Transactions of the Nigerian Association of Mathematical Physics
Volume 7, (*March, 2018*), pp197 – 208

MEASURING THE SPREAD AND CONTROL OF LASSA FEVER IN NIGERIA, USING THE EFFECTIVE BASIC REPRODUCTION NUMBER R_c

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Abstract

The threat of infectious disease(s) is not only a major cause of death and misery to both human and animal populations but also a social and economic impacts as such; this paper presents a deterministic model describing the transmission dynamics of Lassa fever where humans and mastomys interact to infect human, incorporating the use of condom and by the number of mastomys (Child & Adult vectors). Mastomys is a genus of rodent in the family muridae endemic to Africa containing some species such as mastomys natalensis also known as natal multimammate rat referred to as the common African or African soft-furred rat responsible for the spread of the virus. The demographic profile of Nigeria was used in the model to show the effect of control measures at different rates. Numerical simulation were also carried out using maple software to show that effective basic reproduction number R_c is an important tool in determining whether the disease is under control or is spreading within the country.

Keywords: Transmission Dynamics, Lassa fever, Mastomys, Effective Basic Reproduction Number, Differential Equations, Numerical Simulation

1.0 INTRODUCTION

Lassa fever is an acute viral zoonotic illness caused by Lassa virus, an arena virus known to be responsible for a severe hemorrhagic fever characterized by fever, muscle aches, sore throat, nausea, vomiting, and chest and abdominal pain [1]. The virus exhibits asymptomatic infection, with profuse urine in the virus excretion in Mastomys natalensis, the ubiquitous and highly commensal rodent. Mastomys is a genus of rodent in the family muridae endemic to Africa containing some species such as mastomys natalensis also known as natal multimammate rat referred to as the common African or African soft-furred rat [2].

Lassa fever is endemic in West Africa and has been reported from Sierra Leone, Guinea, Liberia, and Nigeria. The number of Lassa fever virus infections per year in West Africa is estimated at 100,000 to 300,000 with approximately 5000 deaths [3]. In spite of the great progress made in recent years in the understanding of the life cycle of arena viruses, including Lassa virus and the new insights gained in the pathogenesis and molecular epidemiology of Lassa fever, as well as the development of the state-of-the-art technologies for diagnosing this life-threatening disease [3]. A rat that is common in endemic areas, known as mastomys natalensis is the natural host of the disease. Contacts with the rats including contamination of food by saliva, urine, excreta or other body fluid can also lead to the infection. Nosocomial transmission may occur through droplets by person-to-person contact or the contamination of needles. Lassa fever may also spread through person-to-person contact. This type of transmission occurs when a person comes into contact with virus in the blood, tissue, secretions, or excretions of an individual infected with the Lassa virus. The virus cannot be spread through casual contact (including skin-to-skin contact without exchange of body fluids). Person-to-person transmission is common in both village and health care settings, where, along with the above-mentioned modes of transmission. The virus also may be spread in contaminated medical equipment, such as reused needles (nosocomial transmission).

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2.0 METHOD OF SOLUTION

2.1 FOMULATION OF THE MODEL

We developed a model, describing the transmission of Lassa fever using ordinary differential equation. The disease free and endemic equilibrium states were addressed and the value of effective basic reproductive number R_c is expressed in terms of parameters, which determines whether the disease is under control or out of control in the population. This model divides the total population of humans into six compartments namely ;$S_H I_H R_H C_v A_v B$.

2.2 MODEL ASSUMPTIONS:

We assumed that the:

i. New births are susceptible S(t) .
ii. Virus does not kill the reservoir host i.e. their death can be natural or accidental.
iii. Infected class is divided into two; Adult reservoir host (A_v) and child vector(C_v).

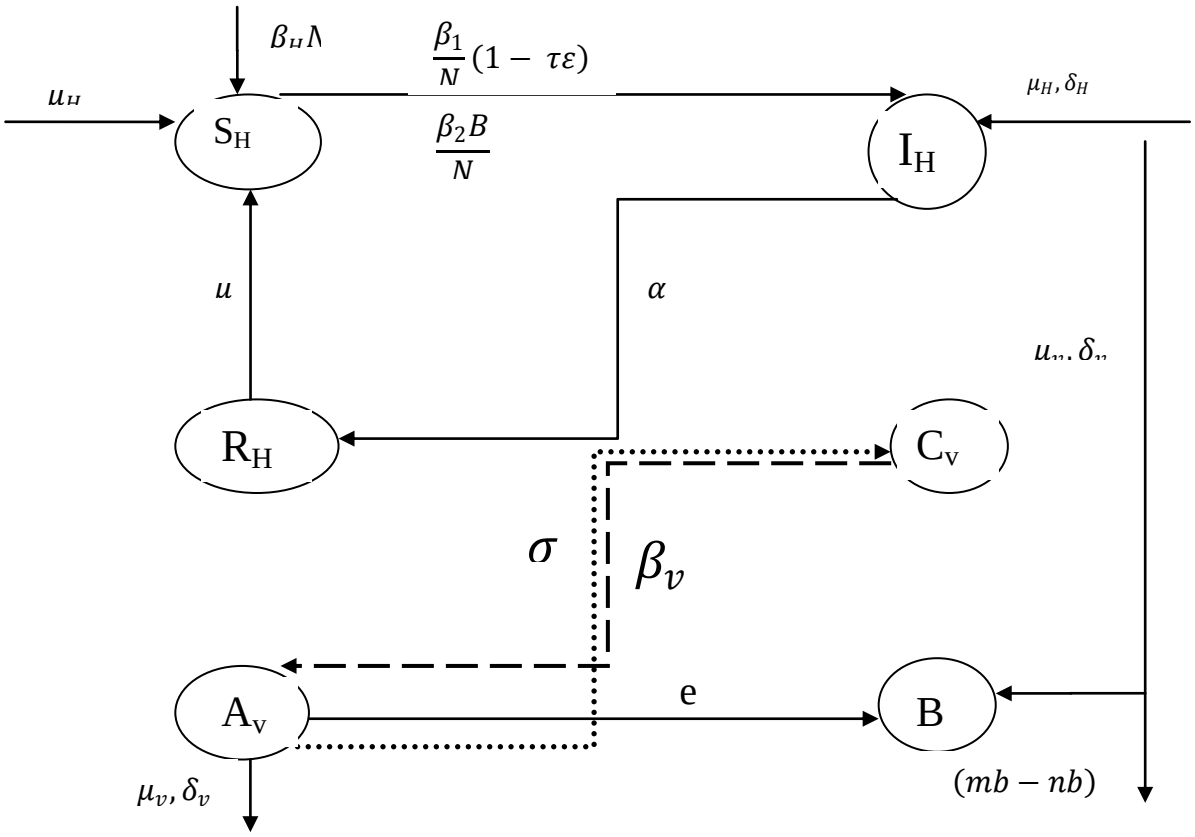

Figure 1: Shows the Schematic Diagram of the Mathematical Model for Lassa Fever Transmission.

3.0 MODEL EQUATIONS

Applying the assumptions, definition of variables and parameters and relationship between the variables and parameters describe in the schematic diagram above, we developed six ordinary differential equations for the transmission and control of Lassa fever in a population. The differential equations are given below;

$$\left.\begin{aligned}
\frac{dS_H}{dt} &= b_H N - \frac{\beta_1(1-\tau\varepsilon)I_H S_H}{N} + \psi R_H - \mu_H S_H - \frac{\beta_2 B S_H}{N} \\
\frac{dI_H}{dt} &= \frac{\beta_1(1-\tau\varepsilon)I_H S_H}{N} + \frac{\beta_2 B S_H}{N} - \mu_H I_H - \gamma I_H - \delta_H I_H \\
\frac{dR_H}{dt} &= \gamma I_H - \mu_H R_H - \psi R_H \\
\frac{dC_V}{dt} &= b_V A_V - \mu_V C_V - \sigma C_V - \delta_V C_V \\
\frac{dA_V}{dt} &= \sigma C_V - \mu_V A_V - \delta_V A_V \\
\frac{dB}{dt} &= eA_V + B(nb - mb)
\end{aligned}\right\} \quad (1)$$

These equations are valid for $N_H > 0$ and all parameters in the model are assumed positive and the total population sizes are:
$N_H = S_H + I_H + R_H$ and $N_V = C_V + A_V$ (2)
Where:

$b_H =$ Per capita birth rate for human,$\gamma =$ Per capita rate of loss of immunity of human.
$\beta_1 =$Contracting rate for the susceptible human population as a result of interaction with infected human population.
$\beta_2 =$ Contracting rate for the susceptible human population as a result of interaction with infected vector population.
$b_v =$ Per capita birth rate of the vector.
$\delta_H =$ The mortality rate of human population due to Lassa fever disease
$\delta_V =$ The mortality rate of vector population due to the hunting of the mastomys,$\mu_H =$ Natural death rate of human population, $\mu_V =$Natural death rate of vector population $\sigma =$ Progression rate from Child vector (C_V) to Adult vector (A_V),$\varepsilon =$ Efficacy of condom usage
$e =$ The contact rate with the contaminated food or water,
$\tau =$ Compliance of condom usage, $mb =$ Loss rate, $nb =$ Growth rate, $\psi =$ The waning of Lassa fever Recovery, $S_H =$ Number of susceptible humans, $R_H =$Those recovered from Lassa fever attack, $C_V =$ Number of Infant vectors, $A_V =$ Number of Adult vectors and, $B =$ Average concentration of virus inside the food or water.

With,
$$\frac{dN_H}{dt} = (b_H - \mu_H)N_H - \delta_H I_H \quad (3)$$
$$\frac{dN_V}{dt} = b_v A_V - (\mu_V + \delta_V)N_v \quad (4)$$
At the equilibrium states;
Let $S_H = S_H^*, I_H = I_H^*, R_H = R_H^*, C_V = C_{V_S}^*, A_V = A_V^*, B = B^*$ (5)
$$\frac{dS_H}{dt} = \frac{dI_H}{dt} = \frac{dR_H}{dt} = \frac{dC_V}{dt} = \frac{dA_V}{dt} = \frac{dB}{dt} = 0 \quad (6)$$
$$\left.\begin{aligned}
&\frac{dS_H}{dt} = b_H N - \frac{\beta_1(1-\tau\varepsilon)I_H^* S_H^*}{N} + \psi R_H^* - \mu_H S_H^* - \frac{\beta_2 B^* S_H^*}{N} = 0\\
&\frac{dI_H}{dt} = \frac{\beta_1(1-\tau\varepsilon)I_H^* S_H^*}{N} + \frac{\beta_2 B^* S_H^*}{N} - \mu_H I_H^* - \gamma I_H^* - \delta_H I_H^* = 0\\
&\frac{dR_H}{dt} = \gamma I_H^* - \mu_H R_H^* - \psi R_H^* = 0\\
&\frac{dC_V}{dt} = b_V A_V^* - \mu_V C_V^* - \sigma C_V^* - \delta_V C_V^* = 0\\
&\frac{dA_V}{dt} = \sigma C_V^* - \mu_V A_V^* - \delta_V A_V^* = 0\\
&\frac{dB}{dt} = eA_V^* + B^*(nb - mb) = 0
\end{aligned}\right\} \quad (7)$$
At the disease-free equilibrium state;
$$I_H^* = C_V^* = A_V^* = B^* = 0 \quad (8)$$
Substitute equation (8) into the first equation of (7)
$$\left.\begin{aligned}
&b_H N - \frac{\beta_1(1-\tau\varepsilon)(0)S_H^*}{N} + \psi R_H^* - \mu_H S_H^* - \frac{\beta_2(0)S_H^*}{N} = 0\\
&-\mu_H S_H^* = -b_H N - \psi R_H^*\\
&S_H^* = \frac{b_H N + \psi R_H^*}{\mu_H}
\end{aligned}\right\} \quad (9)$$
Also substituting equation (8) into the second equation of (7)
$$\left.\begin{aligned}
&\delta(0) - \psi R_H^* - \mu R_H^* = 0\\
&R_H^*(-\psi - \mu) = 0\\
&R_H^* = 0
\end{aligned}\right\} \quad (10)$$
Thus;
$$S_H^* = \frac{b_H N + \psi(0)}{\mu_H} = \frac{b_H N}{\mu_H} \quad (11)$$
Hence, the disease-free equilibrium state is;
$$E_0 = (S_H^*, I_{H*}^*, R_H^*, C_V^*, A_V^*, B^*) \equiv \left(\frac{b_H N}{\mu}, 0,0,0,0,0\right) \quad (12)$$

For disease-endemic equilibrium state;

$$S_H^* > 0, I_H^* > 0, R_H^* > 0, C_H^* > 0, A_V^* > 0, B^* > 0 \quad (13)$$

For human population;

Recall from the third equation of (7)

$$\left.\begin{aligned} &\gamma I_H^* - \mu_H R_H^* - \psi R_H^* = 0 \\ &\gamma I_H^* - R_H^*(\mu_H + \psi) = 0 \\ &R_H^* = \frac{\delta I_H^*}{\mu_H + \psi} \end{aligned}\right\} \quad (14)$$

Also from equation (7):

$$\left.\begin{aligned} &b_H N - \frac{\beta_1(1-\tau\varepsilon)I_H^* S_H^*}{N} + \psi R_H^* - \mu_H S_H^* - \frac{\beta_2 B^* S_H^*}{N} = 0 \\ &b_H N - S_H^*\left(\frac{\beta_1(1-\tau\varepsilon)I_H^* + \mu_H + \beta_2 B^*}{N}\right) + \psi R_H^* - = 0 \\ &- S_H^*\left(\frac{\beta_1(1-\tau\varepsilon)I_H^* + \beta_2 B^*}{N} + \mu_H\right) = -(b_H N + \psi R_H^*) \\ &S_H^* = \frac{N(b_H N + \psi R_H^*)}{\beta_1(1-\tau\varepsilon)I_H^* + N\mu_H + \beta_2 B^* = 0} \end{aligned}\right\} \quad (15)$$

Substituting equation (14) into equation (15), we have;

$$\left.\begin{aligned} &S_H^* = \frac{N(b_H N + \psi(\frac{\gamma I_H^*}{\mu_H + \psi}))}{\beta_1(1-\tau\varepsilon)I_H^* + N\mu_H + \beta_2 B^*} \\ &= \frac{N(b_H N(\mu_H + \psi) + \psi\gamma I_H^*)}{(\mu_H + \psi)} \cdot \frac{1}{\beta_1(1-\tau\varepsilon)I_H^* + N\mu_H + \beta_2 B^*} \\ &S_H^* = \frac{N(b_H N(\mu_H + \psi) + \psi\gamma I_H^*)}{(\mu_H + \psi)(\beta_1(1-\tau\varepsilon)I_H^* + N\mu_H + \beta_2 B^*)} \end{aligned}\right\} \quad (16)$$

Similarly, for the vector population we have from the last equation of (7)

$$\left.\begin{aligned} &eA_V^* + B^*(nb - mb) = 0 \\ &B^* = -\frac{eA_V^*}{nb - mb} \end{aligned}\right\} \quad (17)$$

Also from the fourth equation of (7)

$$\left.\begin{aligned} &b_V A_V^* - \mu_V C_V^* - \sigma C_V^* - \delta_V C_V^* = 0 \\ &b_V A_V^* - (\mu_V + \sigma + \delta_V)C_V^* = 0 \\ &C_V^* = \frac{b_V A_V^*}{\mu_V + \sigma + \delta_V} \end{aligned}\right\} \quad (18)$$

If $I_H^* = 0$

$$R_H^* = \frac{\gamma(0)}{\mu_H + \psi} = 0 \quad (19)$$

Also;

$$\left.\begin{aligned} &S_H^* = \frac{N(b_H N(\mu_H + \psi) + \psi\gamma(0))}{(\mu_H + \psi)(\beta_1(1-\tau\varepsilon)(0) + N\mu_H + \beta_2 B^*} \\ &S_H^* = \frac{N(b_H N(\mu_H + \psi))}{(\mu_H + \psi)(N\mu_H + \beta_2 B^*)} \\ &S_H^* = \frac{b_H N^2}{N\mu_H + \beta_2 B^*} \end{aligned}\right\} \quad (20)$$

Similarly if $A_V^* = 0$

$$B^* = \frac{-e(0)}{nb - mb} = 0 \quad (21)$$

Since

$B^* = 0$,

then

$$\left.\begin{aligned} S_H^* &= \frac{b_H N^2}{N\mu_H + \beta_2(0)} \\ S_H^* &= \frac{b_H N}{\mu_H} \end{aligned}\right\} \quad (22)$$

And $C_V^* = \frac{b_V(0)}{\mu_V + \sigma + \delta_V} = 0$ (23)

Hence the disease-endemic equilibrium state is given by;

$$\left(S_H^*, I_{H*}^*, R_H^*, C_V^*, A_V^*, B^*\right) \equiv \left(\frac{b_H N}{\mu_H}, 0,0,0,0,0\right) \quad (24)$$

To find the value of the effective reproductive number Rc, we must first determine the matrix FV^{-1};

Where; $F = \begin{pmatrix} \frac{\beta_1(1-\tau\varepsilon)S_H}{N} & 0 & 0 & \frac{\beta_2 S_H}{N} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}$ (25)

$V^{-1} = \frac{adj(V)}{|V|}$, so to find V^{-1}, we find V

$V = V^- - V^+$, Where;

$$V^- = \begin{pmatrix} \mu_H + \gamma + \delta_H & 0 & 0 & 0 \\ 0 & \mu_V + \sigma + \delta_V & 0 & 0 \\ 0 & 0 & \mu_V + \delta_V & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix} \& V^+ = \begin{pmatrix} 0 & 0 & 0 & 0 \\ 0 & 0 & b_V & 0 \\ 0 & \sigma & 0 & 0 \\ 0 & 0 & e & nb - mb \end{pmatrix} \quad (26)$$

Thus; $V = V^- - V^+$

$$V = \begin{pmatrix} \mu_H + \gamma + \delta_H & 0 & 0 & 0 \\ 0 & \mu_V + \sigma + \delta_V & -b_V & 0 \\ 0 & -\sigma & \mu_V + \delta_V & 0 \\ 0 & 0 & -e & mb - nb \end{pmatrix} \quad (27)$$

In order to determine the matrix V^{-1}, we use the Gauss-Jordan elimination method as explained in Stroud (2003).

$$V = \left(\begin{array}{cccc|cccc} \mu_H + \gamma + \delta_H & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & \mu_V + \sigma + \delta_V & -b_V & 0 & 0 & 1 & 0 & 0 \\ 0 & -\sigma & \mu_V + \delta_V & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & -e & mb - nb & 0 & 0 & 0 & 1 \end{array}\right)$$

$$= \left(\begin{array}{cccc|cccc} 1 & 0 & 0 & 0 & \frac{1}{\mu_H + \gamma + \delta_V} & 0 & 0 & 0 \\ 0 & 1 & \frac{-b}{\mu_v + \sigma + \delta_V} & 0 & 0 & \frac{1}{\mu_v + \sigma + \delta_V} & 0 & 0 \\ 0 & \frac{-\sigma}{\mu_V + \delta_V} & 1 & 0 & 0 & 0 & \frac{1}{\mu_v + \delta_V} & 0 \\ 0 & 0 & \frac{-e}{mb - nb} & 1 & 0 & 0 & 0 & \frac{1}{mb - nb} \end{array}\right) \begin{matrix} \frac{R_1}{\mu_H + \gamma + \delta_V} \\ \frac{R_2}{\mu_v + \sigma + \delta_V} \\ \frac{R_3}{\mu_V + \delta_V} \\ \frac{R_4}{mb - nb} \end{matrix}$$

$$= \left(\begin{array}{cccc|cccc} 1 & 0 & 0 & 0 & \frac{1}{\mu_H + \gamma + \delta_V} & 0 & 0 & 0 \\ 0 & 1 - \frac{b\sigma}{(\mu + \delta_V)(\mu_V + \sigma + \delta_V)} & 0 & 0 & 0 & \frac{1}{\mu_v + \sigma + \delta_V} & \frac{b}{(\mu_V + \delta_V)(\mu_V + \sigma + \delta_V)} & 0 \\ 0 & \frac{-\sigma}{\mu_V + \delta_V} & 1 & 0 & 0 & 0 & \frac{1}{\mu_v + \delta_V} & 0 \\ 0 & 0 & \frac{-e}{mb - nb} & 1 & 0 & 0 & 0 & \frac{1}{mb - nb} \end{array}\right) R_2 + \frac{b}{\mu_V + \sigma + \delta_V} \cdot R_3$$

$$=\left(\begin{array}{cccc|cccc} 1 & 0 & 0 & 0 & \frac{1}{\mu_H+\gamma+\delta_V} & 0 & 0 & 0 \\ 0 & \frac{(\mu_V+\sigma+\delta_V)-b\sigma}{(\mu_V+\sigma+\delta_V)} & 0 & 0 & 0 & \frac{1}{\mu_v+\sigma+\delta_V} & \frac{b}{(\mu_V+\delta_V)(\mu_V+\sigma+\delta_V)} & 0 \\ 0 & \frac{-\sigma}{\mu_V+\delta_V} & 1 & 0 & 0 & 0 & \frac{1}{\mu_v+\delta_V} & 0 \\ 0 & 0 & \frac{-e}{mb-nb} & 1 & 0 & 0 & 0 & \frac{1}{mb-nb} \end{array}\right) \tag{28}$$

Now let;

$$H=\frac{(\mu_V+\sigma+\delta_V)}{(\mu_V+\sigma+\delta_V)-b\sigma} \tag{29}$$

$$=\left(\begin{array}{cccc|cccc} 1 & 0 & 0 & 0 & \frac{1}{\mu_H+\gamma+\delta_V} & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & \frac{1}{(\mu_V+\sigma+\delta_V)-b\sigma} & \frac{b}{(\mu_V+\delta_V)(\mu_V+\sigma+\delta_V)-b\sigma} & 0 \\ 0 & \frac{-\sigma}{\mu_V+\delta_V} & 1 & 0 & 0 & 0 & \frac{1}{\mu_V+\delta_V} & 0 \\ 0 & 0 & \frac{-e}{mb-nb} & 1 & 0 & 0 & 0 & \frac{1}{mb-nb} \end{array}\right) HR_2$$

$$=\left(\begin{array}{cccc|cccc} 1 & 0 & 0 & 0 & \frac{1}{\mu_H+\gamma+\delta_V} & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & \frac{1}{(\mu_V+\sigma+\delta_V)-b\sigma} & \frac{b}{(\mu_V+\delta_V)(\mu_V+\sigma+\delta_V)-b\sigma} & 0 \\ 0 & 1 & 1 & 0 & 0 & \frac{\sigma}{(\mu_V+\delta_V)(\mu_V+\sigma+\delta_V)-b\sigma} & \frac{(\mu_V+\sigma+\delta_V)}{(\mu_V+\delta_V)(\mu_V+\sigma+\delta_V)-b\sigma} & 0 \\ 0 & 0 & \frac{-e}{mb-nb} & 1 & 0 & 0 & 0 & \frac{1}{mb-nb} \end{array}\right) R_3+\frac{\sigma}{\mu_V+\delta_V}\cdot R_2$$

$$V=\left(\begin{array}{cccc|cccc} 1 & 0 & 0 & 0 & \frac{1}{\mu_H+\gamma+\delta_V} & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & \frac{1}{(\mu_V+\sigma+\delta_V)-b\sigma} & \frac{b}{(\mu_V+\delta_V)(\mu_V+\sigma+\delta_V)-b\sigma} & 0 \\ 0 & 1 & 1 & 0 & 0 & \frac{\sigma}{(\mu_V+\delta_V)(\mu_V+\sigma+\delta_V)-b\sigma} & \frac{(\mu_V+\sigma+\delta_V)}{(\mu_V+\delta_V)(\mu_V+\sigma+\delta_V)-b\sigma} & 0 \\ 0 & 0 & 1 & 1 & 0 & \frac{e\sigma}{(mb-nb)(\mu_V+\delta_V)(\mu_V+\sigma+\delta_V)-b\sigma} & \frac{e(\mu_V+\sigma+\delta_V)}{(mb-nb)(\mu_V+\delta_V)(\mu_V+\sigma+\delta_V)-b\sigma} & \frac{1}{mb-nb} \end{array}\right) R_4+\frac{e}{mb-nb}\cdot R_3 \tag{30}$$

Therefore,

$$V^{-1}=\begin{pmatrix} \frac{1}{\mu_H+\gamma+\delta_V} & 0 & 0 & 0 \\ 0 & \frac{1}{(\mu_V+\sigma+\delta_V)-b\sigma} & \frac{b}{(\mu_V+\delta_V)(\mu_V+\sigma+\delta_V)-b\sigma} & 0 \\ 0 & \frac{\sigma}{(\mu_V+\delta_V)(\mu_V+\sigma+\delta_V)-b\sigma} & \frac{(\mu_V+\sigma+\delta_V)}{(\mu_V+\delta_V)(\mu_V+\sigma+\delta_V)-b\sigma} & 0 \\ 0 & \frac{e\sigma}{(mb-nb)(\mu_V+\delta_V)(\mu_V+\sigma+\delta_V)-b\sigma} & \frac{e(\mu_V+\sigma+\delta_V)}{(mb-nb)(\mu_V+\delta_V)(\mu_V+\sigma+\delta_V)-b\sigma} & \frac{1}{mb-nb} \end{pmatrix} \tag{31}$$

$$FV^{-1}=\begin{pmatrix} \frac{\beta_1(1-\tau\varepsilon)S_H}{N} & 0 & 0 & \frac{\beta_2 S_H}{N} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}\cdot\begin{pmatrix} \frac{1}{\mu_H+\gamma+\delta_V} & 0 & 0 & 0 \\ 0 & \frac{1}{(\mu_V+\sigma+\delta_V)-b\sigma} & \frac{b}{(\mu_V+\delta_V)(\mu_V+\sigma+\delta_V)-b\sigma} & 0 \\ 0 & \frac{\sigma}{(\mu_V+\delta_V)(\mu_V+\sigma+\delta_V)-b\sigma} & \frac{(\mu_V+\sigma+\delta_V)}{(\mu_V+\delta_V)(\mu_V+\sigma+\delta_V)-b\sigma} & 0 \\ 0 & \frac{e\sigma}{(mb-nb)(\mu_V+\delta_V)(\mu_V+\sigma+\delta_V)-b\sigma} & \frac{e(\mu_V+\sigma+\delta_V)}{(mb-nb)(\mu_V+\delta_V)(\mu_V+\sigma+\delta_V)-b\sigma} & \frac{1}{mb-nb} \end{pmatrix}$$

$$FV^{-1}=\begin{pmatrix} \frac{\beta_1(1-\tau\varepsilon)S_H^*}{(\mu_H+\gamma+\delta_V)N} & \frac{\beta_2 S_H^* e\sigma}{N(mb-nb)(\mu_V+\sigma+\delta_V)-b\sigma} & \frac{\beta_2 S_H^* e(\mu_V+\sigma+\delta_V)}{N(mb-nb)(\mu_V+\sigma+\delta_V)-b\sigma} & \frac{\beta_2 S_H^*}{N(mb-nb)} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix} \tag{32}$$

Then;

$$R_c=\frac{\beta_1(1-\tau\varepsilon)S_H^*}{N(\mu_H+\gamma+\delta_V)}=\frac{\beta_1(1-\tau\varepsilon)b_H}{\mu_H(\mu_H+\gamma+\delta_V)} \tag{33}$$

6.0 Result

6.1 Population Data for Nigeria

The total population value of Nigeria is taking to be 162,470,000 and the life expectancy at birth is given as 52.05 for the year 2011 [1]. The birth rate is given as 39.23 births/1000 people and the natural death rate as $\frac{1}{52} = 0.0192$ for the year 2011 [4].

6.2 Data for β_1

The probability of transmission of infection from an infectious human to a susceptible human given that a contact between the two occurs is ρ =0.43 [5] and assuming the average number of contacts is$c = 2$, thus $\beta_1 = \rho \times c$ =0.43× 2 = 0.86.

6.3 Data for β_2

The probability of transmission of infection from a rodent to a susceptible human given that they come in contact with each other is $\rho = 0.05$ [5] and assuming the average number of contacts is $c = 1$,then $\beta_2 = 0.05$

Table 1: The parameter value for Nigeria

Parameters	Values	Detail
μ_H	0.0192	UNICEF
b_H	0.0392	UNICEF
δ_H	0.000011	WHO
γ	0.03836	CDC
ε	0.8	Assumed
$\tau 0 \leq \tau \leq 1$	Assumed	
β_1	0.864.1.2	CDC
β_2	0.054.1.3	CDC
$\delta_V 0 \leq \delta_V \leq 1$		Assumed
mb	0.0175	CDC
nb	0.0233	CDC
b_V	0.0167	WHO
e	0.015	Putz et al
σ	0.6667	Whitney
μ_v	0.0082	Spyghana

6.4 Effective Basic Reproduction Number R_c

From the equation;

$$R_c = \frac{\beta_1(1-\tau\varepsilon)b_H}{\mu_H(\mu_H+\gamma+\delta_V)} \quad (34)$$

Using the parameter values in Table1

When the control measure (compliance to the use of condom) is 0.25

$$R_c = (0.86)(0.0392)(0.8)/((0.0192)(0.0192+0.0383+0..25)) \quad (35)$$

$$= 0.0269696/0.005905 \quad (36)$$

$$R_c = 4.57 \quad (37)$$

When the control measure (compliance to the use of condom) is 0.50

$$R_c = \frac{(0.86)(0.0392)(0.60)}{(0.0192)(0.0192+0.0383+0..50)} \quad (38)$$

$$= 0.0202272/0.010705 \quad (39)$$

$$R_c = 1.89 \quad (40)$$

When the control measure (compliance to the use of condom) is 0.75

$$R_c = \frac{(0.86)(0.0392)(0.4)}{(0.0192)(0.0192+0.0383+0.75)} \quad (41)$$

$$= 0.0134846/0.015505 \quad (42)$$

$$R_c = 0.87 \quad (43)$$

Table 2: Descriptions of effective basic reproduction number and the rate of compliance to the use of condom.

Control measure (compliance to the use of condom) $\tau and \delta_v$	Effective basic reproductive number R_c
0.1	16.04
0.2	5.73
0.3	3.73
0.4	2.61
0.5	1.89
0.6	1.39
0.7	1.02
0.8	0.74
0.9	0.51

Remark
It is very important to note that at equilibrium $R_c = 1$.

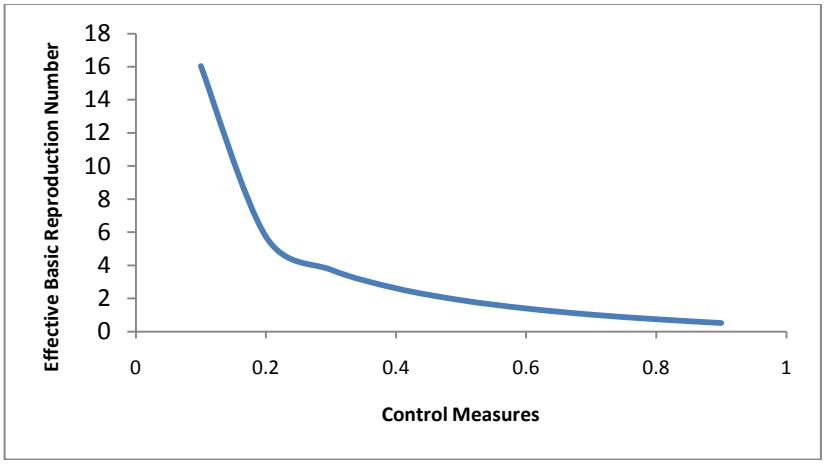

Figure 2: illustrates that as the control measures increases, the effective basic reproduction numberR_c decreases to less than $1(R_c < 1)$.
From the fig. 1 above, the effective basic reproduction number R_c decreases to less than 1 as the rate of control measure increases to 75% and above, this indicates that the disease can only be controlled when there is 75% and above compliance to the use of condom.

The following simulations were conducted using maple software:

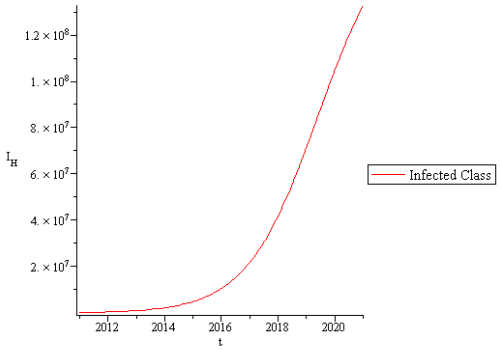

Figure 3: A Numerical Simulation of Lassa Fever for the Model with Initial Conditions:$S_H = 162075000,\ I_H = 200000,\ R_H = 195000,\ C_V = 2500000,\ A_V = 4500000.$
From the numerical simulation in fig.3 above, it shows that the population of the infected human increased as the time increases. Also from table 1, when there is no control measure, the effective basic reproduction number increased significantly which reveals that as a result of no preventive measures, the value of the R_c is greater than 1, this means that the disease is out of control and as a result of that the population of the infected human increased as the time increases, and this is clearly shown in fig.3 above.

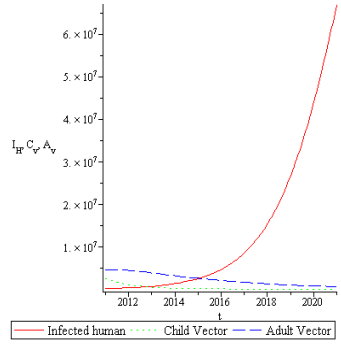

Figure 4a: A Numerical Simulation of Lassa Fever for the Model Using Lower Control measure (0.25) with Initial Conditions:$S_H = 162075000,\ I_H = 200000,\ R_H = 195000,\ C_V = 2500000,\ A_V = 4500000.$

From the numerical simulation in fig.4a above, we discovered that the infected human has increased by a total of 4,652,941 while that of the vector population decreased by a total of 4,927,679, by the year 2016, which is as a result of the fact that the effective basic reproduction number is greater than 1 ($R_c > 1$) as shown in fig. 3, indicating that the rate of the control measures are not adequate to control the spread of the Lassa fever in the country.

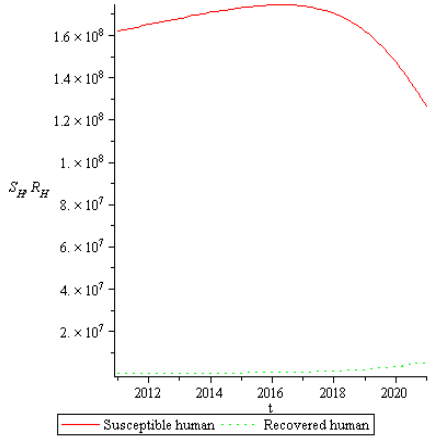

Figure 4b: A Numerical Simulation of Lassa Fever for the Model Using Lower Control measure (0.25) with Initial Conditions:$S_H = 162075000,\ I_H = 200000,\ R_H = 195000,\ C_V = 2500000,\ A_V = 4500000.$

fig.4b indicates that, the population of the susceptible and recovered class has increased by a total number of 12,394,694 and 246,337 respectively, by the year 2016, indicating that the control measures are weak as a result of lower level rate of control measures.

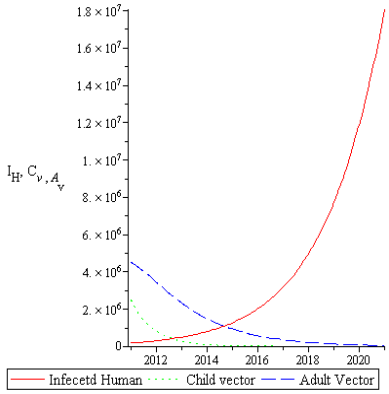

Figure 5a: A Numerical Simulation of the Lassa Fever for Model (3) Using Moderate Control measure (0.5) with Parameter Values Defined in Table 2 and Initial Conditions:$S_H = 162075000,\ I_H = 200000,\ R_H = 195000,\ C_V = 2500000,\ A_V = 4500000.$

Furthermore, fig. 5a shows that the population of infected humans has increased by a total of 1,823,660, while the population of the vectors has reduced by 6,406,270, by the year 2016. Thus from fig.2, ($R_c > 1$) even with 50% rate of control measures, indicating that the disease is out of control.

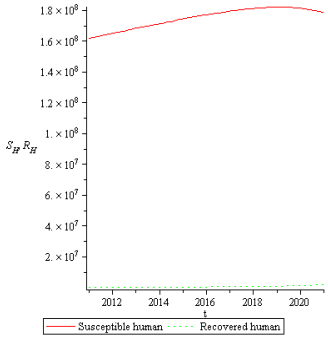

Figure 5b: A Numerical Simulation of Lassa Fever for the Model Using Lower Control measure (0.25) with Initial Conditions:$S_H = 162075000,\ I_H = 200000,\ R_H = 195000,\ C_V = 2500000,\ A_V = 4500000.$

More so, fig.5b signifies that the population of the susceptible and recovered classes has increased by a total of 15,164,123 and 126,225 respectively, by the year 2016 due to moderate rate of control measures, indicating an improvement in controlling the disease.

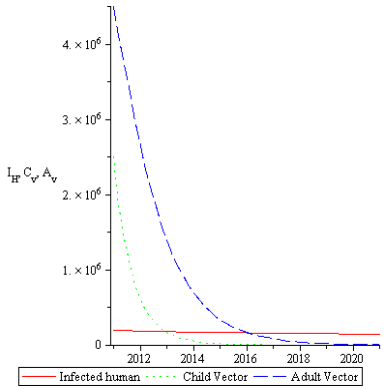

Figure 6a: A Numerical Simulation of Lassa Fever for the Model Using Higher Control measure (0.75) with Initial Conditions:$S_H = 162075000,\ I_H = 200000,\ R_H = 195000,\ C_V = 2500000,\ A_V = 4500000.$

The numerical simulation in fig. 6a indicates that the population of the infected humans, child and adult vectors has decreased as a result of higher rate of control measures. Hence from fig.2, implies that $R_c < 1$ when the control measure is higher than 75%, which means that the disease is under control.

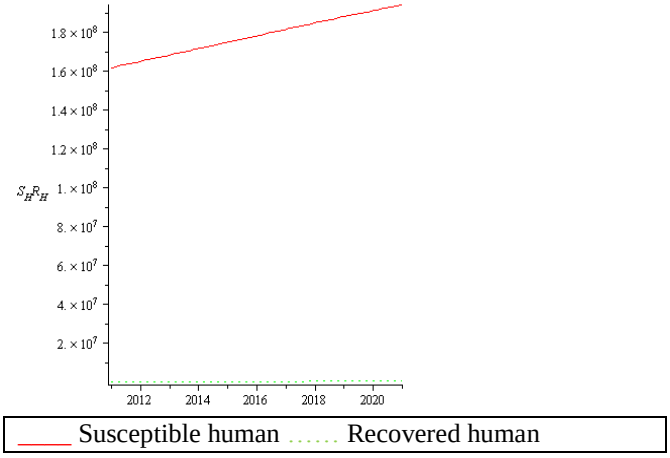

Figure 6b: A Numerical Simulation of Lassa Fever for the Model Using Higher Control measure (0.75) with Parameter Values Defined in Table 2 and Initial Conditions:$S_H = 162075000,\ I_H = 200000,\ R_H = 195000,\ C_V = 2500000,\ A_V = 4500000.$

From the numerical simulation in fig.6b above, it can be seen that the population of the susceptible and recovered class has increased by a total of 16,379,971 and 63,700 as a result of higher rate of control measure been taken to control the spread of Lassa fever in Nigeria.

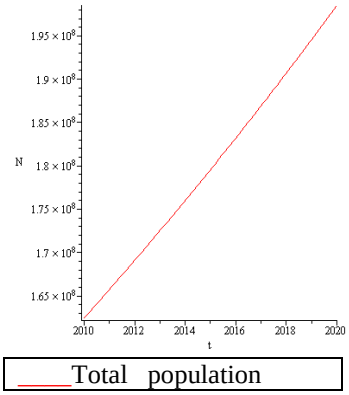

Figure 7: A Numerical Simulation of Lassa Fever for the Model Using Higher Control measure (0.75) with Initial Conditions:$S_H = 162075000,\ I_H = 200000,\ R_H = 195000,\ C_V = 2500000,\ A_V = 4500000.$

From the numerical simulation in fig. 7 above, we observed that the total population of humans has increased by a total of 17,114,028, by the year 2016, this is due to the fact that at higher rate of control measures, $R_c < 1$, which indicates that there will be less number of death due to Lassa fever since the disease is under control and the natural death rate is less than the birth rate.

7.0 Discussion of Results

In this paper, we presented a mathematical model for the spread and control of Lassa Fever. In addition, we also analyzed a 6-dimensional ODE model for the transmission of Lassa fever from the 6-compartment, with 3 variables for human ($S_H, I_H \& R_H$), 2 variables for reservoir host ($C_v \& A_v$) and one variable for the average concentration of virus in the food or water (B). The disease free and endemic equilibrium states were also expressed. The basic reproduction number R_c is computed in terms of parameters and the value of the parameters was later used to determine whether Lassa fever is still endemic in Nigeria. Similarly, in figure 2, $R_c < 1$ at a higher rate of control measure, which means that the disease is under control and when the control measure is at lower rate or moderate rate, then $R_c > 1$.

The numerical simulations in figure 2 shows that the population of the infected human has increases as the time increase due to the fact that there is no measure to control the spread of Lassa fever as displayed in figure 1, hence $R_c > 1$. This means that the disease is out of control.

The numerical simulation in figure 3 and 4 shows the population of the infected human has increased as the time increases, with 25% and 50% control measures respectively. The value of $R_c > 1$, meaning that the disease is still not under control at lower and moderate rate of control measures.

The numerical simulation in figure 5a shows the population of the infected humans, child and adult reservoir host has reduced as a result of higher rate of control measure as verified in figure 1. Thus when the control measure are at higher level, then $R_c < 1$. This implies that the disease is under control within the country.

8.0 Conclusion

We have developed a $S_H I_H R_H C_v A_v B$ model for the dynamics and transmission of Lassa fever which can be applied to study other transmitted diseases such as yellow fever and malaria. We applied this model to compare intervention strategies for Lassa fever spread and control in Nigeria which shows that the most effective strategy is to use condom due to the rate at which humans are killed by the reservoir host, as well as the efficacy of condom and compliance to the condom usage with respect to the value of R_c.

9.0 References

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