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Analysis Of Mathematical Modeling Of Vector Born Infectious Diseases

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Abstract

In this paper, the mathematical model is formulated by the system of non-linear ordinary differential equations. In this model there are four populations, viz. susceptible population, infected populations, susceptible vectors and infected vectors. Here the populations are infected by contacts with infected vectors and vectors are in turn infected by contacts with infected populations. The disease free equilibrium point and endemic equilibrium point has been studied for stability of the mathematical model. The basic reproduction number, $\boldsymbol{R_0}$, is defined on a system of ordinary differential equations. If $\boldsymbol{R_0} < 1$, then the disease free equilibrium point is locally asymptotically stable, and it is unstable if $\boldsymbol{R_0} > 1$. The theoretical results are significant by numerical simulations for disease control and has been observed graphically also.

Keywords: Susceptible population, Susceptible vectors, Infected populations, Infected vectors, Stability, Reproduction number, Asymptotically stable.

1. INTRODUCTION

In the recent mathematical research, mathematical modeling of infectious disease plays an important role to understanding and predicts the prevention of the communicable disease. Through the epidemiological study the causes, effects, the process of transmission of communicable disease either direct or indirect and the methods for its treatment and prevention are obtained. The model formulation requires certain assumptions on variables and parameters. We have used next generation matrix approach as described by Diekmann et al., Hefferman et al. and Baojun, S to define the reproduction number $\boldsymbol{R_0}$. Basic reproductive number ($\boldsymbol{R_0}$) is defined as the average number of secondary infections when an infectious individual entire in susceptible population [1-3]. Also we have use Hurwitz's theorem to study the stability of disease free equilibrium point as described by Ahamad and Perko [4, 5]. Computer simulations techniques are used for the validation of results, quantitative analysis and answering definite questions.

Some communicable diseases such as Chikungunya, Plague, Dengue fever, Kala-azar, Lymphatic filariasis, Japanese Encephalitis and Malaria can be controlled by elimination of vector population responsible for transmission of diseases. Due to climate changes Dengue, Malaria and Yellow fever have emerged and are spreading into new regions. Many communicable diseases such as Chicken pox, Diphtheria, Influenza, Measles, Mumps, Meningococcal-meningitis, Rubella, Polio and Whooping cough can be prevented by active vaccination process. It is obvious that due to environmental pollutions, global warming, ecosystems, traveling will be the main cause to spread of infectious diseases.

Dynamics of various vector borne diseases has been studied by various researchers such as Liming et al., Wang et al., Driessch et al., Martens, Makinnde, Li, M.Y, and Herbert using mathematical model [6-12]. Mishra have studied the transmission dynamics of their research work with the help of SI model [13].

2. FORMULATION OF MODEL

In the proposed mathematical model the population has been classified in two categories, viz. susceptible populations and infected populations. Similarly vector population has been classified into two categories, viz. susceptible vectors and infected vectors. With the contacts of infected vectors the susceptible populations are infected and it goes to the infected class. After some time, the infected populations either die or recover. After recovery the individuals loose the immunity and become again susceptible to the disease. Similarly with the contacts of infected populations the susceptible vectors are infected and that becomes an infected class. Infected vectors are transmitted by contact and then susceptible vectors are infected.

Model in this chapter satisfies following assumptions:

I. The formulation of the model of the proposed population and vector sizes remain constant at any time of the disease. This implies when birth and death rates in the two labels (population and vectors) are balance.
II. The homogeneity of the population as well as that of vector allows the contact in equally changeable.
III. The rates of transfer (not infection) are mean waiting time of the individual in the class and they are average time of the exponentially distributed.

The transmission dynamics diagram of this process is shown in following Figure 1

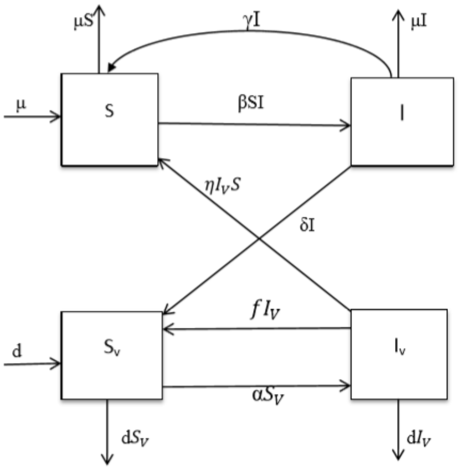

Fig 1: Progression of transmission dynamics

Consider, S(t) be the proportion of populations which are susceptible, I(t) be the proportion of populations which are infected, $S_V(t)$be the proportion of susceptible vector populations and $I_V(t)$ be the proportion of infected vector populations. The dynamical system representing the epidemic spread in proposed population and vector population are then given by the following system of non-linear ordinary differential equations.

$$\frac{dS}{dt} = \mu - \mu S - \beta SI + \gamma I + \eta I_V S \tag{1.1}$$

$$\frac{dI}{dt} = \beta SI - \gamma I - \mu I - \delta S_V I \tag{1.2}$$

$$\frac{dS_V}{dt} = d - dS_V + \delta S_V I - \alpha S_V + fI_V \tag{1.3}$$

$$\frac{dI_V}{dt} = \alpha S_V - \eta I_V S - fI_V - dI_V \tag{1.4}$$

With initial conditions,

S(0)=S_0> 0, I(0) = I_0> 0, $S_V(0) = S_{V0} > 0, I_V(0) = I_{V0} > 0,$ (2)

S(0) +I(0) ≤ 1, $S_V(0) + I_V(0) \leq 1$

where,

β = Contact rate of susceptible individuals and infected population.

γ = Rate at which recovered population becomes susceptible.

μ = Rate of birth and death

δ =Contact rate between vector and infected population

η = Rate of contact of susceptible individuals and infected vector

α = Rate of transfer from susceptible and infected vector

f = Rate of transfer from infected vector to susceptible vector

d = Rate of death

3. THE BASIC REPRODUCTION NUMBER

Define the functions F(I, I_V, S, S_V) and V(I, I_V, S, S_V) be two vector functions of new infections and the rate leaving or entering the infection classes.

where,

$$F(X, Y)_{(0,\,0,\,1,\,\frac{d}{\alpha+d})} = \begin{bmatrix} \beta - \frac{\delta d}{\alpha+d} & 0 \\ 0 & -\eta \end{bmatrix}$$

$$V(X,Y)_{(0,0,\overline{S},\overline{S_V})} = \begin{bmatrix} \gamma+\mu & 0 \\ 0 & d+f \end{bmatrix}$$

Thus the basic reproduction number is

$$\boldsymbol{R_0} = \frac{\boldsymbol{\alpha\beta + d(\beta-\delta)}}{\boldsymbol{(\alpha+d)(\gamma+\mu)}}, \text{ provided } \beta>\delta \tag{3}$$

4. EQUILIBRIUM POINTS OF THE MODEL

The two equilibrium points are as follows:

The equilibrium points E_0 and E_1 of the system of Eqs. (1.1-1.4) is obtained by putting $\frac{dS}{dt} = 0, \frac{dI}{dt} = 0, \frac{dS_V}{dt} = 0, \frac{dI_V}{dt} = 0$

(i)The disease free equilibrium point E_0 ($\overline{S}, \overline{I}, \overline{S}_v, \overline{I}_v$), where

$\bar{S} = 1, \overline{S_V} = \frac{d}{\alpha+d}, \bar{I} = \overline{I_V} = 0$

(ii)The Endemic Equilibrium point E_1 (S^*, I^*, S_V^*, I_V^*), where

$$S^* = \frac{\mu + \gamma I^*}{\mu + \beta I^* - \eta I_V^*}$$

$$I^* = \frac{d+\alpha}{\delta} - \frac{d}{\beta S^* - \gamma - \mu} - \frac{f\alpha}{\delta(\eta S^* + d + f)}$$

$$S_V^* = \frac{\beta S^* - \gamma - \mu}{\delta}$$

$$I_V^* = \frac{\alpha(\beta S^* - \gamma - \mu)}{\delta(\eta S^* + d + f)}$$

Provided, $\beta S^* > \gamma + \mu, \mu + \beta I^* > \eta I_V^*$

5. STABILITY ANALYSIS OF THE MODEL

The Jacobian of the model is:

$$J = \begin{bmatrix} -\mu - \beta I + \eta I_V & -\beta S + \gamma & 0 & \eta S \\ \beta I & \beta S - \gamma - \mu - \delta S_V & -\delta I & 0 \\ 0 & \delta S_V & -d + \delta I - \alpha & f \\ -\eta I_V & 0 & \alpha & -\eta S - f - d \end{bmatrix}$$

5.1. Stability Analysis of Disease Free Equilibrium Point E_0

The Jacobian of the model at E_0 is:

$$J_0 = \begin{bmatrix} -\mu & -\beta+\gamma & 0 & \eta \\ 0 & \beta-\gamma-\mu-\dfrac{\delta d}{\alpha+d} & 0 & 0 \\ 0 & \dfrac{\delta d}{\alpha+d} & -d-\alpha & f \\ 0 & 0 & \alpha & -\eta-f-d \end{bmatrix}$$

The characteristic roots of J_0 are $-\mu, \beta-\gamma-\mu-\frac{\delta d}{\alpha+d}$, and other two have to solve by quadratic equation.

One characteristic root of $J_0$is $-\mu$ which is negative and another characteristic root is $\beta-\gamma-\mu-\frac{\delta d}{\alpha+d}$ is negative if $\beta<\gamma+\mu+\frac{\delta d}{\alpha+d}$ and positive if $\beta>\gamma+\mu+\frac{\delta d}{\alpha+d}$.

Remaining two characteristic roots are obtained by solving following quadratic equation.

$\lambda^2+a_1\lambda+a_2=0$

where,

$a_1 = 2\alpha+\eta+d+f>0$

$a_2 = df+(d+\alpha)(\eta+d)>0$

Therefore, by Hurwitz's theorem both the roots of the equations are negative.

Thus, $\beta<\gamma+\mu+\frac{\delta d}{\alpha+d}$

or, $\beta(\alpha+d)<(\alpha+d)(\gamma+\mu)+\delta d$

or, $\alpha\beta+d(\beta-\delta)<(\alpha+d)(\gamma+\mu)$

or, $\frac{\alpha\beta+d(\beta-\delta)}{(\alpha+d)(\gamma+\mu)}<1$

which is the reproduction number $\boldsymbol{R_0}< 1$.

Therefore, roots of the equation are either negative or have negative real parts only when $\boldsymbol{R_0}< 1$ and has exactly one positive root if $\boldsymbol{R_0}> 1$.

Hence, disease free equilibrium point E_0 is locally asymptotically stable if $\boldsymbol{R_0}< 1$ otherwise unstable if $\boldsymbol{R_0}> 1$.

5.2.Stability Analysis of Endemic Equilibrium Point E_1

The Jacobin of the model at E_1 is

$$J_1 = \begin{bmatrix} -\mu-\beta\left(\dfrac{d+\alpha}{\delta}-\dfrac{d}{A}-\dfrac{f\alpha}{B}\right)+\dfrac{\alpha\eta A}{B} & -\beta S^*+\gamma & 0 & \eta S^* \\ \beta\left(\dfrac{d+\alpha}{\delta}-\dfrac{d}{A}-\dfrac{f\alpha}{B}\right) & 0 & -\delta\left(\dfrac{d+\alpha}{\delta}-\dfrac{d}{A}-\dfrac{f\alpha}{B}\right) & 0 \\ 0 & A & -\dfrac{\delta d}{A}-\dfrac{\delta\alpha f}{B} & f \\ \dfrac{-\alpha\eta A}{B} & 0 & \alpha & -\dfrac{B}{\delta} \end{bmatrix}$$

where,

$A =(\beta S^*-\gamma-\mu)$and

$B = \delta(\eta S^*+d+f)$

The Characteristic equation of the matrix$J_1$is

$$\begin{vmatrix} [-\mu-\beta\left(\frac{d+\alpha}{\delta}-\frac{d}{A}-\frac{f\alpha}{B}\right)+\frac{\alpha\eta A}{B}]-\lambda & -\beta S^*+\gamma & 0 & \eta S^* \\ \beta\left(\frac{d+\alpha}{\delta}-\frac{d}{A}-\frac{f\alpha}{B}\right) & -\lambda & -\delta\left(\frac{d+\alpha}{\delta}-\frac{d}{A}-\frac{f\alpha}{B}\right) & 0 \\ 0 & A & [-\frac{\delta d}{A}-\frac{\delta\alpha f}{B}]-\lambda & f \\ \frac{-\alpha\eta A}{B} & 0 & \alpha & -\frac{B}{\delta}-\lambda \end{vmatrix} = 0$$

The characteristic roots are obtained by solving the following equation.

$$L(\lambda) = \lambda^4 + a_1\lambda^3 + a_2\lambda^2 + a_3\lambda^1 + a_4 = 0 \qquad (4)$$

where,

$$a_1 = \mu + \frac{\beta(\alpha+d)}{\delta} + \frac{d(\beta+\delta)}{A} + \frac{\alpha(\beta f+\delta f-\eta A)}{B}$$

$$\begin{aligned} a_2 = 2\alpha f - \beta d - d &+ \frac{\mu B + \alpha(\beta f-\eta A) + \beta(\alpha+d)A - \beta^2(\alpha+d)S^*}{\delta} + \frac{(\alpha+d)A}{\delta} \\ &+ \frac{dB}{A} + \frac{\mu\delta d}{A} + \frac{\beta d(\alpha+d)}{A} + \frac{\beta^2 dS^*}{A} + \frac{\beta\delta d^2}{A} + \frac{\alpha\delta\mu f}{B} + \frac{\alpha\beta\delta f(\alpha+d)}{B} \\ &+ \frac{\alpha\beta^2 fS^*}{B} + \frac{\alpha\eta^2 S^* A}{B} - \frac{\alpha d\eta}{B} - \frac{\alpha\beta fA}{B} - \frac{\alpha fA}{B} + \frac{\beta dB}{\delta A} + \frac{\beta(\alpha+d)B}{\delta^2} \\ &+ \frac{\alpha^2\beta\delta f^2}{B^2} - \frac{\alpha^2\delta f\eta A}{B^2} + \frac{2\alpha\beta\delta df}{AB} \end{aligned}$$

$$\begin{aligned} a_3 = 2\alpha\mu f + \beta d(\alpha+d) - \alpha\eta d - \mu d &+ \frac{(2\alpha\beta f + A + \beta d)(\alpha+d)}{\delta} + \frac{\alpha\beta^2 fS^*}{\delta} - \frac{dB}{\delta} \\ &- \frac{\alpha fA}{\delta} - \frac{\beta dB}{\delta} - \frac{\alpha\beta fA}{\delta} + \frac{\mu dB}{A} + \frac{\beta(\alpha+d)dB}{A} + \frac{2\alpha\beta df}{A} \\ &- \frac{(\beta+\beta\delta)d^2}{A} - \frac{\beta^2 d(\alpha+d)S^*}{A} + \frac{2\alpha^2\beta f^2}{B} + \frac{\alpha\eta dA}{B} + \frac{\alpha\beta f(\alpha+d)}{B} \\ &+ \frac{\alpha\delta d\eta^2 S^*}{B} + \frac{\alpha^2\delta f\eta^2 S^* A}{B} - \frac{2\alpha\beta fd}{B} - \frac{\alpha\beta fA}{B} - \frac{2\alpha\beta\delta df}{B} \\ &- \frac{\alpha\beta^2 f(\alpha+d)S^*}{B} + \frac{\beta^2 dS^* B}{\delta A} - \frac{\beta d(\alpha+\delta)}{\delta A} \\ &+ \frac{(\alpha+d)(\alpha\beta fA + \alpha\eta A^2)}{\delta B} + \frac{\beta(\alpha+\delta)(\alpha+d)}{\delta^2} + \frac{\beta(\alpha+d)AB}{\delta^2} \\ &- \frac{\beta^2(\alpha+d)S^* A}{\delta^2} + \frac{\beta d^2 B}{A^2} + \frac{\beta^2\delta d^2 S^*}{A^2} + \frac{\alpha^2\eta fA^2}{B^2} + \frac{\alpha^2\beta^2\delta f^2 S^*}{B^2} \\ &- \frac{\alpha^2\beta f^2 A}{B^2} - \frac{\alpha^2\beta\delta f^2 A}{B^2} + \frac{\alpha\beta dfB}{AB} + \frac{2\alpha\beta^2\delta dfS^*}{AB} \end{aligned}$$

$$\begin{aligned} a_4 = {} & \frac{\alpha\eta d A}{\delta} + \frac{\beta d(\alpha+d)B}{\delta} + \frac{\alpha\beta f(\alpha+d)A}{\delta} - \frac{\mu d B}{\delta} - \frac{\mu\alpha f A}{\delta} - \frac{2\alpha\beta d f}{\delta} \\ & - \frac{\alpha\beta^2 f(\alpha+d)S^*}{\delta} + \frac{\alpha\beta^2 d f S^*}{A} - \frac{\beta d^2 B}{A} + \frac{\alpha\delta\gamma\eta d}{B} + \frac{\alpha^2\beta^2 f^2 S^*}{B} \\ & + \frac{\alpha\delta d\eta^2 A}{B} + \frac{\alpha\beta\eta f(\alpha+d)AS^*}{B} + \frac{\alpha^2\delta\eta^2 f A^2}{B} - \frac{\alpha^2\beta f^2 A}{B} \\ & - \frac{\alpha\gamma\eta f(\alpha+d)A}{B} - \frac{\alpha\beta\delta\eta d S^*}{B} - \frac{\alpha^2\beta\delta\eta f A S^*}{B} - \frac{\alpha\eta^2(\alpha+d)S^*}{B} \\ & + \frac{\mu(\alpha+d)AB}{\delta^2} + \frac{\beta d(\alpha+d)B}{\delta^2} + \frac{\alpha\beta f(\alpha+d)A}{\delta^2} - \frac{\beta d(\alpha+\delta)B}{\delta^2} \\ & - \frac{\alpha\beta f(\alpha+\delta)A}{\delta^2} + \frac{\beta(\alpha+d)(\alpha+\delta)AB}{\delta^3} + \frac{\alpha^2\delta\gamma\eta f A}{B^2} - \frac{\beta d^2 B}{\delta A} \\ & + \frac{\alpha^2\eta f A^2}{\delta B} - \frac{\alpha^2\beta f^2 A}{\delta B} - \frac{\alpha\eta(\alpha+d)A^2 B}{\delta^2 B} \end{aligned}$$

6. NUMERICAL SIMULATION

The following table supports the analytical results as depicted below

Parameters	**EEP***	**Coefficients of L(λ)**	$\boldsymbol{a_1 a_2 a_3 - a_3^2 - a_1^2 a_4} > 0$	**Eigenvalues**
$\mu = 0.1$	$S^* = 1.3364$	$a_1 = 6.7553$		-3.3603 + 1.0895i
$\alpha = 0.88$	$I^* = 0.6585$	$a_2 = 12.9031$		-3.3603-1.0895i
$\beta = 0.9$	$S_V^* = 0.4505$	$a_3 = 1.7181$	37.9908	-0.0174 + 0.4368i
$\gamma = 0.9$	$I_V^* = 0.2179$	$a_4 = 2.3845$		-0.0174-0.4368i
$\delta = 0.45$				
$\eta = 0.8$				
$d = 0.3$				
$f = 0.45$				

*EEP = Endemic Equilibrium point

Therefore, by using results of numerical simulation, it is shows that $a_1 > 0$, $a_2 > 0, a_3 > 0, a_4 > 0$ and$a_1 a_2 a_3 - a_3^2 - a_1^2 a_4 > 0$

Thus by the Hurwitz criterion all the roots of Eq. (4) are negative and the endemic equilibrium point is asymptotically stable.

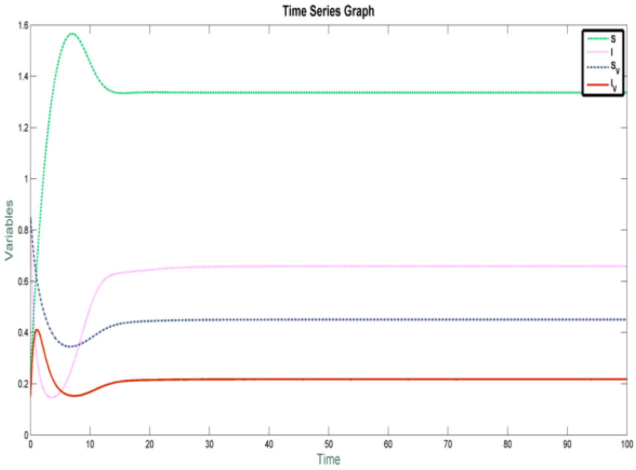

Fig 2: The time series graph shows the relation between time and four compartments susceptible populations, infected populations, susceptible vector and infected vector

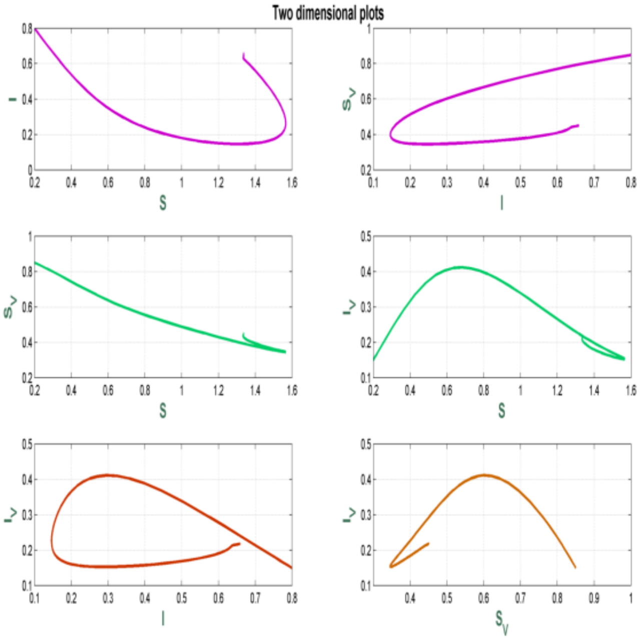

Fig 3: Two dimensional phase plan graph

7. CONCLUSION

In this paper a mathematical model has been proposed and analyzed to study the transmission dynamics of communicable disease. The basic reproduction number $\boldsymbol{R_0}$ has been obtained, the dynamic behavior of the model is determined by the basic reproduction number and it has been observed that disease-free equilibrium E_0 is locally asymptotically stable if $\boldsymbol{R_0} < 1$ and unstable if $\boldsymbol{R_0} > 1$. The endemic equilibrium E_1 exists and under certain condition, all the roots of the characteristic equation have negative real parts and hence according to the Hurwitz criterion, the point E_1 is asymptotically stable.

Thus it is concluded from theoretical results that the spread of disease controlled when the basic reproduction number $\boldsymbol{R_0}$ less than one. This and some other related issues need to be studied further in the near future. Finally with the help numerical simulations above analytical results are shown graphically in the Figure 2 and Figure 3.

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