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The Dynamics of Lassa Fever Transmission and Control

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Abstract: ***We present a Mathematical model for the dynamics of Lassa fever transmission and control. The model is a modified form of the traditional SIR model for infectious disease. The numerical simulation of the disease transmission is carried out using MATLAB ode 45. The effect of the control measure on the susceptible group, the infected group and the recovered group within a period of 100 days are presented.***

Keywords: Lassa Fever, SIR Model, Numerical Simulation

1. Introduction

Lassa fever, 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. 1 in 5 infections result in severe disease, where the virus affects several organs such as the liver, spleen and kidneys. Lassa fever is a zoonotic disease, meaning that humans become infected from contact with infected animals. The animal reservoir, or host, of Lassa virus is a rodent of the genus *Mastomys*, commonly known as the "multimammate rat." *Mastomys* rats infected with Lassa virus do not become ill, but they can shed the virus in their urine and faeces. [1].

Because the clinical course of the disease is so variable, detection of the disease in affected patients has been difficult. When presence of the disease is confirmed in a community, however, prompt isolation of affected patients, good infection prevention and control practices, and rigorous contact tracing can stop outbreaks.

2. Lassa Fever – Nigeria

ProMED report on 13 February 2016 that Nigeria has recorded 176 cases with 108 deaths - a case fatality rate of 61 percent[18]. Of the total, 78 cases have been confirmed, amongst which 49 have died (63%).As of 17 May 2016, 8 states were reporting Lassa fever cases (suspected, probable, and confirmed), deaths and/or following of contacts for the maximum 21-day incubation period. According to a report from WHO Disease outbreak news, 2016, 248 contacts were being followed up in the country as at the time of the report.

3. Challenges in the Management/Control of Lassa Fever

The high virulence and fatality rate of Lassa fever disease is a major concern which is further complicated by the non-specific modes of presentation. The contagious nature of the illness poses a big threat to the medical attendants; other hospital workers and the caregivers who often are exposed to this disease unprotected, prior to diagnoses and establishment of barrier nursing. Furthermore, accidentally imported cases to the rest of the world had been reported with dire consequences making LF a global challenge and not just a problem confined to the developing world. Unavailability of safe vaccines and cost effective/efficient rapid kit for diagnoses nearly half a decade after identifying the disease has hampered the containment of the illness. It is clear that the future lies in effective and safe vaccination of the populace as in the case of yellow fever.

In their work, Lassa fever: the challenges of curtailing a deadly disease Titus Ibekwe recommended a continuing education of the populace on the dangers of the disease, its modes of presentation and the need to seek medical treatment early and an awareness (campaigns) and advocacy on clean and safe environment to promote prevention especially within the endemic areas are necessary. Finally, they recommended that the ultimate aim should be towards producing a functional and safe anti Lassa-fever that could be incorporated into the immunization programs for children and adults respectively.

Fisher-Hoch S. P et al, [15] in their work vaccinated some vaccinated 44 macaques with vaccinia virus-expressed Lassa virus structural proteins separately and in combination, with the object of inducing a predominantly TH1-type immune response. They studied their responses to Lassa fever challenge against unvaccinated ones. Their result showed that an effective, safe vaccine against Lassa virus can and should be made and that its evaluation for human populations is a matter of humanitarian priority.

Geisbert T W, et al [10] developed a replication-competent vaccine against Lassa virus based on attenuated recombinant vesicular stomatitis virus vectors expressing the Lassa viral glycoprotein. They carried out their experiment on monkeys. A single intramuscular vaccination of the Lassa vaccine elicited a protective immune response in nonhuman primates against a lethal Lassa virus challenge. The Lassa vaccine induced strong humoral and cellular immune responses in the four vaccinated and challenged monkeys. Their conclusion

shows that the Lassa vaccine candidate based on recombinant vesicular stomatitis virus is safe and highly efficacious in a relevant animal model that faithfully reproduces human disease.

4. The Basic Reproductive Number

One of the most important concerns about any infectious disease is its ability to invade a population. Many epidemiological models have a disease free equilibrium (DFE) at which the population remains in the absence of the disease. These models usually have a threshold parameter, known as the basic reproductive number R_0. The basic reproductive number is one of the fundamental concepts in mathematical biology. It is defined as "the average number of secondary infections caused by a single infectious individual during their entire infectious lifetime. It is a fundamental parameter that governs the spread of disease, and relates to long term behaviours and the level of vaccination necessary for eradication. If $R_0 < 1$, each individual produces, on average, less than one new infected individual, then the DFE is locally asymptotically stable, and the disease cannot invade the population and hence the disease dies out. If R0>1, each individual produces more than one new infected individual and hence the disease is able to invade the susceptible population then the DFE is unstable and invasion is always possible. For the SIR model with vital dynamics, Ro is defined as the product of birth rate β with transmission rate λ and the duration of infectious period and divide by death rate D.

5. The Mathematical Model

The dynamics of the population infected by an infectious disease is traditionally described mathematically by the system of differential equations..The SIR epidemic model, where the populationis divided into three groups: the susceptible group, denoted by $S(t)$, the infected group, denoted by $I(t)$, and the recovered group, denoted by $R(t)$.

The total population is assumed constant during the short period of time under study, this is given by

$$N = S(t) + I(t) + R(t)$$

It starts with the fact that the population of the susceptible group will be reduced as the infected come into contact with them with a rate of infection. This means that the change in the population of susceptible is equal to the negative product of $\beta$with (t) and (t):

$$\frac{dS}{dt} = -\beta \frac{S(t)I(t)}{N} \quad (1)$$

The population of the infected group changes in two ways:

i. people leave the susceptible group and join the infected group, thus adding to the total population of infected a term $\beta S(t)I(t)$;
ii. People leave the infected group and join the recovered group, reducing the infected population by $-\mu I(t)$. Then, the equation that describes the infected group over time, can be written as

$$\frac{dI}{dt} = \beta \frac{S(t)I(t)}{N} - \mu I(t) \quad (2)$$

and the equation that describes the recovery population is based on the individuals recovered from the virus at rateμ. This means that the recovery group is increased by μ

multiplied by $I(t)$:

$$\frac{dR}{dt} = \mu I(t) \quad (3)$$

Hence the complete set of equations describing the SIR model is given by

$$\frac{dS}{dt} = -\beta \frac{S(t)I(t)}{N}$$

$$\frac{dI}{dt} = \beta \frac{S(t)I(t)}{N} - \mu I(t) \quad (4)$$

$$\frac{dR}{dt} = \mu I(t)$$

The movement of individuals between the compartments is governed by two constants; the rate at which infected individuals give rise to new infections and the rate at which infected individuals progress the final compartment. The first, β, determines the proportion of encounters between an infected and susceptible individual that will result in a new infection; this depends on the infectiousness of the disease. The second, γ, represents the proportion of infected individuals leaving the infected compartment at each time step through recovery or death; this is based on the aetiology of the disease and the typical length of infection.

Ogabi, et al in 2012 in their work on controlling the disease in the northern part of Edo state presented a modified form of the SIR model for Lassa fever transmission of the form

$$\frac{dS}{dt} = -\alpha S(t)I(t) + B - DS(t)$$
$$\frac{dI}{dt} = \alpha S(t)I(t) - (\gamma + D)I(t) \quad (4)$$
$$\frac{dR}{dt} = \gamma I(t) - DR(t))$$

Where B is the birth rate, D is the death rate, α is the transmission rate and γ is the recovery rate of the infectious group after vaccination.

6. Modified Sir Model

A major strategy to control infectious diseases is through vaccination. Now our idea is to study the effect of vaccination on Lassa fever disease. In this section, we improve the SIR model described in equation 4and present the system of equations that describe the Susceptible-Infectious-Recovery (SIR) model with vaccination as:

$$\frac{dS}{dt} = -\beta S(t)I(t) - vS(t)$$
$$\frac{dI}{dt} = \beta S(t)I(t) - \mu I(t) \quad (5)$$

$$\frac{dR}{dt} = \mu I(t) + vS(t)$$

Where β the rate of infection, μ is is the rate of recovery, and $v$is the percentage of individuals vaccinated every day.

7. Numerical Simulation

We simulate the SIR model with vaccination (6) in order to predict the evolution of every group of individuals in case of vaccination. We consider different rates of vaccinations and their effect on the curve of every group. We adopt the data in [13] taking S(0) = 0.5, I(0) =0.3226, R(0) = 0.1774 $\beta = o.5$ and $\mu = o.7$. This gives $R_0 =$ 0.71 such that $R_0 < 1$.

The results are shown in the following figures.

These figures present different rates of vaccination and their effect on the spread of the infection.

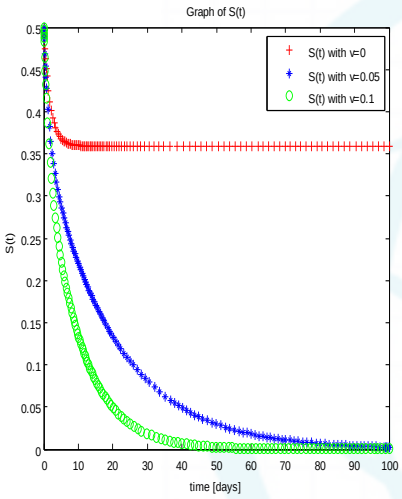

Figure 1: Graph of S(t)with v=0, v=0.05 and v=0.1

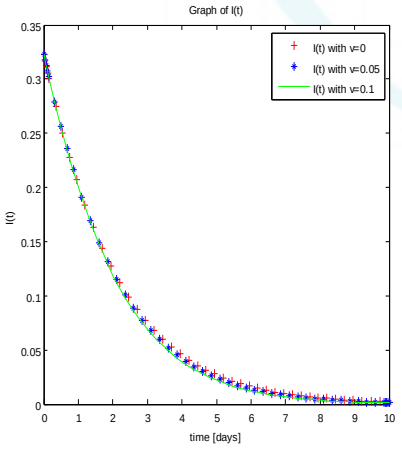

Figure 2: Graph of I(t)with v=0, v=0.05 and v=0.1

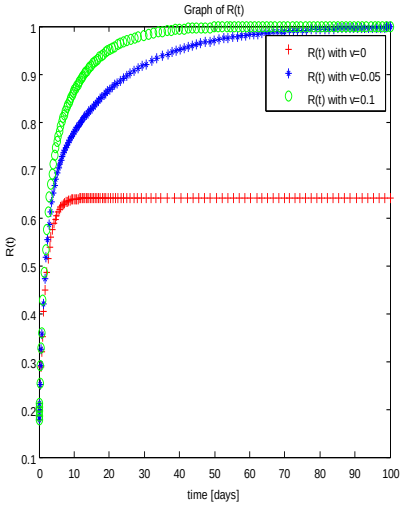

Figure 3: Graph of R(t)with v=0, v=0.05 and v=0.1

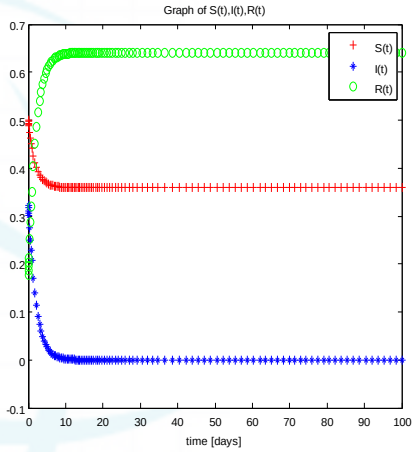

Figure 4: Graph of S(t), I(t) and R(t) with v=0

8. Conclusion

From the graphs, it is observed that the vaccination parameter has significant effect in reducing both the susceptible and the recovered group but no significant difference is seen on the infected group. We therefore conclude that vaccination is a viable control parameter to reduce the susceptible class and increase the recovered group within a short period.

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