# Effects of Vaccination against the Tuberculosis Dynamics from Mother to Child: A Deterministic Mathematical Modeling Approach

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***Abstract*- In this paper, we introduce a deterministic mathematical model which describes the effects of vaccination against the TB disease. We determine the equilibriums points and discuss their stability. The model is refined with the incorporation of mild and severs infection. We examine the parameters reproduction number ($R_0$) responsible for the eradication of disease. Further, we have shown that if the value of reproduction number ($R_0$) is less than 1, the disease is die out and if the value of reproduction number ($R_0$) is greater than 1, the disease will spread.**

***Index Terms*—Modeling, Reproduction number, stability analysis.**

## I. INTRODUCTION

Tuberculosis (TB) is a potentially fatal contagious disease that can affect almost any part of the body but is mainly an infection of the lungs. It is caused by a bacterial microorganism, the tubercle bacillus or Mycobacterium tuberculosis. Although TB can be treated, cured, and can be prevented if persons at risk take certain drugs, scientists have never come close to wiping it out. Few diseases have caused so much distressing illness for centuries and claimed so many lives. It can also affect the central nervous system and kidney etc. One third of the world population is currently affected with tuberculosis bacillus and new infections are occurring at very fast rate. A person can have active and latent (inactive) tuberculosis. Both of this tuberculosis is treatable and curable. In the case of active TB bacteria are active in the body and they weaken the immune system and only people with such type of TB can spread the disease and in the case of latent TB ,people with latent TB does not feel sick and do not have any symptoms.

Castillo-Chavez and Feng [2] focuses on the study of an age-structure model for the disease transmission dynamics of tuberculosis in populations that are subjected to a vaccination program. McCluskey [3] presented a general compartmental model for the spread of an infectious disease. TB progression from latent infection to active disease varies greatly. For instance, people with AID are more likely to develop to active tuberculosis after infection. A patient with AIDS who become infected with Mycrobacterium TB has a 50% chance of developing within 2 months and 5 to 10% chance of developing active disease each year thereafter. Pretorius et al. [4] presented a case study of dynamics of tuberculosis among the small population in South African community having high HIV prevalence. Bhunu and Mushayabasa (2013) formulated and analyzed a deterministic model of co-dynamics of hepatitis C virus and HIV/AIDS in order to assess their impact on the dynamics of each disease in the presence of treatment.

According to World Health Organization (WHO), infants and young children infected with Mycobacterium TB are more likely to develop active TB than older people since their immune system are not yet well developed. Bacillus Calmette Guerin (BCG) is a vaccine used against tuberculosis and is prepared from a strain of weakened live bovine tuberculosis bacillus. BCG vaccine is 80% effective in preventing tuberculosis for duration of 15 years. Whang et al. [7] developed a dynamic SEIR model for tuberculosis (TB) transmission with the time-dependent parameters in South Korea.

Tewa et al. [5] studied two-patched epidemiological model of migrations from one patch to another just by susceptible individuals. Wang et al. [6] formulated a mathematical model of the effects of environmental contamination and presence of volunteers on hospital infections. Bowong and Alaoui [1] provided optimal intervention strategies for tuberculosis in a population**.**

As we know in the case of breast feeding the air space between mother and baby is very small so that it can easily transmit tuberculosis from mother to child, here we study the effect of BCG vaccine in preventing mother to child transmission of TB by using mathematical modeling technique .The model description with transition diagram and equations are presented in section 2. The analysis of the model is carried out in section 3 and stability analysis of disease free equilibrium has been given in section 4. Finally discussion is given in the last section 5.

## II. MODEL FORMULATION

In this paper, the population is divided into five classes. Mycrobacterium immunized class, susceptible, mild infected

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( $M_1$), severe infected ($S_1$) and recovered class. A proportion '$\theta$' of new births were given BCG vaccine at birth to protect them against infection. $(1-\theta)\rho$ be the proportion of new incoming individuals which are not immunized against infection. The first compartment reduces due to the expiration of vaccine efficacy at rate α and also by natural death at rate μ. The susceptible population also reduces at natural death rate μ, and infection with an incident rate of infection β. The same thing happens in the third compartment i.e Mild class. Mild are increases at the rate β resulting from the contact of members of susceptible class with mild class. This class, mild ($M_1$) also reduces by natural death rate μ. In the same way the population dynamics of severe ($S_1$) also increases by incoming of mild population at the rate ω, and reduces by the natural death rate μ. Lastly the recovered class (R) increases by successful care of severe patients (TB) at the rate γ, and decreases by natural death rate μ. δ is the disease induced death rate.

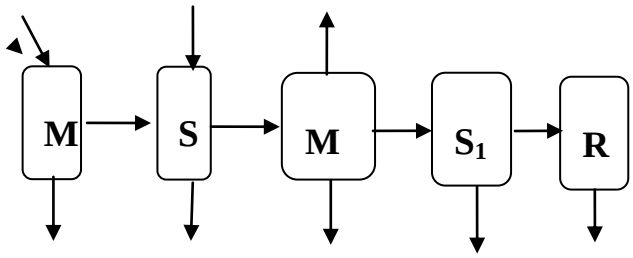


**Fig. 1. Transition diagram exhibits the transmission dynamics of TB.**

**Notations:**

**Following are the notations which are used in the formulation of mathematical model:**

$\theta$ : Portion of individuals which are immunized against infection

$(1-\theta)\rho$ : Portion of individuals which are not immunized against infection.

$\alpha$ : Rate of reduction of mycobacterium vaccine

$\mu$ : Natural death rate which is assumed to be constant.

$\beta$ : Rate of infection from susceptible to mild compartment.

$\delta$ : Death rate induced by disease.

$\gamma$ : Rare at which population is recovered (Recovery rate).

$\omega$ : Infection rate from mild class to severe class.

### A. Model Equations

The relevant model equations are given as following:

$$\frac{dM}{dt} = \theta\rho - (\alpha+\mu)M \qquad (1)$$

$$\frac{dS}{dt} = (1-\theta)\rho + \alpha M - \beta S M_1 - \mu S \qquad (2)$$

$$\frac{dM_1}{dt} = \beta S M_1 - (\delta+\mu+\omega)M_1 - \omega S_1 M_1 \qquad (3)$$

$$\frac{dS_1}{dt} = \omega S_1 M_1 - (\mu+\gamma)S_1 \qquad (4)$$

$$\frac{dR}{dt} = \gamma S_1 - \mu R \qquad (5)$$

## III. THE ANALYSIS

### B. Equilibrium states of the Model:

Let us make the substitution

$$S(t)=v,\ M(t)=u,\ M_1(t)=x,\ S_1(t)=y,\ R(t)=z.$$

Then the system of modified equations becomes:

$$\theta\rho - (\alpha+\mu)u = 0 \qquad (6)$$

$$(1-\theta)\rho + \alpha u - \beta v x - \mu v = 0 \qquad (7)$$

$$\beta v x - (\delta+\mu+\omega)x - \omega x y = 0 \qquad (8)$$

$$\omega x y - (\mu+\gamma)y = 0 \qquad (9)$$

$$\gamma y - \mu z = 0 \qquad (10)$$

On solving the equations (6)-(10), we obtain the followings states:

(I) Disease Free Equilibrium (DEF) state is obtained as

$$(u,v,x,y,z) = \left(\frac{\theta\rho}{\alpha+\mu}, \frac{\theta\rho+\mu\rho(1-\theta)}{\mu(\alpha+\mu)}, 0, 0, 0\right)$$

(II) Endemic Equilibrium (DE) state is

$$(u,v,x,y,z) = \left(\frac{\theta\rho}{\alpha+\mu}, \frac{(\delta+\mu+\omega)+\omega y^*}{\beta}, \frac{\mu+\gamma}{\beta}, \frac{\beta\rho}{\omega}\left(\frac{\alpha\theta+(\alpha+\mu)(1-\theta)}{(\alpha+\mu)(\mu\omega+\beta(\mu+\gamma))}\right) - \frac{(\delta+\mu+\omega)}{\omega}, \frac{\gamma}{\mu}\left[\frac{\beta\rho(\alpha\theta z^*+(\alpha+\mu)(1-\theta))}{(\alpha+\mu)(\mu\omega+\beta(\mu+\omega))} - \frac{(\delta+\mu+\omega)}{\omega}\right]\right)$$

## IV. STABILITY ANALYSIS OF DISEASE FREE EQUILIBRIUM

We investigate the stability of disease free equilibrium states and endemic equilibrium point. As far as the stability of disease free equilibrium is concerned, it is stable point. Let's us examine the behavior of our model near the endemic equilibrium state. We obtain the Transition matrix as follows:

$$J-\lambda I=\begin{bmatrix} -(\alpha+\mu+\lambda) & 0 & 0 & 0 & 0 \\ 0 & -(\mu+\lambda) & 0 & 0 & 0 \\ 0 & 0 & -(\mu+\lambda) & 0 & 0 \\ 0 & 0 & 0 & -(\mu+\gamma+\lambda) & 0 \\ 0 & 0 & 0 & 0 & -(\mu+\delta+\lambda) \end{bmatrix}$$

We obtain the eigen values

$\lambda_1 = -(\alpha + \mu)$,

$\lambda_2 = -\mu$,

$\lambda_3 = -\mu$.

$\lambda_4 = -(\mu + \gamma)$

$$\lambda_5 = \left( \frac{\beta(\alpha\rho + \mu(1-\theta)\rho)}{\mu(\alpha+\mu)} - (\delta + \mu + \omega) \right)$$

Hence all $\lambda_1, \lambda_2, \lambda_3, \lambda_4$ are negative except $\lambda_5$ . Hence the endemic equilibrium state will be stable if following condition holds good

$$\left( \frac{\beta(\alpha\rho + \mu(1-\theta)\rho)}{\mu(\alpha+\mu)} < (\delta + \mu + \omega) \right)$$

## V. DISCUSSION

In this paper a mathematical model of the transmission dynamics of tuberculosis has been formulated. Wherein, we investigate the stability analysis of endemic equilibrium state. Here we have five eigen roots out of which four are negative. For the endemic equilibrium state to be stable the fifth eigen value must also be negative and this is obtained if

$$\lambda_5 = \left( \frac{\beta(\alpha\rho + \mu(1-\theta)\rho)}{\mu(\alpha+\mu)} - (\delta + \mu + \omega) \right)$$

i.e the total removal rate from the infectious class should be greater than the number of latent infections produced throughout the infectious period. Furthermore, these results assumed that the timescale of the disease is short so that the natural birth rate and death rate could be ignored. If the timescale of the diseases is large then the result is doomsday scenario and that will affect the whole population and the vaccination will be failed.

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