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A Mathematical Model of HIV and TB Co-infection

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Abstract

The Human Deficiency Virus (HIV) is the major cause of mortality among individuals also having TB infection. The two diseases interact concurringly in their epidemiological characteristics. A non linear mathematical model with six compartments of Susceptible, Infectious TB, Treated TB, Infectious HIV, Infectious with both HIV and TB and AIDS classes is constructed to examine the interaction between TB and HIV epidemic. The Basic Reproduction Number (BRR) for TB (R_0^T) and HIV (R_0^H) and the overall BRR $R_0 = \max\{R_0^T, R_0^H\}$ is calculated. The model shows three equilibria, viz. a disease-free equilibrium, TB only (HIV-free) equilibrium and HIV only (TB-free) equilibrium. Stability criterion for the three equilibria points is determined. The disease-free equilibrium is found to be globally asymptotically stable if $R_0 \leq 1$. The TB only equilibrium is locally stable if $R_0^T > 1$ along with some other conditions. The HIV only equilibrium is stable if $R_0^H > 1$ along with some other conditions. Numerical simulations presented in the paper examine the role of some essential epidemiological parameters in disease spread.

Keywords: Basic Reproduction Number; Co-infection; Epidemiology; HIV/AIDS; Tuberculosis; Stability.
2020 Mathematics Subject Classification: 34D08, 34D23.

1. Background

The terms 'deadly pair' and 'HIV-TB' are frequently used to describe the situation of co infection caused by HIV/AIDS and TB. The public health burden imposed by these two diseases makes it necessary to use mathematical models to understand the transmission dynamics of the two diseases and to bring the epidemic under control.

1.1 Tuberculosis

TB is an infectious disease which is caused by *Mycobacterium tuberculosis* (MTb). The disease gets transmitted from a person suffering from infectious (active) TB to other people from infected droplets,

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which are created, when a person with active TB sneezes or coughs. The bacterium that causes TB can infect a person and remain passive for many years or their entire lifespan. This results in latent (hidden) infection. Clinical data suggests that after infection, there is a 10% lifetime risk of acquiring clinically evident TB, with a 90% chance that the infection will remain latent [29]. A person advances from the dormant stage to the infectious/active stage when the body's ability to protect itself is compromised.

1.2 HIV/AIDS

AIDS is caused by the Human Immunodeficiency Virus (HIV). The virus primarily infects the CD4+T cells, macrophages and dendritic cells. It is known to directly and indirectly destroy CD4+T cells. Once the virus starts destroying the CD4+T cells and there are less than 200 cells per microlitre (L), cell-mediated immunity is lost. Acute HIV infection advances over time to asymptomatic HIV infection and then to early symptomatic HIV infection and eventually to AIDS, which is determined either on the basis of the amount of CD4+T cells remaining in the blood and/or the presence of specific illnesses [12]. The HIV virus can be passed from mother to child; through sexual contact and through infected blood and blood products.

1.3 Impact of HIV on TB

Since the beginning of the AIDS epidemic, there has been a strong correlation between TB and HIV. HIV has a pronounced effect on the development of TB disease. HIV is the most significant factor that aids the development to active TB in people affected with MTb [25, 10]. A person who is HIV positive and has a latent TB infection has a 50% greater chance of developing active TB than a person who is HIV negative because HIV infection significantly impairs the immune system. HIV also raises the likelihood of recurrent TB illness, which can occur as a result of external re-infection or internal re-activation [17]. There is a higher possibility of TB spreading to the general community with the increase in TB cases amongst the people living with HIV (PLWHA).

1.4 Impact of TB on HIV

TB can also affect HIV infection. In more than 50% of cases in developing countries, TB is the most common and severe opportunistic infection in individuals who are HIV positive [14, 25]. Globally, up to half of HIV/AIDS patients die from TB, which is the main infectious killer of HIV positive people. Studies have found that individuals live with HIV but die from TB [14, 20]. One of the most prevalent, curable infectious HIV-related diseases in PLWHA is tuberculosis (TB). TB is the one of the most prevalent, but, curable disease of PLWHA, but untreated TB shortens the longevity of people with HIV infection [14]. TB accelerates the progression of HIV, by 6-7 times in the HIV viral load in TB patients. Worldwide TB is the most common cause of death in PLWHA.

2. Introduction

The associated spread of two or more infectious illnesses is known as a co-epidemic. A co-epidemic occurs when the spreading of one contagious disease speeds up the transmission of another infectious disease [19]. This situation of a co-epidemic is particularly true in the case of HIV infection, which has formed a lethal combination with TB [1, 4, 9, 11, 18, 23, 24, 26] and malaria [15] each speeding the other's progress. The terms 'deadly pair' and 'HIV-TB' are frequently used to describe the situation of co infection caused by HIV/AIDS and TB. Together TB and HIV continue to be a human catastrophe, inflicting extensive suffering on the global community. In 2020, it was found that approximately 2,14,000 HIV infected persons died from TB [7]. Clinical studies have reported that TB can be the cause of opportunistic infection amongst the PLWHA [14] and HIV is the primary risk factor that stimulates development from latent TB to active TB [25]. There are around two billion MTb bacteria infections worldwide [29]. Every year around 8-10 million people contract TB and 2 million die from it [29]. An estimated 1.3 million people died from TB in 2020 against 1.4 million in 2019 [28]. Just around 10% of those who have TB infection go on to develop active TB over their lifetime, however this number is rising largely as a result of the rise in infections among PLWHA.

In 2021, an estimated 38.4 million people were living with HIV and 6,50,000 died of AIDS [6]. About one third of the PLWHA are co-infected with TB [7]. According to estimates, PLWHA have a 20-37 times higher risk of having TB than people without HIV infection. In 2020, there occurred 9.9 million new cases of TB, of which 7,92,000 (8%) was among the PLWHA and of the 1.3 million who died due to TB, 2,14,000 (16%) were living with HIV [29]. Since 8% of new TB cases and 16% of deaths due to TB being linked with HIV, TB is one of the major cause of mortality and morbidity among the PLWHA and as a reason TB poses a health risk concern for the PLWHA. The study of infectious disease co-epidemics is crucial in apprehending how the two diseases are connected. The vast public health burden occurring due to the two diseases requires the use of mathematical models to deduce the transmission dynamics of the two diseases and to estimate the possible efficacy of different methods to bring the epidemic under control.

Mathematical models for the co-infection with HIV and TB have been studied by [1, 2, 3, 5, 13, 19, 20, 21, 22]. To investigate the connection between TB incidence and HIV prevalence [3] developed a fixed model for Sub-Saharan Africa. Currie [5] studied a compartmental difference equation model of TB and HIV. According to their research, concentrating on TB diagnosis and treatment is the most effective intervention strategy for containing the dual epidemic. Long [13] developed an *SII X SEI* model for the combined disease dynamics of HIV and TB. Their study signifies that exclusively treating HIV or TB may reduce the targeted epidemic, but can thereafter aggravate the other epidemic. Schinazi [19] introduced two mathematical models for South-East Asia and predicted that population having a high TB load might be resistant to HIV infection. Schulzer [20] investigated HIV-TB joint dynamics using actuarial methods. Sharomi [21] analyzed a 15-compartment HIV-TB model with

treatment. Shukla [22] studied an *SIS X SIRS* 5-compartment model and examined its epidemiological significance. Naresh [16] have built a non linear mathematical model to analyze how TB affects the rate at which HIV infection spreads throughout a population. Ayele [1] constructed a mathematical model of HIV with optimal control for Ethiopia by taking into account a compartment for 'aware and unaware susceptibles'.

In this paper, we develop a 6-compartment model of co-epidemics with two diseases HIV and TB with three active infective classes and one treated class. The analysis is both analytical and numerical and it explores how treatment affects the spread of the co-epidemic.

3. Model Formulation

In this model, the human population is divided into six epidemiological classes: Susceptible (X), Infectious TB (Y_I), Treated TB (Y_T), Infectious HIV (Y_H), Infectious with both TB and HIV (Y_{TH}) and AIDS (Y_A). In designing the model, the following assumptions are made:

(i). While TB is an airborne disease, HIV is transmitted mainly via sexual contact, needle sharing and mother-to-child transmission. We neglect vertical transmission (mother- to-child transmission), but we do not differentiate between the other two modes, i.e. a susceptible can get infected with HIV either by sexual contact or needle sharing.

(ii). We assume that the susceptible population cannot simultaneously get infected with TB and HIV. To get to the Y_{TH} class, a person must first enter the Y_I or Y_H class.

(iii). We assume that the individuals in the AIDS class (Y_A) are too sick to remain active sexually and hence do not contribute in HIV transmission.

(iv). We consider successful treatment for TB only.

(v). Inorder to simplify the model, we have not distinguished between latent TB and infectious TB.

(vi). Drug-resistant TB is not incorporated in the model.

(vii). We assume that the chance of infection is the same for X and Y_T classes, viz. for TB it is and for HIV it is.

Considering the above assumptions, the HIV-TB model is given by the following system of ordinary differential equations:

$$\begin{aligned}
\dot{X} &= \Lambda - \beta(Y_I + Y_{TH})\frac{X}{N} - \tau(Y_H + Y_{TH})\frac{X}{N} - \mu X \\
\dot{Y}_I &= \beta(Y_I + Y_{TH})\frac{(X + Y_T)}{N} - \tau(Y_H + Y_{TH})\frac{Y_I}{N} - (\nu + \mu)Y_I \\
\dot{Y}_T &= \nu Y_I - \beta(Y_I + Y_{TH})\frac{Y_T}{N} - \tau(Y_H + Y_{TH})\frac{Y_T}{N} - \mu Y_T
\end{aligned}$$

$$\begin{aligned}
\dot{Y}_H &= \tau(Y_H + Y_{TH})\frac{(X + Y_T)}{N} - \beta(Y_I + Y_{TH})\frac{Y_H}{N} - (\mu + \alpha_1)Y_H \\
\dot{Y}_{TH} &= \tau(Y_H + Y_{TH})\frac{Y_I}{N} + \beta(Y_I + Y_{TH})\frac{Y_H}{N} - (\mu + \alpha)Y_{TH} \\
\dot{Y}_A &= \alpha Y_{TH} - (\mu + d)Y_A + \alpha_1 Y_H \\
\dot{N} &= \Lambda - \mu N - dY_A
\end{aligned} \tag{1}$$

with $X + Y_I + Y_T + Y_H + Y_{TH} + Y_A = N$, where

Λ is the constant recruitment rate,

μ is the natural death rate,

v is the TB treatment rate,

d is the AIDS related death rate,

α is the rate of progression to AIDS for individuals in Y_{TH} class,

α_1 is the rate of progression to AIDS for individuals in Y_H class,

β is the infection rate for transmission of TB and

τ is the infection rate for transmission of HIV.

The region of attraction of the above system is,

$$T = \left\{ (X, Y_I, Y_T, Y_H, Y_{TH}, Y_A) \in \Re^6 : 0 \leq X + Y_I + Y_T + Y_H + Y_{TH} + Y_A \leq \frac{\Lambda}{\mu} \right\}$$

3.1 Basic Reproduction Number (BRR)

The next generation operator method [27] is used to find the $BRRR_0$. The number of secondary cases that an infected person causes in a community that is completely susceptible while they are contagious is known as the BRR. The associated BRR for the HIV-TB model is denoted by R_0 and given by-

$$R_0 = \max\{R_0^T, R_0^H\}$$

where

$R_0^T = \dfrac{\beta}{\nu + \mu}$ is the BRR for TB transmission and$R_0^H = \dfrac{\tau}{\mu + \alpha_1}$ is the BRR for HIV transmission.

3.2 Equilibrium States

In this section we obtain the equilibrium states, by considering the R.H.S. of each of the differential equations in system (1) equal to zero, obtaining the equations:

$$\begin{aligned}
\Lambda - \beta(Y_I + Y_{TH})\frac{X}{N} - \tau(Y_H + Y_{TH})\frac{X}{N} - \mu X = 0 \\
\beta(Y_I + Y_{TH})\frac{(X + Y_T)}{N} - \tau(Y_H + Y_{TH})\frac{Y_I}{N} - (\nu + \mu)Y_I = 0
\end{aligned}$$

$$\begin{aligned}
\nu Y_I - \beta(Y_I + Y_{TH})\frac{Y_T}{N} - \tau(Y_H + Y_{TH})\frac{Y_T}{N} - \mu Y_T &= 0 \\
\tau(Y_H + Y_{TH})\frac{(X + Y_T)}{N} - \beta(Y_I + Y_{TH})\frac{Y_H}{N} - (\mu + \alpha_1)Y_H &= 0 \\
\tau(Y_H + Y_{TH})\frac{Y_I}{N} + \beta(Y_I + Y_{TH})\frac{Y_H}{N} - (\mu + \alpha)Y_{TH} &= 0 \\
\alpha Y_{TH} - (\mu + d)Y_A + \alpha_1 Y_H &= 0 \\
\Lambda - \mu N - dY_A &= 0 \qquad (2)
\end{aligned}$$

Disease Free Equilibrium (DFE)

The disease-free equilibrium is the point at which there are no diseases in the population. It is obtained by setting $Y_I = Y_T = Y_H = Y_{TH} = Y_A = 0$. It is denoted by E_0 and is given by,

$$E_0\left(\frac{\Lambda}{\mu}, 0, 0, 0, 0, 0\right).$$

Quasi Disease Free Equilibria (QDFE)

An equilibrium is known as the quasi disease-free equilibrium if all infected people have either TB or HIV.

TB only (HIV-free) Equilibrium: It is obtained by setting $Y_H = Y_{TH} = Y_A = 0$. It is denoted by E_T and is given by,

$$E_T\left(\frac{\Lambda}{\mu + \beta(1 - \frac{1}{R_0^T})}, \frac{\Lambda(1 - \frac{1}{R_0^T})}{\mu}, \frac{\Lambda\nu(1 - \frac{1}{R_0^T})}{\mu(\beta - \nu)}, 0, 0, 0\right)$$

where $R_0^T = \frac{\beta}{\nu + \mu}$.

HIV only (TB-free) Equilibrium: It is obtained by setting $Y_I = Y_T = Y_{TH} = 0$. It is denoted by E_H and is given by,

$$E_H\left(\frac{\Lambda(\mu + d + \alpha_1)}{\tau(\mu + d) - d\alpha_1}, 0, 0, \frac{\Lambda(\mu + d)(R_0^H - 1)}{\tau(\mu + d) - d\alpha_1}, 0, \frac{\Lambda\alpha_1(R_0^H - 1)}{\tau(\mu + d) - d\alpha_1}\right)$$

where $R_0^H = \frac{\tau}{\mu + \alpha_1}$.

4. Stability Analysis

We state the global stability of the DFE E_0 in the following theorem:

Theorem 4.1. *The equilibrium E_0 is globally stable if $R_0 \leq 1$, alongwith*

$$\max\left\{\frac{\beta}{\mu}, \frac{\tau}{\mu}, \frac{\beta + \tau}{\mu}\right\} < \frac{1}{2},$$

and it is unstable if $R_0 > 1$.

Proof. For proving the global stability of E_0, we build the following Lyapunov function:

$$L = \frac{\mu}{2}\left(X - \frac{\Lambda}{\mu}\right)^2 + \Lambda(Y_I + Y_T + Y_H + Y_{TH} + Y_A).$$

Differentiating we have,

$$\dot{L} = \mu\left(X - \frac{\Lambda}{\mu}\right)\dot{X} + \Lambda(\dot{Y}_I + \dot{Y}_T + \dot{Y}_H + \dot{Y}_{TH} + \dot{Y}_A)$$

Putting values of $\dot{X}$, $\dot{Y}_I$, $\dot{Y}_T$, $\dot{Y}_H$, $\dot{Y}_{TH}$ and $\dot{Y}_A$ from (**??**) into the above equation and simplifying we obtain,

$$\dot{L} = -\mu^2\left(X - \frac{\Lambda}{\mu}\right)^2 - \beta\mu(Y_I + Y_{TH})\frac{X^2}{N} - \tau\mu(Y_H + Y_{TH})\frac{X^2}{N} + \Theta$$

where

$$\Theta = 2\beta\Lambda(Y_I + Y_{TH})\frac{X}{N} + 2\tau\Lambda(Y_H + Y_{TH})\frac{X}{N} - \Lambda\mu(Y_I + Y_T + Y_H + Y_{TH} + Y_A) - d\Lambda Y_A$$

Now we are to prove that $\Theta < 0$. After simplification of the above equation we get,

$$\Theta = \left(\frac{2\beta}{\mu} - 1\right)\Lambda\mu Y_I + \left(\frac{2\tau}{\mu} - 1\right)\Lambda\mu Y_H + \left(\frac{2(\beta+\tau)}{\mu} - 1\right)\Lambda\mu Y_{TH} - \Lambda\mu Y_T - \Lambda(\mu + d)Y_A$$

Hence, $\Theta < 0$ if $\max\left\{\frac{\beta}{\mu}, \frac{\tau}{\mu}, \frac{\beta+\tau}{\mu}\right\} < \frac{1}{2}$. Thus $\dot{L} < 0$ and hence the DFE E_0 is globally asymptotically stable. □

We state the local stability of the TB only equilibrium E_T in the following theorem:

Theorem 4.2. *The TB only equilibrium E_T is locally stable if $R_0^T > 1$ and $R_0^H < 1$, along with*

$$\begin{aligned} &\beta > \nu \\ &\frac{\tau}{\beta} > \frac{\mu + \alpha}{\mu + \alpha_1} \\ &\frac{\tau}{\beta} > \frac{\mu + \alpha_1}{\nu + \mu} \end{aligned} \tag{3}$$

Proof. The Jacobian M corresponding to the system (1) is,

$$M = \begin{pmatrix} -\beta\frac{(Y_I+Y_{TH})}{N} - \tau\frac{(Y_H+Y_{TH})}{N} - \mu & -\beta\frac{X}{N} & 0 & -\tau\frac{X}{N} & -\beta\frac{X}{N} - \tau\frac{X}{N} & 0 \\ \beta\frac{(Y_I+Y_{TH})}{N} & \beta\frac{(X+Y_T)}{N} - \tau\frac{(Y_H+Y_{TH})}{N} - (\nu+\mu) & \beta\frac{(Y_I+Y_{TH})}{N} & -\tau\frac{Y_I}{N} & \beta\frac{(X+Y_T)}{N} - \tau\frac{Y_I}{N} & 0 \\ 0 & \nu - \beta\frac{Y_T}{N} & -\beta\frac{(Y_I+Y_{TH})}{N} - \tau\frac{(Y_H+Y_{TH})}{N} - \mu & -\tau\frac{Y_T}{N} & -\beta\frac{Y_T}{N} - \tau\frac{Y_T}{N} & 0 \\ \tau\frac{(Y_H+Y_{TH})}{N} & -\beta\frac{Y_H}{N} & \tau\frac{(Y_H+Y_{TH})}{N} & \tau\frac{(X+Y_T)}{N} - \beta\frac{(Y_I+Y_{TH})}{N} - \mu - \alpha_1 & \tau\frac{(X+Y_T)}{N} - \beta\frac{Y_H}{N} & 0 \\ 0 & \tau\frac{(Y_H+Y_{TH})}{N} + \beta\frac{Y_H}{N} & 0 & \tau\frac{Y_I}{N} + \beta\frac{(Y_I+Y_{TH})}{N} & \tau\frac{Y_I}{N} + \beta\frac{Y_H}{N} - \mu - \alpha & 0 \\ 0 & 0 & 0 & \alpha_1 & \alpha & -(\mu + d) \end{pmatrix}$$

At the equilibrium point $E_T\left(\frac{\Lambda}{\mu+\beta(1-\frac{1}{R_0^T})}, \frac{\Lambda(1-\frac{1}{R_0^T})}{\mu}, \frac{\Lambda\nu(1-\frac{1}{R_0^T})}{\mu(\beta-\nu)}, 0, 0, 0\right)$, the Jacobian M_1 is given by

$$M_1 = \begin{pmatrix} A_{3\times3} & B_{3\times3} \\ 0_{3\times3} & C_{3\times3} \end{pmatrix}$$

where $0_{3\times3}$ is a zero matrix of order 3×3 and $A_{3\times3}$, $B_{3\times3}$, $C_{3\times3}$ are block matrices given by

$$A_{3\times3} = \begin{pmatrix} -\beta\frac{Y_I}{N}-\mu & -\beta\frac{X}{N} & 0 \\ \beta\frac{Y_I}{N} & 0 & \beta\frac{Y_I}{N} \\ 0 & \nu-\beta\frac{Y_T}{N} & -\beta\frac{Y_I}{N}-\mu \end{pmatrix}$$

$$B_{3\times3} = \begin{pmatrix} -\tau\frac{X}{N} & -\beta\frac{X}{N}-\tau\frac{X}{N} & 0 \\ -\tau\frac{Y_I}{N} & \beta\frac{(X+Y_T)}{N}-\tau\frac{Y_I}{N} & 0 \\ -\tau\frac{Y_T}{N} & -\beta\frac{Y_T}{N}-\tau\frac{Y_T}{N} & 0 \end{pmatrix}$$

$$C_{3\times3} = \begin{pmatrix} \tau\frac{(X+Y_T)}{N}-\beta\frac{Y_I}{N}-\mu-\alpha_1 & \tau\frac{(X+Y_T)}{N} & 0 \\ \tau\frac{Y_I}{N}+\beta\frac{Y_I}{N} & \tau\frac{Y_I}{N}-\mu-\alpha & 0 \\ \alpha_1 & \alpha & -(\mu+d) \end{pmatrix}$$

and the values of X, Y_I and Y_T are given in E_T. Since the lower left block is a zero matrix, the eigen values of M_1 can be found by calculating the eigen values of the block matrices A and C. For stability of E_T, the eigen values of the matrices should be negative. The eigen values of A are negative if $Tr(A)$ is negative and $Det(A)$ is positive under the condition $\beta > \nu$. And the eigen values of C are negative if $Tr(C)$ is negative and $Det(C)$ is positive under the condition $R_0^T > 1$, $R_0^H < 1$ along with the last two conditions of (3). We now show that $Tr(A)$ is negative and $Det(A)$ is positive.

$$\begin{aligned} Tr(A) &= -2\left(\beta\frac{Y_I}{N}+\mu\right) < 0 \ \ and \\ Det(A) &= \left(-\beta\frac{Y_I}{N}-\mu\right)\left\{-\beta\frac{Y_I}{N}(\nu-\beta\frac{Y_T}{N})\right\} - \beta\frac{X}{N}\left(\beta\frac{Y_I}{N}\right)\left(\beta\frac{Y_I}{N}+\mu\right) \\ &= \mu(\beta-\nu)^2+\mu^2(\beta-\nu) \end{aligned}$$

Now $Det(A) > 0$ if $\beta > \nu$. Therefore all eigen values of A are negative. We now show that $Tr(C)$ is negative and $Det(C)$ is positive.

$$\begin{aligned} Tr(C) &= -\beta(1-\frac{\nu+\mu}{\beta})+\tau-3\mu-\alpha_1-\alpha-d \\ &< 0 \ \ if \ \ R_0^H < 1 \end{aligned}$$

$$Det(C) = \left\{\tau\frac{(X+Y_T)}{N}-\beta\frac{Y_I}{N}-\mu-\alpha_1\right\}\left[-(\tau\frac{Y_I}{N}-\mu-\alpha)(\mu+d)\right]+\tau\frac{(X+Y_T)}{N}\left\{(\mu+d)(\tau+\beta)\frac{Y_I}{N}\right\}$$

$$= (\mu + d)\left[\tau(\nu+\mu)\frac{\mu+\alpha}{\beta} + \tau(\nu+\mu)(1-\frac{\nu+\mu}{\beta}) + \beta\tau(1-\frac{\nu+\mu}{\beta})^2 + (1-\frac{\nu+\mu}{\beta})\right.$$
$$\left.\{\tau(\mu+\alpha_1) - \beta(\mu+\alpha)\} - (\mu+\alpha_1)(\mu+\alpha)\right]$$

Now $Det(C) > 0$ if $R_0^T > 1$ and $\frac{\tau}{\beta} > \frac{\mu+\alpha}{\mu+\alpha_1}$ and $\frac{\tau}{\beta} > \frac{\mu+\alpha_1}{\nu+\mu}$. Therefore all eigen values of C are negative. Hence the TB only equilibrium E_T is locally stable. The HIV only equilibrium E_H is locally stable if $R_0^H > 1$. The analytical validation of stability of E_H is challenging, but numerical studies show that, with $R_0^H > 1$ and certain other conditions, E_H is stable. □

In the next section, we prove the stability of E_T and E_H numerically.

5. Numerical Results and Discussion

We evaluate TB's ability to spread in a community where HIV is at equilibrium in order to get a sense of the stability region of the equilibrium point E_H. The BRR of TB infecting a population where HIV is stable is computed using the next generation operator method [27] and is given by

$$R_0^T(E_H) = \frac{\beta\Lambda(\mu+d+\alpha_1)}{(\nu+\mu)\{\tau(\mu+d) - d\alpha_1\}} \mathrm{X} \frac{1}{\left\{\frac{\Lambda(\mu+d+\alpha_1)}{\tau(\mu+d)-d\alpha_1} + \frac{\Lambda(\mu+d)(R_0^H-1)}{\tau(\mu+d)-d\alpha_1} + \frac{\Lambda\alpha_1(R_0^H-1)}{\tau(\mu+d)-d\alpha_1}\right\}}$$

Only HIV persists for $R_0^T(E_H) < 1$, while for $R_0^T(E_H) > 1$, TB and HIV co-exist. Now we compute the stability region of the equilibrium point E_T. The BRR for HIV invading in a population where TB is fixed is computed by [26] and is given by

$$R_0^H(E_T) = \frac{\tau\Lambda}{(\mu+\alpha_1)\{\mu+\beta(1-\frac{1}{R_0^T})\}} \mathrm{X} \frac{1}{\left\{\frac{\Lambda}{\mu+\beta(1-\frac{1}{R_0^T})} + \frac{\Lambda(1-\frac{1}{R_0^T})}{\mu} + \frac{\Lambda\nu(1-\frac{1}{R_0^T})}{\mu(\beta-\nu)}\right\}}$$

Only TB persists for $R_0^H(E_T) < 1$, while for $R_0^H(E_T) > 1$, TB and HIV both co-exist.
To demonstrate the theoretical results obtained in this chapter, the system (1) is solved using the fourth order Runge-Kutta method. A time unit of months is chosen to study the system. The simulation has been performed on system (1) by using two set of parameter values. The actual parameter values used in mathematical models are not always known precisely. Some of the present parameters have been estimated and others have been collected from [13, 21].

5.1 Numerical Simulation A

The parameter (Λ), which measures the recruitment rate, is taken as 4000. The natural death rate parameter (μ) is taken as 0.038. The transmission rate for TB is denoted by β and is chosen as 0.29 and the transmission rate for HIV is denoted by and is taken as 0.47. TB treatment rate is equal to 0.199. AIDS progression rate for individuals in Y_{TH} and Y_H classes, which are τ and α_1 are taken as 0.99 and

0.21 respectively. AIDS induced death rate (d) is chosen to be 0.05. The initial values used for the $X(t)$, $Y_I(t)$, $Y_T(t)$, $Y_H(t)$, $Y_{TH}(t)$ and $Y_A(t)$ classes at time $t = 0$ are $X(0) = 58250$, $Y_I(0) = 8750$, $Y_T(0) = 500$, $Y_H(0) = 5271$, $Y_{TH}(0) = 900$, $Y_A(0) = 9180$ and $N(0) = 82851$.

With change in values of β and τ and rest all parameters values remaining the same, we calculate $R_0^T(E_H)$ for $\beta = 0.21$ and 0.35. We find $R_0^H = 1.41 > 1$ ($\beta = 0.35$), $R_0^T(E_H) = 0.628 < 1$ ($\beta = 0.21$) and $R_0^T(E_H) = 1.04 > 1$ ($\beta = 0.35$). Thus we may conclude that for $R_0^H > 1$, the HIV only equilibrium (TB-free) E_H is stable when $R_0^T(E_H) < 1$ and TB and HIV both co-exist when $R_0^T(E_H) > 1$.

Similarly with changes in values of β and τ and rest all parameters values remaining the same, we calculate $R_0^H(E_T)$ for $\tau = 0.22$ and 0.35. We find $R_0^T = 1.05 > 1$ ($\beta = 0.25$), $R_0^H(E_T) = 0.67 < 1$ ($\tau = 0.22$) and $R_0^H(E_T) = 1.07 > 1$ ($\tau = 0.35$). Thus we may conclude that for $R_0^T > 1$, the TB only equilibrium (HIV-free) E_T is stable when $R_0^H(E_T) < 1$ and TB and HIV both co-exist when $R_0^H(E_T) > 1$.

Figure 1, illustrates the relationship between the BRR for HIV R_0^H and the HIV transmission rate τ. A rise in the transmission rate β brings about a rise in R_0^H.

In Figure 2, the BRR for TB R_0^T is plotted against the TB transmission rate β. It is seen in the figure that with a rise in β, R_0^T increases, resulting in an endemic state of the disease. We plot $R_0^H(E_T)$ and R_0^T against the HIV transmission rate τ in Figure 3. $R_0^H(E_T)$ is the BRR of HIV invading in a population where TB is fixed. For an increasing value of τ, it is observed from the figure that $R_0^H(E_T)$ also increases.

In Figure 4, we study the effect of the TB transmission rate β on $R_0^T(E_H)$ and R_0^H. $R_0^T(E_H)$ is the BRR for TB entering a population with fixed HIV. With a rise in β, the probability of TB to infect a population increases ($R_0^T(E_H)$ increases).

Figure 5 indicates the relationship between the BRR for TB R_0^T and the TB treatment rate ν. A rise in the treatment rate brings about a decline in the BRR. In Figures 6 and 7, the Infectious TB population (Y_I) and the AIDS population (Y_A) respectively are plotted against time for various values of the TB transmission rate β.

It is observed that an increase in β also brings about a rise in the Y_I and Y_A classes, which explains that an increase in the transmission rate β, causes rise in the TB infected population and AIDS patients. We plot the Infectious HIV population (Y_H) and the AIDS population (Y_A) against time for various values of the HIV transmission rate τ in Figures 8 and 9 respectively. It is observed from the figures that with a rise in the HIV transmission rate, the proportion of HIV infected cases and AIDS cases also go up.

We explore various values of the TB treatment rate ν in Figure 10 and 11. We take $\nu = 0.22$, 0.4 and 0.58. It is observed in Figure 10 that when the treatment rate is high, say $\nu = 0.58$, there is a rise in the number of persons in the treated TB (Y_T) class, than the case when the treatment rate is low, say $\nu = 0.22$.

Figure 11 indicates that with a rise in the treatment rate, there is a decline in the Y_{TH} (people infected with both TB and HIV) class.

5.2 Numerical Simulation B

$\Lambda = 50000$, $\mu = 0.0143$, $\beta = 0.35$, $\tau = 0.69$, $\nu = 0.08$, $\alpha = 0.5$, $\alpha_1 = 0.21$, $d = 0.5$, $X(0) = 168558250$, $Y_I(0) = 2018750$, $Y_T(0) = 26562$, $Y_H(0) = 1587563$, $Y_{TH}(0) = 79687$, $Y_A(0) = 529188$ and $N(0) = 172800000$.

Figure 12 illustrates the relationship between the Infectious TB population (Y_I) and the TB transmission rate β. A rise in the transmission rate β brings about a rise in Y_I. We plot the TB and HIV Infected population (Y_{TH}) against time for various values of the HIV transmission rate τ in Figure 13.

It is observed from the figure that with a rise in the HIV transmission rate, the number of TB and HIV infected cases also go up. Figure 14 indicates the relationship between the Treated TB (Y_T) class and the TB treatment rate ν. A rise in the treatment rate brings about a rise in the Y_T class.

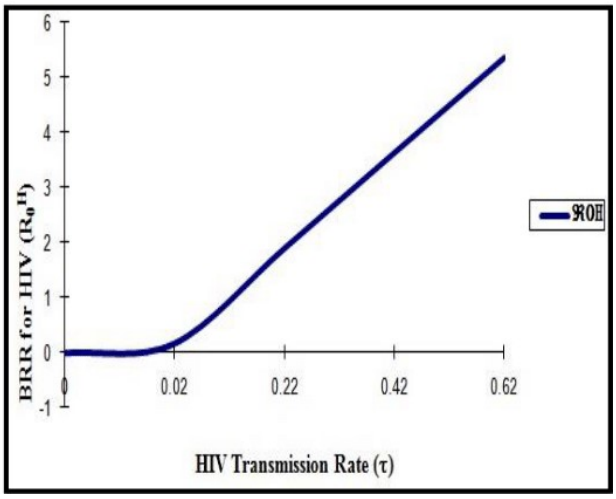

Figure 1: Variation of the Basic Reproduction Number (BRR) for HIV R_0^H for different values of the HIV transmission rate τ (for set A)

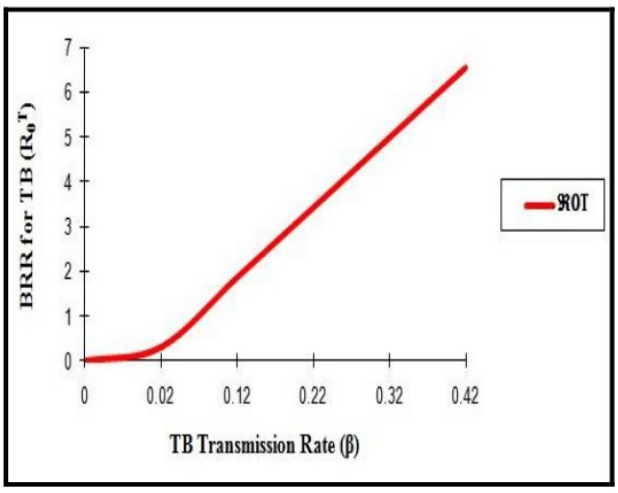

Figure 2: Variation of the Basic Reproduction Number (BRR) for TB R_0^T for different values of the TB transmission rate β (for set A)

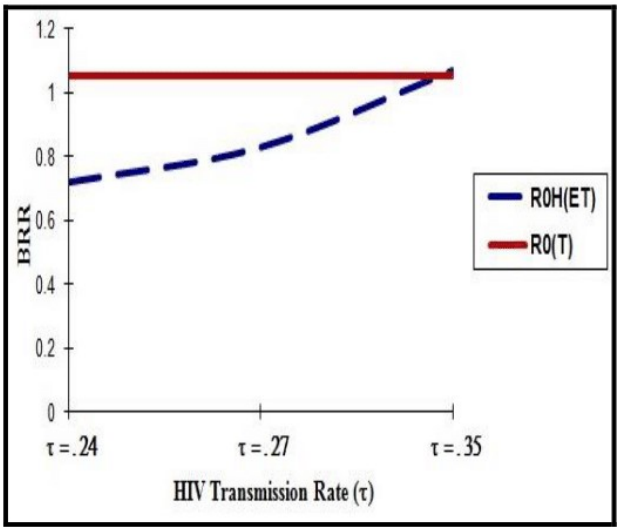

Figure 3: Variation in $R_0^H(E_T)$ and R_0^T for different values of the HIV transmission rate τ (for set A)

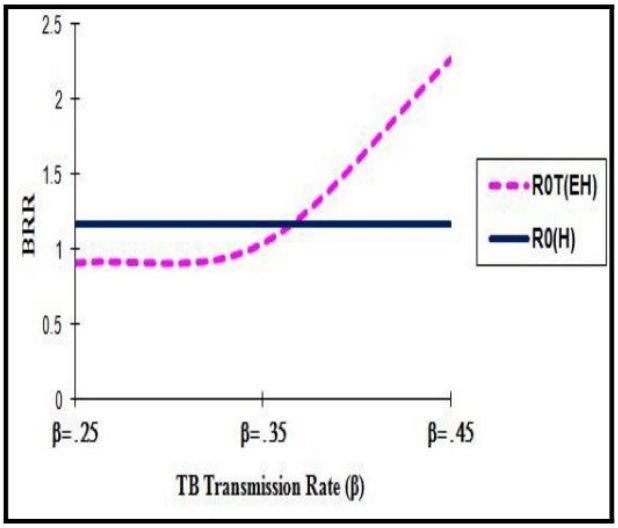

Figure 4: Variation in $R_0^T(E_H)$ and R_0^H for different values of the TB transmission rate β (for set A)

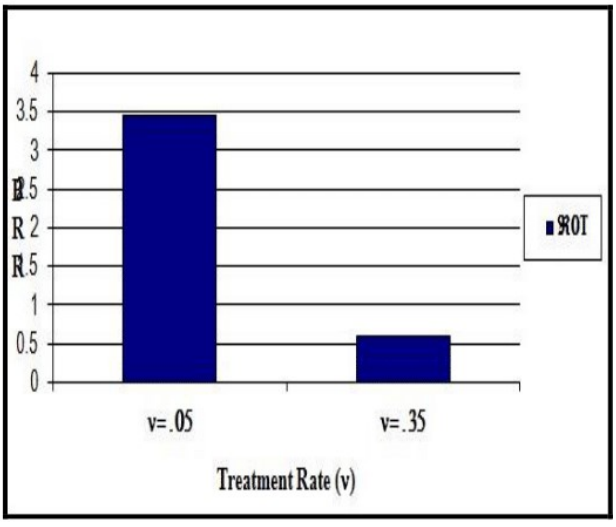

Figure 5: Variation of the Basic Reproduction Number (BRR) for TB R_0^T for different values of the TB treatment rate ν (for set A)

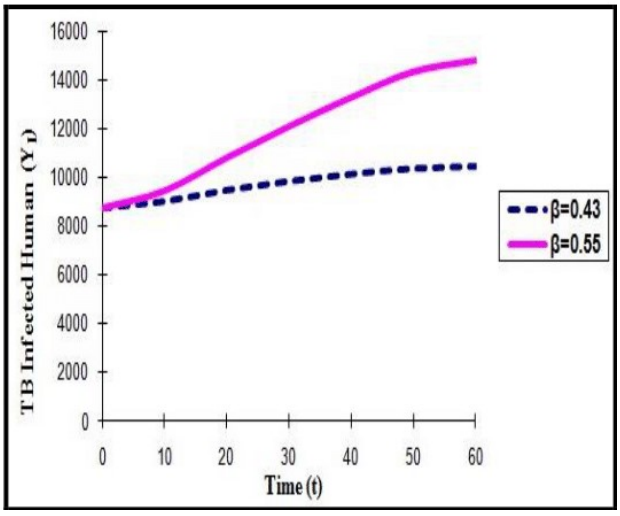

Figure 6: Variation in the TB Infected class Y_I with time for different values of the TB transmission rate β (for set A)

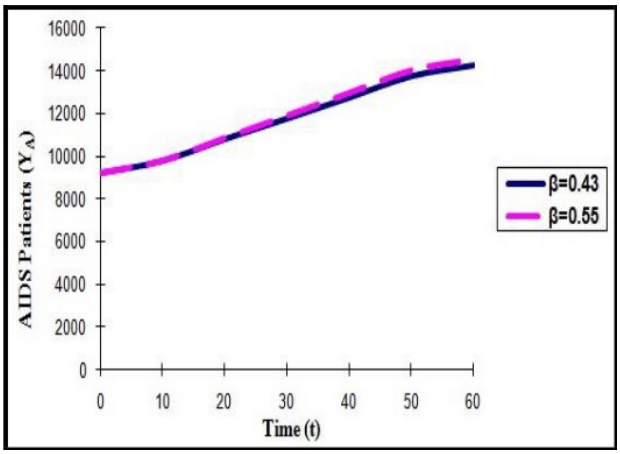

Figure 7: Variation in the AIDS class Y_A with time for various values of the TB transmission rate β (for set A)

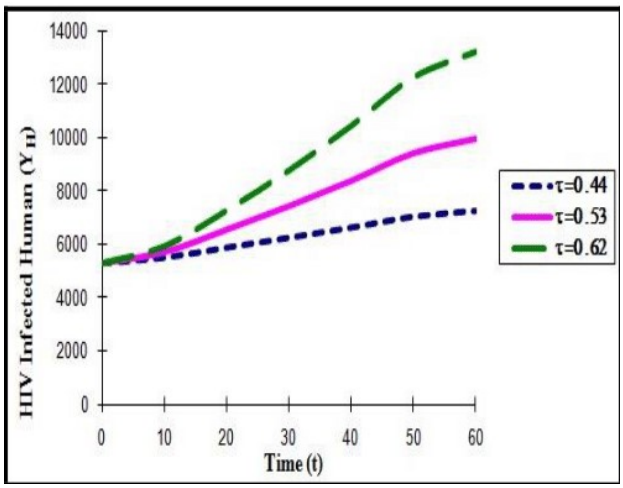

Figure 8: Variation in the HIV Infected class Y_H with time for various values of the HIV transmission rate τ (for set A)

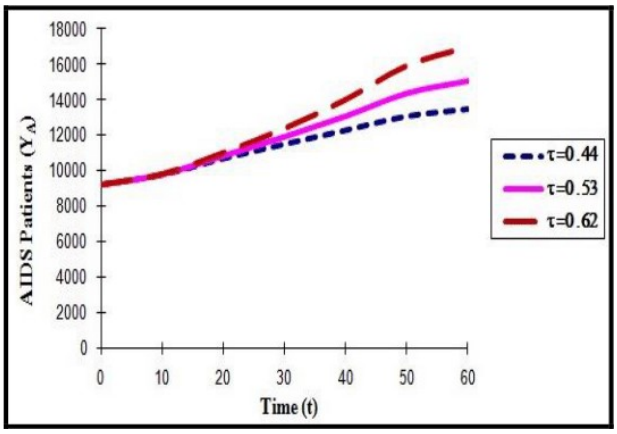

Figure 9: Variation in the AIDS class Y_A with time for various values of the HIV transmission rate τ (for set A)

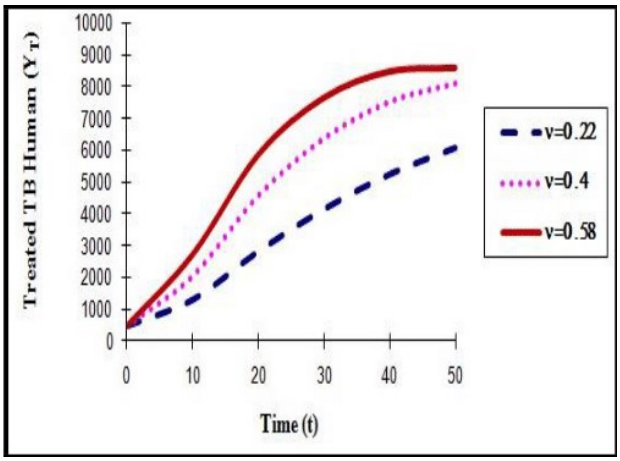

Figure 10: Variation in the Treated TB class Y_T with time for various values of the TB treatment rate ν (for set A)

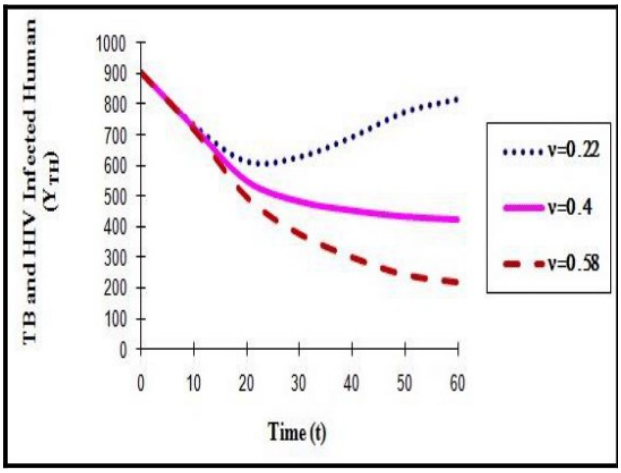

Figure 11: Variation in the TB and HIV Infected class Y_{TH} with time for various values of the TB treatment rate ν (for set A)

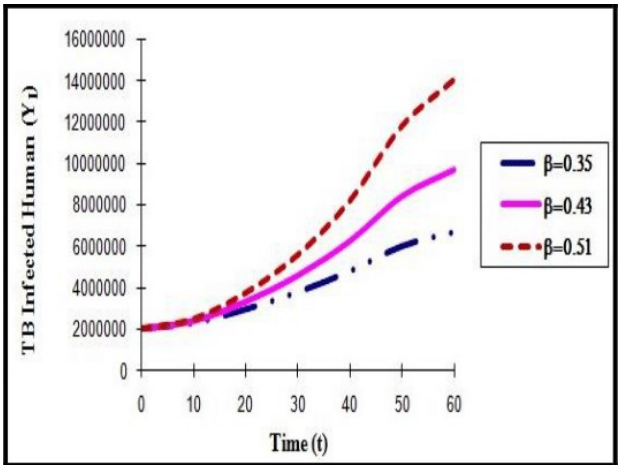

Figure 12: Variation in the TB Infected class Y_I with time for various values of the TB transmission rate β (for set B)

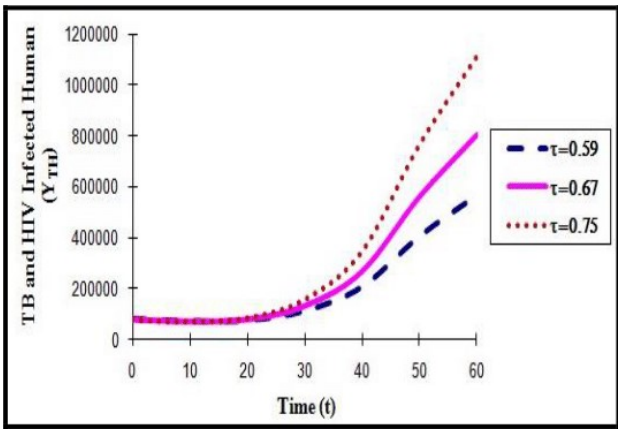

Figure 13: Variation in the TB and HIV Infected class $Y_{TH}$with time for various values of the HIV transmission rate τ (for set B)

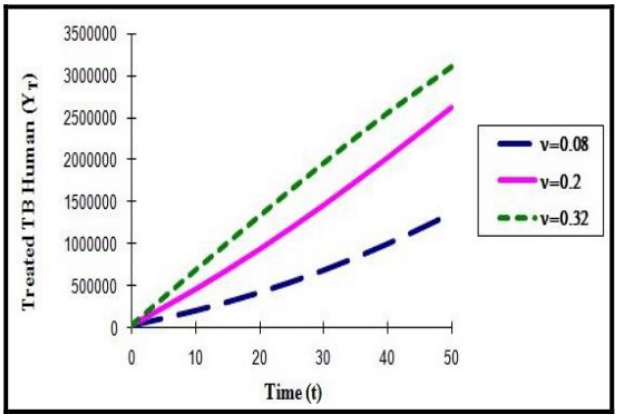

Figure 14: Variation in the Treated TB class Y_T with time for various values of the TB treatment rate ν (for set B)

6. Conclusion

In this paper, a six compartment non-linear mathematical model for TB and HIV has been analyzed. The study is significant as, TB is the main factor contributing to mortality and morbidity associated

with HIV. The HIV-TB co infection model has two BRR. We have computed the BRR for TB (R_0^T) and HIV (R_0^H) and the overall BRR $R_0 = \max\{R_0^T, R_0^H\}$. The model has three equilibria, viz. a disease-free equilibrium, TB only (HIV-free) equilibrium and HIV only (TB-free) equilibrium. We observe that if $R_0 \leq 1$, the disease-free equilibrium is globally asymptotically stable. The TB only equilibrium is locally stable if $R_0^T > 1$ along with some other conditions. The HIV only equilibrium is stable if $R_0^H > 1$ along with some other conditions. The stability of the HIV only equilibrium has been proved through numerical simulations. The simulation finding revealed some useful information on the interaction dynamics between TB and HIV. In Figure 1, we have examined the relation of the HIV transmission rate (τ) and the BRR for HIV (R_0^H). It is found that when τ is greater, $R_0^H >> 1$ which implies that with an increasing HIV transmission rate (τ), the disease gets endemic ($R_0^H >> 1$). Figure 2 studies the relation between the BRR for TB (R_0^T) and the TB transmission rate (β). It is found in the figure that with an increase in β, values of R_0^T also increase rapidly. Figure 10 and 11 show that when the TB treatment rate is high, there is an increase in the number of persons in the Y_T class, while there is a decline in the persons in the Y_{TH} class. In order to simplify the model, certain assumptions were made. We have assumed that individuals in different compartments have the same infection probability for TB (which is β) and for HIV (which is τ). Our model can be significantly expanded by taking into account unequal infection rates for different compartments. We have considered successful treatment for TB only. There is scope for extension of the work considering successful treatment for HIV as well. The numerical findings of the HIV-TB co-epidemic indicate that to lower down TB from spreading devoting finance for TB treatment and TB awareness and control programs can be an effective solution. Besides treatment, prevention programs for HIV and TB can have a greater effect on reducing the BRR and diminish both epidemics.

References

[1] T. K. Ayele, E. F. D. Goufo and S. Mugisha, *Mathematical modeling of HIV/AIDS with optimal control: A case study in Ethiopia*, Res. in Physics, 26(2021).

[2] N. Bacaer, R. Ouifki, C. Pretorius, R. Wood and B. Williams, *Modeling the joint epidemics of TB and HIV in a South African township*, J. Math. Biol., 57(4)(2008), 557-593.

[3] A. Bermejo, H. Veeken and A. Berra, *Tuberculosis incidence in developing countries with high prevalence of HIV infection*, AIDS, 6(10)(1992), 1203-1206.

[4] C. P. Bhunu, W. Garira and Z. Mukandavire, *Modeling HIV/AIDS and Tuberculosis coinfection*, Bull. Math. Biol., 71(7)(2009), 1745-1780.

[5] C. S. M. Currie, B. G. Williams, R. C. H. Cheng and C. Dye, *Tuberculosis epidemics driven by HIV: Is prevention better than cure?*, AIDS, 17(17)(2003), 2501-2508.

[6] —-, Fact Sheet HIV WHO, (2021).

[7] —-, Fact Sheet HIV-TB- WHO, (2022).

[8] J. M. Heffernan, R. J. Smith and L. M. Wahl, *Perspectives on the basic reproduction ratio*, J. R. Soc. Interface, 2(4)(2005), 281-293.

[9] V. Idemyor, *HIV and Tuberculosis co-infection: Inextricably linked liaison*, J. Nat. Med. Ass., 99(12)(2007), 1414-1419.

[10] —-, *Interim Policy On Collaborative TB/HIV Activities*, WHO, WHO/HTM/TB/2004.330 WHO/HTM/HIV/2004.1, (2004).

[11] D. Kirschner, *Dynamics of co-infection with M. Tuberculosis and HIV-1*, Theor. Pop. Biol., 55(1999), 94-109.

[12] M. C. I. Lipman, R. W. Baker and M. A. Johnson, *An Atlas of Differential Diagnosis in HIV Disease*, Second Edition, CRC Press, Parthenon Publishers, (2003).

[13] E. F. Long, N. K. Vaidya and M. L. Brandeau, *Controlling co-epidemics: Analysis of HIV and Tuberculosis infection dynamics*, Operations Research, 56(6)(2008), 1366-1381.

[14] D. J. Martin, J. G. M. Sim and G. J. Sole, *CD4+ Lymphocyte count in African patients co-infected with HIV and TB*, JAIDS, 8(4)(1995), 386-391.

[15] Z. Mukandavire, A. B. Gumel, W. Garira and J. M. Tchuenche, *Mathematical analysis of a model for HIV-malaria co-infection*, Math. Biosci. and Eng., 6(2)(2009), 333-362.

[16] R. Naresh, D. Sharma and A. Tripathi, *Modelling the effect of tuberculosis on the spread of HIV infection in a population with density-dependent birth and death rate*, Math and Comp. Modelling, 50(2009), 1154-1166.

[17] —-, Regional Strategic Plan On HIV/TB, WHO Regional Offce for South-East Asia, (2003).

[18] M. S. Sanchez, J. O. Lloyd-Smith, B. G. Williams, T. C. Porco, S. J. Ryan, M. W. Borgdorff, J. Mansoer, C. Dye and W. M. Getz, *Incongruent HIV and Tuberculosis co-dynamics in Kenya: Interacting epidemics monitor each other*, Epidemics, 1(1)(2009), 14-20.

[19] R. B. Schinazi, *Can HIV invade a population which is already sick?*, Bull. Braz. Math. Soc. (N.S.), 34(3)(2003), 479-488.

[20] M. Schulzer, M. P. Radhamani, S. Grybowski, E. Mak and J. M. Fitzgerald, *A mathematical model for the prediction of the impact of HIV infection on Tuberculosis*, Int. J. Epidemiology, 23(2)(1994), 400-407.

[21] O. Sharomi, C. N. Podder, A. B. Gumel and B. Song, *Mathematical analysis of the transmission dynamics of HIV/TB coinfection in the presence of treatment*, Math. Biosci. and Eng., 5(1)(2008), 145-174.

[22] R. Shukla and V. Kumar, *Designing a novel mathematical model for the analysis of AIDS transmission caused by co-infection of HIV with TB*, Int. J. Systems Biol., 1(2)(2009), 20-31.

[23] V. Sivarman, V. Balu, R. S. Rao and S. K. Amarnath, *Impact of HIV infection on Tuberculosis prevalence: Effectiveness of preventive chemotherapy*, Ind. J. Tuberculosis, 42(3)(1995), 139-143.

[24] S. Swaminathan and G. Narendran, *HIV and tuberculosis in India*, J. Biosci., 33(4)(2008), 527-537.

[25] —–, TB/HIV, A Clinical Manual, WHO, (2004).

[26] P. S. Vaidyanathan and S. Singh, *TB-HIV co-infection in India*, NTI Bull., 39(3-4)(2003), 11-18.

[27] P. Van den Driessche and J. Watmough, *Reproduction numbers and subthreshold endemic equilibrium for compartmental models of disease transmission*, Math. Biosci., 180(1-2)(2002), 29-48.

[28] —–, Global Tuberculosis Report, World Health Organization, (2020).

[29] —–, Global Tuberculosis Report, World Health Organization, (2021).