r = \frac{\beta_1 \Lambda_r}{\mu_r^2}$. (6)

Thus, the effective reproduction number (basic reproduction number with controls) of our model is $R_c = Max\,(R_h, R_r)$.

When there are no controls $i.e.\ \omega = \tau_1 = \tau_2 = 0$, the basic reproduction number is

$R_h = \frac{\alpha\beta_2}{(\alpha+\mu_h)(\mu_h+\delta)}$. (7)

6. Stability of the disease-free equilibrium

Theorem 6.1: If the effective reproduction number $R_c < 1$,the model (1) is locally asymptotically stable at the disease-free equilibrium
$E_0 = \left\{\frac{\Lambda_h}{\mu_h}, 0,0,0,0,\frac{\Lambda_r}{\mu_r}, 0\right\}$ while E_0 is unstable otherwise.

Proof: To prove, we evaluate the Jacobian of the system (1) at the disease-free equilibrium and solve $|J(E_0) - \lambda I| = 0$ as follows:

$$\begin{vmatrix} -\mu_h - \lambda & 0 & -\beta_2(1-\omega) & 0 & \Phi & 0 & -\beta_1(1-\omega) \\ 0 & -(\alpha+\mu_h)-\lambda & \beta_2(1-\omega) & 0 & 0 & 0 & \beta_1(1-\omega) \\ 0 & \alpha & -(\tau_1+\tau_2+\mu_h+\delta)-\lambda & 0 & 0 & 0 & 0 \\ 0 & 0 & \tau_1 & -(\tau_3+\mu_h+\delta)-\lambda & 0 & 0 & 0 \\ 0 & 0 & \tau_2 & \tau_3 & -(\Phi+\mu_h)-\lambda & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & -\mu_r-\lambda & \frac{-\beta_1\Lambda_r}{\mu_r} \\ 0 & 0 & 0 & 0 & 0 & 0 & \frac{\beta_1\Lambda_r}{\mu_r}-\mu_r-\lambda \end{vmatrix} = 0 \quad (8)$$

Clearly, four eigenvalues of (8) are: $\lambda_1 = -\mu_h, \lambda_5 = -(\Phi + \mu_h)$, $\lambda_6 = -\mu_r$, and $\lambda_7 = \mu_r(R_r - 1)$. Clearly $\lambda_1 < 0, \lambda_5 < 0,\ \lambda_6 < 0\ and\ \ \lambda_7 < 0\ \ if\ \ R_r < 1$.

The remaining matrix is given by

$$A = \begin{vmatrix} -a-\lambda & \beta_2 K_1 & 0 \\ e & -b-\lambda & 0 \\ 0 & f & -c-\lambda \end{vmatrix} = 0. \quad (9)$$

The characteristic polynomial is of (9) $A_0\lambda^3 + A_1\lambda^2 + A_2\lambda + A_3 = 0,$ where, $A_0 = 1,\ A_1 = a + b + c, A_2 = ab + ac + bc - e\beta_2 K_1 = ac + bc + ab(1 - R_h),$ and $A_3 = c(ab - e\beta_2 K_1) = abc(1 - R_h)$.

The Routh Hurwitz criterion as used in [1] and [18] will be employed to determine the nature of the roots, which states that all the roots of the polynomial will have negative real parts if and only if

$A_1 > 0,\ A_3 > 0$ and $A_1 A_2 > A_3$.

Clearly that $A_1 > 0,\ \ A_3 > 0$ if $R_h < 1$ and $A_1 A_2 > A_3$ if $R_h < 1$. This completes the proof.

Theorem 6.2: The disease-free equilibrium is globally asymptotically stable if the effective reproduction number $R_c < 1$.

Proof: A comparison theorem as proposed by [10] and used in the works of [13] and [2] shall be used to prove the global stability of the disease-free equilibrium.
The rate of change of variables representing the infected components of the model equations (1) can be re-written as;

$$X' = (F - V)X - J_i X \tag{10}$$

where,

$$X = \begin{pmatrix} E_h \\ I_h \\ J_h \\ I_r \end{pmatrix} \quad , \qquad X' = \begin{pmatrix} E_h' \\ I_h' \\ J_h' \\ I_r' \end{pmatrix},$$

$$\mathrm{F} = \begin{pmatrix} 0 & \beta_2(1-\omega) & 0 & \beta_1(1-\omega) \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \frac{\beta_1 \Lambda_r}{\mu_r} \end{pmatrix}$$

$$V = \begin{pmatrix} (\alpha + \mu_h) & 0 & 0 & 0 \\ -\alpha & (\tau_1 + \tau_2 + \mu_h + \delta) & 0 & 0 \\ 0 & -\tau_1 & (\tau_3 + \mu_h + \delta) & 0 \\ 0 & 0 & 0 & \mu_r \end{pmatrix}$$

$$J_i = \begin{pmatrix} 0 & \frac{\beta_2(1-\omega)S_h}{N_h} & 0 & \frac{\beta_1(1-\omega)S_h}{N_h} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \beta_1 S_r \end{pmatrix} = \left(1 - \frac{S_h}{N_h}\right) \begin{pmatrix} 0 & \beta_2(1-\omega) & 0 & \beta_2(1-\omega) \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & Q\beta_1 \end{pmatrix}, \text{ where}$$

$$Q = \frac{\left(1 - \frac{S_r}{N_r}\right)}{\left(1 - \frac{S_h}{N_h}\right)}.$$

J_i is a non-negative matrix since $S_h(t) \leq N_h(t) \leq \frac{\Lambda_h}{\mu_h}$, $S_r(t) \leq N_r(t) \leq \frac{\Lambda_r}{\mu_r}$ in the invariant set, it follows that

$$X' \leq (F - V)X \tag{11}$$

$$F - V = \begin{pmatrix} -(\alpha + \mu_h) & \beta_2(1-\omega) & 0 & \beta_1(1-\omega) \\ \alpha & -(\tau_1 + \tau_2 + \mu_h + \delta) & 0 & 0 \\ 0 & \tau_1 & -(\tau_3 + \mu_h + \delta) & 0 \\ 0 & 0 & 0 & \frac{\beta_1 \wedge_r}{\mu_r} - \mu_r \end{pmatrix}.$$

All the eigen values of the matrix $(F - V)$ have negative real part whenever $R_c < 1$. See proof of local stability. It follows that the linearized differential in equality (11) is stable whenever $R_c < 1$. Consequently, by comparison theorem we have that $(E_h, I_h, J_h, I_r) \rightarrow$ (0,0,0,0) as t$\rightarrow \infty$. Substituting, $E_h = I_h = J_h = I_r = 0$ into (2) and (3) we have that $N_h(0) \rightarrow S_{h0}$ as t$\rightarrow \infty$. Similarly, $N_r(0) \rightarrow S_{r0}$ as t$\rightarrow \infty$. Hence, we have a positive invariant region. It follows that disease free equilibrium is globally asymptotically stable whenever $R_c < 1$.

7. Sensitivity analysis

Sensitivity analysis is used to determine how "sensitive" a model is to changes in the value of the parameters of the model and to changes in the structure of the model. If the result is negative, then the relationship between the parameters and R_c is inversely proportional. In this case, we will take the modulus of the sensitivity index so that we can deduce the size of the effect of changing that parameter. On the other hand, a positive sensitivity index means R_c varies directly with the parameter [17]. Thus, we use it to discover parameters that have a high impact on R_c and should be targeted by intervention strategies [12, 17]. The sensitivity indices of the respective parameters are derived using the normalized sensitivity index $S_\tau^{R_c}$ defined as $S_\tau^{R_c} = \frac{\partial R_c}{\partial \tau} . \frac{\tau}{R_c}$ [9].

Parameter	Description	Value	Source	Sensitivity index
μ_r	Recruitment rate of rodents	0.0038	Mohammed (2015)	-2
$\wedge_r$	Recruitment rate of humans	0.0250	Mohammed (2015)	+1
β_1	Contact rate of humans	0.8000	Mohammed (2015)	+1
β_2	Contact rate of rodents	0.2000	Adewale (2016)	+1
ω	Rate of public health education	0.5000	Assumed	-1
μ_h	Natural death rate of humans	0.0200	CIA (2015)	-0.9172
α	Rate of progression from exposed to infectious state	0.3000	Assumed	0.8696
τ_1	Isolation rate	0.2000	Adewale (2016)	-0.4759
τ_2	Treatment rate	0.1000	Adewale (2016)	-0.4759
δ	Lassa fever induced death rate	0.0003	Mohammed (2015)	-0.0007

Table 2: Parameters, description, values, sources and sensitivity indices

8. The endemic equilibrium

In the presence of Lassa fever infection, the model equations (1) have a non-trivial equilibrium called the endemic equilibrium $E^*(S_h^*, E_h^*, I_h^*, J_h^*, R_h^*, S_r^*, I_r^*)$ where:

$$S_h^* = \frac{\Lambda_h}{\left[1-\frac{\Phi\alpha\tau_2[(\tau_3+\mu_h+\delta)+\tau_1](1-\omega)\lambda^*}{(\alpha+\mu_h)(\tau_1+\tau_2+\mu_h+\delta)(\tau_3+\mu_h+\delta)(\Phi+\mu_h)}\right]+\mu_h} \quad ,$$

$$E_h^* = \frac{(1-\omega)\Lambda_h\lambda^*}{\left\{\left[1-\frac{\Phi\alpha\tau_2[(\tau_3+\mu_h+\delta)+\tau_1](1-\omega)\lambda^*}{(\alpha+\mu_h)(\tau_1+\tau_2+\mu_h+\delta)(\tau_3+\mu_h+\delta)(\Phi+\mu_h)}\right]+\mu_h\right\}(\alpha+\mu_h)} ,$$

$$I_h^* = \frac{\alpha(1-\omega)\Lambda_h\lambda^*}{\left\{\left[1-\frac{\Phi\alpha\tau_2[(\tau_3+\mu_h+\delta)+\tau_1](1-\omega)\lambda^*}{(\alpha+\mu_h)(\tau_1+\tau_2+\mu_h+\delta)(\tau_3+\mu_h+\delta)(\Phi+\mu_h)}\right]+\mu_h\right\}(\alpha+\mu_h)(\tau_1+\tau_2+\mu_h+\delta)} ,$$

$$J_h^* = \frac{\tau_1\alpha(1-\omega)\Lambda_h\lambda^*}{\left\{\left[1-\frac{\Phi\alpha\tau_2[(\tau_3+\mu_h+\delta)+\tau_1](1-\omega)\lambda^*}{(\alpha+\mu_h)(\tau_1+\tau_2+\mu_h+\delta)(\tau_3+\mu_h+\delta)(\Phi+\mu_h)}\right]+\mu_h\right\}(\alpha+\mu_h)(\tau_1+\tau_2+\mu_h+\delta)(\tau_3+\mu_h+\delta)} \quad ,$$

$$S_r^* = \frac{\mu_r}{\beta_1}, \quad I_r^* = \frac{\mu_r}{\beta_1}(R_r - 1) ,$$

$$R_h^* = \frac{\Phi\tau_2\alpha[(\tau_3+\mu_h+\delta)+\tau_1]\Lambda_h\lambda^*}{\left\{\left[1-\frac{\Phi\alpha\tau_2[(\tau_3+\mu_h+\delta)+\tau_1](1-\omega)\lambda^*}{(\alpha+\mu_h)(\tau_1+\tau_2+\mu_h+\delta)(\tau_3+\mu_h+\delta)(\Phi+\mu_h)}\right]+\mu_h\right\}(\alpha+\mu_h)(\tau_1+\tau_2+\mu_h+\delta)(\tau_3+\mu_h+\delta)(\Phi+\mu_h)},$$

$$\lambda^* = \frac{(\beta_1 I_r+\beta_2 I_h)}{N_h}.$$

The endemic equilibrium satisfies the equation

$f(\lambda^*) = A\lambda^{*2} + B\lambda^* + C = 0$, $\lambda^* = \frac{-B\pm\sqrt{B^2-4AC}}{2A}$, where

$A = \beta_1[\mu_r\Lambda_h(\Phi+\mu_h)(\tau_3+\mu_h+\delta)(\tau_1+\tau_2+\mu_h+\delta) + \mu_r\Lambda_h\alpha(\Phi+\mu_h)(\tau_3+\mu_h+\delta) + \Lambda_h\tau_1\alpha(\Phi+\mu_h) + \mu_r\Lambda_h\tau_1\tau_2\alpha + \beta_1\Lambda_r\Phi\tau_1\tau_2\alpha]$

$$B = \Lambda_h(\alpha+\mu_h)(\tau_1+\tau_2+\mu_h+\delta)(\tau_3+\mu_h+\delta)(\Phi+\mu_h)\left[(1-R_h)+(1-R_r)\frac{\beta_1(1-\omega)}{\Lambda_h}\frac{\mu_r}{\beta_1}\left\{\frac{\tau_2\Phi[(\tau_3+\mu_h+\delta)+\tau_1]}{(\alpha+\mu_h)(\tau_1+\tau_2+\mu_h+\delta)(\tau_3+\mu_h+\delta)(\Phi+\mu_h)}-1\right\}\right],$$

$$C = -\left[\frac{\mu_r}{\beta_1}(R_r-1)\beta_1(\Phi+\mu_h)(\tau_3+\mu_h+\delta)(\tau_1+\tau_2+\mu_h+\delta)(\Phi+\mu_h)\right].$$

In the case of backward bifurcation, multiple endemic equilibrium points must exist. Since all parameter values are positive and between 0 and 1, and A is positive. There are three cases we have to consider of $f(\lambda^*) = 0$ depending on the sign of B and C.

Case 1: $C < 0 \Rightarrow R_r > 1,$ there exists a unique positive root.
Case 2: $B < 0$, and $C = 0 \Leftrightarrow B^2 - 4AC = 0$, there exists a unique positive root.
Case 3: $B < 0, C > 0,\ B^2 - 4AC > 0$, there exist two positive roots.

From case 1 to case 3, we establish the following theorem.

Theorem 8.1: The Lassa fever model has:
precisely one endemic equilibrium if $C < 0$ and $R_r > 1$ and no backward bifurcation;
precisely one endemic equilibrium if $B < 0,\ C = 0$ and $B^2 - 4AC = 0$ and no backward bifurcation;
two endemic equilibria if $B < 0,\ C > 0$ and $B^2 - 4AC > 0$ and it is possible for backward bifurcation;
otherwise, there is none.

8.1. Local stability of the endemic equilibrium

We will investigate the local stability of the endemic equilibrium using center manifold theorem. We make the following change of variables to apply the theorem:

$$S_h = x_1, E_h = x_2, I_h = x_3, J_h = x_4, R_h = x_5, S_r = x_6, I_r = x_7.$$

We now use the vector $X = (x_1, x_2, x_3, x_4, x_5, x_6, x_7)^T$, then, the model equations (1) can be written in the form $\frac{dx}{dt} = F = (f_1, f_2, f_3, f_4, f_5, f_6, f_7)^T$ giving

$$\begin{aligned}
\frac{dx_1}{dt} &= \Lambda_h + \Phi x_5 - \frac{(\beta_1 x_7 + \beta_2 x_3)(1-\omega)x_1}{N_h} - \mu_h x_1 \\
\frac{dx_2}{dt} &= \frac{(\beta_1 x_7 + \beta_2 x_3)(1-\omega)x_1}{N_h} - (\alpha + \mu_h)x_2 \\
\frac{dx_3}{dt} &= \alpha x_2 - (\tau_1 + \tau_2 + \mu_h + \delta +)x_3 \\
\frac{dx_4}{dt} &= \tau_1 x_3 - (\tau_3 + \mu_h + \delta)x_4 \\
\frac{dx_5}{dt} &= \tau_2 x_3 + \tau_3 x_4 - (\Phi + \mu_h)x_5 \\
\frac{dx_6}{dt} &= \Lambda_r - \beta_1 x_6 x_7 - \mu_r x_6 \\
\frac{dx_7}{dt} &= \beta_1 x_6 x_7 - \mu_r x_7
\end{aligned} \tag{12}$$

Taking $\beta_2 = \beta^*$ as our bifurcation constant and solving for β^* when $R_h = 1$ gives

$$\beta^* = \frac{(\alpha + \mu_h)(\tau_1 + \tau_2 + \mu_h + \delta)}{\alpha(1-\omega)}.$$

The Jacobian of the system (12) when $\beta_2 = \beta^*$ and $R_h = 1$ at the DFE is given by

$$J(E_0) = \begin{vmatrix} -\mu_h & 0 & -\beta_2(1-\omega) & 0 & \Phi & 0 & -\beta_1(1-\omega) \\ 0 & -(\alpha+\mu_h) & \beta_2(1-\omega) & 0 & 0 & 0 & \beta_1(1-\omega) \\ 0 & \alpha & -(\tau_1+\tau_2+\mu_h+\delta) & 0 & 0 & 0 & 0 \\ 0 & 0 & \tau_1 & -(\tau_3+\mu_h+\delta) & 0 & 0 & 0 \\ 0 & 0 & \tau_2 & \tau_3 & -(\Phi+\mu_h) & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & -\mu_r & \frac{-\beta_1\Lambda_r}{\mu_r} \\ 0 & 0 & 0 & 0 & 0 & 0 & \frac{\beta_1\Lambda_r}{\mu_r} - \mu_r \end{vmatrix} \quad (13)$$

Let $V = (v_1, v_2, v_3, v_4, v_5, v_6, v_7)$ be the left and eigen vector of (13), then,

$$v_1 = 0, v_2 = v_2 > 0(free), v_3 = \left[\frac{(\alpha+\mu_h)-\beta^*(1-\omega)}{\alpha-(\tau_1+\tau_2+\mu_h+\delta)}\right] v_2 \, , v_4 = 0 \, , v_5 = 0,$$
$$v_6 = 0 \, , \quad v_7 = \frac{\beta_1(1-\omega)v_2}{\left(\mu_r - \frac{\beta_1\Lambda_r}{\mu_r}\right)}.$$

Also, if $W = (w_1, w_2, w_3, w_4, w_5, w_6, w_7)^T$ is the right eigen vector of (13), then,

$$w_1 = \left[\frac{\Phi\tau_1\tau_2}{\mu_h(\tau_3+\mu_h+\delta)(\Phi+\mu_h)} - \frac{\beta^*(1-\omega)}{\mu_h}\right] w_3 \, , \; w_2 = \left[\frac{\beta^*(1-\omega)}{\mu_h} - \frac{(\tau_1+\tau_2+\mu_h+\delta)}{\mu_h}\right] w_3,$$
$$w_3 = w_3 > 0(free) \, , \; w_4 = \frac{\tau_1 w_3}{(\tau_2+\mu_h+\delta)} \, , w_5 = \frac{[\tau_3(\tau_3+\mu_h+\delta)+\tau_1\tau_3]w_3}{(\tau_3+\mu_h+\delta)(\Phi+\mu_h)} \, , w_6 = 0 \, , w_7 = 0.$$

After computing the right and left eigenvectors we have the theorem in [4] to establish the conditions for the existence of backward and forward bifurcation by determining the sign of a and b as indicated in the theorem which is restated as Theorem 8.2 in this work.

Theorem 8.2: Consider the following general system of ordinary differential equations with a parameter β^*.

$$\frac{dx}{dt} = f(x, \beta^*), f: R^n \times R^n \to R^n \; and \; f \epsilon C^2(R^n \times R^n), \quad (14)$$

where 0 is an equilibrium point of the system, that is $f(0, \beta^*) \equiv 0 \; \forall \; \beta^*$ and $A = D_x f(0,0) = \left[\frac{\partial f_i}{\partial x_i}(0,0)\right]$ is linearization matrix of the system evaluated around 0 and with β^* evaluated at 0.

Zero is a simple eigen value of A and other eigen values of A have negative real parts.
Matrix A has a right eigen vector W and a left eigen vector V corresponding to the zero eigen value.
Let f_k be the kth component of f and $a = \sum_{k,i,j=1}^{n} v_k w_i w_j \frac{\partial^2 f_k}{\partial x_i \partial x_j}(0,0)$,

$b = \sum_{k,i=1}^{n} v_k w_i \frac{\partial^2 f_k}{\partial x_i \beta^*}(0,0)$.

The local dynamics of (14) around 0 are completely governed by the signs of a and b.
a > 0, b > 0. When $\beta^* < 0$ with $|\beta^*| << 1$, 0 is locally asymptotically stable, and there exists a positive unstable equilibrium; when $0 < \beta^* << 1$, 0 is unstable and there exists a negative and locally asymptotically stable equilibrium.
a < 0, b < 0. When $\beta^* < 0$ with $|\beta^*| << 1$, 0 is unstable; when $0 < \beta^* << 1$, 0 is locally asymptotically stable, and there exists a positive unstable equilibrium.

(iii) a > 0, b < 0. When $\beta^* < 0$ with $|\beta^*| << 1$, 0 is unstable, and there exists a locally asymptotically stable negative equilibrium; when $0 < \beta^* << 1$, 0 is stable, and a positive unstable equilibrium appears.

(iv) a < 0, b > 0. When β^* changes from negative to positive, 0 changes its stability from stable to unstable. The corresponding negative unstable equilibrium becomes positive and locally asymptotically stable.
Particularly if a>0, b>0, then a backward bifurcation occurs while when a<0, b>0, there is forward bifurcation.

Computation of a and b

Since $v_1 = v_6 = 0$ for $k = 1$ and 6, we consider only $k = 2,3,4,5,7$. The only non-zero second order partial derivatives are: $\frac{\partial^2 f_2(0,0)}{\partial x_1 \partial x_3} = \frac{\beta^*(1-\omega)}{N_h}$, $\frac{\partial^2 f_2(0,0)}{\partial x_1 \partial x_7} = \frac{\beta_1(1-\omega)}{N_h}$

$a = \left[\frac{\Phi\tau_1\tau_3}{\mu_h(\tau_3+\mu_h+\delta)(\Phi+\mu_h)} - \frac{\beta^*(1-\omega)}{N_h\mu_h}\right]\frac{\beta^*(1-\omega)}{N_h} w_3^2 v_2$

Let $p = \frac{\Phi\tau_1\tau_3}{\mu_h(\tau_3+\mu_h+\delta)(\Phi+\mu_h)}$ and $q = \frac{\beta^*(1-\omega)}{N_h\mu_h}$,

$$a = (p-q)\frac{\beta^*(1-\omega)}{N_h} w_3^2 v_2 \ . \tag{15}$$

Similarly, the only non –zero second order partial derivative when calculating b is
$\frac{\partial^2 f_2(0,0)}{\partial x_3 \partial \beta^*} = \frac{(1-\omega)}{N_h}$, $b = v_2 w_3 \frac{\partial^2 f_2(0,0)}{\partial x_3 \partial \beta^*}$, $b = v_2 w_3 \frac{(1-\omega)}{N_h} > 0$.

The sign of *a* in (15) depends on the sign of (p-q), if $p < q$, then $a < 0$, but if $p > q$, then $a > 0$. Thus we have established the following theorem.

Theorem 8.3: (i) If $p < q$,when β^* changes from negative to positive, the disease-free equilibrium changes its stability from stable to unstable. Correspondently, the negative unstable endemic equilibrium becomes positive and locally asymptotically stable when $R_c > 1$.
(ii) If $p > q$, when $\beta^* < 0$ with $|\beta^*| \ll 1$, the disease-free equilibrium is locally asymptotically stable and there exists a positive unstable endemic equilibrium; when $0 < \beta^* \ll 1$, the disease-free equilibrium is unstable and there exists a negative and locally asymptotically stable endemic equilibrium.

9. Numerical Simulations

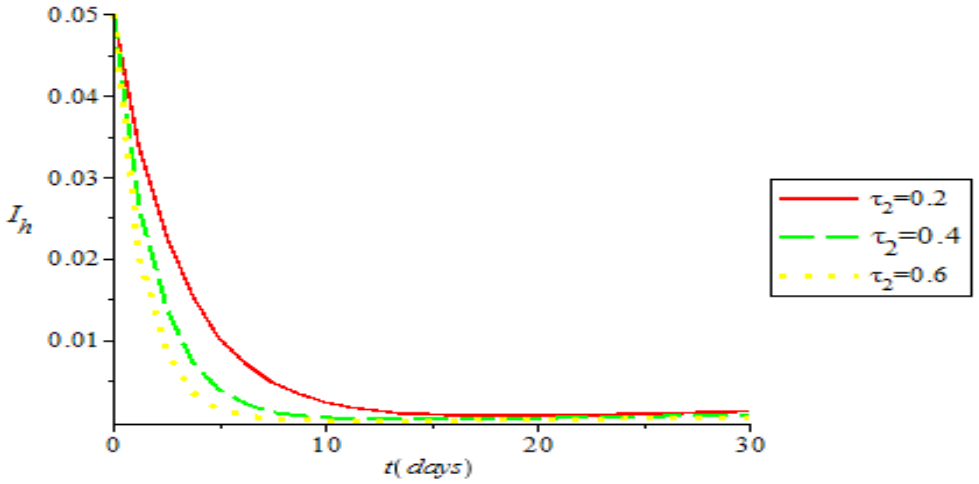

Figure 2: A graph of infectious individuals against time with varying treatment rate.

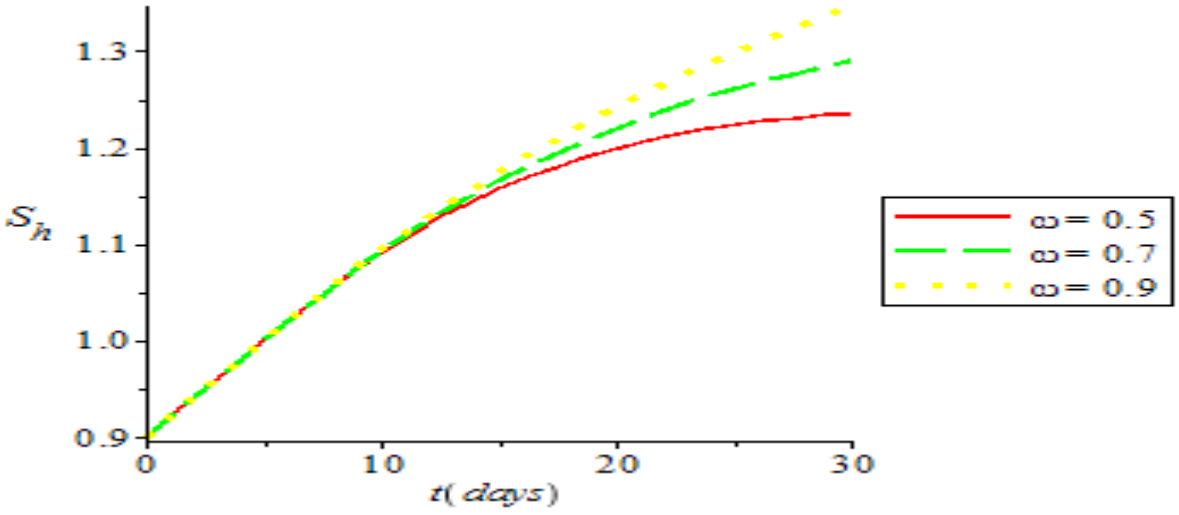

Figure 3: A graph of susceptible individuals against time with varying rate of public health education

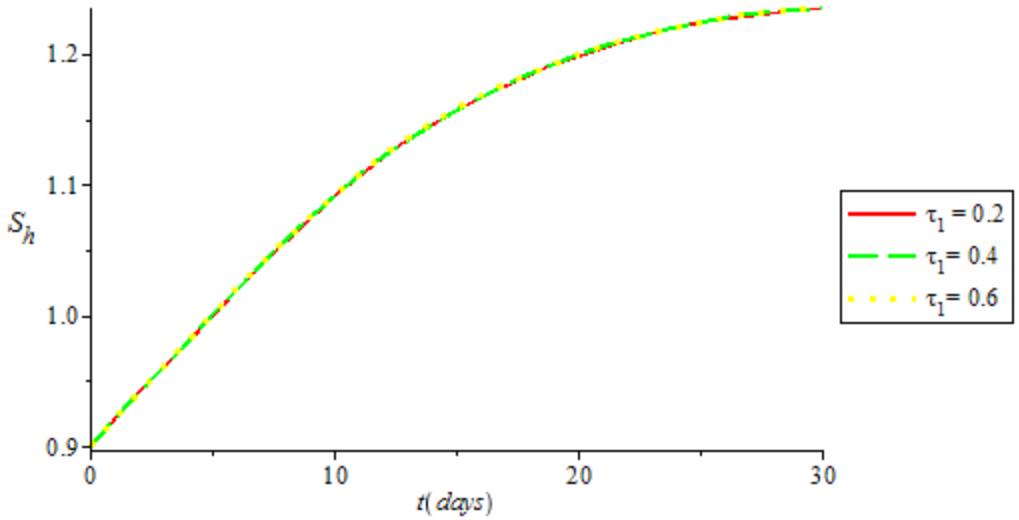

Figure 4: A graph of susceptible individuals against time with varying isolation rate

10. Discussion of results

In Figure 2, we observed the progression of the infectious human population $I_h(t)$ with time in the presence of varying treatment rate τ_2. The infectious human population decreases for all treatment rate. We observe that the infectious human population decreases faster as treatment rate increases. At $\tau_2 = 0.2$ and 0.4, as shown in figure 1, the infectious human population takes 15 to 20 days to attain its minimum while it takes 10 days to attain its minimum at $\tau_2 = 0.6$. This agrees with reality because the more the infectious population is being treated, the lesser it becomes.

Figure 3 shows the progression in susceptible human population $S_h(t)$ with time in the presence of varying public health education campaign rate ω. It is observed that the number of susceptible individuals increases with time for all values of ω . We further observed that increased public health enlightenment reduces the rate at which the susceptible population is being invaded by the disease. When public health enlightenment ω is 0.5 and 0.7, the susceptible population $S_h(t)$ is less than when ω is 0.9. This agrees with reality because an increased public health education campaign will keep people aware of the dangers of the disease, its mode of transmission and preventive strategies there by reducing the infection rate.

In Figure 4, we studied the progression of the Susceptible human population $S_h(t)$ with time in the presence of varying isolation rate τ_1. The susceptible population increases for all isolation rates. This is also in line with reality, because as infectious individuals are being isolated from the susceptible ones, the infection rate reduces there by leading to an increase in the susceptible population.

11. Conclusion

In this work, a deterministic model has been formulated to study the transmission dynamics of Lassa fever disease. The model incorporates three control parameters, isolation τ_1 , treatment $\tau_2$and public health education campaign ω. We obtained an important threshold parameter called the effective reproduction number R_c. It is known that when $R_c < 1$ the disease dies out, and when $R_c > 1$ the disease persists in the population.

Because we are interested in control, we carried out a sensitivity analysis of the effective reproduction number, which shows that the most sensitive parameter to the effective reproduction number R_c is the natural death rate of rodents μ_r followed by the human contact rate β_2, rodents contact rate β_1, recruitment level of rodents Λ_r and the rate of public health education campaign ω while the least sensitive parameter is the Lassa fever induced death rate δ. We conducted numerical simulation and results shows that isolation, treatment and public health education can reduce the number of infections.

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