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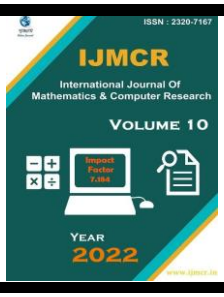

A Mathematical Formulation for Control the Transmission of Dengue Disease

R.N. Shukla[1], A.K. Ray[2]

[1,2] Department of Mathematics M.G.P.G. College, Gorakhpur (U.P.) India – 273001

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Corresponding Author:
A.K. Ray

ABSTRACT

It is transmitted between people by the bite of female adult Aedes mosquitoes. In the present work, we study a mathematical modling which work as a powerful tool for controlling the dengue disease. The aim of the study is to observe the effects of control measures on the dengue disease development. Explicit formula for the metric, basic reproduction number Γ0 is obtained using Next Generation Matrix method. Stability of the disease free equilibrium and sensitivity analysis of model's parameters are discussed in terms of basic reproduction number. It is observed that the disease free equilibrium is locally and globally stable when $\Gamma_0 < 1$ and unstable when $\Gamma_0 > 1$. Numerical results are carried out to illustrate the impact of control measures in the disease transmission. We know the effect of our model on lead & also at global level. Dengue is a masquito–borne viral infection that is usually found in tropical & sub–tropical regions around the world. In recent years, transmission has increased pro–dominantly in urban & semi urban areas & has become a major public health cancern.

KEYWORDS: Mosquitoes, Transmission, Disease, Viruses, Infections ,Immunity.

1. INTRODUCTION

Dengue disease is a masquito borne infectious disease which is threatening about 2.5 billion people of the world's population especially of tropical and subtropical regions around the world (1). Four serologically different viruses (DEN–1, DEN–4) (DEN–3 & DEN–5) cause dengue disease. These viruses are transmitted to humans by the bites of Acdes mosquitoes. A person infected by one of the four serotypes of viruses never DIN get infected by that serotype again but loses immunity to other three serotypes of the viruses (2).

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 researchers [3] [4] [5] [6] [7] [8] [9] have proposed SIR epidemic model [10] to study the factors that influence the spread of disease to support control measures. Many the transmission dynamics of dengue disease. Incubation periods in hosts and vectors have a significant influence in transmission dynamics of dengue disease. So, different mathematical studies [11] [12] [13] of dengue disease have been made to study dengue disease transmission dynamics with incubation periods.

There is no specific medicine to cure dengue disease. Awareness programs can be helpful in reducing the prevalence of the disease. Different epidemic models [14] [15] have been proposed to study the impact of awareness in controlling dengue disease. Prevention of mosquitoes bites is one of the ways to prevent dengue disease. The mosquitoes bite humans during day and night when lights are on. So, to get rid of mosquitoes' bite, people can use mosquito repellents and nets. If infected hosts feel they have symptoms of the disease and approach the doctor in time for the supportive treatment, they can recover fast. This type of awareness can help controlling the disease. Another way of controlling dengue is destroying larval breeding sites of mosquitoes and killing them. Spray of insecticides may be applied to control larvae or adult mosquitoes which can transmit dengue viruses.

In the present work, we have considered followings as control measures:

(i) some susceptible hosts use mosquito repellents to avoid mosquitoes' bite; (ii) some infected hosts seek for the supportive treatment timely and recover fast; (iii) some infected hosts use mosquito repellents to avoid mosquitoes' bite; (iv) spray of insecticides is applied to control mosquito population. (v) Awarenes programs can be helpful in reducing the prevalence of the disease.

2. FORMULATION OF THE MODEL

In present model we consider total human population, N_h which divides infour classes S_h (susceptible), E_h. (exposed), I_h (infectious), Rh (recovered) and total (mosquito)–population, N_m is divided into three classes: S_m (susceptible), E_m (exposed), I_m (infectious). We assume that the fraction u_1 of susceptible hosts use mosquito repellents to avoid mosquitoes bite. So, the fraction $(1 - u_1)$ of susceptible hosts interact with infectious mosquitoes. The fraction u_2 of infectious hosts seek for the timely supportive treatment and recover fast by the rate $r\gamma_h$ $(r > 1)$. The fraction r_1u_1 (r_1 is the proportionality constant) of infectious hosts use mosquito repellents to avoid mosquitoes' bite u_3 is a control variable that represents the eradication effort of insecticide spraying. It follows that the recruitment

rate of mosquito population is reduced by a factor of $1–u_3$. Also, it is assumed that the mortality rate of mosquito population increases at a rate r_2u_3 (r_2 is the proportionality constant).

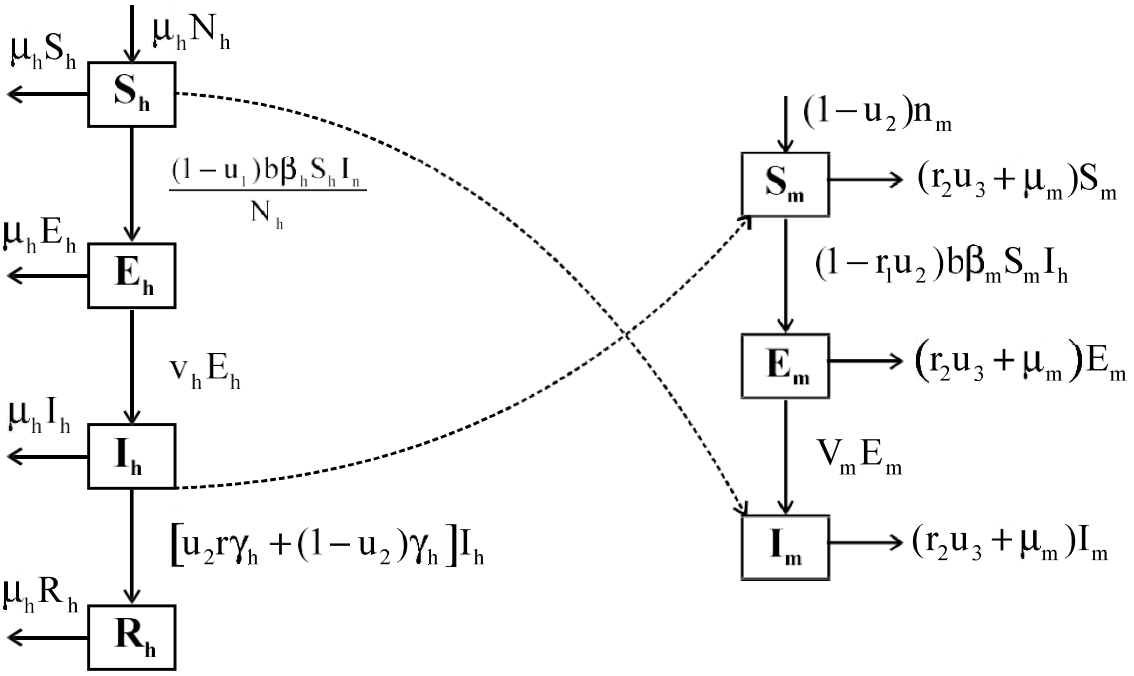

Fig.1. The model in form of flow chart

Fig. 1 describes the dynamics of dengue disease together with control measures. The system of differential equations which describes the present SEIR – SEI vector host model is given by

$$\frac{dS_h}{dt} = \mu_h N_h - (1-u_1)\frac{b\beta_h}{N_h} S_h I_v - \mu_h S_h$$

$$\frac{dE_h}{dt} = (1-u_1)\frac{b\beta_h}{N_h} S_h I_v - (v_h + \mu_h)E_h$$

$$\frac{dI_h}{dt} = v_h E_h - [ru_2\gamma_h + (1-u_2)\gamma_h + \mu_h]I_h$$

$$\frac{dR_h}{dt} = [ru_2\gamma_h + (1-u_2)\gamma_h]I_h - \mu_h R_h$$

$$\frac{dS_m}{dt} = (1-u_3)\pi_m - (1-r_1 u_2)\frac{b\beta_m}{N_h} S_m I_h - (r_2 u_3 + \mu_m)S_m$$

$$\frac{dE_m}{dt} = (1-r_1 u_3)\frac{b\beta_m}{N_h} S_m I_h - (r_2 u_3 + v_m + \mu_m)E_m$$

$$\frac{dI_m}{dt} = v_h I_m - (r_2 u_3 + \mu_m)I_m$$

Parameters of the model are described in Table 1.

Table 1. Model parameters and their description

Symbols	Description
μ_h	death rate of host population
v_h	host's incubation rate
γ_h	recovery rate of host population
β_h	transmission probability from vector to host
π_m	recruitment rate of vector population
μ_m	death rate of vector population
v_m	vector's incubation rate
β_m	transmission probability from host to vector
b	biting rate of vector

Total host population, Nn = Sh + En + In + Rn, total vector population, $N_m = S_m + E_m + I_m$

$$\frac{dN_h}{dt} = 0 \quad \text{and} \quad \frac{dN_m}{dt} = (1-u_3)\pi_m - (r_3u_3 + \mu_n)N_m$$

So, N_h remains constant and N_m approaches the equilibrium $\frac{(1-u_3)\pi_m}{(r_2u_3+\mu_m)}$ at $t\to\infty$.

Introducing the proportions

$$s_h = \frac{S_h}{N_h}, \quad e_h = \frac{E_h}{N_h}, \quad i_h = \frac{I_h}{N_h}, \quad r_h = \frac{R_h}{N_h}, \quad s_m = \frac{S_m}{(1-u_3)\pi_m/(r_2u_3+\mu_m)}$$

$$e_v = \frac{E_m}{(1-u_3)\pi_m/(r_2u_3+\mu_m)}, \quad i_v = \frac{I_m}{(1-u_3)\pi_m/(r_2u_3+\mu_m)}$$

Since $\gamma_h = 1 - s_h - e_h - i_h$ and $s_m = 1 - e_m - i_m$ the system of equations (2.1) can be written as the equivalent five dimensional non–linear system of ODEs:

$$\frac{ds_h}{dt} = \mu_h(1-s_h) - \alpha s_h i_m$$

$$\frac{de_h}{dt} = as_h i_m - \beta i_h$$

$$\frac{di_m}{dt} = v_h e_m - e i_m$$

$$\frac{di_h}{dt} = v_h e_m - \gamma i_h$$

$$\frac{de_m}{dt} = \delta s_m i_h - (e + v_m)e_m$$

$$\frac{di_m}{dt} = v_h e_m - e i_m$$

Here

$$\alpha = \frac{b\beta_h \pi_m (1-u_1)(1-u_3)}{N_h (r_2 u_3 + \mu_m)}, \beta = v_h + \mu_h, \gamma = r u_2 \gamma_h + (1-u_2)\gamma_h + \mu_h, \delta = (1 - r_1 u_2) b\beta_m$$

$$e = r_2 u_3 + \mu_m$$

3. Mathematical Analysis

3.1 Basic Reproduction Number

Definition 3.1.

Basic reproduction number, Γ_0 is the expected number of secondary infections caused by a single infectious individual during their entire infectious lifetime.

Mathematical expression for the basic reproduction number is obtained using Next Generation Matrix Method (16) [17]. The basic reproduction number R_0 is obtained as

$$R_0 = \rho(FV^{-1}) = \sqrt{\frac{a\delta v_h v_m}{\beta\gamma \in (\in + v_m)}} \tag{3.1}$$

$$F = \begin{bmatrix} 0 & 0 & 0 & \alpha \\ 0 & 0 & \delta & 0 \\ \beta & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}, \qquad V = \begin{bmatrix} \beta & 0 & 0 & 0 \\ 0 & \in + v_m & 0 & 0 \\ -v_m & 0 & \gamma & 0 \\ 0 & -v_m & 0 & \in \end{bmatrix}$$

3.2 Equilibrium points of the model

Two possible equilibrium points of the model are $E_0 = (1,0,0,0,0)$ and $E_1 = (s_h^*, e_h^*, i_h^*, e_m^*, i_m^*)$ where,

$$s_h^* = \frac{(\beta_{\gamma\epsilon} + \delta\mu_h v_h)(\in + v_m)}{\delta v_h [\in \mu_h + (\alpha + \mu_h)v_m]}, \quad e_h^* = \frac{\mu_h \beta_{\gamma\in}(\in + v_m)(R_0^2 - 1)}{\beta\delta v_h [\in \mu_h + (\alpha + \mu_h)v_m]}$$

$$i_h^* = \frac{\mu_h \beta_{\gamma\in}(\in + v_m)(R_0^2 - 1)}{\beta\delta_\gamma [\in \mu_h + (\alpha + \mu_h)v_m]}, \quad e_v^* = \frac{\mu_h \beta\gamma \in^2 (R_0^2 - 1)}{\alpha v_m [\beta\gamma \in + \delta\mu_h v_h]}, \quad i_v^* = \frac{\mu_h \beta\gamma \in (R_0^2 - 1)}{\alpha(\beta\gamma \in + \delta\mu_h v_h)}$$

Here, the first equilibrium point is disease free equilibrium (DFE) point which always exists in the absence of infective population. The second point if exists is called endemic equilibrium point. This point exists if $\Gamma_0 > 1$.

Thus, we have Theorem 3.1:

Theorem 3.1 (Existence of Equilibrium Points). System of equations (2.2) always has a discase free equilibrium point. If $\Gamma_0 > 1$, the system of equations (2.2) has a unique endemic equilibrium point.

Theorem 3.2 (Local Stability of DFE). The DFE of the system of equations (2.2) is locally asymptotically stable if $\Gamma_0 < 1$ and unstable if $\Gamma_0 > 1$.

Proof. The Jacobian matrix of the system of equation (2.2) about DFE is obtained as the block structure

$$J = \begin{bmatrix} A & B \\ 0 & F - V \end{bmatrix}$$

Matrix J is triangular matrix. So, the stability of the system of equations (2.2) depends on the matrices on diagonal, $A = [-\mu_h)$ and $F - V$. Matrix A has the eigenvalue $-\mu_h < 0$. Matrix F is non–negative matrix, V is non–singular M– matrix (18). Spectral abscissa of the matrix F–V, $s(F-V) < 0 \Leftrightarrow p\,(FV^{-1}) < 1$ (17). But, $\Gamma_0 = p(FV^{-1})$. Therefore, all the eigenvalues lie in the left half plane if $\Gamma_0 < 1$. Hence, DFE of the system of equations (2.2) is locally asymptotically stable if $\Gamma_0 < 1$.

If $\Gamma_0 > 1$ then $s(F-V) > 0$ showing that at least one eigenvalue lies in the right half plane. So, DFE of the system of equations (2.2) is unstable if $\Gamma_0 > 1$.

Theorem 3.3 (Global Stability of DFE). The DFE of the system of equations (2.2) is globally asymptotically stable if $\Gamma_0 < 1$.

Proof. In the present model, $s_h < 1$ and $s_m < 1$. So, from the system of equations (2.2), for the dynamics of infective population.

$$\frac{de_h}{dt} \leq \alpha i_m - \beta e_h$$

$$\frac{de_m}{dt} \leq \delta i_h - (e + v_m) e_m$$

$$\frac{di_h}{dt} = v_h e_h - \gamma i_m$$

Corresponding linear system of equations of (3.3) is

$$\frac{de_h}{dt} = \alpha i_m - \beta e_h$$

$$\frac{de_m}{dt} = \delta i_m - (e + v_m)e_m$$

$$\frac{di_h}{dt} = v_h e_h - \gamma i_h \qquad (3.4)$$

$$\frac{di_m}{dt} = v_m e_m - \in i_m$$

The system of linear equations (3.4) can be written as

$$\frac{d\vec{u}}{dt} = K\vec{u} \qquad (3.5)$$

where K = F–V and $\vec{u} = [e_h, e_m, i_h, i_m]^T$

If $\Gamma_0 = p\,(FV^{-1}) < 1$, then s(F – V) < 0 [17], thus each positive solution of (3.4) satisfies $\lim_{t\to\infty} e_h = 0$, $\lim_{t\to\infty} e_m = 0$, $\lim_{t\to\infty} i_h = 0$ and $\lim_{t\to\infty} i_m = 0$. DFE of the system of equations (3.4) is globally asymptotically stable since the system is linear. Since all the variables in the system of equations (2.2) are nonnegative, the use of a comparison theorem (19] [20] leads to $\lim_{t\to\infty} e_h = 0$, $\lim_{t\to\infty} e_m = 0$, $\lim_{t\to\infty} i_h = 0$, $\lim_{t\to\infty} i_m = 0$ and $\lim_{t\to\infty} s_h = 1$. Hence, the DFE, (1,0.0,0,0) is globally asymptotically stable if $\Gamma_0 < 1$.

4. Numerical Results and Discussion

In the present work, we have used SEIR – SEI epidemic model with control measures. The simulations are carried out in order to explore the impacts of control measures on the dengue disease dynamics. Following parameter values are used in the model for simulation purpose

N_h = 50111126, π_m = 2500000, 0.1667, μ_h= 0.0045, μ_m= 0.02941, γ_h= 0.328833, 6β_h=0.75 , bβ_m=0.375, v_m= 0.1428 [13]

Fig. 2 shows that many susceptible humans remain uninfected over a time when control measures are implemented. When human becomes aware of control measures such as: using mosquito repellents, applying insecticides, seeking doctor for timely treatment and avoiding mosquitoes' bite, only few humans get infected of the disease (Fig. 3). From Fig 2 and Fig. 3, we see that many hosts can be saved from being infected of the disease when control measures are implemented properly.

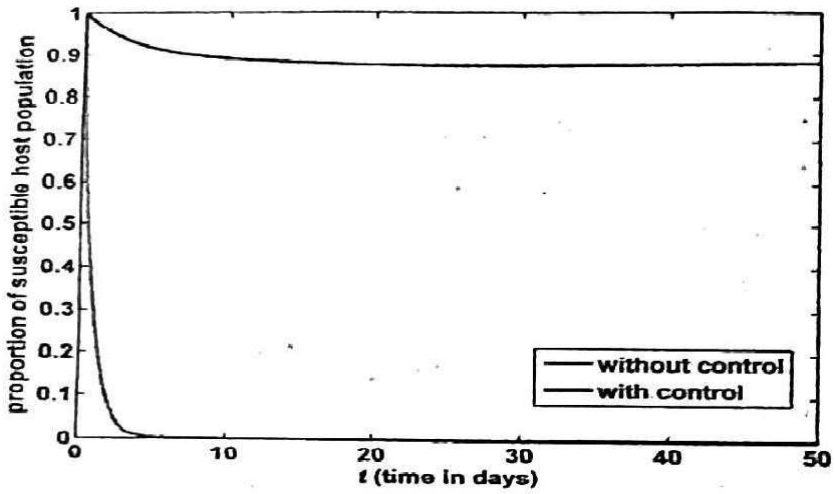

Fig. 2. Dynamics of susceptible hosts with and without implementation of control measures

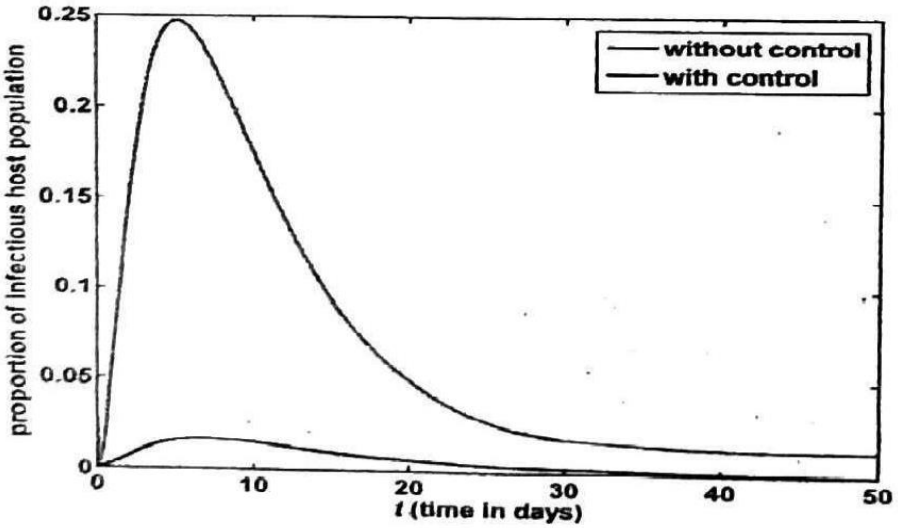

Fig. 3. Dynamics of infectious hosts with and without implementation of control measures

Basic reproduction number, Γ_0 is a metric which tells that the disease dies out if $\Gamma_0 < 1$ and the disease takes hold if $\Gamma_0 > 1$. Figs. 4–6 are simulated to study the impact of control measure in determinig the value of Γ_0. The figures show that Γ_0 decreases with the increase in level of control measures. That means, the prevalence of disease can be reduced with the implementation of control measures. Sufficient increase in level of control measures causes the basic reproduction number to be less than unity.

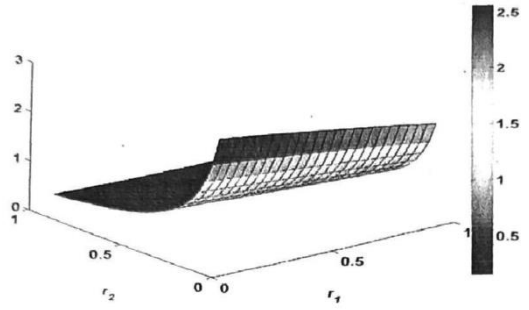

Fig. 4. Basic reproduction number, Γ_0 against control measures, T_1 and r_2

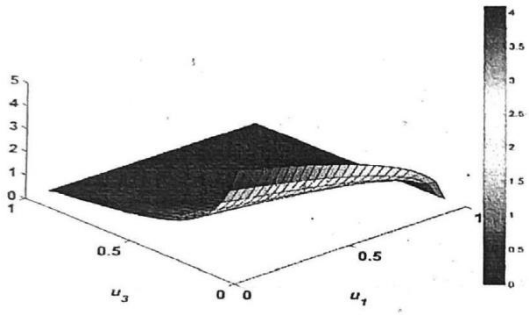

Fig. 5. Basic reproduction number, $\Gamma_0$against control measures, u_1 and u_3

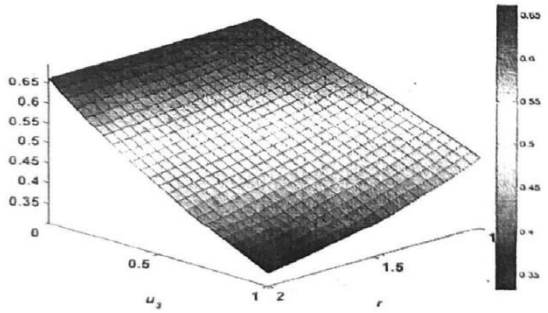

Fig. 6. Basic reproduction number, Γ_0 against control measures, r and u_3

Figs. 7–10 are simulated to describe the sensitivitycof the control measures on the transmission dynamics of dengue disease. The figures show the change in the population of infectious hosts with the change in level of control measures. Among all control measures, the control measures r, u1, 43 are seen more sensitive to the disease transmission. Fig. 10 shows that the most sensitive control measure is us (control variable that represents the eradication effort of insecticide spraying).

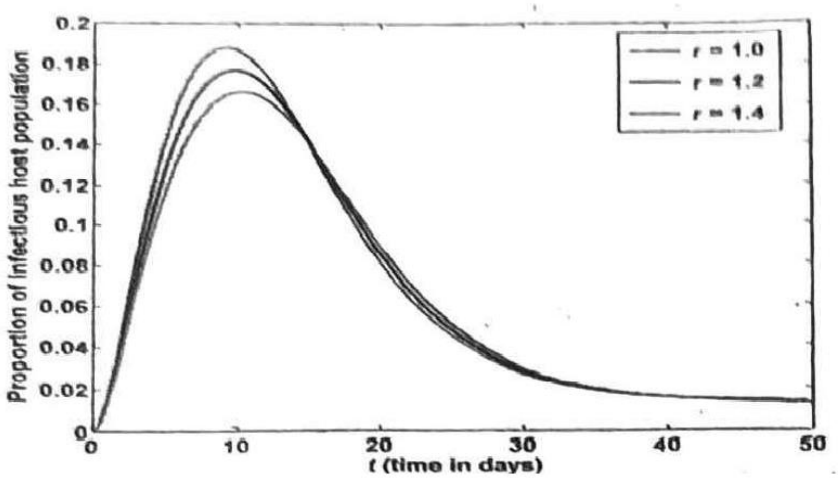

Fig.7. Dynamics of infections hosts with various values of control measure, *r*.

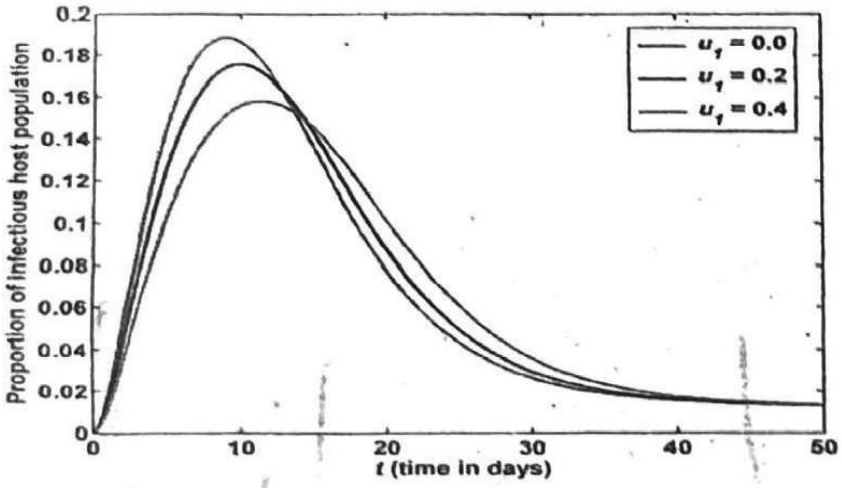

Fig. 8. Dynamics of Infections hosts with various values of control measure, u_1.

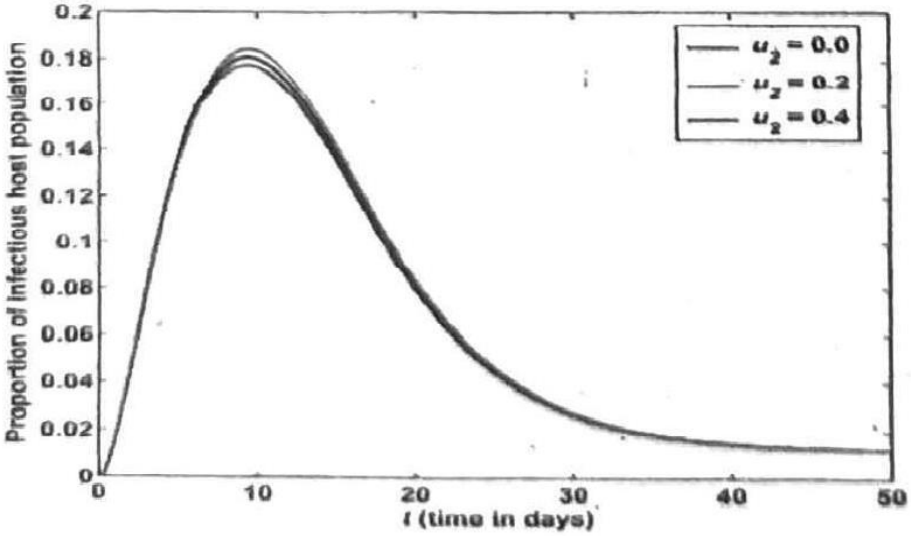

Fig. 9. Dynamics of Infections hosts with various values of control measure, u_1.

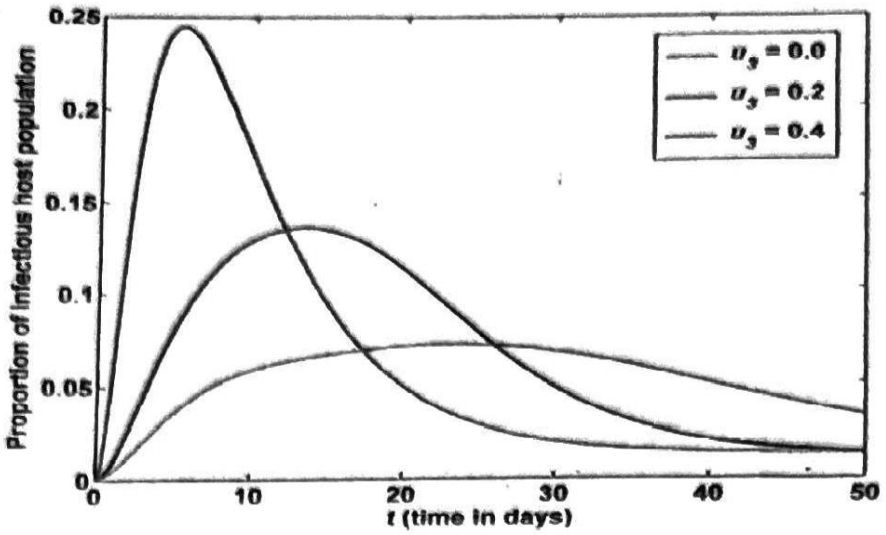

Fig. 10 Dynamics of Infections hosts with various values of control measure, u_3.

CONCLUSION

Dengue disease is becoming more prevalent worldwide and spreading in new areas. So, there is an urgent need to develop mosquito management strategies and control strategies of the discasc. In the present study, we have used to study the influence of control measures in transmission dynamics of dengue disease. There is no effective treatment of dengue disease. So, we have introduced some control measures in the model which can help in reducing of burden of the disease.

Assuming a vaccination program as an option that would enable a proportion p of susceptible humans to be globally immunized against the four serotypes, the stability analysis shows that the population may be protected from epidemics if p satisfies the principle of herd immunity : $\mu_h (\pi - 1) < p$, where R is a function of the model parameters, defined as the number of new infected by an infective in interaction with susceptibles. Otherwise, there will be an endemic equilibrium and the disease will persist. But the problem is precisely in finding a vaccine against the four serotypes, which makes a Strategy based on global immunization irrealistic in the short term. Meanwhile, a search leading to a partial vaccine against each serotype should be more feasible. In this direction, the proposed model shows that the evolution of dengue to dengue haemorrhagic fever can be controlled by a partial vaccine restricted to the people affected by the first epidemic. Torder to illustrate the dynamics of each epidemic and to study different strategies, a simulation was carried out using MATLAB routines with different values of the parameters aplied in each model.

Inplainly two directions can be envisaged to control the disease. The first may act on the number of mosquitoes and the second way consider the number of susceptible humans.

As mentioned in the introduction, Our main purpose was to Gudy the dynamics of dengue disease and its progression to body dengue haemorrhagic fever in order to understand the epidemic phenomenon and to suggest strategies for the Control of the disease in general and the haemorrhagic form in particular. This conclusion agrees with the experiences Yenlized by EA, Newton and P. Reiter using insecticides (3) On the other hand, although the model suggests the reduction Asusceptibles via vaccination, such a strategy is unlikely to be applicable in the short term because it faces some hurdles due to the fact that a vaccine must protect against the four sortypes at the same time. However, we consider this option Sived its eventuality is not excluded in the medium and long term.

In the short term, an intermediate solution would be to combine as much as possible, the environmental prevention and a partial vaccination essentially to avoid the haemorrhagic form of the disease caused by different viruses. This suggestion may help health–care policy makers to tackle environment causes as preventive measures and researchers to investigate and concentrate on the search for a vaccine against each serotype rather than looking for a vaccine against the four serotypes at the same time.

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