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MATHEMATICAL MODEL OF LASSA FEVER TRANSMISSION DYNAMICS IN PREVALENT COMMUNITIES IN NIGERIA: THE CASE STUDY OF ONDO STATE

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Abstract

With the current waive of global health problems and resurgence of many disease around the world. Cholera, Yellow fever,SARS-CoV-2, Monkey pox and Lassa fever resurgence in some West African countries, with Ondo State recording highest number of Lassa fever case in Nigeria. Prompting Nigeria Centre for Disease Control (NCDC), Ondo State Primary Health (OSPH) expert and researchers begin ways to reduce transmission dynamics of Lassa Fever Disease (LFD). In this research, we developed and investigated using System of Ordinary Differential Equation (ODE) mathematical model of Lassa fever disease transmission dynamics, verifying positivity of system of equation as well as feasible region of the model. However, the Disease Free Equilibrium (DFE) of the model is computed and analysed with basic reproduction number R_0 of the model, showing the global stability of the DFE. Furthermore, we determined using model-fitting parameters the condition to attain stability. Finally, numerical simulations shows reduction in transmission with effective pest control measure.

Keywords: Global health, SARS-CoV-2,transmission dynamics, Disease Free Equilibrium, Ordinary Differential Equation.

Introduction

As the world improves daily, and human activities towards making the entire globe a better place so also is the very effect of spread of diseases across the world. Lassa fever(LF) is an aminal-borne, acute viral illness. It is endemic in parts of West Africa including Sierra Leone, Guinea, Liberia and Nigeria. Lassa virus was discovered in 1969 in a community called Lassa in Nigeria. (Richmond and Baglole, 2003). Lassa fever is an acute viral haemorrhagic illness caused by Lassa virus (LV), of the arenavirus family of virus Keenlyside et al. (1983). Mastomys rodents are the carriers of the virus, they live in the rodents system for life, without symptoms and are ejected as excreta and urine.

Once the rodent is infected, its dropping and urine contains the virus for as long as th rodent lives. The high rate of breeding of the mastomys rodents who are usually found in the forest and savanna of Central, East and west of Africa (Keenlyside et al., 1983; Leirs et al., 1996), they easily colonize human abode and areas where food are kept. Improper disposition of food items in Nigeria and other African countries has made Lassa virus easily transmitted to human.

whenever an infected mastomys rodent comes in contact with the food item and the contaminated food item is consumed, transmission occurs. The infection can also be contacted with a direct contact with infected rodent, person-to-person contact with bodily fluids, secretion or excretion of a lassa virus infected individual. Body contacts without the exchange of bodily fluids doesn't not spread the lassa virus. In March 2018, somewhere in Edo State of Nigeria, World Health Organisation (WHO), conducted a sensitization session, reaching out to nearly 9,000 community leaders on the effect of the LV after the infection killed a young father, living behind two sons who show symptoms of the infectious disease.

Although Lassa fever (LF) and Ebola virus disease (EVD) comes up with very similar symptoms. Lassa fever is less likely to spred from peron to persson compared to Ebola which has very high rate of spread and far deadly. Lassa fever comes with bleeding after an incubation period of about 2-21days depending on the immunity of the infected individual. With physical manifestation as fever, general weakness and malaria.

Mathematical modeling holds critical role in the design of prevention and other control measures of infectious diseases. For example, Okuonghae and Okuonghae (2006) formulated a Lassa fever disease dynamics mathematical model of qualifying relative contributions from regular contact with species of vector which carries the virus. Causing Lassa fever and infectious contact with individual is seen as significant in the spread of the disease. Incorporating vaccination effectiveness modeling on a subset of the target population. Bawa et al. (2013) in their study, incorporated standard incidence rate of deterministic model for Lassa fever disease. With concepts of vital dynamics,disease induced death, infection due to humans, reservoirs and aerosol (airborne) transmissions in a population. Obabiyi and Onifade (2017) on their part accessed a mathematical model for LFD focusing on two populations: that of the rodent and human. Using maximum principle theorem, establishing positivity and boundedness of solutions of the system of ODE. Having conditions for attaining disease free equilibrium, endemic equilibrium and stabilities of the system.

There are growing need to improve on understanding Lassa fever disease transmission dynamics, developing effective strategies for prevention and controlling its spread. Optimal control analysis have been a very useful tool in studying and formulating control strategy of infectious diseases (Gupta and Rink, 1973). With several optimal control analysis on diseases such as Malaria (Rafikov et al., 2009; Okosun et al., 2013), Zika (Chaikham and Sawangtong, 2017; Momoh and Fügenschuh, 2018; Djomegni et al., 2021), HIV (Karrakchou et al., 2006; Kutch and Gurfil, 2002) and Ebola (Li et al., 2017; Rachah and Torres, 2015). Lassa Fever Disease (LFD) have recorded about 300,000 clinical infections and as much as about 5,000 deaths yearly in endemic region (Dahmane et al., 2014). The disease have affected so many communities. The reason for the high risk in southern part of Nigeria, Edo and Ondo State leading the number of states numbering to 22 states is majorly because of the primitive way of life, especially the way the farming community dry their agricultural produce. Local farmers depend majourly on spreading farm produce on the road side to get dried by the sunlight as a means to preserve the food item. This practice which exposes the food item to rodents, who come to feast on the food item, thereby dropping feces and urinating on the food, which is then consumed by the human population without proper processing as well as the water for consumption which is got fro streams. LFD is also prevalent in the Southern part of Nigeria because of the orthodox believe and local herbal system of health. Prevalence of LFD which is a public health emergency in Nigeria, report from Jan 2017 to dec 2018, LFD was recorded in 11 states of the country with Edo and Ondo states recording 69% followed by Ebonyi with 11%. Reports from Nigeria Centre for Disease Control (NCDC) showed that the reported cases of LFD is more than 4,000 suspected cases in 23 States with more than 600 confirmed cases and 149 deaths in 2019 (Team et al., 2018, 2019). Which prompted government relevant health agencies, medical researchers and mathematical epidemiologist to come up with solutions to eradicate the disease.

However, Mathematical modeling has been very instrumental in prevention of infectious disease globally and Nigeria in particular. With several studies on mathematical modeling of LFD dynamics, its transmission in so many perspective. (Akanni and Adediipo, 2018) considered sensitivity analysis of dynamical transmission of LFD, with four compartments for the human namely, susceptible, exposed, infectious and the recovered class. while considering SEI for the vector. With all assuming immunity for recovered individuals. But with the prevalence rate of LFD, there are possibilities that a recovered individual can be susceptible again. Hence, in this paper, recovered individual lose immunity at rate σ which is rate at which they return to being susceptible. The σ is very low, because of Optimal control strategies which is put in place. Such as living in a clean environments, following public health guidelines on food intake and waste disposal. Neglecting orthodox medical advice and following medical advise. Recently in the government of Ondo State in Nigeria announced the plan to distribute 10,000 rodent eliminating substance free to residence of LFD prevalent communities. Because of the prevalence and awareness made by government and public health specialist. We assume no recurrence of LFD induced deaths in prevalent communities due to safe disposal of LFD positive corpses.

However, the uniqueness of this study of Lassa virus infection model proposes a stability analysis with control parameters that enables vector elimination, vector-to-human contact reduction and human-to-human contact reduction. Using mathematical model and the stability analysis control Lassa fever transmission dynamics that includes comprehensive medical and hygienic interventions (prompt diagnostic and early treatment of infected humans, clean environmental practices, use of indoor residual spray to control rodents against spread of disease, hygienic agricultural practice and proper disposal of food items, control of bodily contact with body fluids). Mathematical model is formulated in Section 2, while in Section 3, mathematical analysis of the model is presented. While contribution of rodent-human transmission and human-human transmission of

Figure 1: Site of Poor Exposure of Food a major cause of Lassa

Lassa fever disease dynamics, investigating basic reproduction number, Infection control strategy formulation and solution with Numerical Simulations are in Section 4. With conclusion in Section 5.

Model Formation

We consider a SEIR model for humans and an SI model is considered for mastomys rodents with control strategies. Diagram of epidemiological classes of the modeled system is given in Fig. 1,total human population at time t is given as $N_h(t)$, which has four classes: susceptible $S_h(t)$, exposed $E_h(t)$ Infectious $I_h(t)$ and recovered human $R_h(t)$. The vector(mastomys rodents) population $N_v(t)$ has two classes: susceptible $S_v(t)$ and Infected rodents $I_v(t)$,while we assume that rodent infected with Lassa fever (LF) never recovers.

Susceptible individual enters into the system at constant rate π_h through birth and natural death rate μ_h. Susceptible humans get Lassa virus (LV) infection due to contact with infected humans, as well as contacts with infected mastomys rodent at rate

$$\frac{\beta_{vh}}{N_h}$$

. Where β_{vh} is probability of transmission from an infectious mastomys rodent to susceptible human per contact with an infected food item or any contaminant. $\beta_v h$ is the transmission rate from a susceptible. Natural death rate of exposed human is μ_h while they move to the infected class at a rate α_h. Infected individual death at rate d, without any form of recurrence, because due to awareness and government regulation, only approved means of disposal is required. Recovered class with natural death rate μ_h and has propensity of losing immunity at rate ζ, which makes them vulnerable to being reinfected with the disease as they return to the susceptible class at same rate.

Susceptible mastomys rodent $S_v(t)$ have a constant birth rate of λ_v and natural death rate μ_v. $\beta_h v$ is the transmission rate from a susceptible. With the assumption that rodent can be removed either through death by predators or human pest control measures at rate σ_v

The Mathematical Model

The model formulation considers a general population of host and vector respectively. With reference to transmission dynamics of lassa fever disease and states of individuals in the system at time t. The population compartments are divided into classes of individuals who are immunologically naive, such as susceptible class denoted by S_h. Exposed class is denoted by E_h which are set of individuals who are exposed to food items already contaminated with LF or come in contact infectious host. Infected class is denoted by I_h, while recovered individuals as R_h but with temporary immunity. Because likelihood of getting infected if they contract the

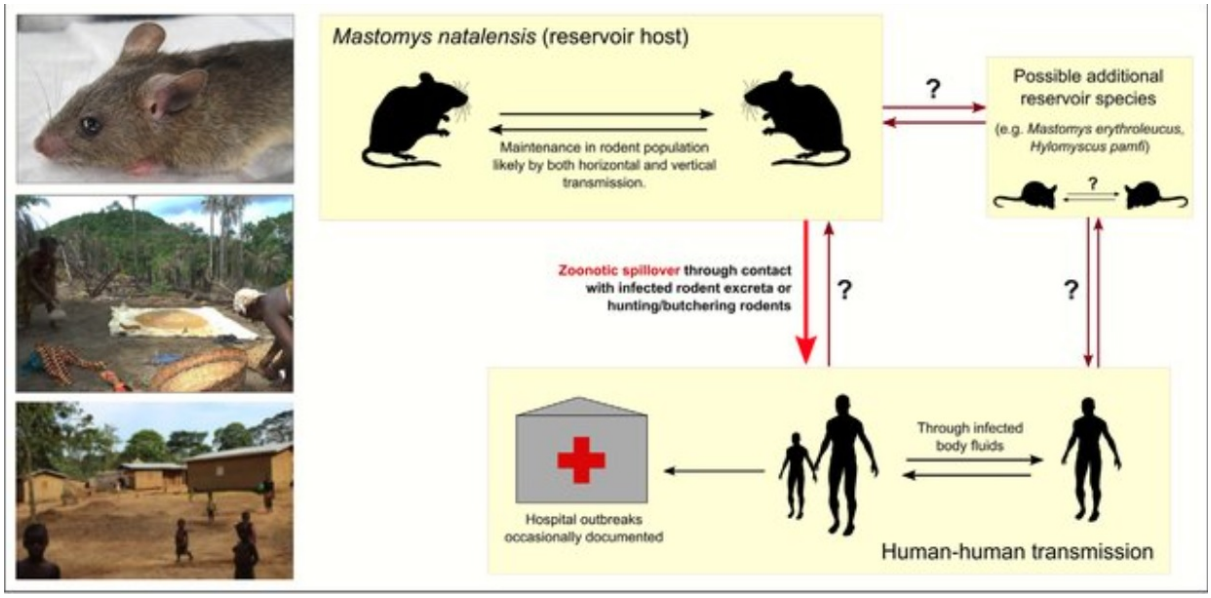

Figure 2: Lassa transmission dynamics

disease again. We assume recovered individuals do not have total or absolute immunity, we also assume lassa fever disease (LFD) is highly infectious which made us consider the use of SEIRS model for the dynamics. The population of human is given by

$$N_h = S_h + E_h + I_h + R_h$$

While the vectors population is given by

$$N_v = S_v + I_v$$

Diagram representing lassa fever disease (LFD) progression flow is given below :

$$\begin{cases} \frac{dS_h}{dt} &= \pi_h - \beta_{vh} S_h I_h - \mu_h S_h + \zeta R_h \\ \frac{dE_h}{dt} &= \beta_{vh} S_h I_h - (\mu_h + \kappa_h) E_h \\ \frac{dI_h}{dt} &= \kappa_h E_h - (\alpha_h + \mu_h + d_h) I_h \\ \frac{dR_h}{dt} &= \alpha_h I_h - \mu_h R_h - \zeta R_h \\ \frac{dS_v}{dt} &= \pi_v - \beta_{hv} S_v I_v - \mu_v S_v \\ \frac{dI_v}{dt} &= \beta_{hv} S_v I_v - (\mu_v + \tau_v) I_v \end{cases} \quad (1)$$

subject to the initial conditions, $S_h \geq 0, E_h \geq 0, I_h \geq 0, R_h \geq 0, S_v \geq 0, I_v \geq 0$

Positivity and Boundedness of Solution

Theorem 1 *The model equation (1) which has a bounded positive solution on the biological feasible region is positively invariant in region* Ω *and analyzed for understanding is defined by* $\left\{(S_h, E_h, I_h, R_h, S_v, I_v) \epsilon R_+^6 : N_h(t) \leqslant \frac{\pi_h}{\mu_h}, N_v(t) \leqslant \frac{\pi_v - \sigma_v I_v}{\mu_v}\right\}$ *with initial conditions* $S_h(0) > 0, E_h(0) \geqslant 0, I_h(0) \geqslant 0, R_h(0) \geqslant 0$ *and* $S_v(0) > 0, I_v(0) \geqslant 0$

The initial solution be given as

$$\{S_h(0), E_h(0), I_h(0), R_h(0), S_v(0), I_v(0)\} \geqslant \Omega$$

We assume positivity, i:e the initial condition satisfies

$$(S_h(0), E_h(0), I_h(0), R_h(0), S_v(0), I_v(0)) \geqslant 0$$

Hence we consider the second equation of our model equation (1)

$$\frac{dE_h}{dt} = \beta_{vh} S_h I_h - U_0 E_h \quad (2)$$

where $U_0 = (\mu_h E_h + \kappa_h)$

$$\frac{dE_h}{dt} + U_0 E_h = \beta_{vh} S_h I_h$$

Integrating Eq.(2) we have

$$E_h = K_0 e^{-U_0(t)} + e^{-U_0(t)} \int \beta_{vh} S_h I_h e^{U_0(t)} dt \geqslant 0 \quad (3)$$

where K_0 is the integrating constant. We consider the first equation of our model equation (1)

$$\frac{dS_h}{dt} = \pi_h - f(I_V(s)) S_h + \zeta R_h \quad (4)$$

where $f(I_v) = \beta_{vh} I_h + \mu_h$ Multiplying with the integrating function $e^{\int f(I_h) dI_h}$ gives

$$e^{\int f(I_h) dI_h} \frac{dS_h}{dt} + f(I_h(s)) e^{\int f(I_h) dI_h} S_h = (\pi_h + \zeta R_h) e^{\int f(I_h) dI_h}$$

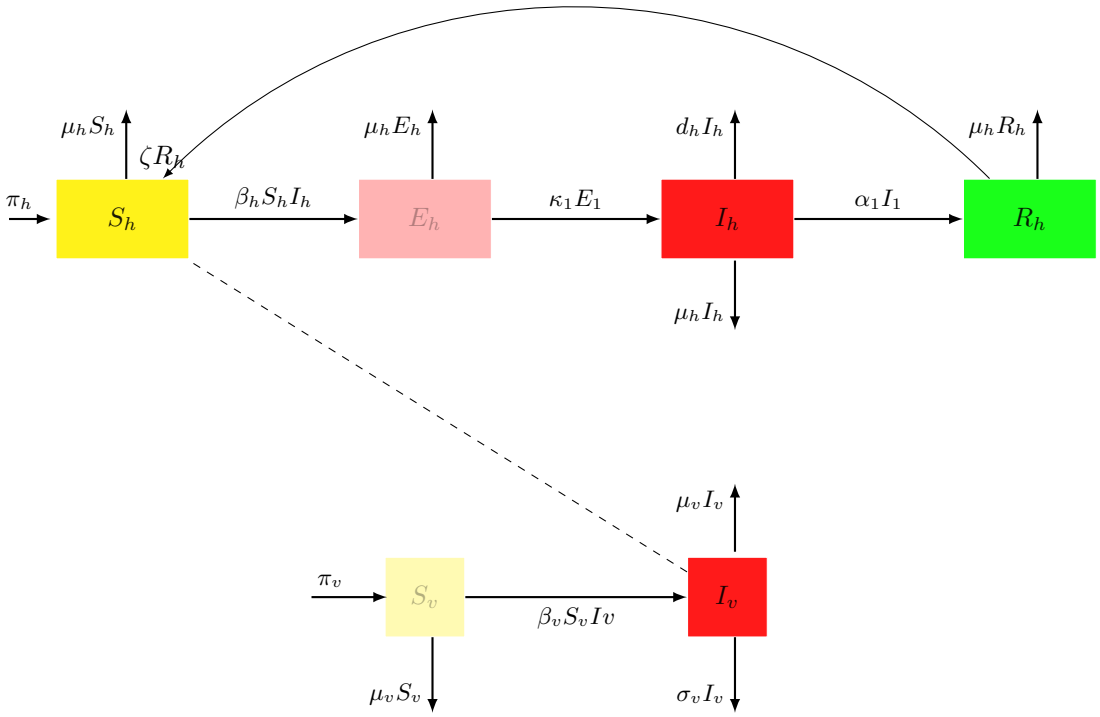

Figure 3: Schematic diagram of the disease dynamics

$$\therefore \frac{d}{dt}(e^{\int f(I_h)dI_h} S_h) = (\pi_h + \zeta R_h)e^{\int f(I_h)dI_h}$$

further integration yields

$$e^{\int f(I_h)dI_h} S_h = K_1 + \int_0^t (\pi_h + \zeta R_h)e^{\int f(I_h)dI_h}$$

$$S_h = K_1 e^{\int f(I_v)dI_v} + e^{\int f(I_v)dI_v} \int_0^t (\pi_h + \zeta R_h)e^{\int f(I_v)dI_v} \geqslant 0 \quad (5)$$

for $t \geq 0$. Hence $S_h \geq 0$ In similar fashion, we obtain the state variable of remaining equation of our model equation. For the vector, we consider the fifth equation of the LFD model,

$$\frac{dS_v}{dt} = \pi_v - U_1 S_v$$

where $U_1 = (\beta_{hv} I_v + \mu_v)$ Multiplying with the integrating function $e^{U_1(t)}$, we have

$$e^{U_1(t)} \frac{dS_v}{dt} + U_1 e^{U_1(t)} S_v = \pi_v e^{U_1(t)}$$

$$\therefore \frac{d}{dt}(e^{U_1(t)} S_v) = (\pi_v) U_1 e^{U_1(t)}$$

Integrating with respect to t yields

$$e^{U_1(t)} S_v = K_2 + \int_0^t (\pi_v) e^{U_1(t)} \geqslant 0$$

$$S_v = K_2 e^{-U_1(t)} + e^{-U_1(t)} \int_0^t (\pi_v) e^{U_1(t)} \geqslant 0 \quad (6)$$

Hence,the entire model solution $\{S_h(t), E_h(t), I_h(t), R_h(t), S_v(t), I_v(t)\}$ of the LFD model is positive for all $t \geq 0$

Theorem 2 *The entire human and vector population of the LFD model which is given as*

$$N_h(t) \leqslant \frac{\pi_h}{\mu_h}, N_v(t) \leqslant \frac{\pi_v - \sigma_v I_v}{\mu_v}$$

satisfying the initial condition of the LFD model with the assumption of the LFD model satisfies

$$N_h(0) \leqslant \frac{\pi_h}{\mu_h}, N_v(0) \leqslant \frac{\pi_v - \sigma_v I_v}{\mu_v}$$

The combined population of human and vector at any given time t which is given by

$$N_h(t) = S_h(t) + E_h(t) + I_h(t) + R_h(t)$$

and

$$N_v(t) = S_v(t) + I_v(t)$$

Hence, the derivatives of the solutions of the system are obtained as $\frac{dN_h(t)}{dt}$ and $\frac{dN_v(t)}{dt}$ which is given as

$$\frac{dN_h(t)}{dt} = \pi_h - \mu_h N_h - d_h I_h \leqslant \pi_h - \mu_h N_h$$

and

$$\frac{dN_v(t)}{dt} = \pi_v - \mu_v N_v - \sigma_v I_v \leqslant \pi_v - \mu_v N_v$$

Table 1: Description of State Variables and Parameters

State Variables	Description
N_h	Total human population.
N_v	Total vector population.
S_h	Total number of Susceptible human population at time t,
S_v	Total number of Susceptible vector population at time t,
E_h	Exposed population of human at time t.
I_h	Infected population of human at time t.
I_v	Infected population of vector at time t.
R_h	Recovered population at time t.
Parameters	Description
π_h	Recruitment rate of human population.
π_v	Recruitment rate of vector population.
μ_h	Natural death rate of human population.
μ_v	Natural death rate of vector population.
α_h	Infection rate.
ζ	Loss of immunity rate of recovered population.
σ_v	Rodent control measure.
β_{hv}	Transmission probability of Susceptible rodent with infected humans.
β_{vh}	Transmission probability of Susceptible humans with infected rodent.
d	Possible disease induced death.
κ_h	Rate at which Lassa Exposed individual becomes Infected.

State variables σ_v and d_h are negligible. Then, applying the Gronwall's inequality gives

$$N_h(t) \leqslant +\frac{\pi_h}{\mu_h}(N_h(0)-\frac{\pi_h}{\mu_h})e^{-\mu_h(t)} whenever N_h(0) \leqslant \frac{\pi_h}{\mu_h}$$

and

$$N_v(t) \leqslant \frac{\pi_v}{\mu_v}+(N_v(0)-\frac{\pi_v}{\mu_v})e^{-\mu_v(t)} whenever N_v(0) \leqslant \frac{\pi_v}{\mu_v}$$

The above shows that the region for the LFD model exists and is bounded.

Equilibrium Points

The model has two equilibrium points for the system of equation (1):

1. The Lassa free Equilibrium (LFE) L_0 occurs when the community do not have prevalent cases of Lassa Fever disease infection. Which is given by $L_0 = (S_h^0, 0, 0, 0, S_v^o, 0)$ where

$$S_h^0 = \frac{\pi_h}{\mu_h}, S_v^o = \frac{\pi_v}{\mu_v} \tag{7}$$

2. The Lassa endemic Equilibrium (LEE) L_1 occurs when their is prevalence of cases of Lassa Fever disease infection in the community. Which is given by $L_1 = (S_h^*, E_h^*, I_h^*, R_h^*, S_v^*, I_v^*)$ where

$$S_h^* = \frac{((\sigma_v + \mu_v)(\mu_h + \kappa_h)(d_h + \mu_h + \alpha_h))U_3}{\kappa_h \beta_{hv}(U_2)} \tag{8}$$

$$S_v^* = \frac{U_3}{\beta_{vh}(U_2)} \tag{9}$$

$$E_h^* = \frac{(d_h + \mu_h + \alpha_h)U_5}{\beta_{hv}(U_2)\kappa_h} \tag{10}$$

$$I_h^* = \frac{-(\zeta + \mu_h)U_1}{\beta_{hv}(U_2)} \tag{11}$$

$$I_v^* = \frac{U_4}{(\mu_v + \sigma_v)(U_3)\beta_{vh}} \tag{12}$$

$$, R_h^* = \frac{(U_1)\alpha_h}{\beta_{hv}(U_2)} \tag{13}$$

where;

$$U_1 = -\mu_v(\mu_v + \sigma_v){\mu_h}^3 - \mu_v(\mu_v + \sigma_v)\times (d_h + \alpha_h + \kappa_h){\mu_h}^2 - \mu_v\kappa_h(\mu_v + \sigma_v)\times (d_h + \alpha_h)\mu_h + \pi_h\pi_v\beta_{hv}\beta_{vh}\kappa_h$$

$$U_2 = (\mu_v + \sigma_v){\mu_h}^4 + (\mu_v + \sigma_v)\kappa_h + (\mu_v + \sigma_v)(\zeta) + (d_h + \alpha_h\sigma_v + (d_h + \alpha_h)\mu_v + \pi_v\beta_{vh}){\mu_h}^3 + (((\mu_v + \sigma_v)(\zeta) + (d_h + \alpha_h)\sigma_v + (d_h + \alpha_h)\mu_v + \pi_v\beta_{vh})\kappa_h + ((d_h + \alpha_h)\sigma_v + (d_h + \alpha_h)\mu_v + \pi_v\beta_{vh})(\zeta) + \pi_v\beta_{vh}(d_h + \alpha_h)){\mu_h}^2 + ((((d_h + \alpha_h)\sigma_v + (d_h + \alpha_h)\mu_v + \pi_v\beta_{vh})(\zeta) + \pi_v\beta_{vh}(d_h + \alpha_h))\kappa_h + (\zeta)\pi_v\beta_{vh}(d_h + \alpha_h))\mu_h + (\zeta)\pi_v\beta_{vh}d_h\kappa_h$$

$$U_3 = {\mu_h}^3\mu_v + \mu_v(\zeta + d_h + \alpha_h + \kappa_h){\mu_h}^2 + (((\zeta + d_h + \alpha_h)\kappa_h + (\zeta)(d_h + \alpha_h))\mu_v + \pi_h\beta_{hv}\kappa_h)\mu_h + (\zeta)\kappa_h\pi_h\beta_{hv} + d_h\mu_v$$

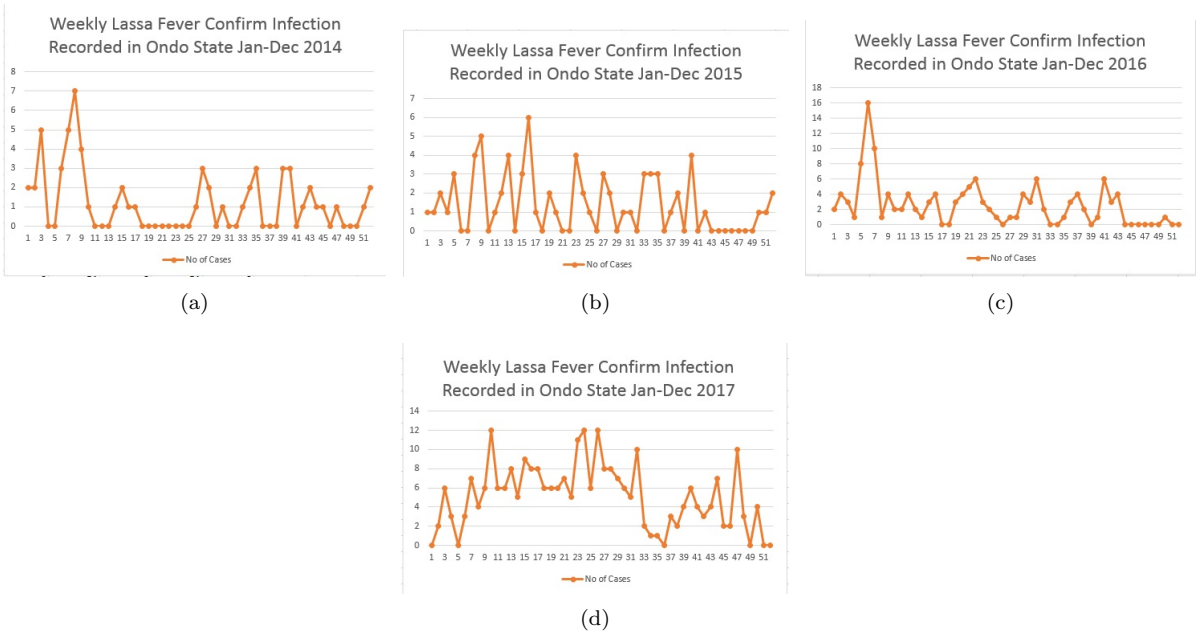

Figure 4: Case of the persistence of Lassa Fever disease for 2014-2017

$$U_4 = -(\zeta+\mu_h)(\mu_v(\mu_v+\sigma_v{\mu_h}^3+\mu_v(\mu_v+\sigma_v)\times (d_h+\alpha_h+\kappa_h){\mu_h}^2+\mu_v\kappa_h(\mu_v+\sigma_v)\times (d_h+\alpha_h)\mu_h-\pi_h\pi_v\beta_{hv}\beta_{vh}\kappa_h)$$

$$U_5 = -\mu_v(\sigma_v+\mu_v){\mu_h}^3+\mu_v(\sigma_v+\mu_v)\times (\kappa_{h+d_h+\alpha_h\mu_h{}^2+\mu_v\kappa_h(d_h+\alpha_h)\times (\sigma_v+\mu_v)\mu_h-\pi_h\pi_v\beta_{hv}\beta_{vh}\kappa_h(\zeta+\mu_h)$$

Basic Reproduction Number

Basic reproduction number R_0 of LFD model equation is transmission index controlled by the interaction between index case and secondary cases. Using next generation matrix described by (Diekmann et al., 1990; Van den Driessche and Watmough, 2002) to calculate basic reproduction of system of equation (1). Such that we define matrices $\mathbb{F}$ and $\mathbb{V}$ as inflow and outflow from compartments, i:e appearance rate of new infection and transfer of infections given below.

$$\mathbb{F} = \begin{pmatrix} \beta_{vh}S_hI_v \\ 0 \\ \beta_{hv}S_vI_h \end{pmatrix}$$

and

$$\mathbb{V} = \begin{pmatrix} (\mu_h+\kappa_h)E_h \\ -\kappa_hE_h+(d_h+\mu_hE_h+\alpha_h)I_h \\ (\mu_v+\sigma_v)I_v \end{pmatrix}$$

Which can be rewritten as

$$\mathbb{F} = \begin{pmatrix} 0 & 0 & \beta_{vh}S_h^* \\ 0 & 0 & 0 \\ 0 & \beta_{hv}S_v^* & 0 \end{pmatrix}$$

$$\mathbb{V} = \begin{pmatrix} \mu_h+\kappa_h & 0 & 0 \\ -\kappa_h & \mu_h+d_h+\alpha_h & 0 \\ 0 & 0 & \sigma_v+\mu_v \end{pmatrix}$$

The largest eigenvalue called spectral radius $\rho(FV^{-1})$ is R_0. Since existence of infection is isolated to human community, reproduction number given below:

$$FV^{-1} = \begin{pmatrix} 0 & 0 & \frac{\beta_{vh}\pi_h}{\mu_h(\mu_v+\sigma_v)} \\ 0 & 0 & 0 \\ \frac{\beta_{hv}\pi_v\kappa_h}{\mu_v(\mu_h+\kappa_h)(d_h+\mu_h+\alpha_h)} & \frac{\beta_{hv}\pi_v}{\mu_v(d_h+\mu_h+\alpha_h)} & 0 \end{pmatrix} \quad (14)$$

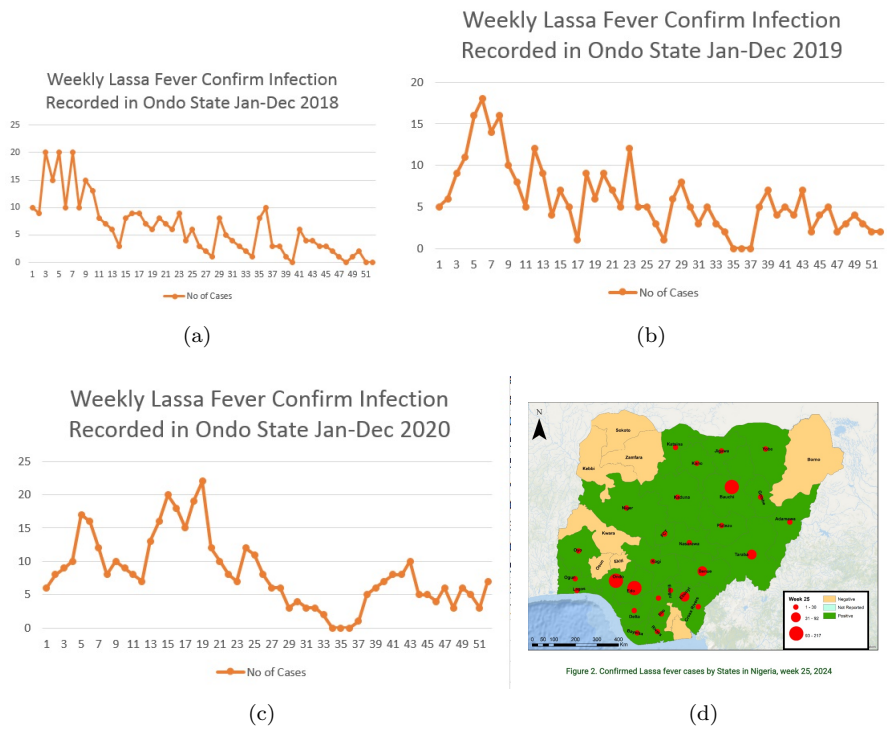

Figure 5: Case of the persistence of Lassa Fever disease for 2018-2024

and has three eigenvalues

$$\lambda^{(1)} = 0, \lambda^{(2)} = \frac{\sqrt{\mu_h \mu_v \left(\mu_h + \kappa_h\right)\left(d_h + \mu_h + \alpha_h\right)\left(\mu_v + \sigma_v\right)\beta_{hv}\pi_v \kappa_h \beta_{vh}\pi_h}}{\mu_v \left(\mu_h + \kappa_h\right)\left(d_h + \mu_h + \alpha_h\right)\mu_h \left(\mu_v + \sigma_v\right)} \tag{15}$$

$$\lambda^{(3)} = -\frac{\sqrt{\mu_h \mu_v \left(\mu_h + \kappa_h\right)\left(d_h + \mu_h + \alpha_h\right)\left(\mu_v + \sigma_v\right)\beta_{hv}\pi_v \kappa_h \beta_{vh}\pi_h}}{\mu_v \left(\mu_h + \kappa_h\right)\left(d_h + \mu_h + \alpha_h\right)\mu_h \left(\mu_v + \sigma_v\right)} \tag{16}$$

Thus, basic reproduction number R_0 the spectral radius is dominant maximum eigenvalue of FV^{-1} which is given by

$$R_0 = \frac{\sqrt{\mu_h \mu_v \left(\mu_h + \kappa_h\right)\left(d_h + \mu_h + \alpha_h\right)\left(\mu_v + \sigma_v\right)\beta_{hv}\pi_v \kappa_h \beta_{vh}\pi_h}}{\mu_v \left(\mu_h + \kappa_h\right)\left(d_h + \mu_h + \alpha_h\right)\mu_h \left(\mu_v + \sigma_v\right)} \tag{17}$$

Hence, basic reproduction number of Lassa fever disease prevalence is average secondary infections caused by single infected individual during his/her entire period of infectiousness in the community.

Stability Analysis

Theorem 3 *The Lassa free equilibrium L_0 is locally asymptotically stable when $R_0 < 1$ and unstable when $R_0 > 1$.*

The Jacobian matrix which is evaluated at L_0 is given by

$$J(L_0) = \begin{pmatrix} -\mu_h & 0 & 0 & \zeta & 0 & -\frac{\beta_{vh}\pi_h}{\mu_h} \\ 0 & -\mu_h - \kappa_h & 0 & 0 & 0 & \frac{\beta_{vh}\pi_h}{\mu_h} \\ 0 & \kappa_h & -d_h - \mu_h - \alpha_h & 0 & 0 & 0 \\ 0 & 0 & \alpha_h & -\zeta - \mu_h & 0 & 0 \\ 0 & 0 & -\frac{\beta_{hv}\pi_v}{\mu_v} & 0 & -\mu_v & 0 \\ 0 & 0 & \frac{\beta_{hv}\pi_v}{\mu_v} & 0 & 0 & -\sigma_v - \mu_v \end{pmatrix} \tag{18}$$

From the values of all the diagonal entries of $|J(L_0)|$ of (18). We use the upper triangular matrix principle

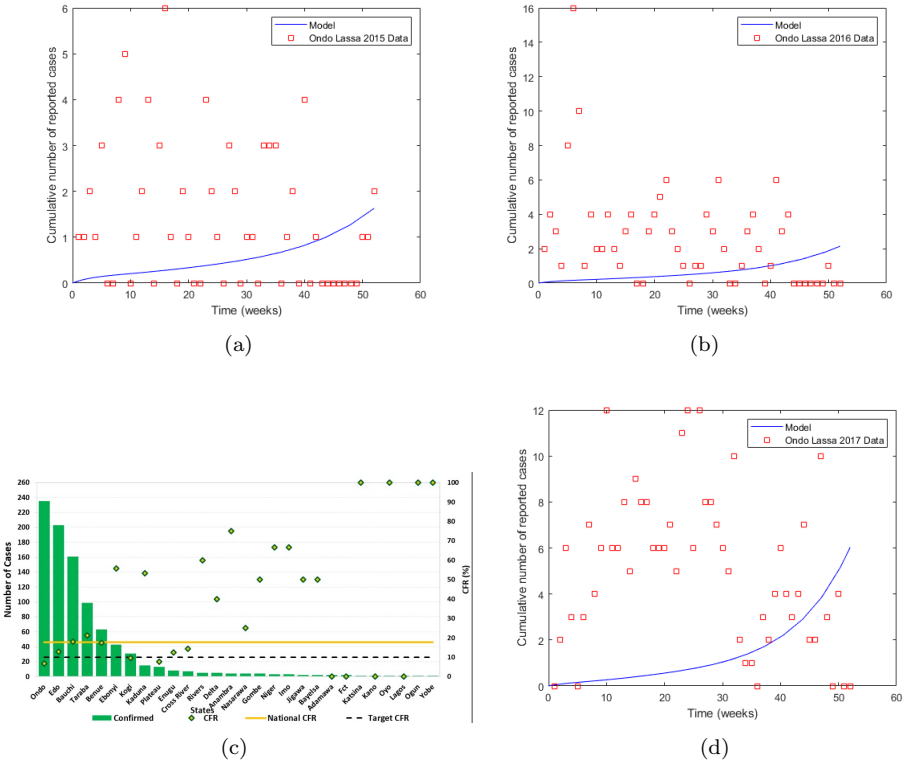

Figure 6: Number of Confirmed cases with case of fatality (CFR) by state, week 25 2024

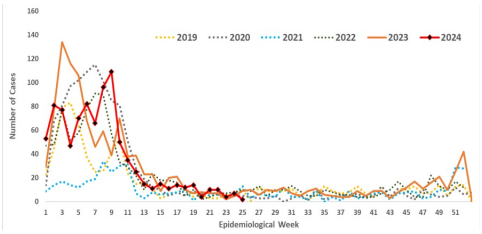

Figure 7: Trend of reported and confirmed cases of Lassa fever disease 2019-2024

Coelho and Milies (1993). Therefore, the determinant $det(\mathbf{J}(\mathbf{L_0}) - \lambda I) = 0$ which is the product of its diagonal entries becomes:

$$J(L_0) = \begin{pmatrix} -\mu_h & 0 & 0 & \zeta & 0 & -\frac{\beta_{vh}\pi_h}{\mu_h} \\ 0 & -\mu_h - \kappa_h & 0 & 0 & 0 & \frac{\beta_{vh}\pi_h}{\mu_h} \\ 0 & 0 & -d_h - \mu_h - \alpha_h & 0 & 0 & 0 \\ 0 & 0 & 0 & -\zeta - \mu_h & 0 & 0 \\ 0 & 0 & 0 & 0 & -\mu_v & 0 \\ 0 & 0 & 0 & 0 & 0 & -\sigma_v - \mu_v \end{pmatrix}$$

Its eigenvalues are

$$\lambda^{(1)} = -\mu_h, \lambda^{(2)} = -\sigma_v - \mu_v, \lambda^{(3)} = -\mu_v, \tag{19}$$

$$\lambda^{(4)} = -\mu_h - \kappa_h, \lambda^{(5)} = -d_h - \mu_h - \alpha_h, \lambda^{(6)} = -\zeta - \mu_h \tag{20}$$

Since the values of $\lambda^{(1)} < 0$, $\lambda^{(2)} < 0$ $\lambda^{(3)} < 0$, $\lambda^{(4)} < 0$, $\lambda^{(5)} < 0$ and $\lambda^{(6)} < 0$ have no positive signs, hence the equilibrium point $R_0 < 1$, then L_0 is asymptotically stable.

Theorem 4 *The Lassa endemic equilibrium L_1 is locally asymptotically stable when $R_0 < 1$ and un-*

Table 2: Description of State Variables, Parameters Values and Reference used.

Parameters	Value	Reference
π_v	500	[Diekmann et al. (1990)]
π_h	2000	[Diekmann et al. (1990)]
β_{vh}	0.7	Assumed
β_{hv}	1.8	Assumed
μ_v	0.6	[Obabiyi and Onifade (2017)]
μ_h	0.2	[Obabiyi and Onifade (2017)]
α_h	0.039	[Obabiyi and Onifade (2017)]
σ_v	0.046	[Obabiyi and Onifade (2017)]
d_h	0.02	[Okuonghae and Okuonghae (2006)]
ζ	0.2	[Okuonghae and Okuonghae (2006)]
κ_h	0.018	[Richmond and Baglole (2003)]

stable when $R_0 > 1$.

The Jacobian matrix which is evaluated at L_1 is given by

$$J(L_1) = \begin{pmatrix} -\beta_{vh}i_v - \mu_h & 0 & 0 & \zeta & 0 & -\beta_{vh}S_h^* \\ \beta_{vh}i_v & -\mu_h - \kappa_h & 0 & 0 & 0 & \beta_{vh}S_h^* \\ 0 & \kappa_h & -d_h - \mu_h - \alpha_h & 0 & 0 & 0 \\ 0 & 0 & \alpha_h & -\zeta - \mu_h & 0 & 0 \\ 0 & 0 & -\beta_{hv}S_v^* & 0 & -\beta_{hv}i_h - \mu_v & 0 \\ 0 & 0 & \beta_{hv}S_v^* & 0 & \beta_{hv}i_h & -\sigma_v - \mu_v \end{pmatrix} \tag{21}$$

Then Eq.(21) becomes

$$J(L_1) = \left[\begin{array}{ccc|ccc} -\beta_{vh}i_v - \mu_h & 0 & 0 & \zeta & 0 & -\beta_{vh}S_h^* \\ \beta_{vh}i_v & -\mu_h - \kappa_h & 0 & 0 & 0 & \beta_{vh}S_h^* \\ 0 & \kappa_h & -d_h - \mu_h - \alpha_h & 0 & 0 & 0 \\ \hline 0 & 0 & \alpha_h & -\zeta - \mu_h & 0 & 0 \\ 0 & 0 & -\beta_{hv}S_v^* & 0 & -\beta_{hv}i_h - \mu_v & 0 \\ 0 & 0 & \beta_{hv}S_v^* & 0 & \beta_{hv}i_h & -\sigma_v - \mu_v \end{array}\right] \tag{22}$$

where

$$A1 = \begin{pmatrix} -\beta_{vh}i_v - \mu_h & 0 & 0 \\ \beta_{vh}i_v & -\mu_h - \kappa_h & 0 \\ 0 & \kappa_h & -d_h - \mu_h - \alpha_h \end{pmatrix}$$

$$A2 = \begin{pmatrix} -\zeta - \mu_h & 0 & 0 \\ 0 & -\beta_{hv}i_h - \mu_v & 0 \\ 0 & \beta_{hv}i_h & -\sigma_v - \mu_v \end{pmatrix}$$

The matrix J(L1) and its eigenvalues a diagonal bloc matrix. Hence, the eigenvalue of first bloc named A1 becomes

$$\lambda^{(1)} = -\mu_h - \kappa_h < 0 \tag{23}$$

$$\lambda^{(2)} = -\beta_{vh}i_v - \mu_h < 0 \tag{24}$$

$$\lambda^{(3)} = -d_h - \mu_h - \alpha_h < 0 \tag{25}$$

While eigenvalue of fourth bloc named A2 becomes

$$\lambda^{(4)} = -\sigma_v - \mu_v < 0 \tag{26}$$

$$\lambda^{(5)} = -\beta_{hv}i_h - \mu_v < 0 \tag{27}$$

$$\lambda^{(6)} = -\zeta - \mu_h < 0 \tag{28}$$

from the values of $\lambda^{(1)} < 0, \lambda^{(2)} < 0, \lambda^{(3)} < 0, \lambda^{(4)} < 0, \lambda^{(5)} < 0, \lambda^{(6)} < 0$, It is clear the L_1 have no positive sign, hence the endemic equilibrium (L_1) is locally asymptotically stable.

Numerical Simulation

In this section, critical Numerical simulations for Lassa fever disease model were performed using

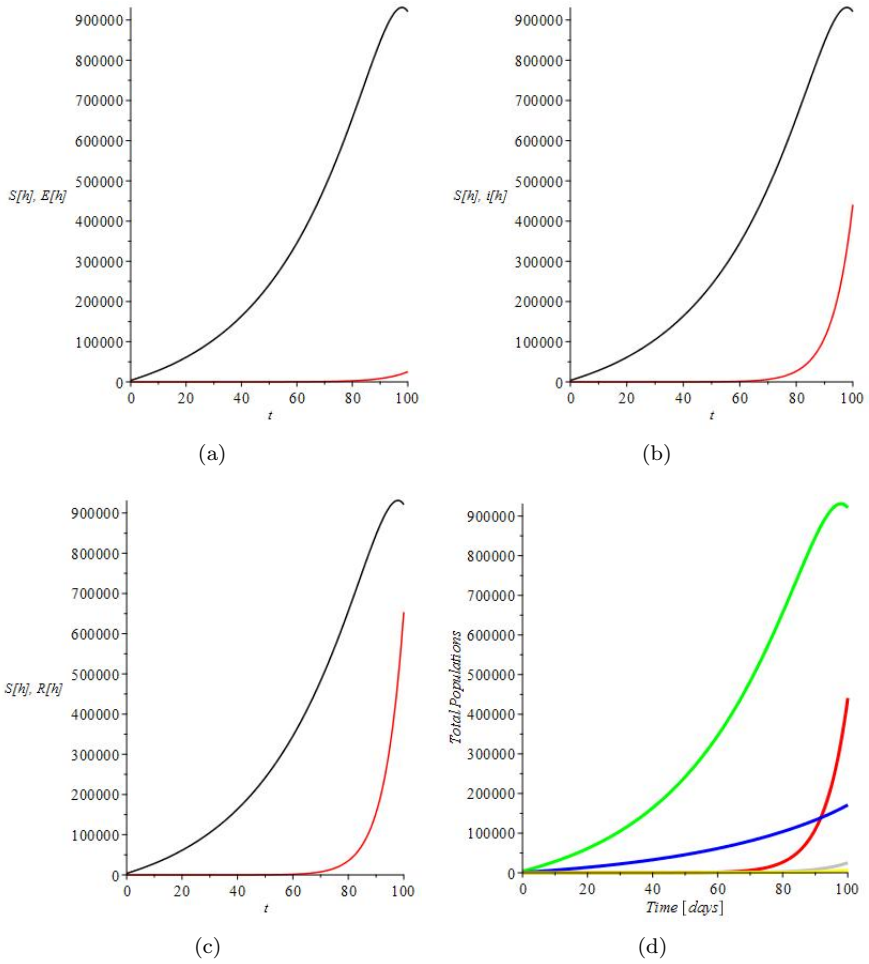

Figure 8: Case of the persistence of Lassa fever disease

parameter values in tables showing prevalence of Lassa with regards to number of recorded cases on weekly basis from January 2014 to December 2020. LFD model parameter sourced from existing literature where available for use, while other model parameter were logically estimated for illustration to fit model analysis. Coupled with Lassa fever infection data spreadsheet for Ondo State, Nigeria sourced from Ondo State Ministry of health and Nigeria Centre for Disease control (NCDC). Program codes with ODE45 were written and implemented on MATLAB encoded solver to simulate Lassa fever disease model system using parameters values.

Our model (i) was applied to study the dynamics of Lassa fever disease in Ondo State, Nigeria. The released weekly outbreak data by the Nigeria Center for Disease Control (NCDC) are used for the fitting. We specifically used cumulative number of reported and active cases for data and model fitting. Which we implemented in our model, conducting numerical simulations for epidemic period starting from when index case was announced in Ondo State.

Model fitting

For our LVD model fitting, we used a genetic algorithm (GA) as function optimizer which was implemented in MATLAB; the GA algorithm enables us find an accurate starting value of estimated parameters and a correct basin of attraction. Enabling adequate use of fmincon function in MATLAB's Optimization Toolbox. By combining these two optimization algorithms for LVD model data fitting, both GA algorithm and fmincon algorithm in MATLAB got more accurate estimation. After which our model fitting was implemented for the cumulative epidemic period from the announcement of the index case in Onso State.

The data used for this analysis is a daily report on the ravaging Lassa fever(LFD) collected from the Nigeria Centre for Disease Control (NCDC) and Ondo State Public Health (OSPH)

DISCUSSIONS

Numerical model parameters of Lassa fever disease (LFD) used in existing in literature with definitive peculiarity of the model and its assumptions, while

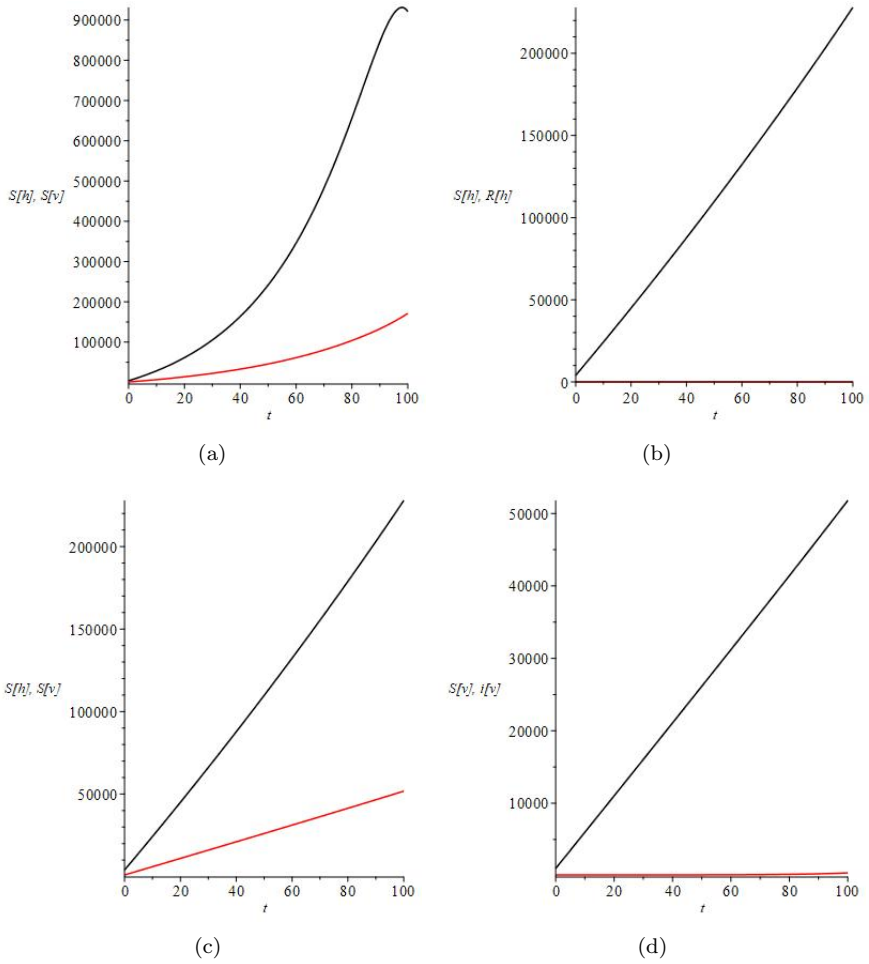

Figure 9: Case of the persistence of Lassa fever Disease with relation to time

other (LFD) model parameters were estimated for purpose of illustrating model analyses to give a logical interpretation. Pictures of dynamical behavior of LFD in specified population, giving the presence of movement of susceptible human in relation to susceptible vector by the numerical simulations of the model (1). Where all the numerical simulations were executed in MAPLE 18

Fig. 6(a) confirmed that number of susceptible human continues to increase rapidly with the exposed human as time progresses because the contact rate on secondary infection will increase as days progresses 100days. While Fig. 6(b) shows that susceptible human and infected human keeps increasing as the days progressing, which in fact signify the number of infected human. Fig. 7 shows the impact of persistence of the disease with relation to time.

CONCLUSION

In this paper, we describe mathematical model of Lassa Fever disease transmission dynamics, our model consist of six compartments with four human population and two vector . Susceptible human are mutually exclusive with Infected vectors who are assumed not to recover and can be removed by predators and by pest control measures by human activities. The Lassa Free Equilibrium (LFE) and Lassa Endemic Equilibrium (LEE) exist in the model which are locally stable at equilibrium. Transmission dynamics shows the effect of the Basic Reproduction number and the graphs also shows the effect of transmission dynamics in relation with time. The solution of the system of equation was tested to be positive and bounded at all time t. We investigated qualitative analysis by deriving the equilibrium points and its stability. The numerical simulation reflects the transmission trend of lassa fever in prevailing communities as seen in the weekly prevalence report showing that fighting against the disease requires effective approach of proper disposal waste and hygienic living as suggested to Ondo State ministry of health and department of public health services for awareness and education.

Declaration of Competing Interest

The authors therefore declares that there is and no knowledge of conflicting and competing financial interests as well as personal relationships that could have affected efforts put on to influence work done in this paper.

References

Akanni, J. and Adediipo, A. (2018). Sensitivity analysis of the dynamical transmission and control of lassa fever virus. *Asian Research Journal of Mathematics*, pages 1–11.

Bawa, M., Abdulrahman, S., Jimoh, O., and Adabara, N. (2013). Stability analysis of the disease–free equilibrium state for lassa fever disease. *Journal of Science, Technology, Mathematics and Education (JOSTMED)*, 9(2):115–123.

Chaikham, N. and Sawangtong, W. (2017). Optimal control of zika virus infection by vector elimination, vector-to-human and human-to-human contact reduction. *Advances in Difference Equations*, 2017(1):177.

Coelho, S. P. and Milies, C. P. (1993). Derivations of upper triangular matrix rings. *Linear algebra and its applications*, 187:263–267.

Dahmane, A., Van Griensven, J., Van Herp, M., Van den Bergh, R., Nzomukunda, Y., Prior, J., Alders, P., Jambai, A., and Zachariah, R. (2014). Constraints in the diagnosis and treatment of lassa fever and the effect on mortality in hospitalized children and women with obstetric conditions in a rural district hospital in sierra leone. *Transactions of the Royal Society of Tropical Medicine and Hygiene*, 108(3):126–132.

Diekmann, O., Heesterbeek, J. A. P., and Metz, J. A. (1990). On the definition and the computation of the basic reproduction ratio r 0 in models for infectious diseases in heterogeneous populations. *Journal of mathematical biology*, 28(4):365–382.

Djomegni, P. T., Olupitan, G., and Goufo, E. D. (2021). A metapopulation model for zika virus disease transmission dynamics between linked communities. *Physica Scripta*, 96(12):124049.

Gupta, N. and Rink, R. (1973). Optimum control of epidemics. *Mathematical Biosciences*, 18(3-4):383–396.

Karrakchou, J., Rachik, M., and Gourari, S. (2006). Optimal control and infectiology: application to an hiv/aids model. *Applied mathematics and computation*, 177(2):807–818.

Keenlyside, R. A., McCormick, J. B., Webb, P. A., Smith, E., Elliott, L., and Johnson, K. M. (1983). Case-control study of mastomys natalensis and humans in lassa virus-infected households in sierra leone. *The American journal of tropical medicine and hygiene*, 32(4):829–837.

Kutch, J. J. and Gurfil, P. (2002). Optimal control of hiv infection with a continuously-mutating viral population. In *Proceedings of the 2002 American Control Conference (IEEE Cat. No. CH37301)*, volume 5, pages 4033–4038. IEEE.

Leirs, H., Verhagen, R., Verheyen, W., Mwanjabe, P., and Mbise, T. (1996). Forecasting rodent outbreaks in africa: an ecological basis for mastomys control in tanzania. *Journal of Applied Ecology*, pages 937–943.

Li, S.-L., Bjørnstad, O. N., Ferrari, M. J., Mummah, R., Runge, M. C., Fonnesbeck, C. J., Tildesley, M. J., Probert, W. J., and Shea, K. (2017). Essential information: Uncertainty and optimal control of ebola outbreaks. *Proceedings of the National Academy of Sciences*, 114(22):5659–5664.

Momoh, A. A. and Fügenschuh, A. (2018). Optimal control of intervention strategies and cost effectiveness analysis for a zika virus model. *Operations Research for Health Care*, 18:99–111.

Obabiyi, O. and Onifade, A. A. (2017). Mathematical model for lassa fever transmission dynamics with variable human and reservoir population. *International Journal of Differential Equations and Applications*, 16(1).

Okosun, K. O., Rachid, O., and Marcus, N. (2013). Optimal control strategies and cost-effectiveness analysis of a malaria model. *BioSystems*, 111(2):83–101.

Okuonghae, D. and Okuonghae, R. (2006). A mathematical model for lassa fever. *Journal of the Nigerian Association of Mathematical Physics*, 10(1).

Rachah, A. and Torres, D. F. (2015). Mathematical modelling, simulation, and optimal control of the 2014 ebola outbreak in west africa. *Discrete Dynamics in Nature and Society*, 2015.

Rafikov, M., Bevilacqua, L., and Wyse, A. (2009). Optimal control strategy of malaria vector using genetically modified mosquitoes. *Journal of Theoretical Biology*, 258(3):418–425.

Richmond, J. K. and Baglole, D. J. (2003). Lassa fever: epidemiology, clinical features, and social consequences. *Bmj*, 327(7426):1271–1275.

Team, N. S. et al. (2018). Lassa fever in nigeria, 2017-2018. *Bulletin of the Nigeria Centre for Disease Control*.

Team, N. S. et al. (2019). Lassa fever in nigeria, 2019. *Bulletin of the Nigeria Centre for Disease Control*.

Van den Driessche, P. and Watmough, J. (2002). Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission. *Mathematical biosciences*, 180(1-2):29–48.