Mathematical Model for the Dynamics of Tuberculosis Disease with Vaccination.

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ABSTRACT

This paper considers the mathematical model for dynamics of TB disease with vaccination, taking into consideration the passively immune infants (M) and the vaccination of the susceptible. We considered a Susceptible-Exposed-Infectious-Recovered (SEIR) model by introduced the passively immune infants resulting to an MSEIR model.

The dynamics of the compartments were described by system of ordinary differential equations which were solved algebraically, and analyzed for stability. It was established that the disease free equilibrium state of the model is stable, when the basic reproduction number $R_0 < 1$, it was also established that the endemic states for the modified model is stable using Bellman and Cooke theorem and that if efforts are made to ensure that more susceptible infants are vaccinated, the breakdown of the susceptible and progression to infectious state is reduced and hence we recommend more vaccination of the susceptible and the treatment of the infected.

(Keywords: Tuberculosis, mathematical model, vaccination, endemic equilibrium, disease free-equilibrium, basic reproduction number)

INTRODUCTION

Mathematical models are derivation of the mathematical relations which describes the features of a system under consideration. It deals with converting real world problems to meaningful mathematical equations in order to find a solution to the problem.

Mathematical modelling for disease transmission in host population is of great practical value in predicting and controlling disease spread. Modelling of infectious diseases has remained a veritable tool used to study the mechanism by which diseases spread, predict the future course of an outbreak and to evaluate strategies to control an epidemic [4]. The earliest account of mathematical modelling on the spread of disease was carried out in 1766 by Daniel Bernoulli who was a trained Physician. He created a mathematical model to defend the practice of inoculating against smallpox [5].

Epidemiology is the study of health and disease in human population. It is the study of the distribution and determinants of health related events in a specified populations and the application of the study to control health problems [1]. Infectious diseases have been a ferocious enemy of man since time immemorial and tuberculosis is one of such dreaded infection.

Tuberculosis or TB (short of *Tubercles bacillus*) is an air borne and highly infectious disease caused by infection with the bacteria Mycobacterium tuberculosis [3]. Tuberculosis is mostly transmitted from an infectious person (active tuberculosis) to susceptible persons by infected droplets created when the person with active TB coughs, spit, laughs or sneezes.

The ravaging and deadly effect of TB and the daunting efforts required to eradicate it, is such that requires urgent global actions; according to [6], one-third of the world's population is infected either latently or actively with tuberculosis and its remains one of the world's deadliest communicable disease. In 2013, an estimated 9 million people developed tuberculosis and 1.5 million died from the disease. More than 90% of new TB cases and deaths occur in developing countries and Nigeria ranks 11thamong the 22 high burden TB countries.

Tuberculosis and Human Immuno-deficiency Virus (HIV) exhibit unique symbiosis despite biological differences, their relationship is synergistic as the presence of one, exacerbates

the other. HIV infected individuals are highly susceptible to acquiring tuberculosis infection [7].

Vaccination is the administration of weakened antigens to produce immunity to a disease. Prevention of tuberculosis relies on screening programs and vaccination usually with Bacillus Calmette-Guerin (BCG) vaccine [2]. While the vaccine protects against severe form of TB in children (TB meningitis and Miliary TB), for the meantime, a vaccine that is effective in preventing TB in adults remains elusive; poor administration of this vaccine and environmental conditions can make the vaccines inefficient.

Tuberculosis diagnosis relies on radiology (commonly chest X-ray), a tuberculin skin test, blood tests as well as microscopic examination and microbiological culture of body fluid such as sputum. Tuberculosis usually attacks the lungs but can also affect the spine, bones, central nervous system and even the skin.

Treatment for Tuberculosis uses antibiotics and requires much longer period of treatment (around 6 to 24 months) to entirely eliminate Mycobacterium from the body. The Directly Observed Treatment Shorts (DOTS) strategy as recommended by W.H.O makes sure diagnosis and medicine are available for all TB patients free of charge and has helped in the control and management of tuberculosis.

METHODOLOGY

In this section we will develop a deterministic model in which the individuals in the population are assigned to different compartments, each representing a specific stage of the epidemic. The model to be considered is a Susceptible-Exposed-Infected-Recovered (SEIR) model which considers the passively immune infants M which will help us understand the dynamics of tuberculosis transmission.

The Model

Our model still contains the basic SEIR model structure except that there is an introduction of passive immune infants M due to the fact that pregnant women antibodies are transfered across her placenta such that the new born infants has temporal immunity.

The Model Diagram

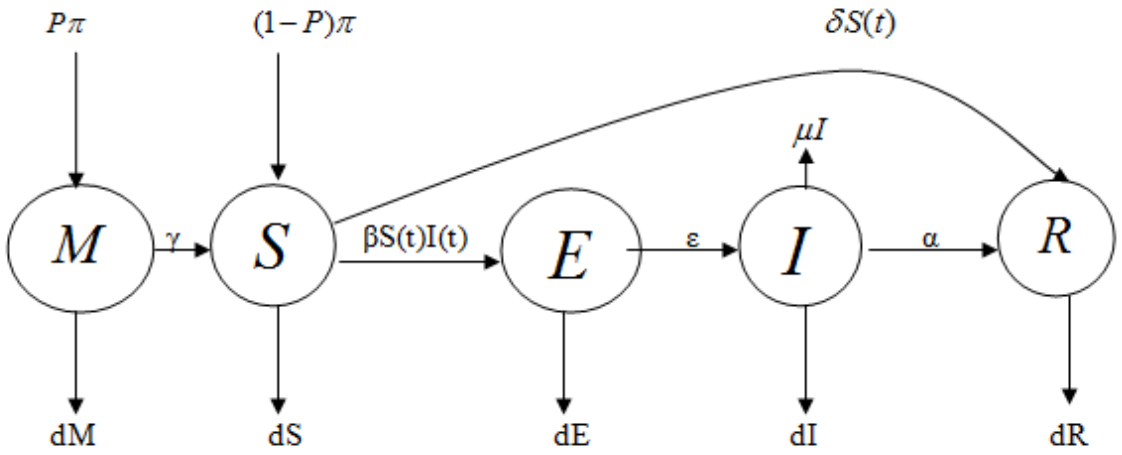

Figure 1: The Modified Model Diagram.

The Model Equations:

$$N(t) = M(t) + S(t) + E(t) + I(t) + R(t)$$

$$\frac{dM(t)}{dt} = p\pi - dM - \gamma M(t) \quad \textbf{(1)}$$

$$\frac{dS(t)}{dt} = \gamma M(t) + (1-p)\pi - dS(t) - \beta S(t)I(t) - \delta S(t) \quad \textbf{(2)}$$

$$\frac{dE(t)}{dt} = \beta S(t)I(t) - \varepsilon E(t) - dE(t) \quad \textbf{(3)}$$

$$\frac{dI(t)}{dt} = \varepsilon E(t) - dI(t) - \mu I(t) - \alpha I(t) \quad \textbf{(4)}$$

$$\frac{dR(t)}{dt} = \alpha I(t) + \delta S(t) - dR(t) \quad \textbf{(5)}$$

The Assumptions of the Model

The assumptions of the Model are given below:

1. It is assumed that the only way of entry into the population is through birth of new born babies and the only way of exit is via death from natural causes or death from TB related causes.

2. It is assumed that a proportion of the new born is immunized against TB infection through vaccination.

3. It is assumed that the immunity conferred on individuals by vaccination wanes after some time at the rate γ.

4. Members of the susceptible class S(t) move into the Exposed class E(t) due to infection at the rate β.

5. The model assumes that certain individuals in the susceptible class that are vaccinated goes to the removed class.

6. Members of the exposed class move to the infectious class due to lack of treatment or immunity breakdown at the rate ε.

7. Members of the infectious class move to the removed class due to treatment/recovery at the rate α.

Definition of Parameters and Variables of the Model

Parameters and Variables	Definitions
$p\pi$	The proportion of new births that is passively immune.
γ	Rate of expiration of vaccine efficacy.
β	Rate of contracting tuberculosis due to interaction between Susceptible S(t) and the infected class I(t).
ε	Progression rate from the exposed class to the infectious class due to lack of treatment or immunity breakdown.
$(1-p)\pi$	Remaining proportion without passive immunity.
α	Recovery rate of the infectious I(t) class due to treatment
μ	Death rate due to tuberculosis infection in the infectious class.
δ	Proportion that becomes immune as a result vaccination of the Susceptible.
dM, dS, dE, dI, dR	Natural death rate for the various population compartments.
M(t)	Passively immune infants.
S(t)	The susceptible class which includes all individual that stands the risk of being infected.
E(t)	The exposed class, which include all those that are infected but not infectious.
I(t)	This is the infectious compartment where those that are Infected are actively infectious.
R(t)	This the recovered compartment which include all individuals that have experienced recovery due to treatment or immune due to vaccination.

Stability Analysis of Equilibrium State

The system exhibits two types of equilibriums; disease – free and endemic equilibrium states.

Stability Analysis of the Disease-Free Equilibrium State

Therefore the disease-free equilibrium state of the model is

$$Eq°(M°, S°, E°, I°, R°) = \left(\frac{p\pi}{d+\gamma}, \frac{\gamma p\pi + (1-p)\pi(d+\gamma)}{(d+\gamma)(d+\delta)}, 0, 0, \frac{\delta\left[\gamma p\pi + (1-p)\pi(d+\gamma)\right]}{d(d+\gamma)(d+\delta)} \right)$$

For us to determine the stability of the Disease-Free Equilibrium State, we examine the behavior of the model population near this equilibrium solution. Here we determine the conditions that must be met for DFE state to be stable, that is, conditions that must be met for the disease to be totally eradicated from the population.

By Jacobian matrix, we obtain the community matrix:

$$J = \begin{pmatrix} -(d+\gamma) & 0 & 0 & 0 & 0 \\ \gamma & -(d+\beta I+\delta) & 0 & -\beta S & 0 \\ 0 & \beta I & -(\varepsilon+d) & \beta S & 0 \\ 0 & 0 & \varepsilon & -(d+\mu+\alpha) & 0 \\ 0 & \delta & 0 & \alpha & -d \end{pmatrix}$$

At the disease-free equilibrium Eq° (M°, S°, E°, I°, R°), the Jacobian matrix becomes:

$$J_0 = \begin{pmatrix} -(d+\gamma) & 0 & 0 & 0 & 0 \\ \gamma & -(d+\delta) & 0 & -\beta\left[\frac{\gamma p\pi + (1-p)\pi(d+\gamma)}{(d+\gamma)(d+\delta)}\right] & 0 \\ 0 & 0 & -(\varepsilon+d) & \beta\left[\frac{\gamma p\pi + (1-p)\pi(d+\gamma)}{(d+\gamma)(d+\delta)}\right] & 0 \\ 0 & 0 & \varepsilon & -(d+\mu+\alpha) & 0 \\ 0 & \delta & 0 & \alpha & -d \end{pmatrix} = 0$$

The characteristic equation $\left|J_0 - I\lambda\right| = 0$ is obtained from the Jacobian determinant. That is;

$$= -(d+\gamma+\lambda)\left\{-(\mathrm{d}+\delta+\lambda)\left[-(\varepsilon+d+\lambda)(d+\mu+\alpha+\lambda)(d+\lambda)+\beta S^0\varepsilon(d+\lambda)\right]\right\} = 0 \qquad \textbf{(6)}$$

Basic Reproduction Number of the Disease-Free Equilibrium State

The basic reproduction number (R_0) is defined as the average number of secondary cases of infection generated by one primary case in a whole susceptible population. The linear stability of Eq° can be established by its basic reproduction number , this is obtained by using Next generation method on Equations 1-5 in the form of matrices F and V.

Let:

F_1 be the rate of appearance of the new infection in a compartment

V_1 be the transfer of individuals out of compartment by another means and

X_O be the disease free equilibrium (Eq^0)

The basic reproduction number is obtained by taking the largest (dominant) Eigen value (spectral radius) of:

$$R_O = \left[\frac{\partial F_i(x_0)}{\partial (x_j)}\right]\left[\frac{\partial V_i(x_o)}{\partial x_j}\right]^{-1}$$

Where;

$$F = \frac{\partial F_i(x_0)}{\partial (x_j)} \text{ and } V = \frac{\partial V_i(x_o)}{\partial x_j}$$

Also

$$V_i(x) = \left[V_i^-(x) - V_i^+(x)\right]$$

Thus;

$$R_O = F * V^{-1} \qquad \textbf{(7)}$$

Hence;

$$\frac{dE}{dt} = \beta SI - (\varepsilon + d)E$$

$$\frac{dI}{dt} = \varepsilon E - (d + \mu + \alpha)I$$

$$F(x) = \begin{bmatrix} \beta SI \\ 0 \end{bmatrix} \text{ the matrix of infectious rate}$$

$$V(x) = \begin{bmatrix} (\varepsilon + d)E \\ -\varepsilon E + (d + \mu + \alpha)I \end{bmatrix} \text{ the matrix of transition rates}$$

Then;

$$FV^{-1} = \begin{bmatrix} \beta\varepsilon\left[\dfrac{\gamma p\pi + (1-p)\pi(d+\gamma)}{(d+\gamma)(d+\delta)(\varepsilon+d)(d+\mu+\alpha)}\right] & \beta\left[\dfrac{\gamma p\pi + (1-p)\pi(d+\gamma)}{(d+\gamma)(d+\delta)(d+\mu+\alpha)}\right] \\ 0 & 0 \end{bmatrix}$$

The spectral radius of FV^{-1} is:

$$P(FV^{-1}) = \frac{\beta\varepsilon\left[\gamma p\pi + (1-p)\pi(d+\gamma)\right]}{(d+\gamma)(d+\delta)(\varepsilon+d)(d+\mu+\alpha)}$$

Hence, the basic reproduction number of the model equation is given by:

$$R_O = \frac{\beta\varepsilon\left[\gamma p\pi + (1-p)\pi(d+\gamma)\right]}{(d+\gamma)(d+\delta)(\varepsilon+d)(d+\mu+\alpha)} \quad \textbf{(8)}$$

For the disease free equilibrium state of the model to be globally asymptotically stable we must have R_O <1, that is,

$$\frac{\beta\varepsilon\left[\gamma p\pi + (1-p)\pi(d+\gamma)\right]}{(d+\gamma)(d+\delta)(\varepsilon+d)(d+\mu+\alpha)} < 1$$

$$\beta\varepsilon\left[\gamma p\pi + (1-p)\pi(d+\gamma)\right] < (d+\gamma)(d+\delta)(\varepsilon+d)(d+\mu+\alpha)$$

$$\Rightarrow \quad \frac{\beta\varepsilon\left[\gamma p\pi + (1-p)\pi(d+\gamma)\right]}{(d+\gamma)(d+\delta)} < (\varepsilon+d)(d+\mu+\alpha) \quad \textbf{(9)}$$

The inequality (9) gives the necessary and sufficient condition for the disease- free equilibrium state of the model to be globally asymptotically stable.

By interpretation, this implies that for the disease equilibrium state to be asymptotically stable, the product of total contraction and total breakdown of the susceptible class given by:

$$\frac{\beta\varepsilon\left[\gamma p\pi + (1-p)\pi(d+\gamma)\right]}{(d+\gamma)(d+\delta)}$$

must be less than the total removal rate from both the Exposed and the infectious compartment given by:

$(\varepsilon+d)(d+\mu+\alpha)$.

Therefore, in order to control tuberculosis, we must ensure that the disease free equilibrium state is stable, that is, we must have the reproduction number R_O<1. We are going to use hypothetical values of each parameter to show that R_0<1.

Hypothetical Values of each Model Parameter used for Numerical Solution

Parameter	Value
$p\pi$	0.25
d	0.10
β	0.12
ε	0.01
μ	0.001
α	0.25
γ	0.01
δ	0.2

R_0<1 when these hypothetical values were substituted into Equation (8) showing that the disease free equilibrium is stable as the value of R_0 obtained is R_0= 0.055067217.

Stability Analysis of Endemic Equilibrium State using Bellman and Cooke Theorem

The result of Bellman and Cooke theorem as applied in Bellman and Cooke (1963) is such that if $H(iy)$, $y \in R$ is separated into its real and imaginary parts $H(iy) = F(y) + iG(y)$, all zeros of $H(z)$ have negative real parts, then the zeros of F(y) and G(y) are real, simple, alternate and

$$F(0)G^{!}(0) - F^{!}(0)G(0) > 0 \quad \textbf{(10)}$$

At the endemic equilibrium state, the characteristic equation is;

$$= -(d+\gamma+\lambda)\begin{Bmatrix} -(d+\delta+\beta I^{*}+\lambda)\left[-(\varepsilon+d+\lambda)(d+\mu+\alpha+\lambda)(d+\lambda)+\beta S^{*}\varepsilon(d+\lambda)\right] \\ +\beta S^{*}(\varepsilon+d+\lambda)\beta I^{*}(d+\lambda) \end{Bmatrix} = 0 \quad \textbf{(11)}$$

From Equation (11) we expand the characteristic equation and resolve into real and imaginary parts. Let λ= (iq)

$$H = (iq) = F(q)+iG(q) \quad \textbf{(12)}$$

$$\begin{aligned} F(q) = &-(5d+\alpha+\gamma+\mu+\delta+\varepsilon-\beta I)q^4+(10d^3+6d^2\alpha+6d^2\gamma+6d^2\mu+6d^2\delta+ \\ &6d^2\varepsilon+3d\alpha\gamma+3d\alpha\delta+3d\alpha\varepsilon+3d\gamma\mu+3d\gamma\delta+3d\mu\delta+3d\gamma\varepsilon+3d\mu\varepsilon+3d\delta\varepsilon+\alpha\gamma\delta \\ &+\alpha\gamma\varepsilon+\alpha\delta\varepsilon+\gamma\mu\delta+\gamma\mu\varepsilon+\gamma\delta\varepsilon+\mu\delta\varepsilon+6d^2\beta I-3dS\beta\varepsilon-S\beta\gamma\varepsilon-S\beta\delta\varepsilon+3d\alpha\beta I \\ &+3d\beta\gamma I+3d\beta\mu I+3d\beta\varepsilon I+\alpha\beta\gamma I+\alpha\beta\varepsilon I+\beta\gamma\mu I+\beta\gamma\varepsilon I+\beta\mu\varepsilon I)q^2-(d^4\alpha+ \\ &d^4\gamma+d^4\mu+d^4\delta+d^4\varepsilon+d^5+d^3\alpha\gamma+d^3\alpha\delta+d^3\alpha\varepsilon+d^3\gamma\mu+d^3\gamma\delta+d^3\mu\delta \\ &+d^3\gamma\varepsilon+d^3\mu\varepsilon+d^3\delta\varepsilon+d^4\beta I+d^2\alpha\gamma\delta+d^2\alpha\gamma\varepsilon+d^2\alpha\delta\varepsilon+d^2\gamma\mu\delta+d^2\gamma\mu\varepsilon \\ &+d^2\gamma\delta\varepsilon+d^2\mu\delta\varepsilon+d^3\alpha\beta I+d^3\beta\gamma I+d^3\beta\mu I+d^3\beta\varepsilon I-d^3S\beta\varepsilon-d^2S\beta\gamma\varepsilon- \\ &d^2S\beta\delta\varepsilon+d^2\alpha\beta\gamma I+d^2\alpha\beta\varepsilon I+d^2\beta\gamma\mu I+d^2\beta\gamma\varepsilon I+d^2\beta\mu\varepsilon I+d\alpha\gamma\delta\varepsilon+d\gamma\mu\delta\varepsilon \\ &-dS\beta\gamma\delta\varepsilon+d\alpha\beta\gamma\varepsilon I+d\beta\gamma\mu\varepsilon I) \end{aligned} \quad \textbf{(13)}$$

$$\begin{aligned} G(q) = &\,q^5+(\alpha\gamma+\alpha\delta+\alpha\varepsilon+\gamma\mu+\gamma\delta+\mu\delta+\gamma\varepsilon+\mu\varepsilon+\delta\varepsilon+4d\alpha+4d\gamma+4d\mu+4d\delta+4d\varepsilon \\ &+10d^2+4d\beta I+\alpha\beta I+\beta\gamma I+\beta\mu I+\beta\varepsilon I-S\beta\varepsilon)q^3-(5d^4+4d^3\alpha+4d^3\gamma \\ &+4d^3\mu+4d^3\delta+4d^3\varepsilon+3d^2\alpha\gamma+3d^2\alpha\delta+3d^2\alpha\varepsilon+3d^2\gamma\mu+3d^2\gamma\delta+3d^2\mu\delta+ \\ &3d^2\gamma\varepsilon+3d^2\mu\varepsilon+3d^2\delta\varepsilon+4d^3\beta I-3d^2S\beta\varepsilon+3d^2\alpha\beta I+3d^2\beta\gamma I+3d^2\beta\mu I \\ &+3d^2\beta\varepsilon I+2d\alpha\gamma\delta+2d\alpha\gamma\varepsilon+2d\alpha\delta\varepsilon+2d\gamma\mu\delta+2d\mu\varepsilon+2d\gamma\delta\varepsilon+2d\mu\delta\varepsilon+\alpha\gamma\delta\varepsilon \\ &+\gamma\mu\delta\varepsilon+\alpha\beta\gamma\varepsilon I+\beta\gamma\mu\varepsilon I-2dS\beta\gamma\varepsilon-2dS\beta\delta\varepsilon-S\beta\gamma\delta\varepsilon+2d\alpha\beta\gamma I+2d\alpha\beta\varepsilon I+2d\beta\gamma\mu I \\ &+2d\beta\gamma\varepsilon I+2d\beta\mu\varepsilon I)q \end{aligned} \quad \textbf{(14)}$$

$$\begin{aligned} F^{1}(q) = &-4(5d+\alpha+\gamma+\mu+\delta+\varepsilon-\beta I)q^3+2(10d^3+6d^2\alpha+6d^2\gamma+6d^2\mu+6d^2\delta+ \\ &6d^2\varepsilon+3d\alpha\gamma+3d\alpha\delta+3d\alpha\varepsilon+3d\gamma\mu+3d\gamma\delta+3d\mu\delta+3d\gamma\varepsilon+3d\mu\varepsilon+3d\delta\varepsilon+\alpha\gamma\delta \\ &+\alpha\gamma\varepsilon+\alpha\delta\varepsilon+\gamma\mu\delta+\gamma\mu\varepsilon+\gamma\delta\varepsilon+\mu\delta\varepsilon+6d^2\beta I-3dS\beta\varepsilon-S\beta\gamma\varepsilon-S\beta\delta\varepsilon+3d\alpha\beta I \\ &+3d\beta\gamma I+3d\beta\mu I+3d\beta\varepsilon I+\alpha\beta\gamma I+\alpha\beta\varepsilon I+\beta\gamma\mu I+\beta\gamma\varepsilon I+\beta\mu\varepsilon I)q \end{aligned} \quad \textbf{(15)}$$

$$G^{1}(q) = 5q^4 + 3(\alpha\gamma + \alpha\delta + \alpha\varepsilon + \gamma\mu + \gamma\delta + \mu\delta + \gamma\varepsilon + \mu\varepsilon + \delta\varepsilon + 4d\alpha + 4d\gamma + 4d\mu + 4d\delta + 4d\varepsilon$$
$$+10d^2 + 4d\beta I + \alpha\beta I + \beta\gamma I + \beta\mu I + \beta\varepsilon I - S\beta\varepsilon)q^2 - (5d^4 + 4d^3\alpha + 4d^3\gamma$$
$$+ 4d^3\mu + 4d^3\delta + 4d^3\varepsilon + 3d^2\alpha\gamma + 3d^2\alpha\delta + 3d^2\alpha\varepsilon + 3d^2\gamma\mu + 3d^2\gamma\delta + 3d^2\mu\delta +$$
$$3d^2\gamma\varepsilon + 3d^2\mu\varepsilon + 3d^2\delta\varepsilon + 4d^3\beta I - 3d^2 S\beta\varepsilon + 3d^2\alpha\beta I + 3d^2\beta\gamma I + 3d^2\beta\mu I$$
$$+ 3d^2\beta\varepsilon I + 2d\alpha\gamma\delta + 2d\alpha\gamma\varepsilon + 2d\alpha\delta\varepsilon + 2d\gamma\mu\delta + 2d\mu\varepsilon + 2d\gamma\delta\varepsilon + 2d\mu\delta\varepsilon + \alpha\gamma\delta\varepsilon$$
$$+\gamma\mu\delta\varepsilon + \alpha\beta\gamma\varepsilon I + \beta\gamma\mu\varepsilon I - 2dS\beta\gamma\varepsilon - 2dS\beta\delta\varepsilon - S\beta\gamma\delta\varepsilon + 2d\alpha\beta\gamma I + 2d\alpha\beta\varepsilon I + 2d\beta\gamma\mu I$$
$$+ 2d\beta\gamma\varepsilon I + 2d\beta\mu\varepsilon I) \quad \textbf{(17)}$$

$$F(0) = -(d^4\alpha + d^4\gamma + d^4\mu + d^4\delta + d^4\varepsilon + d^5 + d^3\alpha\gamma + d^3\alpha\delta + d^3\alpha\varepsilon + d^3\gamma\mu + d^3\gamma\delta + d^3\mu\delta$$
$$+ d^3\gamma\varepsilon + d^3\mu\varepsilon + d^3\delta\varepsilon + d^4\beta I + d^2\alpha\gamma\delta + d^2\alpha\gamma\varepsilon + d^2\alpha\delta\varepsilon + d^2\gamma\mu\delta + d^2\gamma\mu\varepsilon + d^2\gamma\delta\varepsilon + d^2\mu\delta\varepsilon$$
$$+d^3\alpha\beta I + d^3\beta\gamma I + d^3\beta\mu I + d^3\beta\varepsilon I - d^3 S\beta\varepsilon - d^2 S\beta\gamma\varepsilon - d^2 S\beta\delta\varepsilon + d^2\alpha\beta\gamma I +$$
$$d^2\alpha\beta\varepsilon I + d^2\beta\gamma\mu I + d^2\beta\gamma\varepsilon I + d^2\beta\mu\varepsilon I + d\alpha\gamma\delta\varepsilon + d\gamma\mu\delta\varepsilon - dS\beta\gamma\delta\varepsilon + d\alpha\beta\gamma\varepsilon I$$
$$+d\beta\gamma\mu\varepsilon I) \quad \textbf{(18)}$$

$$G(0) = 0 \quad \textbf{(19)}$$

$$F^{1}(0) = 0 \quad \textbf{(20)}$$

$$G^{1}(0) = -(5d^4 + 4d^3\alpha + 4d^3\gamma + 4d^3\mu + 4d^3\delta + 4d^3\varepsilon + 3d^2\alpha\gamma + 3d^2\alpha\delta + 3d^2\alpha\varepsilon + 3d^2\gamma\mu$$
$$+ 3d^2\gamma\delta + 3d^2\mu\delta + 3d^2\gamma\varepsilon + 3d^2\mu\varepsilon + 3d^2\delta\varepsilon + 4d^3\beta I - 3d^2 S\beta\varepsilon + 3d^2\alpha\beta I + 3d^2\beta\gamma I$$
$$+ 3d^2\beta\mu I + 3d^2\beta\varepsilon I + 2d\alpha\gamma\delta + 2d\alpha\gamma\varepsilon + 2d\alpha\delta\varepsilon + 2d\gamma\mu\delta + 2d\mu\varepsilon + 2d\gamma\delta\varepsilon + 2d\mu\delta\varepsilon$$
$$+\alpha\gamma\delta\varepsilon + \gamma\mu\delta\varepsilon + \alpha\beta\gamma\varepsilon I + \beta\gamma\mu\varepsilon I - 2dS\beta\gamma\varepsilon - 2dS\beta\delta\varepsilon - S\beta\gamma\delta\varepsilon + 2d\alpha\beta\gamma I + 2d\alpha\beta\varepsilon I$$
$$+ 2d\beta\gamma\mu + 2d\beta\gamma\varepsilon I + 2d\beta\mu\varepsilon I) \quad \textbf{(21)}$$

Hence, Let $J = F(0)G^{1}(0)$

When J >0 the disease is endemic, we will use Hypothetical values for the various parameters in our equation to establish that the disease endemic equilibrium is stable. According to the World Health Organization vaccination rate is determined when we have:

Vaccination = Success rate * Coverage

Where Coverage is at 80%, we examine Success rate at 25%, and 50%

γ	β	ε	α	μ	π	δ	d	P	J=F(0)G!(0)	Remark
0.2	0.1	0.1	0.1	0.1	0.8	0.2	0.1	0.5	(0.0003302)(0.000115)=0.000000037	Stable
0.2	0.2	0.2	0.1	0.1	0.8	0.2	0.1	0.5	(0.0005396)(0.00982)=0.000004964	Stable
0.2	0.3	0.3	0.1	0.1	0.8	0.2	0.1	0.5	(0.0007363)(0.02541)=0.000018709	Stable
0.2	0.4	0.4	0.1	0.1	0.8	0.2	0.1	0.5	(0.0018604)(0.0481)=0.000089485	Stable

Table 1: Showing the Table of Numerical Simulation at 25% Vaccination of the Susceptible.

γ	β	ε	α	μ	π	δ	d	P	J= F(0)G!(0)	Remark
0.2	0.1	0.1	0.1	0.1	0.8	0.4	0.1	0.5	(0.000768)(0.004115)=0.00000316	Stable
0.2	0.2	0.2	0.1	0.1	0.8	0.4	0.1	0.5	(0.0008816)(0.0058)=0.000005113	Stable
0.2	0.3	0.3	0.1	0.1	0.8	0.4	0.1	0.5	(0.00001449)(0.016569)=0.00000024	Stable
0.2	0.4	0.4	0.1	0.1	0.8	0.4	0.1	0.5	(0.001004)(0.036868)=0.000037015	Stable

Table 2: Showing the Table of Numerical Simulation at 50% Vaccination of the Susceptible.

From the table we varied the values of β, ε and δ to show what happens when the contact rate due to interaction between the susceptible and actively infected person, the progression from exposed to the infectious compartment and the proportion vaccinated at the susceptible that moves to the removed compartment, it will be observed that irrespective of the increase vaccination of the susceptible, with increase progression to the exposed and the infectious class, the disease will remain endemic. This could be addressed by more vaccination of the susceptible and the reduction of the exposed and the infectious via treatment.

CONCLUSION

This work considered the mathematical model of the dynamics of tuberculosis disease with vaccination, involving passively immune infants and the vaccination of the susceptible class. We showed that there exist disease free equilibrium and the endemic equilibrium state using elimination and substitution method.

The analysis of the disease free equilibrium state was conducted using Reproduction number, the result showed that for the disease free equilibrium state to be asymptotically stable, the product of total contraction and total breakdown of the susceptible class should be less than the total removal rate from both the exposed and the infectious classes, when $R_0 < 1$

While the analysis of the endemic equilibrium state was conducted using Bellman and Cooke theorem and the result showed that for the disease endemic equilibrium state to be stable the value of $J > 0$.

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