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Epidemiological Implications of Vertical Transmission and Nonlinear Treatment in Lassa fever: A Mathematical Study

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ABSTRACT

Lassa fever is a viral hemorrhagic disease primarily transmitted through contact with food or household items contaminated by urine or feces of infected rodents. The disease poses a significant health risk in endemic regions, yet the effect of vertical transmission and non-linear treatment on its spread has not been thoroughly explored. To address this, a mathematical model was constructed to assess the effect of vertical transmission and non-linear treatment in the transmission dynamics of Lassa fever. The model was validated through the theory of positivity and boundedness, ensuring that its solution remains biologically meaningful over time. The existence of equilibrium points was examined and the basic reproduction number R_0 was calculated using the next generation matrix operator. Bifurcation analysis is performed using the Center Manifold Theory. The Local and global stability of the model around the Lassa fever free equilibrium is investigated using Jacobian Matrix method and the theorem proposed by Castillo-Chavez. The effect of the parameters of the basic reproduction number R_0 was investigated using normalized forward sensitivity index. Furthermore, it was inferred that decrease in the contact rate and the rate of vertical transmission were instrumental to curtailing the spread of Lassa fever in the population.

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KEYWORDS: Mathematical model; Lassa Fever; Vertical transmission; Nonlinear treatment; Stability; Lyapunov function; Bifurcation.

1. INRODUCTION

The Lassa virus, which belongs to the Arenavirus family, is the cause of Lassa fever, an acute hemorrhagic disease. Usually, the virus is spread to humans by consuming food or household objects tainted with the urine or feces of infected Mastomys rats. In the 1950s, the illness was initially discovered in Africa, more precisely in Sierra Leone. But it wasn't until 1969 that the virus that caused the deaths of two missionary nurses in Nigeria, West Africa, was discovered. The location of Lassa in northern Nigeria, where the first cases were found, inspired the name of the virus (Frame et al. 1970; Buckley et al. 1970).Numerous Lassa virus infection outbreaks have been documented in Nigeria since its discovery, with reports coming from Jos, Onitsha, Zonkwua, Abo Mbaise, Owerri, Epkoma, and Lafia (Carey et al. 1972; Monath 1975). Other West African nations, such as Guinea, Mali, Senegal, Sierra Leone, and Liberia, have also reported Lassa fever outbreaks and consequences (Frame 1970; Monath 1973, 1975). In addition, there are only a few known instances of Lassa virus spreading to other countries, mostly through international travel (Holmes et al. 1990; Higazy et al. 2021; Schmitz et al. 2002; Johnson et al. 1990).

The Lassa virus is categorized as a segmented negative-strand RNA virus and is a member of the Arenavirus family. About 23 viral species make up the Arenavirus family, which is separated into large complexes based on phylogenetic and serological analysis. These complexes include the Old World and New World complexes (Charrel and Lamballerie 2003; Wulff et al. 1978). The antigenicity, geographic distribution, natural hosts, and propensity for human disease development of these virus species vary. Although the majority of arenaviruses do not cause illness in humans, the Lassa virus can cause viral hemorrhagic fever, which manifests as chest, stomach, nausea, vomiting, sore throat, and muscle aches (Centers for Disease Control and Prevention, CDC 2004).While the majority of instances are minor or asymptomatic, extreme cases can have catastrophic consequences. The Lassa virus usually infects humans when they come into contact with the urine or feces of infected Mastomys rats. Furthermore, direct contact with an infected

person's blood, urine, feces, or bodily fluids can spread the virus from person to person. The virus may be transmitted from person to person by contaminated medical equipment in both community and clinical settings (WHO, 2023). Although Lassa hemorrhagic fever outbreaks can happen at any time of year, they tend to happen more frequently during the dry season.Furthermore, it is possible for individuals to transport Lassa fever from an endemic area to a non-endemic area during the incubation period, potentially leading to new outbreaks.

A crucial tool used for studying the dynamical spread of infectious disease in the human population is mathematical modeling (Adepoju and Ibrahim, 2024; Adepoju et al., 2024; Olaniyi et al 2018) and numerous models have been studied to analyze the spread dynamics of Lassa Fever in order to mitigate its dynamical spread. Favour and Okeke (2020) investigated a mathematical model for Lassa Fever transmission and control by buttressing the various stages of infection. Their finding revealed that quarantine system has a great positive effect on the rate of recovery of the infected individuals and also in curbing the risk of infection in the environment which can help safeguard the population. Ibrahim and Attila (2021) investigated mathematical model for Lassa fever transmission dynamics in a seasonal environment with a view to the 2017–2020 epidemic in Nigeria. Omoloye et al. (2021) investigated the modeling and sensitivity analysis of dynamical transmission of Lassa Fever while Olowu and Ako (2021) investigated the impact of reduced infection on Lassa Hemorrhagic Fever transmission dynamics. Ojo and Emile (2020) studied the impact of simulation on the dynamics of Lassa Fever in Nigeria. Their result showed that combined controlled parameters made the total infected human population decline faster and thus reduces Lassa fever's burden on the population. Popoola et al. (2022) addressed the impact of Lassa Fever in West Africa from a mathematical modeling approach.

In another development, Ogwu et al. (2022) studied the effect of Lassa Fever in Nigeria by considering the social and ecological risk factors exacerbating transmission and sustainable management strategies. Musa et al. (2022) investigated mathematical analysis of Lassa fever epidemic with effects of environmental transmission. Madueme et al. (2022) employed the mathematical modeling approach to study the effect of the transmission pathways of Lassa Fever. Abdulrahim et al. (2023) investigated the recurring outbreaks of on Lassa Fever in Nigeria while Omale et al. (2024) investigated various epidemiological aspects of Lassa fever viral infection using a fractional order mathematical model. Ibrahim et al. (2024) investigated the effect of delay techniques on a Lassa Fever epidemic model

It is pertinent to state that this research is aimed at curbing the menace of vertical transmission and the impact of nonlinear treatment in the human population. The organization of this work is as follows: Section 2 presents the full description of the model. The Analytical solution of the model is presented in Section 3 and numerical simulations of the system are performed in Section 4. Concluding remarks are wrapped up in Section 5.

2. MODEL FORMULATION

The total human population denoted by $N_h(t)$ is subdivided into four mutually exclusive classes of Susceptible humans denoted by $S_h(t)$, which describes the population of susceptible human who are prone to Lassa fever; Exposed humans, denoted by $E_h(t)$; Infected humans, denoted by $I_h(t)$ and recovered humans, denoted by $R_h(t)$. Therefore, the total human population is given by

$$N_h(t) = S_h(t) + E_h(t) + I_h(t) + R_h(t) \quad (1)$$

The total rodent population denoted by $(N_r(t))$ on the other hand was divided into susceptible rodents denoted by $(S_r(t))$ and infectious rodents denoted by $(I_r(t))$respectively. Then, the total rodent population is given by

$$N_r(t) = S_r(t) + I_r(t) \quad (2)$$

The susceptible compartment $S_h(t)$ increases due to the recruitment of individuals into the population at a rate π_h. The compartment decreases following the standard incidence rates $\frac{\beta_1 S_h I_r}{N_h}$ and $\frac{\beta_2 S_h I_h}{N_h}$ where β_1 and β_2 are the effective contact with infectious.

The human population is further reduced by the natural death at a rate μ_h. Therefore, the rate of change of the population of susceptible human is given as

$$\frac{dS_h}{dt} = \pi_h - \frac{\beta_1 S_h I_r}{N_h} - \frac{\beta_2 S_h I_h}{N_h} - \mu_h S_h \quad (3)$$

The exposed human compartment is increased by the standard incidences $\frac{\beta_1 S_h I_r}{N_h}$ and $\frac{\beta_2 S_h I_h}{N_h}$ respectively. The population is decreased by the progression of exposed individuals to infectious class at a rate α and further reduced by the natural death at a rate μ_h.

Therefore, the rate of change of the exposed human is given by

$$\frac{dE_h}{dt} = \frac{\beta_1 S_h I_r}{N_h} + \frac{\beta_2 S_h I_h}{N_h} - (\alpha + \mu_h) E_h \qquad (4)$$

In a similar manner, the population of infectious human increases due to progression of exposed individuals to infectious class at a rate α. The population reduces due to natural death rate μ_h and Lassa fever induced death at a rate τ. The population reduces as infectious human are treated at a non-linear rate $\frac{aI_h}{1+bI_h}$. Therefore, the rate change of the population of infectious human is given by

$$\frac{dI_h}{dt} = \alpha E_h - \left(\mu_h + \tau + \frac{a}{1+bI_h}\right) I_h \qquad (5)$$

The recovered human population is increased due to progression of non-linear treatment of infectious human from the infectious class at rate $\frac{aI_h}{1+bI_h}$. Therefore, the rate of change of the population of recovered is given by

$$\frac{dR_h}{dt} = \frac{aI_h}{1+bI_h} - \mu_h R_h \qquad (6)$$

Recruitment into the susceptible rodent population is at a rate π_r. The compartment decrease following the standard incidence rate $\frac{\beta_3 S_r I_r}{N_h}$, where β_3 is the effective contact rate with infectious rodent. The population is further reduced as a result of natural death at a rate μ_r. Therefore, the rate of change of susceptible rodent population is given by

$$\frac{dS_r}{dt} = \pi_r (1 - \rho I_r) - \frac{\beta_3 I_r S_r}{N_r} - (\mu_r + \phi) S_r \qquad (7)$$

The population of infectious rodents increases by standard incidence $\frac{\beta_3 S_r I_r}{N_h}$. The population reduces due to the natural death of rodents at a rate μ_r and induced death at a rate ϕ. Therefore, the rate of change of the population of infectious rodents is given by,

$$\frac{dI_r}{dt} = \pi_r \rho I_r + \frac{\beta_3 I_r S_r}{N_r} - (\mu_r + \phi) I_r \qquad (8)$$

Therefore, the mathematical model governing the transmission dynamics of Lassa fever is presented as follow

$$\begin{aligned}
\frac{dS_h}{dt} &= \pi_h - \frac{\beta_1 S_h I_r}{N_h} - \frac{\beta_2 S_h I_h}{N_h} - \mu_h S_h \\
\frac{dE_h}{dt} &= \frac{\beta_1 S_h I_r}{N_h} + \frac{\beta_2 S_h I_h}{N_h} - (\alpha + \mu_h) E_h \\
\frac{dI_h}{dt} &= \alpha E_h - \left(\mu_h + \tau + \frac{a}{1+bI_h}\right) I_h \\
\frac{dR_h}{dt} &= \frac{aI_h}{1+bI_h} - \mu_h R_h \\
\frac{dS_r}{dt} &= \pi_r (1 - \rho I_r) - \frac{\beta_3 I_r S_r}{N_r} - (\mu_r + \phi) S_r \\
\frac{dI_r}{dt} &= \pi_r \rho I_r + \frac{\beta_3 I_r S_r}{N_r} - (\mu_r + \phi) I_r
\end{aligned} \qquad (9)$$

The state variables (9) are subject to the initial conditions: $S_h > 0, E_h \geq 0, I_h \geq 0, R_h \geq 0, S_r > 0, I_r \geq 0$

Table 1: Description of Variables

Variables	Description
$S_h(t)$	Susceptible humans
$E_h(t)$	Exposed humans
$I_h(t)$	Infected humans
$R_h(t)$	Recovered humans
$S_r(t)$	Susceptible rodents
$I_r(t)$	Infected rodents

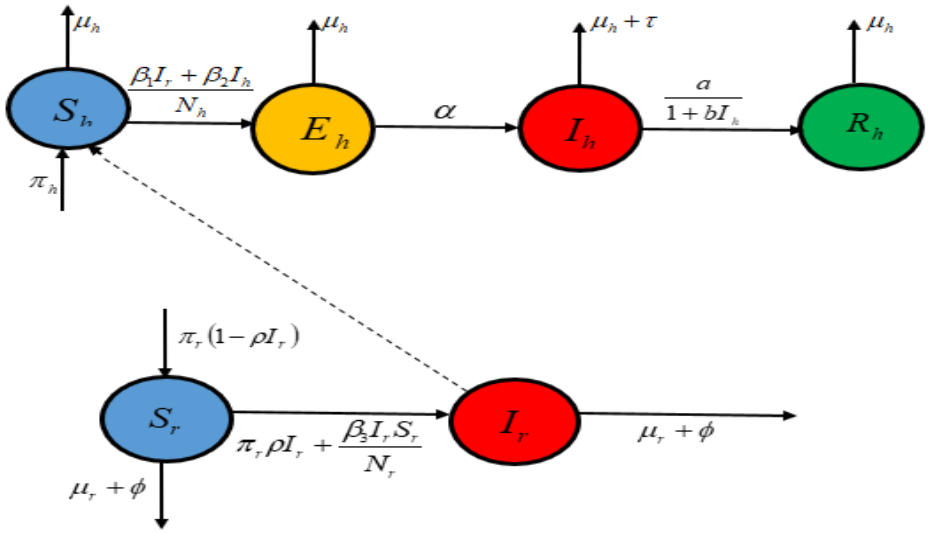

Figure 1: The Schematic Diagram Describing the Dynamic Spread of Lassa Fever

Table 2: Description of parameters of the model

Parameters	Description
π_h	Recruitment rate into human population
β_1	Rodent to human transmission rate
β_2	Human to human transmission rate
β_3	Rodent to rodent transmission rate
μ_h	Natural death rate of human
α	Progression rate from exposed class to infected class
π_r	Recruitment rate into rodent population
μ_r	Natural death rate of rodent
a	Recovery rate in human population
b	Delay in treatment in infected human population
τ	Induced death rate of human
ϕ	Induced death rate of rodent
ρ	Vertical transmission in rodent population

3. ANALYSIS OF THE LASSA FEVER MODEL

3.1 The Invariant region

The Lassa fever model (9) will be analyzed in a biologically feasible region D defined as follows. This region can be shown to be positively invariant and attracting for all positive solution of the Lassa fever model.

$$D_h = \left\{ \left(S_h + E_h + I_h + R_h\right) \in \Re_+^4 : S_h + E_h + I_h + R_h \le \frac{\pi_h}{\mu_h} \right\}$$

$$D_r = \left\{ \left(S_r + I_r\right) \in \Re_+^2 : S_r + I_r \le \frac{\pi_r}{(\mu_r + \phi)} \right\}$$

Theorem 1: Let $\left(S_h, E_h, I_h, R_h, S_r, I_r\right)$ be the solution of Eq.(1) with initial condition in a feasible region $D = D_h \times D_r$ then $D \subset R_+^6$ is positively- invariant.

Proof: Let the total human and rodent population be denoted by N_h and N_r. Then the rate of change of human population gives

$$\frac{dS_h}{dt} = \pi_h - (\lambda_h + \mu_h)S_h$$

So that ,

$$\frac{dN_h}{dt} \le \pi_h - \mu_h N_h$$

Then, by standard technique it follow that

$$N_h(t) = \frac{\pi_h}{\mu_h} + \exp-(\mu_h t)\left[N_h(0) - \frac{\pi_h}{\mu_h} \right]$$

Similarly, the total rodent population gives

$$N_r(t) \le \frac{\pi_r}{(\mu_r + \varphi)} + \exp-(\mu_r + \varphi)t\left[N_r(0) - \frac{\pi_r}{(\mu_r + \varphi)} \right]$$

If $N_h(0) \le \frac{\pi_h}{\mu_h}$ and $N_r(0) \le \frac{\pi_r}{\mu_r + \phi}$, then $N_h(t) \le \frac{\pi_h}{\mu_h}$ and $N_r(t) \le \frac{\pi_r}{\mu_r + \phi}$.Then the region D is positively invariant.

Furthermore, if $N_h(0) \ge \frac{\pi_h}{\mu_h}$ and $N_r(0) \ge \frac{\pi_r}{\mu_r + \phi}$, then the solution enters D in finite time. Hence the feasible region D is attracting.

3.2. Positivity of solutions

Since the mathematical model (9) governing the transmission dynamics of Lassa fever virus considers both human and rodent populations, then it is important that all its state variables and associated parameters are non-negative for all time, t. Hence, the following result holds for all the state variables in the mathematical model

Theorem 2. The solutions of Lassa fever virus model (1) given by the set $S_h, E_h, I_h, R_h, S_r, I_r$ with non-negative initial conditions $S_h(0), E_h(0), I_h(0), R_h(0), S_r(0), I_r(0)$ remain non-negative for every time $t > 0$

Proof. The first compartment of model (1) is considered so that

$$\frac{dS_h}{dt} + (\lambda_h + \mu_h)S_h \qquad (10)$$

This implies that

$$S_h(t) > S_h(0)\exp-\left\{ \int_0^t \lambda_h(\varphi)\,d\varphi + \mu_h t \right\} > 0 \text{ , for all } t > 0. \qquad (11)$$

Following the same procedure, it can be shown that the remaining state variables $E_h(t) > 0$, $I_h(t) > 0$, $R_h(t) > 0$, $S_r(t) > 0$, $I_r(t) > 0$.

3. Equilibrium Points and Stability Analysis

3.3.1.Disease-free Equilibrium

The disease-free equilibrium point is a stable position where the entire population has no infection. Then at steady state, the Lassa fever model (9) has a disease-free equilibrium point.

$$\varepsilon_0 = \left(\frac{\pi_h}{\mu_h}, 0, 0, 0, \frac{\pi_r}{(\mu_r + \phi)}, 0 \right) \tag{12}$$

The basic reproduction number R_0 is calculated using the approach of (Driessche and Watmough, 2002; Chitnis et al. 2008) The transmission matrix f and transition matrix v obtained at Lassa fever free equilibrium ε_0 are given as follows:

$$f = \begin{pmatrix} 0 & \beta_2 & \beta_1 \\ 0 & 0 & 0 \\ 0 & 0 & \beta_3 \end{pmatrix}$$

And

$$v = \begin{pmatrix} k_1 & 0 & 0 \\ -\alpha & K_2 + a & 0 \\ 0 & 0 & K_3 - \pi_r \rho \end{pmatrix}$$

$K_1 = (\alpha + \mu_h), K_2 = (\mu_h + \tau), K_3 = (\mu_r + \phi).$

Then the spectral radius of FV^{-1} is the basic reproduction number given as

$$R_0 = \frac{R_{hh} + R_{rr} + \sqrt{(R_{hh} + R_{rr})^2 - 4(R_{hh} R_{rr})}}{2} \tag{13}.$$

Where $R_{hh} = \frac{\alpha \beta_2}{K_1 (K_2 + a)}$ and $R_{rr} = \frac{\beta_3}{K_3 - \pi_r \rho}$

Theorem 2: The Lassa fever free equilibrium point is locally asymptotically stable whenever the basic reproduction number R_0 is less than unity.

Proof : The Jacobian matrix of Lassa fever model (9) obtained at ε_0 is given as

$$J(\varepsilon_0) = \begin{pmatrix} -\frac{\beta_1 I_r}{N_h} - \frac{\beta_1 I_r}{N_h} - \mu_h & 0 & -\frac{\beta_2 S_r}{N_h} & 0 & 0 & -\frac{\beta_1 S_r}{N_h} \\ \frac{\beta_1 I_r}{N_h} + \frac{\beta_1 I_r}{N_h} & -K_1 & \frac{\beta_2 S_r}{N_h} & 0 & 0 & \frac{\beta_1 S_r}{N_h} \\ 0 & \alpha & -K_2 - \frac{a}{(1+bI_h)^2} & 0 & 0 & 0 \\ 0 & 0 & \frac{a}{(1+bI_h)^2} & -\mu_h & 0 & 0 \\ 0 & 0 & 0 & 0 & -\frac{\beta_3 I_r}{N_r} - K_3 & -\pi_r \rho - \frac{\beta_3 I_r}{N_r} \\ 0 & 0 & 0 & 0 & \frac{\beta_3 I_r}{N_r} & \pi_r \rho + \frac{\beta_3 I_r}{N_r} - K_3 \end{pmatrix} \tag{14}$$

Obviously, three of the eigenvalues of (14) is obtained as $-\mu_h, -\mu_h, -\mu_h$ and the remaining are obtained from the polynomial given by

$$\lambda^3 + \lambda^2 A_1 + \lambda A_2 + A_3 = 0 \tag{15}$$

where

$$A_1 = K_1 + K_2 + a + \left(K_3 - \pi_r \rho\right)\left(1 - R_{rr}\right)$$

$$A_2 = \left(K_1 K_2 + aK_1\right)\left(1 - R_{hh}\right) + \left(K_1 + K_2 + a\right)\left(\left(K_3 - \pi_r \rho\right)\left(1 - R_{rr}\right)\right)$$

$$A_3 = \left(\left(K_1 K_2 + aK_1\right)\left(1 - R_{hh}\right)\right)\left(\left(K_3 - \pi_r \rho\right)\left(1 - R_{rr}\right)\right)$$

Clearly, the polynomial (15) is the solution of the Jacobian matrix (14). Then following Descarte's rule, all the coefficient of the polynomial are positive. It can be concluded that all the eigenvalues of the Jacobian matrix are negative, real and distinct. Hence, the disease-free equilibrium of the Lassa fever model (9) is locally asymptotically stable.

3.3.2 Global stability of Lassa fever free equilibrium

In order to proof the theorem, the comparison test method by Castillo Chavez and Song (2004) is used. This implies that the model (9) must be rewritten in the form

$$\frac{dX}{dt} = F\left(X, Z\right)$$

$$\frac{dZ}{dt} = G\left(X, Z\right), G\left(X, 0\right) = 0 \qquad (16)$$

Where $X \in R_+^3$ and $Z \in R_+^3$. X component represent the uninfected class while Z represent the infected class i.e. $X = \left(S_h, R_h, S_r\right)$ and $Z = \left(E_h, I_{h,} I_r\right)$

Let the Lassa fever free equilibrium of the model be given by $\varepsilon_0 = \left(X^*, 0\right)$ Then the following properties must be satisfied in order to establish the global stability of the model

P_1: For $\frac{dX}{dt} = F\left(X, 0\right)$, X^* is globally asymptotically stable

$P_2 : G\left(X, Z\right) = AZ - \hat{G}\left(X, Z\right) \geq 0,$

Where $A = \partial G / \partial Z$, which is an M-matrix evaluated at $\left(X^*, 0\right)$ with non-negative off diagonal entries.

Theorem 3: The Lassa fever free equilibrium of the model (9) is globally asymptotically stable if the basic reproduction number is less than one $R_0 < 1.$

Proof:

The property P_1 is proved as

$$F\left(X, Z\right) = \begin{pmatrix} \pi_h - \frac{\beta_1 S_h I_h}{N_h} - \frac{\beta_2 S_h I_h}{N_h} - \mu_h S_h \\ \frac{aI_h}{1 + bI_h} - \mu_h R_h \\ \pi_r\left(1 - \rho I_r\right) - \frac{\beta_3 S_r I_r}{N_h} - \left(\mu_r + \phi\right) S_r \end{pmatrix} \qquad (17)$$

Where $\frac{dX}{dt} = F\left(X, 0\right)$ implies that

$$\frac{dS_h}{dt} = \pi_h - \frac{\beta_1 S_h I_r}{N_h} - \frac{\beta_2 S_h I_h}{N_h} - \mu_h S$$

$$\frac{dR_h}{dt} = \frac{aI_h}{1 + bI_h} - \mu_h R_h$$

$$\frac{dS_r}{dt} = \pi_r\left(1 - \rho I_r\right) - \frac{\beta_3 I_r S_r}{N_r} - \left(\mu_r + \phi\right) S_r \qquad (18)$$

Solving by standard technique yields the following result

$$S_h(t) = \frac{\pi_h}{\mu_h} + \ell^{-\mu_h t}\left[S(0) - \frac{\pi_h}{\mu_h}\right]$$

$$S_r(t) = \frac{\pi_r}{(\mu_r + \phi)} + \ell^{-(\mu_r+\varphi)t}\left[S_r(0)\right] - \frac{\pi_r}{(\mu_r + \phi)}$$

$$R_h(0) = R_h(0)\ell^{-\mu_h t}$$

Hence $\{S_h(t), R_h(t), S_r(t)\} \to \left\{\frac{\pi_h}{\mu_h}, 0, \frac{\pi_h}{\mu_r + \phi}\right\}$ irrespective of the initial value of the variables as $t \to \infty$.Therefore, X^* is globally asymptotically stable satisfying P_1

Also, $P_2 : G(X,Z) = AZ - \hat{G}(X, Z)$ is obtained as

$$\begin{pmatrix} \frac{\beta_1 I_r}{N_h}\left(S^*_h - S_h\right) + \frac{\beta_2 I_h}{N_h}\left(S^*_h - S_h\right) \\ -\frac{abI_h}{(1+bI_h)} \\ \frac{\beta_3 I_r}{N_h}\left(S^*_r - S_r\right) \end{pmatrix} \qquad (19)$$

Since $S^*_h > S_h$ and $S^*_r > S_r$. It is obvious that $\hat{G}(X,Z) \geq 0$. Hence the Lassa fever free equilibrium of model (9) is not globally asymptotically stable due to the delay in treatment b.

3.3.3. Existence of endemic equilibrium

The endemic equilibrium state is the point where there is presence of disease in the population. Let the endemic equilibrium point be denoted by E^* and $\lambda_h = \frac{\beta_1 I_r + \beta_2 I_h}{N_h}$ and $\lambda_r = \frac{\beta_3 I_r}{N_r}$ be the force of infection such that $\left(S^*_h, E^*_h, I^*_h, R^*_h, S^*_r, I^*_r\right)$ Then, at steady states

$$\frac{dS^*_h}{dt} = \frac{dE^*_h}{dt} + \frac{dI^*_h}{dt} + \frac{dR^*_h}{dt} + \frac{dS^*_r}{dt} + \frac{dI^*_r}{dt} = 0$$

Solving system (9) simultaneously yields

$$S^*_h = \frac{\pi_h{}^2 R_{rr}(\mu_r + \phi)}{\beta_1\mu_h(R_{rr} - 1)\pi_r + \beta_2\mu_h R_{rr}(\mu_r + \phi)I_h{}^* + \pi_h\mu_h R_{rr}(\mu_r + \phi)}$$

$$E^*_h = \frac{\pi_h\beta_1\mu_h(R_{rr} - 1)\pi_r + \beta_2\mu_h R_{rr}(\mu_r + \phi)I_h{}^*}{\left(\beta_1\pi_r\mu_h(R_{rr} - 1) + \beta_2\mu_h R_{rr}(\mu_r + \phi)I_h{}^* + \pi_h\mu_h R_{rr}(\mu_r + \phi)\right)(\alpha + \mu_h)}$$

$$R^*_h = \frac{aI^*_h}{(1 + bI^*_h)\mu_h} \qquad (20)$$

$$S^*_r = \left[\frac{(\mu_r + \phi)\pi_r - \pi_r{}^2\rho}{\beta_3(\mu_r + \phi)}\right]$$

$$I^*_r = \frac{(R_{rr} - 1)\pi_r}{R_{rr}(\mu_r + \phi)}$$

Table 3 Shows positive root of for $R_{rr}>1$ and $R_{rr}<1$.

Case	Q_1	Q_2	Q_3	Q_4	R_{rr}	No of Signs changed	Positive real roots changed
1	+	+	+	-	$R_{rr}>1$	1	1
2	+	+	+	+	$R_{rr}<1$	0	0
3	+	-	-	-	$R_{rr}>1$	1	1
4	+	-	-	+	$R_{rr}<1$	2	0,2
5	+	+	-	-	$R_{rr}>1$	1	1
6	+	+	-	+	$R_{rr}<1$	2	0,2
7	+	-	+	-	$R_{rr}>1$	3	1,3
8	+	-	+	+	$R_{rr}<1$	2	0,2

The values of I_h^* are obtained from the cubic polynomial

$$I_h^{*3}Q_1+I_h^{*2}Q_2+I_h^*Q_3+Q_4=0 \qquad (21)$$

where

$$Q_1: R_{rr}b(\mu_r+\varphi)(\alpha+\mu_h)\beta_2(\tau+\mu_h)$$

$$Q_2: \beta_2 R_{rr}(\mu_r+\varphi)(\alpha+\mu_h)(\mu_h+\tau+a)+b\pi_r\beta_1(R_{rr}-1)(\alpha+\mu_h)(\mu_h+\tau)$$

$$+(\mu_h+\tau+)\mu_h b(\alpha+\mu_h)-\alpha\pi_h\beta_2 b$$

$$Q_3: \pi_r\beta_1(R_{rr}-1)\left[\mu_h(\alpha+\mu_h)+\tau(\alpha+\mu_h)+a(\alpha+\mu_h)-\alpha\lambda_{h1}b\right]$$

$$+(\tau+a+\mu_h)\mu_h(\alpha+\mu_h)-\alpha\pi_h\beta_2$$

$$Q_4: -\alpha\pi_r\pi_h\beta_1(R_{rr}-1)$$

Theorem 3: The system has a unique endemic equilibrium if $R_{rr}>1$ and cases 1,3,5 are satisfied and could have more than one endemic equilibrium if $R_{rr}>1$ and case 7 is satisfied. Furthermore, system has no endemic equilibrium if $R_{rr}<1$ and case 2 is satisfied and could have two endemic equilibrium if $R_{rr}<1$ and cases 4,6,8 are satisfied.

3.3.4. Bifurcation analysis

Here, the Center Manifold Theory by Castillo Chavez and Song (2004) is used to establish the bifurcation phenomenon of the model whether the model will exhibit forward or backward bifurcation.

The model can be rewritten in the vector form $\frac{dX}{dt}=F(x)$, where $X=(x_1,x_2,...,x_6)$ and $F(x)=(f_1,f_2,...,f_6)^T$, such that $x_1=S_h, x_2=E_h, x_3=I_h, x_4=R_h, x_5=S_r, x_6=I_r$ .Then the model becomes

$$f_1 = \pi_h - \frac{\beta_1 x_1 x_6}{\sum_{i=1}^{4} x_i} - \frac{\beta_2 x_1 x_3}{\sum_{i=1}^{4} x_i} - \mu_h x_1$$

Recall,

$$f_2 = \frac{\beta_1 x_1 x_6}{\sum_{i=1}^{4} x_i} + \frac{\beta_2^* x_1 x_3}{\sum_{i=1}^{4} x_i} - (\alpha + \mu_h) x_2$$

$$f_3 = \alpha x_2 - \left(\mu_h + \tau + \frac{a}{1+bx_3} \right) x_3 \qquad (22)$$

$$f_4 = \frac{ax}{1+bx_3} - \mu_h x_4$$

$$f_5 = \pi_r (1-\rho x_6) - \frac{\beta_3 x_6 x_5}{\sum_{i=5}^{6} x_i} - (\mu_r + \phi) x_5$$

$$f_6 = \pi_r \rho x_6 + \frac{\beta_3 x_6 x_5}{\sum_{i=5}^{6} x_i} - (\mu_r + \phi) x_6$$

$$R_0 = \frac{R_{hh} + R_{rr} + \sqrt{(R_{hh} + R_{rr})^2 - 4(R_{hh} R_{rr})}}{2}$$

Let the bifurcation parameter $\beta_2 = \beta_2^*$ be chosen so that $R_0 = 1$, iff

$$\beta_2 = \beta_2^* = \frac{K_1 (K_2 + a)}{\alpha} \qquad (23)$$

The Jacobian matrix of the system (3.113) evaluated at ε_0 and β_2^* is given by

$$\begin{pmatrix} -\mu_h & 0 & -\frac{K_1(K_2+a)}{\alpha} & 0 & 0 & -\beta_1 \\ 0 & -K_1 & \frac{K_1(K_2+a)}{\alpha} & 0 & 0 & \beta_1 \\ 0 & \alpha & -K_2 - a & 0 & 0 & 0 \\ 0 & 0 & a & -\mu_h & 0 & 0 \\ 0 & 0 & 0 & 0 & -K_3 & -\pi_r \rho - \beta_3 \\ 0 & 0 & 0 & 0 & 0 & \pi_r \rho + \beta_3 - K_3 \end{pmatrix} \qquad (24)$$

Then the resulting eigenvalues are obtained as follows

$$-\mu_h = \lambda, \quad -\mu_h = \lambda, \quad -K_3 = \lambda \quad \lambda = 0, \quad \lambda = -(K_1 + K_2 + a) \qquad (25)$$

Since one of the eigenvalues of the polynomial equals zero, this implies that there exist a simple zero eigenvalues of the Jacobian matrix evaluated at ε_0 and β_2^* while remaining eigenvalues have negative real parts following Descarte's rule of signs.

Let the right eigenvector be denoted by $w = (w_1, w_2, \ldots w_6)$. Then, the right eigenvector corresponding to the simple zero eigenvalue is obtained as follows

$$
\begin{aligned}
&-\mu_h w_1 - \beta_2^* w_3 - \beta_1 w_6 = 0\\
&-k_1 w_2 - \beta_2^* w_3 + \beta_1 w_6 = 0\\
&\alpha w_2 - (k_2 - a) w_3 = 0\\
&a w_3 - \mu_h w_4 = 0\\
&-k_3 w_5 - (\pi_r \rho + \beta_3) w_6 = 0\\
&(\pi_r \rho + \beta_3 - k_3) w_6 = 0
\end{aligned} \qquad (26)
$$

Solving (26) simultaneously, the following result is obtained

$$w_1 = \frac{-\beta_2^* \alpha w_2}{\mu_h (k_2 + a)}$$

$$w_2 = 0 \qquad w_3 = \frac{\alpha w_2}{(k_2 + a)},$$

$$w_4 = \frac{a\alpha w_2}{\mu_h (k_2 + a)} \qquad w_5 = 0,$$

$$w_6 = 0$$

In a similar manner, let $v = (v_1, v_2, v_3, v_4, v_5, v_6)$ be the associated left eigenvector of (24) at $J_{(\varepsilon_{0,\beta_2^*})}$. Then the left eigenvector is given as

$$
\begin{aligned}
&-\mu_h v_1 = 0\\
&-k_1 v_2 + v_3 \alpha = 0\\
&-\beta_2^* v_1 + \beta_2^* v_2 - (k_2 + a) v_3 + a v_4 = 0\\
&-\mu_h v_4 = 0\\
&-k_3 v_5 = 0\\
&-\beta_1 v_1 + \beta_1 v_2 - (\pi_r \rho + \beta_3) v_5 + (\pi_r \rho + \beta_3 - K_3) v_6 = 0
\end{aligned} \qquad (27)
$$

Solving (27) simultaneously yields the following result

$$v_1 = 0, v_2 > 0$$

$$v_3 = \frac{\beta_2^* v_2}{k_2 + a}, \qquad v_4 = 0 \quad , v_5 = 0$$

$$v_6 = \frac{\beta_1 v_2}{\pi_r \rho + \beta_3^* - K_3}$$

Following the approach of Castillo-Chavez and Song (2004),

$$\mathrm{a} = \sum_{i,j,k=1}^{6} v_k w_i w_j \frac{\partial^2 f_k}{\partial x_i \partial x_j}$$

$$\mathrm{b} = \sum_{i=1}^{6} v_k w_i \frac{\partial^2 f_k}{\partial x_i \partial \beta_2 (\varepsilon_0)}$$

The algebraic simplification gives

$$\frac{\partial^2 f_2}{\partial x_2 \partial x_3} = \frac{-\beta_2^*}{x_1}, \quad \frac{\partial^2 f_2}{\partial x_2 \partial x_6} = \frac{-\beta_1}{x_1}, \quad \frac{\partial^2 f_2}{\partial x_3 \partial x_4} = \frac{-\beta_2^*}{x_1}$$

$$\frac{\partial^2 f_2}{\partial x_3 \partial x_5} = \frac{-\beta_2^*}{x_1}, \quad \frac{\partial^2 f_2}{\partial x_3 \partial x_6} = \frac{-\left(\beta_1 + \beta_2^*\right)}{x_1}, \quad \frac{\partial^2 f_2}{\partial x_4 \partial x_6} = \frac{-\beta_1}{x_1}, \quad \frac{\partial^2 f_2}{\partial x_5 \partial x_6} = \frac{-\beta_1}{x_1}$$

$$\frac{\partial^2 f_2}{\partial x^2{}_6} = \frac{-2\beta_1}{x_1}, \quad \frac{\partial^2 f_3}{\partial x^2{}_3} = 2ab, \quad \frac{\partial^2 f_6}{\partial x_5 \partial x_6} = \frac{-2\beta_3}{x_5}, \quad \frac{\partial^2 f_6}{\partial x^2{}_6} = \frac{-2\beta_3}{x_5}$$

Substituting the above expressions into "a'' and "b'' gives

$$\text{a} = \frac{2v_3\alpha^2 w_2^2 ab}{\left(k_2 + a\right)^2} - \frac{\beta_2^* v_2 w_2^2 \alpha}{\left(k_2 + a\right)^2 \pi_h}\left[\mu_h\left(k_2 + a\right) + a\alpha\right]$$

$$\text{b} = \frac{v_2 \alpha w_2}{\left(k_2 + a\right)}$$

The nature of bifurcation of system (9) is determined by sign of coefficient "a'', given that coefficient "b'' is non-negative. If "a'' is non-negative, backward bifurcation occurs.

This coefficient ''a'' is non-negative if and only if

$$\text{b} > \frac{\beta_2^*}{\pi_h}\left[\mu_h\left(k_2 + a\right) + \alpha a\right] \cdot \frac{1}{2a\alpha}$$

$$\text{b} > \frac{\beta_2^*}{2a\alpha\pi_h}\left[\mu_h\left(k_2 + a\right) + \alpha a\right] \qquad (28)$$

Hence the following result was established.

Theorem 3.7: The model (9) exhibits backward bifurcation if (28) holds.

3.3.5. Sensitivity analysis

Sensitivity analysis and simulations are essential for identifying the most effective strategies to reduce Lassa fever's impact by assessing the significance of various factors influencing its spread and prevalence, based on model parameters. The normalized forward sensitivity index quantifies the ratio of the relative change in a variable to the relative change in the corresponding parameter (Chitnis et al. 2008). In this analysis, the sensitivity indices of the basic reproduction number R_0 are evaluated relative to their associated parameters P is defined as:

$$X_P^{R_0} = \frac{\partial R_0}{\partial P} \times \frac{P}{R_0}$$

The sensitivity indices of R_0 relative to the associated parameters is calculated and the result is presented in Table 4. It is observed that the parameters with positive sensitivity indices will increase the basic reproduction number while those with negative sensitivity indices will reduce the basic reproduction number.

Table 4: Sensitivity indices of basic reproduction number relative to its parameters

Parameters	Sensitivity indices
π_r	0.011178862
β_2	9.57623×10^{-13}
β_3	1.00000000
μ_h	-1.0355861×10^{-12}
μ_r	-0.4342818
ρ	0.1117886179
a	$-1.66811734\times10^{-14}$
τ	-8.173775×10^{-13}

ϕ	-0.677507
α	9.1202183×10^{-13}

4. NUMERICAL SIMULATION

As depicted in Figure 4.1, increase in the values of human to human transmission rate. β_2 and increase in the value of progression rate of exposed human to infected class, α, resulted into corresponding increase in the basic reproduction number which will lead to the persistence of the spread of Lassa fever in the population of both human and rodent. Figure 4.2 increase in the value of human induced death rate, τ, and increase in the value of human natural death rate, μ_h, will lead to decrease in the basic reproduction number leading to reduction in the spread of Lassa fever in the human population. Also in Figure 4.3, increase in the value of rodent induced death rate, ϕ, and increase in the value of rodent natural death rate, μ_r, will lead to decrease in the basic reproduction number of the Lassa fever leading to the reduction in the spread of Lassa fever in the population.

Figure 4.5 shows the effect of delay in treatment b on the infected class and Figure 4.6 depicts the effect of vertical transmission ρ on the infected rodents. An increase in the delayed in treatment of infected humans and vertical transmission rate of infected rodents leads to the increase in the population of infectious humans and infectious rodents in the population.

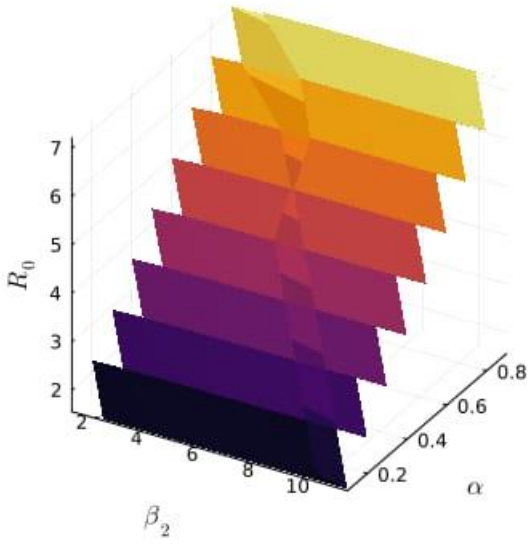

Figure 4.1: Effect of β_2 and α on basic reproduction number

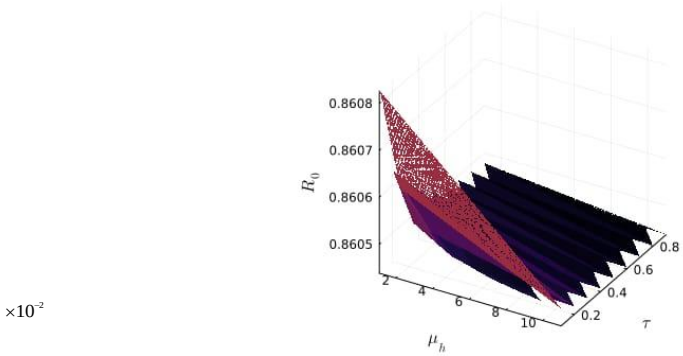

Figure 4.2: Effect of μ_h and τ on basic reproduction number

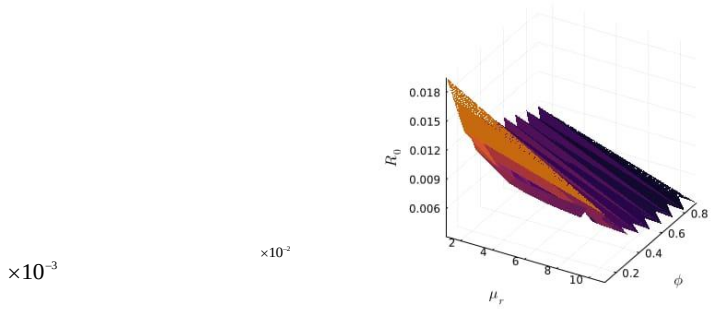

Figure 4.3: Effect of μ_r and ϕ on basic reproduction number

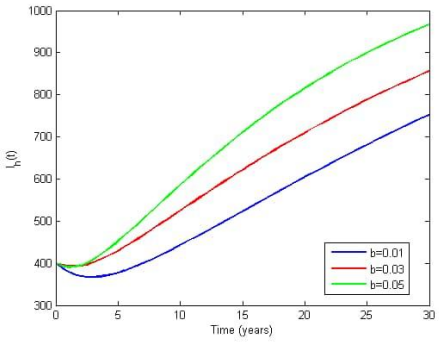

Figure 4.5: Effect of varying values of delay in treatment b in infected human

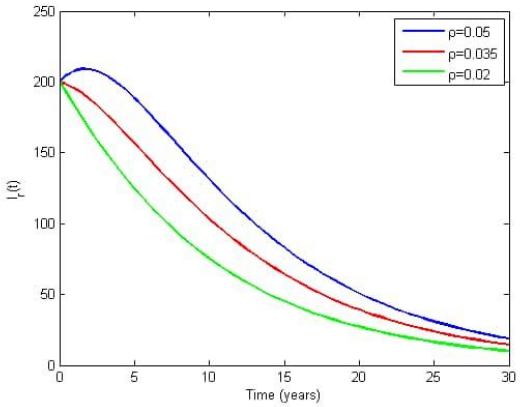

Figure 4.6: Effect of varying values of vertical transmission ρ in infected rodents

5. CONCLUSION

In this study, a mathematical model incorporating vertical transmission and nonlinear treatment was formulated and analyzed using a system of ordinary differential equation to provide deeper insights into the transmission dynamics of Lassa fever in the population. The model was stratified into two populations. Susceptible individuals, exposed individuals, infected individuals and recovered individuals make up the human population. Also, the rodent population is classified into two compartments: Susceptible and infected rodents. The model took into account vertical transmission and nonlinear treatment

The analytical solution of the model yielded the Lassa Fever free equilibrium point. Using the next generation matrix approach, the basic reproduction number was computed. The model was shown to be locally asymptotically stable whenever the basic reproduction number is less than unity by employing the linearized Jacobian method while the M-matrix approach was used to determine the global asymptotic stability of the disease-free equilibrium. The center manifold theory was used to establish the bifurcation analysis and was shown to exhibit backward bifurcation.

Additionally, the influence of the parameters of the basic reproduction number was investigated using the normalized forward sensitivity index. It was deduced that parameters with positive sensitivity indices will mitigate the persistence of Lassa Fever in the population while those with negative indices will help in curbing the menace of Lassa Fever in the human population. Furthermore, efforts should be made by policy makers and healthcare worker to increase the value of parameters with negative indices. The values

used in this study are obtained from already existing literature on Lassa Fever while some are assumed.

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