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Global Analysis of Dengue Fever in a Variable Population

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Abstract

In this paper, a non-linear mathematical model for the transmission dynamics of dengue fever with the presence of therapeutic vaccine in a varying population is designed and rigorously analyzed. We established that the model exists and has a unique solution using theorems on existence and uniqueness of a solution. Using a suitable Lyapunov function, the disease free equilibrium is shown to be globally asymptotically stable whenever the effective reproductive number $\left(R_f\right)$ ***is less than unity,while the endemic equilibrium for the special case when the disease induced death rate is absent or assumed to be negligible is globally asymptotically stable unconditionally whenever it exists.Finally, numerical simulation was carried out to validate the analytical results.***

Key word: Dengue fever, Existence and Uniqueness Solution, Global Analysis.

1.0 Introduction

The epidemiology of the outbreak of dengue fever manifested after the second world war and it claims almost 2.5 billion people all over the world , especially in the tropical countries and became a major epidemic disease in Southeast Asia[1]. There are four antigenically distinct serotypes (DENV1-4) based on neutralization assay. DENV is transmitted to humans mainly by Aedes mosquitoes (*Aedesaegypti*and *Aedesalbopictus*) [1]. The prevalence of dengue disease is high especially in the Asia-Pacific region and the Americas. All four DENV serotypes are now circulating in these areas. With increased international travel and climate change, people are at risk of dengue infection beyond the traditional tropical and subtropical areas. Dengue disease is becoming virulent in nature as one of the deadly vector-borne viral diseases. An estimated 50 million dengue infection cases occur globally with around 500,000 cases of severe dengue and 20,000 deaths per year[2,3].

The viruses are transmitted from*Aedesaegypti* and *Aedesalbopictus*mosquitoes to humans in a viral life cycle that requires both humans and these mosquitoes. There is no human-to-human dengue fever transmission. Once a mosquito is infected, it remains infected for its life span. A human can infect mosquitoes when the human has a high number of viruses in the blood (right before symptoms develop). The viruses belong to the *Flaviviridae* family and have an RNA strand as its genetic makeup. All four serotypes are closely related. However, there are enough antigenic differences between them that if a person becomes immune to one serotype, the person can still be infected by the other three serotypes [4].

The diagnosis of dengue is typically made clinically on the basis of reportedsymptoms and physical examinations; this applies especially in endemicareas. However, early stage of the disease can be difficult to differentiatefrom other viral infections. Dengue fever is caused by a virus and there is no specific medication for treating it yet. For typical dengue, the treatmentis concerned with relief of the symptoms.

There is no specific medication for treatment of a dengue infection. Persons diagnosed of dengue should use analgesics (pain relievers) withacetaminophen and avoid those containing ibuprofen, naproxen, aspirin oraspirin containing drugs. They should also rest, drink plenty of fluids to prevent dehydration, avoid mosquito bites while febrile and consult a physician.

As with dengue, there is no specific medication for dengue hemorrhagic fever
(DHF). If a clinical diagnosis is made early, a health care provider can effectively treat DHF using fluid replacement therapy. Adequate managementof DHF generally requires hospitalization.

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Mathematical modeling can help our understanding and assessment of the present and future risk areas on spread of infectious diseases based on climate data as shown in the case of the malaria cartography [5].
Mathematical modeling uses a set of mathematical equations derived from a theoretical framework and calculates the threshold condition such as, the vectorial capacity for transmitting virus and/or incidences of dengue as a function of time for a particular area. In other words, mathematical modeling can help us not only understand and predict the future spread of infectious diseases but also evaluate strategies on combating dengue [6]. Using computer simulation from mathematical modeling one can produce estimates of disease transmission, e.g. disease incidences under certain assumptions, and threshold for epidemic outbreaks.
There are numerous published results discussing the problem of denguedisease transmission.
Nuraini et al., studied a SIR model for dengue disease transmissionwhere they assumed that two viruses namely strain 1 and strain 2 causethe disease and long lasting immunity from infection caused by one virusmay not be valid with respect to a secondary infection by other virus. Theyalso determined a control measure to reduce the Dengue Hemorrhagic Fever(DHF) patients in the population, or to keep the number of patients at anacceptable level.

Furthermore, Esteva & Vargas formulated a nonlinear system of differential equations that model the dynamics of dengue fever. In theirmodel, they considered the relations between two of the four serotypes ofdengue and analyzed the factors that allow the invasion and the persistence of different serotypes in the human population. The outcome of their research was that the coexistence of both serotypes is possible for a large range of parameters.
The purpose of this paper is to provide a more detailed qualitative analysis to the mathematical model on the transmission dynamics of dengue fever with therapeutic vaccine in a variable population.
This paper is therefore concerned about the improvement on the work of past researchers. We tried to further determine other dynamics of dengue fever as well as its global stability analysis under a variable population.

2.0 Model Description

The model was developed to consist of human and vector (mosquito) populations. The vector can transmit the virus to susceptible humans and can also become infected by an infected human. The human population is governed by the equation

$$N_H(t) = S_H(t) + E_H(t) + I_H(t) + V_H(t) + R_H(t).$$

Where $S_H(t)$ is the susceptible human, $E_H(t)$ istheexposed humans, $I_H(t)$ is theinfected humans, $V_H(t)$ is the vaccinated human and recovered humans is denoted by $R_H(t).$

The vector population is also governed by the equation

$$N_V(t) = S_V(t) + E_V(t) + I_V(t).$$

Where $S_V(t)$, $E_V(t)$ and $I_V(t)$, denote the susceptible, exposed and infected mosquitoes respectively.

The forces of infection for both human and vector population are respectively given by

$$\lambda_H = \frac{C_{HV}(N_H, N_V)}{N_V}(\phi_V E_V + I_V)$$

and

$$\lambda_V = \frac{C_{HV}(N_H, N_V)}{N_V}(\phi_H E_H + \theta\phi_H V_H + I_H)$$

where $0 < \phi_V < 1$ and $0 < \phi_H < 1$ and $0 < \phi_{2H} < 1$ are the modification parameters.

Basic Assumptions of the Model

The following assumptions were considered while constructing the model

1. Recruited individuals are assumed to be susceptible.
2. Only unvaccinatedinfected human $I_H(t)$ experiences disease induced death rate.
3. The model is homogenous and depends on time t.
4. Birth rate is not equal to death rate.

Thus the model for the transmission dynamics of dengue fever with therapeutic vaccine in a variable population is governed by the following system of nonlinear differential equations

$$\begin{aligned}
\dot{S}_H &= \pi_H - S_H(\mu_H + \lambda_H) \\
\dot{E}_H &= \lambda_H S_H - (\mu_H + \sigma_H)E_H \\
\dot{I}_H &= \sigma_H E_H - (\mu_H + \eta_H + \delta_H + \tau_H)I_H + \omega_H V_H \\
\dot{V}_H &= \eta_H I_H - (\mu_H + \alpha_H + \omega_H)V_H \\
\dot{R}_H &= \alpha_H V_H - \mu_H R_H + \tau_H I_H \\
\dot{S}_V &= \pi_V - S_V(\lambda_V + \mu_V) \\
\dot{E}_V &= \lambda_V S_V - (\mu_V + \sigma_V)E_V \\
\dot{I}_V &= \sigma_V E_V - (\mu_V + \delta_V)I_V
\end{aligned} \tag{1}$$

Table 1: Parameter Description

S/N	Parameters	Meanings	Hypothetical Values	Sources
1	C_{HV}	Disease transmission coefficient	0.068	[6]
2	π_H	Recruitment rate of humans	10	[6]
3	π_V	Recruitment rate of mosquitoes	60	[8]
4	σ_H	Progression rate from E_H to I_H class	0.53	[6]
5	σ_V	Progression rate from E_V to I_V class	0.2	[6]
6	μ_H	Natural death rate of humans	0.0195	[6]
7	μ_V	Natural death rate of mosquitoes	0.06	[8]
8	ϕ_H	Modification Parameter associated	0.99	[6]
		with exposed individuals		
9	ϕ_V	Modification Parameter associated	0.78	[6]
		with exposed mosquitoes		
10	τ_H	Recovery rate of infected humans	0.143	[10]
11	η_H	Vaccinated rate of infected humans	(0,1]	[7]
12	ω_H	waning rate of therapeutic vaccine	(0,1]	[7]
13	δ_H	disease-induced death rate of humans	0.001	[9,10]
14	δ_V	disease-induced death rate of mosquitoes	0	[9]
15	α_H	Recovery rate of vaccinated humans	0.25	[11]
16	θ	Modification parameter associated with reduced infection of vaccinated humans	[0,1]	[7]
17	$\phi_{2H} = \theta\phi_H$	Modification parameter associated with infection by vaccinated humans	$\theta\phi_H$	[7]

2.1 Existence and Uniqueness Solution of the Model

In this section,we try to find if the system of equations has a solution and if the solution to the system is unique. We shall use the Lipchtiz condition to verify the existence and uniqueness of equations.

Let

$$\begin{aligned} m_1 &= \pi_H - S_H(\mu_H + \lambda_H) \\ m_2 &= \lambda_H S_H - (\mu_H + \sigma_H)E_H \\ m_3 &= \sigma_H E_H - (\mu_H + \eta_H + \delta_H + \tau_H)I_H + \omega_H V_H \\ m_4 &= \eta_H I_H - (\mu_H + \alpha_H + \omega_H)V_H \\ m_5 &= \alpha_H V_H - \mu_H R_H + \tau_H I_H \\ m_6 &= \pi_V - S_V(\lambda_V + \mu_V) \\ m_7 &= \lambda_V S_V - (\mu_V + \sigma_V)E_V \\ m_8 &= \sigma_V E_V - (\mu_V + \delta_V)I_V \end{aligned} \qquad (2)$$

Theorem 1

Let F denotes the region

$$|t - t_o| \le a, \|x - x_o\| \le b, x = (x_1, x_2, ..., x_n), x_o = (x_{10}, x_{20}, ...x_{n0})$$

and suppose that $f(t,x)$ satisfies the Lipschitz condition

$$\|f(t,x_1) - f(t,x_2)\| \le k\|x_1 - x_2\|.$$

Whenever the pairs (t,x_1) and (t,x_2) belong to F, where k is a positive constant. Then there is a constant $\delta \ge 0$ such that there exists a unique continuous vector solution $x(t)$ of the system in the interval $t - t_o \le \delta$. It is important to note that the condition is satisfied by the requirement that $\frac{\partial f_i}{\partial x_j}$ $i = 1,2,...,8$ be continuous and bounded in F.

Returning to the model equation (2) and considering the region

$$0 \le \alpha R,$$

we look for bounded solution in this region whose partial derivatives satisfy $\delta \le \alpha \le 0$, where α and δ are positive constants.

Theorem 2

Let F denotes the region $0 \le \alpha \le 0$. Then equation (2) have a unique solution. We show that $\frac{\partial f_i}{\partial x_j}$, $i, j = 1,2,3,4,5,6,7,8$ are continuous and bounded in F . We differentiate (2) partially with respect to S_H , E_H , I_H , V_H , R_H , S_V , E_V and I_V respectively.

This gives us the following

$$\left|\frac{\partial m_1}{\partial S_H}\right| = \left|-(\mu_H + \lambda_H)\right| < \infty, \left|\frac{\partial m_1}{\partial E_H}\right| = 0 < \infty, \left|\frac{\partial m_1}{\partial I_H}\right| = 0 < \infty, \left|\frac{\partial m_1}{\partial V_H}\right| = 0 < \infty, \left|\frac{\partial m_1}{\partial R_H}\right| = 0 < \infty,$$

$$\left|\frac{\partial m_1}{\partial S_V}\right| = 0 < \infty, \left|\frac{\partial m_1}{\partial E_V}\right| = \left|-\frac{S_H \phi_V C_{HV}(N_H, N_V)}{N_V}\right| < \infty, \left|\frac{\partial m_1}{\partial I_V}\right| = \left|-\frac{S_H C_{HV}(N_H, N_V)}{N_V}\right| < \infty$$

$$\left|\frac{\partial m_2}{\partial S_H}\right| = \left|\lambda_H\right| < \infty, \left|\frac{\partial m_2}{\partial E_H}\right| = \left|-(\mu_H + \delta_H)\right| < \infty, \left|\frac{\partial m_2}{\partial I_H}\right| = 0 < \infty, \left|\frac{\partial m_2}{\partial V_H}\right| = 0 < \infty, \left|\frac{\partial m_2}{\partial R_H}\right| = 0 < \infty,$$

$$\left|\frac{\partial m_2}{\partial S_V}\right| = 0 < \infty, \left|\frac{\partial m_2}{\partial E_V}\right| = \left|\frac{S_H \phi_V C_{HV}(N_H, N_V)}{N_V}\right| < \infty, \left|\frac{\partial m_2}{\partial I_V}\right| = \left|\frac{S_H C_{HV}(N_H, N_V)}{N_V}\right| < \infty$$

$$\left|\frac{\partial m_3}{\partial S_H}\right| = 0 < \infty, \left|\frac{\partial m_3}{\partial E_H}\right| = \left|\sigma_H\right| < \infty, \left|\frac{\partial m_3}{\partial I_H}\right| = \left|-(\mu_H + \eta_H + \delta_H + \tau_H)\right| < \infty,$$
$$\left|\frac{\partial m_3}{\partial V_H}\right| = \left|\omega_H\right| < \infty, \left|\frac{\partial m_3}{\partial R_H}\right| = 0 < \infty, \left|\frac{\partial m_3}{\partial S_V}\right| = 0 < \infty, \left|\frac{\partial m_3}{\partial E_V}\right| = 0 < \infty, \left|\frac{\partial m_3}{\partial I_V}\right| = 0 < \infty$$

$$\left|\frac{\partial m_4}{\partial S_H}\right| = 0 < \infty, \left|\frac{\partial m_4}{\partial E_H}\right| = 0 < \infty, \left|\frac{\partial m_4}{\partial I_H}\right| = \left|\eta_H\right| < \infty, \left|\frac{\partial m_4}{\partial V_H}\right| = \left|-(\mu_H + \alpha_H + \omega_H)\right| < \infty,$$
$$\left|\frac{\partial m_4}{\partial R_H}\right| = 0 < \infty, \left|\frac{\partial m_4}{\partial S_V}\right| = 0 < \infty, \left|\frac{\partial m_4}{\partial E_V}\right| = 0 < \infty, \left|\frac{\partial m_4}{\partial I_V}\right| = 0 < \infty$$
$$\left|\frac{\partial m_5}{\partial S_H}\right| = 0 < \infty, \left|\frac{\partial m_5}{\partial E_H}\right| = 0 < \infty, \left|\frac{\partial m_5}{\partial I_H}\right| = \left|\tau_H\right| < \infty, \left|\frac{\partial m_5}{\partial V_H}\right| = \left|\alpha_H\right| < \infty,$$
$$\left|\frac{\partial m_5}{\partial R_H}\right| = \left|-\mu_H\right| < \infty, \left|\frac{\partial m_5}{\partial S_V}\right| = 0 < \infty, \left|\frac{\partial m_5}{\partial E_V}\right| = 0 < \infty, \left|\frac{\partial m_5}{\partial I_V}\right| = 0 < \infty$$

$$\left|\frac{\partial m_6}{\partial S_H}\right| = 0 < \infty, \left|\frac{\partial m_6}{\partial E_H}\right| = \left|\frac{-S_V \phi_H C_{HV}(N_H, N_V)}{N_V}\right| < \infty, \left|\frac{\partial m_6}{\partial I_H}\right| = \left|\frac{-S_V C_{HV}(N_H, N_V)}{N_V}\right| < \infty,$$
$$\left|\frac{\partial m_6}{\partial V_H}\right| = \left|\frac{-\theta\phi_H S_V C_{HV}(N_H, N_V)}{N_V}\right| < \infty, \left|\frac{\partial m_6}{\partial R_H}\right| = 0, \left|\frac{\partial m_6}{\partial S_V}\right| = \left|-(\lambda_V + \mu_V)\right| < \infty, \left|\frac{\partial m_6}{\partial E_V}\right| = 0 < \infty, \left|\frac{\partial m_6}{\partial I_V}\right| = 0 < \infty$$

$$\left|\frac{\partial m_7}{\partial S_H}\right| = 0 < \infty, \left|\frac{\partial m_7}{\partial E_H}\right| = \left|\frac{\phi_H C_{HV}(N_H, N_V)}{N_V}\right| < \infty, \left|\frac{\partial m_7}{\partial I_H}\right| = \left|\frac{C_{HV}(N_H, N_V)}{N_V}\right| < \infty,$$
$$\left|\frac{\partial m_7}{\partial V_H}\right| = \left|\frac{\theta\phi_H C_{HV}(N_H, N_V)}{N_V}\right| < \infty, \left|\frac{\partial m_7}{\partial R_H}\right| = 0 < \infty, \left|\frac{\partial m_7}{\partial S_V}\right| = \left|\lambda_V\right| < \infty,$$
$$\left|\frac{\partial m_7}{\partial E_V}\right| = \left|-(\mu_V + \sigma_V)\right| < \infty, \left|\frac{\partial m_7}{\partial I_V}\right| = 0 < \infty$$

$$\left|\frac{\partial m_8}{\partial S_H}\right| = 0 < \infty, \left|\frac{\partial m_8}{\partial E_H}\right| = 0 < \infty, \left|\frac{\partial m_7}{\partial I_H}\right| = 0 < \infty, \left|\frac{\partial m_8}{\partial V_H}\right| = 0 < \infty,$$
$$\left|\frac{\partial m_8}{\partial R_H}\right| = 0 < \infty, \left|\frac{\partial m_8}{\partial S_V}\right| = 0 < \infty, \left|\frac{\partial m_8}{\partial E_V}\right| = \left|\sigma_V\right| < \infty, \left|\frac{\partial m_8}{\partial I_V}\right| = \left|-(\mu_V + \delta_V)\right| < \infty$$

Since all the partial derivatives of the system equation (2) exists, then they are finite and bounded. Hence, by Theorem (2), the model system (2) has a unique solution.

The two biological relevant equilibria of the model are,

1. The disease free equilibriumis given by

$$\varepsilon_\circ = (\bar{S}_H, \bar{E}_H, \bar{I}_H, \bar{V}_H, \bar{R}_H, \bar{S}_V, \bar{E}_V, \bar{I}_V) = \left(\frac{\pi_H}{\mu_H}, 0, 0, 0, 0, \frac{\pi_V}{\mu_V}, 0, 0\right)$$

2. The component of the endemic equilibrium denoted by ε_1 satisfies the following

$$S_H^* = \frac{\pi_H}{\mu_H + \lambda_H^*}, \quad E_H^* = \frac{\lambda_H^* \pi_H}{(\mu_H + \lambda_H^*)Q_1},$$

$$I_H^* = \frac{\sigma_H \lambda_H^* \pi_H Q_3}{Q_1(\mu_H + \lambda_H^*)(Q_2 Q_3 - \omega_H \eta_H)}, \quad V_H^* = \frac{\sigma_H \lambda_H^* \pi_H \eta_H}{Q_1(\mu_H + \lambda_H^*)(Q_2 Q_3 - \omega_H \eta_H)},$$

$$R_H^* = \frac{\sigma_H \lambda_H^* \pi_H (\alpha_H \eta_H + \tau_H Q_3)}{\mu_H Q_1(\mu_H + \lambda_H^*)(Q_2 Q_3 - \omega_H \eta_H)} \quad S_V^* = \frac{\pi_H}{\mu_V + \lambda_V^*},$$

$$E_V^* = \frac{\lambda_V^* \pi_V}{(\mu_V + \lambda_V^*)Q_4} \quad I_V^* = \frac{\sigma_V \lambda_V^* \pi_V}{(\mu_V + \lambda_V^*)Q_4 Q_5},$$

$$N_H^* = \frac{(a_1 \lambda_H^* + a_2)\pi_H}{Q_1 \mu_H (\mu_H + \lambda_H^*)(Q_2 Q_3 - \omega_H \eta_H)} \quad \lambda_H^* = \frac{C_{HV}(\varphi_V E_V^* + I_V^*)}{N_H^*},$$

$$\lambda_V^* = \frac{C_H V}{N_H^*}(\varphi_H E_H^* + \theta \varphi_H V_H^* + I_H^*)$$

where $a_1 = \mu_H(Q_2 Q_3 - \omega_H \eta_H) + \sigma_H[Q_3(\mu_H + \tau_H) + \eta_H(\mu_H + \alpha_H)]$, $a_2 = \mu_H\left(Q_2 Q_3 - \omega_H \eta_H\right)$

$Q_1 = \mu_H + \sigma_H, Q_2 = \mu_H + \eta_H + \delta_H + \tau_H, Q_3 = \mu_H + \alpha_H + \omega_H, Q_4 = \mu_V + \sigma_V, Q_5 = \mu_V + \delta_V$ Since $Q_2 Q_3 - \omega_H \eta_H > 0, a_1 > 0, a_2 > 0.$

The effective reproduction number denoted by R_f is given by

$$R_f = \frac{C_{HV}\sqrt{A_1 A_2 A_3}}{A_1}$$

where

$A_1 = \pi_H \mu_V Q_1 Q_4 Q_5 (Q_2 Q_3 - \eta_H \omega_H), A_2 = \pi_V \mu_H (\sigma_V + \phi_V Q_5), A_3 = \pi_H (Q_2 Q_3 - \eta_H \omega_H) + \sigma_H (\theta \phi_H \eta_H + Q_3)$

From [7], the following Theorems (3-5) were established for model (1).

Theorem 3.

The disease-free equilibrium ε_o, of the model (1), is locally asymptotically stable if $R_f < 1$ and unstable if $R_f > 1$.

Theorem 4.

The model (1) has a unique endemic equilibrium if and only if $R_f > 1$.

Theorem 5.

The endemic equilibrium ε_1 of the model (1) is locally asymptotically stable if $R_f > 1$ and unstable if $R_f < 1.$

3.0 Global Stability Analysis of the Model's Equilibria

Theorem 6:

The disease-free equilibrium ε_o, of model (1) is generally asymptotically stable for $R_f < 1$ and unstable for $R_f > 1$.

Proof

Consider the lyapunov function

$$L_1 = K_1 E_H + K_2 I_H + K_3 V_H + K_4 E_V + K_5 I_V$$

Where $K_1 = R_f^2$, $K_2 = \frac{C_{HV}^2 \pi_V \mu_H [Q_3 + \phi_{2H} \eta_H][Q_5 \phi_V + \sigma_V]}{\phi_H \mu_V Q_4 Q_5 [Q_2 Q_3 - \omega_H \eta_H]}$

$$K_3 = \frac{C_{HV}^2 \pi_V \mu_H [Q_2 \phi_{2H} + \omega_H][Q_5 \phi_V + \sigma_V]}{\phi_H \mu_V Q_4 Q_5 [Q_2 Q_3 - \omega_H \eta_H]}$$

$$K_4 = \frac{C_{HV}(Q_5\phi_V + \sigma_V)}{Q_4Q_5},\ \ K_5 = \frac{C_{HV}}{Q_5}$$

The lyapunov derivative is given by

$$\dot{L}_1 = K_1\dot{E}_H + K_2\dot{I}_H + K_3\dot{V}_H + K_4\dot{E}_V + K_5\dot{I}_V$$

(where a dot represents differentiation with respect to t)

$$\dot{L}_1 = R_f[\lambda_H S_H - Q_1E_H] + \frac{C_{HV}\pi_V\mu_H[Q_3+\phi_{2H}\eta_H][Q_5\phi_V+\sigma_V]}{\pi_H\mu_V Q_4Q_5[Q_2Q_3-\omega_H\eta_H]}[\sigma_H E_H - Q_2I_H + \omega_H V_H]$$

$$+\frac{C_{HV}^2\pi_V\mu_H[Q_2\phi_{2H}+\omega_H][Q_5\phi_V+\omega_V]}{\pi_H\mu_V Q_4Q_5[Q_2Q_3-\omega_H\eta_H]}[\eta_H I_H - Q_3V_H] + \frac{C_{HV}[Q_5\phi_V+\sigma_V]}{Q_4Q_5}[\lambda_V S_V - Q_4E_V]$$

$$+\frac{C_{HV}}{Q_5}[\sigma_V E_V - Q_5I_V]$$

$$\dot{L}_1 = \left\{-R_f^2Q_1 + \frac{C_{HV}^2\pi_V\mu_H[Q_3+\phi_{2H}\eta_H][Q_5\phi_V+\sigma_V]\sigma_H}{\pi_H\mu_V Q_4Q_5[Q_2Q_3-\omega_H\eta_H]} + \frac{C_{HV}^2(Q_5\phi_V+\sigma_V)S_V\phi_V}{Q_4Q_5N_H}\right\}E_H$$

$$+\left\{\frac{C_{HV}^2\pi_V\mu_H[Q_2\phi_{2H}+\omega_H][Q_5\phi_V+\sigma_V]\eta_H}{\pi_H\mu_V Q_4Q_5[Q_2Q_3-\omega_H\eta_H]} - \frac{C_{HV}^2\pi_V\mu_H[Q_3+\phi_{2H}\eta_H][Q_5\phi_V+\sigma_V]Q_2}{\pi_H\mu_V Q_4Q_5[Q_2Q_3-\omega_H\eta_H]}\right.$$

$$\left.+\frac{C_{HV}^2(Q_5\pi_V+\sigma_V)S_V}{Q_4Q_5N_H}\right\}I_H + \left\{\frac{R_f^2C_{HV}S_H}{N_H} - \frac{C_{HV}Q_5}{Q_5}\right\}I_V$$

$$+\left\{\frac{C_{HV}^2\pi_V\mu_H[Q_3+\phi_{2H}\eta_H][Q_5\phi_V+\sigma_V]\omega_H}{\pi_H\mu_V Q_4Q_5[Q_2Q_3-\omega_H\eta_H]} - \frac{C_{HV}^2\pi_V\mu_H[Q_2\phi_{2H}+\omega_H][Q_5\phi_V+\sigma_V]Q_3}{\pi_H\mu_V Q_4Q_5[Q_2Q_3-\omega_H\eta_H]}\right.$$

$$\left.+\frac{C_{HV}^2[Q_5\phi_V+\sigma_V]\phi_{2H}S_V}{Q_4Q_5N_H}\right\}V_H + \left\{\frac{R_f^2C_{HV}\phi_V S_H}{N_H} - \frac{C_{HV}(Q_5\phi_V+\sigma_V)Q_4}{Q_4Q_5} + \frac{C_{HV}\sigma_V}{Q_5}\right\}E_V$$

$$\dot{L}_1 \le \left\{-R_f^2Q_1 + \frac{C_{HV}^2\pi_V\mu_H[Q_3+\phi_{2H}\eta_H][Q_5\phi_V+\sigma_V]\sigma_H}{\pi_H\mu_V Q_4Q_5[Q_2Q_3-\omega_H\eta_H]} + \frac{C_{HV}^2(Q_5\phi_V+\sigma_V)\pi_V\mu_H\phi_V}{Q_4Q_5\pi_H\mu_V}\right\}E_H + \left\{R_f^2C_{HV} - C_{HV}\right\}I_V$$

$$+\left\{\frac{C_{HV}^2\pi_V\mu_H[Q_2\phi_{2H}+\omega_H][Q_5\phi_V+\sigma_V]\eta_H}{\pi_H\mu_V Q_4Q_5[Q_2Q_3-\omega_H\eta_H]} - \frac{C_{HV}^2\pi_V\mu_H[Q_3+\phi_{2H}\eta_H][Q_5\phi_V+\sigma_V]Q_2}{\pi_H\mu_V Q_4Q_5[Q_2Q_3-\omega_H\eta_H]}\right.$$

$$\left.+\frac{C_{HV}^2[Q_5\pi_V+\sigma_V]\pi_V\mu_H}{Q_4Q_5\pi_H\mu_V}\right\}I_H$$

$$+\left\{\frac{C_{HV}^2\pi_V\mu_H[Q_3+\phi_{2H}\eta_H][Q_5\phi_V+\sigma_V]\omega_H}{\pi_H\mu_V Q_4Q_5[Q_2Q_3-\omega_H\eta_H]} - \frac{C_{HV}^2\pi_V\mu_H[Q_2\phi_{2H}+\omega_H][Q_5\phi_V+\sigma_V]Q_3}{\pi_H\mu_V Q_4Q_5[Q_2Q_3-\omega_H\eta_H]}\right.$$

$$\left.+\frac{C_{HV}^2[Q_5\phi_V+\sigma_V]\phi_{2H}\pi_V\mu_H}{Q_4Q_5\pi_H\mu_V}\right\}V_H + \left\{R_f^2C_{HV}\phi_V - \frac{C_{HV}[Q_5\phi_V+\sigma_V]}{Q_5} + \frac{C_{HV}\sigma_V}{Q_5}\right\}E_V$$

Since $S_H \le N_H \le \frac{\pi_H}{\mu_H}, S_V \le \frac{\pi_V}{\mu_V}$

After many tedious algebraic simplifications, we have

$$\dot{L}_1 \le C_{HV}(\phi_V E_V + I_V)[R_f^2 - 1]$$

Thus, $\dot{L}_1 \leq 0$ when $R_f \leq 1$ and $\dot{L}_1 = 0$ if and only if $E_V = I_V = 0.$ It follows from Lasalle's Invariance principle [10], that every solution to the system (1) with initial conditions in F approaches E_o as $t \to \infty$. Thus, since the region F is positively invariant, the disease-free equilibrium is globally asymptotically stable in F if $R_f \leq 1.$

3.1 Global Stability Analysis of Endemic Equilibrium:Special Case

Let $\varepsilon_2 = \varepsilon_1 |_{\delta_H = \delta_V = 0} = (S_H^{**}, E_H^{**}, I_H^{**}, V_H^{**}, R_H^{**}, S_V^{**}, E_V^{**}, I_V^{**})$ denote the unique positive endemic equilibrium point of model (1), i.e, (the equilibrium where at least one of the infected components of the model is non zero) will be consider as special case where the disease-induced death rate is assumed to be negligible or absent (i.e, $\delta_H = \delta_V = 0$). Thus, we note that the components of ε_2 satisfies the following

$S_H^{**} = S_H^* \mid_{\delta=0}, E_H^{**} = E_H^* \mid_{\delta=0}, I_H^{**} = I_H^* \mid_{\delta=0}, V_H^{**} = V_H^* \mid_{\delta=0}, R_H^{**} = R_H^* \mid_{\delta=0},$

$S_V^{**} = S_V^* \mid_{\delta=0}, E_V^{**} = E_V^* \mid_{\delta=0}, I_V^{**} = I_V^* \mid_{\delta=0}$

The effective reproduction number for this special case is denoted by R_{fs} and is expressed as

$$R_{fs} = \frac{C_{HV}\sqrt{A_{10}A_{20}A_{30}}}{A_{10}}$$

where

$$A_{10} = \pi_H \mu_V Q_1 Q_4 Q_{50}(Q_{20}Q_3 - \omega_H \eta_H), A_{20} = \pi_V \mu_H (\sigma_V + \phi_V Q_{50})$$

$$A_{30} = \pi_H (Q_{20}Q_3 - \omega_H \eta_H) + \sigma_H (\theta \varphi_H \eta_H + Q_3), Q_{20} = \mu_H + \eta_H + \tau_H, Q_{50} = \mu_V$$

Theorem 7

The endemic equilibrium point at special case ε_2 is globally asymptotically stable unconditionally whenever it exists.

Proof

Consider the Lyapunov function

$$L_2 = \frac{1}{2}[(S_H - S_H^{**}) + (E_H - E_H^{**}) + (I_H - I_H^{**}) + (V_H - V_H^{**}) + (R_H - R_H^{**})]^2$$

$$+ \frac{1}{2}[(S_V - S_V^{**}) + (E_V - E_V^{**}) + (I_V - I_V^{**})]^2 \quad (3)$$

with Lyapunov derivative given by

$$\dot{L}_2 = [(S_H - S_H^{**}) + (E_H - E_H^{**}) + (I_H - I_H^{**}) + (V_H - V_H^{**}) + (R_H - R_H^{**})][S_H + I_H + E_H + V_H + R_H])$$

$$+ [(S_V - S_V^{**}) + (E_V - E_V^{**}) + (I_V - I_V^{**})][\dot{S}_V + \dot{E}_V + \dot{I}_V] \quad (4)$$

Since $N_H = S_H + I_H + E_H + V_H + R_H$ and $N_V = S_V + I_V + E_V$, we have the following at special case $(i.e, \delta_H = \delta_V = 0)$

$$\dot{N}_H = \dot{S}_H + \dot{E}_H + \dot{I}_H + \dot{V}_H + \dot{R}_H = \pi_H - \mu_H (S_H + I_H + E_H + V_H + R_H)$$

and

$$\dot{N}_V = \dot{S}_V + \dot{E}_V + \dot{I}_V = \pi_V - \mu_V (S_V + I_V + E_V).$$

Thus,

$$\pi_H = \mu_H (S_H^{**} + E_H^{**} + I_H^{**} + V_H^{**} + R_H^{**})$$

and

$$\pi_V = \mu_V (S_V^{**} + E_V^{**} + I_V^{**})$$

So, (4) becomes

$$\dot{L}_2 = [(S_H - S_H^{**}) + (E_H - E_H^{**}) + (I_H - I_H^{**}) + (V_H - V_H^{**}) + (R_H - R_H^{**})][\mu_H (S_H^{**} + E_H^{**} + I_H^{**} + V_H^{**} + R_H^{**})$$

$$-\mu_H(S_H+E_H+I_H+R_H)]$$
$$+[(S_V-S_V^{**})+(E_V-E_V^{**})+(I_V-I_V^{**})][\mu_V(S_V^{**}+E_V^{**}+I_V^{**})-\mu_V(S_V+E_V+I_V)]$$
$$\dot{L}_2=-\mu_H[(S_H-S_H^{**})+(E_H-E_H^{**})+(I_H-I_H^{**})+(V_H-V_H^{**})+(R_H-R_H^{**})]^2$$
$$-\mu_V[(S_V-S_V^{**})+(E_V-E_V^{**})+(I_V-I_V^{**})]\le 0$$

Thus, we conclude the proof that model (1) is globally asymptotically stable at ε_2 unconditionally whenever it exists.

4.0 Numerical Simulation and Discussion

In this section, some numerical solutions of the model for different initial population sizes is presented using the various values of the parameters stated in Table.1 and to validate that these solutions are in agreement with the qualitative results obtained in previous section . Thus we choose different initial population sizes such that the total human population $N_H=S_H+E_H+I_H+V_H+R_H=500$ and vector population, $N_V=S_V+E_V+I_V=1000$ are as follows

1____ $S_H(0)=450, E_H(0)=20, I_H(0)=15, V_H(0)=5, R_H(0)=10, S_V(0)=700, E_V(0)=100, I_V(0)=200,$

2____ $S_H(0)=420, E_H(0)=27, I_H(0)=40, V_H(0)=10, R_H(0)=3, S_V(0)=900, E_V(0)=80, I_V(0)=20,$

3____ $S_H(0)=400, E_H(0)=60, I_H(0)=30, V_H(0)=15, R_H(0)=5, S_V(0)=850, E_V(0)=76, I_V(0)=74,$

4____ $S_H(0)=454, E_H(0)=30, I_H(0)=10, V_H(0)=6, R_H(0)=0, S_V(0)=790, E_V(0)=108, I_V(0)=102.$

In Fig.1, the eight figures depict the numerical solution curve of the system (1) for $\theta=0.2, \eta_H=0.8, \omega_H=0.2$, thus $R_f=0.7433<1$.

Figure 1(a), shows that the number of susceptible individuals at first decreases,then it increases and decreases to approach $\overline{S}_H$ while figure 1(f) shows that the cumulative number of susceptible mosquitoes increases to approach $\overline{S}_V$.

In figures 2(b)-2(e) and 2(h),the cumulative number of exposed individuals, infected individuals, vaccinated individuals, recovered individuals, exposed mosquitoes and infected mosquitoes approaches $\overline{E}_H, \overline{I}_H, \overline{V}_H, \overline{R}_H, \overline{E}_V$ and $\overline{I}_V$ respectively (i.e. zero). We note that the solution curves of these figures tend to the equilibrium ε_0 for any initial values when $R_f>1$.

Thus, the system (1) is locally-globally asymptotically stable about ε_0 for the aforementioned parameter value.

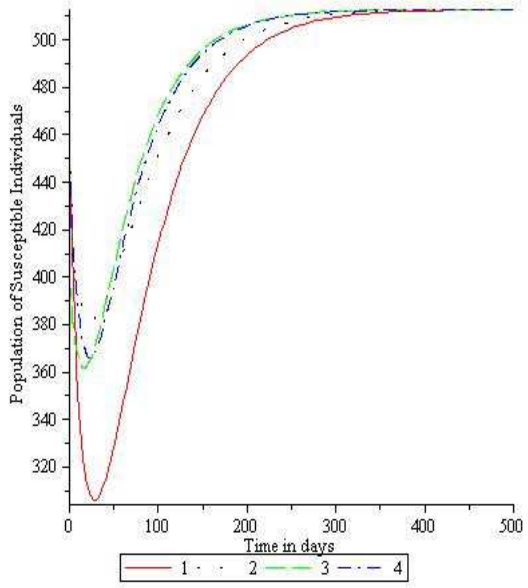

Fig.(1a)

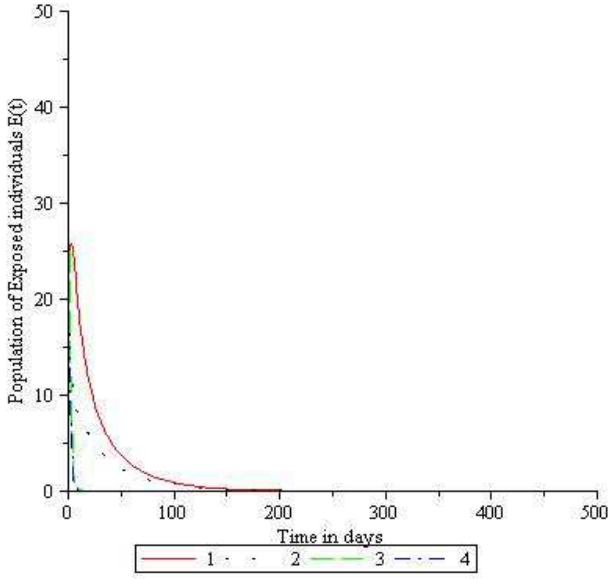

Fig.(1b)

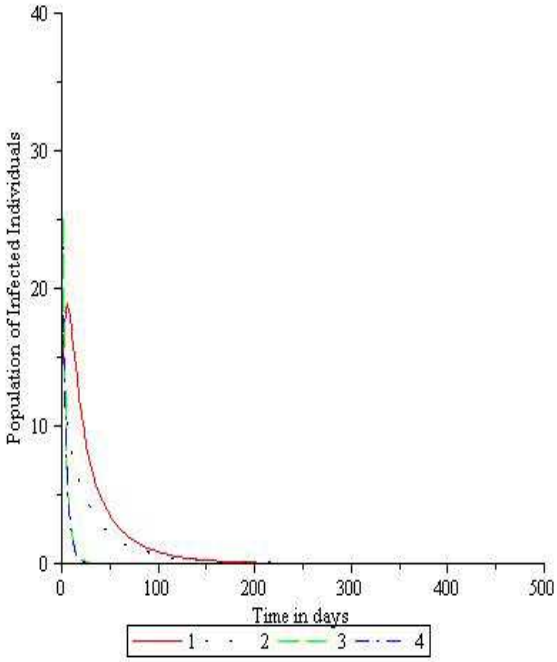

Fig.(1c)

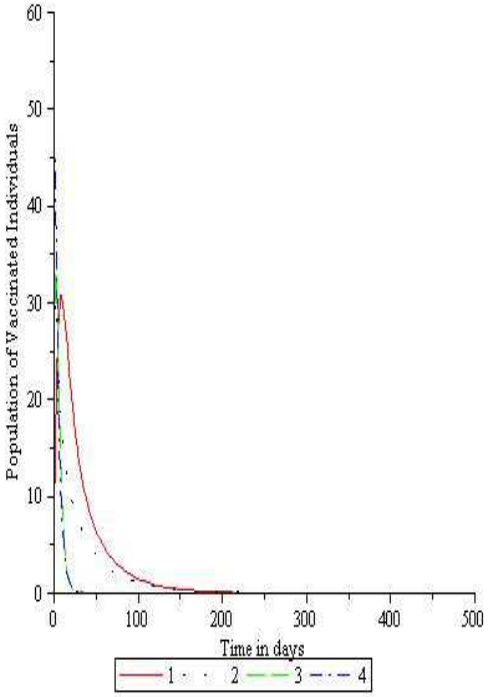

Fig. (1d)

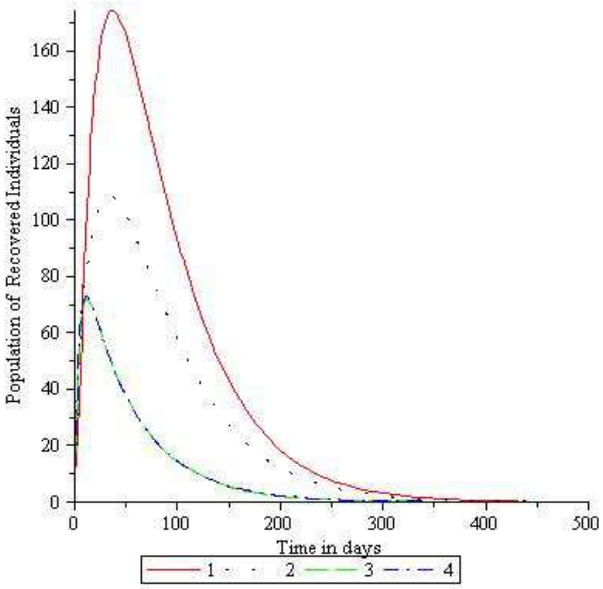

Fig. (1e)

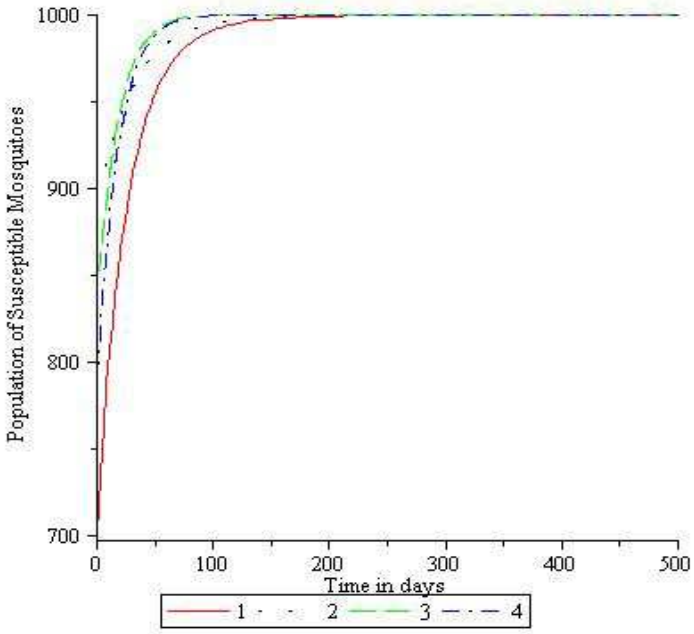

Fig. (1f)

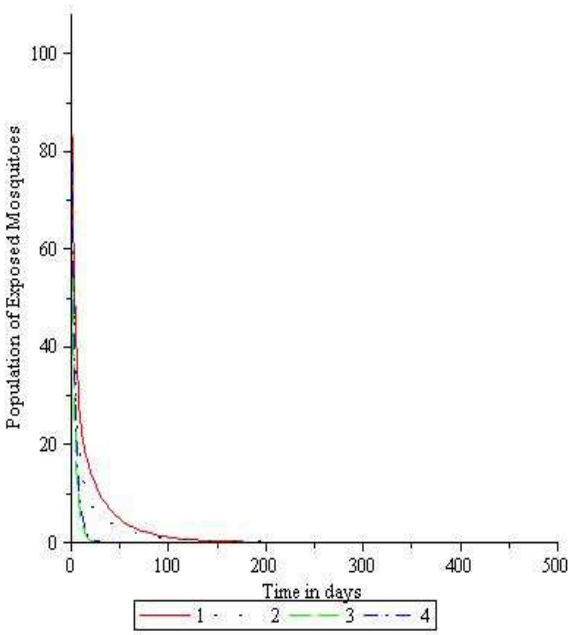

Fig. (1g)

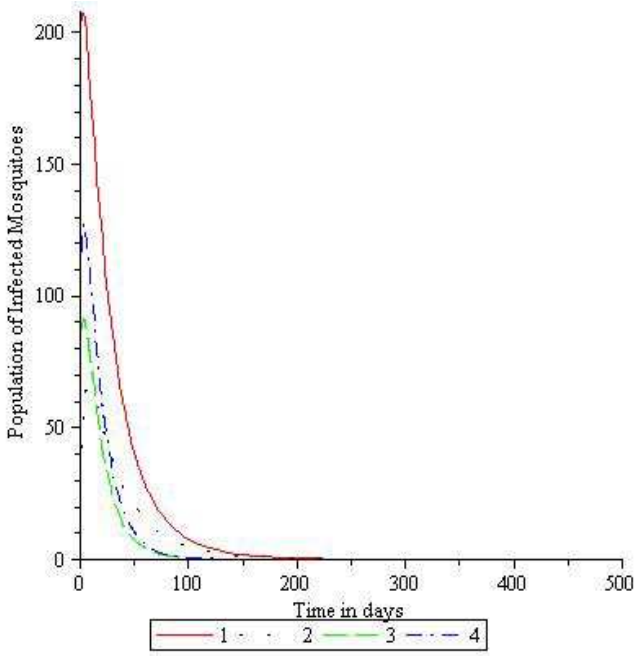

Fig. (1h)

Fig. 1. Time plots of system (1) with different initial conditions for $R_f < 1$:

(a) Susceptible human population; (b) Exposed human population; (c) Infected human population; (d) Vaccinated human population (e) Recovered human population; (f) Susceptible mosquitoes population;
(g) Exposedmosquitoes population; (h) infected mosquitoes population.

In Fig.2, the eight figures depict the numerical solution curve of the system (1) for $\theta = 0.8, \eta_H = 0.2, \omega_H = 0.9, \delta_H = \delta_V = 0$, thus $R_f\,|_{\delta_H=\delta_V=0} = 1.0030 > 1$.

Figure 2(a), shows that the number of susceptible individuals at first decreases,then it increases and decreases to approach $S^*\,|_{\delta_H=\delta_V=0}$ In figures 2(b)-2(h),the cumulative number of exposed individuals, infected individuals, vaccinated individuals, recovered individuals, susceptible mosquitoes, exposed mosquitoes and infected mosquitoes approaches $E_H^*\,|_{\delta_H=\delta_V=0}$, $I_H^*\,|_{\delta_H=\delta_V=0}$, $V_H^*\,|_{\delta_H=\delta_V=0}$, $R_H^*\,|_{\delta_H=\delta_V=0}$, $S_V^*\,|_{\delta_H=\delta_V=0}$, $E_V^*\,|_{\delta_H=\delta_V=0}$ and $I_V^*\,|_{\delta_H=\delta_V=0}$ respectively. We note that the solution curves of these Figures tend to the equilibrium $\varepsilon_1\,|_{\delta_H=\delta_V=0}$ for any initial values when $R_f\,|_{\delta_H=\delta_V=0} > 1$ .Thus, the system (1) is locally-globally asymptotically stable about $\varepsilon_1\,|_{\delta_H=\delta_V=0}$ for the aforementioned parameter value.

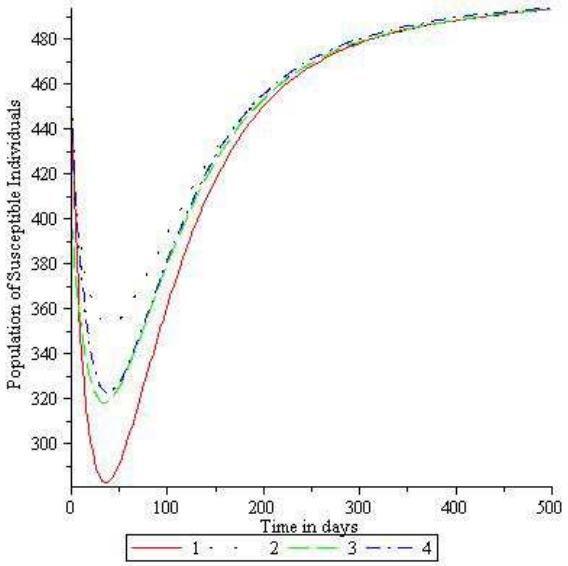

Fig. (2a)

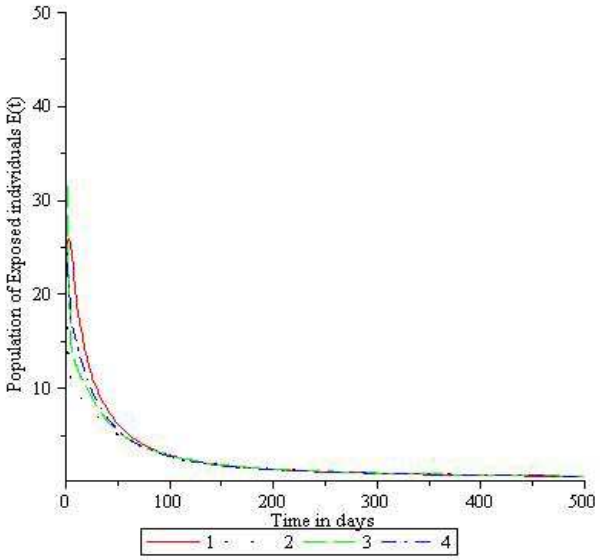

Fig. (2b)

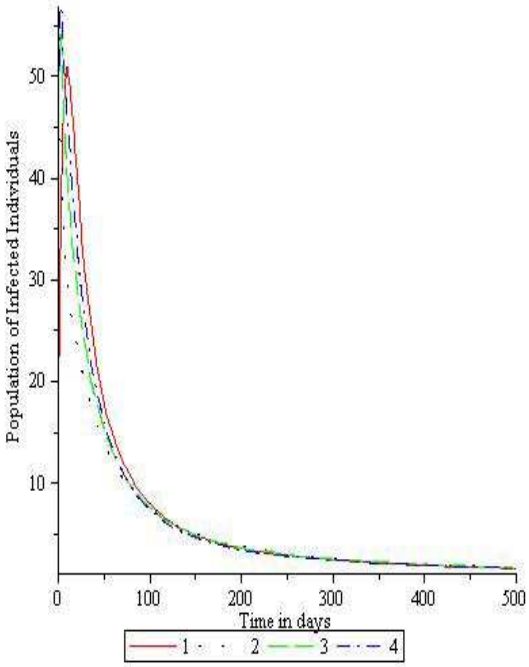

Fig. (2c)

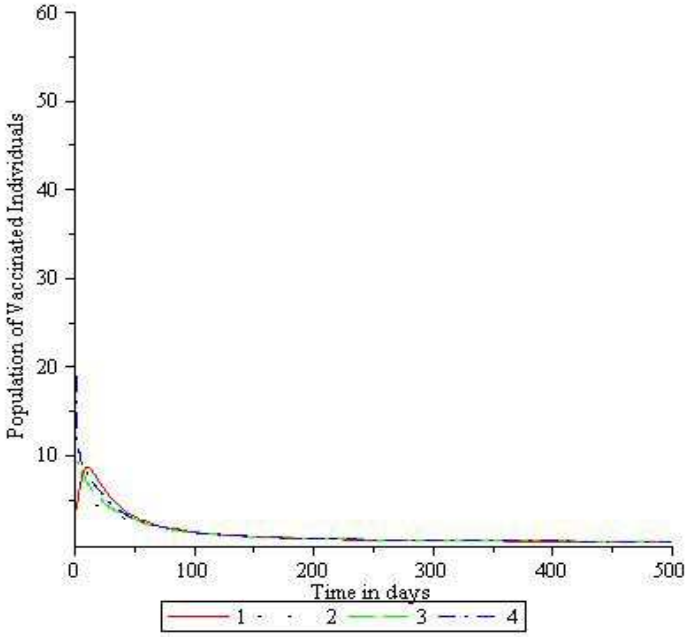

Fig. (2d)

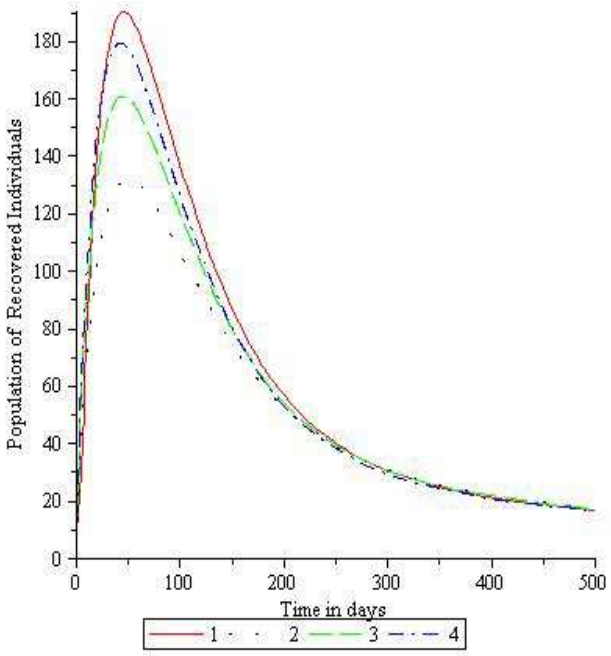

Fig. (2e)

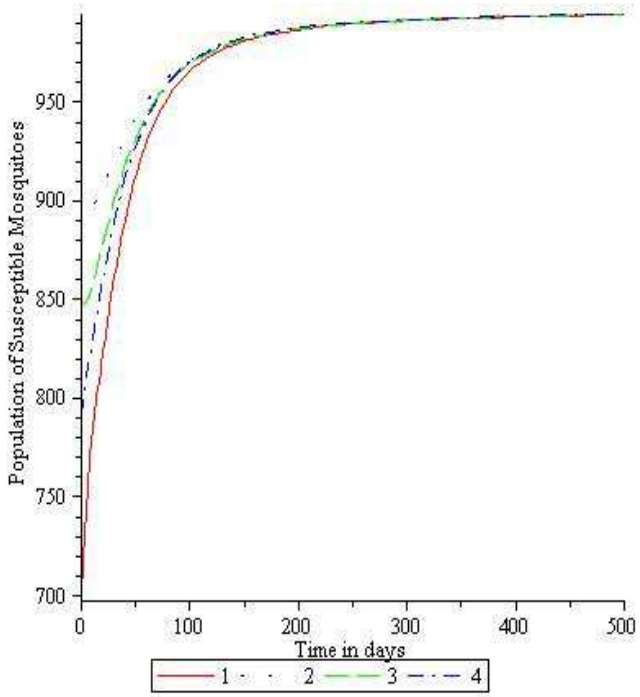

Fig. (2f)

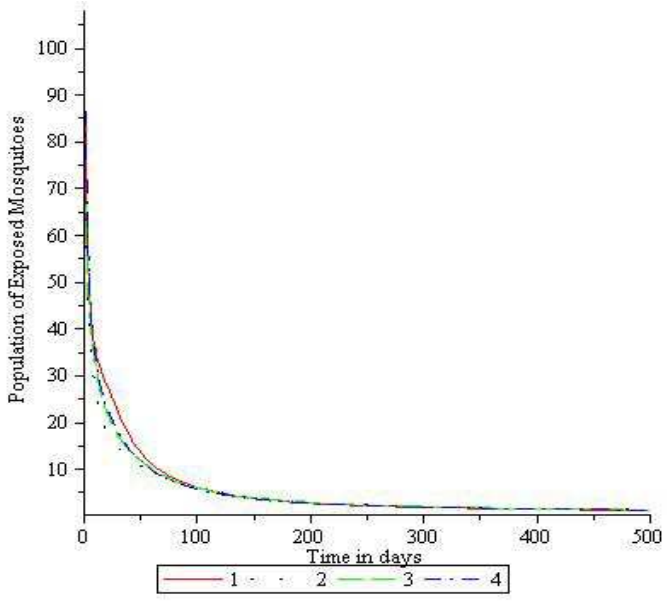

Fig. (2g)

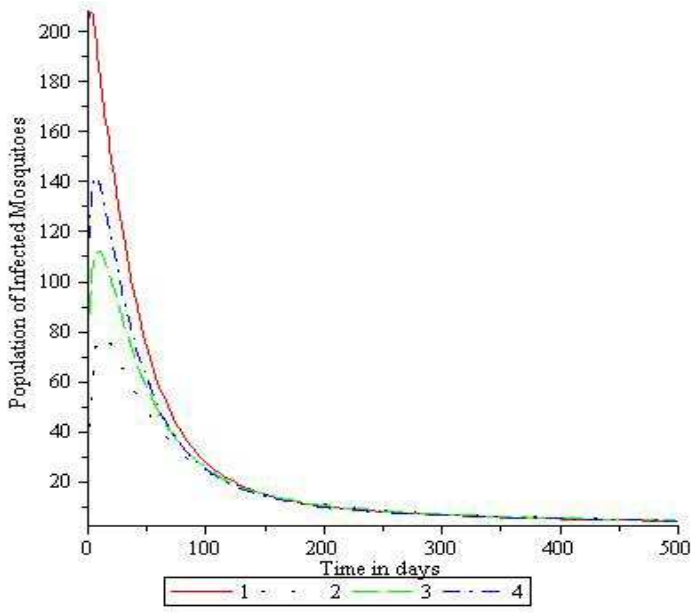

Fig. (2h)

Fig. 2. Time plots of system (1) with different initial conditions for $R_f\,|_{\delta_H=\delta_V=0}>1$: (a) Susceptible human population; (b) Exposed human population; (c) Infected human population; (d) Vaccinated human population (e) Recovered human population; (f) Susceptible mosquitoes population;
(g) Exposedmosquitoes population; (h) Infectedmosquitoes population.

5.0 Conclusion

In this paper,we designed a non-linear mathematical model of eight disjoint epidemiological compartments which describes the role of therapeutic vaccine in the spread of dengue fever in a variable population. The model was shown to exist and have unique solution using formulated Theorems on existence and uniqueness of a solution. With the aid of effective reproductive number R_f , the global behavior of the dengue fever dynamics was established for disease free equilibrium and the endemic equilibrium at special case (i.e. when disease induced death rate for human and mosquitoes is assumed negligible or ignored) by constructing suitable Lyapunov functions. The disease free equilibrium ε_0 is globally asymptotically stable whenever $R_f < 1.$ This means that eradication of dengue fever is independent of initial human and mosquitoes population. On the other hand the endemic equilibrium for special case (i.e. when $\delta_H = \delta_V = 0$), $\varepsilon_1 |_{\delta_H=\delta_V=0}$ is globally asymptotically stable whenever $R_f |_{\delta_H=\delta_V=0} > 1$. This means that dengue fever will continue to persist. Some numerical simulations were performed to show that the analytical results are in good agreement with the quantitative results.

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