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STABILITY AND BIFURCATION ANALYSIS OF ENDEMIC EQUILIBRIUM OF A MATHEMATICAL MODEL OF YELLOW FEVER INCORPORATING SECONDARY HOST

[1*]*Somma S. A.*,[2]*Akinwande N. I.*,[3]*Jiya M.*,[4]*Abdulrahman S.and*[5]*Ogwumu O. D.*

[1,2,3]Department of Mathematics, Federal University of Technology, P. M. B. 65, Minna, Nigeria.
[4]Department of Mathematics, Federal University, BirninKebbi, Nigeria.
[5]Department of Mathematics and Statistics, Federal University Wukari, Wukari, Nigeria.

Abstract

In this paper we used the Centre Manifold theorem to analyzed the local stability of Endemic Equilibrium (EE). We obtained the endemic equilibrium point in terms of forces of infection and use it to analyze for the bifurcation of the model. We carried out the bifurcation analysis of the model with four forces of infection which resulted into bifurcation diagram. The forces of infection of vector-primary host and vector-secondary host transmissions were plotted against basic reproduction number. The bifurcation diagram revealed that the model exhibit forward bifurcation.

Keywords: Stability, bifurcation, endemic equilibrium, yellow fever.

1. Introduction

In a dynamical system, bifurcation occurs when a small smooth change made to the parameter values (the bifurcation parameters) of a system causes a sudden qualitative or topological change in its behaviour. Bifurcations occur in both continuous systems and discrete systems [1]. A slight variation in parameter can caused a change in the differential system. The change in a parameter can also cause the stable equilibrium to change to unstable equilibrium [2].

Mathematical modelling of epidemics is aim at understanding the spread and control of an infectious disease within a host population [3, 4]. The basic reproduction number, R_0 played a key role by providing the condition for the eradication or persistence of the epidemics [5, 6, 7]. Indeed, assessing the direction of the transcritical bifurcation arising at $R_0 = 1$ is a primary issue in epidemic modelling. For many compartmental epidemic models, if R_0 is greater than unity, then the disease will spread and possibly persist within the host population; if R_0 is less than the unity, then the infection cannot sustain itself [3, 4, 8]. When this happens, the bifurcation at the criticality is said to be a trans critical forward bifurcation. However, in some cases the dynamics may be more complex. This happens, in particular, when the model exhibits the phenomenon of backward bifurcation [8, 9]. This occurrence implies that a stable endemic equilibrium may also exist when R_0 is less than unity. From the epidemiological point of view, this phenomenon has important public health implications because reducing R_0 below the unity is no longer sufficient to guarantee disease elimination; the basic reproduction number must be reduced under a smaller threshold in order to avoid endemic states and get the elimination[10].

Yellow fever is an acute viral disease. In most cases symptoms include fever, chills, loss of appetite, nausea, muscle pains particularly in the back, and headaches. The disease is caused by the yellow fever virus and is spread by the bite of the female mosquito. It only infects humans, other primates and several species of mosquito [11]. In cities it is primarily spread by mosquitoes of the *Aedesaegypti* species. The virus is an Ribonucleic acid (RNA) virus of the genus *Flavivirus* [12].Basically Yellow Fever Virus (YFV) is spread through the bite of the mosquito *Aedes aegypti,* however different mosquitoes, for example, the tiger mosquito (*Aedesalbopictus*) can likewise serve as a carrier for this infection. To confirm a suspected case blood sample testing with Polymerase Chain Reaction (PCR) is required [13].

Yellow fever virus (YFV) is mainly transmitted through the bite of the yellow fever mosquito *Aedesaegypti*, but other mosquitoes such as the tiger mosquito (*Aedesalbopictus*) can also serve as a vector for this virus. Like other Arboviruses which are transmitted via mosquitoes, the yellow fever virus is taken up by a female mosquito when it ingests the blood of an infected human or other primate. Viruses reach the stomach of the mosquito, and if the virus concentration is high enough, the virus can infect epithelial cells and replicate there [14].

Corresponding Author: Somma S.A., Email: sam.abu@futminna.edu.ng, Tel: +2348068037304

In persons who develop symptoms, the incubation period (time from infection until illness) is 3–6 days. The initial symptoms include sudden onset of fever, chills, severe headache, back pain, general body aches, nausea, and vomiting, fatigue, and weakness. After a brief remission of hours to a day, roughly 15% of cases progress to develop a more severe form of the disease. The severe form is characterized by high fever, jaundice, bleeding, and eventually shock and failure of multiple organs [15]. Surviving the infection provides lifelong immunity [16].

In [17] the model of yellow fever epidemics was formulated which involves the interactions of two principal communities; hosts (humans) and Vectors *(aedesaegypti* mosquitoes). The host community was divided into three compartments of Susceptible $S(t)$, Infected $I(t)$ and Recovered $R(t)$ while the vector community was partitioned into two compartments of Susceptible $N(t)$ and Infective or virus carriers $M(t)$ where $t \geq 0$ is the time. He analyzed the local stability of the model

ıcobian matrix and implicit function.

they formulated a model and incorporated the biology of the urban vector of yellow fever, the mosquito *Aedesaegypti*, es of the disease in the host (humans). From the epidemiological point of view, the mosquito follows a Susceptible, d, Infective (SEI) sequence. In their, model the adult populations are subdivided according to their status with respect irus. They assumed that there is no vertical transmission of the virus and eggs, larvae, pupae and non parous adults are susceptible. The humans are subdivided in sub-populations according to their status with respect to the illness as: ible (S), exposed (E), infective (I), in remission (r), toxic (T) and recovered (R).

:hey formulated a mathematical model of yellow fever dynamics incorporating secondary host and two equilibrium :xist; Disease Free Equilibrium (DFE) and Endemic Equilibrium (EE). In [20] they obtained the Disease Free rium (DFE) points, computed the basic reproduction number and analyzed the local and global stabilities.

paper, we obtained the Endemic Equilibrium (EE) point in terms of forces of infection and analyze the local stability entre manifold theorem as used in[21, 22]. We carried out the bifurcation analysis of the model with four forces of n which resulted into bifurcation diagram where forces of infection of vector to primary host transmission λ_{vh}^{**} and vector to secondary host transmission λ_{vm}^{**} were plotted against the basic reproduction number of vector to primary host transmission R_{vh} and basic reproduction number vector to secondary host transmission R_{vm}, respectively.

2. Materials and Methods

Model Formulation

The schematic diagram of the model is shown in figure 2. 1. The dash line from infected human class, I_h, to the non-carrier vector, V_1, shows that the infected human individuals infect the non-carrier vector population while the dash line from carrier vector, V_2, to the susceptible human population, S_h, shows the transfer of the virus from infected mosquito to susceptible human. So also, the dash line from infected monkey class, I_m, to the non-carrier vector, V_1, shows that the infected monkey infect the non-carrier vector population while the dash line from carrier vector, V_2, to the susceptible monkey population, S_m, shows the transfer of the virus from carrier vector to susceptible monkey.

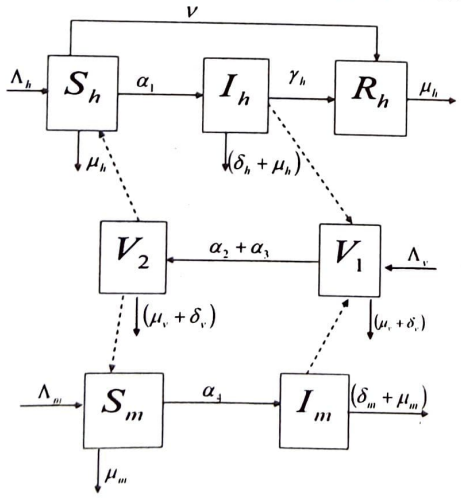

Figure 2.1: Schematic Diagram of the Model

Assumptions of the Model

The details of the model formulation is given in [19] and [20].

The following assumptions were made:

(i) The susceptible vaccinated individuals move to recovered/immune class;

(ii) The recovery rate, γ_h of humans include the treatment and natural healing of the infected individuals;

(iii) The vaccinated and recovered susceptible and infected individuals become permanently immune to the disease for life;

(iv) The natural death rate of vectors μ_v include the death due to absence of blood meal;

(v) The infected secondary host died with the infection since they do not have access to vaccination and treatment;

(vi) The forces of infection of vector-human transmission $\frac{\alpha_1 S_h V_2}{N_h}$ and human-vector transmission $\frac{\alpha_2 V_1 I_h}{N_h}$ as no effect on the forces of infection of vector-secondary host transmission $\frac{\alpha_4 S_m V_2}{N_m}$ and secondary host -vector transmission $\frac{\alpha_2 V_1 I_m}{N_m}$ and vice visa because the contact between the humans and secondary host cannot cause the transmission of the virus.

$$\frac{dS_h}{dt} = \Lambda_h - \frac{\alpha_1 S_h V_2}{N_h} - (\nu + \mu_h) S_h \tag{2.1}$$

$$\frac{dI_h}{dt} = \frac{\alpha_1 S_h V_2}{N_h} - (\gamma_h + \mu_h + \delta_h) I_h \tag{2.2}$$

$$\frac{dR_h}{dt} = \nu \delta_h + \gamma_h I_h - \mu_h R_h \tag{2.3}$$

$$\frac{dV_1}{dt} = \Lambda_v - \frac{\alpha_2 V_1 I_h}{N_h} - \frac{\alpha_3 V_1 I_m}{N_m} - (\mu_v + \delta_v) V_1 \tag{2.4}$$

$$\frac{dV_2}{dt} = \frac{\alpha_2 V_1 I_h}{N_h} + \frac{\alpha_3 V_1 I_m}{N_m} - (\mu_v + \delta_v) V_2 \tag{2.5}$$

$$\frac{dS_m}{dt} = \Lambda_m - \frac{\alpha_4 S_m V_2}{N_m} - \mu_m S_m \tag{2.6}$$

$$\frac{dI_m}{dt} = \frac{\alpha_4 S_m V_2}{N_m} - (\mu_m + \delta_m) I_m \tag{2.7}$$

Where,

$$N_h = S_h + I_h + R_h \tag{2.8}$$

$$N_v = V_1 + V_2 \tag{2.9}$$

$$N_m = S_m + I_m \tag{2.10}$$

Table 2.1: Notation and definition of variables and parameter

Symbol	Description
$S_h(t)$	Number of susceptible humans at time t
$I_h(t)$	Number of infectious humans at time t
$R_h(t)$	Number of recovered/Immune human at time t
$V_1(t)$	Number of non-carrier vectors at time t
$V_2(t)$	Number of carrier vectors at time t
$S_m(t)$	Number of susceptible secondary host at time t
$I_m(t)$	Number of infectious secondary host at time t
N_h	Total human population at time t
N_v	Total vector population at time t
N_m	Total secondary vector population at time t
α_1	Effective virus Transmission rate from mosquito to humans

α_2 Effective virus Transmission rate from humans to mosquito
α_3 Effective virus Transmission rate from secondary host to mosquito
α_4 Effective virus Transmission rate from mosquito to secondary host
Λ_h Recruitment number of human population
Λ_v Recruitment number of mosquito population
Λ_m Recruitment number of secondary vector population
δ_h Disease-induced death rate of humans
δ_v Death rate of mosquito due to application of insecticide
δ_m Disease-induced death rate of secondary host
μ_h Natural death rate of human population
μ_v Natural death rate of mosquito population
μ_m Natural death rate of secondary host population
γ_h Recovery rate of human population due to drug administration
ν vaccination rate for the human population

Disease Free Equilibrium (DFE) Points

The DFE is given as

$$E^0 = \left(S_h^0, I_h^0, R_h^0, V_1^0, V_2^0, S_m^0, I_m^0\right) = \left(\frac{\Lambda_h}{A_1}, 0, \frac{\Lambda_h \nu}{\mu_h A_1}, \frac{\Lambda_v}{A_3}, 0, \frac{\Lambda_m}{\mu_m}, 0\right) \tag{2.11}$$

Basic Reproduction Number, R_0

The basic reproduction number is the average number of secondary infections caused by a single infectious individual during his/her entire infectious life time. Applying next generation matrix operator to compute the Basic Reproduction Number of the model [7 23, 24]. The basic reproduction number is obtained by dividing the whole population into n compartments in which there are $m < n$ infected compartments. Let x_i, $i = 1, 2, 3, \ldots, m$ be the numbers of infected individuals in the i^{th} infected compartment at time t.

The largest eigenvalue or spectral radius of FV^{-1} is the basic reproduction number of the model.

$$FV^{-1} = \left[\frac{\partial F_i(E^0)}{\partial x_i}\right]\left[\frac{\partial V_i(E^0)}{\partial x_i}\right]^{-1} \tag{2.12}$$

Where F_i is the rate of appearance of new infection in compartment i, V_i is the transfer of infections from one compartment i to another and E^0 is the disease-Free Equilibrium.

$$F = \begin{bmatrix} 0 & \frac{\alpha_1 \mu_h}{A_1} & 0 \\ \frac{\alpha_2 A_5 \mu_h}{A_3} & 0 & \frac{\alpha_3 A_6 \mu_m}{A_3} \\ 0 & \alpha_4 & 0 \end{bmatrix} \tag{2.13}$$

Where

$$A_5 = \frac{\Lambda_v}{\Lambda_h} \text{ and } A_6 = \frac{\Lambda_v}{\Lambda_m}$$

$$V = \begin{bmatrix} A_2 & 0 & 0 \\ 0 & A_3 & 0 \\ 0 & 0 & A_4 \end{bmatrix} \tag{2.14}$$

$$V^{-1} = \begin{bmatrix} \frac{1}{A_2} & 0 & 0 \\ 0 & \frac{1}{A_3} & 0 \\ 0 & 0 & \frac{1}{A_4} \end{bmatrix} \quad (2.15)$$

multiplying (2.13) by (2.15) gives

$$FV^{-1} = \begin{bmatrix} 0 & \frac{\alpha_1 \mu_h}{A_1 A_3} & 0 \\ \frac{\alpha_2 A_5 \mu_h}{A_2 A_3} & 0 & \frac{\alpha_3 A_6 \mu_m}{A_3 A_4} \\ 0 & \frac{\alpha_4}{A_4} & 0 \end{bmatrix} \quad (2.16)$$

The characteristic equation of (2.16) is given by

$$\lambda\left[\lambda^2 - \left[\frac{\alpha_3\alpha_4 A_6 \mu_m}{A_3^{\,2} A_4} + \frac{\alpha_1\alpha_2 A_5 \mu_h^{\,2}}{A_1 A_2 A_3^{\,2}}\right]\right] = 0 \quad (2.17)$$

Therefore,

$$\lambda_1 = 0,\ \lambda_2 = \sqrt{\left[\frac{\alpha_3\alpha_4 A_6 \mu_m}{A_3^{\,2} A_4} + \frac{\alpha_1\alpha_2 A_5 \mu_h^{\,2}}{A_1 A_2 A_3^{\,2}}\right]} \text{ and } \lambda_3 = -\sqrt{\left[\frac{\alpha_3\alpha_4 A_6 \mu_m}{A_3^{\,2} A_4} + \frac{\alpha_1\alpha_2 A_5 \mu_h^{\,2}}{A_1 A_2 A_3^{\,2}}\right]} \quad (2.18)$$

Hence,

λ_2 is the spectral radius of $\rho(FV^{-1})$

$$R_0 = \sqrt{\frac{\alpha_1\alpha_2 A_5 \mu_h^{\,2}}{A_1 A_2 A_3^{\,2}} + \frac{\alpha_3\alpha_4 A_6 \mu_m}{A_3^{\,2} A_4}} \quad (2.19)$$

There are two host populations and one vector in the model, and it was shown from the schematic diagram in Figure 2.1 that the vector transmits the infection to human host and secondary host (monkey). Hence, the Basic Reproduction Number can be represented as,

$$R_0 = \sqrt{R_{vh} + R_{vm}} \quad \text{or} \quad R_0^{\,2} = R_{vh} + R_{vm} \quad (2.20)$$

Such that

$$R_{vh} = \frac{\alpha_1\alpha_2 A_5 \mu_h^{\,2}}{A_1 A_2 A_3^{\,2}} \quad (2.21)$$

which is the basic reproduction number of vector-primary host compartments and represents the infection from vector to human and human to vector in the absence of secondary host (monkeys).

and

$$R_{vm} = \frac{\alpha_3\alpha_4 A_6 \mu_m}{A_3^{\,2} A_4} \quad (2.22)$$

which is the basic reproduction number of vector-secondary host compartments and represents the infection from vector to monkey and monkey to vector in the absence of primary host (humans).

Endemic Equilibrium Point (EEP) in Terms of Forces of Infection

The Endemic Equilibrium Point (EEP) in terms of forces of infectionare computed for the bifurcation analysis.

Let,

$$E^{**} = (S_h, I_h, R_h, V_1, V_2, S_m, I_m) = (S_h^{**}, I_h^{**}, R_h^{**}, V_1^{**}, V_2^{**}, S_m^{**}, I_m^{**}) \quad (2.23)$$

bethe Endemic Equilibrium points

$$\Lambda_h - S_h^{**}\lambda_{vh}^{**} - A_1 S_h^{**} = 0 \quad (2.24)$$

$$S_h^{**}\lambda_{vh}^{**} - \Lambda_1 I_h^{**} = 0 \tag{2.25}$$

$$\Lambda_2 S_h^{**} + \gamma_h I_h^{**} - \mu_h R_h^{**} = 0 \tag{2.26}$$

$$\Lambda_v - V_1^{**}\lambda_{hv}^{**} - V_1^{**}\lambda_{mv}^{**} - \Lambda_3 V_1^{**} = 0 \tag{2.27}$$

$$V_1^{**}\lambda_{hv}^{**} + V_1^{**}\lambda_{mv}^{**} - \Lambda_3 V_2^{**} = 0 \tag{2.28}$$

$$\Lambda_m - S_m^{**}\lambda_{vm}^{**} - \mu_m S_m^{**} = 0 \tag{2.29}$$

$$S_m^{**}\lambda_{vm}^{**} - \Lambda_4 I_m^{**} = 0 \tag{2.30}$$

Where,

$$\lambda_{vh}^{**} = \frac{\alpha_1 V_2^{**}}{N_h^{**}},\ \lambda_{hv}^{**} = \frac{\alpha_2 I_h^{**}}{N_h^{**}},\ \lambda_{mv}^{**} = \frac{\alpha_3 I_m^{**}}{N_m^{**}} \text{ and } \lambda_{vm}^{**} = \frac{\alpha_4 V_2^{**}}{N_m^{**}} \tag{2.31}$$

λ_{vh}^{**} is the force of infection of vectors (mosquitoes) to primary host (humans)

λ_{hv}^{**} is the force of infection of primary host (humans) to vectors (mosquitoes)

λ_{mv}^{**} is the force of infection of secondary host (monkeys) to vectors (mosquitoes)

λ_{vm}^{**} is the force of infection of vectors (mosquitoes) to secondary host (monkeys)

Solving (2.24) to (2.30) gives the endemic equilibrium point in terms of forces of infection:

$$\begin{pmatrix} S_h^{**} \\ I_h^{**} \\ R_h^{**} \\ V_1^{**} \\ V_2^{**} \\ S_m^{**} \\ I_m^{**} \end{pmatrix} = \begin{pmatrix} \frac{\Lambda_h}{\Lambda_1 + \lambda_{vh}^{**}} \\ \frac{\Lambda_h \lambda_{vh}^{**}}{\Lambda_2(\Lambda_1 + \lambda_{vh}^{**})} \\ \frac{\Lambda_h(\Lambda_2 \nu + \gamma\lambda_{vh}^{**})}{\Lambda_2 \mu_h(\Lambda_1 + \lambda_{vh}^{**})} \\ \frac{\Lambda_v}{\Lambda_3 + \lambda_{hv}^{**} + \lambda_{mv}^{**}} \\ \frac{\Lambda_v(\lambda_{hv}^{**} + \lambda_{mv}^{**})}{\Lambda_3(\Lambda_3 + \lambda_{hv}^{**} + \lambda_{mv}^{**})} \\ \frac{\Lambda_m}{\mu_m + \lambda_{vm}^{**}} \\ \frac{\Lambda_m \lambda_{vm}^{**}}{\Lambda_4(\mu_m + \lambda_{vm}^{**})} \end{pmatrix} \tag{2.32}$$

The total population of human at endemic equilibrium in terms of forces of infection is given as

$$\left.\begin{aligned} N_h^{**} &= S_h^{**} + I_h^{**} + R_h^{**} \\ N_h^{**} &= \frac{\Lambda_h}{\Lambda_1 + \lambda_{vh}^{**}} + \frac{\Lambda_h \lambda_{vh}^{**}}{\Lambda_2(\Lambda_1 + \lambda_{vh}^{**})} + \frac{\Lambda_h(\Lambda_2 \nu + \gamma\lambda_{vh}^{**})}{\Lambda_2 \mu_h(\Lambda_1 + \lambda_{vh}^{**})} \\ N_h^{**} &= \frac{\Lambda_h(\Lambda_1\Lambda_2 + \Lambda_2\lambda_{vh}^{**})}{\Lambda_2 \mu_h(\Lambda_1 + \lambda_{vh}^{**})} \end{aligned}\right\} \tag{2.33}$$

Where $\Lambda_2 = (\mu_h + \gamma)$

The total population of secondary host at endemic equilibrium in terms of forces of infection is given as

$$\left.\begin{aligned} N_m^{**} &= S_m^{**} + R_m^{**} \\ N_m^{**} &= \frac{\Lambda_m}{\mu_m + \lambda_{vm}^{**}} + \frac{\Lambda_m \lambda_{vm}^{**}}{\Lambda_4(\mu_m + \lambda_{vm}^{**})} \\ N_m^{**} &= \frac{\Lambda_m(\Lambda_4 + \lambda_{vm}^{**})}{\Lambda_4(\mu_m + \lambda_{vm}^{**})} \end{aligned}\right\} \tag{2.34}$$

Substituting (2.32) and (2.33) into first equation of (2.31) gives

$$\lambda_{vh}^{**} = \frac{\alpha_1 \Lambda_v \Lambda_h \mu_h(\Lambda_1 + \lambda_{vh}^{**})(\lambda_{hv}^{**} + \lambda_{mv}^{**})}{\Lambda_3(\Lambda_3 + \lambda_{hv}^{**} + \lambda_{mv}^{**})(\Lambda_1\Lambda_2 + \Lambda_2\lambda_{vh}^{**})} \tag{2.35}$$

$$\lambda_{hv}^{**} = \frac{\alpha_2 \lambda_{vh}^{**} \mu_h}{\Lambda_1\Lambda_2 + \Lambda_2\lambda_{vh}^{**}} \tag{2.36}$$

$$\lambda_{mv}^{**} = \frac{\alpha_3 \lambda_{vm}^{**}}{\Lambda_4 + \lambda_{vm}^{**}} \tag{2.37}$$

$$\lambda_{mv}^{**} = \frac{\alpha_4 A_3 A_6 \left(\lambda_{hv}^{**} + \lambda_{mv}^{**}\right)\left(\mu_m + \lambda_{vm}^{**}\right)}{A_3\left(A_3 + \lambda_{hv}^{**} + \lambda_{mv}^{**}\right)\left(A_4 + \lambda_{vm}^{**}\right)} \tag{2.38}$$

Note that, λ_{mv}^{**} and λ_{vm}^{**} are the force of infections of secondary host to mosquitoes and mosquitoes to secondary host respectively. It was assumed that, the infected secondary host cannot infect humans even if they have contact, since the means of transmission is through mosquito bite. Hence, they are taken as zero in the force of infections of mosquitoes to human and human to mosquitoes, i.e. $\lambda_{hv}^{**} = \lambda_{vm}^{**} = 0$.

Therefore, (2.35) becomes

$$\lambda_{vh}^{**} = \frac{\alpha_1 A_2 A_5 \mu_h \lambda_{hv}^{**}\left(A_1 + \lambda_{vh}^{**}\right)}{A_3\left(A_3 + \lambda_{hv}^{**}\right)\left(A_1 A_2 + A_7 \lambda_{vh}^{**}\right)} \tag{2.39}$$

Substituting (2.36) into (2.39) gives

$$\left(A_3^2 A_7^2 + \alpha_2 A_3 A_7 \mu_h\right)\lambda_{vh}^{**2} + \left(2A_1 A_2 A_3^2 A_7 + \alpha_2 A_1 A A_3 \mu_h - \alpha_1 \alpha_2 A_2 A_5 \mu_h^2\right)\lambda_{vh}^{**} + \left(A_1^2 A_2^2 A_3^2 - \alpha_1 \alpha_2 A_1 A_2 A_5 \mu_h^2\right) = 0 \tag{2.40}$$

$$G_1 \lambda_{vh}^{**2} + G_2 \lambda_{vh}^{**} + G_3 = 0$$

Where, (2.41)

$$\left.\begin{aligned} G_1 &= A_3^2 A_7^2 + \alpha_2 A_3 A_7 \mu_h \\ G_2 &= 2A_1 A_2 A_3^2 A_7 + \alpha_2 A_1 A A_3 \mu_h - \alpha_1 \alpha_2 A_2 A_5 \mu_h^2 \\ G_3 &= A_1^2 A_2^2 A_3^2 \left(1 - R_{vh}\right) \end{aligned}\right\} \tag{2.42}$$

Note also that, λ_{vh}^{**} and λ_{hv}^{**} are the force of infections of mosquitoes to human and human to mosquitoes respectively. It was assumed that, the infected secondary host cannot infect humans even if they have contact, since the means of transmission is through mosquito bite. Hence, they aretaken as zero in the force of infections of secondary host to mosquitoes and mosquitoes to secondary host, i.e. $\lambda_{vh}^{**} = \lambda_{hv}^{**} = 0$.

Therefore, (2.38) becomes

$$\lambda_{mv}^{**} = \frac{\alpha_3 \lambda_{vm}^{**}}{\left(A_4 + \lambda_{vm}^{**}\right)} \tag{2.43}$$

Substituting (2.37) into (2.43) gives

$$\left(A_3^2 + \alpha_3 A_3\right)\lambda_{vm}^{**2} + \left(2A_3^2 A_4 + \alpha_3 A_3 A_4 - \alpha_3 \alpha_4 A_4 A_6\right)\lambda_{vm}^{**} + \left(A_3^2 A_4^2 - \alpha_3 \alpha_4 A_4 A_6 \mu_m\right) = 0 \tag{2.44}$$

$$H_1 \lambda_{vm}^{**2} + H_2 \lambda_{vm}^{**} + H_3 = 0 \tag{2.45}$$

Where,

$$\left.\begin{aligned} H_1 &= A_3^2 + \alpha_3 A_3 \\ H_2 &= 2A_3^2 A_4 + \alpha_3 A_3 A_4 - \alpha_3 \alpha_4 A_4 A_6 \\ H_3 &= A_3^2 A_4^2 \left(1 - R_{vm}\right) \end{aligned}\right\} \tag{2.46}$$

The quadratic equation (2.41) and (2.45) can be analyze for the possibility of multiple equilibria whenever the associated reproduction number is greater than or less than unity. The coefficient G_1 is always positive and G_3 is positive if $R_{vh} < 1$ and negative if $R_{vh} > 1$. Hence, this leads to the following remark:

Remark 2.1

The model equation (2.1) to (2.7) has

i. Precisely one unique endemic equilibrium if $G_3 < 0$, $R_{vh} > 1$,

ii. Precisely one unique endemic equilibrium if $G_2 < 0$ and $G_3 = 0$ or $G_2^2 - 4G_1G_3 = 0$,

iii. Precisely two endemic equilibria if $G_3 > 0$, $G_2 < 0$ and $G_2^2 - 4G_1G_3 > 0$, $R_{vh} < 1$ and

iv. No endemic equilibrium otherwise.

Remark 2.2

The model equation (2.1) to (2.7) has

i. Precisely one unique endemic equilibrium if $H_3 < 0$, $R_{vm} > 1$,

ii. Precisely one unique endemic equilibrium if $H_2 < 0$ and $H_3 = 0$ or $H_2^2 - 4H_1H_3 = 0$,

iii. Precisely two endemic equilibria if $H_3 > 0$, $H_2 < 0$ and $H_2^2 - 4H_1H_3 > 0$, $R_{vm} < 1$ and

iv. No endemic equilibrium otherwise.

Local Stability of Endemic Equilibrium

From the result above, the following theorem is stated which will be proved by using Centre Manifold Theorem and bifurcation diagram.

Theorem 2.1: The endemic equilibrium point E^*, exist if $G_3 > 0$, $G_2 < 0$, $G_2^2 - 4G_1G_3 > 0$ and $R_{vh} > 1$, and is locally stable if $R_{vh} > 1$ and unstable if $R_{vh} < 1$.

Using the Center Manifold theory as used by [21] to investigate the likelihood of backward or forward bifurcation of the model. This is accomplished by renaming the factors as follows

Let

$$S_h = y_1,\ I_h = y_2,\ R_h = y_3,\ V_1 = y_4,\ V_2 = y_5,\ S_m = y_6,\ I_m = y_7 \tag{2.47}$$

where

$$y_1 + y_2 + y_3 = 1,\quad y_4 + y_5 = 1,\quad y_6 + y_7 = 1 \tag{2.48}$$

By using vector notation

$$Y = (y_1, y_2, y_3, y_4, y_5, y_6, y_7)^T, \tag{2.49}$$

the model (2.1) to (2.7) can be re-written in the form of

$$\frac{dY}{dt} = F(y), \tag{2.50}$$

with

$$F = (f_1, f_2, f_3, f_4, f_5, f_6, f_7)^T \tag{2.51}$$

as follows;

$$\frac{dy_1}{dt} = f_1 = \Lambda_h - \frac{\alpha_1 y_1 y_5}{N_h} - A_1 y_1 \tag{2.52}$$

$$\frac{dy_2}{dt} = f_2 = \frac{\alpha_1 y_1 y_5}{N_h} - A_2 y_2 \tag{2.53}$$

$$\frac{dy_3}{dt} = f_3 = \nu y_1 + \gamma_h y_2 - \mu_h y_3 \tag{2.54}$$

$$\frac{dy_4}{dt} = f_4 = \Lambda_v - \frac{\alpha_2 y_4 y_2}{N_h} - \frac{\alpha_3 y_4 y_7}{N_m} - A_3 y_4 \tag{2.55}$$

$$\frac{dy_5}{dt} = f_5 = \frac{\alpha_2 y_4 y_2}{N_h} + \frac{\alpha_3 y_4 y_7}{N_m} - A_3 y_5 \tag{2.56}$$

$$\frac{dy_6}{dt} = f_6 = \Lambda_m - \frac{\alpha_4 y_6 y_5}{N_h} - \mu_m y_6 \tag{2.57}$$

$$\frac{dy_7}{dt} = f_7 = \frac{\alpha_4 y_6 y_5}{N_h} - A_4 y_7 \tag{2.58}$$

The Jacobian matrix of the model at DFE is given as

$$J(E_0) = \begin{bmatrix} -A_1 & 0 & 0 & 0 & -\alpha_1 B_1 & 0 & 0 \\ 0 & -A_2 & 0 & 0 & \alpha_1 B_1 & 0 & 0 \\ \nu & \gamma_h & -\mu_h & 0 & 0 & 0 & 0 \\ 0 & -\alpha_2 B_2 & 0 & -A_3 & 0 & 0 & -\alpha_3 B_3 \\ 0 & \alpha_2 B_2 & 0 & 0 & -A_3 & 0 & \alpha_3 B_3 \\ 0 & 0 & 0 & 0 & -\alpha_4 B_4 & -\mu_m & 0 \\ 0 & 0 & 0 & 0 & \alpha_4 B_4 & 0 & -A_4 \end{bmatrix} \tag{2.59}$$

The following theorem will be used to determine whether the model system (2.1) – (2.7) exhibit a backward or forward bifurcation at $R_0 = 1$

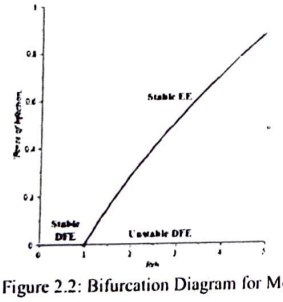

Figure 2.2: Bifurcation Diagram for Mosquitoes to Human Infection

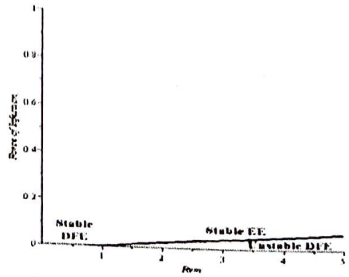

Figure 2.3: Bifurcation Diagram for Mosquitoes to Secondary Host Infection

Theorem 2.2:[22], consider the following general system of ordinary differential equations with a parameter ϕ such that $\frac{dy}{dt} = f(y, \phi)$, $f : \Re^n \times \Re \to \Re^n$ and $f \in c^2(\Re^n \times \Re)$ where 0 is an equilibrium point of the system (i.e. $f(0, \phi) \equiv 0$) for all ϕ and

i. $M = \Delta_y f(0, 0) = \left[\frac{\partial f_i}{\partial y_j}(0, 0)\right]$ is the linearization matrix of the system around the equilibrium 0 with ϕ evaluated at 0.

ii. Zero is a simple eigenvalues of M and all other eigenvalues of M have negative real parts.

iii. Matrix M has a right eigenvectors r and left eigenvectors l corresponding to zero eigenvalues.

Let f_k be the k^{th} component of f and

$$a = \sum_{k,i,j=1}^{n} l_k r_i r_j \frac{\partial^2 f_k}{\partial y_i \partial y_j}(0, 0) \tag{2.60}$$

$$b = \sum_{k,i,j=1}^{n} l_k r_j \frac{\partial^2 f_k}{\partial y_i \partial \alpha_1}(0, 0) \tag{2.61}$$

The local dynamics of the system around the equilibrium point is determined by the signs of a and b particularly, if $a > 0$ and $b > 0$, then a backward bifurcation occurs at $\phi = 0$.

The local dynamics of (2.41) are totally governed by the signs of a and b.

Suppose $\alpha_1 = \alpha^*$ is the chosen bifurcation parameter and when $R_0 = 1$ and solve for α_1 from

$$R_0 = \sqrt{\frac{\alpha_1 \alpha_2 A_5 \mu_h^2}{A_1 A_2 A_3^2} + \frac{\alpha_3 \alpha_4 A_6 \mu_m}{A_3^2 A_4}} \tag{2.62}$$

$$1 = \sqrt{\frac{\alpha_1 \alpha_2 A_5 \mu_h^2}{A_1 A_2 A_3^2} + \frac{\alpha_3 \alpha_4 A_6 \mu_m}{A_3^2 A_4}} \tag{2.63}$$

$$\alpha 1 = \alpha^* = \frac{A_1 A_2 A_3^2 A_4 - \alpha_3 \alpha_4 A_1 A_2 A_6 \mu_m}{\alpha_2 A_4 A_5 \mu_h^2}$$

Thus, the centre manifold theory can be used to analyze the dynamics of (2.1)-(2.7) at $\alpha_1 = \alpha^*$. It can be shown that the Jacobian matrix (2.59) at $\alpha_1 = \alpha^*$ has a right eigenvector associated with the zero eigenvalues given by

$$r = (r_1, r_2, r_3, r_4, r_5, r_6, r_7)^T, \tag{2.64}$$

Multiplying (2.59) by (2.64) and equate to zero gives

Right eigenvectors are: (2.65)

$$r_1 = -\frac{\alpha_1 B_1}{A_1} r_5 \tag{2.66}$$

$$r_2 = \frac{\alpha_1 B_1}{A_2} r_5 \tag{2.67}$$

$$r_3 = \frac{(A_1 \alpha_1 \gamma_h B_1 - A_2 \alpha_1 \nu B_1)}{A_1 A_2 \mu_h} r_5 \tag{2.68}$$

$$r_4 = -\frac{(A_4 \alpha_1 \alpha_2 B_1 B_2 + A_2 \alpha_3 \alpha_4 B_3 B_4)}{A_2 A_3 A_4} r_5 \tag{2.69}$$

$$r_6 = -\frac{\alpha_4 B_4}{\mu_m} r_5 \tag{2.70}$$

$$r_7 = \frac{\alpha_4 B_4}{A_4} r_5$$

where $r_5 > 0$ and is called a free right eigenvector.

Furthermore, the Jacobian matrix (2.59) has left eigenvector associated with the zero eigenvalues at $\alpha_1 - \alpha^*$. Given by (2.71)

$$l = (l_1, l_2, l_3, l_4, l_5, l_6, l_7)^T,$$

Taking the transpose of (2.59) and multiplying by (2.71) and equate to zero gives (2.72)

The left eigenvectors are: (2.73)

$$l_1 = l_3 = l_4 = l_6 = 0$$

$$l_2 = \frac{B_2 \alpha_2}{A_2} l_5 \tag{2.74}$$

$$l_7 = \frac{B_3 \alpha_3}{A_4} l_5$$

For which $l_5 > 0$ is a free left eigenvector.

The computation of a and b

From the model system (2.1) – (2.7) the associated non-zero partial derivatives of F at DFE are given by

$$\frac{\partial^2 f_1}{\partial y_1 \partial y_5} = -\frac{\alpha_1}{N_h} \tag{2.75}$$

$$\frac{\partial^2 f_2}{\partial y_1 \partial y_5} = \frac{\alpha_1}{N_h} \tag{2.76}$$

$$\frac{\partial^2 f_4}{\partial y_4 \partial y_2} = -\frac{\alpha_2}{N_h}, \quad \frac{\partial^2 f_4}{\partial y_4 \partial y_7} = -\frac{\alpha_3}{N_m} \tag{2.77}$$

$$\frac{\partial^2 f_5}{\partial y_4 \partial y_2} = \frac{\alpha_2}{N_h}, \quad \frac{\partial^2 f_5}{\partial y_4 \partial y_7} = \frac{\alpha_3}{N_m} \tag{2.78}$$

$$\frac{\partial^2 f_6}{\partial y_6 \partial y_5} = -\frac{\alpha_4}{N_m} \tag{2.79}$$

$$\frac{\partial^2 f_7}{\partial y_6 \partial y_5} = \frac{\alpha_4}{N_m} \tag{2.80}$$

From (2.60) andconsidering (2.75) to (2.80), it follows that,

$$a = l_2 r_1 r_5 \frac{\alpha_1}{N_h} + l_5 r_2 r_4 \frac{\alpha_2}{N_h} + l_5 r_4 r_7 \frac{\alpha_3}{N_m} + l_7 r_5 r_6 \frac{\alpha_4}{N_m} \tag{2.81}$$

Substituting (2.65), (2.66), (2.68), (2.69), (2.70), (2.73) and (2.74) into (2.81) gives

$$a = -l_5 r_5^2 \left[\frac{\alpha_1^2 \alpha_2 B_1 B_2}{A_1 A_2 N_h} + \frac{\alpha_1 \alpha_4^2 B_1 B_4}{A_4 \mu_m N_m} \right] - l_5 r_5^2 \frac{(A_4 \alpha_1 \alpha_2 B_1 B_2 + A_2 \alpha_1 \alpha_4 B_1 B_4)}{A_2 A_3 A_4} \left[\frac{\alpha_1 \alpha_2 B_1}{A_2 N_h} + \frac{\alpha_1 \alpha_4 B_4}{A_4 N_m} \right] \tag{2.82}$$

From (2.82)

$$a < 0 \tag{2.83}$$

The value of b is also obtained from (2.61)

For the sign of b, the associated non-zero partial derivatives of F at DFE are

$$\frac{\partial^2 f_1}{\partial \alpha_1 \partial y_5} = -\frac{y_1}{N_h} = -\frac{\Lambda_h}{A_1 N_h} \tag{2.84}$$

$$\frac{\partial^2 f_2}{\partial \alpha_1 \partial y_5} = \frac{y_1}{N_h} = \frac{\Lambda_h}{A_1 N_h} \tag{2.85}$$

Since $y_1 = \frac{\Lambda_h}{A_1}$

Therefore,

$$b = l_1 \sum_{j=1}^{2} r_j \frac{\partial^2 f_1}{\partial y_5 \partial \alpha_1} + l_2 \sum_{j=1}^{2} r_j \frac{\partial^2 f_2}{\partial y_5 \partial \alpha_1} \tag{2.86}$$

$$b = -l_1 r_5 \frac{\Lambda_h}{A_1 N_h} + l_2 r_5 \frac{\Lambda_h}{A_1 N_h} \tag{2.87}$$

But $l_1 = 0$

Therefore,

$$b = l_2 r_5 \frac{\Lambda_h}{A_1 N_h} \tag{2.88}$$

Substituting (2.73) into (2.88) gives

$$b = \frac{\alpha_2 B_2 \Lambda_h}{A_1 A_2 N_h} l_5 r_5 \tag{2.89}$$

Since $l_5 > 0$ and $r_5 > 0$ then $b > 0$

Hence, the endemic equilibrium is local stable $a < 0$.

Figure 2.2 and 2.3 clearly show the existence of a unique stable equilibrium and the model undergoes the phenomenon of forward bifurcation. The diagrams exhibits a globally stable disease-free equilibrium when $R_{vh} < 1$, $R_{vm} < 1$ and an unstable state if $R_{vh} > 1, R_{vm} > 1$ while it is evident that a unique stable endemic equilibrium emerges from the bifurcation point $R_{vh} = 1$, $R_{vm} = 1$ and increases rapidly when $R_{vh} > 1$ and $R_{vm} > 1$. It is clear that the disease-free state exists for all R_{vh} and R_{vm} while an endemic equilibrium only exists for $R_{vh} > 1$ and $R_{vm} > 1$.

3. Result and Discussion

In figure 2.2, the two equilibrium points exchange stabilities depending on the value of basic reproduction number of mosquitoes to human, R_{vh}. A transcritical/forward bifurcation in the equilibrium points occur at $R_{vh}=1$.If, $R_{vh}<1$ the disease free equilibrium (DFE) is stable. But if $R_{vh}>1$, the endemic equilibrium exists and it is stable while the disease free equilibrium is a saddle point. Thus there is a forward bifurcation because in the neighbourhood of the bifurcation point, the force of infection of mosquitoes to human, λ_{vh}^{**} is an increasing function of R_{vh}.

In figure 2.3, the two equilibrium points exchange stabilities depending on the value of basic reproduction number of mosquitoes to secondary host, R_{vm}. A transcritical/forward bifurcation in the equilibrium points occur at $R_{vm}=1$.If, $R_{vm}<1$ the disease free equilibrium (DFE) is stable. But if $R_{vm}>1$, the endemic equilibrium exists and it is stable while the disease free equilibrium is a saddle point. Thus there is a forward bifurcation because in the neighbourhood of the bifurcation point, the force of infection of mosquitoes to secondary host, λ_{vm}^{**} is an increasing function of R_{vm}.

4. Conclusion

In this paper, the mathematical model of yellow fever dynamics was developed using a system of first order ordinary differential equation. The local stability analysis showed that, the Endemic Equilibrium (EE) is stable since $a<0, b>0$. Bifurcation analysis showed that the model exhibited forward bifurcation which implies there is no co-existence of stable endemic equilibrium at $R_{vh}<1$ and $R_{vm}<1$, to this effect the disease can be put under control or eradicated from the population.

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