A MATHEMATICAL MODEL OF YELLOW FEVER DISEASE DYNAMICS INCORPORATING SPECIAL SATURATION INTERACTIONS FUNCTIONS

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Abstract

We proposed an Mathematical Model of Yellow Fever Disease Dynamics Incorporating Special Saturation Process functions, obtained the equilibrium states of the model equations and analyzed same for stability. Conditions for the elimination of the disease in the population are obtained as constraint inequalities on the parameters using the basic reproduction number R_0. Graphical simulations are presented using some demographic and epidemiological data.

Keywords: Basic Reproduction Number, Equilibrium States, Saturation Process, Stability

1. Introduction

We present a model of five ordinary differential equations representing the dynamics of Yellow Fever Infection in a host population of humans enabled by vector populations of mosquitoes which facilitate the transmission of the causative virus. We obtain the Disease Free Equilibrium state and analyze same for stability using the Reproduction number.

In the urban Yellow Fever infection dynamics, the virus incubation period in the host is from 3 to 6 days after an effective interacting bite of a virus carrying vector. The host is humans while the vector is the *aedes egypti* specie of mosquitoes. The Yellow Fever infection is characterized by the sudden onset of fever, chills, intense headache, lumbosacral and generalized muscular pain, nausea, vomiting and lethargy. All these result in a short remission of the fever, and the development of haemorrhagic signs, jaundice, bleeding from the nose and gums, black vomit and stool, anuria (failure to pass urine), hypertension, shock and death within 10 days if not treated, (Tomori, 1988). It is worthy of note that after surviving a Yellow Fever infection, the host will have a life-long immunity. Also, the infant have natural immunity for the first nine months of birth so all the offspring of the host are born as susceptible. The dynamics of Yellow Fever though has some similarity with Malaria yet has its own peculiarity as outlined above.

According to Monath (1989), Van der *et al.* (1999), Figueiredo (2000), Souza (2010) and Auguste *et al.* (2010), Yellow fever virus (YFV) is the prototype species for the genus *Flavivirus*. Historically, YFV is one of the most important human arboviral pathogens. It continues to cause large sporadic epidemics in Africa but typically emerges as epizootics among nonhuman primates in South America with or without associated human cases. Several phylogenetic studies have shown that YFV is locally maintained during these interepizootic periods in Peru, Bryant *et al.* (2003), Brazil, Vasconcelos *et al.* (2004), and Auguste *et al.* (2010). Yellow fever virus

undergoes regionally independent evolution within some countries, (Bryant *et al.* 2003). The sporadic emergence of YFV in the Americas has been strongly associated with infection of red howler monkeys *Alouatt aseniculus*, which are particularly susceptible to disease, (Auguste *et al.* 2015).

In section 3, the notations and definitions of parameters and variables together with the set of the model equations are presented. In section three, we obtain the Disease Free Equilibrium state of the model equations, obtained the Reproduction number and analyze the state for stability or otherwise. The concluding remark is presented in section 5.

2. Literature Review

Yellow fever virus (YFV) is mainly transmitted through the bite of the yellow fever mosquito *Aedes aegypti*, but other mosquitoes such as the tiger mosquito (*Aedes albopictus*) 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, (Fontenille *et al*. 1997).

Akinwande (1996), formulated a model of yellow fever epidemics, which involves the interactions of two principal communities; hosts (humans) and Vectors *(aedes aegypti* 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 using Jacobian matrix and implicit function.

Fernandez *et al.* (2013), formulated a model and incorporated the biology of the urban vector of yellow fever, the mosquito *Aedes aegypti*, the stages of the disease in the host (humans). From the epidemiological point of view, the mosquito follows a SEI sequence (Susceptible, Exposed, Infective). In their, model the adult populations are subdivided according to their status with respect to the virus. They assumed that there is no vertical transmission of the virus and eggs, larvae, pupae and non parous adults are always susceptible. The humans are subdivided in sub-populations according to their status with respect to the illness as: susceptible (S), exposed (E), infective (I), in remission (r), toxic (T) and recovered (R).

Hui-Ming *et al.* (2008), considered an epidemic model of a vector-borne disease which has direct mode of transmission in addition to the vector-mediated transmission. The incidence term is assumed to be of the bilinear mass-action form. They include both a baseline ordinary differential equation (ODE) version of the model, and, a differential-delay model with a discrete time delay. The delay in the differential-delay model accounts for the incubation time the vectors need to become infectious. They studied the effect of that delay on the stability of the equilibria.

3. Methodology

3.1 Model Formulation

At time instant $t \geq 0$ the host community is separated into three disjoint compartments namely Susceptible $S(t)$, the Infected $I(t)$ and Recovered/Immune $R(t)$ while the vector community is partitioned into two compartments namely virus carriers $M(t)$ and non-virus carriers $N(t)$.

An effective bite among the interacting compartments is defined as the bite that results in the transmission of virus; essentially between $N(t)$ and $I(t)$ on one hand and $M(t)$ and $S(t)$ on the other. Using the method adopted by Sowunmi (1987), we construct the interaction functions as follow:

3.2 Construction of Virus Transmission Interaction Saturation Functions

Let

p = the probability that a member of the Susceptible hosts $S(t)$ is effectively bitten by a virus carrier member from the $M(t)$ compartment.

q = the probability that a member of the Infected hosts $I(t)$ is effectively bitten by a non-virus carrier member from the $N(t)$ compartment.

$(1-p)^{-1} = a$, $(1-q)^{-1} = b$; $0 \le p, q \le 1$ and $1 \le a, b < \infty$. (3.1)

Thus $1-p$ is the probability that no effective bite takes place between $S(t)$ and $M(t)$ while

$1-q$ is the probability that no effective bite takes place between $I(t)$ and $N(t)$.

Then

$(1-p)^{M(t)}$ gives the proportion of the susceptible host members who are not bitten effectively at time $t \ge 0$, and

$(1-q)^{I(t)}$ gives the proportion of the non-vector carrier members which did not bite effectively at time $t \ge 0$.

Let

$$(1-p)^{M(t)} = \exp[-\alpha_1 M(t)],\ \alpha_1 = \log a \quad (3.2)$$

The proportion of the susceptible class who are effectively bitten at time $t \ge 0$ will be given by

$$B(\alpha_{1,} M(t)) = 1 - \exp[-\alpha_1 M(t)] \quad (3.3)$$

Also

$$(1-q)^{I(t)} = \exp[-\alpha_2 I(t)],\ \alpha_2 = \log b \quad (3.4)$$

the proportion of the non-virus carrier class which effectively bite at time $t \ge 0$ will be given by

$$B(\alpha_{2,} I(t)) = 1 - \exp[-\alpha_2 I(t)] \quad (3.5)$$

The virus transmission interaction function between $S(t)$ and $M(t)$ is thus given by

$$f_1(S,M) = B(\alpha_{1,}M(t))S(t) = (1-\exp[-\alpha_1 M(t)])S(t) \quad (3.6)$$

And between $N(t)$ and $I(t)$ is given by

$$f_2(N,I) = B(\alpha_{2,}I(t))N(t) = (1-\exp[-\alpha_2 I(t)])N(t) \quad (3.7)$$

These functions are saturation functions, we have that

$$f_1(S,0) = f_1(0,M) = 0$$

$$f_2(I,0) = f_2(0,N) = 0$$

Also

$f_1(S,M) \to S$, as $M \to \infty$

$f_2(I,N) \to N$, as $I \to \infty$

3.3 Definition of Parameters & Variables

β_1 = natural per capita birth rate for the host population.

μ_1 = natural per capita death rate for the host population.

γ = per capita immunization rate

α = per capita recovery rate

δ = per capita death rate from infection in the host population.

w = per capita loss of immunity rate in the Recovered/Immune host compartment.

β_2 = natural per capita birth rate for the vector population.

μ_2 = natural per capita death rate for the vector population.

θ = proportion of the infants/eggs of $M(t)$ with virus

$S(t)$ = Susceptible host compartment.

$I(t)$ = Infected host compartment.

$R(t)$ = Recovered/Immune host compartment.

$N(t)$ = Non-Virus-Carrying vector compartment.

$M(t)$ = Virus-Carrying vector compartment.

t = time

3.4 The Model Equations

$$\frac{dS(t)}{dt} = \beta_1 - \left(\mu_1 + \gamma + B(\alpha_1, M(t))\right)S(t) + wR(t) \tag{3.8}$$

$$\frac{dI(t)}{dt} = B(\alpha_1, M(t))S(t) - \left(\mu_1 + \delta + \alpha\right)I(t) \tag{3.9}$$

$$\frac{dR(t)}{dt} = \alpha I(t) + \gamma S(t) - \left(\mu_1 + w\right)R(t) \tag{3.10}$$

$$\frac{dN(t)}{dt} = \theta\beta_2 + \mu_2 M(t) - B(\alpha_2, I(t))N(t) \tag{3.11}$$

$$\frac{dM(t)}{dt} = (1-\theta)\beta_2 - \mu_2 M(t) + B(\alpha_2, I(t))N(t) \tag{3.12}$$

$$B(\alpha_1, M(t)) = 1 - \exp(-\alpha_1 M(t)) \tag{3.13}$$

$$B(\alpha_2, I(t)) = 1 - \exp(-\alpha_2 I(t)) \tag{3.14}$$

3.5 Computation of the Reproduction Number

In this section we compute the Reproduction number for the system of equations (3.8) – (3.14).

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 as used by Diekmann *et al*, (1990) and improved by Driessche and Watmough (2002). 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.

At equilibrium state let

$$S(t) = x,\ R(t) = y,\ I(t) = z,\ N(t) = p,\ M(t) = q \tag{3.15}$$

Now, R_0 is the spectral radius (highest eigen value) of FV^{-1}, where F (infection terms) and V (transition terms) are Jacobian matrix obtained from the infected classes of the model equations, i.e. equations (3.9) and (3.12).

Thus,

$$F = \begin{pmatrix} 0 & x\alpha_1 e^{-\alpha_1 q} \\ p\alpha_2 e^{-\alpha_2 z} & 0 \end{pmatrix} \tag{3.16}$$

And

$$V = \begin{pmatrix} (\mu_1 + \delta + \alpha) & 0 \\ 0 & \mu_2 \end{pmatrix} \tag{3.17}$$

So that,

$$V^{-1} = \frac{1}{\mu_2(\mu_1 + \delta + \alpha)} \begin{pmatrix} \mu_2 & 0 \\ 0 & (\mu_1 + \delta + \alpha) \end{pmatrix} \tag{3.18}$$

i.e.

$$V^{-1} = \begin{pmatrix} \frac{1}{(\mu_1 + \delta + \alpha)} & 0 \\ 0 & \frac{1}{\mu_2} \end{pmatrix} \tag{3.19}$$

Then,

$$FV^{-1} = \begin{pmatrix} 0 & x\alpha_1 e^{-\alpha_1 q} \\ p\alpha_2 e^{-\alpha_2 z} & 0 \end{pmatrix} \begin{pmatrix} \frac{1}{(\mu_1 + \delta + \alpha)} & 0 \\ 0 & \frac{1}{\mu_2} \end{pmatrix} \tag{3.20}$$

i.e.

$$FV^{-1} = \begin{pmatrix} 0 & \frac{x\alpha_1 e^{-\alpha_1 q}}{\mu_2} \\ \frac{p\alpha_2 e^{-\alpha_2 z}}{(\mu_1 + \delta + \alpha)} & 0 \end{pmatrix} \tag{3.21}$$

Now, to get the eigenvalues, we have

$$\left| FV^{-1} - \lambda \right| = 0$$

i.e.

$$\begin{vmatrix} 0 - \lambda & \frac{x\alpha_1 e^{-\alpha_1 q}}{\mu_2} \\ \frac{p\alpha_2 e^{-\alpha_2 z}}{(\mu_1 + \delta + \alpha)} & 0 - \lambda \end{vmatrix} = 0 \tag{3.22}$$

which gives

$$\lambda = \pm \sqrt{\frac{x\alpha_1 e^{-\alpha_1 q} p\alpha_2 e^{-\alpha_2 z}}{\mu_2 (\mu_1 + \delta + \alpha)}} \tag{3.23}$$

Thus, Reproduction number R_o is given by the highest eigenvalue, i.e.

$$R_0 = \sqrt{\frac{x\alpha_1 e^{-\alpha_1 q} p\alpha_2 e^{-\alpha_2 z}}{\mu_2(\mu_1 + \delta + \alpha)}} \tag{3.24}$$

Setting $z = q = 0$ in (3.15) at Disease Free State, we have

$$R_0 = \sqrt{\frac{xp\alpha_1\alpha_2}{\mu_2(\mu_1 + \delta + \alpha)}} \tag{3.25}$$

If $R_o < 1$ we have that

$$\alpha_1 < \frac{\mu_2(\mu_1 + \delta + \alpha)}{xp\alpha_2} = \alpha_{1\max} \tag{3.26}$$

The inequality (3.17) gives an upper bound on the susceptible hosts infection per capita which guarantees the stability of the Disease Free State resulting in the imminent removal of the infection from the population.

4 Results and Discussion

4.1 Graphical Profiles

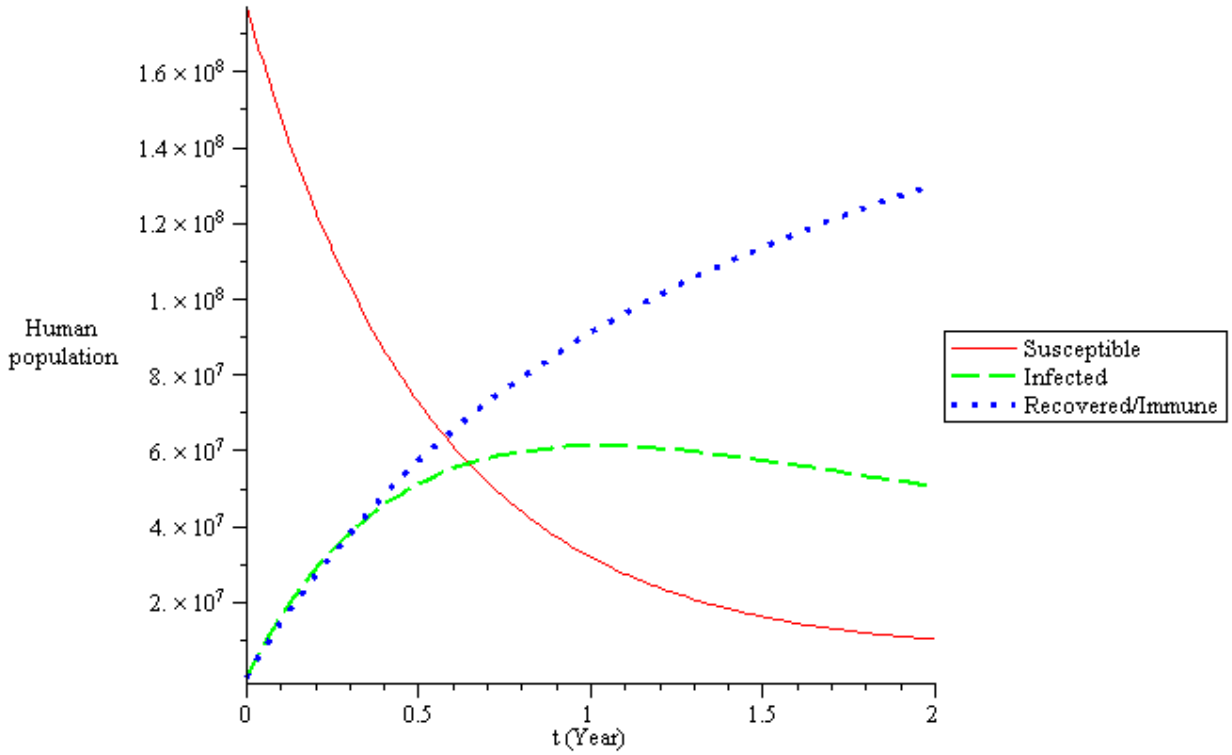

Figure 4.1: Effect of High Immunization Rate γ

Figure 4.1, is the effect of high immunization rate on the entire human population. It was observed that, the susceptible population decreases while the recovered/immune increases, this is because the susceptible individuals that are successfully immunized moved to recovered class. The increase of infected population was not high because only few susceptible were infected.

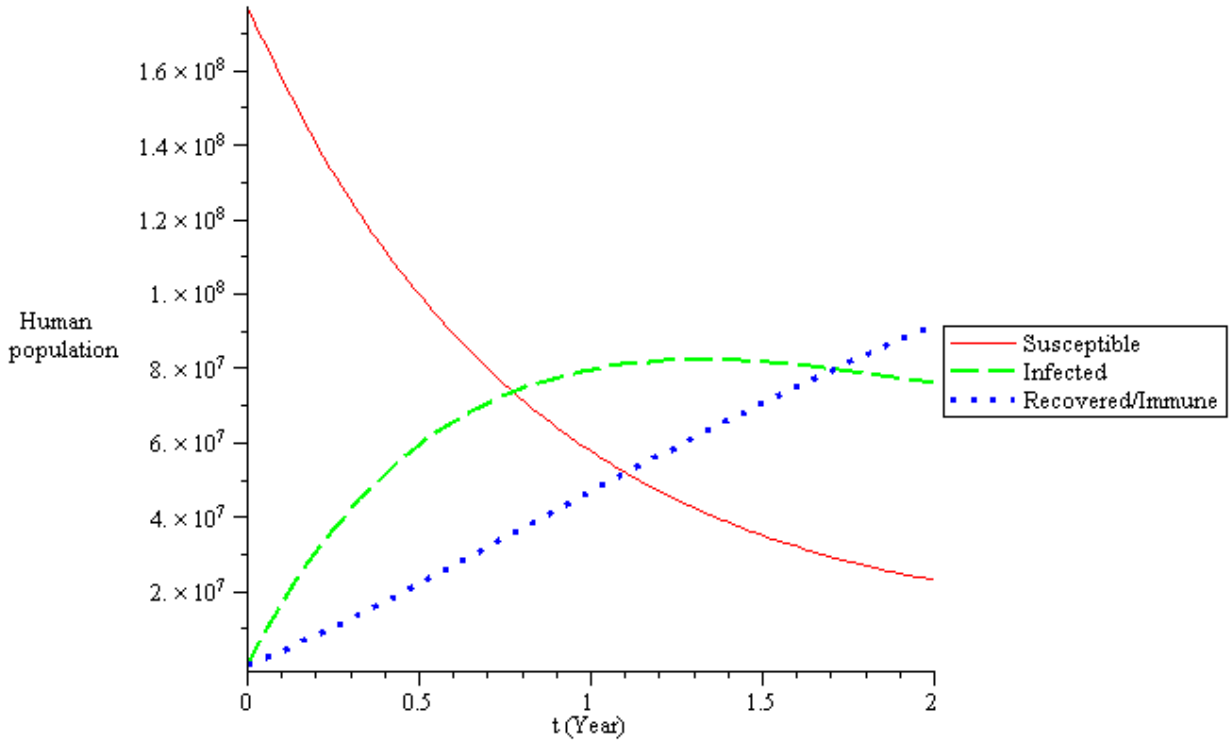

Figure 4.2: Effect of Low Immunization Rate γ

Figure 4.2, is the effect of low immunization rate on the entire human population. It was observed that, the susceptible population decreases while the recovered/immune increases. But the decrease and increase on susceptible and recovered are not the same as that of high immunization rate. It was also shown that, the increase of infected population was high compare to that of figure 4.1, this is because only more susceptible were infected with low immunization rate.

5 Conclusion

The basic reproduction number R_0 was computed and used to determine an upper bound for the biting/infection rate α_1 . For the effective control of the disease, the biting/infection rate $\alpha_1 < \alpha_{1\max}$. The effect of high and low immunization rate γ on the entire human population was presented graphically, and it was observed that with high immunization rate the susceptible human population decreases and the recovered/immune population increases. Therefore the immunization rate γ should be kept high in order to eliminate the disease from the population.

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