

A Mathematical Model of a Yellow Fever Dynamics with Vaccination

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Abstract

In this paper, a mathematical model describing the dynamics of yellow fever epidemics, which involves the interactions of two principal communities of Hosts (Humans) and vectors (mosquitoes) is considered. The existence and uniqueness of solutions of the model were examined by actual solution. We conduct local stability analysis for the model. The results show that it is stable under certain conditions. The system of equations describing the phenomenon was solved analytically using parameter-expanding method coupled with direct integration. The results are presented graphically and discussed. It is discovered that improvement in Vaccination strategies will eradicate the epidemics.

Keywords: Yellow fever, model, vaccination, epidemics

1.0 Introduction

Yellow fever (YF), a hemorrhagic fever caused by a *Flavivirus*, family *Flaviviridae* [1, 2], is characterized by fever, chills, losses of appetite, nausea, muscle pains particularly in the back, and headaches [3]. There are more than 200,000 infections and 30,000 deaths every year [3]. About 90% of YF cases occur in Africa [4], and a billion people live in an area of the world where the disease is common [3]. It also affects tropical areas of South America, but not Asia [3, 5, 6]. The number of cases of yellow fever has been increasing in the last 30 years [3, 7], probably due to fewer people being immune, more people living in cities, people moving frequently, and changing climate [3]. The origin of the disease is Africa, from where it spread in South America through the slave trade in the 17th century [8, 9]. The yellow fever virus was the first human virus discovered [10], and its family comprises approximately 70 viruses [2], most of which are transmitted by arthropod insects (hence the name arthropod borne viruses or arboviruses). A safe and effective vaccine against yellow fever exists and some countries require vaccinations for travelers [3]. In rare cases (less than one in 200,000 to 300,000 doses), the vaccination can cause yellow fever vaccine-associated viscerotropic disease (YEL-AVD), which is fatal in 60% of cases, probably due to the genetic morphology of the immune system. Another possible side effect is an infection of the nervous system, which occurs in one in 200,000 to 300,000 cases, causing yellow fever vaccine-associated neurotropic disease (YEL-AND), which can lead to meningoencephalitis, fatal in less than 5% of cases [6]. In some rare circumstances, however, the fatality rate of vaccine induced diseases can reach alarming proportions, as observed recently by Mascheretti et al. [11], who found 1 death per million doses applied in a Southeastern Brazilian region.

This present study investigates the criteria under which the effectiveness of vaccination could lead to the stability of the equilibrium point. We establish the conditions for existence and uniqueness of the solution of models, conducted local stability analysis of the models and provide an analytical solution via parameter-expanding method.

2.0 Model Formulation

Following [12], the equations describing yellow fever epidemics are:

$$\frac{dS_h}{dt} = \beta_1 N - (\mu_1 + \delta)S_h - \alpha_1 I_m S_h \quad (1)$$

$$\frac{dI_h}{dt} = -(\mu_1 + \alpha + \rho)I_h + \alpha_1 I_m S_h \quad (2)$$

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$$\frac{dR_h}{dt} = -\mu_1 R_h + \delta S_h + \alpha I_h \tag{3}$$

$$\frac{dS_m}{dt} = \beta_2 (S_m + (1 - \theta) I_m) - \mu_2 S_m - \alpha_2 S_m I_h \tag{4}$$

$$\frac{dI_m}{dt} = \theta \beta_2 I_m - \mu_2 I_m + \alpha_2 S_m I_h \tag{5}$$

$$N_h(t) = S_h(t) + I_h(t) + R_h(t) \tag{6}$$

As initial condition based on our assumptions, we choose

$$S_h(0) = S_{h0}, \quad I_{h0}(0) = I_{h0}, \quad R_h(0) = R_{h0}, \quad S_m(0) = S_{m0}, \quad I_m(0) = I_{m0} \tag{7}$$

Where

Variables	Parameters
$S_h(t)$ - the density of susceptible humans	β_1 - the natural birthrate for hosts
$I_h(t)$ - the density of infected humans	β_2 - the natural birthrate for vectors
$R_h(t)$ - the density of recovered humans	μ_1 - the natural mortality rate for hosts
$S_m(t)$ - the density of susceptible mosquitoes	μ_2 - the natural mortality rate for vectors
$I_m(t)$ - the density of infected mosquitoes	α - the recovery rate
	α_1 - the effective biting interaction rate between $S_h(t)$ and $I_m(t)$ compartments
	α_2 - the effective biting interaction rate between $S_m(t)$ and $I_h(t)$ compartments
	ρ - the death rate from infection
	θ - the proportion of the offsprings of $I_m(t)$ that is infected vertically
	δ - the vaccination rate

3.0 Method of Solution

3.1 Existence and Uniqueness of Solution

Theorem 1: Let $\rho = 0$. Then the equations (1) – (5) with initial conditions (7) has a unique Solution for all $t \geq 0$.

Proof: Let $\rho = 0$, $\phi(t) = S_h(t) + I_h(t) + R_h(t)$ and $\varphi(t) = S_m(t) + I_m(t)$. We obtain

$$\frac{d\phi}{dt} = (\beta_1 - \mu_1)\phi, \quad \phi(0) = (S_{h0} + I_{h0} + R_{h0}) = \phi_0 \tag{8}$$

$$\frac{d\varphi}{dt} = (\beta_2 - \mu_2)\varphi, \quad \varphi(0) = (S_{m0} + I_{m0}) = \varphi_0 \tag{9}$$

By direct integration, we obtain the solution of problem (8) and (9) as

$$\phi(t) = \phi_0 e^{(\beta_1 - \mu_1)t} \quad \text{and} \quad \varphi(t) = \varphi_0 e^{(\beta_2 - \mu_2)t} \tag{10}$$

Then, we obtain

$$S_h(t) = \phi_0 e^{(\beta_1 - \mu_1)t} - (I_h(t) + R_h(t)) \tag{11}$$

$$I_h(t) = \phi_0 e^{(\beta_1 - \mu_1)t} - (S_h(t) + R_h(t)) \tag{12}$$

$$R_h(t) = \phi_0 e^{(\beta_1 - \mu_1)t} - (S_h(t) + I_h(t)) \tag{13}$$

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ERROR: undefined
OFFENDING COMMAND: ife
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STACK:
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{userdict }
{currentglobal exch true setglobal globaldict }
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true
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