Mathematical Understanding of Dynamical Model for the Transmission of Endemic Tuberculosis in Bangladesh

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Abstract
The paper deals with the mathematical analysis of a dynamical model of Tuberculosis (TB) transmission in Bangladesh. Bangladesh is the 6th among the 22 TB high burden countries in the world that account for 80% of all new TB cases arising each year. So, this communicable diseases cause a major public health hazard in Bangladesh. In this study, we propose a compartmental dynamic TB model where the total populations are categorized into five compartments according to their biological features. We investigate the impact of various stages of the compartments by analyzing the disease free equilibrium, basic reproduction, stability of the model and endemic equilibrium. It is shown that the model is locally asymptotically stable disease free equilibrium when the basic reproduction number is less than unity and unique endemic equilibrium when the basic reproduction number is greater than unity. The graphical representation of this model shows the interaction among the five stages of our proposed model. The mathematical analysis is conducted through matrix method, next generation matrix method and Routh-Hurwitz criterion and the numerical simulations of the model illustrate the analytical findings.

Keywords: Dynamical systems, Compartmental model, TB Transmission, Stability analysis, Numerical simulation.

Mathematics Subject Classifications (MSC): 34D05, 34D20, 92D25.

1. Introduction

TB is a major public health concern because of its devastating effect on overall population and the ability to spread out like deadly weapons in Bangladesh. In South-East Region of Asia, Bangladesh is the most vulnerable of TB infection as it is highly densely populated country with a number of unclean slums which play an important role for the prevalence of TB ([12], [13]). One person dies of TB in every ten minutes and one is infected in every two minutes in Bangladesh and this severe situation has placed Bangladesh in the 6th position in the world in terms of burden of TB patients [7]. The outbreaks of TB infections in Bangladesh are assumed to be the most alarming and thus the significantly different in epidemiologic and clinical features [4] because of the fact that they have been occurring every year since the first detection of TB virus and its devastating infections in Bangladesh (see Table 1). The transmission rate of TB vector agents depends on age dependent contract rates on the basis of host biological feature. When the individuals get the transmission of these infectious diseases is not completely known. One can be infected with symptoms or without symptoms ([2], [7], [16]). But whatever the different families of these virus is, the ultimate result is the epidemic form and public health hazard. The consecutive prevalence and the increasing mortality rate is statistically shown in the

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Table 1. We see from the Table 1 that in the year 1994, 2007 and 2015, the mortality rate is less than 1% that is very low and under control but in the year 2003, 2004, 2010 and 2011, the mortality rate is above 20%-30% which is obviously an alarming threat for the public health of Bangladesh as well as the world. Under the Mycobacterial Disease Control Unit (MBDC) of the Director General of Health Services (DGHS), the National Tuberculosis Control Program (NTP) is working with a mission of eliminating TB from Bangladesh. Besides different health institute of Bangladesh like International Center for Diarrhoeal Disease Research, Bangladesh (ICDDR,B), Institute of Epidemiology, Disease
Control and Research (IEDCR) and Bangladesh Rural Advancement Committee (BRAC) are jointly carrying out their effective research work with various national and international health organizations to control TB outbreak in Bangladesh but the proper steps of treatment strategies should be enacted from Govt. as well as public health workers. Otherwise it may create serious public health threat if the outbreak becomes more widespread than our statistical analysis. We offer people to read ([2], [13], [16], [17], [22], [23], [24] and the references within) for more and detail study on TB virus.

In this paper, we incorporate dynamical model for the transmission of endemic tuberculosis in Bangladesh. Five compartmental stages are considered in the form of SEIR-type to understand their interaction and behavior in respect of Bangladesh. Dynamic models of infectionous virus are discussed in ([1], [8]). For some other infectionous and communicable diseases ([19], [4], [6]) discuss in detail. The main aim of this study is to modify the TB sub model Proposed in [8] by introducing modification parameter and the values of parameters in respect of Bangladesh and thus we modified a new dynamic model of TB prevalence in respect of ordinary differential equation. We analyze the model mathematically and show the dynamic behavior with numerical analysis.

The world along with Bangladesh is burden with TB for its massive spread out throughout the world. Mycobacterium is a genus of Actinobacteria, given its own family, the Mycobacteriaceae. There are over 150 species in this genus including pathogens known to cause serious disease in human body [9]. A molecular clock dates this ancestral strain to 40,000 years old when automatically modern humans were spreading out of Africa to Europe and Asia [14]. In Bangladesh the population density is very high and malnutrition, overcrowding, extreme poverty, lack of knowledge etc. are main causes for infection with MTB. TB is acquired through interactions with infectious individual interactions that include primarily the sharing of a common close environment [19]. The TB scenario in rural area and town area in Bangladesh is not same. Town area is more acute for having extreme pollution, factories, vehicles etc. The slum dwellers and the factory workers are at high risk of TB disease. The male are getting more infection comparing female in city area showing the detected case of male and female ratio is 1.6: 1. In urban area pulmonary tuberculosis revealed 29.7% resistance and 4.9% are new cases of MDR [25]. The exact TB burden is not clear in Bangladesh. Bangladesh is one of the highest TB burden among 22 countries in the world that account for 80% of all new TB cases arising each year and the 27 countries that account for 85% of the global MDR-TB burden [16]. The proportion of MDR-TB was 2.3% among new and 13.8% among previously treated TB patients ($P < 0.001$). The overall proportion of MDR-TB was 3.2%-3.5% in males and 2.3% in females. By age, the MDR-TB rate was highest (5.2%) in those aged 65 years [2]. More over 319252 new cases including 143,000 sputum smear positive TB cases and 70,000 TB related deaths occur annually ([21],[23]). New multidrug resistant TB case is 1.6% and adult TB cases HIV (+) is 0.1% [23]. Though the transmission of TB has biological and epidemical significance, the study of it has not yet been enough advances. The purpose of our paper is quite specific and significant.

In Bangladesh the causes of the TB are quite clear. Although TB cannot be transmitted easily but huge numbers of people are getting affected with it. People living in congested area inhaling

contagious air blowing from industrial area, over smoking, come to touch with untreated active tuberculosis person and so on. Contract may occur through infected people coughing, sneezing, speaking, laughing, or singing. A possible transmission Diagram of TB virus is shown in Fig. 1. However public awareness and knowledge of TB transmission can play a vital role to reduce TB prevalence in Bangladesh and the purpose of this paper is to take part in reducing TB spreading through this study.

Table 1: The Original Data on Tuberculosis in Bangladesh from 1993 to 2015 ([17, 23])

Year	Reported cases	Reported Deaths	Death Rate (%)	Remarks
1993	9233	278	3.02	------
1994	27556	231	0.84	Less Mortality Rate
1995	15175	292	1.93	------
1996	14341	317	2.21	------
1997	16064	331	2.06	------
1998	18570	454	2.44	------
1999	18737	380	2.03	------
2000	19368	407	2.10	------
2001	8570	454	5.29	------
2002	18737	330	1.76	------
2003	1368	307	22.44	High Mortality Rate
2004	1101	314	28.51	High Mortality Rate
2005	17855	387	2.17	------
2006	17627	326	1.89	------
2007	16259	112	0.69	Less Mortality Rate
2008	9368	407	4.34	------
2009	4558	417	9.15	------
2010	1042	452	43.38	High Mortality Rate
2011	1484	498	33.55	High Mortality Rate
2012	1160	244	12.41	------
2013	1855	187	10.08	------
2014	17628	426	2.42	------
2015	193521	519	0.27	Less Mortality Rate

2. Model Formulation

Modeling is the best way to present and understand the behavior of infectious diseases like TB. The different stages of TB virus are taken according to their biological feature and infectious scenario within the whole time period. The total population of model is divided into five compartments that are susceptible individual (y), means the individuals that are capable of transmitting or get infection by the vector agents [4], Latent TB individual (y_1), means the persons having latent TB infection with no symbol of TB [21], Exposed to TB (y_2), Symptom of TB (y_3) and those who have recovered with temporal immunity (y_4). We assume that susceptible individuals are recruited at a constant rate A. The exposed to TB class is influenced at a constant rate ν_1. Since we know that individuals infected with TB cannot fully recover then we assume that individuals would not completely recover from TB but would be exposed. Susceptible individuals acquire TB infection following contract with an infectious individual at a rate λ. It is assumed that in different subgroups all individuals suffer from natural death at a

constant rate μ. Individuals who suffer from TB may naturally recover and enter the recovery class at a constant rate r_1. The force of infection is given by,

$$\lambda = \frac{\beta c}{N}(y_1 + y_3) \tag{1}$$

In (1) β is the probability that one individual being infected with one infectious individual and c is per capita contact rate. Individuals infected with TB develop active TB at a constant rate k_1. The individuals also develop TB at rate $\psi\lambda$ with $\psi > 1$. The death rate d_1 is related to TB and r_2 is relapsing rate for the individuals with symptom of TB. The total population size $N(t)$ at time t is given by

$$N(t) = y(t) + y_1(t) + y_2(t) + y_3(t) + y_4(t) \tag{2}$$

The transmission diagram for the TB model is given in Fig. 1.

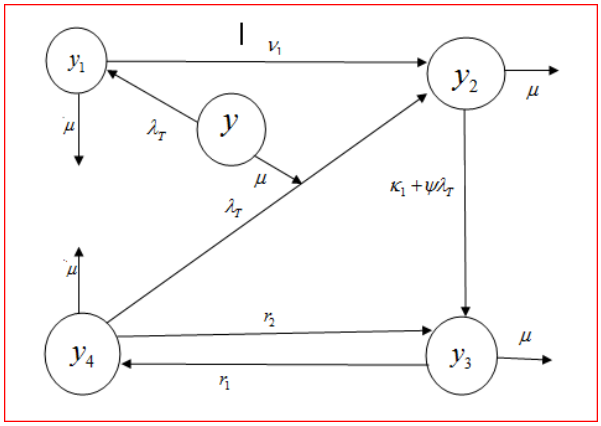


Fig. 1: Transmission diagram of TB among its various compartments

On the basis of the above transmission diagram the following TB model is constructed.

$$\begin{aligned}
\frac{dy}{dt} &= A - \lambda_T y - \mu y \\
\frac{dy_1}{dt} &= \lambda_T y - (\mu + v_1) y_1 \\
\frac{dy_2}{dt} &= v_1 y_1 + \lambda_T y_4 - (\psi\lambda_T + \mu + k_1) y_2 \\
\frac{dy_3}{dt} &= (k_1 + \psi\lambda_T) y_2 + r_2 y_4 - (\mu + r_1 + d_1) y_3 \\
\frac{dy_4}{dt} &= r_1 y_3 - (r_2 + \lambda_{T1} + \mu) y_4
\end{aligned} \tag{3}$$

The initial conditions of this model are

$$y(0) = y_0 \geq 0, y_1(0) = y_{1_0} \geq 0, y_2(0) = y_{2_0} \geq 0,$$
$$y_3(0) = y_{3_0} \geq 0, y_4(0) = y_{4_0} \geq 0.$$

Considering the biological perspectives of this model we assume the initial conditions.

Theorem 1 [10]: *The region* $\mathbb{R}_+^5$ *is positive everywhere for model* (3) *for all* $t \geq 0$ *i.e. there is no negative value for the state variables.*

Proof: Let us consider that there exists a first time variable t_1 then

$t_1 = \sup\{t > 0 : \mathrm{y} \geq 0, \mathrm{y}_1 \geq 0, \mathrm{y}_2 \geq 0, \mathrm{y}_3 \geq 0, \mathrm{y}_4 \geq 0 \in [0, \mathrm{t}]\}$

Then the first equation of the model (1) is

$$\frac{dy}{dt} = A - \lambda y - \mu y \qquad (4)$$

where $\lambda = \frac{\beta c}{N}(y_1 + y_3)$

Now from the equation (4) we have

$$\frac{dy}{dt} + (\lambda + \mu) y = A$$

The integrating factor of the above equation is $I.F = \exp\left(\int_0^{t_1} (\mu + \lambda)\, dt\right) = \exp\left(\mu t_1 + \int_0^{t_1} \lambda\, dt\right).$

So we have, $\frac{d}{dt}\left(y(t) \times \exp\left(\mu t_1 + \int_0^{t_1} \lambda\, dt\right)\right) = A \times \exp\left(\mu t_1 + \int_0^{t_1} \lambda\, dt\right).$

Now we get from the above equation

$$\Rightarrow y(t_1) = y(0) \times \exp\left(-\left(\mu t_1 + \int_0^{t_1} \lambda dt\right)\right) +$$

$$\exp\left(-\left(\mu t_1 + \int_0^{t_1} \lambda dt\right)\right) \times \int_0^{t_1} A \times \left(\mu\xi + \int_0^{\xi} \lambda(\theta)\, d\theta\right) d\xi \geq 0$$

This is true for other four compartments. Hence complete the theorem**.**

Theorem 2 [8]: *All the solutions starting in* Ω *approach enter or stay in* Ω *for all times.*

Proof: The rate of change of total population is equal to the addition of the equations in (3). Hence the rate of change of $N(t)$ is given by

$$\begin{aligned}\frac{dN}{dt} &= A - \mu y - \mu y_1 - \mu y_2 - \mu y_3 - d_1 y_3 - \mu y_4 \\ &= A - \mu(y - y_1 - y_2 - y_3 - y_4) - d_1 y_3 \\ &= A - \mu N - d_1 y_3.\end{aligned}$$

Consider the initial conditions in $\mathbb{R}_+^5$ and $t \geq 0$ from the above equation we get

$$\frac{dN}{dt} \le A - \mu N \Rightarrow \frac{d}{dt}\left(Ne^{\mu t}\right) \le Ae^{\mu t}$$

$$\Rightarrow N(t)e^{\mu t} - N(0) \le \frac{A}{\mu}\left(e^{\mu t} - 1\right)$$

$$\Rightarrow N(t)e^{\mu t} - N(0) \le \frac{A}{\mu}e^{\mu t}.$$

Now for $t \ge 0$

$$N(t) \le \frac{A}{\mu} + N(0)e^{-\mu t}.$$

If $\left(y^*, y_1^*, y_2^*, y_3^*, y_4^*\right)$ is an Ω limit point of a region in $\mathbb{R}_+^5$ such that there exists a subsequence, $t_i \to \infty$,then $\lim_{t\to\infty}\left(y(t_i), y_1(t_i), y_2(t_i), y_3(t_i), y_4(t_i)\right) = \left(y^*, y_1^*, y_2^*, y_3^* y_4^*\right)$

So, $\lim_{t\to\infty} N(t_i) = N^* = \left(y^*, y_1^*, y_2^*, y_3^*, y_4^*\right)$

by evaluating $t = t_i$ at $t \to \infty$ we have $N^* = \frac{A}{\mu}$.

Now we can say that $\left(y^*, y_1^*, y_2^*, y_3^*, y_4^*\right) \in \Omega$, or $\left(y^*, y_1^*, y_2^*, y_3^* y_4^*\right) \in \mathbb{R}_+^5$

Hence the Theorem 2 is proved.

3. Model Analysis

3.1 *Disease Free Equilibrium*

In case of disease free equilibrium point of the model (3), all the compartments are zero except the susceptible individuals. Now put $\frac{dy}{dt} = 0$ in the first equation of the model (3) and then get,

$$A - \mu y = 0$$

$$\Rightarrow y = \frac{A}{\mu}.$$

Hence the disease free equilibrium point for the model (3) is $\left(\frac{A}{\mu}, 0, 0, 0, 0\right)$.

3.2 *Basic Reproduction Number*

We take the model (3) excluding the susceptible individuals to find the basic reproduction number of the TB model.

$$\begin{aligned}
\frac{dy_1}{dt} &= \lambda y - (\mu + v_1) y_1 \\
\frac{dy_2}{dt} &= v_1 y_1 + \lambda y_4 - (\psi\lambda + \mu + k_1) y_2 \\
\frac{dy_3}{dt} &= (k_1 + \psi\lambda) y_2 + r_2 y_4 - (\mu + r_1 + d_1) y_3 \\
\frac{dy_4}{dt} &= r_1 y_3 - (r_2 + \lambda + \mu) y_4
\end{aligned} \tag{5}$$

We find out the positive individuals and negative individuals separately from the equation (5) and construct the infection matrix for the TB sub model.

$$F = \begin{pmatrix} \lambda y \\ 0 \\ 0 \\ 0 \end{pmatrix} \tag{6}$$

From the equation (6) we have

$$v = v^- - v^+$$

$$= \begin{pmatrix} (\mu + v_1) y_1 \\ (k_1 + \psi\lambda + \mu) y_2 - v_1 y_1 - \lambda y_4 \\ (\mu + r_1 + d_1) y_3 - (k_1 + \psi\lambda) y_2 - r_2 y_4 \\ (r_2 + \lambda + \mu) y_4 - r_1 y_3 \end{pmatrix} \tag{7}$$

We put the disease free equilibrium point $\left(\frac{A}{\eta}, 0, 0, 0, 0\right)$ in (6) and get the Jacobin matrix,

$$F = \begin{pmatrix} \beta c & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix} \tag{8}$$

Again we calculate the Jacobian matrix of (7) at the disease free equilibrium point $\left(\frac{A}{\eta}, 0, 0, 0, 0\right)$,

$$v = \begin{pmatrix} (\mu + v_1) & 0 & 0 & 0 \\ -v_1 & k_1 + \mu & 0 & 0 \\ 0 & k_1 & \mu + r_1 + d_1 & -r_2 \\ 0 & 0 & -r_1 & r_2 + \mu \end{pmatrix}$$

The inverse of this matrix is

$$v^{-1}=\begin{pmatrix} \frac{1}{\mu+v_1} & 0 & 0 & 0 \\ \frac{v_1}{(k_1+\mu)(\mu+v)} & \frac{1}{k_1+\mu} & 0 & 0 \\ -c_1(k_1\mu v_1+k_1v_1r_2) & -c_1(k_1\mu+k_1v_1)(\mu+r_2) & c_2(\mu+r_2) & c_2r_2 \\ -c_1r_1k_1v_1 & -c_1(r_1\mu k_1+k_1v_1r_2) & c_2r_1 & c_2(r_1+\mu+d_1) \end{pmatrix} \quad (9)$$

where

$$c_1=\frac{1}{(k_1+\mu)(v_1+\mu)\left((r_1+\mu+d_1)(\mu+r_2)-r_1r_2\right)}$$

$$c_2=(r_1+\mu+d_1)(\mu+r_2)-r_1r_2$$

Now we construct the next generation matrix by multiplying (8) and (9),

$$Fv^{-1}=\begin{pmatrix} \frac{\beta c}{\mu+v_1} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}. \quad (10)$$

Let λ be the Eigen value and I be the corresponding identity matrix of (10), then the characteristic equation is

$$\Rightarrow \begin{vmatrix} \frac{\beta c}{\mu+v_1}-\lambda & 0 & 0 & 0 \\ 0 & -\lambda & 0 & 0 \\ 0 & 0 & -\lambda & 0 \\ 0 & 0 & 0 & -\lambda \end{vmatrix}=0 \quad (11)$$

By factoring out the matrix (11) we get the value of λ and the reduced matrix,

$$\lambda_1=0,\lambda_2=0 \text{ and } \begin{vmatrix} \frac{\beta c}{\mu+v_1}-\lambda & 0 \\ 0 & -\lambda \end{vmatrix}=0$$

$$\Rightarrow -\lambda\left(\frac{\beta c}{\mu+v_1}-\lambda\right)=0$$

$$\therefore \lambda_3=0 \text{ and } \lambda_4=\frac{\beta c}{\mu+v_1}.$$

Hence the basic reproduction number of the TB sub model (3) is

$$R = \max\left(0, \frac{\beta c}{\mu + v_1}\right)$$
$$= \frac{\beta c}{\mu + v_1}.$$

3.3 *Stability Analysis of the Model*

For the stability analysis of the disease free equilibrium point of the system (3) let,

$$\begin{aligned} u &= A - \lambda y - \mu y \\ v &= \lambda y - (\mu + v_1) y_1 \\ w &= v_1 y_1 + \lambda y_3 - (\psi\lambda + \mu + k_1) y_2 \\ x &= (k_1 + \psi\lambda) y_2 + r_2 y_4 - (\mu + r_1 + d_1) y_3 \\ z &= r_1 y_3 - (r_2 + \lambda_{T1} + \mu) y_4 \end{aligned} \qquad (12)$$

Now we construct the jacobian matrix of the system (12),

$$J = \begin{pmatrix} -\mu - \lambda & 0 & 0 & 0 & 0 \\ \lambda & -(\mu + v_1) & 0 & 0 & 0 \\ 0 & v_1 & -(\psi\lambda + \mu + k_1) & \beta & \lambda \\ 0 & 0 & k_1 + \psi\lambda & -(\mu + r_1 + d_1) & r_2 \\ 0 & 0 & 0 & r_1 & -(\lambda + r_2 + \mu) \end{pmatrix} \qquad (13)$$

Theorem 3 [8]: *The disease free equilibrium of TB model is locally asymptotically stable if* $R < 1$ *and unstable if* $R > 1$.

Proof: In the system (14) we put the disease free equilibrium point $\left(\frac{A}{\mu}, 0, 0, 0, 0\right)$ and get,

$$J(w_0) = \begin{pmatrix} -\mu & 0 & 0 & 0 & 0 \\ 0 & -(\mu + v_1) & 0 & 0 & 0 \\ 0 & v_1 & -(\mu + k_1) & \beta & 0 \\ 0 & 0 & k_1 & -(\mu + r_1 + d_1) & r_2 \\ 0 & 0 & 0 & r_1 & -(r_2 + \mu) \end{pmatrix} \qquad (14)$$

Let λ be the Eigen value and I be the identity matrix, of (14) and then the characteristic equation is

$$\begin{vmatrix} -\mu-\lambda & 0 & 0 & 0 & 0 \\ 0 & -(\mu+v_1)-\lambda & 0 & 0 & 0 \\ 0 & v_1 & -(\mu+k_1)-\lambda & \beta & 0 \\ 0 & 0 & k_1 & -(\mu+r_1+d_1)-\lambda & r_2 \\ 0 & 0 & 0 & r_1 & -(r_2+\mu)-\lambda \end{vmatrix} = 0 \qquad (15)$$

By factoring out the matrix (15) thrice we have

$\lambda_1 = -(r_2+\mu),\ \lambda_2 = -\mu,\ \lambda_3 = -(\mu+v_1).$

The reduced matrix of (15) is

$$\begin{vmatrix} -(\mu+\kappa_1)-\lambda & \beta \\ \kappa_1 & -(\mu+v_1)-\lambda \end{vmatrix} = 0$$

This matrix results in terms of R as

$$\lambda^2 + (2\mu+\kappa_1+v_1)\lambda + (1-R)(\mu+v_1)(\mu+\kappa_1) - \beta\kappa_1 = 0 \qquad (16)$$

The eigenvalues λ_4 and λ_5 of the equation (16) are negative or have negative real parts when $0<1-R$ or $R<1$. Hence $\lambda_1,\ \lambda_2,\ \lambda_3,\ \lambda_4$ and λ_5 are all negative or have negative real parts when $R<1$. So disease free equilibrium point is locally asymptotically stable when $R<1$.
This holds the proof.

3.4 *Endemic Equilibrium point*

We solve the equation (3) in terms of the force infection $\lambda^* = \dfrac{\beta c(y_1^* + y_3^*)}{N^*}$ to get the endemic equilibrium point of the TB model.
Equating the R.H.S of the equations of (3) to zero we have,

$$\begin{aligned} &A-\lambda y-\mu y = 0 \\ &\lambda y-(\mu+v_1)y_1 = 0 \\ &v_1y_1+\lambda y_4-(\psi\lambda+\mu+k_1)y_2 = 0 \\ &(k_1+\psi\lambda)y_2+r_2y_4-(\mu+r_1+d_1)y_3 = 0 \\ &r_1y_3-(r_2+\lambda+\mu)y_4 = 0 \end{aligned} \qquad (17)$$

Now we solve the system (17) we have,

$$y^* = \frac{A}{\lambda^*+\mu}, \mathrm{y}_1^* = \frac{v_1y^*}{(\mu+v_1)}, \mathrm{y}_3^* = \frac{E_{T0}^*(\mu+\lambda+r_2)(\psi\lambda^*+\mu+\kappa_1)-v_1y_1^*}{(\psi\lambda^*+\mu+\kappa_1)}, \mathrm{y}_4^* = \frac{y_3^*}{(\mu+\lambda+r_2)},$$

$$y_2^* = \frac{v_1y_1^*}{(\psi\lambda^*+\mu+\kappa_1)} + \frac{v_1y_1^*r_1\lambda^*(\psi\lambda^*+\kappa_1)}{(\psi\lambda^*+\mu+\kappa_1)} \times \frac{1}{((\mu+r_1+d_1)(\mu+\lambda+r_2)-r_2r_1)-\lambda r_1(\psi\lambda^*+\kappa_1)}.$$

Hence the endemic equilibrium is given by $E_T^* = (y^*, \mathrm{y}_1^*, \mathrm{y}_2^*, \mathrm{y}_3^*, \mathrm{y}_4^*)$.

4. Numerical Results and Discussion

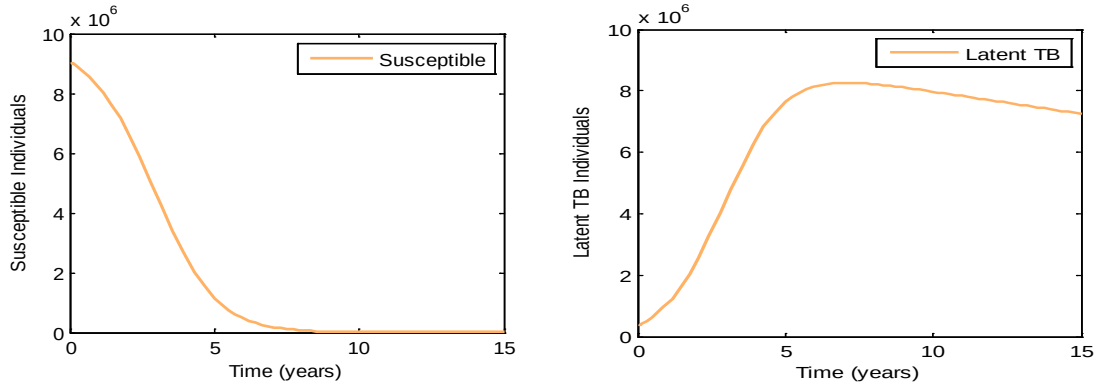
In this section the results of numerical implementations are given and the parameters which are used are given in Table 2. We use the results that are found in the numerical analysis for the graphs of Fig. 2 as proportion of the whole population. It shows the effect of β on the basic reproduction R. The time period considered is 15 years along the horizontal axis and the vertical axis represents the infected individuals and their behavior.

Table 2: The values of parameters and their descriptions.

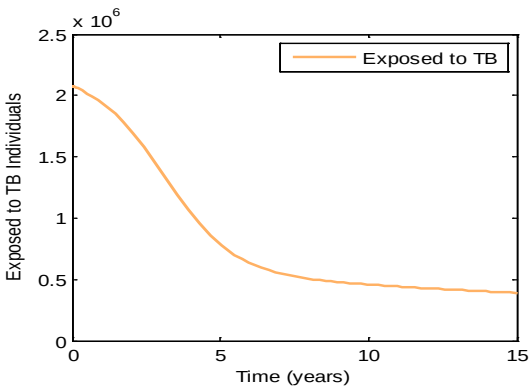
Symbol of parameters	Descriptions of parameters	Values of parameters $\left(yr^{-1}\right)$
A	Recruitment rate of Susceptible Individuals	100 (estimated)
c	Contact Rate	3.0*
d_1	Death Rate Related to TB	0.1(estimated)
β	Contact Rate of TB	0.35(.30-.70) [10]
r_1	Natural Recovery Rate	0.2*
r_2	Relapsing Rate for the Individuals with Symptom of TB	0.00001*
ψ	Modification Parameter	0.71 [10]
κ_1	TB Propagation Rate	0.000113 [10]
v_1	Rate of Propagation from Latent TB Class to Active Class	0.009*
μ	Natural Mortality	0.01(estimated)

*The values are calculated using the data of TB patients in Bangladesh.

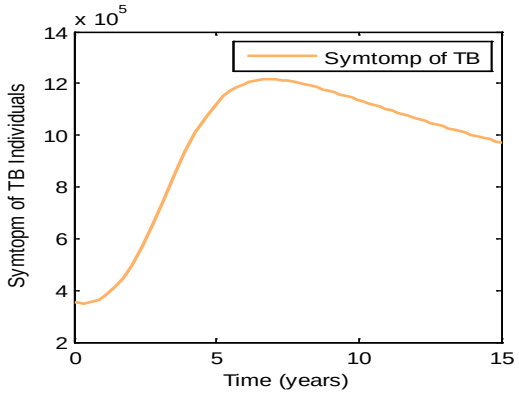
Now the numerical simulation of the model (3) is performed using the values of the parameters presented in Table 2 and the results are shown in Fig. 2.



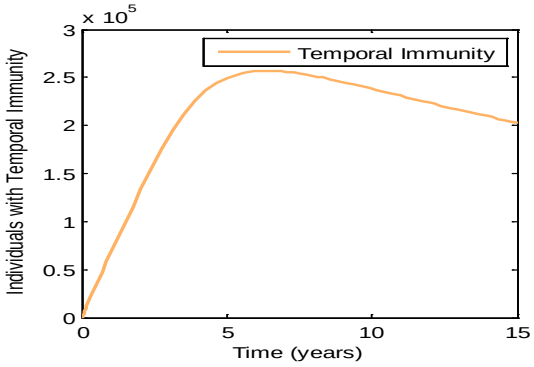
(a) (b)



(c)



(d)

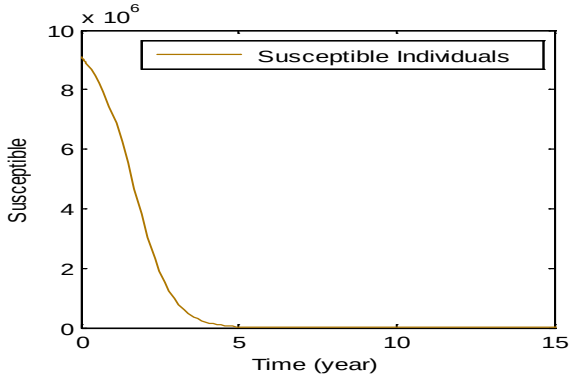


(e)

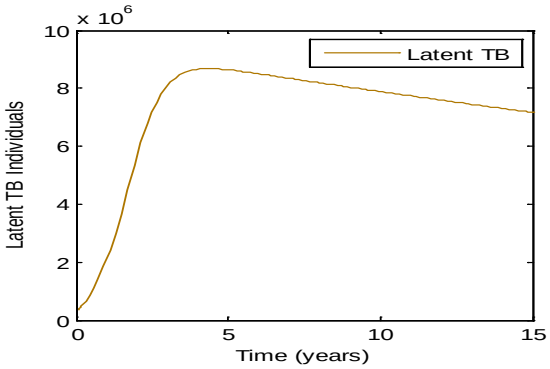
Fig. 2: Dynamic behaviors of the susceptible (y), the latent TB (y_1), exposed to TB (y_2), symptom of TB (y_3) and individuals with temporal immunity (y_4) for the parameters value of Table 2 where $\beta = 0.35$.

Fig. 2 is the graphical demonstration of the behavior of populations in different stages of TB over a period of 15 years. Fig. 2(a) shows the individuals reduce over the half of the total time scale. Due to birth or recruitment the susceptible reaches a stable state where it remains constant. Fig. 2(b) describes that the latent TB individuals increase about 6-7 years over a time period of 15 years and get asymptotical stable label. Fig. 2(c) shows the dramatically degradation of exposed to TB individuals. Fig. 2(d) describes that the symptom of TB individuals increase apparently fast and after 5 or 6 years it starts to decrease for the whole time period. Fig. 2(e) shows that an increasing feature in proportion with people recovered from TB.

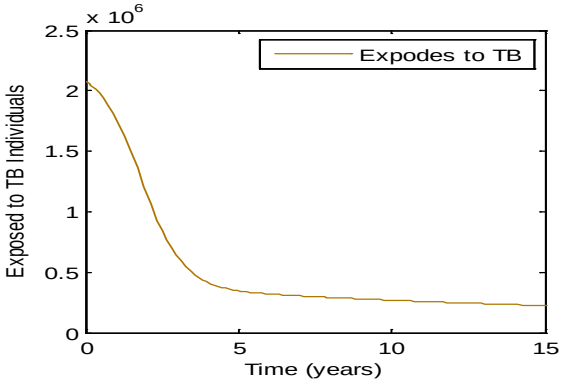
We again solve the model taking all the values of the parameters in Table 2 same but comparatively a bigger value of the $\beta = 0.60$. The results found from this computational investigation are shown in Fig. 3.



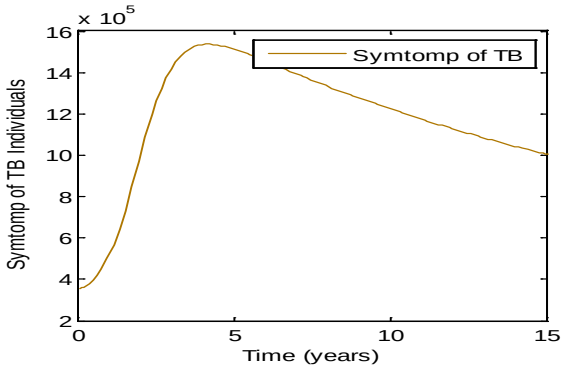
(a)



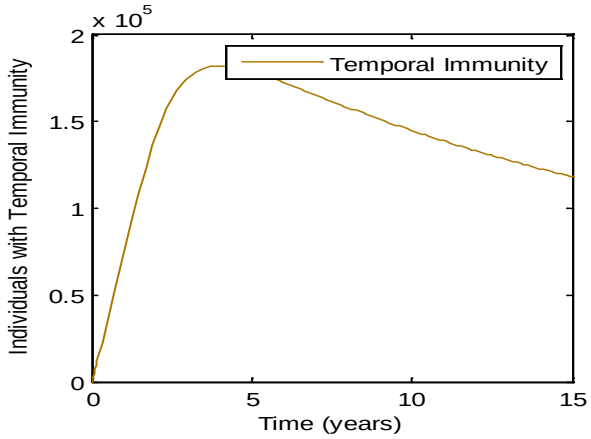
(b)



(c)



(d)



(e)

Fig. 3: Dynamic behaviors of the susceptible (y), the latent TB (y_1), exposed to TB (y_2), symptom of TB (y_3) and individuals with temporal immunity (y_4) for the parameters value of Table 2 where $\beta = 0.60$.

In Fig. 3 the dynamic characteristics of TB model are illustrated for the increasing value of β and the impact of variation of β is clear from the Figs. 2 and 3. From Fig. 3(a) we see that the susceptible individuals show decreasing behavior and after 4 years it gets asymptotically stable position. In Fig. 3(b) we see that the susceptible stage and the latent TB stage are opposite over the time period because latent TB stage shows the increasing feature for the first 5 years and

then it gradually reaches to stable position. Fig. 3(c) shows the decreasing behavior but this downward happens faster for the increasing value of β. This dramatically change takes 6 years for the lower value of β and 4 years for the higher value of β. In Fig. 3(d) the symptom to TB individuals carry out their increasing feature for first 5 years and starts to decreasing. We see from the Fig. 3(e) that the temporal immunity is slower for the increasing value of β.

5. Conclusions

Bangladesh is highly TB infected zone among the Asian countries. If TB endemic cannot be controlled immediately we have to face crucial health problem with a great loss of life and wealth. We reformulate a general mathematical model of ordinary differential equations (ODEs) for the TB model. The total population is divided into five compartments. Then we make a relation for disease free equilibrium point, basic reproduction number and endemic equilibrium point. We analyze the stability of the model. Since one-third of the people of Bangladesh have latent TB, a big percentage is infected with TB but it is in the latent stage. We find that the parameter β affects the basic reproduction number and the basic reproduction number shows a linear relationship with the TB model. From the graph we find that y_1 and y_3 has very fast increasing feature, so if we control these two class the TB infection may be reduced according to this model. Through theorem we clear that the disease free equilibrium of TB model is locally asymptotically stable if $R<1$ and unstable if $R>1$. In result section it is clear that all the stages except the temporal immunity stage in Fig. 3 are more dynamic than in Fig. 2. This result comes out for the variation of β, that is if β increases the prevalence of TB accelerates but for the temporal immunity it does not.

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