Modeling the Role of Treatment and Counseling in an HIV/AIDS and Tuberculosis Sub Model

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Abstract

This study presents a co infection deterministic model defined by a system of ordinary differential equations for HIV/AIDS, malaria and tuberculosis. The HIV/AIDS tuberculosis (TB) co infection sub model is analyzed to determine the conditions for the stability of the equilibria points and assess the role of treatment and counseling in controlling the spread of the co -infections. The disease free equilibrium is locally asymptotically stable when the reproduction number is less than unity but exhibits the phenomenon of backward bifurcation. The study shows that in the absence of HIV/AIDS, the TB virus would not establish itself in the susceptible human population if there is effective TB treatment. However in the presence of HIV/AIDS, TB treatment alone
without effective HIV/AIDS counseling is not sufficient to eradicate the TB problem. It is also noted that HIV/AIDS will establish itself in a host population of the susceptibles even in the absence of TB.

**Keywords:** HIV/AIDS - TB and Malaria, equilibria, stability, bifurcation, sensitivity, counseling, treatment

1 Background Information

HIV/AIDS remains one of the leading causes of death in the world with its effects most devastating in sub saharan Africa. One of the key factors that fuels the high incidence of HIV/AIDS in Sub saharan Africa is its dual infection with malaria and tuberculosis [5].

Audu et al. [1] investigated the possible impact of co infections of tuberculosis and malaria on the $CD4^+$ cell counts of HIV/AIDS patients and established the following: The healthy control group recorded a median $CD4^+$ cell counts of 789 cells/ul (789 cells per mm$^3$ of blood); subjects infected with HIV/AIDS only recorded a median $CD4^+$ cell counts of 386 cell/ul; subjects co infected with HIV/AIDS and TB recorded a median $CD4^+$ cell counts of 268 cell/ul; subjects co infected with HIV/AIDS and malaria recorded a median $CD4^+$ cell counts of 211 cell/ul and those co infected with HIV/AIDS, malaria and TB recorded the lowest median $CD4^+$ cell counts of 182 cell/ul. Motivated by this finding, a deterministic model exploring the joint dynamics of the simultaneous co infections of HIV/AIDS, TB and malaria incorporating treatment and counseling is presented. The paper represents the first deterministic mathematical model incorporating HIV/AIDS, TB and Malaria co infections within a single model and an analysis of the HIV/AIDS TB sub model.

2 Model Formulation and Description

To study the dynamics of HIV/AIDS, malaria and TB co infection, a deterministic model is formulated described by a system of ordinary differential equations. The model sub-divide the human population into the following epidemiological classes: $S_H(t)$ - Susceptible population at time $t$, $I_M(t)$ - Malaria infectives at time $t$, $I_H(t)$ - HIV cases at time $t$, $I_A(t)$ - AIDS cases at time $t$, $I_T(t)$ - TB cases at time $t$. $I_{HM}(t)$ - Those co infected with malaria and HIV at time $t$, $I_{AM}(t)$ - Those co infected with malaria and AIDS at time $t$, $I_{MT}(t)$ - Those co infected with malaria and TB at time $t$, $I_{HT}(t)$ - Those co infected with HIV and TB at time $t$, $I_{AT}(t)$ - Those co infected with AIDS and TB at time $t$, $I_{HMT}(t)$ - Those co infected with HIV, Malaria and TB at time $t$, $I_{AMT}(t)$ - Those co infected with AIDS, Malaria and TB at time $t$. The total human population ($N_H(t)$) is therefore denoted by: $N_H(t) = S_H(t) + I_M(t) + I_H(t) +$
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\[ I_A(t) + I_T + I_{HM}(t) + I_{AM}(t) + I_{MT}(t) + I_{HT}(t) + I_{AT}(t) + I_{HMT}(t) + I_{AMT}(t). \]

The vector (mosquito) population at time \( t \) denoted by \( N_V(t) \) is sub-divided into the following classes: \( S_V(t) \) - Vector susceptibles at time \( t \), \( I_V(t) \) - Vector infectives at time \( t \). The total vector population \( N_V(t) \) is given by \( N_V(t) = S_V(t) + I_V(t) \).

### 2.1 Definition of Parameters

It is assumed that susceptible humans are recruited into the population at a constant rate either by birth or recovery from malaria and TB. They acquire infection with either HIV/AIDS, malaria or TB and move to the infectious classes. Susceptible mosquitoes are recruited into the mosquito population at a constant rate. They acquire malaria infection following a blood meal feeding on infected malaria humans, becomes infectious and move to the infectious class. The recruitment rate of humans into the susceptible population is denoted by \( \Lambda_H \) while that of vectors (mosquitoes) is denoted by \( \Lambda_V \) and are both assumed to be constant. The natural death rate of humans is given by \( d_n \) while that of vectors is given by \( d_v \). The death rates due to AIDS, malaria and TB in humans are \( d_a, d_m \) and \( d_t \) respectively. The parameters \( d_{am}, d_{mt}, dat \) and \( d_{amt} \) account for the combined death rates in the \( I_{AM}, I_{MT}, I_{AT} \) and \( I_{AMT} \) classes respectively. The parameters \( r_m \) and \( r_t \) are the recovery rates from malaria and TB respectively due to effective treatment. It is assumed that the recovered individuals do not acquire temporary immunity to either or both diseases thus become susceptible again. The model assumes that susceptible humans cannot simultaneously get infected with malaria, HIV/AIDS and TB since the transmission mechanics are completely different for the three diseases. The model further assumes that humans acquire HIV/AIDS through sexual contacts between an infective and a susceptible. The average force of infection for HIV/AIDS denoted \( \lambda_{ah} \) is given by

\[
\lambda_{ah} = \frac{\beta_a(1-\delta)c_1(I_H + I_{HM} + I_{HT})}{N_H} \tag{2.1.1}
\]

where \( \beta_a \) is the average transmission probability of HIV/AIDS between an infective and a susceptible per sexual contact and \( c_1 \) is the per capita number of sexual contacts of susceptible humans with HIV/AIDS infected individuals per unit time. The parameter \( \delta \) measures the effectiveness of counseling through condom use and a reduction in the number of sexual partners, where \( 0 \leq \delta \leq 1 \). Effective counseling reduces the value of the parameter \( c_1 \). The model assumes that the classes \( I_{HMT}, I_A, I_{AM}, I_{AT} \) and \( I_{AMT} \) do not transmit the virus due to acute ill health and noticeable AIDS symptoms. Define \( \alpha_1 \) as the number of bites per human per mosquito (biting rate of mosquitoes), \( \beta_m \) as the transmission probability of malaria in humans per bite thus the force of
infection with malaria for humans, denoted $\lambda_{mh}$ is given by

$$\lambda_{mh} = \frac{\alpha_1 \beta_m I_V}{N_H} \tag{2.1.2}$$

whereas the average force of infection with malaria for vectors, denoted $\lambda_{mv}$ is given by

$$\lambda_{mv} = \frac{\alpha_1 \beta_v (I_M + I_{HM} + I_{MT} + I_{AM} + I_{HMT} + I_{AMT})}{N_H} \tag{2.1.3}$$

where $\beta_v$ is the transmission probability of malaria in vectors from any infected human. Finally the average force of infection for TB denoted $\lambda_{th}$ is given by

$$\lambda_{th} = \frac{\beta_t c_2 (I_T + I_{HT} + I_{MT} + I_{AM} + I_{HMT} + I_{AMT})}{N_H} \tag{2.1.4}$$

where $\beta_t$ is the transmission probability of TB in humans and $c_2$ is the average per capita contact rate of susceptible humans with TB infected individuals.

The rate of progression from HIV to AIDS for the untreated HIV cases is $p$. The parameters $\theta_1p$, $\theta_2p$ and $\theta_3p$ account for increased rates of progression to AIDS for individuals co infected with HIV - TB, HIV - malaria and HIV - malaria - TB respectively where $\theta_1 < \theta_2 < \theta_3$. Define $\alpha$ as the proportion of the HIV/AIDS infectives receiving effective treatment. This involves the administration of ARV’S that keeps the HIV patients from progressing to AIDS while transferring the AIDS patients back to the HIV classes. The modification parameters $e_{mh}$, $e_{ht}$ and $e_{mt}$ account for the reduced susceptibility to infection with HIV for individuals in the $I_M$, $I_T$ and the $I_{MT}$ classes respectively due to reduced sexual activity as a result of ill health where $e_{mh} < 1$, $e_{ht} < 1$, $e_{mt} < 1$. The parameters $e_{ma}$, $e_{ha}$, $e_{hm}$, $e_{at}$, $e_{ht}$, $e_{mt}$, $e_{am}$, account for the increased susceptibility to infection with malaria for individuals already infected with AIDS, HIV - TB and AIDS - TB respectively due to suppressed immune system where $e_{ma} > 1$, $e_{ha} > 1$, $e_{hm} > 1$, $e_{at} > 1$, $e_{ht} > 1$, $e_{mt} > 1$, $e_{am} > 1$. It is also clear that $e_{ma} < e_{at}$ and $e_{ha} < e_{ht}$. The parameters $e_{h}^t$, $e_{a}^t$, $e_{mh}^t$, and $e_{am}^t$ account for the increased susceptibility to infection with TB for individuals already infected with HIV, AIDS, HIV - malaria and AIDS - malaria respectively due to suppressed immune system where $e_{h}^t > 1$, $e_{a}^t > 1$, $e_{hm}^t > 1$, $e_{am}^t > 1$. Again $e_{h}^t < e_{hm}^t$ and $e_{a}^t < e_{am}^t$. 
2.2 The model equations

\[
\frac{dS_H(t)}{dt} = \Lambda_H - \lambda_m S_M(t) + r_t I_H(t) - \lambda_a H_S(t) \tag{2.2.1}
\]

\[
-\lambda_m S_H(t) - \lambda_a H_S(t) - d_n S_H(t)
\]

\[
\frac{dI_M(t)}{dt} = \lambda_m H_M(t) + r_t H_M(t) - \lambda_a I_M(t) - e^h_m \lambda_h I_M(t)
\]

\[
-\lambda_a H_I(t) - d_n I_M(t) - d_m I_M(t).
\]

\[
\frac{dI_H(t)}{dt} = \lambda_a H_I(t) + r_t H_M(t) + r_t I_H(t) - (1 - \alpha) P_H(t)
\]

\[
-\lambda_h H_I(t) - e^h_a \lambda_h I_H(t) - d_n I_H(t) + \alpha I_A(t).
\]

\[
\frac{dI_A(t)}{dt} = (1 - \alpha) P_I(t) + r_t I_A(t) + r_t I_H(t) - e^m_a \lambda_I A(t)
\]

\[
-\lambda_a I_H(t) - d_a I_A(t) - d_m I_A(t) - \alpha I_A(t).
\]

\[
\frac{dI_T(t)}{dt} = \lambda_h I_H(t) + r_m I_H(t) - e^m_a \lambda_I I_M(t) - \lambda_m I_H(t)
\]

\[
-\lambda_a I_I(t) - d_n I_H(t) - r_t I_I(t).
\]

\[
\frac{dI_HH(t)}{dt} = e^m_a \lambda_m H_H(t) + e^m_a \lambda_a I_M(t) - r_t H_H(t) - e^m_s \lambda_s I_M(t) +
\]

\[
\alpha I_H(t) - d_n I_H(t) - (1 - \alpha) \theta_2 P_{AM}(t) - d_m I_H(t).
\]

\[
\frac{dI_AM(t)}{dt} = (1 - \alpha) \theta_2 I_A(t) + e^m_a \lambda_m I_A(t) - r_m I_A(t) - d_m I_A(t) - \alpha I_A(t)
\]

\[
+ r_t I_A(t) - e^m_a \lambda_a I_A(t) - d_a I_A(t) - d_m I_A(t) - \alpha I_A(t).
\]

\[
\frac{dI_MT(t)}{dt} = \lambda_I I_I(t) + r_m I_I(t) - e^m_a \lambda_I I_M(t) - \lambda_m I_I(t)
\]

\[
-\lambda_I I_A(t) - d_n I_I(t) - d_m I_I(t) - d_m I_I(t).
\]

\[
\frac{dI_HT(t)}{dt} = e^m_a \lambda_I I_H(t) + r_m I_H(t) + e^m_a \lambda_I H_H(t) - e^m_s \lambda_s H_H(t) - (1 - \alpha) \theta_3 P_I_H(t)
\]

\[
-\lambda_I I_I(t) - d_n I_H(t) - r_I I_I(t) + \alpha I_H(t).
\]

\[
\frac{dI_AT(t)}{dt} = e^m_a \lambda_I I_A(t) + r_m I_A(t) + (1 - \alpha) \theta_1 P_I_H(t) - \alpha I_A(t)
\]

\[
- e^m_a \lambda_I I_A(t) - d_n I_A(t) - d_m I_A(t) - d_m I_A(t) - r_I I_A(t) - d_I I_A(t).
\]

\[
\frac{dI_HMT(t)}{dt} = e^m_a \lambda_I I_H(t) + e^m_s \lambda_s I_H(t) + e^m_a \lambda_I I_M(t) + \alpha I_A(t)
\]

\[
- r_m I_H(t) - d_m I_H(t) - d_n I_H(t) - (1 - \alpha) \theta_3 P_I_H(t) - d_m I_H(t) - r_I I_H(t) - d_m I_H(t).
\]

\[
\frac{dI_AMT(t)}{dt} = e^m_a \lambda_I I_A(t) + e^m_a \lambda_I I_M(t) + (1 - \alpha) \theta_3 P_I_H(t)
\]

\[
- r_m I_A(t) - d_m I_A(t) - d_n I_A(t) - \alpha I_A(t) - d_m I_A(t) - r_I I_A(t) - d_m I_A(t).
\]

\[
\frac{dS_V(t)}{dt} = \Lambda_V - \lambda_m S_V(t) - d_a S_V(t)
\]

\[
\frac{dI_V(t)}{dt} = \lambda_m S_V(t) - d_v I_V(t).
\]
2.3 Positivity and Boundedness of solutions

The model system 2.2.1 describes living populations therefore the associated state variables are non-negative for all time $t \geq 0$. The solutions of this model with positive initial data therefore remain positive for all time $t \geq 0$.

3 HIV/AIDS-TB model

The model of HIV/AIDS-TB is obtained by setting $I_M = I_{MH} = I_{MA} = I_{MT} = I_{MHT} = I_{MAT} = I_V = S_V = 0$. The total human population is given by $N_H = S_H + I_H + A + I_T + I_{HT} + I_{TA}$. The model equations are given by:

$$\frac{dS_H(t)}{dt} = \Lambda_H + r_I I_T(t) - \lambda_{ah} S_H(t) - \lambda_I H(t) - d_n S_H(t) \quad (3.0.1)$$

$$\frac{dI_H(t)}{dt} = \lambda_{ah} S_H(t) + r_I I_{HT}(t) - (1 - \alpha) p I_H(t) - e_I \lambda_I H(t) - d_n I_H(t) + \alpha I_A(t).$$

$$\frac{dI_A(t)}{dt} = (1 - \alpha) p I_H(t) + r_I I_{AT}(t) - e_I \lambda_I A(t) - d_n I_A(t) - d_a I_A(t) - \alpha I_A(t).$$

$$\frac{dI_T(t)}{dt} = \lambda_I S_H(t) - e_I \lambda_I I_T(t) - d_n I_T(t) - d_t I_T(t) - r_I I_T(t).$$

$$\frac{dI_{HT}(t)}{dt} = e_I \lambda_I I_T(t) + e_I \lambda_I I_{HT}(t) - (1 - \alpha) \theta_I p I_{HT}(t)$$

$$- d_a I_{HT}(t) - d_t I_{HT}(t) - r_I I_{HT}(t) + \alpha I_{AT}(t).$$

$$\frac{dI_{AT}(t)}{dt} = e_I \lambda_I I_A(t) + (1 - \alpha) \theta_I p I_{HT}(t) - \alpha I_{AT}(t)$$

$$- d_a I_{AT}(t) - d_t I_{AT}(t) - r_I I_{AT}(t) - d_a I_{AT}(t) - d_t I_{AT}(t).$$

$$\frac{dN_H}{dt} = \Lambda_H - d_n N_H - (d_t A_{AT} + d_a B_{AT} + d_a I_{AT}).$$

$$A_{AT} = (I_A + I_T + I_{HT}), \quad B_{AT} = (I_A + I_{AT}).$$

The forces of infection are given by:

$$\lambda_{ah} = \frac{\beta_a (1 - \delta) c_1 (I_H + I_{HT})}{N_H}, \quad \lambda_t = \frac{\beta_t c_2 (I_T + I_{HT} + I_{AT})}{N_H}.$$

3.1 Invariant region

The model system 3.0.1 is dissipative (all solutions are uniformly bounded in a proper subset $\{\Omega_{HT} \subset \mathbb{R}_+^6\}$). Let $(S_H, I_H, I_A, I_T, I_{HT}, I_{AT}) \in \mathbb{R}_+^6$, be any solution with non-negative initial conditions. It can be easily shown that, all the feasible solutions of system 3.0.1 enter the region $\{\Omega_{HT} \in \mathbb{R}_+^6 : N_H \leq \frac{\Lambda_H}{d_n}\}$. Thus, $\Omega_{HT}$ is positively invariant and attracting and it is sufficient to consider it’s solutions in $\Omega_{HT}$. Existence, uniqueness and continuation results for system 3.0.1 hold in this region. Therefore all solutions of system 3.0.1 starting in
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Ω_{HT} remain in Ω_{HT} for all \( t \geq 0 \). All parameters and state variables for model system 3.0.1 are assumed to be non-negative for \( t \geq 0 \).

3.2 Disease-free equilibrium point of the model

The disease-free equilibrium of the system 3.0.1, is given by \( E_0 = (s_0^H, I_0^H, I_0^A, I_0^T, I_0^{HT}, I_0^{AT}) = (\frac{\mu}{d_n}, 0, 0, 0, 0, 0) \). To study the stability of the disease-free equilibrium, the basic reproduction number \( (R_{HT}) \) which governs the qualitative dynamics of the model 3.0.1 is first obtained. Define \( F_i \) as the rate of appearance of new infections in the class or compartment \( i \) and \( V_i = V_i^- - V_i^+ \), where \( V_i^- \) is the rate of transfer of individuals out of compartment \( i \), and \( V_i^+ \) is the rate of transfer of individuals into compartment \( i \) by all other means. Therefore:

The Jacobian of \( F_i \) and \( V_i \) at the disease-free equilibrium denoted by \( F \) and \( V \) respectively is given by:

\[
F = \begin{pmatrix}
\beta_a(1 - \delta)c_1 & 0 & 0 & \beta_a(1 - \delta)c_1 & 0 \\
0 & 0 & 0 & 0 & 0 \\
0 & 0 & \beta t c_2 & \beta t c_2 & \beta t c_2 \\
0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0
\end{pmatrix}
\]

and

\[
V = \begin{pmatrix}
y_1 & -\alpha & 0 & -r_t & 0 \\
-(1 - \alpha)p & y_2 & 0 & 0 & -r_t \\
0 & 0 & y_3 & 0 & 0 \\
0 & 0 & 0 & y_4 & -\alpha \\
0 & 0 & 0 & -(1 - \alpha)\theta_1 p & y_5
\end{pmatrix}
\]

Where \( y_1 = (1 - \alpha)p + d_n, \ y_2 = d_a + d_n + \alpha, \ y_3 = d_a + d_t + r_t \)
\( y_4 = (1 - \alpha)\theta_1 p + d_n + d_t + r_t, \ y_5 = \alpha + d_a + d_n + d_t + d_at + r_t \).

The TB reproduction number \( R_T \) (under treatment) is given by

\[
R_T = \frac{\beta t c_2}{d_n + d_t + r_t}
\]

and the HIV reproduction number \( (R_H) \) is given by

\[
R_H = \frac{\beta_a(1 - \delta)c_1\{d_a p(\alpha - 1) + (\alpha - 1)\alpha y_2 p \theta_1 + (y_4(y_5 y_2 + d_n r_t))\}}{(\alpha - 1)\alpha \pi_1 \theta - d_n p r_t + \alpha p r_t + y_4(y_5 \pi_1 - d_n \pi_2)}
\]

\[
\pi_1 = \alpha d_n + d_a d_n + d_n^2 + d_a p - \alpha d_n p + d_n p - \alpha d_n p
\]
\( \pi_2 = -d_n r_t - p r_t + \alpha p r_t \). The reproduction number for the system 3.0.1 is given by \( R_{HT} = \max\{R_T, R_H\} \).

Lemma 3.1. The DFE of the HIV/AIDS-TB model 3.0.1 is locally asymptotically stable (LAS) if \( R_{HT} < 1 \), and unstable otherwise.

Lemma 3.1 follows from Theorem two by Van, P. and Watmough, J. (2002).
3.3 Parameter values for the HIV/AIDS TB model

<table>
<thead>
<tr>
<th>symbol</th>
<th>parameter</th>
<th>value ($yr^{-1}$)</th>
<th>reference</th>
</tr>
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<tbody>
<tr>
<td>$\Lambda_H$</td>
<td>Recruitment rate of humans</td>
<td>$0.4 \times 40 \times 10^b$</td>
<td>[4]</td>
</tr>
<tr>
<td>$d_n$</td>
<td>Natural death rate of humans</td>
<td>0.016667</td>
<td>[4]</td>
</tr>
<tr>
<td>$d_a$</td>
<td>HIV/AIDS-induced death rate</td>
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<td>[7]</td>
</tr>
<tr>
<td>$p$</td>
<td>Progression rate from HIV to AIDS (untreated)</td>
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<td>[3]</td>
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<tr>
<td>$\alpha$</td>
<td>Proportion of the HIV/AIDS victims treated</td>
<td>0.68</td>
<td>[5]</td>
</tr>
<tr>
<td>$\beta_a$</td>
<td>Transmission probability of HIV/AIDS</td>
<td>0.019</td>
<td>[3]</td>
</tr>
<tr>
<td>$c_1$</td>
<td>Per capita number of sexual contacts</td>
<td>9</td>
<td>[5]</td>
</tr>
<tr>
<td>$\delta$</td>
<td>Effectiveness of HIV/AIDS counseling</td>
<td>Variable</td>
<td></td>
</tr>
<tr>
<td>$r_m$</td>
<td>Proportion of TB victims treated</td>
<td>0.6</td>
<td>[7]</td>
</tr>
<tr>
<td>$d_t$</td>
<td>Death rate due to TB</td>
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<td>[2]</td>
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<tr>
<td>$c_2$</td>
<td>Contact rate of susceptible humans with TB infectives</td>
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<td>[2]</td>
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<tr>
<td>$\beta_t$</td>
<td>Transmission probability of TB in humans</td>
<td>0.027</td>
<td>[2]</td>
</tr>
<tr>
<td>$\theta_2$</td>
<td>Increased Progression rate from HIV to AIDS due to TB</td>
<td>2</td>
<td>Estimated</td>
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3.4 The role of treatment and counseling

From equation 3.2.2, ARV treatment and counseling for HIV/AIDS patients has no effect on the spread of TB. The reproduction threshold, $R_T$, is analyzed to determine whether treating people with TB can lead to the effective control or elimination of TB in the population. A plot of $R_T$ as a function of TB treatment $r_t$ is depicted in Figure 1. This figure (figure 1) shows that, in the
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absence of HIV/AIDS, an effective strategy for treating people with TB may be adequate to eliminate TB in the community, since it brings $R_T$ down to a level less than one.

A plot of TB incidence against time in years in the absence of HIV/AIDS without TB treatment and with TB treatment is shown in figure 2a and 2b respectively. These figures (figure 2a and 2b) show that TB treatment ($r_t = 0.7$) is very effective in controlling the disease.

However the inclusion of HIV/AIDS into the population worsens the TB problem as shown in figure 3. Figure 3 shows that in the presence of HIV/AIDS, TB treatment alone without HIV/AIDS counseling is not sufficient to control the TB problem. With effective counseling for the HIV/AIDS infectives, the TB problem will be eliminated as shown in figure 4.
3.5 Global stability of disease-free equilibrium (DFE)

To ensure that elimination of the HIV/AIDS - TB co infections is independent of the initial sizes of the sub-populations, it is necessary to show that the DFE is globally asymptotically stable. The global asymptotic stability (GAS) of the disease-free state of the model is investigated using the theorem by [1]. The model is rewritten as follows:

\[
\frac{dX}{dt} = H(X, Z) \tag{3.5.1}
\]
\[
\frac{dZ}{dt} = G(X, Z), \quad G(X, 0) = 0 \tag{3.5.2}
\]

where the components of the column-vector \(X \in \mathbb{R}^m\) denote the uninfected population and the components of \(Z \in \mathbb{R}^n\) denote the infected population. \(U_0 = (X^*, 0)\) denotes the disease-free equilibrium of this system. The fixed point \(U_0 = (X^*, 0)\) is a globally asymptotically stable equilibrium for this system provided that \(R_0 < 1\) (locally asymptotically stable) and the following two conditions satisfied:

(H1) For \(\frac{dX}{dt} = H(X, 0), X^*\) is globally asymptotically stable

(H2) \(G(X, Z) = PZ - \tilde{G}(X, Z), \quad \tilde{G}(X, Z) \geq 0\) for \((X, Z) \in \Omega_H\),

where \(P = D_Z G(X^*, 0)\) is an M-matrix (the off diagonal elements of \(P\) are non negative) and \(\Omega_H\) is the region where the model makes biological sense. The disease-free equilibrium is now denoted as \(U^0 = (X^*, 0)\), \(X^* = \left(\frac{\Lambda_H}{d_m}, \frac{\Lambda_V}{d_c}\right)\)

**Theorem 3.2.** The fixed point \(U^0 = (X^*, 0)\) is a globally asymptotically stable equilibrium of system 3.0.1 provided that \(R_{HT} < 1\) and the assumptions H1 and H2 are satisfied.

**Proof.** From the system 3.0.1
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\[ H(X, 0) = \left( \begin{array}{c} \Lambda_H - d_n \\ \Lambda_V - d_v \end{array} \right) \]

\[ G(X, Z) = PZ - \hat{G}(X, Z) \]

\[ P = \begin{pmatrix} \beta_1 (1 - \delta) c_1 - y_1 & \alpha & 0 & r_t + \beta_1 (1 - \delta) c_1 & 0 \\ (1 - \alpha)p & -y_2 & 0 & 0 & r_t \\ 0 & 0 & \beta_2 c_2 - y_3 & \beta_4 c_2 & \beta_4 c_2 \\ 0 & 0 & 0 & -y_4 & \alpha \\ 0 & 0 & 0 & (1 - \alpha) r_1 p & -y_5 \end{pmatrix} \]

where: \( y_1 = r_m + d_n + d_m, y_2 = \beta_2 c_1 - (1 - \alpha)p + d_n, y_3 = d_a + d_n + \alpha \)

\( y_4 = r_m + d_n + (1 - \alpha)p \theta_1 - d_n, y_5 = r_m + d_m + \alpha + d_n + d_a \)

\( \hat{G} = \begin{pmatrix} G_1(X, Z) \\ G_2(X, Z) \\ G_3(X, Z) \\ G_4(X, Z) \\ G_5(X) \end{pmatrix} = \begin{pmatrix} \lambda_{a_h} (1 - \frac{S_h}{N_h}) + e_h^{a_h} \lambda_{a_h} I_H \\ e_a^{a_h} \lambda_{a_h} I_A \\ \lambda_{th} (1 - \frac{S_h}{N_h}) + e_t^{a_h} \lambda_{a_h} I_T \\ -\left( e_t^{a_h} \lambda_{a_h} I_T + e_t^{a_h} \lambda_{a_h} I_H \right) \\ -\left( e_a^{a_h} \lambda_{a_h} I_A \right) \end{pmatrix} \)

Notice that \( \hat{G}_4(X, Z) < 0, \hat{G}_5(X, Z) < 0 \) and so the conditions of \( H1 \) and \( H2 \) are not met so \( U^0 \) may not be globally asymptotically stable when \( R_{HT} < 1 \). This implies that there is the possibility of future disease outbreaks when the conditions favouring the outbreaks are prevailing.

This result is numerically illustrated in figure 5 and figure 6 representing the graphs of the total infectives against time in years.

In figure 5, \( R_T = 0.6061 \) and \( R_H = 0.7015 \). The global disease free equilibrium is stable and there is no possibility of further disease outbreaks in future.

Figure 6 ( \( R_T = 0.954717 \) and \( R_H = 0.997303 \)), shows the phenomenon of backward bifurcation, where multiple stable equilibria co-exist when \( R_{HT} < 1 \).
This implies that the classical epidemiological requirement for the eradication of the disease whenever $R_{HT} < 1$ is no longer sufficient, though necessary.

4 Conclusion

In the absence of HIV/AIDS, the TB virus would not establish itself in the susceptible human population if there is effective TB treatment, however in the presence of HIV/AIDS, TB treatment alone without HIV/AIDS counseling is not sufficient to eradicate the TB problem. It is also noted that HIV/AIDS will establish itself in a host population of the susceptible population even in the absence of TB. The HIV/AIDS TB co infection model exhibits the phenomenon of backward bifurcation which posses a challenge to the design of effective control measures.

Acknowledgements. The authors are very grateful to Prof. Adiel M. Magana of Chuka University - Kenya, for many excellent comments that have enhanced the model as well as the clarity of the paper.

References


Received: November 1, 2015; Published: May 5, 2020