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Disease Dynamics of Dengue Transmission: A Mathematical Approach

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Abstract: Dengue remains one of the most serious and widespread mosquito-borne viral infections in human beings, with serious health problems or even death. About 50 to 100 million people are newly infected annually, with almost 2.5 billion people living at risk and resulting in 20,000 deaths. Dengue virus infection is especially transmitted through bites of Aedes mosquitos, hugely spread in tropical and subtropical environments, mostly found in urban and semiurban areas. In this research article, a mathematical model of dengue is proposed and analysed. Here a four dimensional mathematical model is considered. The dynamical behaviour of the system is studied analytically. Existence condition and stability analysis are performed. Our aim is to control the disease dengue by using control therapeutic approach.

Keywords: Dengue, Aedes Mosquito, Viral infections, Mathematical model.

I. INTRODUCTION

Dengue fever (DF) and Dengue Haemorrhagic Fever (DHF) are increasingly important public health problems in the tropic and subtropics areas. Dengue has been recognized in over 100 countries and 2.5 billion people live in areas where dengue is endemic [1]. Dengue is a viral disease transmitted by the bite of an Aedes mosquito infected with one of the four dengue virus serotypes (DEN-1, DEN-2, DEN-3 and DEN-4) [2,3]. Dengue can affect almost all age groups (infant to adult), and symptoms appear 3–14 days after the infected mosquito bite [3]. A person recovers from one of the dengue serotype having life-long immunity to that serotype but prone to infection from other three serotypes.

About 12 weeks' time the person becomes more susceptible to develop dengue hemorrhagic fever or dengue shock syndrome [4]. In recent decades, the burden of dengue increases rapidly and according to WHO there may be 50–100 million dengue cases occur each year worldwide [2]. To understand the dengue transmission dynamics fully, it is of utmost importance to realize the blood feeding behavior of Aedes mosquito. Recent entomological studies on Aedes aegypti revealed that mosquito did not feed randomly on host blood, but they use their prior experience about a host location and a host defensiveness to select a host to feed on [5,6,7,8,9,10,11]. Furthermore, on human population also, the memory plays a key role in dengue transmission. In epidemic and endemic area's awareness about dengue will lessen the contact rate between host and mosquitoes [12,13]. Thus, in dengue transmission, a future state depends upon the full history of the transmission process [14].

Different mathematical models have been proposed and analyzed to understand the transmission dynamics of infectious diseases. In recent years, modeling has become a valuable tool in the analysis of dengue disease transmission dynamics and to determine the factors that influence the spread of disease to support control measures. Many researchers have proposed SIR epidemic model to study the transmission dynamics of dengue disease [15, 16,17,18,19,20,21,22]. Incubation periods in hosts and vectors have a significant influence in transmission dynamics of dengue disease. So, different mathematical studies [23,24,25] of dengue disease have been made to study dengue disease transmission dynamics with incubation periods.

The original model used by Esteva and Vargas [26], did not include the intrinsic and extrinsic incubation periods of dengue virus in human and vector populations. Their model considered the transmission between the human and vector populations. The human population is separated into susceptible, infectious and recovered classes. The vector population is divided into susceptible and infectious classes. In our study, the length of time during the dengue virus circulating in the blood of human and vector populations are considered. The infected human and infected vector classes are included into the model. There is the difference between infected and infectious classes for the human and vector populations. The infected classes cannot transmit dengue virus until they become to be infectious class.

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Fig.1 A schematic illustration of the interaction between the virus and target cells [27].

II. DEVELOPMENT OF MATHEMATICAL MODEL

We consider that prey population is facing an infectious disease, where the predator feeds on both healthy and infected preys. Let, $S_{\rm H}$ is the susceptible human population, $I_{\rm H}$ is the infected human population, $S_{\rm V}$ is the susceptible vector population, $I_{\rm V}$ is the infected vector population, $H_{\rm V}$ is the Human Vaccinated.

$$\begin{aligned} \frac{dS_H}{dt} &= (1-r)\lambda_H - d_1S_H \\ \frac{dI_H}{dt} &= \frac{\beta_H S_H I_V}{N_H} - \gamma I_H - d_1 I_H \\ \frac{dS_V}{dt} &= \lambda_V - \frac{\beta_V I_H}{N_V} - d_2 S_V \\ \frac{dI_V}{dt} &= \frac{\beta_V S_V I_H}{N_V} - d_2 I_V \\ \frac{dH_V}{dt} &= r\lambda_H - \frac{(1-\alpha_2)\beta_{H_V} S_V}{N_H} - d_3 H_V \end{aligned}$$

where, $\lambda_{\rm H}$ is Birth rate of human population, d₁ is nature death rate(mosquito)of susceptible infected human population, d₂ is death rate of vector population, d₃ is death rate of human after vaccinated, γ is death rate due to infection, $\lambda_{\rm V}$ is constant recruitment rate of population, $\beta_{\rm H}$ is transmission rate of dengue virus from vector to human, $\beta_{\rm V}$ is transmission rate of dengue virus from human to vector, $\beta_{V_{\rm H}}$ is transmission rate of dengue virus from vector to human after vaccination, $\beta_{H_{\rm V}}$ is transmission rate of dengue virus

from infected human to vector after vaccination.



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III. EXISTENCE AND LOCAL STABILITY ANALYSIS OF THE EQUILIBRIUM POINTS

There are four equilibrium points of the aggregated system, trivial equilibrium point $E_0(0,0,0,0,0,0)$, planer equilibrium points

$$\underbrace{(1-r)\lambda_{H}}_{E_{1}(1-r)\lambda_{H}} \underbrace{\lambda_{V}}_{0,0} \underbrace{(1-r)\lambda_{H}}_{0,0} \underbrace{\lambda_{V}}_{d_{2},0,0} \underbrace{(1-r)\lambda_{H}}_{d_{3},0} \underbrace{(1-r)\lambda_{H}}_{0,0} \underbrace{(1-r)\lambda_{H}}_{d_{3},0} \underbrace{(1-r)\lambda_{H}}_{d_{1},0} \underbrace{(1-r)\lambda_{H}}_{d_{1},0} \underbrace{(1-r)\lambda_{H}}_{d_{2},0} \underbrace{(1-r)\lambda_{H}}_{d$$

interior equilibrium point is $E^*(S_{H}^*, I_{H}^*, S_{V}^*, I_{V}^*, H_{V}^*)$.

Lemma 1: The equilibrium point E0(0,0,0,0,0,0) is always unstable.

Lemma 2: The System (1) around $E_1(\frac{(1-r)\lambda_H}{d_1}, 0, \frac{\lambda_V}{d_2}, 0, 0)$, is locally asymptotically stable (LAS).

Proof : The eigen values of the corresponding Jacobian matrix are $-d_1$, $-d_2$, $-d_3$ and the other two eigen values satisfy the equation $\lambda^2 - (a_{22}+a_{24})\lambda + (a_{22}a_{24}-a_{24}a_{42}) = 0$,

i.e., if
$$\frac{-\gamma}{d_1+d_2} < 0$$
 and $\frac{d_2\gamma+d_1d_2}{\beta_H\beta_V} > 0$.

Therefore, the E₁ is LAS. **Lemma 3:** The System around E₂($\frac{(1-r)\lambda_H}{d_1}$, 0, $\frac{\lambda_V}{d_2}$, 0, $\frac{r\lambda_H}{d_3}$), is locally asymptotically stable (LAS).

Proof : The eigen values of the corresponding Jacobian matrix are $-d_1$, $-d_2$, $-d_3$ and the other two eigen values satisfy the equation: $\lambda^2 - (a_{22}+a_{24}) \lambda + (a_{22}a_{24}-a_{24}a_{42}) = 0$,

i.e., if
$$\frac{-\gamma}{d_1+d_2} < 0$$
 and $\frac{d_2 \gamma + d_1 d_2}{\beta_H \beta_V} > 0$.

Therefore, the E_2 is **LAS**.

$$\underline{(1-r)\lambda_H - I_H(\gamma + d_1)} \qquad \underline{\lambda_V - d_2 I_V}$$

Lemma 4: The System around $E_3(d_1, I_H, d_2, I_V, 0)$ is locally asymptotically stable (LAS). **Proof :** The roots of the characteristic equation

 $A_0\lambda^4 + A_1\lambda^3 + A_2\lambda^2 + A_3\lambda + A_4 = 0$ of the Jacobian Matrix satisfy the Routh-Hurwitz criteria i.e. $A_i > 0$ (where, i=0,1,2,3,4), $A_1A_2 - A_0A_3 > 0$,

 $\begin{array}{c} A_1A_2A_3 - A_1{}^2A_4 - A_0A_3{}^2 > 0, \\ \text{where,} \quad A_0 = 1 \\ A_1 = \Upsilon + 2d_1 + 2d_2 \\ A_2 = \Upsilon d_1 + 2\Upsilon d_2 + 4d_1d_2 + d_1{}^2 + d_2{}^2 - \beta_H\beta_V \\ A_3 = 2\Upsilon d_1d_2 + 2d_1{}^2d_2 + d_1d_2{}^2 + \Upsilon d_2{}^2 - d_1\beta_H\beta_V + d_2\beta_H\beta_V \\ \text{And} \quad A_4 = \Upsilon d_1d_2{}^2 + d_1{}^2d_2{}^2 - d_1d_2\beta_H\beta_V \\ \text{the fifth value of } \lambda \text{ is } -d_3. \\ \text{Therefore, the } E_3 \text{ is conditionally LAS.} \end{array}$

Lemma 5: The System around the interior equilibrium point $E^*(S_H^*, I_H^*, S_V^*, I_V^*, H_V^*)$ is locally asymptotically stable(LAS). **Proof :** The roots of the characteristic equation

 $\begin{array}{l} A_0\lambda^4 + A_1\lambda^3 + A_2\lambda^2 + A_3\lambda + A_4 = 0 \mbox{ of the Jacobian Matrix satisfy the Routh-Hurwitz criteria i.e. } A_i > 0 \mbox{ (where, } i=0,1,2,3,4), \\ A_1A_2 - A_0A_3 > 0 \mbox{,} \\ A_1A_2A_3 - A_1^2A_4 - A_0A_3^2 > 0. \\ \mbox{where, } A_0 = 1 \\ A_1 = \Upsilon + 2d_1 + 2d_2 \\ A_2 = \Upsilon d_1 + 2\Upsilon d_2 + 4d_1d_2 + d_1^2 + d_2^2 - \beta_H\beta_V \\ A_3 = 2\Upsilon d_1d_2 + 2d_1^2d_2 + d_1d_2^2 + \Upsilon d_2^2 - d_1\beta_H\beta_V + d_2\beta_H\beta_V \\ \mbox{And} \qquad A_4 = \Upsilon d_1d_2^2 + d_1^2d_2^2 - d_1\beta_H\beta_V \\ \mbox{the fifth value of } \lambda \mbox{ is } -d_3. \\ \mbox{Therefore, the } E^* \mbox{ is conditionally LAS.} \end{array}$

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IV. CONCLUSION

The last two years have been really challenging the COVID-19 pandemic changed so much about the way we lived and worked. Now, just as we're starting to ease back into regular life, we're hearing media stories about dengue as an emerging threat. It's spread through the infected mosquitoes during day time. The best way to protect yourself is using mosquito nets if sleeping during the day and use coils. So far one vaccine (Dengvaxia) has been approved and licensed in some countries.

A deterministic mathematical model was developed for the transmission dynamics of Dengue virus. It was shown that the model is mathematically and epidemiologically well posed. Environment and vaccination strategies are discussed especially in the case of the succession of two epidemics with two different viruses. The equilibrium of the model equation was obtained and analysed analytically.

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