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Lassa fever and its Control Measures

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Abstract
Mathematical Models have been very useful in understanding the spread and control of diseases. We will use Mathematical model to investigate the dynamics of spread of Lassa fever in human population. We will examine the contributions from regular contact with the species of rodents that carry the virus that cause Lassa fever and infections contract with persons suffering from the disease is seen as significant in the spread of the disease. We examined the factors that influence equilibrium prevalence, the steady states of the model are also examined for epidemic and endemic situations. Among several intervention measures, control of the rodents carrying the virus, isolation policy for persons infected with the virus and introducing vaccines to the human population are some of the best strategies against the spread of the disease.
Keywords: Mathematical Model; *L*assa fever*;* steady states; epidemic; endemic.

1. Introduction

When infectious disease starts to spread in any given population, the most important thing in the mind of the people is how best to combat the outbreak or at least control the number of infections. Vaccination, quarantining the infective and antiviral drugs which are some of the control measures are costly and time consuming, so any means that will help to predict the outcome is highly welcome.

Mathematical models are useful and powerful tool for investigating human infectious diseases, providing useful predictions about the potential transmission of the disease and the effectiveness of possible control measures. As a result of this, the relationship between mathematics and epidemiology has been on the increase. For the mathematician, epidemiology provides new and exciting branches, while for the epidemiologist, mathematical modeling provide an important research tool in the study of the evolution of diseases.

In 1760, Daniel Bernoulli proposed a smallpox model which was useful in understanding the disease and this model is considered by many as the first epidemiological mathematical model. The theoretical papers provided by Kermack and McKendrinck, between 1927 and 1933 on infectious disease models, have had a great influence in the development of mathematical epidemiology models (Helena 2012, . McCormick et al 1986). Mathematical models are increasingly being used to clarify the transmission of several diseases, so that the researcher can gain important knowledge of the underlying aspects of the infectious diseases spread out and also to evaluate the potential impact of control programs in reducing morbidity and mortality (Harper, 2004).

After the Second World War, the strategy of public health has been to focused on the control and elimination of the organisms that causes diseases. Furthermore, malaria, tuberculosis, dengue and yellow fever have re-emerged as a result of climate Changes and has spreads into new regions (Hethcote, 2000)).

The successful containment of the emerging diseases is not just linked to medical infrastructure but also on the capacity to recognize its transmission characteristics and apply optimal medical and logistic policies. Public health often asks information such as (Anderson and May, 1991) how many people will be infected, how many require hospitalization, what is the maximum number of people ill at a given time and how long will the epidemic last.

A comprehensive survey was carry out by (Anderson and May, 1991) on the use of Mathematics to study infectious diseases, and since that revelation there has been a great increase in the number of mathematical epidemiology papers in circulation. Many infectious diseases are spread by vectors, which transfer pathogens from humans to humans, humans to animals or vice versa. The emergence of such vector-borne diseases seems especially to have stimulated recent interest. One of the early known vector-borne disease models studies carried out, was done (Rogers et al 2003). Many other authors have also studied various vector-borne diseases, such as malaria (Eunha Shim 2012, Jacob C Koella.1991), West Nile virus (Gustavo Cruz-Pacheco et al 2005), and dengue fever (Lourdes Esteva and Cristobal Vargas, 1998)

The focus of researcher now is in the use of models with control measures for disease eradication and control. (Lourdes Esteva and Cristobal Vargas 1998) focuses, is how best a persons should make use of social distancing and self-protective behaviors during an epidemic (Althouse et al. 2010) provided a quantitative framework for making allocation decisions in the presence of different externalities associated with control measures such as vaccination or antibiotic treatment.(Mbah et al. 2012) looked at the effects of both imitation behavior and contact heterogeneity on vaccination coverage and disease dynamics. Unfortunately, there are very limited control measures for most of the vector-borne diseases. Vaccines, is only available for only a few diseases such as yellow fever, Japanese encephalitis, tick-borne encephalitis, tularemia, plague, but are not widely used. Some widespread diseases, such as West Nile virus, malaria, Lassa and dengue fever, don't have

vaccine till now. People have to depend on vector control programs such as the removal of breeding sites generated by humans in households, parricidal control, and Marathon spraying to target adult vector populations. Other controls rely on shortening the mean vector life span. However, these methods appear not to be sufficiently effective, as the frequency of these diseases outbreaks appears to be increasing in some areas. As a consequence of a lack of efficient control measures, mathematical models of vector-borne disease seldom incorporate the ideas of how to curb the disease, and mostly focus on the dynamic transmission of the diseases by using various approaches.

2. Related work

Many pathogens have the ability to infect different species. Lassa fever virus is an important example; this virus infects a species of rodent in West Africa, and can cause a severe disease in people. Lassa fever virus is transmitted from rodent-to-rodent, rodent-to-human, human-to-human and perhaps human-to-rodent. So far, the relative importance of these routes has not been assessed (Richmond and Baglole, 2003).

It is a known fact that disease spread through four basic infectious agents which are *viruses, bacteria, protozoa* and *helminthes*. (Enns 2011). There are also four basic ways of transmission of disease by these infectious agents. They are Human to human, Human to environment to human, Reservoir to humans, Reservoir to vector to human. The term vector refers to insects and reservoir refers to other non-human vectors such as dogs, foxes and rats (Eze et al 2010).

Lassa fever is a virus transmitted disease; it is under Reservoir to human as mentioned above. The incubation period of Lassa fever is 1 to 3 weeks. The disease is endemic in West Africa mostly Nigeria, Liberia, Sierra Leone and Guinea. The earliest record of the disease was in the 1950s but the virus was isolated by the Centre for Disease Control (CDC), Atlanta, USA, in 1969, from a sample taken from a missionary worker in Lassa village in northern Nigeria (Fisher-Hoch 1995). Humans are infected with this disease by eating foods that is contaminated with saliva, urine or excreta of the hosted Lassa virus rat. Nosocomial transmission may occur through droplets by person to person contact or the contamination of needles (Fisher-Hoch 1995). The symptoms and signs of the disease are similar to the symptoms and signs of malaria, typhoid and yellow fever. The symptoms and signs include fever, nausea, vomiting, chest pain, puffy face, puffy cheeks, edema, dehydration, conjunctiva injection, fainting attacks, bleeding from orifices, hypotension, shock and coma (Harper 2004, McCormick et al 1986, Okuonghae and Okuonghae 2006).

It has the potential to cause tens of thousands of deaths and after recovery, the virus remains in the body fluids, including semen (Timothy C Reluga 2010). The mortality rates for Lassa virus are typically estimated at 15% to 20%. Some studies estimate mortality as high as 45%. One survey of Lassa infection viscous mortality rates indicates that less than 1% of all Lassa-virus infections in West Africa will eventually result in fatal disease. The mortality rates for Lassa appear to be much higher in people of non-African stock. (Richmond and Baglole , 2003). Lassa virus also causes high fatal mortality and high mortality in pregnant women. The mortality rate is 92% for fetuses in early pregnancy, 75% for fetuses in the third trimester and100% in the neonatal period for full-term babies. High concentrations of the virus have been found in both fetal tissue and in the placenta (Timothy C Reluga 2010).

The health workers and policy makers have been battling with this disease in various areas and looking for way to put an end to this problem. A mathematical model can be of great help to give better solution to this problem. The disease transmission can be represented by a dynamical nonlinear system.

3. Research Objectives and Approach

The objectives of this work are to show how a nonlinear mathematical model will aid in implementing health policy and to show the rate of spread of Lassa fever. Also, how the solution of system of ordinary differential equations of SEIS model can be used to control the spread of Lassa fever.

We make use of modeling approach to analyze data from published outbreaks and the number of Lassa fever hospitalized patients.

4. Current Work and Preliminary Results

The model will be an SEIS model coupled to a population of the rodent species Mastomys-natalensis. The rational for using an SEIS is as a result of recovered individuals could become susceptible to the disease again.
In this model effort will be made to ensure that the basic variables involved in the disease dynamics are captured.
The mathematical model is:

$$\left.\begin{aligned}
\frac{dS}{dt} &= bN - \mu S - \beta SI - \alpha RS + \gamma I \\
\frac{dE}{dt} &= \beta SI - \eta E - \mu E \\
\frac{dI}{dt} &= \alpha RS + \beta SI - \gamma I - \mu I \\
\frac{dR}{dt} &= rR(1 - \tfrac{R}{K}) - dR
\end{aligned}\right\} \quad 1.1$$

S(0)=N, E(0)=0, I(0)>0, R(0)=0.

The symbols used in the model are listed in Table 1 and a diagrammatic representation of the model is in Figure 1.

Table 1: Symbols used in the mathematical model

S	Number of susceptible
E	Number of those who are exposed to Lassa fever
I	Number of those who are infected with Lassa fever
R	Population of rodents carrying the virus
N	Total population of humans
B	Human birth rates per day
D	Death rate of the rodents per day
R	Growth rate of the rodents per day
K	Carrying capacity of the environment for the rodents
μ	Human death rate per day
β	contact rate of infection from susceptible to exposed per day
α	Infectious contact rate with rodent per day
γ	Rate at which infected recover from Lassa per day
η	Contact rate of infection from exposed to infected class per day

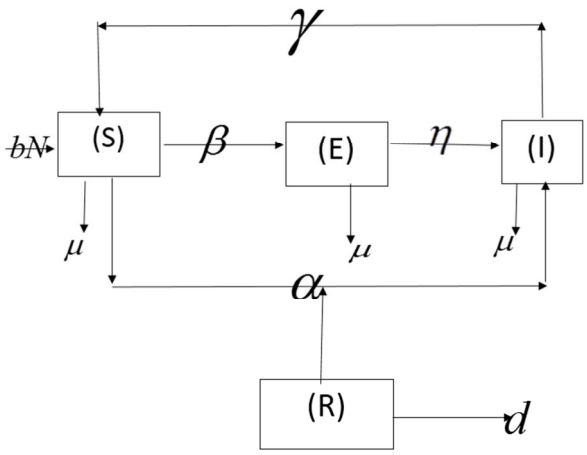

Figure 1: Diagrammatic representation of the model

Equation 1.1 describes the dynamics of susceptible, exposed and infected individuals as well as the rodent population. The first equation in (1.1) describes the dynamics of susceptible. The population is of constant size N. the susceptible are renewed at a rate b and die at rate μ. The susceptible become infected with the disease due to contacts with rodents (as a result of eating the rodents, food contaminated with rodent's fasces, urine and saliva) at rate α and also due to infectious contacts with individuals suffering from Lassa fever at rate β. Since we are using the SEIS model, recovered individuals get back to the susceptible pool at rate γ (recovering rate).

The second equation in (1.1) describes the dynamics of the exposed people in the given population; those exposed to Lassa fever. The equation shows that the expose population increases as susceptible become infected (the first term in the second equation) and decreases at the rate at which they die.

The third equation in (1.1) describes the dynamics of the infected people in the given population; those

suffering from Lassa fever. The equation shows that the infected population increases as susceptible become infected (the first two terms in the third equation) and decreases as they recover from the disease and the rate at which they die.

The fourth equation in (1.1) describes the dynamics of the rodent population. We use logistic growth equation to describe the population of the rodents, with K being the environmental carrying capacity for the rodents and r the growth rate. The rodents die (either naturally or by outright killing) at the rate d.

All individuals in human classes die at the same rate μ . For the sake of the model, we assume that the birth and the death rate are equal.

Equilibrium Analysis

We have to perform the equilibrium and the stability analysis of the model for a better understanding of the dynamics of the disease. We set each of the four derived equations in (1.1) equal to zero and solve for S, E, I and R. This gives the fixed points, or equilibrium solutions; that gives values of S, E, I and R for which the system will no longer change (that is all the derivatives or rate of change will be zero).

Stability Analysis

We need to compute the linearization of the system, to determine the population behavior near the equilibrium solutions. We will get this from the Jacobian matrix of the system.

From the system of equations in (1.1), the Jacobian matrix is as below.

$$\begin{pmatrix} -\mu-\beta I-\alpha R & 0 & -\beta S+\gamma & -\alpha S \\ \beta I & -\eta-\mu & 0 & 0 \\ \alpha R+\beta I & 0 & \beta S-\gamma-\mu & \alpha S \\ 0 & 0 & 0 & r\left(1-\frac{R}{K}\right)-\frac{rR}{K}-d \end{pmatrix} \quad 1.2$$

We will work out the stability analysis using the Jacobian in 1.2 above.

Lassa free population.

When (S^*, E^*, I^*, R^*) = (N, 0, 0, 0) this is a disease free equilibrium point.

For the points (S^*, E^*, I^*, R^*) = (N, 0, 0, 0), the Jacobian matrix of the system is the matrix below

$$\begin{pmatrix} -\mu & 0 & -\beta N+\gamma & -\alpha N \\ 0 & -\eta-\mu & 0 & 0 \\ 0 & 0 & \beta N-\gamma-\mu & \alpha N \\ 0 & 0 & 0 & r-d \end{pmatrix} \quad 1.3$$

The eigenvalues of the Jacobian are $\lambda_1=-\mu, \lambda_2=-\eta-\mu, \lambda_3=\beta N-\gamma-\mu, \lambda_4=r-d$

For the stability of the disease Free State, all eigenvalues of (1.3) must be negative. This is only possible if and only if

$$\gamma+\mu>\beta N \quad 1.4$$

$$d>r \quad 1.5$$

If (1.4) and (1.5) are achieved, then the disease dies out.

From (1.4) we can obtain threshold condition. Which is given as

$$N<\frac{\gamma+\mu}{\beta} \quad 1.6$$

The critical susceptible pool is given as

$$S_c=\frac{\gamma+\mu}{\beta} \quad 1.7$$

If the initial susceptible, $S_i > S_c$, then the disease will spread and there will be an epidemic. From (1.7) the basic reproduction number for the infection is given by

$$R_o = \frac{\beta}{\gamma + \mu} S_c \qquad 1.8$$

If $R_o > 1$, a disease outbreak will occur, but if $R_o < 1$ the number of Lassa cases will reduce and will in fact return to zero.

6. Conclusions

Effort must be made to reduce the spread of Lassa fever by reducing the basic reproduction number $R_{o,}$ it must be below 1, if it is more than 1 the disease will not die out. To achieve this, the transmission rate must be very Low. The contacts rate of sick individual with other must be low to prevent the transmission rate. Good health policy must be implemented.

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