A SEIRS Model of Tuberculosis Infection Model with Vital Dynamics, Early Treatment for Latent Patients and Treatment of Infective

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Abstract

Tuberculosis is one of the most destructive bacteria in human being and the second cause of mortality after HIV/AIDS in the whole world. In this research work, a SEIRS of mathematical model for the transmission of tuberculosis incorporating vital dynamics, early therapy of patient with tuberculosis were studied and a model for treatment of infective as controls was developed. The effective reproduction number and the disease-free equilibrium was also analysed for the stability. The results revealed that the two controls reduce effective number below unity. Furthermore, it shows that early therapy of patient with tuberculosis is more effective in mitigating the spread of tuberculosis burden.

Index Terms: Tuberculosis Transmission; Control Strategy; Disease Free Equilibrium; Effective Reproduction Number; Stability.

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1. Introduction

Tuberculosis (TB) is an airborne disease caused by Mycobacterium tuberculosis (Mtb) bacterial [10]. It has been known since 1000 B.C., so it not a new disease. About 3 million death worldwide attributed to tuberculosis every year [4].

Since TB is a disease of respiratory transmission, optimal conditions for transmission include:

– Overcrowding
– Poor personal hygiene
– Poor public hygiene.

Most cases of TB infection are in developing countries [7]. Transmission of TB result through the tiny droplets released into air via cough and sneezes from one person to another, it's a communicable disease. The bacteria usually attack the lungs.

In addition, according to the World Health Organization, one-third of the world's population is infected, either latently or actively, with tuberculosis [1]. There are more cases of tuberculosis in the world today than in previous time in human [17].

Tuberculosis: Signs and Symptoms
. Cough that lasts for more than 2 weeks
. Fever
. Night sweats
. Feeling weak & 8red
. Losing weight (without trying)
. Loss of appetite
. Chest pains
. Coughing up blood

The study of tuberculosis transmission dynamics has been of great interest to both applied mathematicians and biologists because of its universal threat to humanity [25].

A number of theoretical studies have been carried out on the mathematical modelling of tuberculosis transmission dynamics [1,5, 9,11-15,17, 18, 24, 25].

[2] modeled tuberculosis transmission that incorporates treatment and chemoprophylaxis. They assumed that latency infected individuals developed active tuberculosis disease as a result of endogenous re-activation, exogenous reinfection and disease relapse. Their results showed that treatment of infective is more effective in the first years of implementation as treatment results in clearing active TB immediately and there after chemoprophylaxis will do better in controlling the number of infective due to reduced progression to active TB.

The main principal aim of the current work is to improved on the SIR model of tuberculosis initially studied by [25]. TB have a long incubation period or latent at which an individuals is infected but cannot spread the infection [26,27]due to the long incubation period exposed class has been incorporated in to the model by [25].

By considering the work of authors mentioned above, we developed and analyzed a new mathematical model of tuberculosis infection to complements and extend their works by incorporating the following factors that are very important in the transmission of tuberculosis infection.

- Vital dynamics with unequal birth rate and death rate
- Temporary immunity for describing the spread of infectious disease
- Standard incidence rate
- Disease induced death due to tuberculosis
- Treatment of both latency and infective.

The reminder of this paper is organized as follows. In section (2), we formulate the model (3) we analysed the model to obtained the effective basic reproduction number and establishing the condition for local and global stability of the disease free equilibrium of the model and finally we discuss the results in section (4).

2. Material and Method

A mathematical model for tuberculosis infection is developed by making improvement on the previous models as actual source and can be seen from figure 1.
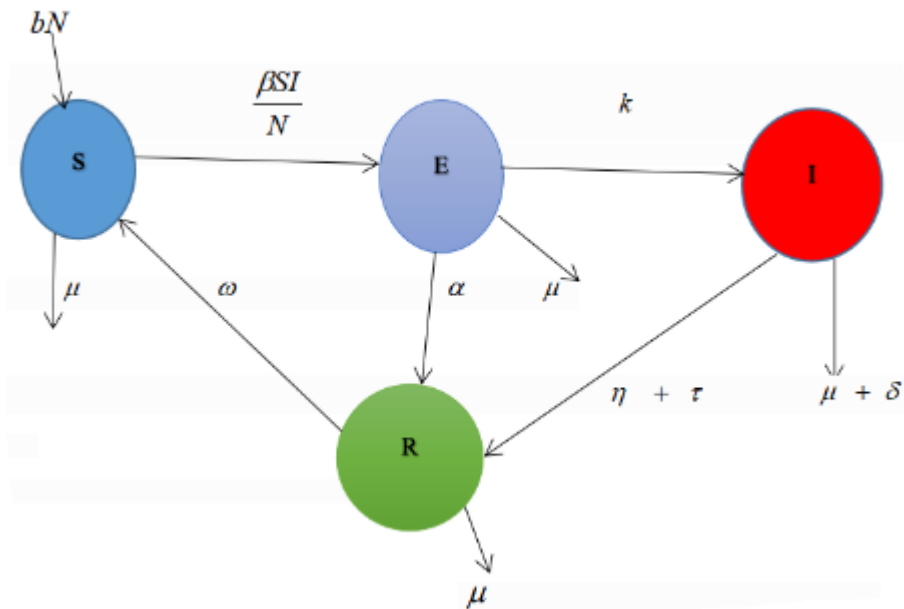

Fig. 1: Schematic diagram for Tuberculosis transmission with early treatment of latent patient and treatment of infection.

2.1. Model Assumption

A model the spread of tuberculosis was developed with the following assumption.
- Homogeneous mixing, susceptible individuals acquire tuberculosis infection following contact rate with an infective individual
- Treatment are offered to both latency infected and infectious
- The infection does not confer immunity to the cure and as such the recovered components are returned back to the susceptible compartment at a given rate (ω)
- The total population is compartmentalized in to four (4) epidemiological classes as shown in figure (1)

2.2 . Model Equation

The corresponding mathematical model equations are described by a system of ordinary differential equation given below:

$$\frac{dS}{dt} = bN - \frac{\beta SI}{N} + \omega R - \mu S$$

$$\frac{dE}{dt} = \frac{\beta SI}{N} - (k + \alpha + \mu)E$$

$$\frac{dI}{dt} = kE - (\eta + \tau + \mu + \delta)I \tag{1}$$

$$\frac{dR}{dt} = (\eta + \tau)I + \alpha E - (\omega + \mu)R$$

2.3. Symbols for State Variables

S — Number of susceptible individuals

E — Number of exposed individuals

I — Number of infected individuals

R — Number of recovered individuals

N — Total population

1.2.4. Symbols for Parameters

b — Per capital birth rate of humans

μ — Per capital natural death rate of humans

β — Transmission rate

k — Progression from E to I

η — Natural recovery from tuberculosis

τ — Recovery due to treatment

δ — Tuberculosis-induced death rate by I

α — Treatment rate for exposed individuals

ω — Loss (waning) of immunity by recovered individuals.

based on biological considerations, model system (1) will be studied in the following region

$$= \left\{ (S, E, I, R) \in R_+^4 : N \leq \frac{bN}{\mu} \right\} \tag{2}$$

which can be shown to be positively invariant with respect to the model system (1).

4. Disease Free Equilibrium (E_f) and Model Analysis

The disease free equilibrium state is a steady state solution where there is no disease [24]. To obtained disease free equilibrium, the right hand sides of system model (1) is set to zero and the state variables S, E, I and R are solved.

$$\frac{dS}{dt} = 0 \Rightarrow bN - \frac{\beta SI}{N} + \omega R - \mu S = 0$$

$$\frac{dE}{dt} = 0 \Rightarrow \frac{\beta SI}{N} - (k + \alpha + \mu)E = 0 \tag{3}$$

$$\frac{dI}{dt} = 0 \Rightarrow kE - (\eta + \tau + \mu + \delta)I = 0$$

$$\frac{dR}{dt} = 0 \Rightarrow (\eta + \tau)I + \alpha E - (\omega + \mu)R = 0$$

If E=0,I=0, and R = 0 , then equation (3) becomes

$$S = \frac{bN}{\mu}, E = 0, I = 0, R = 0$$

Therefore, substituting with E=I=R=0, we obtained disease free equilibrium

$$\left(S^*, E^*, I^*, R^*\right) = \left(\frac{bN}{\mu}, 0, 0, 0\right) \tag{4}$$

3.1.. Basic Reproduction Number, R_0

Consideration of stability of a disease-free equilibrium gives certain conditions under which disease will die out or stay in the population called the basic reproduction number, R_0. A better widely accepted and used method in finding R_0 that reflect its biological meaning is the next generation operator approach described by [16] and subsequently analysed by [3]. Using this approach we obtain the basic reproduction number, R_0 of the model system (1) which is the spectral radius (ρ) of the next generation matrix, K .

i.e.

$$R_0 = \rho K , \text{ where } K = FV^{-1}$$

$$F = \begin{pmatrix} 0 & \dfrac{\beta b}{\mu} \\ 0 & 0 \end{pmatrix} \tag{5}$$

$$V^{-1} = \begin{pmatrix} \dfrac{1}{(\tau + \eta + \delta + \mu)} & 0 \\ \dfrac{k}{(k + \alpha + \mu)(\tau + \eta + \delta + \mu)} & \dfrac{1}{(k + \alpha + \mu)} \end{pmatrix} \tag{6}$$

$$Rc = \frac{\beta k b}{\mu(k + \alpha + \mu)(\eta + \tau + \delta + \mu)} \tag{7}$$

$$R_o = \frac{\beta k b}{\mu(k + \mu)(\eta + \delta + \mu)} \tag{8}$$

4. Result and Discussion

In this section, we do numerical simulation of model system (1) using maple software. The numerical values that we used for the simulation are presented in Table (1). Most of the parameters values in Table (1) are from the literature.

Table 1: Values of Parameters of the Model

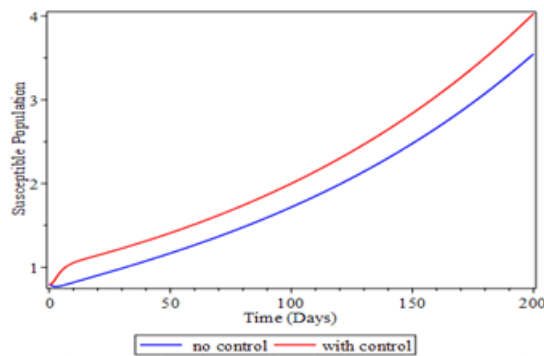| S/N	Parameters	Value	Source
1	b	0.027	[25]
2	μ	0.02 year^{-1}	[21]
3	β	0.35(0.1-0.6)0.02 year^{-1}	[22]
4	δ	0.3	[21]
5	τ	(0-1)	Varying
6	α	(0-1)	Varying
7	k	0.025	[23]
8	ω	0.4	[20]
9	η	0.2	[21]

Fig 2. The total number of susceptible individuals without any control which gives Rc=1.3889 with control gives Rc=0.0276

Figure 2 shows the graphical profile of susceptible population without any intervention and in the presence of intervention for the period of 200 days. It can be seen that the number of susceptible individuals decrease without any intervention and increases sharply in the presence of intervention.
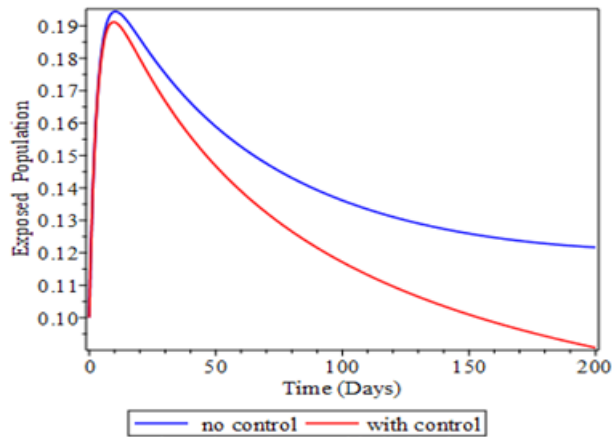

Fig 3. The total number of exposed individuals without any control which gives Rc=1.3889 with control gives Rc=0.0276

Figure 3 shows the numerical simulation of the exposed individuals without control and in the presence of control. It is observed that without control the number of exposed individuals gradually increase and with control the exposed individuals drops to zero.
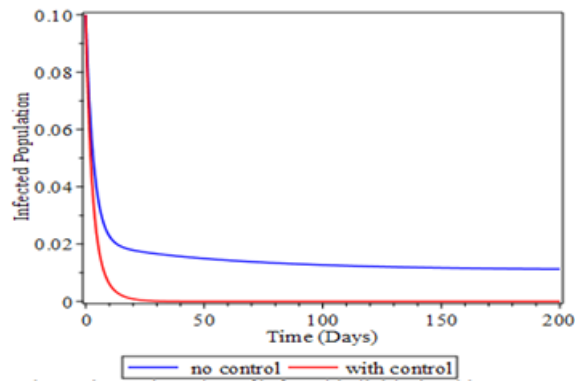

Fig 4. The total number of infected individuals without any control which gives Rc=1.3889 with control gives Rc=0.0276

Figure 4 shows the simulation of infected individuals as a function of time with both absence and presence of control. It can be observed that the number infected individuals decreases very rapidly to zero level and stayed there indicating that there is no more tuberculosis burden and at this time it has been shown in figure 5 that the number of the recovered individuals have gradually increased.
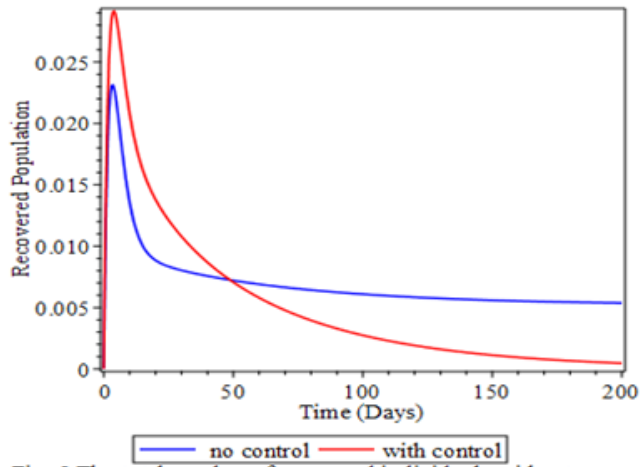
Fig 5. The total number of recovered individuals without any control which gives Rc=1.3889 with control gives Rc=0.0276
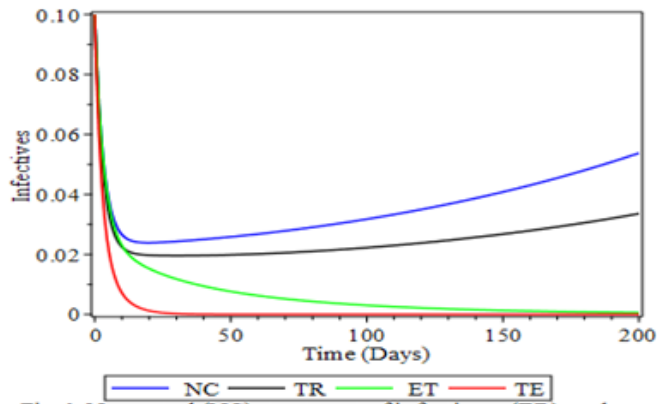

Fig 6. No control(NC), treatment of infectivess(TR), early treatment of latently tuberculosis patient(ET) and both treatment of infectives and early treament of latently tuberculosis patients(TE)

    Figure 6 present the dynamics of infected population with four different situation by testing the model without any control, with treatment of infective only, with early therapy of patients with the disease and with both treatment of infective and early therapy of patients.

    Rt denote effective basic reproduction number with respect to treatment of infective only while Re represent effective basic reproduction number with respect to early therapy of patients with tuberculosis.
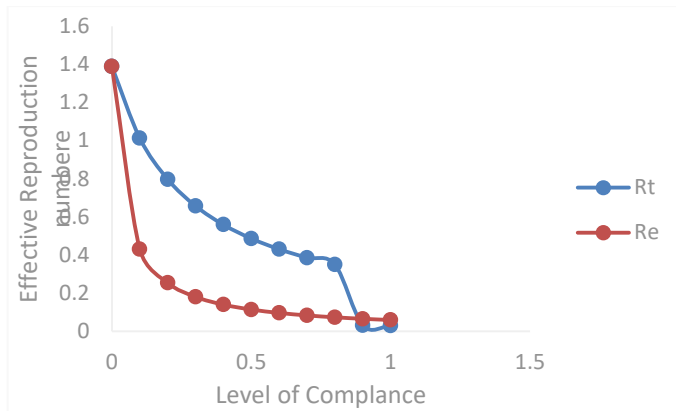
Figure 7 shows the trend of R_t and R_e of effective basic reproduction numbers obtained by varying level of compliance from (0-1).

Table 2: Values of effective basic reproduction number with respect to level of complance

Level of complance	Rt	Re
0	1.3889	1.3889
0.1	1.0135	0.431
0.2	0.7979	0.2551
0.3	0.6579	0.1812
0.4	0.5597	0.1404
0.5	0.487	0.1147
0.6	0.431	0.0969
0.7	0.3866	0.0839
0.8	0.3505	0.074
0.9	0.0321	0.06613
1	0.0295	0.0598

6. Conclusion

This paper present and studied a deterministic models of tuberculosis infection by incorporating some important factors that plays a significant role in tuberculosis transmission which include vital dynamics, early therapy of patient with tuberculosis and treatment of infective. To considered the effect of early early therapy of latently infected and treatment of infected individuals, figure 2,3,4 and 5 are plotted with presence and absence of control. It is observed that the number of susceptible individuals increase sharply when control are applied and exposed individuals slowly.

Our result reveals that the two (2) controls reduced effective basic reproduction number below the unity. It further show that early therapy of patients with tuberculosis is more effective. And finally obtained simulations results confirm both early therapy of patients with tuberculosis and treatment of infective control the epidemics of tuberculosis, although the two combined intervention offered the most effective.

There is a need for future research work on the comparing the model with bilinear incidence rate, incorporation of vaccination, public health education, isolation of infected individuals and also to perform sensitivity analysis to know which parameter is more sensitive.

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