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Modeling the Effect of Variation of Recruitment Rate on the Transmission Dynamics of Tuberculosis

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Abstract: *In this Paper, the effect of the variation of recruitment rate on the transmission dynamics of tuberculosis was studied by modifying an existing model. While the recruitment rate into the susceptible class of the existing model is constant, in our modified model we used a varying recruitment rate. The models were analyzed analytically and numerically and these results were compared. The Disease Free Equilibrium (DFE) state of the existing model was found to be* $\left(\frac{\Lambda}{\mu},0,0,0\right)$*, the DFE of the modified model was found to be* $(S^*,0,0,0)$ *where* S^* *is arbitrary. While all the eigenvalue of the existing model are negative, one of the eigenvalues of the modified model is zero. The basic reproduction number* R_o *of both models are established to be the same. The numerical experiments show a gradual decline in the infected and exposed populations as the recruitment rates increase in both models but the decline is more in the modified model than in the existing model. This implies that eradication will be achieved faster using the model with a varying recruitment rate.*

Keywords*: tuberculosis, variation, recruitment rate, constant, effect, reproduction number, stability*

I. Introduction

Tuberculosis commonly called TB is a contagious and airborne disease caused by mycobacterium tuberculosis. It is a estimated that nearly 1/3 of the world population acts as a reservoir of the disease [7,1].It is a disease of poverty affecting mostly young adults in their most productive years. Majority of TB deaths occur in the developing world. The death toll as a result of the disease in 2009 alone is put at about 1.7 million people, that is approximately 4700 people in a day [11].

Mycobacterium Tuberculosis is transmitted when a susceptible individual inhales air containing the nuclei carrying the tubercle bacilli released by infectious individuals when they talk, sing sneeze, cough or spit. Once inhaled, the bacteria eventually reach the lungs and spread throughout the body. It can attack any part of the body, but only active pulmonary and laryngeal tuberculosis pose a risk of transmission. Approximately 10% of the individuals who inhale the droplets become infectious while the remaining may remain in the latent or exposed class for various durations, some may never develop active tuberculosis. Those in the latent class have annual 10 – 20% risk of progressing to active TB. Other category of individuals at greater risk of developing active TB are children under four years of age, those with weakened immunity due to conditions such as HIV/AIDS, malnutrition, certain cancers and those recently infected by mycobacterium tuberculosis [2,3].

Tuberculosis can be prevented and can also be cured. The preventive measures include: avoiding overcrowded places especially those with poor ventilation network, the use of ultraviolet lighting to kill the bacteria in confined places, early detection and early treatment of TB patients, vaccinations such as BCG to mention but a few. The effective treatment of the disease mostly involves the use of a combination of drugs for a period of 6 to 9 months [2, 3]. Non – adherence to the treatment of the disease results in the resurgence of the resistant strains of the disease making it even more difficult to cure. This led the World Health Organization WHO to adopt a global control strategy to help in reducing this menace and promote proper treatment of patients with tuberculosis known as the Direct Observation Therapy Strategy (DOTS). This has evolved a process that makes it compulsory for patients to complete their treatment through the use of a nurse or a surrogate who delivers and supervises the patient to take his/her drugs at and as when due rather than relying on the patient to take the drugs by himself or herself [4].

II. Role of Mathematical Models

Several organizations and disciplines have contributed immensely in the global fight against tuberculosis among which is mathematical modeling. The first mathematical model for the study of transmission

dynamics of tuberculosis was developed by [10]. Their model comprises of a linear equation with three compartments. From then on, several models of the disease were developed. The models which immediately followed the first were mostly concerned with cost-effectiveness of different types of interventions. Revelle et. al.,(1969)[9] argued that vaccination was cost-effective in countries with high TB burdens. Most models of tuberculosis are of the SEIR type and each has its peculiar area(s) of interest. All these models are aimed at contributing to the understanding of tuberculosis with a view to preventing, controlling and possibly eradicating the disease. Another common thing with tuberculosis models is the constant recruitment into the susceptible class of the models. It is a known fact that the world's population has almost tripled between 1950 and 2005 and although the growth rate in the developed countries is almost on the decline, the growth rate in the developing countries where tuberculosis is endemic is on the increase and geometrical at that. According to the Population Reference Bureau most of the annual growth rate of 1.2 of the world's population from 2005 to 2030 will occur in less developed countries in Africa, Asia and Latin America [8]. These are the places where tuberculosis is endemic. We therefore propose the use of varying recruitment rates into the susceptible classes of tuberculosis models which we hope will give us a better understanding of the disease.

The model for the transmission dynamics that we will use in this paper is a modified version of the model by Feng et. al., (2000)[5]. We incorporated a varying recruitment rate into the existing model instead of the constant recruitment and analyzed both the existing and the modified for the existence of the disease free equilibrium states, stability of the DFEs, determine their basic reproduction numbers R_o and perform numerical simulation and compare the results obtained.

2.1 Definition of Terms

Definition 2.1.1 Susceptible: This is an individual who is not infected by the disease but can be infected if exposed to the disease.

Definition 2.1.2 Exposed: This is an individual who has been infected by the disease but is not infectious (i.e. he/she cannot transmit the disease).

Definition 2.1.3 Infective: This is an individual who has already been infected by the disease and is capable of transmitting the disease.

Definition 2.1.4 Recruitment rate: This the rate at which people are added to the population.

Definition 2.1.5 Basic Reproduction Number (R_o): The expected number of secondary cases produced by a single infection introduced into a completely susceptible population.

Definition 2.1.6 CDC: Centers for Disease Control

III. Model Parameters

S (t)	=	Number of susceptible individuals at time t
E (t)	=	Number of exposed individuals at time t
I (t)	=	Number of infected individuals at time t
T (t)	=	Number of treated individuals at time t
N (t)	=	the total population size at time t (N=S+E+I+T)
b	=	natural birth rate (b>0)
Λ	=	Constant recruitment rate used in the original model
β	=	Average number of susceptible individuals infected by one infectious individual per contact per unit of time
σ	=	Average number of treated individuals infected by one infectious individual per contact per unit of time
c	=	the per-capita contact rate
μ	=	the per capita natural death rate
k	=	the rate at which and individual leaves the latent class by becoming infectious
d	=	the per-capita disease-induced death rate
r	=	the per-capita treatment rate
ρ	=	the level of re-infection

3.1 Model Equations

Below is the model with a constant recruitment rate as in Feng et al., 2000:

$$\frac{dS}{dt} = \Lambda - \beta cS\frac{I}{N} - \mu S \qquad (3.1.1)$$

$$\frac{dE}{dt} = \beta cS\frac{I}{N} - \rho\beta cE\frac{I}{N} - (\mu + k)E + \beta cT\frac{I}{N} \quad (3.1.2)$$

$$\frac{dI}{dt} = \rho\beta cE\frac{I}{N} + kE - (\mu + r + d)I \quad (3.1.3)$$

$$\frac{dT}{dt} = rI - \beta cT\frac{I}{N} - \mu T \quad (3.1.4)$$

Our modified model with a varying recruitment rate takes the following form:

$$\frac{dS}{dt} = bN - \beta cS\frac{I}{N} - \mu S \quad (3.1.5)$$

$$\frac{dE}{dt} = \beta cS\frac{I}{N} - \rho\beta cE\frac{I}{N} - (\mu + k)E + \beta cT\frac{I}{N} \quad (3.1.6)$$

$$\frac{dI}{dt} = \rho\beta cE\frac{I}{N} + kE - (\mu + r + d)I \quad (3.1.7)$$

$$\frac{dT}{dt} = rI - \beta cT\frac{I}{N} - \mu T \quad (3.1.8)$$

$$N = S + E + I + T \quad (3.1.9)$$

3.2 Existence of the Disease-free Equilibrium State of the Existing Model

Here we will investigate the existence of the disease free equilibrium state of the existing model which we will denote as W_0, a state in which there are no exposed, infected and treated individuals i.e. the disease is absent. We assume that all the parameters are non-negative and we determine an equilibrium state by setting the right-hand sides of the equations (3.1.1)-(3.1.4) to zero.

$$\Lambda - \beta cS\frac{I}{N} - \mu S = 0 \quad (3.2.1)$$

$$\beta cS\frac{I}{N} - \rho\beta cE\frac{I}{N} - (\mu + k)E + \sigma\beta cT\frac{I}{N} = 0 \quad (3.2.2)$$

$$\rho\beta cE\frac{I}{N} + kE - (\mu + r + d)I = 0 \quad (3.2.3)$$

$$rI - \sigma\beta cT\frac{I}{N} - \mu T = 0 \quad (3.2.4)$$

At the disease-free equilibrium state W_0,

$E = I = T = 0$

Putting these into equations (3.2.1) - (3.2.4) gives

$\Lambda - \mu S = 0$, from which we have $S = \frac{\Lambda}{\mu}$

$E = I = T = 0$

Therefore, disease-free equilibrium state $W_O = \left(\frac{\Lambda}{\mu}, 0, 0, 0\right)$

3.3 Stability of the Disease-Free Equilibrium State of the Existing Model

Here we analyze the stability of the disease free equilibrium of the existing model by computing the Jacobian of equations (3.2.1)-(3.2.4).

$$F_1 = \Lambda - \beta cS\frac{I}{S + E + I + T} - \mu S, \quad (3.3.1)$$

$$F_2 = \beta cS\frac{I}{S+E+I+T} - \rho\beta cE\frac{I}{S+E+I+T} - (\mu+k)E + \sigma\beta cT\frac{I}{S+E+I+T}, \quad (3.3.2)$$

$$F_3 = \rho\beta cE\frac{I}{S+E+I+T} + kE - (\mu+r+d)I, \quad (3.3.3)$$

$$F_4 = rI - \sigma\beta cT\frac{I}{S+E+I+T} - \mu T, \quad (3.3.4)$$

Then

$$\frac{\partial F_1}{\partial S} = -\beta c\frac{I}{S+E+I+T} + \beta cS\frac{I}{(S+E+I+T)^2} - \mu$$

$$\frac{\partial F_1}{\partial E} = \beta cs\frac{I}{(S+E+I+T)^2}$$

$$\frac{\partial F_1}{\partial I} = -\beta c\frac{S}{(S+E+I+T)} + \beta cS\frac{I}{(S+E+I+T)^2}$$

$$\frac{\partial F_1}{\partial T} = \beta cS\frac{I}{(S+E+I+T)^2}$$

$$\frac{\partial F_2}{\partial S} = \frac{\beta cI}{(S+E+I+T)} - \frac{\beta cSI}{(S+E+I+T)^2} + \frac{\rho\beta cEI}{(S+E+I+T)^2} - \frac{\sigma\beta cTI}{(S+E+I+T)^2}$$

$$\frac{\partial F_2}{\partial E} = \frac{-\beta cSI}{(S+E+I+T)^2} - \frac{\rho\beta cI}{(S+E+I+T)} + \frac{\rho\beta CEI}{(S+E+I+T)^2} - (\mu+k) - \frac{\sigma\beta cTI}{(S+E+I+T)^2}$$

$$\frac{\partial F_2}{\partial I} = \frac{\beta cS}{(S+E+I+T)} - \frac{\beta cSI}{(S+E+I+T)^2} - \frac{\rho\beta cE}{(S+E+I+T)} + \frac{\rho\beta cEI}{(S+E+I+T)^2} + \frac{\sigma\beta cT}{(S+E+I+T)} - \frac{\sigma\beta cTI}{(S+E+I+T)^2}$$

$$\frac{\partial F_2}{\partial T} = \frac{-\beta cSI}{(S+E+I+T)^2} + \frac{\rho\beta cEI}{(S+E+I+T)^2} + \frac{\sigma\beta cI}{(S+E+I+T)} - \frac{\sigma\beta cTI}{(S+E+I+T)^2}$$

$$\frac{\partial F_3}{\partial S} = \frac{-\rho\beta cEI}{(S+E+I+T)^2}$$

$$\frac{\partial F_3}{\partial E} = \frac{\rho\beta cI}{(S+E+I+T)} - \frac{\rho\beta cEI}{(S+E+I+T)^2} + k$$

$$\frac{\partial F_3}{\partial I} = \frac{\rho\beta cI}{(S+E+I+T)} - \frac{\rho\beta cEI}{(S+E+I+T)^2} - (\mu+r+d)$$

$$\frac{\partial F_3}{\partial T} = \frac{-\rho\beta cEI}{(S+E+I+T)^2}$$

$$\frac{\partial F_4}{\partial S} = \frac{-\sigma\beta cTI}{(S+E+I+T)^2}$$

$$\frac{\partial F_4}{\partial E} = \frac{-\sigma\beta cTI}{(S+E+I+T)^2}$$

$$\frac{\partial F_4}{\partial I} = r - \frac{\sigma\beta cT}{(S+E+I+T)} + \frac{\sigma\beta cTI}{(S+E+I+T)^2}$$

$$\frac{\partial F_4}{\partial T} = -\frac{\sigma\beta cI}{(S+E+I+T)} + \frac{\sigma\beta cTI}{(S+E+I+)^2} - \mu$$

Evaluating the Jacobian at W_0 we get

$$Jw_0 = \begin{bmatrix} -\mu & 0 & -\beta c & 0 \\ 0 & -(\mu+k) & \beta c & 0 \\ 0 & k & -(\mu+r+d) & 0 \\ 0 & 0 & r & -\mu \end{bmatrix}$$

The characteristics equation is given by

$$|Jw_0 - \lambda I| = \begin{vmatrix} -\mu-\lambda & 0 & -\beta c & 0 \\ 0 & -(\mu+k)-\lambda & \beta c & 0 \\ 0 & k & -x-\lambda & 0 \\ 0 & 0 & r & -\mu-\lambda \end{vmatrix}$$

$$(-\mu-\lambda)(-\mu-\lambda)\begin{vmatrix} -(\mu+k)-\lambda & \beta c \\ k & -x-\lambda \end{vmatrix} = 0$$

where $x = (\mu+r+d)$

$$(-\mu-\lambda)(-\mu-\lambda)\begin{vmatrix} -(\mu+k)-\lambda & \beta c \\ k & -x-\lambda \end{vmatrix} = 0$$

$$\lambda_1 = -\mu$$

$$\lambda_2 = \frac{-(\mu+k+x)+\sqrt{(\mu+k+x)^2 - 4(\mu+k)x[1-R_O]}}{2}$$

$$\lambda_3 = \frac{-(\mu+k+x)-\sqrt{(\mu+k+x)^2 - 4(\mu+k)x[1-R_O]}}{2}$$

$$\lambda_4 = -\mu$$

where $R_o = \frac{k\beta c}{(\mu+k)x}$

If $1-R_o > 0,$

then $R_o < 1$ and

$$\lambda_2 < \frac{-(\mu+k+x)}{2} + \frac{\sqrt{(\mu+k+x)^2}}{2} = 0$$

$$\lambda_3 < \frac{-(\mu+k+x)}{2} - \frac{\sqrt{(\mu+k+x)^2}}{2} = -(\mu+k+x)$$

Therefore, $\lambda_2 < 0$ and $\lambda_3 < 0$, thus establishing $\lambda_1 < 0,\ \lambda_2 < 0,\ \lambda_3 < 0,\ \lambda_4 < 0$

3.4 Existence of the Disease-free Equilibrium State of the Modified Model

Here we will investigate the existence of the disease free equilibrium state of the modified model which we will denote as Z_O, a state in which there are no exposed, infected and treated individuals i.e. the disease is absent. We assume that all the parameters are non-negative and we determine an equilibrium state by setting the right-hand sides of the equations (3.1.5)-(3.1.8) to zero.

$$b(S+E+I+T)-\beta cS\frac{I}{S+E+I+T}-\mu S=0 \quad (3.4.1)$$

$$\beta cS\frac{I}{S+E+I+T}-\rho\beta cE\frac{I}{S+E+I+T}-(\mu+k)E+\sigma\beta cT\frac{I}{S+E+I+T}=0 \quad (3.4.2)$$

$$\rho\beta cE\frac{I}{S+E+I+T}+kE-(\mu+r+d)I=0 \quad (3.4.3)$$

$$rI-\sigma\beta cT\frac{I}{S+E+I+T}-\mu T=0 \quad (3.4.4)$$

At the disease-free equilibrium state Z_O,

$$E=I=T=0$$

Substituting these into equations (3.4.1) - (3.4.4)

$$bS-\mu S=0$$

$$(b-\mu)S=0$$

$$S\neq 0, b=\mu$$

S^* Is arbitrary

The disease-free equilibrium state $(S^*,0,0,0)$

3.5 Stability of the Disease-Free Equilibrium State of the Modified Model

Here we analyze the stability of the disease free equilibrium of the modified model by computing the Jacobian of equations (3.4.1)-(3.4.4).

$$F_1=b(S+E+I+T)-\beta cS\frac{I}{S+E+I+T}-\mu S=0 \quad (3.5.1)$$

$$F_2=\beta cS\frac{I}{S+E+I+T}-\rho\beta cE\frac{I}{S+E+I+T}-(\mu+k)E+\sigma\beta cT\frac{I}{S+E+I+T}=0 \quad (3.5.2)$$

$$F_3=\rho\beta cE\frac{I}{S+E+I+T}+kE-(\mu+r+d)I=0 \quad (3.5.3)$$

$$F_4=rI-\sigma\beta cT\frac{I}{S+E+I+T}-\mu T \quad (3.5.4)$$

The Jacobian matrix of the system is given by

$$\frac{\partial F_1}{\partial S}=b-\beta c\frac{I}{S+E+I+T}+\beta cS\frac{I}{(S+E+I+T)^2}-\mu$$

$$\frac{\partial F_1}{\partial E}=b+\beta cs\frac{I}{(S+E+I+T)^2}$$

$$\frac{\partial F_1}{\partial I}=b-\beta c\frac{S}{(S+E+I+T)}+\beta cS\frac{I}{(S+E+I+T)^2}$$

$$\frac{\partial F_1}{\partial T} = b + \beta cS\frac{I}{(S+E+I+T)^2}$$

$$\frac{\partial F_2}{\partial S} = \frac{\beta cI}{(S+E+I+T)^2} - \frac{\beta cSI}{(S+E+I+T)^2} + \frac{\rho\beta cEI}{(S+E+I+T)^2} - \frac{\sigma\beta cTI}{(S+E+I+T)^2}$$

$$\frac{\partial F_2}{\partial E} = \frac{-\beta cSI}{(S+E+I+T)} - \frac{\rho\beta cI}{(S+E+I+T)} + \frac{\rho\beta CEI}{(S+E+I+T)^2} - (\mu+k) - \frac{\sigma\beta cTI}{(S+E+I+T)^2}$$

$$\frac{\partial F_2}{\partial I} = \frac{\beta cS}{(S+E+I+T)} - \frac{\beta cSI}{(S+E+I+T)^2} - \frac{\rho\beta cE}{(S+E+I+T)} + \frac{\rho\beta cEI}{(S+E+I+T)^2} + \frac{\sigma\beta cT}{(S+E+I+T)} - \frac{\sigma\beta cTI}{(S+E+I+T)^2}$$

$$\frac{\partial F_2}{\partial T} = \frac{-\beta cSI}{(S+E+I+T)^2} + \frac{\rho\beta cEI}{(S+E+I+T)^2} + \frac{\sigma\beta cI}{(S+E+I+T)} - \frac{\sigma\beta cTI}{(S+E+I+T)^2}$$

$$\frac{\partial F_3}{\partial S} = \frac{-\rho\beta cEI}{(S+E+I+T)^2}$$

$$\frac{\partial F_3}{\partial E} = \frac{\rho\beta cI}{(S+E+I+T)} - \frac{\rho\beta cEI}{(S+E+I+T)^2} + k$$

$$\frac{\partial F_3}{\partial I} = \frac{\rho\beta cI}{(S+E+I+T)} - \frac{\rho\beta cEI}{(S+E+I+T)^2} - (\mu+r+d)$$

$$\frac{\partial F_3}{\partial T} = \frac{-\rho\beta cEI}{(S+E+I+T)^2}$$

$$\frac{\partial F_4}{\partial S} = \frac{-\sigma\beta cTI}{(S+E+I+T)^2}$$

$$\frac{\partial F_4}{\partial E} = \frac{-\sigma\beta cTI}{(S+E+I+T)^2}$$

$$\frac{\partial F_4}{\partial I} = r - \frac{\sigma\beta cT}{(S+E+I+T)} + \frac{\sigma\beta cTI}{(S+E+I+T)^2}$$

$$\frac{\partial F_4}{\partial T} = -\frac{\sigma\beta cI}{(S+E+I+T)} + \frac{\sigma\beta cTI}{(S+E+I+)^2} - \mu$$

Evaluating the Jacobian matrix at Z_O

$$J_{Z_O} = \begin{bmatrix} 0 & b & b-\beta c & b \\ 0 & -(\mu+k) & \beta c & 0 \\ 0 & k & -(\mu+r+d) & 0 \\ 0 & 0 & r & -\mu \end{bmatrix}$$

The characteristics equation is given by

$$\left|J_{Z_O} - \lambda I\right| = \begin{vmatrix} -\lambda & b & b-\beta c & b \\ 0 & -(\mu+k)-\lambda & \beta c & 0 \\ 0 & k & -x-\lambda & 0 \\ 0 & 0 & r & -\mu-\lambda \end{vmatrix}$$

where $x = (\mu + r + d)$

$$(-\lambda)(-\mu-\lambda)\begin{vmatrix} -(\mu+k)-\lambda & \beta c \\ k & -x-\lambda \end{vmatrix} = 0$$

$$\lambda_1 = 0$$

$$\lambda_2 = \frac{-(\mu+k+x)+\sqrt{(\mu+k+x)^2 - 4(\mu+k)x[1-R_O]}}{2}$$

$$\lambda_3 = \frac{-(\mu+k+x)-\sqrt{(\mu+k+x)^2 - 4(\mu+k)x[1-R_O]}}{2}$$

$$\lambda_4 = -\mu$$

where $R_o = \frac{k\beta c}{(\mu+k)x}$

If $1 - R_o > 0,$

then $R_o < 1$ and

$$\lambda_2 < \frac{-(\mu+k+x)}{2} + \frac{\sqrt{(\mu+k+x)^2}}{2} = 0$$

$$\lambda_3 < \frac{-(\mu+k+x)}{2} - \frac{\sqrt{(\mu+k+x)^2}}{2} = -(\mu+k+x)$$

Therefore, $\lambda_2 < 0$ and $\lambda_3 < 0$, thus establishing $\lambda_1 = 0,\ \lambda_2 < 0,\ \lambda_3 < 0,\ \lambda_4 < 0$

That is the disease-free equilibrium state of the modified model is marginally stable [6].

IV. Numerical Experiments

We performed numerical experiments on both models using the ode45 solver with data obtained from literatures including Feng et. al.,(2000). The epidemical parameters used are: ∧=417, b=0.1668, N=25000, μ=0.0167, k=0.005, β=80, r=2, σ=0.9, ρ =0.4, d=0.1, N=25000, S(0)=13250, E(0)=10500, I(0)=1000 and T(0)=250. The results show that there were decline in the exposed and infected populations in both models as the recruitment rates increase but the decline in the modified model was more than that of the existing model in all cases. This implies that eradication will be faster with models with varying recruitment rates than with models constant recruitment rates.

V. Conclusion

In this paper, we modified the model by Feng et. al.,2000 by replacing the constant recruitment rate in their model with a varying recruitment rate in our modified model. We studied both models and established their disease-free equilibrium states, stability, basic reproduction number and performed numerical experiments. We discovered that they have different DFE states. While that of the existing model was $\left(\frac{\Lambda}{\mu},0,0,0\right)$, the DFE of the modified model was $(S^*,0,0,0)$ where S^* is arbitrary. The stability analysis show that the eigenvalues of the existing model have negative real parts while that of modified model has one zero. The basic reproduction number of both models are the same. In the numerical experiments, we used ode45, a mathlab functions which uses the Runge-Kutta scheme to solve non-stiff ordinary differential equations. The numerical results show that eradication can be achieved faster with the model with a varying recruitment rate than the one with a constant recruitment rate.

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