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**Mathematical Model for the Transmission Dynamics of Lassa Fever
 Disease with Contact Tracing and Effective Quarantine**

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ABSTRACT

In this paper, we developed a mathematical model to study transmission dynamics of Lassa fever with contact tracing and effective quarantine as control strategies. The model is sub divided into eight mutually exclusive classes namely: Susceptible human S_H , Humans suspected to have had contact with the infected C_H , Infected humans I_H , Quarantined humans Q_H , Recovered humans R_H , Dead humans D , Susceptible rodents S_R and Infected rodents I_R . We established the positivity of the solution for the model equations, more also, we obtained the invariant region of the system. The disease-free equilibrium point was established and the model threshold parameter (Reproduction Number) was examined using next-generation operator method. The model analytical result shows that diseases free equilibrium is local asymptotically stable at $R_0 < 1$ and unstable at $R_0 > 1$. We also established that the model is globally asymptotically stable using Castillo-Chavez method. The simulated results show that effective contact tracing and quarantining reduces the spread of Lassa fever. We therefore conclude that every effort must be put in place by the agencies concern to ensure that early contact tracing and effective quarantining is encouraged as this play a very vital role in controlling the spread of the virus.

Keywords: lassa fever, contact tracing, quarantine, local stability, global stability.

1. INTRODUCTION

Lassa fever is an acute viral illness cause by Lassa virus and a zoonotic disease which is transmitted from an infected animal to human, person to person and occurs in the dry season as a result of dust particles from dead rats. The virus is known as Mastomy (Mastomy Natalensis), it can also be defined as a viral disease that attacks the liver, nervous system, spleen and kidney. It is an acute viral hemorrhagic fever (VHF) first isolated in a town called Lassa in the Yedseram River Valley in the present Borno State of Northern Nigeria in 1969 (Tara, 2004). The first victim is Laura Wine, 65 years old female nurse who works at Lassa Mission Hospital (McCormick, Webb, Krebs, Johnson & Smith, 1998). Lassa fever is endemic in Nigeria, Liberia, Sierra Leone, Guinea and other West African countries, 2-3 million people with 5000-10000 fatalities annually. Since its initial discovery in Lassa-Nigeria, rural and

nosocomial outbreaks of Lassa fever have occurred repeatedly in other parts of Nigeria: Jos, Onitsha, Zorikwa, and Ekpoma (Tomori, Fabiyi, Sorungbe, Smith & McCormick, 1998). Promed (2006) reported outbreaks in some cities of West African countries of Sierra Leone, Liberia, Guinea. In Côte d'Ivoire, Ghana, Togo and Benin, no outbreak has ever been recorded, though isolated cases show evidence of viral circulation (Günther, Weisner, Roth, Grewing, Asper, Drosten et al., 2001). Lassa fever therefore appears to have 2 geographically separate endemic areas: The Mano River region (Guinea, Sierra Leone, and Liberia) in the West, and Nigeria in the East. However, Some Lassa fever cases have been "imported" into the U.S. and U.K. through travelers who acquired the disease elsewhere (Tara, 2004). Definitive diagnosis requires testing that is available only in reference

laboratories. Laboratory specimens may be hazardous and must be handled with extreme care. Lassa virus infections can only be diagnosed definitively in the laboratory using the following tests: i. reverse transcriptase polymerase chain reaction (RT-PCR) assay; ii. antibody enzyme-linked immunosorbent assay (ELISA); iii. antigen detection tests; iv. virus isolation by cell culture (Richmond and Bangole, 2003). Though first described in the 1950s, the virus causing Lassa disease was not identified until 1969. The virus is a single-stranded RNA virus belonging to the virus family Arenaviridae. About 80% of people who become infected with Lassa virus have no symptoms. One in five infections results in severe disease, where the virus affects several organs such as the liver, spleen, and kidneys (World Health Organization, 2017). The incubation period of Lassa fever ranges from 6–21 days. The onset of the disease, when it is symptomatic, is usually gradual, starting with fever, general weakness, and malaise. After a few days, headache, sore throat, muscle pain, chest pain, nausea, vomiting, diarrhoea, cough, and abdominal pain may follow. In severe cases facial swelling, fluid in the lung cavity, bleeding from the mouth, nose, vagina or gastrointestinal tract and low blood pressure may develop (WHO, 2016). The effect of acquiring immunity, be it permanent or temporal have been of great interest to researchers, aimed at gaining better insight into the complex transmission dynamics of infectious diseases (El-Doma, 2006).

2. MATHEMATICAL FORMULATION

In this paper, we divide the human population into six (6) compartments: the susceptible human S_H , these are those who could contract the virus; C_H , individuals that are suspected to have had contact with the virus; the infected I_H , these refers to those who have had contact with the virus and are now infected and also capable of

infecting others; the quarantined Q_H , are people who are being observed if they would show symptoms of the disease; those who do not show symptoms go back to the susceptible class, while those that become symptomatic are treated; if they recover the move to the recovered class R_H and then back to the susceptible class; those who couldn't recover move to D ; the recovered class R_H these group of people have been treated and confirmed to have no trace of the virus hence have temporal immunity; whereas D represents their dead bodies, these category could not recover, they are also capable of transmitting the disease. The vector population *mastomys natalensis* is divided into susceptible rodents S_R and rodents I_R . The susceptible humans population is increased by recruitment (birth) at a constant rate β_1 , ψ is the quarantine rate of humans who were successfully contact traced while ϵ refers to the rate at which humans who had contact with the virus but were not successfully contact traced progress to the infectious class without being quarantined. The susceptible human population decreases due to transmission by infected humans, infected rats, and the dead humans who were not properly buried; this is denoted by $\alpha_1 S_H I_H + \alpha_2 S_H I_R + \alpha_3 S_H D$ and the natural death rate μ_H . The susceptible rat population increases by recruitment (birth) at constant rate β_2 The susceptible rat population decreases due to transmission by infected humans and dead humans who were not properly buried denoted by $\alpha_1 S_R I_H + \alpha_3 S_R D$, natural death of rats at rate μ_R . The epidemiological flow for the Lassa fever model with contact traced humans, quarantine humans and rats compartments is presented in figure 1.

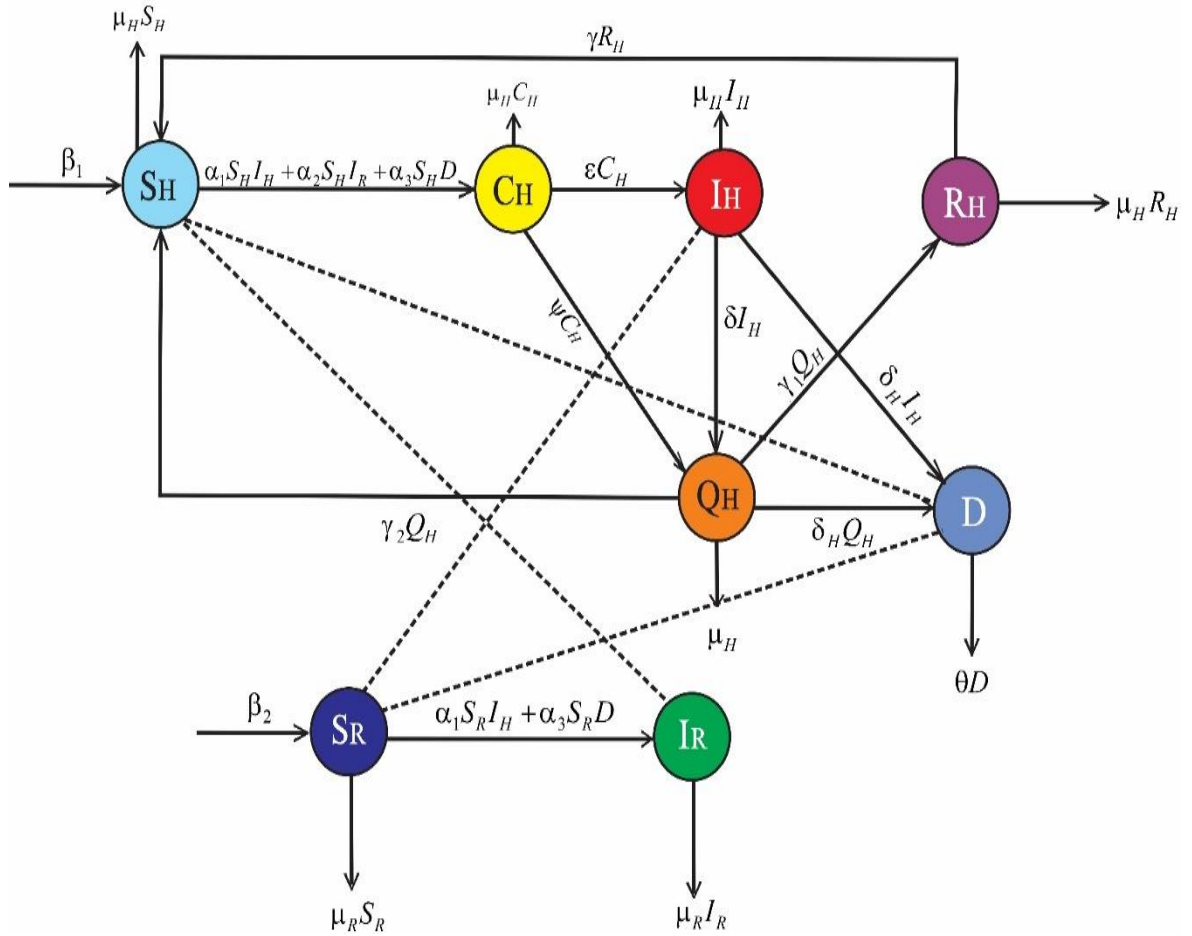


Figure 1. The epidemiological flow for the Lassa fever model.

2.1 Model equations

$$\left. \begin{aligned}
 \frac{dS_H}{dt} &= \beta_1 + \gamma_2 Q_H + \gamma R_H - (\alpha_1 S_H I_H + \alpha_2 S_H I_R + \alpha_3 S_H D) - \mu_H S_H \\
 \frac{dC_H}{dt} &= \alpha_1 S_H I_H + \alpha_2 S_H I_R + \alpha_3 S_H D - (\varepsilon + \psi + \mu_H) C_H \\
 \frac{dI_H}{dt} &= \varepsilon C_H - (\delta + \delta_H + \mu_H) I_H \\
 \frac{dQ_H}{dt} &= \psi C_H + \delta I_H - (\gamma_1 + \gamma_2 + \delta_H + \mu_H) Q_H \\
 \frac{dR_H}{dt} &= \gamma_1 Q_H - (\gamma + \mu_H) R_H \\
 \frac{dD}{dt} &= \delta_H I_H + \delta_H Q_H - \theta D \\
 \frac{dS_R}{dt} &= \beta_2 - (\alpha_1 I_H + \alpha_3 D) S_R - \mu_R S_R \\
 \frac{dI_R}{dt} &= (\alpha_1 I_H + \alpha_3 D) S_R - \mu_R I_R
 \end{aligned} \right\} \quad (1)$$

where initial conditions are:

$$\{S_H(0) > 0, C_H(0) > 0, I_H(0) > 0, Q_H(0) > 0, R_H(0) > 0, D(0) > 0, S_R(0) > 0, I_R(0) > 0\} \in \mathbb{R}_+^8$$

Table1: Variables and parameters for the Lassa fever model.

Symbol	Description
S_H	Susceptible humans at time t .
C_H	Humans suspected to have had contact with the infected at time t .
Q_H	Quarantined humans at time t .
I_H	Infected humans at time t .
R_H	Recovered humans at time t .
D	Dead humans at time t .
R_H	Recovered humans at time t .
S_R	Susceptible rodents at time t .
I_R	Infected rodents at time t .
α_1	Rate of transmission by infected humans.
α_2	Rate of transmission by infected rodents.
α_3	Rate of transmission by dead bodies of humans not properly buried.
ε	Rate of progression to the infected class by humans suspected to have had contact with the infected but not successfully contact traced.
γ	Rate at which recovered humans become susceptible.
γ_1	Humans recovery rate.
γ_2	Rate at which the quarantined that shows no symptoms.
ψ	Quarantine rate of humans successfully contact traced.
θ	Rate of proper burial.
δ	Quarantine rate of infected humans who could not be contact traced before showing symptoms.
δ_H	Disease induced death rate.
μ_H	Natural death rate for humans.
μ_R	Natural death rate for rodents.

3. MODEL ANALYSIS

3.1 Invariant region

Lemma 1

Let $(S_H, C_H, I_H, Q_H, R_H, D, S_R, I_R)$ be the solution of the model equations (1) with the initial conditions and biological feasible region given by the set $\Omega = \Omega_H \cup \Omega_R$ where

$$\Omega_H = \left\{ (S_H, C_H, I_H, Q_H, R_H, D) \in \mathbb{R}_+^6 : N_H \leq \frac{\beta_1}{\mu_H} \right\}$$

$$\Omega_R = \left\{ (S_R, I_R) \in R_+^2 : N_b \leq \frac{\beta_2}{\mu_R} \right\}$$

It has been verified that the model is biologically feasible.

3.2 Positivity of solution

It is necessary to prove that all solutions of system (1) with positive initial conditions will remain positive for all times $t > 0$.

$$\{S_H(0) > 0, C_H(0) > 0, I_H(0) > 0, Q_H(0) > 0, R_H(0) > 0, D(0) > 0, S_R(0) > 0, I_R(0) > 0\} \in \mathbb{R}_+^8$$

Then the solution set $\{S_H(t), C_H(t), I_H(t), Q_H(t), R_H(t), D(t), S_R(t), I_R(t)\}$ is positive for all time $t > 0$.

The proof for has also been verified and we conclude that the system (1) with positive initial conditions will remain positive for all times $t > 0$.

3.3 Disease free equilibrium

$$\text{At equilibrium, } \frac{dS_H}{dt} = \frac{dC_H}{dt} = \frac{dI_H}{dt} = \frac{dQ_H}{dt} = \frac{dR_H}{dt} = \frac{dD}{dt} = \frac{dS_R}{dt} = \frac{dI_R}{dt} = 0.$$

Therefore, the disease free equilibrium state (DFE) for the Lassa fever model denoted by E_0 is

$$E_0 = \left(\frac{\beta_1}{\mu_H}, 0, 0, 0, 0, 0, \frac{\beta_2}{\mu_R}, 0 \right)$$

3.4 Model reproduction number

The basic reproduction number of transmission dynamics of lassa fever disease with quarantine is denoted by R_0 . It is an important parameter that is used to study the behavior of epidemiological models. It is defined as the average number of secondary infections infected by an infective individual during an infective period provided that the all members of the population are susceptible. We apply the next generation matrix technique by Diekman, Heesterbeek and Metz (1990) to obtain the basic reproduction number

for Lassa fever Disease R_0 by considering the infected compartments of the system (1).

Let F_i be the rate of appearance of new infection in the i compartment and V_i be the rate of transfer of individuals out of i , given the disease free equilibrium, then R_0 is the spectral radius (largest Eigen values) of the next generation matrix denoted by $G = FV^{-1}$. $R_0 = \rho FV^{-1}$

$$R_0 = \frac{\frac{\alpha_1\beta_1D_2 + \alpha_3\beta_1D_4}{\mu_H} + \sqrt{4\left(\frac{\alpha_1\beta_2D_2 + \alpha_3\beta_2D_4}{\mu_R}\right)\left(\frac{\alpha_2\beta_1D_{11}}{\mu_H}\right) + \left(\frac{\alpha_1\beta_1D_2 + \alpha_3\beta_1D_4}{\mu_H}\right)^2}}{2} \tag{2}$$

3.5 Local stability of the disease free equilibrium

Theorem 1.

The disease free equilibrium point E_o is locally asymptotically stable if $R_o < 1$ and unstable if $R_o > 1$

Proof

Let

$$\left. \begin{aligned} F_1 &= \beta_1 + \gamma_2 Q_H + \gamma R_H - (\alpha_1 I_H + \alpha_2 I_R + \alpha_3 D + \mu_H) S_H \\ F_2 &= (\alpha_1 I_H + \alpha_2 I_R + \alpha_3 D) S_H - (\varepsilon + \psi + \mu_H) C_H \\ F_3 &= \varepsilon C_H - (\delta + \delta_H + \mu_H) I_H \\ F_4 &= \psi C_H + \delta I_H - (\gamma_1 + \gamma_2 + \mu_H + \delta_H) Q_H \\ F_5 &= \gamma_1 Q_H - (\gamma + \mu_H) R_H \\ F_6 &= \delta_H I_H + \delta_H Q_H + \theta D \\ F_7 &= \beta_2 - (\alpha_1 I_H + \alpha_3 D) S_R - \mu_R S_R \\ F_8 &= \alpha_1 S_R I_H + \alpha_3 S_R D - \mu_R I_R \end{aligned} \right\} \quad (3)$$

Given

$$|J(E_o) - \lambda I| = 0 \quad (4)$$

The Jacobean matrix J for the system (3) is

$$J(E_o) = \begin{bmatrix} -\mu_H & 0 & -\frac{\alpha_1 \beta_1}{\mu_H} & \gamma_2 & \gamma & -\frac{\alpha_3 \beta_1}{\mu_H} & 0 & -\frac{\alpha_2 \beta_1}{\mu_H} \\ 0 & -(\varepsilon + \psi + \mu_H) & \frac{\alpha_1 \beta_1}{\mu_H} & 0 & 0 & \frac{\alpha_3 \beta_1}{\mu_H} & 0 & \frac{\alpha_2 \beta_1}{\mu_H} \\ 0 & \varepsilon & -(\delta + \delta_H + \mu_H) & 0 & 0 & 0 & 0 & 0 \\ 0 & \psi & \delta & -(\gamma_1 + \gamma_2 + \delta_H + \mu_H) & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \gamma_1 & -(\gamma + \mu_H) & 0 & 0 & 0 \\ 0 & 0 & \delta_H & \delta_H & 0 & -\theta & 0 & 0 \\ 0 & 0 & -\frac{\alpha_1 \beta_2}{\mu_R} & 0 & 0 & -\frac{\alpha_3 \beta_2}{\mu_R} & -\mu_R & 0 \\ 0 & 0 & \frac{\alpha_1 \beta_2}{\mu_R} & 0 & 0 & \frac{\alpha_3 \beta_2}{\mu_R} & 0 & -\mu_R \end{bmatrix} \quad (5)$$

Substituting (5) into equation (4) we obtain

$$\begin{vmatrix}
 -\mu_H - \lambda & 0 & -\frac{\alpha_1 \beta_1}{\mu_H} & \gamma_2 & \gamma & -\frac{\alpha_3 \beta_1}{\mu_H} & 0 & -\frac{\alpha_2 \beta_1}{\mu_H} \\
 0 & -(\varepsilon + \psi + \mu_H) - \lambda & \frac{\alpha_1 \beta_1}{\mu_H} & 0 & 0 & \frac{\alpha_3 \beta_1}{\mu_H} & 0 & \frac{\alpha_2 \beta_1}{\mu_H} \\
 0 & \varepsilon & -(\delta + \delta_H + \mu_H) - \lambda & 0 & 0 & 0 & 0 & 0 \\
 0 & \psi & \delta & -(\gamma_1 + \gamma_2 + \delta_H + \mu_H) - \lambda & 0 & 0 & 0 & 0 \\
 0 & 0 & 0 & \gamma_1 & -(\gamma + \mu_H) - \lambda & 0 & 0 & 0 \\
 0 & 0 & \delta_H & \delta_H & 0 & -\theta - \lambda & 0 & 0 \\
 0 & 0 & -\frac{\alpha_1 \beta_2}{\mu_R} & 0 & 0 & -\frac{\alpha_3 \beta_2}{\mu_R} & -\mu_R - \lambda & 0 \\
 0 & 0 & \frac{\alpha_1 \beta_2}{\mu_R} & 0 & 0 & \frac{\alpha_3 \beta_2}{\mu_R} & 0 & -\mu_R - \lambda
 \end{vmatrix} = 0 \quad (6)$$

From equation (6) we have $\lambda_1 = -\mu_H$, $\lambda_2 = -\mu_R$, $\lambda_3 = -(\gamma + \mu_H)$

Thus, equation (6) reduces to

$$\begin{vmatrix}
 -A - \lambda & B & 0 & F & H \\
 \varepsilon & -C - \lambda & 0 & 0 & 0 \\
 \psi & \delta & -E - \lambda & 0 & 0 \\
 0 & \delta_H & \delta_H & -\theta - \lambda & 0 \\
 0 & M & 0 & G & -\mu_R - \lambda
 \end{vmatrix} = 0 \quad (7)$$

where

$$\left. \begin{aligned}
 A &= (\varepsilon + \psi + \mu_H) \\
 B &= \frac{\alpha_1 \beta_1}{\mu_H}, \quad M = \frac{\alpha_4 \beta_2}{\mu_R} \\
 C &= (\delta + \delta_H + \mu_H), \quad F = \frac{\alpha_3 \beta_1}{\mu_H} \\
 E &= (\gamma_1 + \gamma_2 + \delta_H + \mu_H) \\
 G &= \frac{\alpha_5 \beta_2}{\mu_R}, \quad H = \frac{\alpha_2 \beta_1}{\mu_H}
 \end{aligned} \right\} \quad (8)$$

Therefore, the characteristics of equation (7) gives

$$m_5 \lambda^5 + m_4 \lambda^4 + m_3 \lambda^3 + m_2 \lambda^2 + m_1 \lambda + m_0 = 0 \quad (9)$$

where

$$m_5 = 1$$

$$m_4 = A + C + E + \theta + \mu_R$$

$$m_3 = E\mu_R + AE + \theta E + C\mu_R + AC + \theta C + EC + A\mu_R + \theta\mu_R + A\theta$$

$$m_2 = (AE\mu_R + \theta E\mu_R + \theta AE + AC\mu_R + \theta C\mu_R + \theta AC + CE\mu_R + ACE + \theta CE + \theta A\mu_R + B + \delta_H F\varepsilon - \psi F\delta)$$

$$m_1 = (\theta AE\mu_R + \theta AC\mu_R + \theta AEC + \theta CE\mu_R + \theta ACE + MH + B\mu_R + B\theta + GH\delta_H\varepsilon + F\delta_H\varepsilon\mu_R + EF\varepsilon\delta_H + H\delta_H - F(\varepsilon\delta_H + \psi\delta_H\mu_R + C\delta\psi))$$

$$m_0 = EF\delta_H\varepsilon\mu_R + EGH\delta_H\varepsilon + B\theta\mu_R + MH\theta + \theta CEH\mu_R + H\delta_H\mu_R - \delta_H(F\varepsilon\delta\mu_R + CF\psi\mu_R + GH)$$

We apply Routh-Hurwitz criterion on (9) which states that all roots of the polynomial have negative real part if and only if the coefficient A_i are positive and the determinant of the matrices $H_i > 0$ for $i = 0, 1, 2, 3, 4, 5$. Thus

$$H = \begin{vmatrix} m_4 & m_2 & m_0 & 0 & 0 \\ m_5 & m_3 & m_1 & 0 & 0 \\ 0 & m_4 & m_2 & m_0 & 0 \\ 0 & m_5 & m_3 & m_1 & 0 \\ 0 & 0 & m_4 & m_2 & m_0 \end{vmatrix} = \begin{vmatrix} m_4 & m_2 & m_0 & 0 & 0 \\ 1 & m_3 & m_1 & 0 & 0 \\ 0 & m_4 & m_2 & m_0 & 0 \\ 0 & 1 & m_3 & m_1 & 0 \\ 0 & 0 & m_4 & m_2 & m_0 \end{vmatrix}$$

Therefore,

$$H_1 = m_4 = A + C + E + \theta + \mu_R > 0$$

$$H_2 = \begin{vmatrix} m_4 & m_2 \\ 1 & m_3 \end{vmatrix} = m_3m_4 - m_2 > 0$$

$$m_3m_4 > m_2$$

$$H_3 = \begin{vmatrix} m_4 & m_2 & m_0 \\ 1 & m_3 & m_1 \\ 0 & m_4 & m_2 \end{vmatrix} = -m_4 \begin{vmatrix} m_4 & m_0 \\ 1 & m_1 \end{vmatrix} + m_2 \begin{vmatrix} m_4 & m_2 \\ 1 & m_3 \end{vmatrix}$$

$$m_5m_4 + m_2m_3m_4 > m_1m_4^2 + m_2^2$$

$$H_4 = \begin{vmatrix} m_4 & m_2 & m_0 & 0 \\ 1 & m_3 & m_1 & 0 \\ 0 & m_4 & m_2 & m_0 \\ 0 & 1 & m_3 & m_1 \end{vmatrix}$$

$$m_1 m_2 m_3 m_4 + m_0 m_1 m_4 + m_0 m_2 m_3 + m_0 m_1 m_4 > m_0 m^2_3 m_4 + m^2_1 m^2_4 + m^2_0$$

$$H_5 = \begin{vmatrix} m_4 & m_2 & m_0 & 0 & 0 \\ 1 & m_3 & m_1 & 0 & 0 \\ 0 & m_4 & m_2 & m_0 & 0 \\ 0 & 1 & m_3 & m_1 & 0 \\ 0 & 0 & m_4 & m_2 & m_0 \end{vmatrix}$$

$$m_0 m_1 m_2 m_3 m_4 + m_0 m^2_1 m^2_4 + m^2_0 m_2 m_3 + m^2_0 m_1 m_4 > m^2_0 m^2_3 m_4 + m^2_0 m_1 m_4 + m_0 m_1 m_2^2 + m_0^3$$

Therefore, all the eigen values of the polynomial (9) have negative real parts, implying that $\lambda_4 < 0, \lambda_5 < 0, \lambda_6 < 0, \lambda_7 < 0$ and $\lambda_8 < 0$. Since all the values of $\lambda_i < 0$, for $i = 1, 2, 3, 4, 5, 6, 7, 8$. when $R_0 < 1$, we conclude that the disease-free equilibrium point is locally asymptotically stable.

3.6 Global stability of the disease free equilibrium point

For global stability of the DFE, the technique used by Castillo-Chavez, Feng and Huang (2002) was employed. The model is re-written as follows:

$$\left. \begin{aligned} \frac{dX}{dt} &= K(X, Z) \\ \frac{dZ}{dt} &= G(X, Z), G(X, 0) = 0 \end{aligned} \right\} \tag{10}$$

Where $X \in \mathbb{R}^3$ and $X = \{S_H, R_R, S_R\}$ denotes the number of uninfected individuals and $Z \in \mathbb{R}^5$ where

$Z = \{C_H, I_H, Q_H, D, I_R\}$ denotes the number of infected individuals. $E^0 = \left(\frac{\beta_1}{\mu_H}, 0, 0, 0, 0, \frac{\beta_2}{\mu_R}, 0 \right)$

denotes the disease free equilibrium point of this system, where $X^* = \left(\frac{\beta_1}{\mu_H}, \frac{\beta_2}{\mu_R} \right)$

$$(11)$$

Condition (10) may be met to guaranteed global asymptotic stability

(H_1) : For $\frac{dX}{dt} = K(X, 0)$, X^* is globally asymptotic stable

(H₂): For $G(X, Z) = AZ - \hat{G}(X, Z), \hat{G}(X, Z) \geq 0 \forall (X, Z) \in \Gamma$ where $A = D_Z G(X^*, 0)$ is an M matrix and Γ is the region where the model has biological meaning.

Theorem 2

If system (1) satisfies condition (10), then the fixed point $E^0 = \left(\frac{\beta_1}{\mu_H}, 0, 0, 0, 0, 0, \frac{\beta_2}{\mu_R}, 0 \right)$ is a globally asymptotically stable equilibrium of the system (1) provided that $R_0 < 1$ and the conditions (H₁) and (H₂) are satisfied:

Proof

Consider $K(X, 0) = \begin{bmatrix} \beta_1 - \mu_H S_H & 0 \\ \beta_2 - \mu_R S_R & 0 \end{bmatrix}$ and $G(X, Z) = AZ - \hat{G}(X, Z)$

$$A = \begin{bmatrix} -(\varepsilon + \psi + \mu_H) & \alpha_1 S_H & 0 & \alpha_3 S_H & \alpha_2 S_H \\ \varepsilon & -(\delta + \delta_H + \mu_H) & 0 & 0 & 0 \\ \psi & \delta & -(\gamma_1 + \gamma_2 + \delta_H + \mu_H) & 0 & 0 \\ 0 & \delta_H & \delta_H & -\theta & 0 \\ 0 & \alpha_1 S_R & 0 & \alpha_3 S_R & -\mu_R \end{bmatrix} \tag{12}$$

and

$$Z = \begin{bmatrix} C_H \\ I_H \\ Q_H \\ D \\ I_R \end{bmatrix} \tag{13}$$

$$G(X, Z) = \begin{bmatrix} \alpha_1 S_H I_H + \alpha_2 S_H I_R + \alpha_3 S_H D - (\varepsilon + \psi + \mu_H) C_H \\ \varepsilon C_H - (\delta + \delta_H + \mu_H) I_H \\ \psi C_H + \delta I_H - (\gamma_1 + \gamma_2 + \delta_H + \mu_H) Q_H \\ \delta_H I_H + I_H Q_H - \theta D \\ (\alpha_1 I_H + \alpha_3 D) S_R - \mu_R I_R \end{bmatrix} \tag{14}$$

Given

$$\hat{G}(X, Z) = AZ - G(X, Z) \tag{15}$$

Substituting equations (12), (13) and (14) into (15) we have

$$\hat{G}(X, Z) = \begin{bmatrix} \alpha_1 S_H I_H + \alpha_2 S_H I_R + \alpha_3 S_H D - (\varepsilon + \psi + \mu_H) C_H \\ \varepsilon C_H - (\delta + \delta_H + \mu_H) I_H \\ \psi C_H + \delta I_H - (\gamma_1 + \gamma_2 + \delta_H + \mu_H) Q_H \\ \delta_H I_H + I_H Q_H - \theta D \\ (\alpha_1 I_H + \alpha_3 D) S_R - \mu_R I_R \end{bmatrix} \tag{16}$$

$$- \begin{bmatrix} \alpha_1 S_H I_H + \alpha_2 S_H I_R + \alpha_3 S_H D - (\varepsilon + \psi + \mu_H) C_H \\ \varepsilon C_H - (\delta + \delta_H + \mu_H) I_H \\ \psi C_H + \delta I_H - (\gamma_1 + \gamma_2 + \delta_H + \mu_H) Q_H \\ \delta_H I_H + I_H Q_H - \theta D \\ (\alpha_1 I_H + \alpha_3 D) S_R - \mu_R I_R \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}$$

Since all the conditions are satisfied, $\hat{G}(X, Z) = 0$, the DFE, E^0 is globally asymptotically stable.

4. NUMERICAL SIMULATION

In this section, we present the graphical solutions to the proposed model. The graphs are generated using the parameters and variables value presented in Table 2. The graphs are divided into two sub-sections namely: Dynamics of the

compartments with respect to time; Effects of quarantine rate on the transmission dynamics of Lassa fever; Effect of isolation centre on the transmission dynamics of Lassa fever.

Table 2: Parameters and variable values used for simulations

Parameter/Variable	Value	References
β_1	0.038,	[12]
β_2	0.56	[12]
α_1	0.0712, 0.62	[13]
α_2	0.6	[13]
α_3	0.5	[12]
δ_H	0.2, 0.01,	[12]
δ	0.3	[13]
ψ	0.1, 0.5, 0.75, 0.9	Assumed
θ	0.5	Assumed

ε	0.8, 0.72	[13]
γ	0.17	[13]
μ_H	0.02	[12]
μ_R	0.6	Assumed
γ_1	0.9	Assumed
γ_2	0.4	Assumed
C_H	100	Assumed
Q_H	50	Assumed
I_R	25	Assumed
S_R	20000	Assumed
R_H	20	Assumed
D	10	Assumed
S_H	10000	Assumed
I_H	30	Assumed

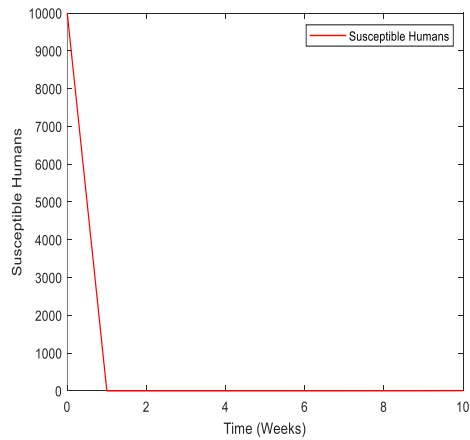


Figure 2: Diagram showing the dynamics susceptible humans.

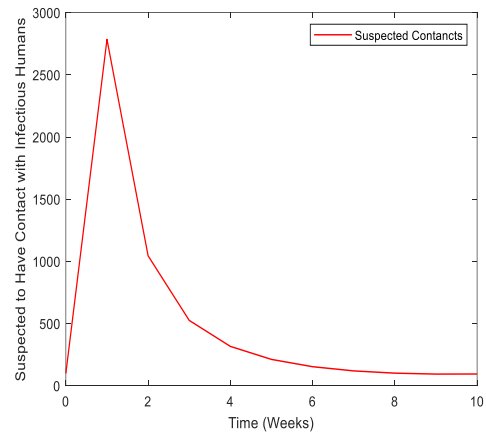


Figure 3: Diagram showing the dynamics humans that are suspected to have had contact with infectious humans.

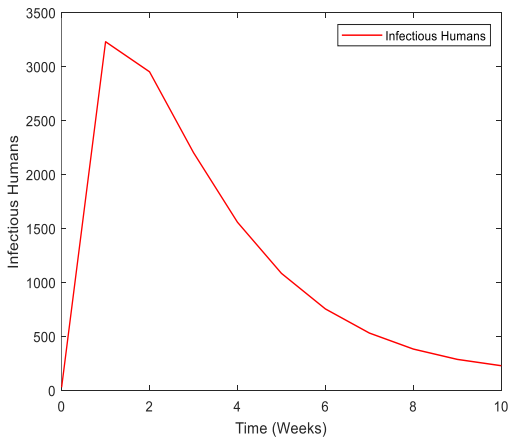


Figure 4: Diagram showing the dynamics infectious humans.

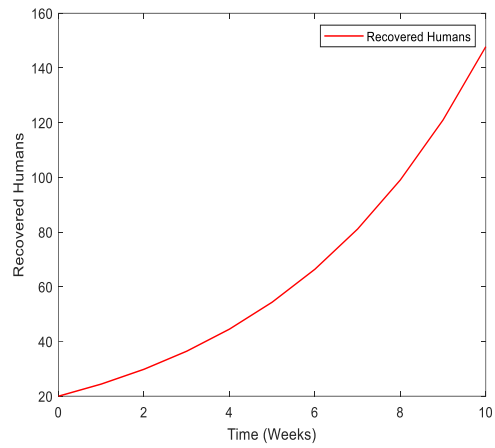


Figure 6: Diagram showing the dynamics recovered humans.

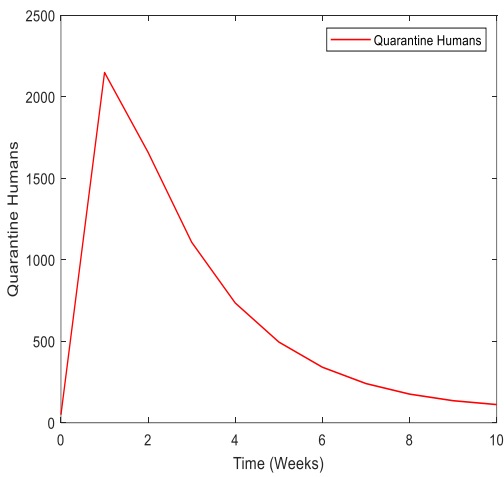


Figure 5: Diagram showing the dynamics quarantine humans.

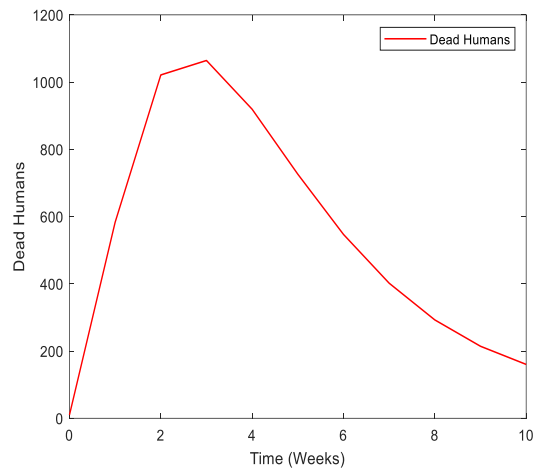


Figure 7: Diagram showing the dynamics recovered humans.

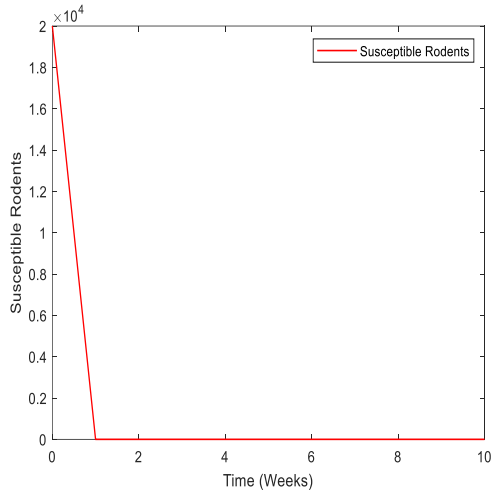


Figure 8: Diagram showing the dynamics susceptible rodents.

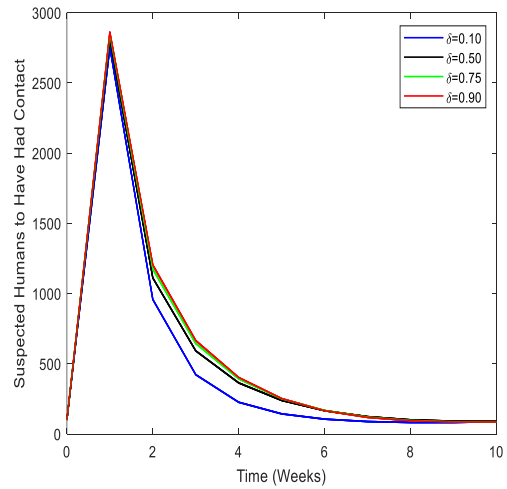


Figure 10: Diagram showing the effects of isolation of infectious human on suspected to have had contact with infectious humans.

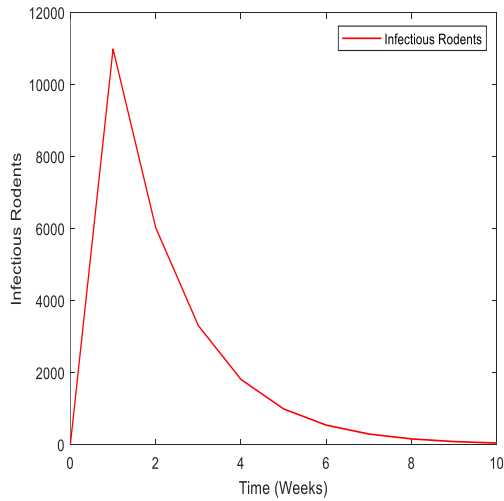


Figure 9: Diagram showing the dynamics infectious rodents.

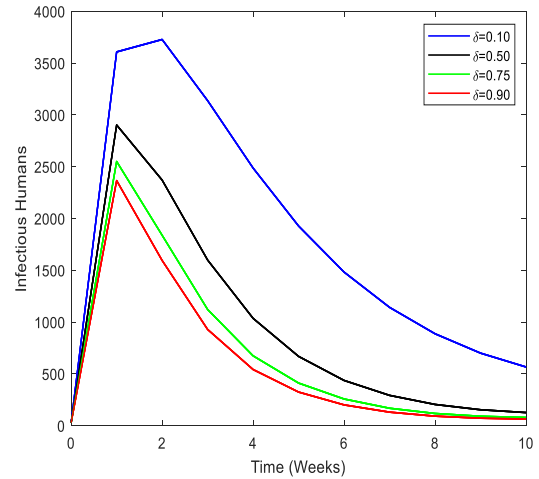


Figure 11: Diagram showing the effects of isolation of infectious human on infectious humans.

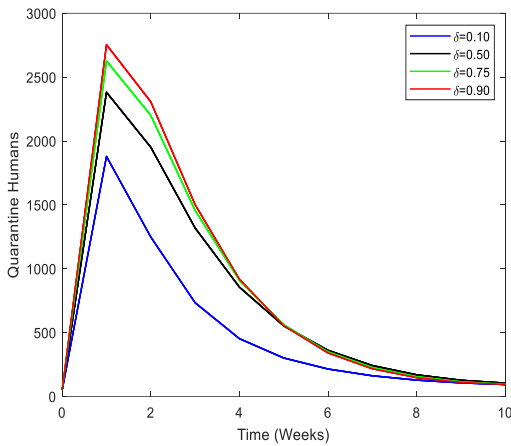


Figure 12: Diagram showing the effects of isolation of infectious human on quarantine humans.

Figure (2) shows the dynamics of the susceptible population. At the onset of the outbreak, the susceptible human population drops rapidly and this is due to the high infectious nature of the virus more also, there was no intervention then. Figure (3) depicts the dynamics of those that are suspected to have had contact with infected individuals. The result of the outbreak, governmental bodies and health agents began the process of contact tracing this resulted into the rapid rise in the compartment of those suspected to have had contact with the virus. Figure (4) represents the dynamics of infected population. The population rose drastically at the onset before quarantining and treatment measures were put in place. Figure (5) depicts the dynamics of the quarantined individuals. The population increases significantly at a rapid rate until it reaches its peak due to much effort put into quarantining of individuals who were successfully contact traced. Figure (6) depicts the population of recovered individuals. There is gradual rise in recovered population due to effective treatment. Figure (7) represents the dynamics of the dead compartment. There is rapid rise in the death compartment but the number began to drop as intervention measures came into place. Figure 8 shows a rapid drop in rodents population due to the high infectious nature of the virus. In figure (9), we observed that infected population of the rodents rose rapidly at

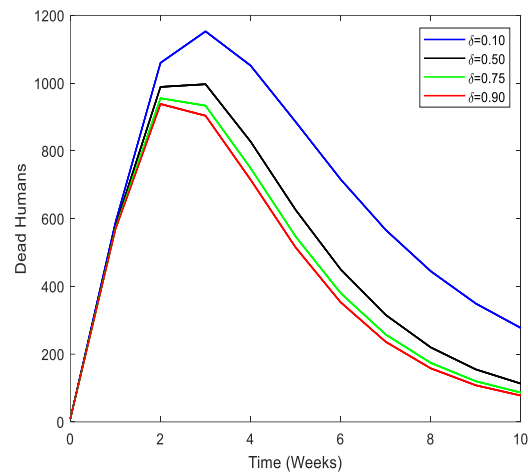


Figure 13: Diagram showing the effects of isolation of infectious human on dead humans.

the onset of the outbreak while in figure (10) the more individuals are effectively quarantined, the death reduces. Figure (11) depicts the dynamics of infectious humans when isolation rate is varied. When individuals are confirmed to be infected, they are taken to the to the isolation centre for treatment hence from our graph, we see the drop in the infectious class due to isolation. Figure (12) shows the positive impact of isolation on the quarantine compartment as we increase the rate of isolation, there is also an increase in the quarantine compartment. Figure (13) shows that infected individuals are treated thereby reducing the number of people that would have died; clearly from the graph, as the rate of isolation increases, there is a reduction in the number of deaths.

5.0 CONCLUSION

In this paper, we developed a mathematical model for the transmission dynamics of Lassa fever incorporating contact tracing and effective quarantine as control measures. We carried out analytical studies on the proposed model. The disease free equilibrium state (DFE) for the model was obtained. The next generation matrix method was used to obtain the reproduction number for the Lassa fever model.

We obtained the invariant region, we established the positivity of solutions for the system

equations. The analytical results showed that the disease-free equilibrium point is locally asymptotically stable when $R_0 < 1$ indicating that Lassa fever eradication is possible within the population. We also obtained the global stability of the disease-free equilibrium and results showed that the disease-free equilibrium point is globally asymptotically stable when $R_0 \leq 1$.

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- Numerical simulations for the model shows that Lassa fever will be eradicated if effort is intensified in bringing down the transmission rate of Lassa fever with contact tracing and effective quarantining of those suspected to have had contacts with infected individuals.
- 6.0 CONFLICT OF INTEREST**
- The authors declare that there is no conflict of interest regarding this paper.
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