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Analysis of a Mathematical Model to Investigate the Dynamics of Dengue Fever

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ABSTRACT: In this paper, we formulated a compartmental model to investigate the dynamics of dengue fever in a population with some measure of disease control. We qualitatively and quantitatively analyzed the model and found that the model has a disease free equilibrium (DFE), an endemic equilibrium point and undergoes the phenomenon of backward bifurcation. It was also discovered that Dengue can be eliminated irrespective of the initial size of the infected population whenever the effective reproduction number is less than one. Numerical simulations were carried out on the model and effective control measures were proposed that will result in reducing the burden of the disease in the population. © JASEM

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Dengue, a mosquito-transmitted disease caused by any of four closely-related virus serotypes (DEN-1-4) of the genus Flavivirus, is endemic in at least 100 countries in Africa, the Americas, the Eastern Mediterranean and subtropical regions of the world, inhibited by over 2.5 billion people (Garba*, et al.,* 2008) . In developing countries population growth is an important factor that contributes to the increase in the incidence of communicable diseases which affects mainly the urban poor, with infants and children among the groups particularly at risk (Nuraini *et al,* 2009). Urbanization and population growth increase the demand on the basic essential services such as housing, water supply, etc., and at the same time induce conditions that increase the transmission of some vector-borne diseases (Nuraini *et al.,* 2009). Dengue is a viral, vector borne disease, spread by the Aedes Aegypti mosquito. It was estimated that about 50 million infections occur annually in over 100 countries. There is no specific treatment for curing dengue patients (Nuraini *et al*., 2009). Hospital treatment, in general, is given as supportive care which includes bed rest and analgesics (Nuraini *et al*., 2009).

Dengue virus is one of the most difficult arboviruses to isolate (Nuraini *et al*., 2009). There are four serotypes of the dengue virus; Den-1, Den-2, Den-3, Den-4, and each of the serotypes has numerous virus strains (Nuraini *et al*., 2009). Infection with one dengue serotypes may provide long life immunity to that serotype, but there is no complete cross-protective immunity to other serotype (Gubler, 1998). Identification of the primary target cells of dengue viruses' replication in the infected human body has proven to be extremely difficult (Nuraini *et al*., 2009).

The incubation period of the disease in an infected host is 3-14 days (average 4-7 days) (Nuraini *et al*., 2009). At the end of the incubation period, the patient may experience a sudden onset of fever (Nuraini *et al*, 2009). Viraemia is the presence of the virus in the blood stream (Nuraini *et al*., 2009). It is detected using the mosquito inoculation technique. Viraemia is assumed to become detectable on the second or the third day before the onset of symptoms and ends on the last days of illness (Nuraini *et al*., 2009). It usually peaks at the time of or shortly after the onset of illness (Gubler *et al.,* 1981). Susceptible mosquitoes can be infected when they bite dengue infected hosts during the febrile viremic stage (Nuraini *et al*., 2009). It is usually believed that dengue viruses quickly clear in human body within approximately 7 days after the day of sudden onset of fever (Vaughn *et al*., 1994). Naturally this clearing process is done by the immune system which is as a result of complex dynamics reactions (Nuraini *et al*., 2009). Over the last decade mathematical models have been formulated to evaluate the dynamics of Dengue Fever. In this paper, a mathematical model is formulated and analysed to investigate the dynamics of Dengue Fever in a population in order to reduce the public health burden of the disease.

MATERIALS AND METHODS

Let N_H (t) and N_V (t) denote the total number of humans and vectors at time t, respectively. The model sub-divides these populations into a number of mutually-exclusive compartments, as given below.

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The total population of human and vectors is divided into the following mutually exclusive epidemiological classes, namely, susceptible humans ($S_H(t)$), humans with dengue in latent stage ($E_1(t)$), humans with dengue ($I_I(t)$), humans treated of dengue ($R_1(t)$), susceptible vectors ($S_V(t)$), vectors with latent dengue ($E_V(t)$), vectors with dengue ($I_V(t)$), Hence, we have that,

$$N_H(t) = S_H(t) + E_1(t) + I_1(t) + R_1(t)$$

and

$$N_V(t) = S_V(t) + E_V(t) + I_V(t)$$

Susceptible humans are recruited at a rate Λ_H while the susceptible vectors are recruited at a rate Λ_V.
Susceptible humans contract dengue at a rate

$$\lambda_{DV} = \frac{\beta_{VH}\left(\eta_v E_v + I_v\right)}{N_H},$$

where $\eta_v < 1$, this accounts for the relative infectiousness of vectors with latent dengue E_V compared to vectors in the I_V class.
Susceptible vectors acquire dengue infection from infected humans at a rate

$\lambda_{DH} = \frac{\beta_{HV}(\eta_A E_1 + \eta_B I_1)}{N_H}$,

Where $\eta_A < \eta_B$, this accounts for the relative infectiousness of humans with latent dengue E_1 compared to humans in the I_1 class.

Derivation of Model Equations: Singly infected individuals with latent dengue progress to active dengue at a rate γ_1. Natural human death occurs at a rate μ_H in the classes S_H,, E_1, I_1, R_1, respectively and those in I_1 class undergo an additional dengue induced death, at rate δ_{D1}. Natural vector death occurs, at a rate μ_V, in the classes S_V, E_V *and* I_V, while the vectors in the I_V class undergoes additional dengue induced death, at a rate δ_{HV}, although this is negligible as infected vectors are not deemed to be suffering dengue. Exposed vectors progress to the infectious stage at the rate γ_V.

The above assumptions result in the following system of nonlinear ordinary differential equations:

$$\begin{aligned}
\dot{S}_H &= \Lambda_H - \mu_H S_H - \lambda_{DV} S_H, \\
\dot{E}_1 &= \lambda_{DV} S_H - (\gamma_1 + \mu_H) E_1, \\
\dot{I}_1 &= \gamma_1 E_1 - (\tau_1 + \mu_H + \delta_{D1}) I_1, \\
\dot{R}_1 &= \tau_1 I_1 - \mu_H R_1, \\
\dot{S}_V &= \Lambda_V - \lambda_{DH} S_V - \mu_V S_V, \\
\dot{E}_V &= \lambda_{DH} S_V - (\gamma_V + \mu_V) E_V, \\
\dot{I}_V &= \gamma_V E_V - (\mu_V + \delta_{HV}) I_V,
\end{aligned} \qquad (1)$$

Table 1: Description of the state variables of the model 1

Variable	Description
S_H	Susceptible human population
E_1	Human population with dengue in latent stage
I_1	Human population with dengue (Dengue only)
R_1	Human population treated of dengue (Dengue only)
S_V	Susceptible vectors population
E_V	Exposed vectors
I_V	Infectious vectors

Table 2: Description of Parameters of the Model (1)

Parameter	Description	Values	Unit	Reference
Λ_H,Λ_V	Recruitment rate into the population of susceptible humans,vectors respectively.	500,10000000	Year^{-1}	Garba et al, 2008.
μ_H,μ_v	Natural death for humans, vectors respectively.	0.02041,36.5	Year^{-1} Year^{-1}	Okuonghae and Omosigho (2011).
β_{VH}	Effective contact rate for dengue from vectors to humans	5	Year^{-1}	Garba et al, 2008.
β_{HV}	Effective contact rate for dengue from humans to vectors	4	Year^{-1}	Garba et al, 2008.
τ_1, τ_2	Dengue treatment rate for I_1,E_1.	2.5,1.5	Ind^{-1} Year^{-1}	Garba et al, 2008.
γ_1	Progression rate to active dengue	0.3254	Year^{-1}	Garba et al, 2008.
γ_V	Progression rate to active dengue (vectors)	0.03	Year^{-1}	Garba et al, 2008.
δ_{D1}	Disease induced death Dengue	0.365	Year^{-1}	Okuonghae and Omosigho, (2011).
δ_{HV}	Disease induced death dengue (vectors)	*0*	Year^{-1}	Garba et al, 2008.
k_V	Progression rate to active dengue (vectors)	0.05	Year^{-1}	Garba et al, 2008.
$,\eta_V$, η_A,η_B	Modification parameters for E_v, E_1, I_1	0.4,1.2,0.5,0.6,1,0.6,1 .1,1,	Year^{-1}	Okuonghae and Omosigho, (2011)
P_{D1}	Fraction of newly infected humans with latent dengue	0.6	Year^{-1}	Garba et al, 2008.

Analysis of the Model

Boundedness and Positivity of Solutions

Consider the region $D_2 = \left\{\left(S_H, E_1, I_1, R_1, S_V, E_V, I_V\right) \epsilon \mathbb{R}_+^7 : N_H \leq \frac{\Lambda_H}{\mu_H}, N_V \leq \frac{\Lambda_V}{\mu_V}\right\}$. It can be shown that the set D_2 is positively invariant and an attractor of all positive solution of the system **(1).**

Lemma 1 *The region D_2 is positively invariant for the system (1)*

Proof: The rate of change of the total human population is given as

$$\dot{N}_H = \dot{S}_H + \dot{E}_1 + \dot{I}_1 + \dot{R}_1 = \Lambda_H - \mu_H N_H - \delta_{D1} I_1 \quad (2)$$

By standard comparison theorem, $\dot{N}_H \leq \Lambda_H - \mu_H N_H$ (3)

So we have $\dot{N}_H + \mu_H N_H \leq \Lambda_H$. (4)

Using the integrating factor method

$$\dot{N}_H e^{\mu_H t} + \mu_H N_H e^{\mu_H t} \leq \Lambda_H e^{\mu_H t} \quad (5)$$

$$\frac{d}{dt}\left(\dot{N}_H e^{\mu_H t}\right) \leq \Lambda_H e^{\mu_H t} \quad (6)$$

$$\int d(\dot{N}_H e^{\mu_H t}) \leq \int \Lambda_H e^{\mu_H t} dt \quad (7)$$

$$N_H e^{\mu_H t} \leq \frac{\Lambda_H}{\mu_H} e^{\mu_H t} + D \quad (8)$$

$$at\ t = 0, D = N_H(0) - \frac{\Lambda_H}{\mu_H} \quad (9)$$

$$N_H e^{\mu_H t} \leq \frac{\Lambda_H}{\mu_H} e^{\mu_H t} + N_H(0) - \frac{\Lambda_H}{\mu_H} \quad (10)$$

$$N_H = N_H(0)e^{-\mu_H t} + \frac{\Lambda_H}{\mu_H}[1 - e^{-\mu_H t}] \tag{11}$$

and the rate of change of the total vector population

$$\dot{N}_V = \Lambda_V - \mu_V N_V - \delta_{HV} I_V \tag{12}$$

By standard comparison theorem,

$$\dot{N}_V \leq \Lambda_V - \mu_V N_V \tag{13}$$

Similarly, using the integrating factor method, we have

$$N_V = N_V(0)e^{-\mu_V t} + \frac{\Lambda_V}{\mu_V}[1 - e^{-\mu_V t}] \tag{14}$$

In particular $N_H(t) \leq \frac{\Lambda_H}{\mu_H}$ if $N_H(0) \leq \frac{\Lambda_H}{\mu_H}$ and $N_V(t) \leq \frac{\Lambda_V}{\mu_V}$ if $N_V(0) \leq \frac{\Lambda_V}{\mu_V}$, respectively.

So, D_2 is a positively invariant set under the flow described in (1). Hence, no solution path leaves through the boundary of D_2. Also, since solution paths cannot leave D_2, solutions remain non-negative for non-negative initial conditions. Solutions exist for all time t. In this region, the model (1) is said to be well posed mathematically and epidemiologically.

Positivity of Solutions

Lemma 2.*Let the initial data for the model* ***(1)*** *be* $S_H(t) > 0,\ E_1(t) > 0, I_1(t) > 0, R_1(t) > 0, S_V(t) > 0, E_V(t)$ *and* $I_V(t) > 0$ *then the solution* $S_H(t)$, $E_1(t)$, $I_1(t)$, $R_1(t)$, $S_V(t), E_V(t)$, *and* $I_V(t)$ *with positive initial data will remain positive for all time t > 0.*

Proof*:* Let $t_1 = sup\{t > 0: S_H(t) > 0, E_1(t) > 0, I_1(t) > 0, R_1(t) > 0, S_V(t) > 0, E_V(t) > 0,\ I_V(t) > 0\} > 0$

$$\dot{S}_H = \Lambda_H - \lambda_{DV} S_H - \mu_H S_H = \Lambda_H - (\lambda_{DV} + \mu_H) S_H \tag{15}$$

To solve the ODE using the integrating factor method

$$I.F = exp\left[\mu_H t + \left\{\int_0^t \lambda_{DV}(\tau)d(\tau)\right\}\right] \tag{16}$$

$$\frac{d}{dt}\left[S_H(t)exp\left\{\mu_H t + \int_0^t \lambda_{DV}(\tau)d(\tau)\right\}\right] = \Lambda_H\left[exp\left\{\mu_H t + \int_0^t \lambda_{DV}(\tau)d(\tau)\right\}\right] \tag{17}$$

$$S_H(t_1)exp\left\{\mu_H t_1 + \int_0^{t_1} \lambda_{DV}(\tau)d(\tau)\right\} = S_H(0) + \int_0^{t_1} \Lambda_H\left[exp\{\mu_H y + \int_0^y \lambda_{DV}(\tau)d(\tau)\}\right]dy \tag{18}$$

$$S_H(t_1) = S_H(0)exp\left\{-\mu_H t_1 - \int_0^{t_1} \lambda_{DV}(\tau)d(\tau)\right\} + \left[exp\left\{-\mu_H t_1 - \int_0^{t_1} \lambda_{DV}(\tau)d(\tau)\right\}\right]\int_0^{t_1} \Lambda_H\left[exp\left\{\mu_H y + \int_0^y \lambda_{DV}(\tau)d(\tau)\right\}\right]dy > 0$$

for $\dot{E}_1 = \lambda_{DV} S_H - (\gamma_1 + \mu_H) E_1$ we have that $\dot{E}_T \geq -(\gamma_1 + \mu_H) E_1$,

for $\dot{I}_1 = \gamma_1 E_1 - (\tau_1 + \mu_H + \delta_{D_1}) I_1$ we have that $\dot{I}_1 \geq -(\tau_1 + \mu_H + \delta_{D_1}) I_1$,

for $\dot{R}_1 = \tau_1 I_1 - \mu_H R_1$ we have that $\dot{R}_1 \geq -\mu_H R_1$,

for $\dot{S}_V = \Lambda_V - \lambda_{DH} S_V - \mu_V S_V$ we have that $\dot{S}_V \geq -(\lambda_{DH} + \mu_V) S_V$,

for $\dot{E}_V = \lambda_{DH} S_V - (\gamma_V + \mu_V) E_V$ we have that $\dot{E}_V \geq -(\gamma_V + \mu_V) E_V$,

for $\dot{I}_V = \gamma_V E_V - (\mu_V + \delta_{HV}) I_V$ we have that $\dot{I}_V \geq -(\mu_V + \delta_{HV}) I_V$.

Similarly, we can show that $S_H(t) > 0,\ E_1(t) > 0, I_1(t) > 0, R_1(t) > 0, S_V(t) > 0, E_V(t) > 0,$ *and* $I_V(t) > 0$.

Local Stability of Disease-Free Equilibrium (DFE) of the Model: The model (1) has a disease-free equilibrium, obtained by setting the right hand side of the model to zero and also setting the disease classes to zero we obtain

$$\xi_2 = \left(S_H^*, E_1^*, I_1^*, R_1^*, S_v^*, E_v^*, I_v^*\right) = \left(\frac{\Lambda_H}{\mu_H}, 0,0,0, \frac{\Lambda_v}{\mu_v}, 0,0\right) \qquad (20)$$

The stability of ξ_2 is established using the next generation operator method on the system (1). Using the notation in van den Driessche and Watmough (2002) the matrices F_1 and V_1 for the new infection terms and the remaining transfer terms, are respectively given as

$$F_1 = \begin{pmatrix} 0 & 0 & \beta_{VH}\eta_V & \beta_{VH} \\ 0 & 0 & 0 & 0 \\ \frac{\beta_{HV}\eta_A S_V}{N_H} & \frac{\beta_{HV}\eta_B S_V}{N_H} & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix} \qquad (21)$$

And,

$$V_1 = \begin{pmatrix} g_3 & 0 & 0 & 0 \\ -\gamma_1 & g_4 & 0 & 0 \\ 0 & 0 & g_5 & 0 \\ 0 & 0 & -\gamma_V & g_6 \end{pmatrix} \qquad (22)$$

Where, $g_3 = \mu_H + \gamma_1, g_4 = \tau_1 + \mu_H + \delta_{D1}, g_5 = \gamma_V + \mu_V, g_6 = \mu_V + \delta_{HV}$

The spectral radius given by $\rho(F_1 V_1^{-1}) = \sqrt{\frac{\Lambda_V \beta_{HV}\beta_{VH}\mu_H(g_4\eta_A + \gamma_1\eta_B)(\gamma_V + g_6\eta_V)}{\Lambda_H g_3 g_4 g_5 g_6 \mu_V}} = R_D$ (23)

The value R_D is the effective reproduction number.

Lemma 3 *The DFE of the system (1) is locally asymptotically stable if $R_D < 1$ and unstable if $R_D > 1$.*

The threshold quantity R_D is the effective or control reproduction number for the Dengue model. By Lemma 3, biologically speaking, Dengue is eliminated from the population when $R_D < 1$ if the initial sizes of the subpopulations of the model are in the region of attraction of ξ_2.

However, the disease free equilibrium may not be globally asymptotically stable even if $R_D < 1$ in the case when a backward bifurcation occurs. That is, there is the presence of a stable EEP co-existing with the DFE.

Existence of Endemic Equilibrium Point (EEP) of the model

Let the EEP of model (1) be denoted by $\xi_{(1,D)} = (S_H^{**}, E_1^{**}, I_1^{**}, R_1^{**}, S_V^{**}, E_V^{**}, I_V^{**})$. The equations in (1) are solved in terms of the force of infection at steady state and they are given as

$$S_H^{**} = \frac{\Lambda_H}{\mu_H + \lambda_{DV}^{**}}, \qquad (24)$$

$$E_1^{**} = \frac{\Lambda_H \lambda_{DV}^{**}}{(\mu_H + \lambda_{DV}^{**})(\gamma_1 + \mu_H)}, \qquad (25)$$

$$I_1^{**} = \frac{\gamma_1 \lambda_{DV}^{**} \Lambda_H}{(\mu_H + \lambda_{DV}^{**})(\gamma_1 + \mu_H)(\tau_1 + \mu_H + \delta_{D1})}, \qquad (26)$$

$$R_1^{**} = \frac{\tau_1\gamma_1\lambda_{DV}^{**}\Lambda_H}{(\mu_H + \lambda_{DV}^{**})(\gamma_1 + \mu_H)(\tau_1 + \mu_H + \delta_{D1})\mu_H}, \tag{27}$$

$$S_V^{**} = \frac{\Lambda_V}{(\mu_V + \lambda_{DH}^{**})}, \tag{28}$$

$$E_V^{**} = \frac{\lambda_{DH}^{**}\Lambda_V}{(\mu_V + \lambda_{DH}^{**})(\gamma_V + \mu_V)}, \tag{29}$$

$$I_V^{**} = \frac{\gamma_V\lambda_{DH}^{**}\Lambda_V}{(\mu_V + \lambda_{DH}^{**})(\gamma_V + \mu_V)(\mu_V + \delta_{HV})}, \tag{30}$$

$$N_H^{**} = \frac{\begin{array}{c}\Lambda_H\mu_H(\gamma_1 + \mu_H)(\tau_1 + \mu_H + \delta_{D1}) + \lambda_{DV}^{**}\Lambda_H(\tau_1 + \mu_H + \delta_{D1})\mu_H + \\ \gamma_1\lambda_{DV}^{**}\Lambda_H\mu_H + \tau_1\gamma_1\lambda_{DV}^{**}\Lambda_H\end{array}}{\mu_H(\mu_H + \lambda_{DV}^{**})(\gamma_1 + \mu_H)(\tau_1 + \mu_H + \gamma + \delta_{D1})}, \tag{31}$$

now,

$$\lambda_{DH}^{**} = \frac{\beta_{HV}(\eta_A E_1^{**} + \eta_B I_1^{**})}{N_H^{**}} \text{ and } \lambda_{DV}^{**} = \frac{\beta_{VH}(\eta_V E_V^{**} + I_V^{**})}{N_H^{**}}$$

Substituting the values of E_1^{**}, I_1^{**}, N_H^{**} to λ_{DH}^{**} and E_V^{**}, I_V^{**}, N_H^{**} to λ_{DV}^{**} we have

$$\lambda_{DH}^{**} = \frac{\beta_{HV}\mu_H(g_4\eta_A + \gamma_1\eta_B)\lambda_{DV}^{**}}{\mu_H g_3 g_4 + (\mu_H g_4 + \gamma_1\mu_H + \tau_1\gamma_1)\lambda_{DV}^{**}} \tag{32}$$

and

$$\lambda_{DV}^{**} = \frac{\begin{array}{c}\beta_{VH}\Lambda_V\mu_H(\eta_V g_6 + \gamma_V)g_3 g_4(\mu_H + \lambda_{DV}^{**})\lambda_{DH}^{**} \\ \Lambda_H\mu_H g_3 g_4 g_5 g_6\mu_V + (\Lambda_H\mu_H g_4 g_5 g_6\mu_H + (\Lambda_H\gamma_1\mu_H + \tau_1\gamma_1\Lambda_H)g_5 g_6\mu_V)\lambda_{DV}^{**} \\ +(\Lambda_H\mu_H g_3 g_4 g_5 g_6 + (\Lambda_H\mu_H g_4 g_5 g_6 + (\Lambda_H\gamma_1\mu_H + \tau_1\gamma_1\Lambda_H)g_5 g_6)\lambda_{DV}^{**})\lambda_{DH}^{**}\end{array}} \tag{33}$$

substituting λ_{DH}^{**} to λ_{DV}^{**} we have

$$A_1\lambda_{Dv}^{**2} + A_2\lambda_{Dv}^{**} + A_3 = 0 \tag{34}$$

where

$$\begin{array}{l}A_1 = (\mu_H g_4 + \gamma_1\mu_H + \tau_1\gamma_1)\Lambda_H\mu_H^2 g_4 g_5 g_6 + g_5 g_6\mu_v(\mu_H g_4 + \gamma_1\mu_H + \tau_1\gamma_1)(\Lambda_H\gamma_1\mu_H + \tau_1\gamma_1\Lambda_H) \\ \qquad +\beta_{Hv}\mu_H^2(g_4\eta_A + \gamma_1\eta_B)\Lambda_H g_4 g_5 g_6 + \beta_{Hv}\mu_H(g_4\eta_A + \gamma_1\eta_B)g_5 g_6(\Lambda_H\gamma_1\mu_H + \tau_1\gamma_1\Lambda_H) \\ A_2 = (\mu_H g_4 + \gamma_1\mu_H + \tau_1\gamma_1)\Lambda_H g_3 g_4 g_5 g_6\ \mu_v + \Lambda_H\mu_H^3 g_3 g_4^2 g_5 g_6 + \\ \mu_H g_3 g_4 g_5 g_6\mu_v\ (\Lambda_H\gamma_1\mu_H + \tau_1\gamma_1\Lambda_H) + \beta_{Hv}\mu_H^2(g_4\eta_A + \gamma_1\eta_B)\Lambda_H \\ g_3 g_4 g_5 g_6 - \beta_{Hv}\beta_{vH}\Lambda_H\mu_H^2 g_3 g_4(\eta_v g_6 + \gamma_v)(g_4\eta_A + \gamma_1\eta_B),\end{array} \tag{36}$$

$$A_3 = \Lambda_H \mu_H g_3^2 g_4^2 g_5 g_6 \mu_v - \beta_{Hv}\beta_{vH}\Lambda_v \mu_H^2 g_3 g_4 (\eta_v g_6 + \gamma_v)(g_4\eta_A + \gamma_1\eta_B)$$
$$= \Lambda_H \mu_H g_3^2 g_4^2 g_5 g_6 \mu_v \left[1 - \frac{\Lambda_v \beta_{Hv}\beta_{vH}\mu_H (\eta_v g_6 + \gamma_v)(g_4\eta_A + \gamma_1\eta_B)}{\Lambda_H g_3 g_4 g_5 g_6 \mu_v}\right] \quad (37)$$
$$A_3 = \Lambda_H \mu_H g_3^2 g_4^2 g_5 g_6 \mu_v \left[1 - (R_D)^2\right]$$

where $g_3 = \mu_H + \gamma_1, g_4 = \tau_1 + \mu_H + \delta_{D1}, g_5 = \gamma_1 + \mu_v g_6 = \mu_v + \delta_{Hv}$ (38)

Hence, we now claim the following

***Theorem 1*:** The Dengue model (1) has a unique positive equilibrium if R_D>1.

Bifurcation Analysis of the model: T*heorem* ***2*:** The model (1) undergoes backward bifurcation phenomenon at $R_D = 1$ under certain condition.
***Proof*:** The proof is based on the Centre manifold Theorem.

Let $x_1 = S_H, x_2 = E_1, x_3 = I_1, x_4 = R_1, x_5 = S_V, x_6 = E_V, x_7 = I_V$. Further, let $\hat{f} = [f_1, \cdots, f_7]^T$ denote the vector field of the model (1). Thus, the model (1) can be written as:

$$\frac{dx_1}{dt} = \Lambda_H - \mu_H x_1 - \frac{\beta_{VH}(\eta_V x_6 + x_7)x_1}{x_1 + x_2 + x_3 + x_4},$$

$$\frac{dx_2}{dt} = \frac{\beta_{VH}(\eta_V x_6 + x_7)x_1}{x_1 + x_2 + x_3 + x_4} - (\gamma_1 + \mu_H)x_2,$$

$$\frac{dx_3}{dt} = \gamma_1 x_2 - (\tau_1 + \mu_H + \delta_{DI})x_3,$$
$$\frac{dx_4}{dt} = \tau_1 x_3 - \mu_H x_4, \quad (39)$$

$$\frac{dx_5}{dt} = \Lambda_V - \frac{\beta_{HV}(\eta_A x_2 + \eta_B x_3)x_5}{x_1 + x_2 + x_3 + x_4} - \mu_V x_5,$$

$$\frac{dx_6}{dt} = \frac{\beta_{HV}(\eta_A x_2 + \eta_B x_3)x_5}{x_1 + x_2 + x_3 + x_4} - (\gamma_V + \mu_V)x_6,$$
$$\frac{dx_7}{dt} = \gamma_V x_6 - (\mu_V + \delta_{HV})x_7,$$

The Jacobian of the transformed system (39), evaluated at the *DFE*, is given by:

$$J(\xi_2)=\begin{bmatrix} -\mu_H & 0 & 0 & 0 & 0 & -\beta^*_{vH}\eta_v & -\beta^*_{vH} \\ 0 & -g_3 & 0 & 0 & 0 & \beta^*_{vH}\eta_v & \beta^*_{vH} \\ 0 & \gamma_1 & -g_4 & 0 & 0 & 0 & 0 \\ 0 & 0 & \tau_1 & -\mu_H & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & -\mu_V & 0 & 0 \\ 0 & \beta^*_{vH}\eta_A x^*_5 & \beta^*_{vH}\eta_B x^*_5 & 0 & 0 & -g_5 & 0 \\ 0 & 0 & 0 & 0 & 0 & \gamma_v & -g_6 \end{bmatrix}, \quad ($$

40)

Suppose $\beta_{VH}=\beta^*_{VH}$ is chosen as the bifurcation parameter at $R_D=1$, we have that

$$\beta^*_{VH}=\frac{\Lambda_H g_3 g_4 g_5 g_6 \mu_V}{\Lambda_V \beta_{HV}\mu_H\left(g_4\eta_A+\gamma_1\eta_B\right)\left(\gamma_V+g_6\eta_V\right)}$$

The right eigenvector of $J(\xi_2)_{\beta_{VH}=\beta^*_{VH}}$ is given by

$w=\left(w_1,w_2,w_3,w_4,w_5,w_6,w_7\right)$ where,

$$\begin{aligned} &w_1=-\frac{\beta_{Hv}\beta^*_{vH}x^*_5 w_3\left(\eta_A+\gamma_1\eta_B\right)}{\gamma_1 g_5\mu_H}<0, w_2=\frac{w_3}{\gamma_1}, \\ &w_3=w_3>0 \\ &w_4=\frac{\tau_1 w_3}{\mu_H}, w_5=0, w_6=\frac{\beta_{Hv}x^*_5 w_3\left(\eta_A+\gamma_1\eta_B\right)}{\gamma_1 g_5} \\ &w_7=\frac{\beta_{Hv}x^*_5\gamma_v w_3\left(\eta_A+\gamma_1\eta_B\right)}{\gamma_1 g_5 g_6} \end{aligned} \tag{41}$$

The above right eigenvector were obtained by solving (42) below.

$$\begin{aligned} &-\mu_H w_1-\beta^*_{vH}\eta_v w_5-\beta^*_{vH}w_6=0, \\ &-g_3 w_2+\beta^*_{vH}\eta_v w_5+\beta^*_{vH}\eta_v w_6=0, \\ &\gamma_1 w_2-g_4 w_3=0, \\ &\tau_1 w_3-\mu_H w_4=0, \\ &-\mu_v w_5=0, \\ &\beta_{Hv}\eta_A x^*_5 w_2+\beta_{Hv}\eta_B x^*_5 w_3-g_5 w_6=0, \\ &\gamma_v w_6-g_6 w_7=0, \end{aligned} \tag{42}$$

Similarly, $J(\xi_2)_{\beta_{VH}=\beta^*_{VH}}$ has a left eigenvector,

$v=\left(v_1,v_2,v_3,v_4,v_5,v_6,v_7\right)$ where,

$$
\begin{aligned}
&v_1 = 0, v_2 = \left(\gamma_1\eta_B + \eta_A g_4\right)\frac{v_3}{\eta_B g_3},\\
&v_3 = v_3 > 0, v_4 = 0, v_5 = 0\\
&v_6 = \frac{g_3 v_3}{\beta_{Hv}\eta_B x_5^*}, v_7 = \frac{\beta_{vH}^*\left(\gamma_1\eta_B + \eta_A g_4\right)v_3}{\eta_B g_3 g_6}
\end{aligned}
\tag{43}
$$

The above eigenvectors were obtained by solving (44) below.

$$
\begin{aligned}
&-\mu_H v_1 = 0,\\
&-g_3 v_2 + \gamma_1 v_3 + \beta_{Hv}\eta_A x_5^* v_6 = 0,\\
&-g_4 v_3 + \tau_1 v_4 + \beta_{Hv}\eta_B x_5^* v_6 = 0,\\
&-\mu_H v_4 = 0,\\
&-\mu_H v_5 = 0,\\
&-\beta_{vH}^*\mu_v v_1 + \beta_{vH}^*\eta_v v_2 - g_3 v_6 + \gamma_v v_3 v_7 = 0,\\
&-\beta_{vH}^* v_1 + \beta_{vH} v_2 - g_6 v_7 = 0.
\end{aligned}
\tag{44}
$$

Computation of the bifurcation coefficient a and b for the Model: For the system (39), the associated non-zero partial derivatives required for the calculation of the backward bifurcation coefficients are given by

$$
\begin{aligned}
&\frac{\partial^2 f_2}{\partial x_2\partial x_6} = \frac{\partial^2 f_2}{\partial x_6\partial x_2} = \frac{-\beta_{VH}^*\eta_V\mu_H}{\Lambda_H},\\
&\frac{\partial^2 f_2}{\partial x_2\partial x_7} = \frac{\partial^2 f_2}{\partial x_7\partial x_2} = \frac{-\beta_{VH}^*\mu_H}{\Lambda_H},\\
&\frac{\partial^2 f_2}{\partial x_3\partial x_6} = \frac{\partial^2 f_2}{\partial x_6\partial x_3} = \frac{-\beta_{VH}^*\eta_V\mu_H}{\Lambda_H},\\
&\frac{\partial^2 f_2}{\partial x_3\partial x_7} = \frac{\partial^2 f_2}{\partial x_7\partial x_3} = \frac{-\beta_{VH}^*\mu_H}{\Lambda_H},\\
&\frac{\partial^2 f_2}{\partial x_4\partial x_6} = \frac{\partial^2 f_2}{\partial x_6\partial x_4} = \frac{-\beta_{VH}^*\eta_V\mu_H}{\Lambda_H},\\
&\frac{\partial^2 f_2}{\partial x_4\partial x_7} = \frac{\partial^2 f_2}{\partial x_7\partial x_4} = \frac{-\beta_{VH}^*\mu_H}{\Lambda_H},\\
&\frac{\partial^2 f_6}{\partial x_1\partial x_2} = \frac{\partial^2 f_6}{\partial x_2\partial x_1} = \frac{-\beta_{VH}\eta_A\mu_H^2\Lambda_V}{\Lambda_H^2\mu_V},\\
&\frac{\partial^2 f_6}{\partial x_1\partial x_3} = \frac{\partial^2 f_6}{\partial x_3\partial x_1} = \frac{-\beta_{VH}\eta_B\mu_H^2\Lambda_V}{\Lambda_H^2\mu_V},\\
&\frac{\partial^2 f_6}{\partial x_2^2} = \frac{-2\beta_{HV}\eta_A\mu_H^2\Lambda_V}{\Lambda_H^2\mu_V},
\end{aligned}
\tag{45}
$$

$$\frac{\partial^2 f_6}{\partial x_2 \partial x_3} = \frac{\partial^2 f_6}{\partial x_3 \partial x_2} = \frac{-\beta_{VH}\mu_H^2 \Lambda_V (\eta_A + \eta_B)}{\Lambda_H^2 \mu_V},$$

$$\frac{\partial^2 f_6}{\partial x_2 \partial x_4} = \frac{\partial^2 f_6}{\partial x_4 \partial x_2} = \frac{-\beta_{VH}\eta_B \mu_H^2 \Lambda_V}{\Lambda_H^2 \mu_V},$$

$$\frac{\partial^2 f_6}{\partial x_3^2} = \frac{-2\beta_{HV}\eta_B \mu_H^2 \Lambda_V}{\Lambda_H^2 \mu_V},$$

$$\frac{\partial^2 f_6}{\partial x_3 \partial x_4} = \frac{\partial^2 f_6}{\partial x_4 \partial x_3} = \frac{-\beta_{HV}\eta_B \mu_H^2 \Lambda_V}{\Lambda_H^2 \mu_V},$$

$$\frac{\partial^2 f_2}{\partial x_6 \partial \beta_{VH}^*} = \eta_V,$$

$$\frac{\partial^2 f_2}{\partial x_7 \partial \beta_{VH}^*} = 1.$$

Since we know that,

$$a = \sum_{k,\delta,j=1}^{7} v_k w_i w_j \frac{\partial^2 f_k}{\partial x_i \partial x_j}(0,0), \tag{46}$$

$$b = \sum_{k,i=1}^{7} v_k w_i \frac{\partial^2 f_k}{\partial x_i \partial \beta_{vH}^*}(0,0), \tag{47}$$

we now have that,

$$a = 2v_2 w_2 w_6 \frac{\partial^2 f_2}{\partial x_2 \partial x_6}(0,0), + 2v_2 w_2 w_7 \frac{\partial^2 f_2}{\partial x_2 \partial x_7}(0,0) + 2v_2 w_3 w_6 \frac{\partial^2 f_2}{\partial x_3 \partial x_6}(0,0)$$

$$+ 2v_2 w_2 w_7 \frac{\partial^2 f_2}{\partial x_3 \partial x_7}(0,0) + 2v_2 w_4 w_6 \frac{\partial^2 f_2}{\partial x_4 \partial x_6}(0,0) + 2v_2 w_4 w_7 \frac{\partial^2 f_2}{\partial x_4 \partial x_7}(0,0)$$

$$+ 2v_6 w_1 w_2 \frac{\partial^2 f_6}{\partial x_1 \partial x_2}(0,0) + 2v_6 w_1 w_2 \frac{\partial^2 f_6}{\partial x_1 \partial x_3}(0,0) + v_2 {w_2}^2 \frac{\partial^2 f_6}{\partial {x_2}^2}(0,0) \tag{48}$$

$$+ 2v_6 w_2 w_3 \frac{\partial^2 f_6}{\partial x_2 \partial x_3}(0,0) + 2v_6 w_2 w_4 \frac{\partial^2 f_6}{\partial x_2 \partial x_4}(0,0) + v_6 {w_3}^2 \frac{\partial^2 f_6}{\partial {x_3}^2}(0,0) + 2v_6 w_3 w_4 \frac{\partial^2 f_6}{\partial x_3 \partial x_4}(0,0),$$

which leads to

$$a = K_1 - (K_2 + K_3), where, \tag{49}$$

$$\mathrm{K}_1 = \frac{2g_3 g_4^2 g_6 v_3 w_3 (\eta_A + \gamma_1 \eta_B)}{\Lambda_H \gamma_1 (g_4 \eta_A + \gamma_1 \eta_B)(\gamma_V + g_6 \eta_V)} \left[\frac{\eta_A}{\eta_B} + w_3 \right], \tag{50}$$

$$\mathrm{K}_2 = \frac{2g_4 g_6 v_3 w_3^2 (\eta_A + \gamma_1 \eta_B)}{\eta_B \gamma_1 \mu_H (\gamma_V + g_6 \eta_V)} \left[\mu_H \left[\frac{1}{\gamma_V}(\eta_V + \gamma_V) + \eta_V + \frac{\gamma_V}{g_6} \right] + \tau_1 \left(\eta_V + \frac{\gamma_V}{g_6} \right) \right], \tag{51}$$

$$\mathrm{K}_3 = \frac{2g_4 v_3 w_3^2 \mu_H}{\Lambda_H^2}\left[\frac{1}{\eta_B \gamma_1}\left(\frac{\eta_A \mu_H}{\gamma_1} + \eta_A + \eta_B + \tau_1 \eta_A\right) + 1 + \tau_1\right]. \tag{52}$$

And

$$b = \sum_{k,i=1}^{7} v_k w_i \frac{\partial^2 f_k}{\partial x_i \partial \beta_{vH}^*}(0,0),$$

Also we have that,

$$b = v_2 w_6 \frac{\partial^2 f_2}{\partial x_6 \partial \beta_{vH}^*}(0,0) + v_2 w_7 \frac{\partial^2 f_2}{\partial x_7 \partial \beta_{vH}^*}(0,0) \tag{53}$$

$$b = \frac{(\gamma_1 \eta_B + \eta_A g_4)(\eta_A + \gamma_1 \eta_B)\beta_{Hv} x_5^* w_3}{\eta_B g_3 g_5 \gamma_1}\left[\eta_v + \frac{\gamma_v}{g_6}\right]. \tag{54}$$

It follows from (49) that the bifurcation coefficient, a, is positive whenever,

$K_1 > K_2 + K_3$ (55)

Thus, the model (1) undergoes a backward bifurcation at $R_D=1$ whenever the inequality (55) holds.

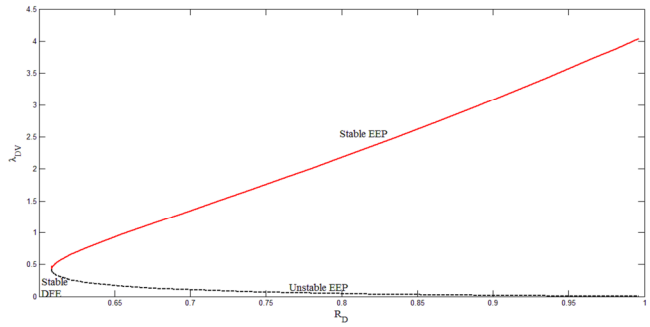

Fig. 3: Backward bifurcation diagram for the model (1) showing the force of infection λ_{DV} as a function of the control reproduction number R_D with all the parameters used as stated in Table (2) except $\beta_{VH} = 2$ and $\beta_{HV} = 1$ so that $R_D < 1$.

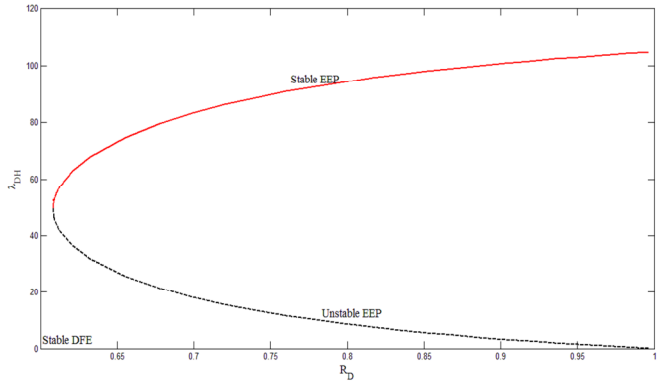

Fig. 4: Backward bifurcation diagram for the model (1) showing the force of infection λ_{DH} as a function of the control reproduction number R_D with all the parameters used as stated in Table (2) except $\beta_{VH} = 2$ and $\beta_{HV} = 1$ so that$R_D < 1$.

Simulations

Table 3: Parameter Information Using the parameter values in Table 3, we carried out some simulations of model (1).

Parameter	Values	Unit	References
Λ_H	500	Year^{-1}	Garba et al, 2008.
Λ_V	10^7	Year^{-1}	Garba et al, 2008.
μ_H	O.O2041	Year^{-1}	Okuonghae and Omosigho (2011)
μ_V	36.5	Year^{-1}	Okuonghae and Omosigho (2011)
β_{VH}	5	Year^{-1}	Garba et al, 2008.
β_{HV}	4	Year^{-1}	Gubler,1998
τ_1	2.5	Ind^{-1} Year^{-1}	Garba et al, 2008.
γ_1	0.3254	Year^{-1}	Gubler,1998
γ_V	0.03	Year^{-1}	Garba et al, 2008.
δ_{D1}	0.365	Year^{-1}	Gubler,1998
δ_{HV}	0	Year^{-1}	Gubler,1998
K_V	0.02	Year^{-1}	Garba et al, 2008.
$\eta_i(i = A, B)$	0.6,1	Year^{-1}	Garba et al, 2008.
η_V	0.5	Year^{-1}	Garba et al, 2008.

RESULTS AND DISCUSSION

Biologically speaking, Dengue is eliminated from the population when $R_D < 1$ if the initial sizes of the populations of the model are in the region of attraction of ξ_2. However, the disease free equilibrium may not be globally asymptotically stable even if $R_D < 1$ in the case when a backward bifurcation occurs. That is, there is the presence of a stable EEP co-existing with the DFE. The model undergoes the phenomenon of backward bifurcation at $R_D=1$ whenever the inequality (55) holds.

*Conclusion***:** In this paper, a mathematical model is proposed and analyzed to study the transmission dynamics of Dengue fever in a human population with treatment. Analyzing the models revealed that: The model undergoes a phenomenon of backward bifurcation if a certain condition shown in inequality (55) holds. The model possesses the disease free equilibrium and it also has an endemic equilibrium. Finally, the results from the numerical simulations show that treatment is crucial for an effective public health control of dengue fever.

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