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STABILITY ANALYSIS OF A DENGUE DISEASE TRANSMISSION MODEL WITH INTRACELLULAR DELAY

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ABSTRACT. In this paper, an analytical investigation of a dengue disease transmission model with delay effect is studied. We find the basic reproduction number $\bar{R_0}$ for this model using Next Generation Method. All possible equilibrium points are established. The global stability of the viral free equilibrium E_1 is studied by constructing a suitable Lyapunov's function and the infected equilibrium E_2 is studied using Routh-Hurwitz criterion. Numerical simulations are carried out to illustrate the results.

1. INTRODUCTION

Dengue fever and dengue hemorrhagic fever are the most common mosquito borne infectious diseases spreading rapidly in tropical regions of the world. Dengue is transmitted to humans through the bite of infected Aedes mosquito, principally Aedesaegypti of the genus Flavivirus from the family Flaviviridae. It is been observed that there are four active antigenically distinct serotypes: DENV-1, DENV-2, DENV-3 and DENV-4 [1-2] which develop infections of varying severity in human population. There exists a possibility of some serotypes being more successful at infecting a host population, or more pathogenic, or both [3] because of the variations in the susceptibility and transmission of dengue

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infection [4-5]. The dynamics of interaction between the host and vector can be analysed using compartmental models which are the most commonly used sort of epidemic models.

A general model with only one virus and the population of susceptible and infectious humans assumed as a constant was considered by Esteva and Varga [6]. The authors also studied the models where the human population was growing exponentially and has constant disease rate [7]; two serotypes of virus and variable human [8]; the impact of vertical transmission and interrupted feeding on the dynamics of the disease [9].

Natural delays that arise in the dynamics of vector borne diseases play a very important role in the study of the dengue dynamics and virus transmission behaviour. It explains the dynamical behaviour of the susceptible hosts; the infected hosts and the virus carrying Aedes mosquitoes from the mathematical view which can help us to understand the model law for the prevalence of dengue fever. This in turn helps in better controlling of the spread of dengue virus.

Assume that Ω is a bounded region. Let N_h and N_m represent the human and vector population respectively. Let S_h, I_h and R_h denote the susceptible human population, infected population and recovered population respectively. The mosquito population consists of the number of susceptible mosquitoes S_m and the number of infectives I_m.

It is assumed that the human population has a constant birth and death rate μ_h. As only a fraction of eggs and larvae from its large pool develop into adult mosquitoes, a constant recruitment rate $\mathbf{A}$ is considered which is independent of the actual number of adult mosquitoes. The susceptible hosts have the probability of getting infected with the dengue virus at a rate $\frac{\beta_h b I_m}{N_h}$, where β_h is the transmission probability from infectious mosquitoes to susceptible humans; $\mathbf{b}$ is the average number of bites per infected mosquito per day.

The infected host population has a death rate given by $\mu_h I_h$ and the recovery rate of the host population after infection is $\gamma_h I_h$. Also with the changing times, there will be a change in the total recovered host population (R_h). The difference between the recovered hosts from infection $(\gamma_h I_h)$ and the total mortality in healthy host $(\mu_h R_h)$ gives the rate changes for a healthy population in the total time.

Variations in the group S_m gives the probability of the the susceptible population being bitten by the dengue infected mosquitoes at a rate $\frac{\beta_m b I_h}{N_h}$, where β_m is the transmission probability from humans to mosquitoes and μ_m is the per capita mortality rate of mosquitoes. The mathematical model that defines the host-vector interaction is given as follows:

$$\begin{aligned}
\frac{dS_h}{dt} =& \mu_h - \mu_h S_h(t) - \frac{b\beta_h}{N_h} I_m(t) S_h(t) \\
\frac{dI_h}{dt} =& e^{-Q\tau} \frac{b\beta_h}{N_h} S_h(t-\tau) I_m(t-\tau) - (\mu_h + \gamma_h) I_h(t) \\
\frac{dR_h}{dt} =& \gamma_h I_h(t) - \mu_h R_h(t).
\end{aligned}$$

The mosquito population is given by

$$\begin{aligned}
\frac{dS_m}{dt} =& \mu_m N_m - \frac{b\beta_m}{N_h} I_h(t) S_m(t) - \mu_m S_m(t) \\
\frac{dI_m}{dt} =& \frac{\beta_m b}{N_h} I_h(t) S_m(t) - \mu_m I_m(t),
\end{aligned}$$

with the condition

$$\begin{aligned}
S_h + I_h + R_h =& N_h \Rightarrow R_h = N_h - S_h - I_h, \\
S_m + I_m = N_m =& \frac{A}{\mu_m} \Rightarrow S_m = N_m - I_m = \frac{A}{\mu_m} - I_m.
\end{aligned}$$

Hence, the model for the human and vector population is given as follows:

$$\begin{aligned}
\frac{dS_h}{dt} =& \mu_h N_h - \frac{\beta_h b}{N_h} I_m(t) S_h(t) - \mu_h S_h(t) \\
\frac{dI_h}{dt} =& e^{-Q\tau} \frac{\beta_h b}{N_h} I_m(t-\tau) S_h(t-\tau) - (\mu_h + \gamma_h) I_h(t) \\
\frac{dI_m}{dt} =& \frac{\beta_m b}{N_h} I_h(t) S_m(t) - \mu_m I_m(t) \\
S_h =& \frac{S_h}{N_h}, i_h = \frac{I_h}{N_h}, i_m = \frac{I_m}{N_m} = \frac{I_m}{\frac{A}{\mu_m}}
\end{aligned}$$

Thus, the dynamics of dengue transmission is described by the following system of differential equations:

$$
\begin{aligned}
\frac{ds_h}{dt} &= \mu_h(1 - s_h(t)) - \alpha s_h(t) i_m(t) \\
\frac{di_h}{dt} &= e^{-Q\tau}\alpha s_h(t-\tau) i_m(t-\tau) - \beta i_h(t) \\
\frac{di_m}{dt} &= b\beta_m(1 - i_m(t)) i_h(t) - \mu_m i_m(t),
\end{aligned} \tag{1.1}
$$

where, $\alpha = \frac{b\beta_h A}{\mu_m N_h}$, $\beta = (\mu_h + \gamma_h)$, $Q = (\mu_m + \mu_h)$.

2. BASIC PROPERTIES

Let $C([-\tau, 0], R^3_+)$denote the Banach space of continuous functions mapping the interval $[-\tau, 0]$ into R^3_+ with the topology of uniform convergence, i.e., for $\Phi \in C^+$ the norm of Φ is defined as $\|\Phi\| = sup_{-\tau \le \theta \le 0}\{|\Phi_1(\theta)|, |\Phi_2(\theta)|, |\Phi_3(\theta)|\}$.

The initial conditions of the system (1.1) are

$$
S_h(\theta) = \Phi_1(\theta) \ge 0, i_h(\theta) = \Phi_2(\theta) \ge 0, i_m(\theta) = \Phi_3(\theta) \ge 0, \tag{2.1}
$$

where

$$
R^3_+ = \{(s_h, i_h, i_m) \in R^3 : s_h \ge 0, i_h \ge 0, i_m \ge 0\},
$$

$$
\Phi_1 \ge 0, \Phi_2 \ge 0, \Phi_3 \ge 0, \theta \in [-\tau, 0],
$$

$$
\Phi_1(0) \ge 0, \Phi_2(0) \ge 0, \Phi_3(0) \ge 0.
$$

From the fundamental theorem of functional differential equations [10], it can be seen that the system (1.1) has a unique solution$(s_h(t), i_h(t), i_m(t))$ satisfying the initial condition (1.2) for all time $t \ge 0$.

Theorem 2.1. *Consider the initial data* $s_h(\theta) = \Phi_1(\theta) \ge 0, i_h(\theta) = \Phi_2(\theta) \ge 0, i_m(\theta) = \Phi_3(\theta) \ge 0$ *for all* $\theta \in [-\tau, 0)$*, with* $\Phi_1(0) > 0, \Phi_2(0) > 0$ *and* $\Phi_3(0) > 0$*. Then the solutions* $s_h(t), i_h(t), i_m(t)$ *of the system (1.1) are positive for all* $t \ge 0$*.*

Proof. First we prove that $s_h(t)$ is positive. Let us assume the contrary i.e., let $t_1 > 0$ be the first time such that $s_h(t_1) = 0$. By the first equation of (1.1), we have $s'_h(t_1) = \mu_h > 0$. This means $s_h(t) < 0$ for $t \in (t_1 - \varepsilon, t_1)$ where ε is an arbitrarily small positive constant. This leads to a contradiction. It follows that $s_h(t)$ is always positive.

Solving $i_h(t_1) > 0, i_m(t_1) > 0$ for all time $t_1 > 0$, we have

$$i_h(t_1) = exp[-\beta t_1][i_h(0) + \int_0^{t_1} \alpha s_h(\theta - \tau) i_m(\theta - \tau) exp[\beta\theta] d\theta] > 0$$

$$i_m(t_1) = i_m(0) exp[-\mu_m t_1 - \int_0^{t_1} (b\beta_m i_h(t_1)) i_m(\theta) d\theta]$$

$$+ \exp[-\mu_m t_1 - \int_0^{t_1} (b\beta_m i_h(t_1)) i_m(\theta) d\theta]$$

$$\int_0^{t_1} (b\beta_m i_h(t_1)) \exp[\mu_m u + \int_0^{u} (b\beta_m i_h(t_1)) i_m(\theta) d\theta] du > 0.$$

Let $t_1 \in [0, \tau]$, we have $\theta - \tau \in [0, \tau]$ for all $\theta \in [0, \tau]$. As we have $s_h(\theta) = \Phi_1(\theta), i_h(\theta) = \Phi_2(\theta), i_m(\theta) = \Phi_3(\theta)$ and from (1.5) we deduce that $i_m(t) \geq 0, t_1 \in [0, \tau]$. From equations (3) and (4), we see that $s_h(t)$ and $i_h(t)$ are all non - negaive on the interval $[0, \tau]$.

Next, we consider the arguments for ultimate boundedness. □

Theorem 2.2. *Let $(s_h(t), i_h(t), i_m(t))$ be the solution of the system (1.1) satisfying the conditions (1.2) then $(s_h(t), i_h(t), i_m(t))$ are all bounded for all $t > 0$, where the solution exists.*

Proof. Let $N(t) = s_h(t) + i_h(t) + i_m(t)$. The invariant region where solution exist is obtained as follows

$$0 < \liminf N(t) \leq \limsup N(t) \leq k, \qquad (t \to \infty).$$

□

Since $N(t) > 0$ on $[-\tau, 0], N(t) > 0$ for all $t \geq 0$. Hence, from the evolution of the system (1.1) and from the relation $N(t) = s_h(t) + i_h(t) + i_m(t)$, N(t) cannot increase to infinity in the infinite time. The system solutions are bounded and the solutions exist globally for all $t \geq 0$ in the invariant and compact set

$$\Phi = (s_h, i_h, i_m) \in R_+^3; s_h + i_h + i_m = N \leq k.$$

3. Equilibrium points and local stability analysis

We now consider the equilibrium points of the system (1.1).

3.1. **Disease free equilibrium E_1.**

$$E_1 = (\hat{s_h}, 0, 0) = (1, 0, 0).$$

This is used to find the basic reproduction number which is defined as the average of secondary infections generated by a single infected individual when it is introduced into a completely susceptible population. The basic reproduction number $\bar{R}_0$ is obtained by next generation method [11]. The next generation matrix is obtained from sub system of (1.1) considering the states-at-infection (i_h and i_m). In matrix form, the dynamical system (1.1) is written as

$$\frac{d}{dt}x_p = f_p(x) - v_p(x), p = 1, 2, 3.$$

Here, the disease compartments are i_h and i_m and

$$F_{DFE} = \begin{bmatrix} 0 & \alpha e^{-Q\tau} \\ 0 & 0 \end{bmatrix}, V_{DFE} = \begin{bmatrix} \beta & 0 \\ -b\beta_m & \mu_m \end{bmatrix},$$

and

$$V^{-1} = \begin{bmatrix} \frac{1}{\beta} & 0 \\ \frac{b\beta_m}{\beta} & \frac{1}{\mu_m} \end{bmatrix}.$$

The next generation matrix is FV^{-1}.The spectral radius of a matrix is represented by $\rho(A)$. This is the dominant eigen value. So, $\rho(FV^{-1}) = \sqrt{R_0}$. The square root is due to the two generations necessary for an infected vector to reproduce itself [12].

We can see that the basic reproduction number $\bar{R}_0$ equals the spectral radius of the following matrix

$$M_0 = \begin{bmatrix} 0 & \frac{\alpha e^{-Q\tau}}{\mu_m} \\ \frac{b\beta_m}{\mu_h+\gamma_h} & 0 \end{bmatrix},$$

and hence $R_0 = \frac{b^2\beta_h\beta_m\frac{A}{\mu_m}e^{-Q\tau}}{N_h\mu_m(\mu_h+\gamma_h)}$. The quantity $\bar{R}_0 = \sqrt{R_0}$ is called the basic reproduction number of the disease.

3.2. **The endemic equilibrium E_2.**

$$E_2 = (\hat{s}_h, \bar{i}_h, \bar{i}_m)$$

$$E_2 = \left(\frac{\beta' e^{-Q\tau} + M}{\beta' e^{-Q\tau} + MR_0}, \frac{(R_0 - 1)e^{-Q\tau}}{\beta' e^{-Q\tau} + MR_0}, \frac{\beta' e^{-Q\tau}(R_0 - 1)}{R_0(\beta' e^{-Q\tau} + M)}\right),$$

where $M = \frac{\mu_h+\gamma_h}{\mu_h}$ and $\beta' = \frac{b\beta_m}{\mu_m}$. When $R_0 \leq 1$,the steady state value E_1 lies in Ω and when $R_0 > 1$, the endemic equilibrium E_2 also lies in Ω.

Let $E^*(s_h^*, i_h^*, i_m^*$ be an arbitrary equilibrium. Then the characteristic equation about E^* is given by

$$\Delta = \begin{vmatrix} -\mu_h - \alpha i_m^* - \lambda & 0 & -\alpha s_h^* \\ \alpha e^{-Q\tau} i_m^* e^{-\lambda\tau} & -\beta - \lambda & \alpha e^{-Q\tau} s_h^* e^{-\lambda\tau} \\ 0 & b\beta_m - b\beta_m i_m^* & -b\beta_m i_h^* - \mu_m - \lambda \end{vmatrix}. \tag{3.1}$$

There exist two types of possible non-negative equilibrium points namely
(a) $E_1 = (\bar{s}_h, 0, 0)$, the disease free equilibrium (DFE).
(b) $E_2 = (\bar{s}_h, \bar{i}_h, \bar{i}_m)$, the positive or endemic equilibrium.

Theorem 3.1.

(1) If $R_0 < 1$, then the infection free steady state E_1 is locally asymptotically stable for any time delay $\tau \geq 0$.

(2) If $R_0 > 1$, then E_1 is unstable for any time delay $\tau \geq 0$.

Proof. For E_1, equation (1.3) reduces to

$$-(\mu_h + \lambda)[\lambda^2 + \lambda(\mu_h + \mu_m + \gamma_h) + \mu_m(\mu_h + \gamma_h) - \alpha b\beta_m e^{-Q\tau} s_h^* e^{-\lambda\tau}] = 0$$
$$\rightarrow (-\mu_h - \lambda)(\lambda^2 + p_1\lambda + p_2 + p_3 e^{-\lambda\tau}) = 0,$$

where, $p_1 = \mu_h + \mu_m + \gamma_h, p_2 = \mu_m(\mu_h + \gamma_h), p_3 = -R_0\mu_m(\mu_h + \gamma_h)$. It is clear that equation (7) has the characteristic root $\lambda = -\mu_h < 0$.

Next, we consider the transcendental polynomial

$$(\lambda^2 + p_1\lambda + p_2 + p_3 e^{-\lambda\tau}) = 0 \tag{3.2}$$

when $R_0 < 1$ and $\tau = 0$, we have $p_1 > 0$, $p_2 + p_3 = (\mu_h + \gamma_h)\mu_m(1 - R_0)$, for $R_0 < 1$ the infection free steady state E_1 of the system (1.1) is locally asymptotically stable.

If equation (1.4) has pure imaginary root $\lambda = i\omega$, for some $\omega > 0, \tau > 0$ we have from equation (1.4) $\omega^4 + (p_1^2 - 2p_2)\omega^2 + (p_2^2 - p_3^3) = 0$. Now, $p_1^2 - 2p_2 = \beta^2 + \mu_m^2 > 0$, $p_2^2 - p_3^2 = (\mu_h + \gamma_h)^2\mu_m^2(1 - R_0^2)$. Notice that $p_2^2 - p_3^2 > 0$ when when $R_0 < 1$. Hence, equation (1.4) contains no purely imaginary roots for all $\tau > 0$.

So, the viral free equilibrium E_1 is locally asymptotically stable when $R_0 < 1$ and for any time delay $\tau \geq 0$.

Let us denote g by $g(\lambda) = \lambda^2 + p_1\lambda + p_2 + p_3e^{-\lambda\tau} = 0$ where $p_1 = \mu_h + \mu_m + \gamma_h, p_2 = \mu_m(\mu_h+\gamma_h), p_3 = -R_0\beta\mu_m$, when $R_0 > 1$, $g(0) = \mu_m(\mu_h+\gamma_h)(1-R_0) < 0$ and $\lim_{t\to\infty} g(\lambda) = +\infty$.

It follows from the continuity of the function $g(\lambda)$ on $(-\infty, +\infty)$ that the equation $g(\lambda) = 0$ has at least one positive root. Hence, the characteristic equation (1.4) has at least one positive real root. So,E_1 is unstable. For $R_0 > 1$ the steady state E_1 becomes unstable and the positive steady state E_2 happens to be the unique equilibrium in the interior of the feasible region. □

3.3. **Existence of endemic equilibrium.**

Theorem 3.2. *If $\tau = 0$ and $R_0 > 1$,then the infected steady state E_2 is locally asymptotically stable.*

Proof. The characteristic polynomial from (1.3) is

$$\lambda^3 + a_1\lambda^2 + a_2\lambda + a_3 + e^{-\lambda\tau}(b_1\lambda + b_2) = 0, \tag{3.3}$$

where

$$a_1 = \frac{\mu_h(\beta' e^{-Q\tau} + MR_0)}{\beta' e^{-Q\tau} + M} + M\mu_h + \frac{\mu_m R_0(\beta' e^{-Q\tau} + M)}{\beta' e^{-Q\tau} + MR_0}$$
$$a_2 = \frac{M\mu_h^2(\beta' e^{-Q\tau} + MR_0)}{\beta' e^{-Q\tau} + M} + \mu_h\mu_m R_0 + \frac{M\mu_h\mu_m R_0(\beta' e^{-Q\tau} + M)}{\beta' e^{-Q\tau} + MR_0}$$
$$a_3 = M\mu_h^2\mu_m R_0 \quad \text{and} \quad b_1 = -M\mu_m\mu_h, b_2 = -M\mu_h^2\mu_m.$$

Equation (1.5) takes the general form

$$P(\lambda,\tau) + Q(\lambda,\tau)e^{-\lambda\tau} = 0, \tag{3.4}$$

with

$$P(\lambda,\tau) = \lambda^3 + a_1\lambda^2 + a_2\lambda + a_3, Q(\lambda,\tau) = b_1\lambda + b_2,$$

when $\tau = 0$, equation (1.3) takes the form $\lambda^3 + a_1\lambda^2 + (a_2 + b_1)\lambda + (a_3 + b_2) = 0$ where, $a_2 + b_1 = \frac{M\mu_h^2(\beta' e^{-Q\tau}+MR_0)}{\beta' e^{-Q\tau}+M} + \mu_h\mu_m R_0 + \frac{M\mu_h\mu_m R_0(\beta' e^{-Q\tau}+M)}{\beta' e^{-Q\tau}+MR_0} - M\mu_m\mu_h > 0$ $a_3 + b_2 = M\mu_h^2\mu_m(R_0 - 1) > 0$.

We see that $a_1 > 0, a_3 + b_2 > 0, a_1(a_2 + b_1) - (a_3 + b_2) > 0$. Hence, by Routh-Hurwitz criterion, it follows that E_2 locally asymptotically stable.

In the following when $\tau > 0$, we investigate the existence of purely imaginary roots $\lambda = i\omega(\omega > 0)$ to equation (1.3).

Substituting $\lambda = i\omega$ into equation (1.3) and separating the real and imaginary parts, we get

$$\omega^3 - a_2\omega = b_1\omega\cos\omega\tau - b_2\sin\omega\tau,$$
$$a_1\omega^2 - a_3 = b_1\omega\sin\omega\tau + b_2\cos\omega\tau$$

Let

$$F(\omega,\tau) = |P(i\omega,\tau)|^2 - |Q(i\omega,\tau)|^2$$
$$F(\omega,\tau) = \omega^6 + c_1\omega^4 + c_2\omega^2 + c_3,$$

where

$$c_1 = a_1^2 - 2a_2 = \frac{\mu_h^2(\beta' e^{-Q\tau} + MR_0)^2}{(\beta' e^{-Q\tau} + M)^2} + M^2\mu_h^2 + \frac{\mu_m^2 R_0^2(\beta' e^{-Q\tau} + M)^2}{(\beta' e^{-Q\tau} + MR_0)^2}$$
$$c_2 = a_2^2 - 2a_1a_3 - b_1^2 = \frac{\mu_h^4 M^2(\beta' e^{-Q\tau} + MR_0)^2}{(\beta' e^{-Q\tau} + M)^2}$$
$$+ \mu_h^2\mu_m^2 R_0^2 + \frac{\mu_m^2 M^2\mu_h^2 R_0^2(\beta' e^{-Q\tau} + M)^2}{(\beta' e^{-Q\tau} + MR_0)^2} - \mu_h^2 M\mu_m^2$$
$$c_3 = a_3^2 - b_2^2 = (\mu_h^2 M\mu_m)^2(R_0^2 - 1).$$

Then $\lambda = i\omega$ is a root of the equation (1.3) if and only if $F(\omega,\tau) = 0$. Let $z = \omega^2$, then the polynomial function F can be written as $F(\omega,\tau) = h(\omega^2,\tau)$ and

$$h(z,\tau) = z^3 + c_1z^2 + c_2z + c_3 = 0. \tag{3.5}$$

Noticing that $c_1 > 0, c_2 > 0, c_3 > 0$, for all $\tau > 0$, equation (1.7) has no positive roots, and thus the characteristic equation (1.5) has no purely imaginary roots. Also, $P(0,\tau) + Q(0,\tau) = a_3 + b_2 > 0$ for all $\tau > 0$ implies that zero is not the root of equation (1.5). Summarizing the above, we obtain the following conclusion. □

Theorem 3.3. *When $R_0 > 1$, the infected equilibrium E_2 of the system (1) is locally asymptotically stable. From biological point of view, the locally asymptotic stability characterizes the chronic infection of the infected individuals. The results prove that the time delay has no effect on the local asymptotic properties of the endemic equilibrium state E_2.*

3.4. **Global stability of E_1.** Suppose $R_0 \leq 1$, then E_1 is globally asymptotically stable in Ω. Define a Lyapunov funtional $V : C \times C \times C \to R$:

$$V = \frac{\alpha e^{-Q\tau}}{\mu_m} i_m + i_h + \alpha e^{-Q\tau} \int_{t-\tau}^{t} s_h(\theta) i_m(\theta) d\theta.$$

Taking the time derivative of V,

$$V' = \frac{\alpha e^{-Q\tau} b\beta_m}{\mu_m}(1 - i_m)i_h - \alpha e^{-Q\tau} i_m - (\mu_h + \gamma_h)i_h + \alpha e^{-Q\tau} s_h(t) i_m(t)$$

implying

$$V = -(\mu_h + \gamma_h)i_h[1 - R_0(1 - i_m)] - \alpha e^{-Q\tau} i_m(1 - s_h)$$

and $V' \leq 0$ in Ω and $(1 - s_h)i_m = 0, i_h = 0$ for $R_0 < 1; (1 - s_h)i_m = 0, i_m i_h = 0$ for $R_0 = 1$.

Hence, from Lyapunov-LaSalle theorem, we see that E_1 is globally asymptotically stable for $R_0 \leq 1$.

3.5. **Permanence.** In fact, for the system (1.1) we have

Theorem 3.4. *There is an $M > 0$ such that for any positive solution $(s_h(t), i_h(t), i_m(t))$ of the system (1.1), $s_h(t) < M, i_h(t) < M, i_m(t) < M$ for all large t.*

Proof. Set $V_1(t) = e^{-Q\tau} s_h(t - \tau) + i_h(t)$. Then $V_1'(t) = e^{-Q\tau} s_h'(t - \tau) + i_h'(t) = -\mu e^{-Q\tau} s_h(t - \tau) - \beta i_h(t) + \mu_h e^{-Q\tau} \leq -\delta_h V_1(t) + \mu_h e^{-Q\tau}$, where $\delta_h = \min\{\mu_h, \beta\}$. Hence, we get boundedness $V_1(t)$, that is there exists $t_2 > 0$ and $M_1 > 0$ such that $V_1(t) < M_1$ for $t > t_2$. Then $i_h(t)$ has an ultimately upper bound. It follows from the third equation of the system (1.1) that $i_m(t)$ has an ultimately upper bound, say, their maximum is an M. Then the assertion of Theorem 1.6 now follows. This completes the proof. This shows that the system (1.1) is dissipative. □

Definition 3.1. *System (1.1) is said to be uniformly persistent if there is an $\eta > 0$, such that $\liminf_{t\to+\infty} s_h(t) \geq \eta$, $\liminf_{t\to+\infty} i_h(t) \geq \eta$, $\liminf_{t\to+\infty} i_m(t) \geq \eta$ for any initial conditions of the system satisfying $s_h(t) > 0, i_h(t) > 0, i_m(t) > 0$.*

Theorem 3.5. *System (1.1) is said to be permanent if $R_0 > 1$. In order to prove Theorem 1.7, we present he permanence theory for infinite dimensional system as given by Hale et al. [13]*

The semi group $Y(t)$ is said to be point dissipative in X if there is a bounded non empty set B in X such that, for any $x \in X$, there is a $y_0 = y_0(x, B)$ such that

$Y(t)x \in B$ for $t \geq t_0$. Let X be a complete metric space. Suppose that X^0 is open and dense in $X, X^0 \subset X, X_0 \subset X, X^0 \cap X_0 = \phi$. Assume that Y(t) is C^0 - semi group on X satisfying

$$Y(t) : X^0 \to X^0$$
$$Y(t) : X_0 \to X_0 \tag{3.6}$$

Let $Y_b(t) = Y(t)|_{X_0}$ and A_b be the global attractor for $Y_b(t)$.

Lemma 3.1. *Suppose that Y(t) satisfies (1.4) and we have the following:*

(i) There is a $t_0 \geq 0$ such that Y(t) is compact for $t > t_0$.

(ii) Y(t)is point dissipative in X.

(iii) $\bar{A}_b = \cup_{x \in A_b} \omega(x)$ is isolated and has an acyclic covering $\bar{M}$, where $\bar{M} = \{M_1, M_2, M_3, ..., M_n\}$

(iv) $W^s(M_i) \cap X_0 = \phi$, for $i = 1, 2, \ldots, n$.

Then X_0 is a uniform repellor with respect to X^0, i.e., there is an $\epsilon > 0$ such that for any $x \in X^0$, $\lim_{t \to +\infty} \inf d(Y(t)x, X_0) \geq \epsilon$,where is the distance of Y(t)x from X_0.

Proof. We start with proving that the boundary planes of R^3_+ repel the positive solutions of the system (1.1) uniformly. Let us define

$$C_0 = \{(\phi_1, \phi_2, \phi_3) \in C([-\tau, 0], R^3_+) : \phi_1(\theta) \neq 0, \phi_2(\theta) = \phi_3(\theta) = 0, (\theta \in [-\tau, 0])\}.$$

If $C^0 = intC([-\tau, 0], R^3_+)$,it suffices to show that there exists an $\epsilon_0 > 0$ such that for any solution u_t of the system (1.1) initiating from C^0 $\liminf_{t \to +\infty} d(u_t, C^0) \geq \epsilon_0$. To this end, we verify below that the conditions of Lemma 1.8 are satisfied. It is easy to see that C^0 and C_0 are positive invariant. Moreover, conditions (i) and (ii) of Lemma 1.8 are clearly satisfied. Thus, we only need to verify conditions (iii) and (iv). There is a constant solution E_1 in C_0 to $s_h(t) = \hat{s}_h, i_h(t) = i_m(t) = 0$. If $(s_h(t), i_h(t), i_m(t))$ is a solution of the system (1.1) initiating from C_0, then $s_h(t) \to \hat{s}_h, i_h(t) \to 0, i_m(t) \to 0$ as $t \to \infty$. It is obvious that E_1 is an isolated invariant.

Now, we show that $W^s(E_1) \cap C^0 = \phi$.

Assuming the contrary, there exists a positive solution $(\tilde{s}_h(t), \tilde{i}_h(t), \tilde{i}_m(t))$ of the system such that $(\tilde{s}_h(t), \tilde{i}_h(t), \tilde{i}_m(t)) \to (\tilde{s}_h(t), i_h(t), i_m(t))$ as $t \to +\infty$. Let us choose $\epsilon > 0$ small enough such that $\tilde{s}_h(t) - \epsilon > \bar{s}_h$. Let $t_0 > 0$ be sufficiently large such that $\tilde{s}_h - \epsilon < \tilde{s}_h(t) < \tilde{s}_h + \epsilon$ for $t_0 - \tau$.

Linearising the system (1.1)at the DFE $(\hat{s}_h, 0, 0)$, we get the following time-delayed system for the disease compartments as:

$$\begin{aligned} \tilde{i}'_m(t) &= b\beta_m \tilde{i}_h(t) - \mu_m \tilde{i}_m(t) \\ \tilde{i}'_h(t) &= \alpha e^{-Q\tau}(\hat{s}_h - \epsilon)\tilde{i}_m(t) - \beta \tilde{i}_h(t), \end{aligned} \tag{3.7}$$

for $\epsilon > 0$ small enough, let $\lambda_1(\epsilon)$ be the principle eigen value of the system (1.5). Since $R_0 > 1$, we can see that $\lambda_1(0) > 0$ [14, Corrollary 1]. Thus we can restrict ϵ small enough so that, $\lambda_1(\epsilon) > 0$. For this small ϵ, there exists $\delta = \delta(\epsilon)$ such that

$$\begin{aligned} \frac{i_m}{i_m + i_h + s_h} &> 1 - \epsilon \\ \frac{i_m + i_h}{i_m + i_h + s_h} &> \hat{s}_h - \epsilon > 0. \end{aligned}$$

We have for $t > t_0$:

$$\begin{aligned} \tilde{i}'_m(t) &\geq b\beta_m \tilde{i}_h(t) - \mu_m \tilde{i}_m(t) \\ \tilde{i}'_h(t) &\geq \alpha e^{-Q\tau}(\hat{s}_h - \epsilon)\tilde{i}_m(t) - \beta \tilde{i}_h(t) \end{aligned}$$

Let us consider $v = (v_1, v_2)^T$ is the positive eigen vector associated with $\lambda_1(\epsilon)$ for the system (1.5).

Choose $l > 0$ small enough such that $lv_1 e^{\lambda_1(\epsilon)t} \leq \bar{i}_m(t_0 + \theta)$ and $lv_2 e^{\lambda_1(\epsilon)t} < \bar{i}_h(t_0 + \theta)$ for $\theta \in [-\tau, 0]$. Clearly, $le^{\lambda_1(\epsilon)t}(v_1, v_2)^T$ satisfies (1.5) for $t \geq t_0$. Then by comparison principle, we get $(i_m(t), i_h(t)) \geq le^{\lambda_1(\epsilon)t}(v_1, v_2)$, for all $t \geq t_0 + \tau$. Since the semi-flow of the system (1.5) is monotone and $\lambda_1(\epsilon) > 0$, letting $t \to +\infty$, we obtain $\lim_{t\to+\infty} i'_m(t) = +\infty, \lim_{t\to+\infty} i'_m(t) = +\infty$, a contradiction.

Hence, E_1 is an isolated invariant set in C_0 and $W^s(E_1) \cap C^0 = \phi$. Moreover there is no subset of $\{E_1\}$ that forms a cycle in C_0, i.e., to say that C_0 repels the positive solutions of the system (1.1) uniformly. By [15, Theorem 3], it then follows that $\exists \eta > 0$ such that $\liminf_{t\leftarrow+\infty}\{s_h(t), i_h(t), i_m(t)\} \geq \eta$, which implies the uniform persistence. Hence, incorporating this in Theorem 1.7, it follows that the system (1.1) is permanent.

3.6. **Global stability of E_2.** We assume that when $R_0 > 1$, the endemic-infection equilibrium E_2 is the only equilibrium point in the interior of the feasible region Ω. We Construct a global Lyapunov functional.

Let $g(z) = z - 1 - lnz$. Define a Lyapunov functional $V : C \times R \times C \to R$:

$$V(s_h(t), i_h(t), i_m(t)) = \bar{s}_h g\left(\frac{s_h(t)}{\bar{s}_h}\right) + \bar{i}_h g\left(\frac{i_h(t)}{\bar{i}_h}\right) + \frac{\beta e^{Q\tau}}{b\beta_m}\bar{i}_m g\left(\frac{i_m(t)}{\bar{i}_m}\right) + \alpha\bar{s}_h\bar{i}_m \int_0^\tau g\left(\frac{s_h(t-\theta)i_m(t-\theta)}{\bar{s}_h\bar{i}_m}\right) d\theta.$$

Calculating the time derivative of along the positive solutions of the system (1.1), we get

$$\begin{aligned} V'|_{(1.1)} &= \mu_h - \mu_h\frac{\bar{s}_h}{s_h} - \mu_h s_h + \mu_h\bar{s}_h + \alpha\bar{s}_h i_m(t) - \alpha\bar{i}_h\frac{s_h(t-\tau)i_m(t-\tau)}{i_h(t)} \\ &+ \beta\bar{i}_h e^{Q\tau} - \frac{\beta e^{Q\tau}}{b\beta_m}\mu_m i_m(t) - \beta e^{Q\tau}\bar{i}_m\frac{i_h(t)}{i_m(t)} + \frac{(\mu_h+\gamma_h)}{b\beta_m}\mu_m\bar{i}_m + \frac{\beta}{b\beta_m}\mu_m\bar{i}_m \\ &- [\beta e^{Q\tau} i_m(t)i_h(t) - \beta e^{Q\tau} i_h(t)\bar{i}_m] + \alpha\bar{s}_h\bar{i}_m lns_h(t-\tau)i_m(t-\tau) \\ &- \alpha\bar{s}_h\bar{i}_m lns_h(t)i_m(t). \end{aligned}$$

Using $\mu_h = \mu_h\bar{s}_h + \alpha\bar{s}_h\bar{i}_m, \alpha\bar{s}_h\bar{i}_m = \beta e^{Q\tau}\bar{i}_h$, $\alpha\bar{s}_h = \frac{\beta(\mu_m + b\beta_m\bar{i}_h)e^{Q\tau}}{b\beta_m}$ we get

$$\begin{aligned} \mu_h &\leq \mu_h\bar{s}_h\left[2 - \frac{s_h(t)}{\bar{s}_h} - \frac{\bar{s}_h}{s_h(t)}\right] - \alpha\bar{s}_h\bar{i}_m g\left[\frac{\bar{i}_h s_h(t-\tau)i_m(t-\tau)}{\bar{s}_h\bar{i}_m i_h(t)}\right] \\ &- \alpha\bar{s}_h\bar{i}_m g\left[\frac{\bar{s}_h}{s_h(t)}\right] - \alpha\bar{s}_h\bar{i}_m\left[\frac{\bar{i}_m i_h(t)}{\bar{i}_h i_m(t)}\right]. \end{aligned}$$

We see that $g : R_+ \to R$ has the global minimum at z=1 and g(z)=0. Hence $\bar{s}_h, \bar{i}_h, \bar{i}_m > 0$ ensures that $\frac{dV}{dt} \leq 0$ and V=0 if and only if $(s_h(t), i_h(t), i_m(t)) = (\bar{s}_h, \bar{i}_h, \bar{i}_m)$. Hence, it also follows from stability theorems [1.16] that the infected equilibrium E_2 is stable for any time delay $\tau \geq 0$ under the condition $R_0 > 1$ i.e., all positive solutions in Ω converge to E_2. From Lyapunov LaSalle invariance principle, it shows that E_2 is globally stable when $R_0 > 1$.

□

4. NUMERICAL SIMULATIONS

In this section, we have carried out numerical simulations to illustrate the analytical results for disease free equilibrium and endemic equilibrium points.

4.1. **Population dynamics when $\bar{R}_0 < 1$.** For the condition $\bar{R}_0 < 1$, we fix the parameter values as $\mu_h = 0.098; \beta_m = 0.98; \beta_h = 0.075; b = 0.9; \gamma_h = 0.143; \mu_m = 0.35; N = 2300; A = 282; Q = \mu_h + \mu_m; \tau = 1.60;$ the basic reproduction number $\bar{R}_0 = 0.6566$. The disease - free equilibrium E_1 is globally asymptotically stable as illustrate in Figure 1.

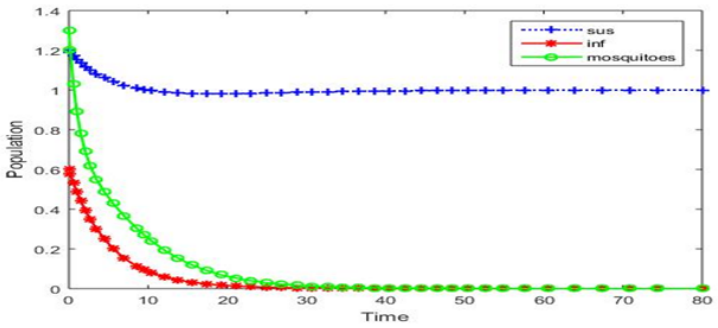

Figure 1 Stable variations of populations against time when $\tau = 3.5$ and $\tilde{R}_0 < 1$.

TABLE 1. Value of $\bar{R}_0$ with μ_m parameter and the other parameters remain the same for E_1.

S.No.	γ_h	μ_m	$\bar{R}_0$
1	0.143	0.35	0.6566
2	0.143	0.55	0.4464
3	0.143	0.75	0.3257
4	0.143	0.95	0.2465

When mortality rate of the mosquitoes increases, the basic reproduction number will decrease. Thus the rate of spread of disease in the population can be achieved by the decrease in basic reproduction number as mentioned in Table 1 for $\bar{R}_0 < 1$. Figure 2 shows the effects that occur in each population if the mosquito death rate increases.

4.2. **Population dynamics when $\bar{R}_0 > 1$.** : For $\bar{R}_0 > 1$, we fix the parameter values as $\mu_h = 0.0098; \beta_m = 0.98; \beta_h = 0.075; b = 0.9; \gamma_h = 0.43; \mu_m = 0.9;$ $N = 2300; A = 982; Q = \mu_h + \mu_m; \tau = 160;$ the basic reproduction number $\bar{R}_0 = 1.2361$. The endemic equilibrium is globally asymptotically stable as illustrated

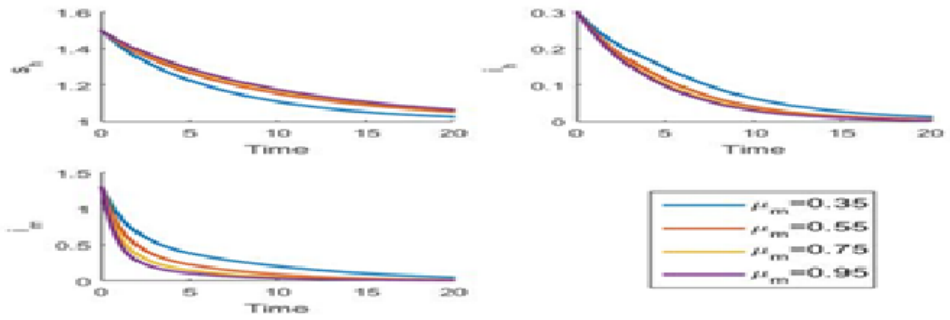

Figure 2 Numerical simulations indicating variations in each population with mosquito mortality rate in the disease free case.

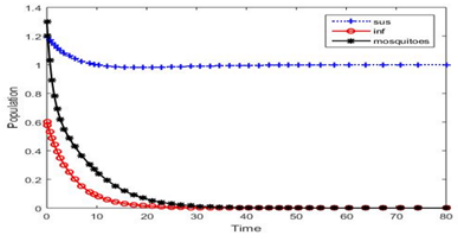

Figure 3. Stable variations of the populations against time for the system (1) when $\tilde{R}_0 > 1$

in Figure 3.

TABLE 2. Value of $\bar{R}_0$ with μ_m parameter and the other parameters remain the same for E_2.

S.No.	γ_h	μ_m	$\bar{R}_0$
1	0.43	0.29	3.5479
2	0.43	0.4	2.7664
3	0.43	0.6	1.9248
4	0.43	0.9	1.2361

The increased mortality rate of mosquitoes decreases the basic reproduction number as mentioned in Table 2 for $\bar{R}_0 > 1$. Figure 4 shows the changes in each populations of the system (1.1) if the mosquito death rate increases.

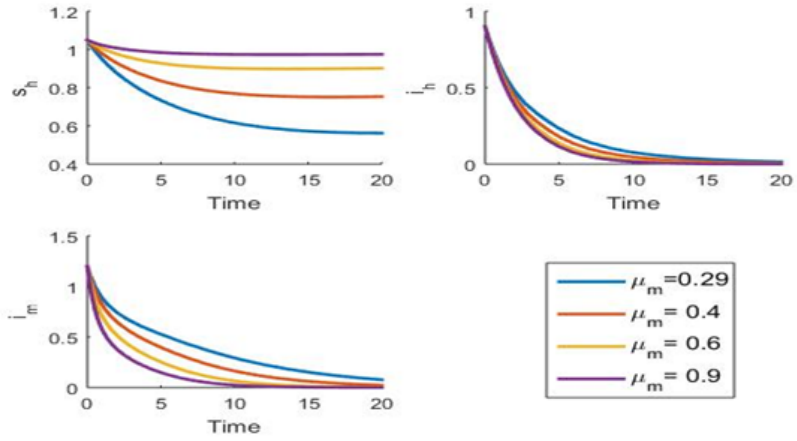

Fig 4: Numerical Simulation indicating variations in each population which mosquito mortality rate in the endemic case.

5. Conclusion

In this chapter, we proposed and investigated a dynamic model for dengue disease transmission, where we have also included the time delay that stands for the fixed latent periods of mosquitoes. For the model system (1), we found the basic reproduction ratio $\bar{R}_0$, which is determined as the spectral radius of the next generation operator. Analytical results are derived which are supported by the numerical simulations. The occurrence of infection in vectors and hosts depends directly on the basic reproduction number and the relationship is non-linear. The model has a stable positive equilibrium when the basic reproduction number is greater than one.

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