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BIFURCATION ANALYSIS OF A MATHEMATICAL MODEL FOR TB-DENGUE CO-INFECTION

[1]Andrawus, J., [2]Nwankwo, A. and [2]*Okuonghae, D.

[1]Department of Mathematics, Federal University, Dutse, Jigawa State, Nigeria
[2]Department of Mathematics, University of Benin, Benin City, Nigeria
*daniel.okuonghae@uniben.edu

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ABSTRACT

Tuberculosis (TB) and Dengue are two diseases that have resulted in high mortality, mostly in developing countries. In this work, we investigate the causes of the backward bifurcation phenomenon in a mathematical model describing the dynamics of Tuberculosis-Dengue co-infection in a population where both diseases are endemic, a phenomenon characterized by the coexistence of a stable disease-free equilibrium with a stable endemic equilibrium, when the associated reproduction number is less than unity. The analyses showed that, for the TB-only model, exogenous reinfection and the reinfection of previously treated individuals are the causes of the backward bifurcation phenomenon, while for the Dengue-only model, disease-induced deaths in infected humans will lead to the backward bifurcation in the system. In co-infection scenarios where tuberculosis is having a larger disease burden than dengue, it is shown that the exogenous reinfection of latently infected TB individuals and the reinfection of previously treated individuals for TB will lead to the backward bifurcation phenomenon. The implication of these results is that for the reproduction numbers of the model to be useful for designing robust public health control measures against both diseases, concerted efforts must be geared towards minimizing the incidences of exogenous reinfection of latently infected TB cases, reinfection of previously treated individuals for TB and disease-induced deaths due to dengue infection.

1. INTRODUCTION

Tuberculosis (TB) is an airborne disease caused by *Mycobacterium tuberculosis*. According to the World Health Organization (WHO), about 9 million persons were infected with TB in 2013, with about 1.5 million deaths reported (WHO, 2014).

Dengue is a viral, vector borne disease, spread by the Aedes Aegypti mosquito (Nuraini *et al*., 2009). It was estimated that about 50 million infections occur annually in over 100 countries (WHO, 2005). 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).

There are 22 Tuberculosis (TB) high burden countries worldwide, and together they account for about 80% of the world's tuberculosis (TB) infection (International SOS, 2015). India accounts for over 20% of the world's multi-drugs resistant tuberculosis (MDR-TB) cases (International SOS, 2015). Dengue fever risk is present throughout India, including most metropolitan cities and towns (International SOS, 2015).

Mathematical models have long been used in understanding the underlying factors affecting the dynamics of infectious diseases (for example, see Okuonghae and Omosigho (2011) and Okuonghae and Ikhimwin (2016) for some TB mathematical models). Generally, the dynamics of most epidemiological models is often characterized by the basic reproduction number, usually written as R_o. The reproduction number measures the average number of new cases generated by a typical infected individual introduced into a completely susceptible population (Hethcote, 2000). Typically, when $R_o>1$, the disease will persist in the population and the endemic equilibrium will, generally, be locally asymptotically stable. When $R_o< 1$, then the disease will die out with time (even with the influx of a small number of infected individuals into the population), so that the disease free equilibrium (DFE) is locally asymptotically stable. However, in some cases, when $R_o<1$, the stable DFE will co-exist with a stable endemic equilibrium and an unstable endemic equilibrium, resulting to the phenomenon called backward bifurcation (see Gumel (2012) for some causes of the backward bifurcation phenomenon).

In this work, we will investigate the causes of the backward bifurcation in a mathematical model describing the dynamics of TB-Dengue co-infection in a population.

2. MODEL FORMULATION

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.

The total population of human and vectors is divided into the following mutually exclusive epidemiological classes, namely, susceptible humans ($S_H(t)$), humans with latent TB ($E_T(t)$), humans with active stage TB ($I_T(t)$), humans treated of active TB ($T_T(t)$), humans with latent dengue ($E_1(t)$), humans with dengue ($I_I(t)$), humans treated of dengue ($R_1(t)$), susceptible vectors ($S_V(t)$), vectors at the latent stage of dengue ($E_V(t)$), vectors infectious with dengue ($I_V(t)$), humans with latent TB and latent dengue ($E_2(t)$), humans with latent TB and infectious dengue ($E_3(t)$), humans with active TB and latent dengue ($E_4(t)$), and humans with active TB and dengue ($I_2(t)$). Hence, we have that,

$$N_H(t)=S_H(t)+E_T(t)+I_T(t)+T_T(t)+E_1(t)+I_1(t)+R_1(t)+E_2(t)+E_3(t)+E_4(t)+I_2(t) \quad (1)$$

and

$$N_V(t)=S_V(t)+E_V(t)+I_V(t) \quad (2)$$

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

$$\lambda_T = \frac{\beta_T \left(I_T + \eta_{T1} E_4 + \eta_{T2} I_2 \right)}{N_H}, \tag{3}$$

where β_T is the TB infectious contact rate, and η_{T1} and η_{T2} account for the relative infectiousness of those in E_4 and I_2 classes compared to those in I_T class; we assume that $\eta_{T2} > \eta_{T1} > 1$. Susceptible humans contract dengue at a rate given by Equation (4)

$$\lambda_{DV} = \frac{\beta_{VH} \left(\eta_v E_v + I_v \right)}{N_H} \tag{4}$$

where $\eta_v < 1$ 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 given by Equation (5)

$$\lambda_{DH} = \frac{\beta_{HV}(\eta_A E_1 + \eta_B I_1 + \eta_C E_2 + \eta_D E_3 + \eta_E E_4 + \eta_F I_2)}{N_H}. \tag{5}$$

The modification parameters $\eta_B, \eta_C, \eta_{D,}$ and η_F account for the relative infectiousness of those in the I_1, E_2, E_3 and I_2 classes compared to those in the E_1 and E_4 classes, where $\eta_A = \eta_E < 1$.

2.1. Derivation of Model Equations

Individuals in the E_T, E_2 and E_3 classes can be exogenously re-infected at the rate $\sigma_1 \lambda_T, \sigma_2 \lambda_T$ and $\sigma_3 \lambda_T$, respectively, where σ_1, σ_2 and σ_3 are modification parameters. A fraction P_{T1} $(0 \leq P_{T1} \leq 1)$ of susceptible and treated individual's progress faster to the I_T class while a fraction $\left(1 - P_{T2}\right)$ $(0 \leq P_{T2} \leq 1)$ of those treated for dengue progress faster to the I_T class. Also, a fraction $\left(1 - P_{D1}\right)$ $(0 \leq P_{D1} \leq 1)$ of individuals in the E_1 class progress faster to the E_4 class and $\left(1 - P_{D2}\right)$ $(0 \leq P_{D2} \leq 1)$ of those in the I_1 class progress faster to the I_2 class.

Active TB is treated at a rate r_1, r_2 and r_3 for those in the classes I_T, E_4 and I_2 classes, respectively, while dengue is treated at a rate τ_1, τ_2 and τ_3 for those in I_1, E_3 and I_2 classes respectively. Singly infected individuals with latent TB progress to active TB at a rate k_1; while dually infected individuals in the E_2 class progress to the E_4 class at the rate k_2. Individuals in the E_3 class progress to the I_2 class at the rate k_3. Singly infected individuals with latent dengue progress to active dengue at a rate γ_1 while dually infected individuals in the E_2 class progress to the E_3 class at the rate γ_2. Infected individuals in the E_4 class progress to the I_2 class at a rate γ_3.

Natural death in humans occurs at a rate μ_H in the classes S_H, E_T, I_T, T_T, E_1, I_1, R_1, E_2, E_3, E_4 *and* I_2 while those in the I_T, E_4 and I_2 classes undergo an additional TB induced death at the rates d_{T1}, d_{T2} and d_{T3}, respectively. Individuals in the I_1, E_3 and I_2 classes undergo an additional dengue induced death, at rates δ_{D1}, δ_{D2} and δ_{D3}, respectively. Treated individuals have a relative difference in susceptibility to TB after a previous infection compared to wholly susceptible

individuals (with $\varepsilon \geq 0$ being the modification parameter accounting for this relative difference in susceptibility). 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 affected by 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:

$$\dot{S}_H = \Lambda_H - \lambda_T S_H - \mu_H S_H - \lambda_{DV} S_H, \tag{6}$$

$$\dot{E}_T = (1 - P_{T1})\lambda_T S_H + (1 - P_{T1})\epsilon\lambda_T T_T - \sigma_1\lambda_T E_T - (\mu_H + k_1)E_T - \lambda_{DV} E_T + P_{T2}\lambda_T R_1 + \tau_1 E_2, \tag{7}$$

$$\dot{I}_T = P_{T1}\lambda_T S_H + P_{T1}\epsilon\lambda_T T_T - (\mu_H + d_{T1} + r_1)I_T + \sigma_1\lambda_T E_T - \lambda_{DV} I_T + (1 - P_{T2})\lambda_T R_1 + \tau_3 I_2 + k_1 E_T, \tag{8}$$

$$\dot{T}_T = r_1 I_T - \epsilon\lambda_T T_T - \mu_H T_T - \lambda_{DV} T_T, \tag{9}$$

$$\dot{E}_1 = \lambda_{DV} S_H + \lambda_{DV} T_T - (\gamma_1 + \mu_H)E_1 - \lambda_T E_1 + r_2 E_4, \tag{10}$$

$$\dot{I}_1 = \gamma_1 E_1 - (\tau_1 + \mu_H + \delta_{D1})I_1 - \lambda_T I_1 + r_3 I_2, \tag{11}$$

$$\dot{R}_1 = \tau_1 I_1 - \mu_H R_1 - \lambda_T R_1, \tag{12}$$

$$\dot{S}_V = \Lambda_V - \lambda_{DH} S_V - \mu_V S_V, \tag{13}$$

$$\dot{E}_V = \lambda_{DH} S_V - (\gamma_V + \mu_V)E_V, \tag{14}$$

$$\dot{I}_V = \gamma_V E_V - (\mu_V + \delta_{HV})I_V, \tag{15}$$

$$\dot{E}_2 = \lambda_{DV} E_T + P_{D1}\lambda_T E_1 - (\gamma_2 + k_2 + \mu_H)E_2 - \sigma_2\lambda_T E_2, \tag{16}$$

$$\dot{E}_3 = \gamma_2 E_2 + P_{D2}\lambda_T I_1 - (k_3 + \tau_2 + \delta_{D2} + \mu_H)E_3 - \sigma_3\lambda_T E_3, \tag{17}$$

$$\dot{E}_4 = (1 - P_{D1})\lambda_T E_1 + \lambda_{DV} I_T + k_2 E_2 - (d_{T2} + r_2 + \gamma_3 + \mu_H)E_4 + \sigma_2\lambda_T E_2, \tag{18}$$

$$\dot{I}_2 = (1 - P_{D2})\lambda_T I_1 - (\tau_3 + r_3 + \delta_{D3} + d_{T3} + \mu_H)I_2 + k_3 E_3 + \gamma_3 E_4 + \sigma_3\lambda_T E_3. \tag{19}$$

Table 1 gives the description of the state variables of the model (6) – (19).

Table 1: Description of the state variables of the model (6) – (19)

Variable	Description
S_H	Susceptible human population
E_T	Human population with TB in latent stage (TB only)
I_T	Human population with TB in active stage (TB only)
T_T	Human population treated of TB (TB only)
E_1	Human population with dengue in latent stage (Dengue only)
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
E_2	Dually infected humans with latent TB and latent dengue
E_3	Dually infected humans with dengue and latent TB
E_4	Dually infected human with active TB and latent dengue
I_2	Dually infected human with active TB and dengue

3. ANALYSIS OF SUB-MODELS

Before analyzing the complete model (6) – (19), it is instructive to gain insight into the occurrence of the backward bifurcation phenomenon for the TB-only model and the dengue- only model.

3.1. TB-only Model

The TB only model is derived in (6) – (19) by setting $E_1 = R_1 = S_V = E_V = I_V = E_2 = E_3 = E_4 = I_2 = 0$. Hence we have

$$\frac{dS_H}{dt} = \Lambda_H - \lambda_T S_H - \mu_H S_H, \tag{20}$$

$$\frac{dE_T}{dt} = (1-P_{T1})\lambda_T S_H + (1-P_{T1})\in \lambda_T T_T - \sigma_1\lambda_T E_T - (\mu_H + k_1)E_T, \tag{21}$$

$$\frac{dI_T}{dt} = P_{T1}\lambda_T S_H + P_{T1}\in \lambda_T T_T - (\mu_H + d_{T1} + r_1)I_T + \sigma_1\lambda_T E_T + k_1 E_T, \tag{22}$$

$$\frac{dT_T}{dt} = r_1 I_T - \in \lambda_T T_T - \mu_H T_T, \tag{23}$$

where $\lambda_T = \frac{\beta_T I_T}{N_H}$ and $N_H = S_H + E_T + I_T + T_T$.

Consider the region $D_1 = \{(S_H, E_T, I_T, T_T)\epsilon\mathbb{R}_+^4 : N_H \leq \frac{\Lambda_H}{\mu_H}\}$. It can be shown that the set D_1 is positively invariant and a global attractor of all positive solution of the system (20) – (23). We claim the following.

Lemma 1: *The region D_1 is positively invariant for the system* (20) – (23).

Proof: The rate of change of the total population is give as

$$\dot{N}_H(t) = \dot{S}_H + \dot{E}_T + \dot{I}_T + \dot{T}_T = \Lambda_H - \mu_H(S_H + E_T + I_T + T_T) - d_{T1}I_T$$

$$\dot{N}_H(t) = \Lambda_H - \mu_H N_H - d_{T1}I_T.$$

Since the right-hand side of (20) – (23) is bounded by $\Lambda_H - \mu_H N_H$, standard comparison theorem (Lakshmikantham *et al.*, 1989) can be used to show that

$$N_H \leq N_H(0)e^{-\mu_H t} + \frac{\Lambda_H}{\mu_H}[1 - e^{-\mu_H t}].$$

If $N_H(0) \leq \frac{\Lambda_H}{\mu_H}$ then $N_H(0) \leq \frac{\Lambda_H}{\mu_H}$. Thus, D_1 is a positively invariant set under the flow described in (20) – (23). Hence, no solution path leaves through and boundary of D_1. In this region, the model (20) – (23) is said to be well posed mathematically and epidemiologically.

We now prove the positivity of solutions of the model (20) – (23). We claim the following.

Lemma 2: *Let the initial data for the model (20) – (23) be $S_H(t) > 0$, $E_T(t) > 0, I_T(t) > 0,$ and $T_T(t) > 0$ then the solution $S_H(t)$, $E_T(t)$, $I_T(t)$, and $T_T(t)$ with positive initial data will remain positive for all time t > 0.*

Proof: Let $t_1 = sup\{t > 0 : S_H(t) > 0, E_T(t) > 0, I_T(t) > 0, T_T(t) > 0\} > 0$

$\dot{S}_H = \Lambda_H - \lambda_T S_H - \mu_H S_H = \Lambda_H - (\lambda_T + \mu_H)S_H,$

which, when solved, leads to

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

Hence, S_H is positive for all time, t. Similarly, we can show that $E_T(t) > 0, I_T(t) > 0, and\ T_T(t) > 0$ for all time, t.

3.1.1. Local stability of disease-free equilibrium (DFE) of the TB-only model

The model (20) – (23) has a disease-free equilibrium obtained by setting the right hand side of the model to zero given by:

$$\xi_1 = \left(S_H^*, E_T^*, I_T^*, T_T^*\right) = \left(\frac{\Lambda_H}{\mu_H}, 0, 0, 0\right).$$

The linear stability of ξ_1 is established using the next generation operator method on the system (20) – (23) (van den Driessche and Watmough, 2002). Using the notation in van den Driessche and Watmough (2002), the matrices F and V, for the new infection terms and the remaining transfer terms respectively, are given by:

$$F = \begin{pmatrix} 0 & (1-P_{T1})\beta_T \\ 0 & P_{T1}\beta_T \end{pmatrix}, \text{ and } V = \begin{pmatrix} g_1 & 0 \\ -k_1 & g_2 \end{pmatrix}.$$

It follows that the effective reproduction number of the model (20) – (23), denoted by R_T, is given by:

$$R_T = \rho(FV^{-1}) = \frac{\beta_T\left(g_1 P_{T1} + k_1(1-P_{T1})\right)}{g_1 g_2},$$

where $\rho(FV^{-1})$ is the spectral radius of the matrix FV^{-1}. The next result follows from Theorem 2 in van den Driessche and Watmough (2002).

Lemma 3: *The DFE, ξ_1, of the model* (20) – (23) *is locally asymptotically stable (LAS) if* $R_T < 1$, *and unstable if* $R_T > 1$.

The threshold quantity, $R_{T,}$ is the effective reproduction number for the TB sub-model. It represents the average number of secondary TB infections generated by a typical infected individual in a completely susceptible population where treatment for TB is available. Epidemiologically speaking, Lemma 3 implies that TB can be eliminated from the population when $R_T < 1$ if the initial sizes of the sub-population of the sub-model are in the basin of attraction of ξ_1. Hence, a small influx of TB-infected individuals into the community will not generate large TB outbreaks, and the disease will die out with time.

3.1.2. Backward bifurcation analysis of the TB-only model

It is instructive to characterize the type of bifurcation model (20) – (23) may undergo. We claim the following result, with the proof (based on the Centre manifold Theorem (Castillo-Chavez and Song, 2004)) given below.

Theorem 1: The model (20) – (23) does not undergo a backward bifurcation at $R_T = 1$ whenever parameters $\sigma_1 = 0\ and\ \epsilon = 0$.

Proof:

Let $x_1 = S_H, x_2 = E_T, x_3 = I_T, x_4 = T_T$. Further, let $\hat{f} = [f_1, ..., f_4]^T$ denote the vector field of (20) – (23). Thus, the model (20) – (23) can be re-written as:

$$\frac{dx_1}{dt} = \Lambda_H - \frac{\beta_T x_3 x_1}{x_1 + x_2 + x_3 + x_4} - \mu_H x_1, \tag{24}$$

$$\frac{dx_2}{dt} = \frac{(1-P_{T1})\beta_T x_3 x_1}{x_1 + x_2 + x_3 + x_4} + \frac{(1-P_{T1}) \in \beta_T x_3 x_4}{x_1 + x_2 + x_3 + x_4} - \frac{\sigma_1 \beta_T x_3 x_2}{x_1 + x_2 + x_3 + x_4} g_1 x_2, \tag{25}$$

$$\frac{dx_3}{dt} = \frac{P_{T1}\beta_T x_3 x_1}{x_1 + x_2 + x_3 + x_4} + \frac{P_{T1} \in \beta_T x_3 x_4}{x_1 + x_2 + x_3 + x_4} - g_2 x_3 + \frac{\sigma_1 \beta_T x_3 x_2}{x_1 + x_2 + x_3 + x_4} + k_1 x_2, \tag{26}$$

$$\frac{dx_4}{dt} = r_1 x_3 - \frac{\in \beta_T x_3 x_4}{x_1 + x_2 + x_3 + x_4} - \mu_H x_4, \tag{27}$$

The Jacobian of the transformed system (24) – (27), evaluated at the *DFE* (ξ_1), is given by

$$J(\xi_0) = \begin{bmatrix} -\mu_H & 0 & -\beta_T^* & 0 \\ 0 & -g_1 & (1-P_{T1})\beta_T^* & 0 \\ 0 & k_1 & -(P_{T1}\beta_T^* + g_2) & 0 \\ 0 & 0 & r_1 & -\mu_H \end{bmatrix}.$$

Consider the case when $R_T = 1$. Furthermore, let $\beta_T = \beta_T^*$ be the bifurcation parameter. Solving for β_T from$R_T = 1$ gives $\beta_T = \beta_T^* = \frac{g_1 g_2}{g_1 P_{T1} + k_1(1-P_{T1})}$.

The right eigenvector of $J(\xi_1)\big|_{\beta_T = \beta_T^*}$ is given by

$w = (w_1, w_2, w_3, w_4)^T$ where,

$$w_1 = -\frac{g_1}{k_1(1-P_{T1})\mu_H} < 0,$$

$$w_2 = \frac{(1-P_{T1})\beta_T^*}{-g_1(P_{T1}\beta_T^* - g_2)} > 0,$$

$$w_3 = \frac{g_1}{k_1(1-P_{T1})\beta_T^*} > 0,$$

$$w_4 = \frac{r_1 g_1}{k_1(1-P_{T1})\mu_H \beta_T^*} > 0.$$

Furthermore, $J(\xi_1)\big|_{\beta_T = \beta_T^*}$ has a left eigenvector, given by

$v = (v_1, v_2, v_3, v_4)$ where,

$$v_1 = 0, \quad v_2 = \frac{k_1}{-g_1(P_{T1}\beta_T^* - g_2)} > 0$$

$$v_3 = \frac{g_1}{k_1(1-P_{T1})\beta_T^*} > 0, \; v_4 = 0$$

It follows from Theorem 4.1 in Castillo-Chavez and Song (2004), if we compute the associated non-zero partial derivatives of $F(x)$ (evaluated at the DFE ξ_1), that the associated bifurcation coefficients, a and b, defined by:

$$a = \sum_{k,i,j=1}^{4} v_k w_i w_j \frac{\partial^2 f_k}{\partial x_i \partial x_j}(0,0),$$

and

$$b = \sum_{k,i=1}^{4} v_k w_i \frac{\partial^2 f_k}{\partial x_i \partial x \beta_T^*}(0,0)$$

are computed to be

$$\begin{aligned} a = {} & \frac{2v_2}{x_1^*}[-(1-P_{T1})\beta_T^* w_2 w_3 - \sigma_1 \beta_T^* w_2 w_3 - (1-P_{T1})\beta_T^* w_3^2 + (\varepsilon - 1)(1-P_{T1})\beta_T^* w_3 w_4] + \\ & \frac{2v_3}{x_1^*}[-P_{T1}\beta_T^* w_2 w_3 + \sigma_1 \beta_T^* w_2 w_3 - P_{T1}\beta_T^* w_3^2 + (\varepsilon - 1)P_{T1}\beta_T^* w_3 w_4] \end{aligned} \tag{28}$$

and

$$b = \frac{(g_1 P_{T1} + k_1(1-P_{T1}))}{g_2^2}\left[\frac{1}{g_1} + \frac{P_{T1}(g_1 P_{T1} + k_1(1-P_{T1}))}{k_1^2(1-P_{T1})^2}\right] > 0.$$

Since the bifurcation coefficient b is positive, it follows from Theorem 4.1 in Castillo-Chavez and Song (2004) that model (20) – (23), or the transformed model (24) – (27), will undergo a backward bifurcation if the backward bifurcation coefficient, a, given by (28), is positive.

Setting $\varepsilon = 0$ and $\sigma_1 = 0$, results in $a < 0$. Thus, it follows that Theorem 4.1 of Castillo Chavez and Song (2004) that the model (20) – (23) will not undergo a backward bifurcation if $\varepsilon = 0$ and $\sigma_1 = 0$. Hence, in the absence of exogenous re-infection ($\sigma_1 = 0$) and reinfection of treated individuals, there will be no backward bifurcation at $R_T = 1$; only the DFE will exist when $R_T < 1$. Figure 1 shows the bifurcation diagram for the TB-only model (2). Here, we can see the coexistence of the stable DFE with one stable EEP and an unstable EEP, when $R_T < 1$.

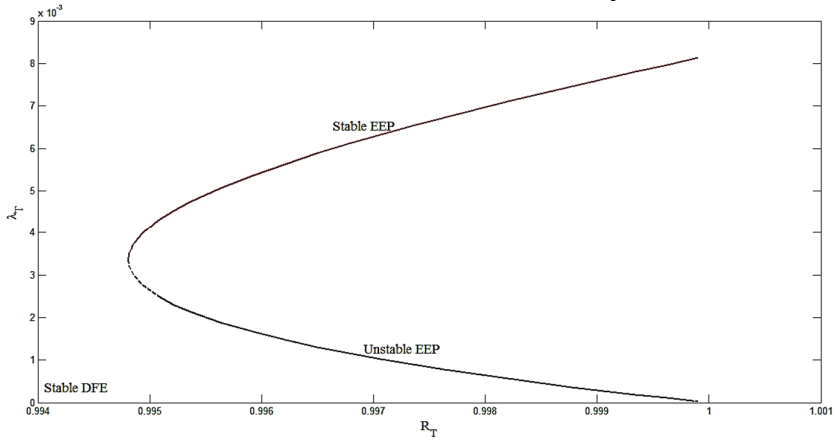

Figure 1: Backward Bifurcation Diagram for the Model (20) – (23) showing the force of infection λ_T as a function of the control reproduction number R_T.

3.2. Dengue-only Model

The dengue only model is derived from system (6) – (19) by setting $E_T = I_T = T_T = E_2 = E_3 = E_4 = I_2 = 0$. This leads to the following sub-model:

$$\frac{dS_H}{dt} = \Lambda_H - \mu_H S_H - \lambda_{DV} S_H, \tag{29}$$

$$\frac{dE_1}{dt} = \lambda_{DV} S_H - (\gamma_1 + \mu_H) E_1, \tag{30}$$

$$\frac{dI_1}{dt} = \gamma_1 E_1 - (\tau_1 + \mu_H + \delta_{D1}) I_1, \tag{31}$$

$$\frac{dR_1}{dt} = \tau_1 I_1 - \mu_H R_1, \tag{32}$$

$$\frac{dSv}{dt} = \Lambda_V - \lambda_{DH} S_V - \mu_V S_V, \tag{33}$$

$$\frac{dE_V}{dt} = \lambda_{DH} S_V - (\gamma_V + \mu_V) E_V, \tag{34}$$

$$\frac{dI_V}{dt} = \gamma_V E_V - (\mu_V + \delta_{HV}) I_V, \tag{35}$$

with

$$\lambda_{DV} = \frac{\beta_{VH}(\eta_v E_v + I_v)}{N_H}, \lambda_{DH} = \frac{\beta_{HV}(\eta_A E_1 + \eta_B I_1 + \eta_C E_2 + \eta_D E_3 + \eta_E E_4 + \eta_F I_2)}{N_H}, \; N_H = S_H + E_1 + I_1 + R_1$$

and $N_V = S_V + E_V + I_V$.

Consider the region $D_2 = \left\{(S_H, E_1, I_1, R_1, S_V, E_V, I_V) \epsilon \mathbb{R}_+^7 : N_H \leq \frac{\Lambda_H}{\mu_H}, N_V \leq \frac{\Lambda_V}{\mu_V}\right\}$. Using the approaches used in Section 3.1, it can be shown that the set D_2 is positively invariant and an attractor of all positive solution of the system (29) – (35). Hence, we claim the following

Lemma 4. *The region D_2 is positively invariant for the system* (29) – (35).

Lemma 5. *Let the initial data for the model* (29) – (35) *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.*

3.2.1. Local stability of disease-free equilibrium (DFE) of the Dengue-only model

The model (29) – (35) has a disease-free equilibrium, obtained by setting the right hand side of the model to zero, given by

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

The stability of ξ_2 is established using the next generation operator method on the system (29) – (35) (van den Driessche and Watmough, 2002). Following the procedure, as implemented in Section 3.1.1, we have that the effective reproduction number is given by

$R_D = \sqrt{\frac{\Lambda_V \beta_{HV} \beta_{VH} \mu_H (g_4 \eta_A + \gamma_1 \eta_B)(\gamma_V + g_6 \eta_V)}{\Lambda_H g_3 g_4 g_5 g_6 \mu_V}}$,

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 next result follows from Theorem 2 in van den Driessche and Watmough (2002).

Lemma 6. *The DFE of the system* (29) – (35) *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 only sub-model. The implication of Lemma 6 is that Dengue can be eliminated from the population when $R_D < 1$ if the initial sizes of the subpopulations of the sub-model are in the region of attraction of ξ_2.

3.2.2. Backward Bifurcation Analysis of the Dengue-only Model

It is instructive to characterize the type of bifurcation model (29) – (35) may undergo. We claim the following result, with the proof (based on the Centre manifold Theorem (Castillo Chavez and Song, 2004)) given below.

Theorem 2: The model (29) – (35) undergoes backward bifurcation phenomenon at $R_D = 1$ when $\delta_{D1} = 0$.

Proof:

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 (29) – (35). Thus, the model (29) – (35) can be written as:

$$\frac{dx_1}{dt} = \Lambda_H - \mu_H x_1 - \frac{\beta_{VH}(\eta_V x_6 + x_7)x_1}{x_1 + x_2 + x_3 + x_4}, \tag{36}$$

$$\frac{dx_2}{dt} = \frac{\beta_{VH}(\eta_V x_6 + x_7)x_1}{x_1 + x_2 + x_3 + x_4} - (\gamma_1 + \mu_H)x_2, \tag{37}$$

$$\frac{dx_3}{dt} = \gamma_1 x_2 - (\tau_1 + \mu_H + \delta_{DI})x_3, \tag{38}$$

$$\frac{dx_4}{dt} = \tau_1 x_3 - \mu_H x_4, \tag{39}$$

$$\frac{dx_5}{dt} = \Lambda_V - \frac{\beta_{HV}(\eta_A x_2 + \eta_B x_3)x_5}{x_1 + x_2 + x_3 + x_4} - \mu_V x_5, \tag{40}$$

$$\frac{dx_6}{dt} = \frac{\beta_{HV}(\eta_A x_2 + \eta_B x_3)x_5}{x_1 + x_2 + x_3 + x_4} - (\gamma_V + \mu_V)x_6, \tag{41}$$

$$\frac{dx_7}{dt} = \gamma_V x_6 - (\mu_V + \delta_{HV})x_7, \tag{42}$$

The Jacobian of the transformed system (36) – (42), evaluated at the *DFE,* ξ_2 , is given by:

$$J(\xi_2)=\begin{bmatrix} -\mu_H & 0 & 0 & 0 & 0 & -\beta^*_{vH}\eta_v & -\beta^*_{vH} \\ 0 & -g_3 & 0 & 0 & 0 & \beta^*_{vH}\eta_v & \beta^*_{vH} \\ 0 & \gamma_1 & -g_4 & 0 & 0 & 0 & 0 \\ 0 & 0 & \tau_1 & -\mu_H & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & -\mu_V & 0 & 0 \\ 0 & \beta^*_{vH}\eta_A x_5^* & \beta^*_{vH}\eta_B x_5^* & 0 & 0 & -g_5 & 0 \\ 0 & 0 & 0 & 0 & 0 & \gamma_v & -g_6 \end{bmatrix},$$

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

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

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

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

$$w_1=-\frac{\beta^{*2}_{VH}x_5^* w_2(g_4\eta_A+\gamma_1\eta_B)}{x_1^* g_4 g_5 g_6 \mu_H}(\gamma_V+\eta_V g_6)<0, w_2=w_2>0, w_3=\frac{\gamma_1 w_2}{g_4},$$

$$w_4=\frac{\tau_1 w_3}{\mu_H}, w_5=-\frac{\beta_{VH}x_5^* w_2}{\mu_V x_1^* g_4}(g_4+\gamma_1\eta_B), w_6=\frac{\beta^*_{VH}x_5^* w_2(g_4\eta_A+\gamma_1\eta_B)}{g_4 g_5 x_1^*},$$

$$w_7=\frac{\beta^*_{VH}x_5^*\gamma_V w_2(g_4\eta_A+\gamma_1\eta_B)}{g_4 g_5 g_6 x_1^*}.$$

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

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

$$v_1=0, v_2=v_2>0, v_3=v_3>0, v_4=0, v_5=0$$

$$v_6=\frac{\beta^*_{VH}v_2(\eta_V g_6+\gamma_V)}{g_5 g_6}, v_7=\frac{\beta^*_{vH}\eta_B x_5^*(\eta_V g_6+\gamma_V)v_2}{x_1^* g_4 g_5 g_6}.$$

It follows from Theorem 4.1 in Castillo Chavez and Song (2004), if we compute the associated non-zero partial derivatives of $F(x)$ (evaluated at the DFE ξ_2), that the associated bifurcation coefficients, a and b, defined by

$$a=\sum_{k,i,j=1}^{4} v_k w_i w_j \frac{\partial^2 f_k}{\partial x_i \partial x_j}(0,0),$$

and

$$b=\sum_{k,i=1}^{4} v_k w_i \frac{\partial^2 f_k}{\partial x_i \partial x \beta^*_T}(0,0)$$

are computed to be

$$a = \frac{-2v_2}{x_1^{*2}\mu_H g_4^2 g_5 g_6}[w_2^2(\mu_H g_4 + \gamma_1\mu_H + \tau_1\gamma_1)\beta_{VH}^2 x_5^*(g_4 + \eta_B\gamma_1)(\eta_V g_6 + \gamma_V)] + \frac{2v_2\beta_{VH}^2(\eta_V g_6 + \gamma_V)}{x_1^{*2} g_5 g_6}[\frac{x_5^* w_2^2 \delta_{D1}\gamma_1}{g_4\mu_H} + \frac{\eta_B x_5^*\gamma_1^2 w_2^2\delta_{D1}}{g_4^2\mu_H} - \frac{x_1^*\beta_{VH}x_5^* w_2^2(g_4+\eta_B\gamma_1)^2}{\mu_V x_1^* g_4^2}] \quad (43)$$

and

$$b = \frac{2\beta_{VH}^* x_5^* w_2(g_4 + \eta_B\gamma_1)(\eta_V g_6 + \gamma_V)w_2 v_2 x_5^*}{g_4 g_5 g_6 x_1^*} > 0.$$

Since the bifurcation coefficient b is positive, it follows from Theorem 4.1 in Castillo Chavez and Song (2004) that model (29) – (35), or the transformed model (36) – (42), will undergo a backward bifurcation if the backward bifurcation coefficient, a, given by (43), is positive.

Setting $\delta_{D1} = 0$, leads to

$$a = \frac{-2v_2}{x_1^{*2}\mu_H g_4^2 g_5 g_6}[w_2^2(\mu_H g_4 + \gamma_1\mu_H + \tau_1\gamma_1)\beta_{VH}^2 x_5^*(g_4 + \eta_B\gamma_1)(\eta_V g_6 + \gamma_V)] - \frac{2v_2\beta_{VH}^2(\eta_V g_6 + \gamma_V)}{x_1^{*2} g_5 g_6}\frac{x_1^*\beta_{VH}x_5^* w_2^2(g_4+\eta_B\gamma_1)^2}{\mu_V x_1^* g_4^2}] < 0.$$

Thus, it follows that Theorem 4.1 of Castillo Chavez and Song (2004) that the model (29) – (35) will not undergo a backward bifurcation if $\delta_{D1} = 0$. Hence, in the absence of disease-induced death in humans, there will be no backward bifurcation in the Dengue-only model at $R_D = 1$; only the DFE will exist when $R_D < 1$. Figure 2 shows the bifurcation diagram for the Dengue-only model (29) – (35). Here, we can see the coexistence of the stable DFE with one stable EEP and an unstable EEP, when $R_D < 1$.

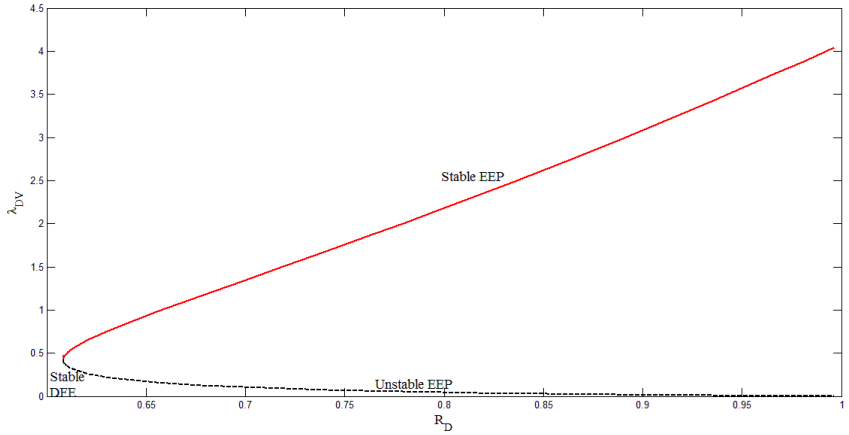

Figure 2: Backward bifurcation diagram for the model (29) – (35) showing the force of infection λ_{DV} as a function of the control reproduction number R_D.

4. ANALYSIS OF FULL MODEL

Consider the region

$$D = \{(S_H, E_T, I_T, T_T, E_1, I_1, R_1, S_V, E_V, I_V, E_2, E_3, E_4, I_2) \epsilon \mathbb{R}_+^{14} : N_H \leq \frac{\Lambda_H}{\mu_H}, N_V \leq \frac{\Lambda_V}{\mu_V}\}.$$

Using the approaches in Section 3.1, it can be shown that the set D is positively invariant and an attractor of all positive solution of the system (6) – (19). Hence, we claim the following.

Lemma 7. *The region D is positively invariant for the system* (6) – (19).
Lemma 8. *Let the initial data for the model* (6) – (19) *be* $S_H(t) > 0, E_T(t) > 0, I_T(t) > 0, T_T(t) > 0, E_1(t) > 0, I_1(t) > 0, R_1(t) > 0, S_V(t) > 0, E_V(t) > 0, I_V(t) > 0, E_2(t) > 0, E_3(t) > 0, E_4(t) > 0, and\ I_2(t) > 0$ *then the solution* $S_H(t), E_T(t), I_T(t), T_T(t), E_1(t), I_1(t), R_1(t), S_V(t), E_V(t), I_V(t), E_2(t), E_3(t), E_4(t), and\ I_2(t)$ *with positive initial data will remain positive for all time t > 0.*

4.1. Local Stability of disease-free equilibrium (DFE) of TB-Dengue Model

The model (6) – (19) has a disease-free equilibrium obtained by setting the right hand side of the model to zero given by

$$\xi_3 = (S_H^*, E_T^*, I_T^*, T_T^*, E_1^*, I_1^*, R_1^*, S_V^*, E_V^*, I_V^*, E_2^*, E_3^*, E_4^*, I_2^*) = (\frac{\Lambda_H}{\mu_H}, 0,0,0,0,0,0, \frac{\Lambda_V}{\mu_V}, 0,0,0,0,0,0)$$

The linear stability of ξ_3 is established using the next generation operator method on the system (6) – (19) (van den Driessche and Watmough, 2002). Following a similar procedure in Section 3.1.1, the effective reproduction number of the TB-Dengue model (6) – (19) is obtained as R_C = max $\{R_T, R_D\}$, where $R_T = \dfrac{\beta_T\left(g_1 P_{T1} + k_1(1-P_{T1})\right)}{g_1 g_2}$,

$R_D = \sqrt{\dfrac{\Lambda_v \beta_{Hv} \beta_{vH} \mu_H \left(g_4\eta_A + \gamma_1\eta_B\right)\left(\gamma_v + g_6\eta_v\right)}{\Lambda_H g_3 g_4 g_5 g_6 \mu_v}}$, and

$g_1 = \mu_H + k_1, g_2 = \mu_H + d_{T1} + r_1, g_3 = \gamma_1 + \mu_H . g_4 = \tau_1 + \mu_H + \delta_{D1}, g_5 = \gamma_V + \mu_V, g_6 = \mu_V + \delta_{HV},$

$g_7 = \gamma_2 + k_2 + \mu_H, g_8 = k_3 + \tau_2 + \delta_{D2} + \mu_H, g_9 = d_{T2} + r_2 + \gamma_3 + \mu_H, g_{10} = \tau_3 + r_3 + \delta_{D3} + d_{T3} + \mu_H,$

$N_H^* = \dfrac{\Lambda_H}{\mu_H}$, and $S_V^* = \dfrac{\Lambda_V}{\mu_V}$.

The control reproduction number, associated with the *DFE* (ξ_3) of the model (6) – (19), denoted by R_C. The following results follows from Theorem 2 in from van den Driessche and Watmough (2002).

Lemma 9: *The DFE,* ξ_3 *of the model* (6) – (19) *is locally asymptotically stable (LAS) if* $R_C < 1$ *and unstable if* $R_C > 1$.

4.2. Bifurcation Analysis of TB-Dengue Model

It is instructive to characterize the type of bifurcation the complete TB-Dengue model (6) – (19) may undergo. We claim the following result, with the proof (based on the Centre manifold Theorem (Castillo Chavez and Song, 2004)) given below.

Theorem 3. T*he model* (6) – (19) *does not undergoes backward bifurcation phenomenon at* $R_C = 1$ *whenever* $\sigma_1 = \epsilon = 0$.

Proof: Let

$x_1 = S_H, x_2 = E_T, x_3 = I_T, x_4 = T_T, x_5 = E_1, x_6 = I_1, x_7 = R_1, x_8 = S_v, x_9 = E_v,$

$x_{10} = I_v, x_{11} = E_2, x_{12} = E_3, x_{13} = E_4, x_{14} = I_2$

Further, let $\hat{f} = [f_1, f_2, ..., f_{14}]^T$ denote the vector field of the model (6) – (19). Thus, the model (6) – (19) can be re-written as:

$$\frac{dx_1}{dt} = \Lambda_H - \frac{\beta_T(x_3 + \eta_{T1}x_{13} + \eta_{T2}x_{14})x_1}{N_H} - \frac{\beta_{vH}(\eta_v x_9 + x_{10})x_3}{N_H} - \mu_H x_1, \tag{44}$$

$$\frac{dx_2}{dt} = \frac{(1-P_{T1})\beta_T(x_3 + \eta_{T1}x_{13} + \eta_{T2}x_{14})x_1}{N_H} + \frac{(1-P_{T1})\in \beta_T(x_3 + \eta_{T1}x_{13} + \eta_{T2}x_{14})x_4}{N_H}$$
$$- \frac{\sigma_1\beta_T(x_3 + \eta_{T1}x_{13} + \eta_{T2}x_{14})x_2}{N_H} - g_1x_2 - \frac{\beta_{vH}(\eta_v x_9 + x_{10})x_2}{N_H} + \frac{P_{T2}\beta_T(x_3 + \eta_{T1}x_{13} + \eta_{T2}x_{14})x_7}{N_H} + \tau_2 x_{13}, \tag{45}$$

$$\frac{dx_3}{dt} = \frac{P_{T1}\beta_T(x_3 + \eta_{T1}x_{13} + \eta_{T2}x_{14})x_1}{N_H} + \frac{P_{T1}\in \beta_T(x_3 + \eta_{T1}x_{13} + \eta_{T2}x_{14})x_4}{N_H} - g_2x_3$$
$$+ \frac{\sigma_1\beta_T(x_3 + \eta_{T1}x_{13} + \eta_{T2}x_{14})x_2}{N_H} - \frac{\beta_{vH}(\eta_v x_9 + x_{10})x_3}{N_H} + \frac{(1-P_{T2})\beta_T(x_3 + \eta_{T1}x_{13} + \eta_{T2}x_{14})x_7}{N_H}$$
$$-\tau_3x_{14} + k_1x_2, \tag{46}$$

$$\frac{dx_4}{dt} = r_1x_3 - \frac{\in \beta_T(x_3 + \eta_{T1}x_{13} + \eta_{T2}x_{14})x_4}{N_H} - \mu_H x_4 - \frac{\beta_{vH}(\eta_v x_9 + x_{10})x_4}{N_H} \tag{47}$$

$$\frac{dx_5}{dt} = \frac{\beta_{vH}(\eta_v x_9 + x_{10})x_1}{N_H} + \frac{\beta_{vH}(\eta_v x_9 + x_{10})x_4}{N_H} - g_3x_5 + r_2x_{13} - \frac{\beta_T(x_3 + \eta_{T1}x_{13} + \eta_{T2}x_{14})x_5}{N_H}, \tag{48}$$

$$\frac{dx_6}{dt} = \gamma_1x_5 - g_4x_6 - \frac{\beta_T(x_3 + \eta_{T1}x_{13} + \eta_{T2}x_{14})x_6}{N_H} + \gamma_3x_{14}, \tag{49}$$

$$\frac{dx_7}{dt} = \tau_1x_6 - \mu_H x_7 - \frac{\beta_T(x_3 + \eta_{T1}x_{13} + \eta_{T2}x_{14})x_7}{N_H} \tag{50}$$

$$\frac{dx_8}{dt} = \Lambda_v - \frac{\beta_{Hv}(\eta_A x_5 + \eta_B x_6 + \eta_c x_9 + \eta_D x_{12} + \eta_E x_{13} + \eta_F x_{14})x_8}{N_H} - \mu_v x_8, \tag{51}$$

$$\frac{dx_9}{dt} = \frac{\beta_{Hv}(\eta_A x_5 + \eta_B x_6 + \eta_c x_9 + \eta_D x_{12} + \eta_E x_{13} + \eta_F x_{14})x_8}{N_H} - g_5x_9, \tag{52}$$

$$\frac{dx_{10}}{dt} = \gamma_v x_9 - g_6x_{10}, \tag{53}$$

$$\frac{dx_{11}}{dt} = \frac{\beta_{vH}(\eta_v x_9 + x_{10})x_2}{N_H} - \frac{P_{D1}\beta_T(x_3 + \eta_{T1}x_{13} + \eta_{T2}x_{14})x_5}{N_H} - g_7x_{11} - \frac{\sigma_2\beta_T(x_3 + \eta_{T1}x_{13} + \eta_{T2}x_{14})x_{11}}{N_H}, \tag{54}$$

$$\frac{dx_{12}}{dt} = \gamma_2 x_{11} + \frac{P_{D2}\beta_T(x_3 + \eta_{T1}x_{13} + \eta_{T2}x_{14})x_6}{N_H} - g_8 x_{12} - \frac{\sigma_3\beta_T(x_3 + \eta_{T1}x_{13} + \eta_{T2}x_{14})x_{12}}{N_H} \quad (55)$$

$$\frac{dx_{13}}{dt} = \frac{(1-P_{D1})\beta_T(x_3 + \eta_{T1}x_{13} + \eta_{T2}x_{14})x_5}{N_H} + \frac{\beta_{vH}(\eta_v x_9 + x_{10})x_3}{N_H} + k_2 x_{11} - g_9 x_{13} + \frac{\sigma_2\beta_T(x_3 + \eta_{T1}x_{13} + \eta_{T2}x_{14})x_{11}}{N_H} \quad (56)$$

$$\frac{dx_{14}}{dt} = \frac{(1-P_{D2})\beta_T(x_3 + \eta_{T1}x_{13} + \eta_{T2}x_{14})x_6}{N_H} - g_{10}x_{14} + k_3 x_{12} + \gamma_3 x_{13} + \frac{\sigma_3\beta_T(x_3 + \eta_{T1}x_{13} + \eta_{T2}x_{14})x_{12}}{N_H}, \quad (57)$$

where,

$g_1 = \mu_H + k_1, g_2 = \mu_H + d_{T1} + r_1, g_3 = \gamma_1 + \mu_H . g_4 = \tau_1 + \mu_H + \delta_{D1}, g_5 = \gamma_v + \mu_v, g_6 = \mu_v + \delta_{Hv}, g_7 = \gamma_2 + k_2 + \mu_H, g_8 = k_3 + \tau_2 + \delta_{D2} + \mu_H, g_9 = d_{T2} + r_2 + \gamma_3 + \mu_H, g_{10} = \tau_3 + r_3 + \delta_{D3} + d_{T3} + \mu_H$ and $N_H = x_1 + x_2 + x_3 + x_4 + x_5 + x_6 + x_7 + x_{11} + x_{12} + x_{13} + x_{14}$

The Jacobian of the transformed system (44) – (57), evaluated at the *DFE* (ξ_3), is given by:

$$J(\xi_0) = \begin{bmatrix}
-\mu_H & 0 & -\beta_T^* & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -q_1 & -q_2 \\
0 & -g_1 & q_3 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & q_4+\tau_1 & q_5 \\
0 & k_1 & q_6 - g_2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & q_7 & q_8+\tau_3 \\
0 & 0 & \gamma_1 & -\mu_H & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & \beta_{rH} & 0 & -g_3 & 0 & 0 & 0 & q_9 & 0 & 0 & 0 & \gamma_2 & 0 \\
0 & 0 & 0 & 0 & \gamma_1 & -g_4 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -\gamma_3 \\
0 & 0 & 0 & 0 & 0 & \tau_1 & -\mu_H & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & -q_{10} & -q_{11} & 0 & -\mu_V & -q_{12} & 0 & 0 & -q_{13} & -q_{14} & -q_{15} \\
0 & 0 & 0 & 0 & q_{10} & q_{11} & 0 & 0 & q_{12} - g_5 & 0 & 0 & q_{13} & q_{14} & q_{15} \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \gamma_V & -g_6 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -g_7 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \gamma_2 & -g_8 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & k_2 & 0 & -g_9 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & k_3 & \gamma_3 & -g_{10}
\end{bmatrix}$$

where,

$q_1 = \beta_T^*\eta_{T1}$, $q_1 = \beta_T^*\eta_{T2}$, $q_3 = (1-P_{T1})\beta_T^*$, $q_4 = (1-P_{T1})\beta_T^*\eta_{T1}$, $q_5 = (1-P_{T1})\beta_T^*\eta_{T2}$, $q_6 = P_{T1}\beta_T^*$, $q_7 = \eta_{T1}P_{T1}\beta_T^*$, $q_8 = \eta_{T2}P_{T1}\beta_T^*$, $q_9 = \eta_V\beta_{VH}$, $q_{10} = \frac{\eta_A\beta_{HV}x_8^*}{x_1^*}$, $q_{11} = \frac{\eta_B\beta_{HV}x_8^*}{x_1^*}$, $q_{12} = \frac{\eta_C\beta_{HV}x_8^*}{x_1^*}$, $q_{13} = \frac{\eta_D\beta_{HV}x_8^*}{x_1^*}$, $q_{14} = \frac{\eta_E\beta_{HV}x_8^*}{x_1^*}$, $q_{15} = \frac{\eta_F\beta_{HV}x_8^*}{x_1^*}$.

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Consider the case when $R_T > R_D$ and $R_C = 1$. Furthermore, let $\beta_T = \beta_T^*$ be a bifurcation parameter. Solving for β_T from $R_T = 1$ gives

$$\beta_T = \beta_T^* = \frac{g_1 g_2}{g_1 P_{T1} + k_1 (1 - P_{T1})}.$$

The right eigenvector of $J(\xi_3)\Big|_{\beta_T = \beta_T^*}$ is given by

$w = (w_1, w_2, w_3, w_4, w_5, w_6, w_7, w_8, w_9, w_{10}, w_{11}, w_{12}, w_{13}, w_{14})^T$, where,

$$w_1 = \frac{\beta_T^* w_3}{\mu_H}, w_2 = \frac{(1 - P_{T1})\beta_T^* w_3}{g_1}, w_3 = w_3 > 0, w_4 = \frac{r_1 w_3}{\mu_H}, w_5 = \frac{\beta_{vH} w_3}{g_3}, w_6 = \frac{\gamma_1 \beta_{vH} w_3}{g_3 g_4},$$

$$w_7 = \frac{\tau_1 \gamma_1 \beta_{vH} w_3}{\mu_H g_3 g_4}, w_8, = w_9, = w_{10}, = w_{11}, = w_{12}, = w_{13}, = w_{14} = 0$$

Furthermore, the Jacobian, $J(\xi_3)\Big|_{\beta_T = \beta_T^*}$, has a left eigenvectors, given by

$v = (v_1, v_2, v_3, v_4, v_5, v_6, v_7, v_8, v_9, v_{10}, v_{11}, v_{12}, v_{13}, v_{14})$, where,

$v_1 = v_4 = v_5 = v_6 = v_7 = v_8 = v_9 = v_{10} = 0,$

$$v_2 = \frac{k_1 v_3}{g_1},$$

$v_3 = v_3 > 0,$

$$v_{11} = \frac{v_3 \left(g_1 g_9 k_3 \gamma_2 \tau_3 + g_8 k_2 \left(g_{10} k_1 \tau_2 + g_1 \gamma_3 \tau_3\right) + \left(k_1 (1 - P_{T1}) + g_1 P_{T1}\right) \left(g_9 k_3 \gamma_2 + g_8 k_2 \left(g_{10} \eta_{T1} + \gamma_3 \eta_{T2}\right)\right) \beta_T^*\right)}{g_1 g_7 g_8 g_9 g_{10}},$$

$$v_{12} = \frac{k_3 v_3 \left(g_1 \tau_3 + \left(k_1 (1 - P_{T1}) + g_1 P_{T1}\right) \eta_{T2} \beta_T^*\right)}{g_1 g_8 g_{10}},$$

$$v_{13} = \frac{v_3 \left(g_{10} k_1 \tau_2 + g_1 \gamma_3 \tau_3 + \left(k_1 (1 - P_{T1}) + g_1 P_{T1}\right) \left(g_{10} \eta_{T1} + \gamma_3 \eta_{T2}\right) \beta_T^*\right)}{g_1 g_9 g_{10}},$$

$$v_{14} = \frac{v_3 \left(g_1 \tau_3 + \left(k_1 (1 - P_{T1}) + g_1 P_{T1}\right)\right) \eta_{T2} \beta_T^*}{g_1 g_{10}}.$$

It follows from Theorem 4.1 in Castillo Chavez and Song (2004), if we compute the associated non-zero partial derivatives of $F(x)$ (evaluated at the DFE ξ_3), that the associated bifurcation coefficients, a and b, defined by

$$a = \sum_{k,i,j=1}^{4} v_k w_i w_j \frac{\partial^2 f_k}{\partial x_i \partial x_j}(0,0),$$

and

$$b = \sum_{k,i=1}^{4} v_k w_i \frac{\partial^2 f_k}{\partial x_i \partial x \beta_T^*}(0,0)$$

are computed to be

$$a = \frac{2k_1v_3(1-P_{T1})w_2^2g_2}{\Lambda_H(g_1P_{T1}+k_1(1-P_{T1}))}\left[\frac{g_2\sigma_1\mu_H(1+g_1)}{(g_1P_{T1}+k_1(1-P_{T1}))}+r_1\in\right]-\frac{2k_1v_3w_3^2g_2(1-P_{T1})}{\Lambda_H(g_1P_{T1}+k_1(1-P_{T1}))}$$
$$\left[\mu_H+r_1+\frac{\beta_{vH}\mu_H}{g_3}+\frac{(1-P_{T1})g_2\mu_H}{g_1P_{T1}+k_1(1-P_{T1})}+\frac{\gamma_1\beta_{v\,H}^2\eta_v\mu_H}{g_1g_3g_4}+\frac{\tau_1\gamma_1\beta_{v\,H}^2}{g_1g_3g_4}+\frac{\gamma_1\beta_{vH}\mu_H}{g_3g_4}+\frac{\tau_1\gamma_1\beta_{vH}}{g_3g_4}\right]$$
$$-\frac{2v_3w_2^2}{\Lambda_H(g_1P_{T1}+k_1(1-P_{T1}))}\left[\frac{(1-P_{T1})g_2^2g_1g_1P_{T1}\mu_H}{g_1P_{T1}+k_1(1-P_{T1})}+P_{T1}\mu_Hg_1g_3+\right.$$
$$\left.r_1P_{T1}g_1g_2+\frac{\tau_1\gamma_1\beta_{vH}P_{T1}g_1g_2}{g_3g_4}+\frac{\beta_{vH}P_{T1}\mu_Hg_1g_2}{g_3}\left(1+\frac{\gamma_1}{g_4}\right)\right] \quad (58)$$
$$-\frac{2v_3w_3^2\gamma_1\beta_{vH}^2\eta_v\mu_H}{\Lambda_Hg_3g_4}-\frac{2w_3^2\gamma_1\beta_{vH}k_3v_3(\tau_1+\eta_{T2}g_2)P_{D2}\mu_Hg_1g_2}{\Lambda_Hg_3g_6g_8g_{10}(g_1P_{T1}+k_1(1-P_{T1}))}$$
$$-\frac{2w_3^2\beta_{vH}v_3P_{D1}\mu_Hg_2(g_1g_9k_3\gamma_2\tau_3+g_8k_2(g_{10}k_1\tau_2+g_1\gamma_3\tau_3)+(k_1(1-P_{T1})+g_1P_{T1})(g_9k_3\gamma_2+g_8k_3(g_{10}\eta_{T1}+\gamma_3\eta_{T2}))g_2)}{\Lambda_Hg_3g_9g_{10}(g_1P_{T1}+k_1(1-P_{T1}))^2g_8}$$
$$-\frac{2w_3^2\beta_{vH}v_3(g_{10}k_1\tau_2+g_1\gamma_3\tau_3+(g_{10}\eta_{T1}+\gamma_3\eta_{T2})g_1g_2)(1-P_{T1})\mu_Hg_1g_2}{\Lambda_Hg_3g_9g_{10}(g_1P_{T1}+k_1(1-P_{T1}))}.$$

and

$$b = \frac{v_3w_3\mu_H}{\Lambda_H}\left[\frac{k_1(1-P_{T1})}{g_1}+P_{T1}\right].$$

Since the bifurcation coefficient b is positive, it follows from Theorem 4.1 in Castillo Chavez and Song (2004) that the TB-Dengue model (6) – (19), or the transformed model (44) – (57), will undergo a backward bifurcation if the backward bifurcation coefficient, a, given by (58), is positive. Thus, it follows from Theorem 4.1 of Castillo Chavez and Song (2004) that the model (6) – (19) does not undergoes a backward bifurcation phenomenon at $R_C = 1,$ if $R_T > R_D$, whenever $\sigma_1 = \in = 0$. This implies that if TB is driving the co-endemicity of both diseases, then the system (6) – (19) will not under the backward bifurcation phenomenon when there are no cases of exogenous re-infection and individuals treated for tuberculosis do not get re-infected.

5. CONCLUSION

In this work, backward bifurcation analysis was carried out on a mathematical model for the population dynamics of TB-Dengue coinfection in a population where both diseases are endemic. The results show that the effective reproduction number, though necessary for disease control, may not be sufficient for producing robust public health control strategies for effective control of both diseases if certain parameters are not effectively monitored. We observe that incidences of TB exogenous reinfection as well as cases where previously treated individuals gets re-infected with TB can cause a backward bifurcation in the system. In the case of Dengue, incidences of disease-induced deaths can lead to a backward bifurcation in the system, hereby making it difficult to control the disease. It was also observed that, when the TB burden is higher than that for Dengue in the population, then

exogenous reinfection of latently infected individuals and reinfection of previously treated individuals will also lead to a backward bifurcation. Hence, public health policies must take into consideration these important parameters when planning health control measures in a population where TB and dengue are endemic.

6. CONFLICT OF INTEREST

There is no conflict of interest associated with this work.

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