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MODELING AND ANALYSIS OF A VECTOR-HOST EPIDEMIC MODEL WITH SATURATED INCIDENCE RATE UNDER TREATMENT

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ABSTRACT

Global stability of an epidemic model for vector-borne disease was studied by Yang et al. [7]. A reinvestigation of the model with a saturated incidence rate and a treatment function proportionate to infectious population *I* is presented to understand the effect of the capacity for treatment. An equivalent system is obtained, which has two equilibriums: a disease-free equilibrium and an endemic equilibrium. The stability of these two equilibriums can be controlled by the basic reproduction number $\Re_0$. The global stability of the disease-free equilibrium state is established by Lyapunov method and a geometric approach is used for the global stability of the endemic equilibrium state. The model has a globally asymptotically stable disease-free solution whenever the basic reproduction number $\Re_0$ is less than or equal unity and has a unique positive globally asymptotically stable endemic equilibrium whenever $\Re_0$ exceeds unity. Numerical examples are given for the model with different values of the parameters. Graphical presentations are also provided. The details are supplemented by numerical results given in annexure.

KEYWORDS: Epidemic Model, Vector-Borne Disease, Saturated Incidence, Equilibrium Point, Stability, Reproduction Number, Treatment Function

AMS Subject Classification: 92D25, 92D30.

1. INTRODUCTION

The main purpose of this paper is to study the dynamics of Vector-borne disease and understand the effect of the capacity for treatment. Vector-borne diseases are infectious diseases caused by viruses, bacteria, protozoa or rickettsia which are primarily transmitted by disease transmitting biological agents (anthropoids), called vectors, who carry the disease without getting it themselves. Globally, malaria is the most prevalent vector-borne disease whose vectors are the mosquitoes. The mosquitoes are vectors of a number of infectious diseases most prominent among which are dengue (the second most important vector-borne disease), yellow fever, St Louis Encephalitis, Japanese Encephalitic, and West Nile Fever, caused by the West Nile Virus. The literature dealing with the mathematical theory and dynamics of vector-borne diseases are quite extensive. Many mathematical models concerning the emergence and reemergence of the vector-host infectious disease have been proposed and analyzed in the literature [9, 10]. The mathematical models of epidemiology for the West Nile virus and for dengue have been investigated in [1, 3] and [10, 11].

Mathematical modeling became considerable important tool in the study of epidemiology because it helped us

to understand the observed epidemiological patterns, disease control and provide understanding of the underlying mechanisms which influence the spread of disease and may suggest control strategies. The model formulation and its simulation with parameter estimation allow us to test for sensitivity and comparison of conjunctures. Treatment plays an important role to control or decrease the spread of diseases. Kar et al. [16,17] and Ujjainkar et al. [4] proposed an epidemic model with treatment function. Wei et al. [6] investigated an epidemic model of a vector-borne disease with direct transmission and the vector-mediated transmission. The global stability of an epidemic model for vector-borne disease was studied by Yang et al. [7]. Here we have reanalyzed the model [7] with saturated incidence and a treatment function proportionate to infectious population *I*. The only mode of transmission in this model is through the vector.

The paper is organized as follows: In Section 2, a vector-host epidemic model with vector transmissions is presented, where the dynamics of the hosts and vectors are described by *SIR* and *SI* model, respectively. Equilibrium points and reproduction number are obtained in Section 3. The analysis of stability of the equilibrium of the model is investigated in Section 4 and Section 5. Numerical analysis and conclusion are given in Section 6 and Section 7.

2. THE MATHEMATICAL MODEL

In this section, a vector-host epidemic model with vector transmissions is presented and investigated, where the dynamics of the human hosts and vectors are described by *SIR* and *SI* model, respectively. The total host population $N_1(t)$ is partitioned into three distinct epidemiological subclasses which are susceptible, infectious and recovered, with sizes denoted by $S(t)$, $I(t)$ and $R(t)$, respectively, and the total vector population $N_2(t)$ is divided into susceptible and infectious, with the sizes denoted by $M(t)$ and $V(t)$, respectively.

The dynamics of this infectious disease in the host and vector populations are described by the following system of nonlinear differential equations:

$$\begin{aligned}
\frac{dS}{dt} &= b_1 - \frac{\lambda_1 SV}{(1+\alpha_1 V)} - \mu_1 S, \\
\frac{dI}{dt} &= \frac{\lambda_1 SV}{(1+\alpha_1 V)} - \gamma I - \mu_1 I - rI, \\
\frac{dR}{dt} &= \gamma I - \mu_1 R + rI, \\
\frac{dM}{dt} &= b_2 - \lambda_2 MI - \mu_2 M, \\
\frac{dV}{dt} &= \lambda_2 MI - \mu_2 V.
\end{aligned} \tag{2.1}$$

With the initial Conditions $S(0) = S_0$, $I(0) = I_0$, $R(0) = R_0$, $M(0) = M_0$ and $V(0) = V_0$.

The parameters in the model stand for

b_1 = Recruitment rate constant in the host population

b_2 = Recruitment rate constant in the vector population

μ_1 = Death rate constant in the host population

μ_2 = Death rate constant in the vector population

γ = Recovery rate constant in the host population

λ_1 = Transmission rate from infected vector population to susceptible host population

λ_2 = Transmission rate from infected host population to susceptible vector population

α_1 =Constant parameter

r = Treatment rate constant in the host population.

It is assumed that all parameters are positive. The total dynamics of host population can be determined from the differential equation $dN_1/dt = b_1 - \mu_1 N_1$ which is derived by adding first three equations of system (2.1). The total dynamics of vector population can be determined from the differential equation $dN_2/dt = b_2 - \mu_2 N_2$ which is derived by adding last two equations of system (2.1). It is easily seen that both for the host population and for the vector population the corresponding total population sizes are asymptotically constant: $\lim_{t\to\infty} N_1 = b_1/\mu_1$ and $\lim_{t\to\infty} N_2 = b_2/\mu_2$. This implies that in our model we can assume without loss of generality that $N_1 = b_1/\mu_1$, $N_2 = b_2/\mu_2$ for all t ≥ 0 provided that $S(0)+I(0)+R(0) = b_1/\mu_1$, $M(0)+V(0) = b_2/\mu_2$.

Therefore, we attact system (2.1) by studying the subsystem given by

$$\begin{aligned}
\frac{dS}{dt} &= b_1 - \frac{\lambda_1 SV}{(1+\alpha_1 V)} - \mu_1 S,\\
\frac{dI}{dt} &= \frac{\lambda_1 SV}{(1+\alpha_1 V)} - \gamma I - \mu_1 I - rI,\\
\frac{dV}{dt} &= \lambda_2\left(\frac{b_2}{\mu_2} - V\right) I - \mu_2 V.
\end{aligned} \tag{2.2}$$

From biological considerations, we study the system (2.2) in the closed set

$$\Gamma = \{(S, I, V) \in R_+^3 : 0 \le S + I \le b_1/\mu_1, 0 \le V \le b_2/\mu_2, S \ge 0, I \ge 0\},$$

Where R_+^3 denotes the nonnegative cone of R^3 including its lower dimensional faces. Obviously Γ is positively invariant set of (2.2).We denote by $\partial\Gamma$ and Γ^0 the boundary and the interior of Γ in R^3, respectively.

3. MATHEMATICAL ANALYSIS OF THE MODEL

Equilibrium points of model (2.2) can be obtained by equating right hand side to zero. The system (2.2) has two

equilibrium states: the disease-free equilibrium $E_0 = (\frac{b_1}{\mu_1}, 0, 0) \in \partial\Gamma$ and a unique endemic equilibrium $E^* = (S^*, I^*, V^*) \in \Gamma^0$ with

$$S^* = \frac{(\gamma + \mu_1 + r)(1 + \alpha_1 V^*) I^*}{\lambda_1 V^*}, \tag{3.1}$$

$$I^* = \frac{\lambda_1\lambda_2 b_1 b_2 - \mu_1\mu_2^2(\gamma + \mu_1 + r)}{\lambda_2(\gamma + \mu_1 + r)[\lambda_1 b_2 + \mu_1(\mu_2 + \alpha_1 b_2)]}, \tag{3.2}$$

$$V^* = \frac{\lambda_2 b_2 I^*}{\mu_2(\mu_2 + \lambda_2 I^*)}. \tag{3.3}$$

The dynamics of the disease are described by the basic reproduction number $\Re_0$ .The threshold quantity $\Re_0$ is called the reproduction number, which is defined as the average number of secondary infections produced by an infected individual in a completely susceptible population. The basic reproduction number of model (2.2) is given by the expression

$$\Re_0 = \frac{\lambda_1\lambda_2 b_1 b_2}{\mu_1\mu_2^2(\gamma + \mu_1 + r)}. \tag{3.4}$$

For $\Re_0 \le 1$, the only equilibrium is disease-free equilibrium E_0 in $\partial\Gamma$ and for $\Re_0 > 1$, there is a unique endemic equilibrium E^* in Γ^0 .

4. STABILITY OF THE DISEASE-FREE EQUILIBRIUM

In this section we discuss the stability of the disease-free equilibrium E_0 .

Theorem 4.1: *The disease-free equilibrium E_0 of* (2.2) *is locally asymptotically stable in* Γ *if* $\Re_0 < 1$*; it is unstable if* $\Re_0 > 1$.

Proof: To discuss the stability of the system (2.2) the variational matrix is

$$J = \begin{pmatrix} -\left(\frac{\lambda_1 V}{1 + \alpha_1 V} + \mu_1\right) & 0 & -\frac{\lambda_1 S}{(1 + \alpha_1 V)^2} \\ \frac{\lambda_1 V}{1 + \alpha_1 V} & -(\gamma + \mu_1 + r) & \frac{\lambda_1 S}{(1 + \alpha_1 V)^2} \\ 0 & \lambda_2\left(\frac{b_2}{\mu_2} - V\right) & -(\lambda_2 I + \mu_2) \end{pmatrix}.$$

At the equilibrium point $E_0 = (\frac{b_1}{\mu_1}, 0, 0)$, the variational matrix becomes

$$J(E_0)=\begin{pmatrix} -\mu_1 & 0 & -\frac{\lambda_1 b_1}{\mu_1} \\ 0 & -(\gamma+\mu_1+r) & \frac{\lambda_1 b_1}{\mu_1} \\ 0 & \frac{\lambda_2 b_2}{\mu_2} & -\mu_2 \end{pmatrix}$$

Its characteristic equation is

$$(\lambda+\mu_1)[\lambda^2+(\gamma+\mu_1+r+\mu_2)\lambda+\mu_2(\gamma+\mu_1+r)-\frac{\lambda_1\lambda_2 b_1 b_2}{\mu_1\mu_2}]=0$$

$$\Rightarrow(\lambda+\mu_1)[\lambda^2+(\gamma+\mu_1+r+\mu_2)\lambda+\mu_2(\gamma+\mu_1+r)(1-\Re_0)]=0 \tag{4.1}$$

By Descartes rule of sign all roots of equation (4.1) are negative if $\Re_0<1$ .Thus, if $\Re_0<1$ then the disease-free equilibrium E_0 is locally asymptotically stable; Otherwise, if $\Re_0>1$ then it is unstable.

Theorem 4.2: *If* $\Re_0\le 1$, *then the disease - free equilibrium* E_0 *is globally asymptotically stable in* Γ.

Proof: To establish the global stability of the disease-free equilibrium, we construct the following Lyapunov function:

$$L=\mu_1\mu_2 I+\lambda_1 b_1 V.$$

Clearly, $L\ge 0$ along the solutions of the system (2.2) and is zero if and only if both I and V are zero. Calculating the time derivative of *L* along the solutions of system (2.2), we obtain

$$\begin{aligned}
\dot{L} &= \mu_1\mu_2\dot{I}+\lambda_1 b_1\dot{V} \\
&= \mu_1\mu_2\left[\frac{\lambda_1 SV}{(1+\alpha_1 V)}-(\gamma+\mu_1+r)I\right]+\lambda_1 b_1\left[\lambda_2\left(\frac{b_2}{\mu_2}-V\right)I-\mu_2 V\right] \\
&\le \mu_1\mu_2\lambda_1\frac{b_1}{\mu_1}V-\left[\mu_1\mu_2(\gamma+\mu_1+r)-\frac{\lambda_1\lambda_2 b_1 b_2}{\mu_2}\right]I-\lambda_1\lambda_2 b_1 VI-\lambda_1 b_1\mu_2 V \\
&= -I\left[\mu_1\mu_2(\gamma+\mu_1+r)(1-\Re_0)+\lambda_1\lambda_2 b_1 V\right] \\
&\le 0,
\end{aligned}$$

Where in the first inequality we have used the fact that $\frac{1}{(1+\alpha_1 V)}\le 1$ and $S\le\frac{b_1}{\mu_1}$ in Γ. In addition, the last inequality follows from the assumption that $\Re_0\le 1$. Thus $\dot{L}(t)$ is negative if $\Re_0\le 1$.When $\Re_0<1$, the derivative $\dot{L}$ = 0 if and only if I = 0, while in the case $\Re_0=1$ the derivative $\dot{L}$ = 0 if and only if I = 0 or V = 0. Consequently, the

largest compact invariant set in $\{(S, I, V) \in \Gamma: \dot{L} = 0\}$ when $\Re_0 \leq 1$, is the singleton $\{E_0\}$. Hence, LaSalle's invariance principle [8] implies that E_0 is globally asymptotically stable in Γ. This completes the proof.

STABILITY OF THE ENDEMIC EQUILIBRIUM

In this section we discuss the stability of the endemic equilibrium E^* .

Theorem 5.1: *If* $\Re_0 > 1$, *then the endemic equilibrium* E^* *of* (2.2) *is locally asymptotically stable in* Γ^0.

Proof: At the equilibrium point E^*, the variational matrix becomes

$$J(E^*) = \begin{pmatrix} -\left(\frac{\lambda_1 V^*}{1+\alpha_1 V^*} + \mu_1\right) & 0 & -\frac{\lambda_1 S^*}{\left(1+\alpha_1 V^*\right)^2} \\ \frac{\lambda_1 V^*}{1+\alpha_1 V^*} & -(\gamma+\mu_1+r) & \frac{\lambda_1 S^*}{\left(1+\alpha_1 V^*\right)^2} \\ 0 & \lambda_2\left(\frac{b_2}{\mu_2} - V^*\right) & -\left(\lambda_2 I^* + \mu_2\right) \end{pmatrix}$$

Its characteristic equation is

$$\lambda^3 + a_1\lambda^2 + a_2\lambda + a_3 = 0, \tag{5.1}$$

Where

$$a_1 = \frac{\lambda_1 V^*}{1+\alpha_1 V^*} + 2\mu_1 + \gamma + r + \mu_2 + \lambda_2 I^* \geq 0,$$

$$\begin{aligned} a_2 &= \left[\frac{\lambda_1 V^*}{1+\alpha_1 V^*} + \mu_1\right](\gamma+\mu_1+r) + \left[\frac{\lambda_1 V^*}{1+\alpha_1 V^*} + 2\mu_1 + \gamma + r\right](\mu_2 + \lambda_2 I^*) \\ &\quad - \frac{\lambda_1\lambda_2 S^*}{\left(1+\alpha_1 V^*\right)^2}\left(\frac{b_2}{\mu_2} - V^*\right) \\ &\geq \left[\frac{\lambda_1 V^*}{1+\alpha_1 V^*} + 2\mu_1 + \gamma + r\right]\lambda_2 I^* + \left[\frac{\lambda_1 V^*}{1+\alpha_1 V^*} + \mu_1\right](\gamma+\mu_1+\mu_2+r) \\ &\quad + \mu_2(\gamma+\mu_1+r) - \frac{\lambda_1\lambda_2 S^*}{\left(1+\alpha_1 V^*\right)}\left(\frac{b_2}{\mu_2} - V^*\right) \\ &= \left[\frac{\lambda_1 V^*}{1+\alpha_1 V^*} + 2\mu_1 + \gamma + r\right]\lambda_2 I^* + \left[\frac{\lambda_1 V^*}{1+\alpha_1 V^*} + \mu_1\right](\gamma+\mu_1+\mu_2+r) \qquad [\textit{from } (2.2)] \\ &\geq 0 \end{aligned}$$

$$
\begin{aligned}
a_3 &= \left[\frac{\lambda_1 V^*}{1+\alpha_1 V^*}+\mu_1\right](\gamma+\mu_1+r)(\mu_2+\lambda_2 I^*) \\
&\quad -\frac{\mu_1\lambda_1\lambda_2 S^*}{(1+\alpha_1 V^*)^2}\left(\frac{b_2}{\mu_2}-V^*\right) \\
&\geq (\gamma+\mu_1+r)\left[\frac{\lambda_1\lambda_2 V^* I^*}{(1+\alpha_1 V^*)}+\frac{\lambda_1\mu_2 V^*}{(1+\alpha_1 V^*)}+\mu_1\lambda_2 I^*\right] \\
&\quad +\mu_1\mu_2(\gamma+\mu_1+r)-\frac{\mu_1\lambda_1\lambda_2 S^*}{(1+\alpha_1 V^*)}\left(\frac{b_2}{\mu_2}-V^*\right) \\
&= (\gamma+\mu_1+r)\left[\frac{\lambda_1\lambda_2 V^* I^*}{(1+\alpha_1 V^*)}+\frac{\lambda_1\mu_2 V^*}{(1+\alpha_1 V^*)}+\mu_1\lambda_2 I^*\right] \qquad [\,from\ (2.2)] \\
&\geq 0
\end{aligned}
$$

It can be easily seen that $a_1, a_2, a_3 \geq 0$. By Descartes rule of sign all roots of equation (5.1) are negative. Thus, the endemic equilibrium E^* is locally asymptotically stable in Γ^0.

Now, we analyze the global behavior of the endemic equilibrium E^*. Here, we use the geometrical approach of Li and Muldowney [14] to investigate the global stability of the endemic equilibrium E^* in the feasible region Γ. We have omitted the detailed introduction of this approach and we refer the interested readers to see [14]. We summarize this approach below.

Let $x \mapsto f(x) \in R^n$ be a C^1 function for x in an open set $D \subset R^n$. Consider the differential equation

$$x' = f(x). \tag{5.2}$$

Denote by $x(t, x_0)$ the solution of (5.2) such that $x(0, x_0) = x_0$. We have following assumptions:

(H_1) D is simply connected;

(H_2) There exists a compact absorbing set $K \subset D$;

(H_3) Equation (5.2) has unique equilibrium $\bar{x}$ in D.

Let $P : x \mapsto P(x)$ be a nonsingular $\binom{n}{2} \times \binom{n}{2}$ matrix-valued function which is C^1 in D and a vector norm $|\cdot|$ on R^N, where $N = \binom{n}{2}$. Let μ be the Lozinskiĭ measure with respect to the $|\cdot|$.

Define a quantity $\overline{q_2}$ as

$$\overline{q_2} = \limsup_{t\to\infty} \sup_{x_o \to K} \frac{1}{t}\int_0^t \mu(B(x(s,x_0)))ds, \tag{5.3}$$

Where $B = P_f P^{-1} + PJ^{[2]}P^{-1}$, the matrix P_f is obtained by replacing each entry *p* of *P* by its derivative in the direction of *f*, $\left(p_{ij}\right)_f$, and $J^{[2]}$ is the second additive compound matrix of the Jacobian matrix *J* of (5.2). The following result has been established in Li and Muldowney [14].

Theorem 5.2: *Suppose that* (H_1), (H_2) *and* (H_3) *hold, the unique endemic equilibrium* E^* *is globally stable in* Γ^0 *if* $\overline{q_2} < 0$.

Obviously Γ^0 is simply connected and E^* is unique endemic equilibrium for $\Re_0 > 1$ in Γ^0. To apply the result of the above theorem for global stability of endemic equilibrium E^*, we first state and prove the following result.

Lemma 5.3: *If* $\Re_0 > 1$, *then the system* (2.2) *is uniformly persistent in* Γ^0.

System (2.2) is said to be uniformly persistent [2] if there exists a constant c > 0, independent of initial data in Γ^0, such that any solution (*S*(*t*), *I*(*t*), *V*(*t*)) of (2.2) satisfies

$$\liminf_{t\to\infty} S \geq c\,,\ \liminf_{t\to\infty} I \geq c\ ,\ \liminf_{t\to\infty} V \geq c$$

Provided $(S(0), I(0), V(0)) \in \Gamma^0$.

The uniform persistence of (2.2) can be proved by applying a uniform persistence result in [5, Theorem 4.3], and using a similar argument as in the proof of proposition 3.3 of [13]. The proof is omitted.

The boundedness of Γ^0 and the above lemma imply that (2.2) has a compact absorbing set $K \subset \Gamma^0$ [2]. Now we shall prove that the quantity $\overline{q_2} < 0$.

Let *x* = (S, I, V) and *f*(*x*) denote the vector field of (2.2). The Jacobian matrix *J* = $\dfrac{\partial f}{\partial x}$ associated with a general solution *x*(*t*) of (2.2) is

$$J = \begin{pmatrix} -\left(\dfrac{\lambda_1 V}{1+\alpha_1 V} + \mu_1\right) & 0 & -\dfrac{\lambda_1 S}{(1+\alpha_1 V)^2} \\ \dfrac{\lambda_1 V}{1+\alpha_1 V} & -(\gamma+\mu_1+r) & \dfrac{\lambda_1 S}{(1+\alpha_1 V)^2} \\ 0 & \lambda_2\left(\dfrac{b_2}{\mu_2} - V\right) & -(\lambda_2 I + \mu_2) \end{pmatrix},$$

and its second additive compound matrix $J^{[2]}$ is,

$$J^{[2]} = \begin{pmatrix} a_{11}+a_{22} & a_{23} & -a_{13} \\ a_{32} & a_{11}+a_{33} & a_{12} \\ -a_{31} & a_{21} & a_{22}+a_{33} \end{pmatrix},$$

$$J^{[2]} = \begin{pmatrix} -\left(\frac{\lambda_1 V}{1+\alpha_1 V}+2\mu_1+\gamma+r\right) & \frac{\lambda_1 S}{(1+\alpha_1 V)^2} & \frac{\lambda_1 S}{(1+\alpha_1 V)^2} \\ \lambda_2\left(\frac{b_2}{\mu_2}-V\right) & -(\frac{\lambda_1 V}{1+\alpha_1 V}+\mu_1+\lambda_2 I+\mu_2) & 0 \\ 0 & \frac{\lambda_1 V}{1+\alpha_1 V} & -(\gamma+\mu_1+r+\lambda_2 I+\mu_2) \end{pmatrix}.$$

Set the function $P(x) = P(S, I, V) = \text{diag}\left\{1, \frac{I}{V}, \frac{I}{V}\right\}$, then $P_f P^{-1} = diag\left\{0, \frac{I'}{I} - \frac{V'}{V}, \frac{I'}{I} - \frac{V'}{V}\right\}$. The matrix $B = P_f P^{-1} + PJ^{[2]}P^{-1}$ can be written in block form as

$$B = \begin{pmatrix} B_{11} & B_{12} \\ B_{21} & B_{22} \end{pmatrix},$$

With $B_{11} = -\left(\frac{\lambda_1 V}{1+\alpha_1 V}+2\mu_1+\gamma+r\right)$,

$$B_{12} = \left(\frac{\lambda_1 SV}{(1+\alpha_1 V)^2 I}, \frac{\lambda_1 SV}{(1+\alpha_1 V)^2 I}\right),$$

$$B_{21} = \begin{pmatrix} \frac{\lambda_2 I}{V}\left(\frac{b_2}{\mu_2}-V\right) \\ 0 \end{pmatrix},$$

$$B_{22} = \begin{pmatrix} \frac{I'}{I} - \frac{V'}{V} - \left(\frac{\lambda_1 V}{1+\alpha_1 V}+\mu_1+\lambda_2 I+\mu_2\right) & 0 \\ \frac{\lambda_1 V}{1+\alpha_1 V} & \frac{I'}{I} - \frac{V'}{V} - (\gamma+\mu_1+r+\lambda_2 I+\mu_2) \end{pmatrix}.$$

Consider the norm in R^3 as $|(u, v, w)| = \max(|u|, |v| + |w|)$ where (u, v, w) denotes the vector in R^3. Let μ denote the Lozinski˘*i* measure with respect to this norm. Using the method of estimating μ in [15], we have

$$\mu(B) \le \sup(g_1, g_2), \tag{5.4}$$

Where $g_1 = \mu_{10}(B_{11}) + |B_{12}|$, $g_2 = \mu_{10}(B_{22}) + |B_{21}|$.

$|B_{12}|$, $|B_{21}|$ are matrix norms with respect to the l_1 vector norm, and μ_{10} denotes the Lozinskiĭi measure with respect to the l_1 norm.

From system (2.2) we can write

$$\frac{I'}{I} = \frac{\lambda_1 SV}{(1+\alpha_1 V)\mathrm{I}} - (\gamma + \mu_1 + r), \tag{5.5}$$

$$\frac{V'}{V} = \lambda_2 \left(\frac{b_2}{\mu_2} - V \right) \frac{I}{V} - \mu_2, \tag{5.6}$$

Since B_{11} is a scalar, its Lozinskiĭı measure with respect to any vector norm in R^1 will be equal to B_{11}. Thus

$$\mu_{10}(B_{11}) = B_{11} = -\left(\frac{\lambda_1 V}{1+\alpha_1 V} + 2\mu_1 + \gamma + r \right).$$

Also $|B_{12}| = \dfrac{\lambda_1 SV}{(1+\alpha_1 V)^2 I}$.

On substituting the values of $\mu_{10}(B_{11})$ and $|B_{12}|$, g_1 will become

$$g_1 = -\left(\frac{\lambda_1 V}{1+\alpha_1 V} + 2\mu_1 + \gamma + r \right) + \frac{\lambda_1 SV}{(1+\alpha_1 V)^2 I}$$

$$\leq -\left(\frac{\lambda_1 V}{1+\alpha_1 V} + 2\mu_1 + \gamma + r \right) + \frac{\lambda_1 SV}{(1+\alpha_1 V) I}$$

$$= -\left(\frac{\lambda_1 V}{1+\alpha_1 V} + 2\mu_1 + \gamma + r \right) + \frac{I'}{I} + (\gamma + \mu_1 + r) \qquad \text{[From (5.5)]}$$

$$= \frac{I'}{I} - \left(\frac{\lambda_1 V}{1+\alpha_1 V} + \mu_1 \right)$$

$$\leq \frac{I'}{I} - \mu_1. \tag{5.7}$$

Now $|B_{21}| = \dfrac{\lambda_2 I}{V}\left(\dfrac{b_2}{\mu_2} - V \right)$. To calculate $\mu_{10}(B_{22})$, we add the absolute value of the off- diagonal elements to the diagonal one in each column of B_{22}, and then take the maximum of two sums, see [18], which leads to

$$\mu_{10}(B_{22}) = \sup\left\{ \frac{I'}{I} - \frac{V'}{V} - \left(\frac{\lambda_1 V}{1+\alpha_1 V} + \mu_1 + \lambda_2 I + \mu_2 \right) + \frac{\lambda_1 V}{1+\alpha_1 V}, \frac{I'}{I} - \frac{V'}{V} - (\gamma + \mu_1 + r + \lambda_2 I + \mu_2) \right\},$$

$$= \sup\left\{\frac{I^{'}}{I}-\frac{V^{'}}{V}-(\mu_1+\lambda_2 I+\mu_2), \frac{I^{'}}{I}-\frac{V^{'}}{V}-(\gamma+\mu_1+r+\lambda_2 I+\mu_2)\right\}$$

$$= \frac{I^{'}}{I}-\frac{V^{'}}{V}-(\mu_1+\lambda_2 I+\mu_2).$$

On substituting the values of $\mu_{10}(B_{22})$ and $|B_{21}|$, g_2 will becomes

$$g_2 = \frac{\lambda_2 I}{V}\left(\frac{b_2}{\mu_2}-V\right)+\frac{I^{'}}{I}-\frac{V^{'}}{V}-(\mu_1+\lambda_2 I+\mu_2)$$

$$= \frac{V^{'}}{V}+\mu_2+\frac{I^{'}}{I}-\frac{V^{'}}{V}-(\mu_1+\lambda_2 I+\mu_2) \qquad \text{[From (5.6)]}$$

$$= \frac{I^{'}}{I}-(\mu_1+\lambda_2 I)$$

$$\leq \frac{I^{'}}{I}-\mu_1. \qquad (5.8)$$

Using equations (5.7) and (5.8) in equation (5.4), we have

$$\mu(B) \leq \sup(g_1, g_2) \leq \frac{I^{'}}{I}-\mu_1. \qquad (5.9)$$

Along each solution $x(t, x_0)$ to (2.2) such that $x_0 \in K$, the absorbing set, we have

$$\frac{1}{t}\int_0^t \mu(B)dt \leq \frac{1}{t}\log\frac{I(t)}{I(0)}-\mu_1, \qquad (5.10)$$

Which further implies that

$$\overline{q_2} \leq \limsup_{t\to\infty} \sup_{x_o\to K} \frac{1}{t}\log\frac{I(t)}{I(0)}-\mu_1$$

$$= -\mu_1$$

$$< 0$$

i.e. $\overline{q_2}$ < 0. Therefore all the conditions of Theorem (5.2) are satisfied. Hence unique endemic equilibrium E^* is globally stable in Γ^0 .

NUMERICAL SIMULATIONS

In this section, we give numerical simulations supporting the theoretical findings. When we choose the values of

the parameters as: $b_1 = 200,\ b_2 = 300,\ \mu_1 = 0.5,\ \mu_2 = 0.6,\ \gamma = 0.4,\ \lambda_1 = 0.01,\ \lambda_2 = 0.02,\ \alpha_1 = 0.1,\ r = 0.4$ for the model then $E^*(S^* = 335.7049, I^* = 24.72888, V^* = 225.9217)$ exists and $\Re_0 = 51.28 > 1$. Our simulation shows endemic equilibrium E^* is asymptotically stable (see figure 1). To see the dependence of the steady state value I^* of the infective population on the parameter '*r*', we have plotted figure 2 for different values of '*r*', keeping all others parameter values same as for figure 1 and see that the infective population decreases as the parameter '*r*' increases. Further, we have also plotted figure 3, 4, 5 to see the dependence of steady state value of the susceptible and infective population on the parameter α_1, keeping all others parameter values same as for figure 1 and noted that the susceptible population increases and infective population decreases as α_1 increases. The details are supplemented by numerical results given in annexure.

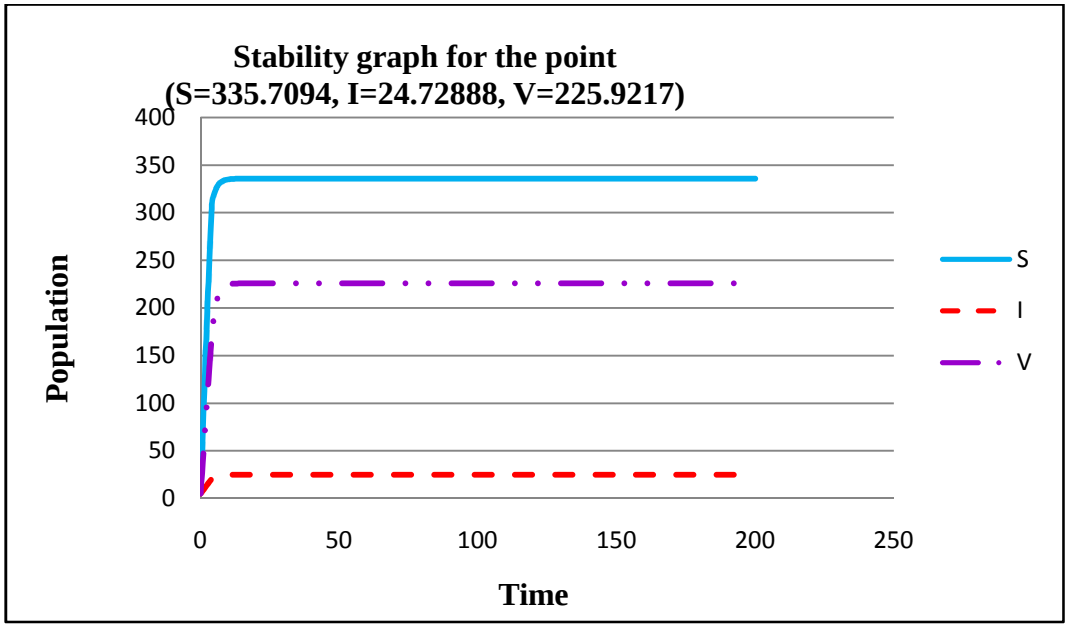

Figure 1

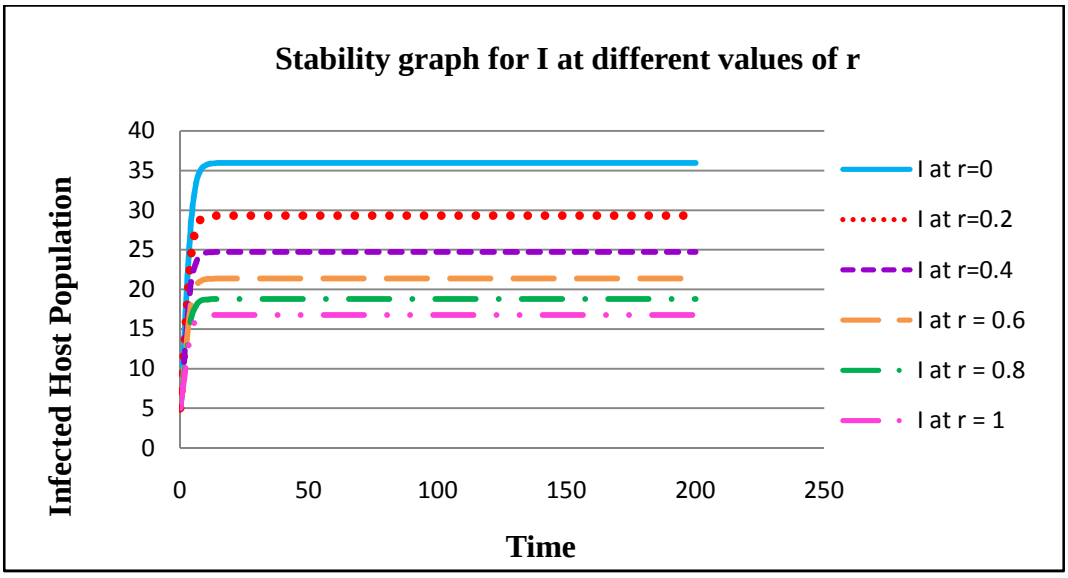

Figure 2

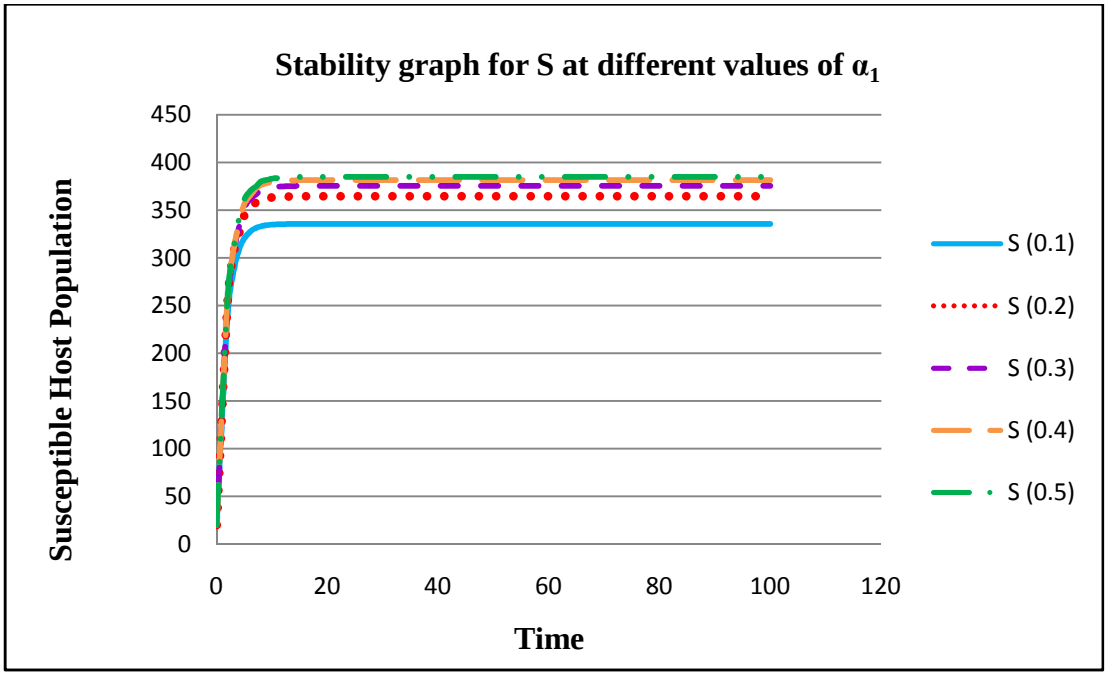

Figure 3

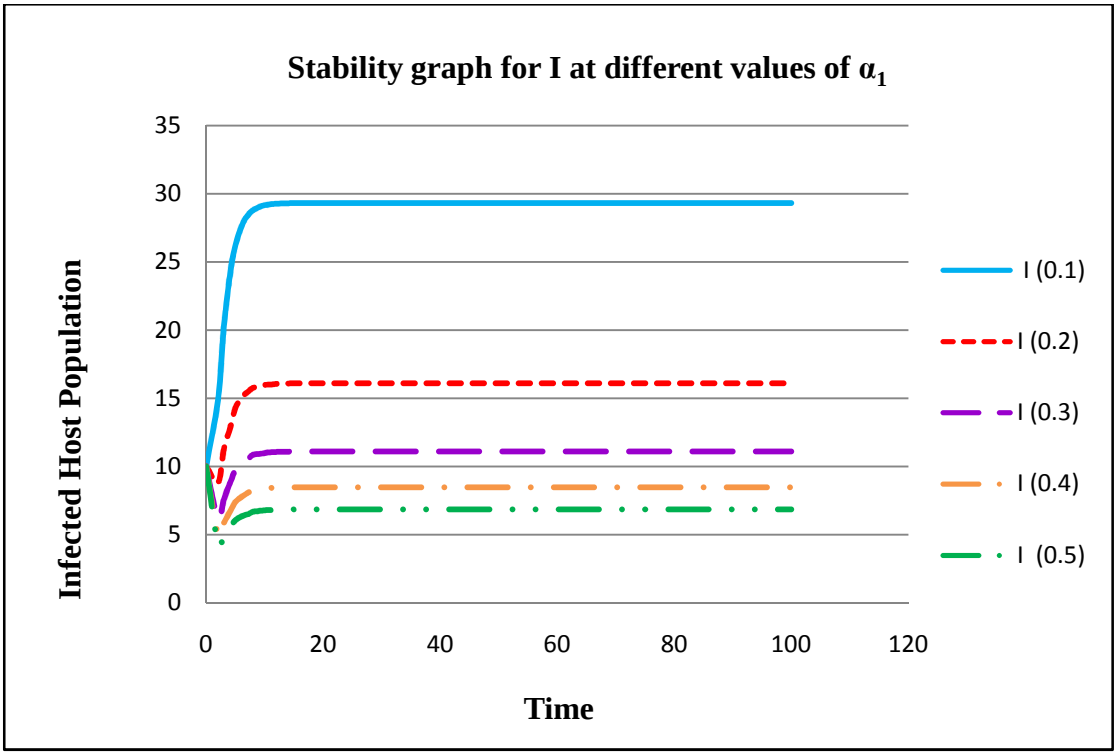

Figure 4

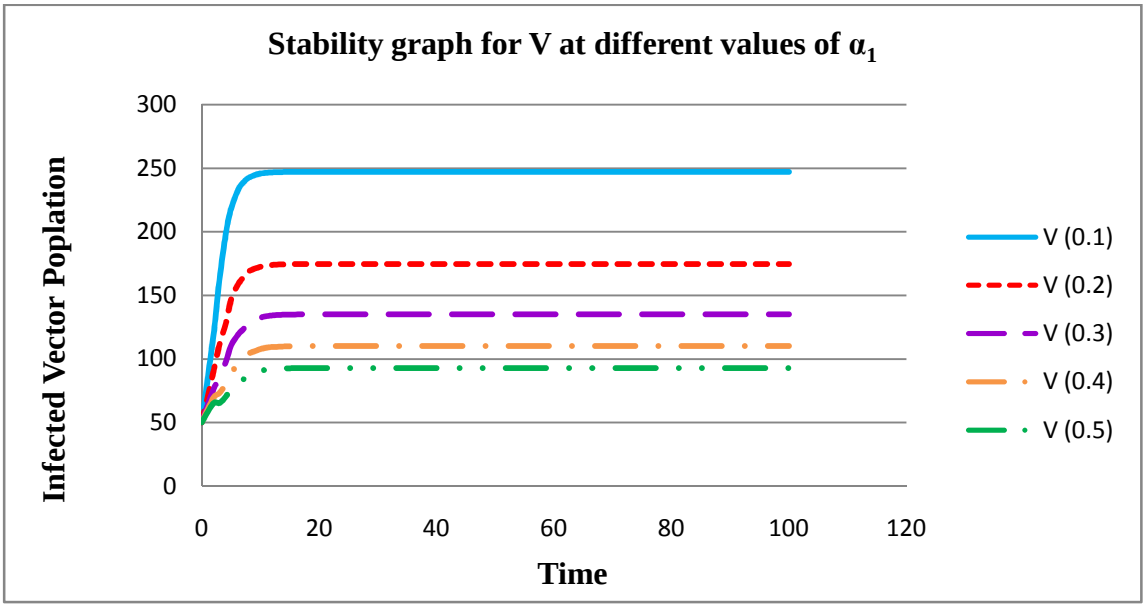

Figure 5

CONCLUSIONS

In this paper, we have studied a vector-host epidemic model with saturated incidence and a treatment function proportionate to infectious population *I*. The global stability of the disease-free equilibrium state is established by Lyapunov method and a geometric approach is used for the global stability of the endemic equilibrium state. The basic reproduction number is obtained and it completely determines the dynamics of the ODE model. The model has a globally asymptotically stable disease-free solution whenever the basic reproduction number $\Re_0$ is less than or equal unity and has a unique positive globally asymptotically stable endemic equilibrium whenever $\Re_0$ exceeds unity. However, it is clear that when the disease is endemic, the steady state value I^* of the infective individuals decreases as the treatment function and α_1 increases, and I^* approaches zero as the treatment function and α_1 tends to infinity. Thus, it will be of great importance for public health management to maintain the treatment and saturation effects. In the absence of the treatment function and with $\alpha_1 = 0$, the result is perfectly in agreement with Yang et al. [7].

Annexure

b_1	b_2	μ_1	μ_1	γ	λ_1	λ_2	α_1	r	$\Re_0$	S^*	I^*	V^*
200	300	0.5	0.6	0.4	0.01	0.02	0.1	0	74.07407	335.3115	35.93807	272.5138
200	300	0.5	0.6	0.4	0.01	0.02	0.1	0.2	60.60606	335.5082	29.31446	247.1106
200	300	0.5	0.6	0.4	0.01	0.02	0.1	0.4	51.28205	335.7049	24.72888	225.9217
200	300	0.5	0.6	0.4	0.01	0.02	0.1	0.6	44.44444	335.9016	21.36612	207.9787
200	300	0.5	0.6	0.4	0.01	0.02	0.1	0.8	39.21569	336.0984	18.7946	192.5889
200	300	0.5	0.6	0.4	0.01	0.02	0.1	1	35.08772	336.2951	16.76445	179.2435
200	300	0.5	0.6	0.4	0.01	0.02	0.1	0.2	60.60606	335.5082	29.31446	247.1106
200	300	0.5	0.6	0.4	0.01	0.02	0.2	0.2	60.60606	364.5586	16.10975	174.6892
200	300	0.5	0.6	O.4	0.01	0.02	0.3	0.2	60.60606	375.5652	11.10672	135.0962
200	300	0.5	0.6	0.4	0.01	0.02	0.4	0.2	60.60606	381.3555	8.474795	110.1344
200	300	0.5	0.6	0.4	0.01	0.02	0.5	0.2	60.60606	384.9272	6.851271	92.95841

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