Deterministic Model for Eradicating Tuberculosis in the Present of Vaccination and Treatment Strategy without Migration Effect

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Abstract: **- In this study, we proposed a mathematical model for the vaccination and treatment strategy to eradicate tuberculosis with absent of migration effect, where we modified the existing model by excluding the migrants effect, incorporate efficacy of vaccination, treatment and new babies were considered 100% vaccinated. Existence and uniqueness of solution of the modified model was carried out and it shows that the solution exists and it is unique. The stability analysis of the disease free equilibrium shows that the disease-free equilibrium (DFE) is locally asymptotically stable. The effective reproductive number R_e was computed under different conditions. In the case where there is treatment and vaccination we found Re to be 0.22235. The results show that mycobacterium tuberculosis can be eradicated if mass vaccination and treatment actions are properly initiated and enforced. Therefore, migrant that are infected should be strongly be discourage from leaving his/her resident country before treatment to ensure fast eradication of mycobacterium tuberculosis.**

Keywords**: tuberculosis, vaccination, treatment, migration**

I. INTRODUCTION

In deterministic models, individuals in the population are assigned to different subgroups or classes, each representing a specific stage of the epidemic. Letters such as M, S, E, I and R are often used to represent different stages [1].

The transition rates from one class to another are mathematically expressed as derivatives, hence the model is formulated using differential equations. While building TB models, it must be assumed that the population size in a compartment is differentiable with respect to time and the epidemic process is deterministic [2].

Tuberculosis is an airborne infection caused by Mycobacterium Tuberculosis (MTB). [3] opined that MTB or TB (short for tubercle bacillus) is a common, and in many cases lethal infectious disease caused by various strains of mycobacteria, usually mycobacterium tuberculosis. TB typically attacks the lungs, but can also affect other parts of the body. It is spread through the air when people who have active TB infection cough, sneeze, laugh or sing or otherwise propel their saliva into the air [4]. Most infections are asymptomatic and latent, but about one in ten infections eventually progress to active disease which, if left untreated, kills more than 50% of those infected [5].

Tuberculosis is treated by killing the bacterial using antibiotics. The treatment usually last at least six months in duration and sometimes longer, up to twenty-four months. It involves different antibiotics to increase effectiveness while preventing the bacteria from becoming resistant to the medicine [6].

Not everyone infected with TB becomes sick. As a result, two TB-related conditions exist: latent TB infection and active TB disease. Both latent TB infection and active TB disease can be treated [7].

Treatment completion is determined by the number of doses ingested over a given period of time. Although basic TB regimens are broadly applicable, there are modifications that should be made under special circumstances (such as people with HIV infection, drug resistance, pregnant women or treatment of children) [1].Pre-exposure vaccines, also known as pre-infection vaccines, are given before infection with the pathogen, usually at birth as neonatal vaccines. Pre-exposure vaccines speed up the development of immune response, therefore preventing further infections from becoming symptomatic [8]. [6], presented an SEIR model which incorporated treatment of infectious individuals and chemoprophylaxis (treatment for the latently infected). The model assumed that the latently infected individuals develop active disease as a result of endogenous re-activation, exogenous re-infection and disease relapse. The study showed that chemoprophylaxis will do better in controlling the number of infectious due to reduced progression to active TB.

[9], studied the role of vaccination of newborn babies against TB infection and treatment of both latently and actively

infected individuals in controlling the spread of TB using mathematical model based on the standard SEIR model. The disease-free equilibrium state of the model was established and its stability analysis using the Routh-Hurwitz theorem. The result of the analysis showed that tuberculosis can be totally eradicated if effort is made to ensure that the total contraction and the total breakdown of the latent class should be less than the total removal rate from both the latent and the infectious class. From these studies, we can conclude that vaccination, treatment and immigration all have effects on the spread of TB. While we can see vaccination and treatment curbing the spread of the disease, the overall effect is neutralized, if not aggravated, by immigration of infective in such a way that disease persists in the host population. Further studies are required to determine which factor plays the bigger role in the spreading/controlling of TB in order to maintain the balance and keep the disease under control.

II. METHOD

Mathematical models have played a key role in the formulation of TB control strategies and the establishment of interim goals for intervention programs. Many types of epidemic models exist. They include: the stochastic models, the deterministic (compartmental) models such as the SIR, SIS, SIRS, SEIS, SEIR, MSEIR, models, (Where S=Susceptible class; I=Infective class; M=passively immune class; E=Exposed class; and R=Recovered class) .

Our model is a deterministic MSEIR type model where the population is partitioned into components or classes based on the epidemiological state of the individuals, and it is assumed that the epidemic process is deterministic.

2.1 The Modified Model

We modified the work of [9] by incorporating incorporate efficacy of vaccination, treatment and assuming 100% vaccination for the new-births. The modified model based on the following assumptions: That the individuals that make up the population can be grouped into different compartments according to their epidemiological state, the population size in a compartment changes with time, all new-births are immunized against TB infection and enter the vaccinated class, M, and there is migration in the population. That is, there are immigrants and emigrants. In addition, it is assumed that there is no vertical transmission of TB. That is, no transmission from mother to new-born, hence all new-births are previously uninfected. The immunity conferred on individuals by vaccination wanes after some time at a given rate, the population mixes homogeneously. That infection does not confer permanent immunity on the individuals and susceptible individual once infected develops latent infection. Those latently infected individuals are treated and are recovered or the infection develops to active TB. Furthermore, every individual can die a natural death. That all immigrants are either vaccinated and are immune or they are unvaccinated and are susceptible. Lastly, the latently infected and infectious individuals are restricted from entering the population.

2.2 Model Variables and Parameters

The following variables and parameters shall be used in this model:

M(t): the number of individuals who are immunized/vaccinated against TB at time t.

S(t): the number of susceptible individuals. That is, the individuals who can catch the disease because they have no immunity to the infectious agent so might become infected if exposed.

L(t): the number of latently infected individuals at time t.

I(t): the number of infectious individuals at time t.

R(t): the number of individuals who have been treated and have recovered from the infection at time t.

β: the rate of new-births in the population

f: the efficacy of the vaccine in preventing initial infection.

Υ: Average immigration rate into the population

K: the rate at which susceptible individuals develop latent infection

q: the rate of expiration of vaccine (rate at which immunity wanes)

ψ: the rate at which active TB is treated.

ε: recovery rate of latent infection due to treatment

α: average emigration rate

e: efficacy of treatment in curing infected persons

m: the rate at which latently infected become actively infected

π: the rate at which recovered individuals become susceptible to TB again

μ: natural mortality rate

μ_τ: TB induced deaths

η: Proportion of immigrants vaccinated and are immune

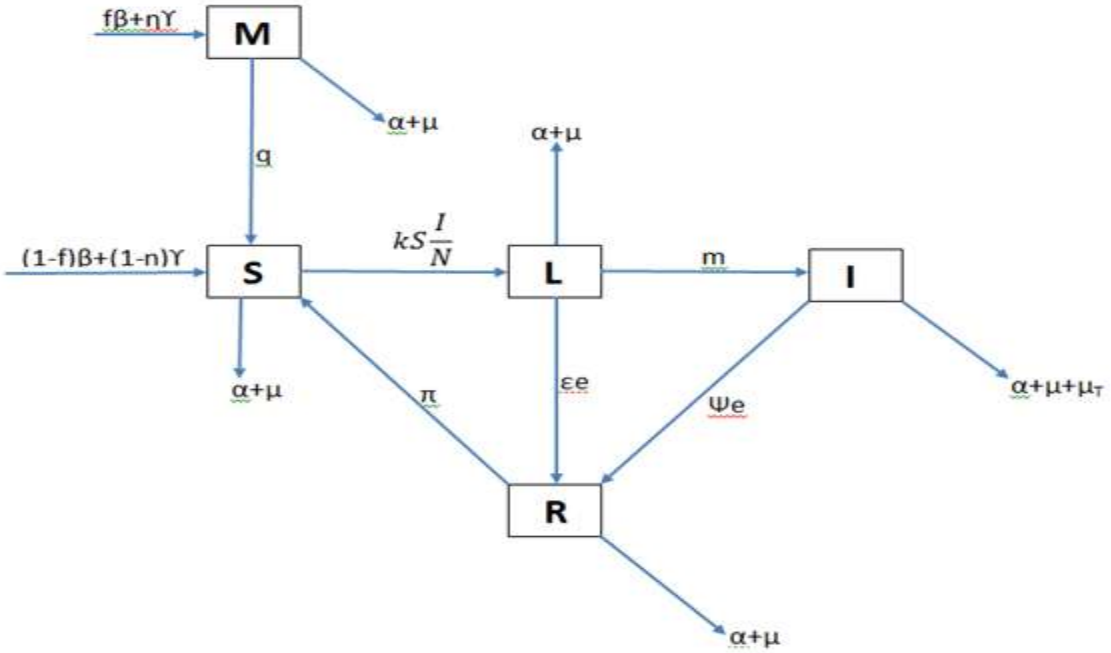

Figure 2: SCHEMATIC PRESENTATION OF THE MODIFIED MODEL

2.3 The Modified Model Equation

This section presents the modified model equations by a system of differential equations thus:

$$\frac{dM}{dt} = f\beta + n\Upsilon - \alpha M - \mu M - qM$$
$$= f\beta + n\Upsilon - (\alpha + \mu + q)M \quad (1)$$

$$\frac{dS}{dt} = (1-f)\beta + (1-n)\Upsilon - \mu S - \alpha S + qM + \pi R - kS\frac{I}{N}$$
$$= (1-f)\beta + (1-n)\Upsilon - (\mu + \alpha)S + qM + \pi R - kS\frac{I}{N} \quad (2)$$

$$\frac{dL}{dt} = kS\frac{I}{N} - \alpha L - \mu L - mL - \varepsilon L$$
$$= kS\frac{I}{N} - (\alpha + \mu + m + \varepsilon)L \quad (3)$$

$$\frac{dI}{dt} = mL - \alpha I - \psi eI - (\mu + \mu_\tau)I$$
$$= mL - (\alpha + \psi e + \mu + \mu_\tau)I \quad (4)$$

$$\frac{dR}{dt} = \psi eI + \varepsilon L - \alpha R - \mu R - \pi R$$
$$= \psi eI + \varepsilon L - (\alpha + \mu + \pi)R \quad (5)$$

$$N(t) = M(t) + S(t) + L(t) + I(t) + R(t) \quad (6)$$

$$M(0) \geq 0, S(0) \geq 0, L(0) \geq 0, I(0) \geq 0, R(0) \geq 0$$

The system of equations (1) to (5) are the deterministic model equations which will be used to determine the existence and uniqueness of solution, the Disease-Free Equilibrium (DFE) for the disease as well as calculate the effective reproductive number R_e which determines whether the disease can be eliminated or not.

2.4 Methods of Solution and Analysis

2.4.1 Existence and Uniqueness of Solution

To prove the existence and uniqueness of solution of the system of equations in section 2.3, we shall use the method described by [10].

Consider the system of equations below

$$\left.\begin{aligned} x_1' &= f_1(t, x_1, x_2, \dots, x_n),\ x_1(t_0) = x_{10} \\ x_2' &= f_2(t, x_1, x_2, \dots, x_n),\ x_2(t_0) = x_{20} \\ &\vdots \\ x_n' &= f_n(t, x_1, x_2, \dots, x_n),\ x_n(t_0) = x_{n0} \end{aligned}\right\} \quad (7)$$

We may write (7) in compact form as

$$x' = f(t, x), x(t_0) = x_0 \quad (8)$$

Theorem1:

Let D denotes the region $|t - t_0| \leq a, ||x - x_0|| \leq b, x = (x_1, x_2 \dots, x_n)$ (9)

Suppose that $f(t, x)$ satisfies the Lipschitz condition

$\|f(t, x_1) - f(t, x_2)\| \leq k\|x_1 - x_2\|$, where the pairs $(t, x_1), (t, x_2) \in D$, k is a positive constant. Then, there is a constant $\delta > 0$ such that there exist a unique continuous vector solution $\underline{x}(t)$ of the system (8) in the interval $|t - t_0| \leq \delta$.

It is important to note that Lipschitz condition is satisfied by the requirement that $\frac{\partial f_i}{\partial x_j}$, $i,j = 1,2,\ldots,n$ are continuous and bounded in D.

2.4.2 Equilibrium and Stability Analysis for the Existing Model

We shall use the formulation of Disease Free Equilibrium (DFE) and stability analysis presented in [10] to find the DFE for the formulated model and carryout stability analysis.

Consider the equation (8).

Definition 3.31: An equilibrium solution or fixed point, or steady-state solution of the system (8) is a constant solution x of the equation [11].

At the equilibrium point, the derivatives in the equations (1) to (5) are equal to zero. That is, $M^{'} = S^{'} = L^{'} = I^{'} = R^{'} = 0$. In the absence of any infections (DFE), $L = I = 0$.

To determine the stability of the model, we shall evaluate the DFE of the system.

Theorem 2: Suppose that x^* is an equilibrium solution of (8), i.e. $f(x^*) = 0$, then

- $x^*$is locally asymptotically stable (LAS) if all the eigenvalues of J_{x^*} have negative real parts.
- If at least one eigen value has positive real part then x^* is unstable. The eigenvalues are the roots of the characteristic equation of the Jacobian matrix, J, where $J = \left[\frac{\partial f_i}{\partial x_j}\right], i,j = 1,2,\ldots,n.$

III. RESULTS

In this chapter, the researcher consider the modified model of section 2.3 in details by carrying out the existence and stability analysis of the disease-free equilibrium (DFE) state and determines the basic reproductive number R_0 for the formulated model.

3.1 Existence and Uniqueness of Solution

We shall prove the existence and uniqueness of solution or otherwise of model equations (1) to (5) using the formulation of [11]. Specifically, we shall use ***Theorem 3.31*** presented in ***Section 3.3***of this work.

Proof:

Let

$f_1 = f\beta + n\Upsilon - (\alpha + \mu + q)M$

$f_2 = (1-f)\beta + (1-n)\Upsilon - (\mu + \alpha)S + qM + \pi R - kS\frac{I}{N}$

$f_3 = kS\frac{I}{N} - (\alpha + \mu + m + \varepsilon e)L$

$f_4 = mL - (\alpha + \psi e + \mu + \mu_\tau)I$

$f_5 = \psi eI + \varepsilon eL - (\alpha + \mu + \pi)R.$

It suffices to show that $\frac{\partial f_i}{\partial x_j}$, $i,j = 1,2,\ldots,n$ are continuous and bounded in the region D defined by equation (9).

Consider the partial derivatives below:

$\left|\frac{\partial f_1}{\partial M}\right| = |-(\alpha + \mu + q)| < \infty$

$\left|\frac{\partial f_1}{\partial S}\right| = \left|\frac{\partial f_1}{\partial L}\right| = \left|\frac{\partial f_1}{\partial I}\right| = \left|\frac{\partial f_1}{\partial R}\right| = 0 < \infty$

$\left|\frac{\partial f_2}{\partial M}\right| = |q| < \infty$

$\left|\frac{\partial f_2}{\partial S}\right| = \left|-(\alpha + \mu) - k\frac{I}{N}\right| < \infty$

$\left|\frac{\partial f_2}{\partial L}\right| = 0 < \infty$

$\left|\frac{\partial f_2}{\partial I}\right| = |\pi| < \infty$

$\left|\frac{\partial f_2}{\partial R}\right| = |-kS| < \infty$

$\left|\frac{\partial f_3}{\partial M}\right| = \left|\frac{\partial f_3}{\partial R}\right| = 0 < \infty$

$\left|\frac{\partial f_3}{\partial S}\right| = \left|k\frac{I}{N}\right| < \infty$

$\left|\frac{\partial f_3}{\partial I}\right| = |kS| < \infty$

$\left|\frac{\partial f_3}{\partial L}\right| = |-(\alpha + \mu + m + \varepsilon e)| < \infty$

$\left|\frac{\partial f_4}{\partial M}\right| = \left|\frac{\partial f_4}{\partial R}\right| = \left|\frac{\partial f_4}{\partial S}\right| = 0 < \infty$

$\left|\frac{\partial f_4}{\partial L}\right| = |m| < \infty$

$\left|\frac{\partial f_4}{\partial I}\right| = |-(\alpha + \psi e + \mu + \mu_T)| < \infty$

$\left|\frac{\partial f_5}{\partial M}\right| = \left|\frac{\partial f_5}{\partial S}\right| = 0 < \infty$

$\left|\frac{\partial f_5}{\partial L}\right| = |\varepsilon e| < \infty$

$\left|\frac{\partial f_5}{\partial I}\right| = |\psi e| < \infty$

$\left|\frac{\partial f_5}{\partial R}\right| = |-(\alpha + \mu + \pi)| < \infty$

Clearly, all these partial derivatives are continuous and bounded. Hence by ***Theorem 3.31*** there exists a unique solution of the model equation (1)-(5) in the region D.

3.2 Existence and Stability of Disease-Free Equilibrium State of the Modified Model

The existence and stability of the DFE state of the modified model is investigated in this section

3.2.1 Equilibrium Solution

Let $E(M,S,L,I,R)$ be the equilibrium point of the system described by the equations (1) to (5). At the equilibrium state we have:

$$\frac{dM}{dt}=\frac{dS}{dt}=\frac{dL}{dt}=\frac{dI}{dt}=\frac{dR}{dt}=0$$

That is,

$$f\beta+n\Upsilon-(\alpha+\mu+q)M=0 \quad (10)$$

$$(1-f)\beta+(1-n)\Upsilon-(\mu+\alpha)S+qM+\pi R-kS\frac{I}{N}=0 \quad (11)$$

$$kS\frac{I}{N}-(\alpha+\mu+m+\varepsilon)L=0 \quad (12)$$

$$mL-(\alpha+\psi e+\mu+\mu_{\tau})I=0 \quad (13)$$

$$\psi eI+\varepsilon L-(\alpha+\mu+\pi)R=0 \quad (14)$$

In order to obtain the disease-free equilibrium state, we solve the system of equations (10) to (14) simultaneously.

3.2.2 Existence of Trivial Equilibrium State

Let $E_0(M_0,S_0,L_0,I_0,R_0)$ be the trivial equilibrium state for the model. That is, when $M=S=L=I=R=0$. so that$E_0(M_0,S_0,L_0,I_0,R_0)=(0,0,0,0,0)$. But no such equilibrium exists for the model since the population cannot go extinct so long as new babies are born into the population and there is migration into the population. In other words, so long as the recruitment terms $f\beta$ and $(1-f)\beta$ are not both zero and also $\eta\Upsilon$ and $(1-\eta)\Upsilon$ cannot be both zero, the population will never go extinct; and so $E_0(M_0,S_0,L_0,I_0,R_0)\neq(0,0,0,0,0)$.

3.2.3 The Diseease-Free Equilibrium State

The disease-free equilibrium state is the state of total eradication of the disease. Let $E^0(M^0,S^0,L^0,I^0,R^0)$ be the DFE state for the model. For disease-free equilibrium state, the disease states of the model must be zero. That is, the infectious class, I and the latently infected class, L must be zero. Mathematically, for the DFE state $L^0=I^0=0$.

Now, substituting $L^0=I^0=0$ into the system of equations (10) to (14) we obtain the following: From (10),

$$f\beta+n\Upsilon-(\alpha+\mu+q)M=0$$

$$\Rightarrow \quad (\alpha+\mu+q)M=f\beta+n\Upsilon$$

$$\Rightarrow \quad M=\frac{f\beta+n\Upsilon}{\alpha+\mu+q},$$

That is,

$$M^0=\frac{f\beta+n\Upsilon}{\alpha+\mu+q} \quad (15)$$

From ((11),

$$(1-f)\beta+(1-n)\Upsilon-(\mu+\alpha)S+qM+\pi R-kS\frac{I}{N}=0$$

For$I=0$, we have:

$$(1-f)\beta+(1-n)\Upsilon-(\mu+\alpha)S+qM+\pi R=0 \quad (*)$$

But $M^0=\frac{f\beta+n\Upsilon}{\alpha+\mu+q}$, substituting into (*) yields:

$$(1-f)\beta+(1-n)\Upsilon-(\mu+\alpha)S+\frac{q(f\beta+n\Upsilon)}{\alpha+\mu+q}+\pi R=0 \quad (16)$$

From (4.13),

$$kSI-(\alpha+\mu+m+\varepsilon e)L=0$$

For $I=L=0$,the equation vanishes.

Similarly, equation (4.14) vanishes on substituting$I=L=0$, since it depends entirely on *I* and *L* only.

From equation (4.15),

$$\psi eI+\varepsilon eL-(\alpha+\mu+\pi)R=0$$

$\Rightarrow \quad 0+0-(\alpha+\mu+\pi)R=0$ (since I=L=0)

$\Rightarrow \quad (\alpha+\mu+\pi)R=0 \quad (**)$

Either $\alpha+\mu+\pi=0$ Or$R=0$

But $\alpha+\mu+\pi$ cannot be zero since α,μ,π are positive constants. i.e. $(\alpha+\mu+\pi)\neq 0$

$\Rightarrow$ For (**) to be true, then necessarily, $R=0$.

Therefore, $R^0=0$ (17)

If $R=0$, equation (4.17) becomes

$$(1-f)\beta+(1-n)\Upsilon-(\mu+\alpha)S+\frac{q(f\beta+n\Upsilon)}{\alpha+\mu+q}+\pi(0)=0$$

$$\Rightarrow \quad S=\frac{\{(1-f)\beta+(1-n)\Upsilon\}(\alpha+\mu+q)+q(f\beta+n\Upsilon)}{(\alpha+\mu)(\alpha+\mu+q)}$$

$$\Rightarrow \quad S^0=\frac{q(\beta+\Upsilon)+(\alpha+\mu)\{(1-f)\beta+(1-\eta)\Upsilon\}}{(\alpha+\mu)(\alpha+\mu+q)} \quad (18a)$$

Therefore, the DFE state for the model is

$$E_0(M_0,S_0,L_0,I_0,R_0)=$$

$$(\frac{f\beta+n\Upsilon}{\alpha+\mu+q},$$

$$\frac{q(\beta+\Upsilon')+(\alpha+\mu)\{(1-f)\beta+(1-\eta)\Upsilon'\}}{(\alpha+\mu)(\alpha+\mu+q)},0,0,0)$$

3.2.4 Stability Analysis of the Disease- Free Equilibrium State

To determine the stability or otherwise of the disease-free equilibrium stateE^0, we examine the behavior of the model equations near this equilibrium solution. Here we examine the condition(s) that must be met for the disease-free equilibrium state to be stable. In other words, we determine the conditions that must be met if the disease is to be totally eradicated from the population.

Recall the system of equations of this model at equilibrium as given in equations (10)-(14)

We now linearize the system of equations, to get the Jacobian matrix, J as;

$$J=\begin{bmatrix} -(\alpha+\mu+q) & 0 & 0 & 0 & 0 \\ q & -(\alpha+\mu)-k\frac{I}{N} & 0 & -kS & \pi \\ 0 & kI & -(\alpha+\mu+m+\varepsilon) & kS & 0 \\ 0 & 0 & m & -(\alpha+\psi e+\mu+\mu_\tau) & 0 \\ 0 & 0 & \varepsilon & \psi e & -(\alpha+\mu+\pi)R \end{bmatrix} \quad (18b)$$

At the disease-free equilibrium

$E^0(M^0,S^0,L^0,I^0,R^0)=(\frac{f\beta+n\Upsilon'}{\alpha+\mu+q},\frac{q(\beta+\Upsilon')+(\alpha+\mu)\{(1-f)\beta+(1-\eta)\Upsilon'\}}{(\alpha+\mu)(\alpha+\mu+q)},0,0,0),$

The Jacobian Matrix (18b) becomes

$$J_{E^0}=\begin{bmatrix} -(\alpha+\mu+q) & 0 & 0 & 0 & 0 \\ q & -(\alpha+\mu) & 0 & \frac{-k\{q(\beta+\Upsilon')+(\alpha+\mu)[(1-f)\beta+(1-\eta)\Upsilon']\}}{(\alpha+\mu)(\alpha+\mu+q)} & \pi \\ 0 & 0 & -(\alpha+\mu+m+\varepsilon) & \frac{k\{q(\beta+\Upsilon')+(\alpha+\mu)[(1-f)\beta+(1-\eta)\Upsilon']\}}{(\alpha+\mu)(\alpha+\mu+q)} & 0 \\ 0 & 0 & m & -(\alpha+\psi e+\mu+\mu_T) & 0 \\ 0 & 0 & \varepsilon & \psi e & 0 \end{bmatrix}$$

Where the quantity $\frac{q(\beta+\Upsilon')+(\alpha+\mu)[(1-f)\beta+(1-\eta)\Upsilon']}{(\alpha+\mu)(\alpha+\mu+q)}=s^o$

The Eigen values are calculated from the characteristics equation $|J_{E^o}-\lambda I|=0$ where I is a5×5 identity matrix. That is,

$$|J_{E^o}-\lambda I|=\begin{vmatrix} -(\alpha+\mu+q)-\lambda & 0 & 0 & 0 & 0 \\ q & -(\alpha+\mu)-\lambda & 0 & -ks^o & \pi \\ 0 & 0 & -(\alpha+\mu+m+\varepsilon)-\lambda & ks^o & 0 \\ 0 & 0 & m & -(\alpha+\psi e+\mu+\mu_\tau)-\lambda & 0 \\ 0 & 0 & \varepsilon & \psi e & -(\alpha+\mu+\pi)-\lambda \end{vmatrix} = 0$$

For simplicity of appearance and computational advantage, we let $c = \alpha + \mu$. Then we obtain the following

$$|J_{E^o} - \lambda I| = (-(c+q)-\lambda)\begin{vmatrix} -c-\lambda & 0 & -ks^o & \pi \\ 0 & -(c+m+\varepsilon)-\lambda & ks^o & 0 \\ 0 & m & -(c+\psi e+\mu_\tau)-\lambda & 0 \\ 0 & \varepsilon & \psi e & -(c+\pi)-\lambda \end{vmatrix} = 0$$

$$= (-(c+q)-\lambda)(-c-\lambda)\begin{vmatrix} -(c+m+\varepsilon)-\lambda & ks^o & 0 \\ m & -(c+\psi e+\mu_\tau)-\lambda & 0 \\ \varepsilon & \psi e & -(c+\pi)-\lambda \end{vmatrix} = 0$$

$$= (-(c+q)-\lambda)(-c-\lambda)(-(c+\ \pi)-\lambda)\begin{vmatrix} -(c+m+\varepsilon)-\lambda & ks^o \\ m & -(c+\psi e+\mu_\tau)-\lambda \end{vmatrix} = 0 \quad (19)$$

From equation (19),

Either$\big(-(c+q)-\lambda\big)(-c-\lambda)(-(c+\ \pi)-\lambda) = 0$ (20)

Or

$$\begin{vmatrix} -(c+m+\varepsilon)-\lambda & ks^o \\ m & -(c+\psi e+\mu_\tau)-\lambda \end{vmatrix} = 0 \quad (21)$$

From equation (21)

$$\left.\begin{aligned} \lambda_1 &= -(c+q) \\ \lambda_2 &= -c \\ \lambda_3 &= -(c+\pi) \end{aligned}\right\} \quad (22)$$

From equation (22), we see that the first three (3) Eigen values $\lambda_1, \lambda_2\ and\ \lambda_3$ are all negative.

Using ***theorem 3.32,*** we see that the DFE of this model will be asymptotically stable iff the remaining Eigen values, $\lambda_4\ and\ \lambda_5$ are also negative.

Now, we consider equation (21). For local asymptotic stability (LAS) of the DFE, we require the remaining two eigenvalues $\lambda_4\ and\ \lambda_5$ to be negative.

Theorem 4.1

Let A be an$n \times n$ matrix. Then:

i. The matrix A has n eigenvalues (including each according to its multiplicity).
ii. The sum of the n eigenvalues of A is the same as the trace of A.
iii. The product of the n eigenvalues of A is equal to the determinant of A.

Using ***heorem 4.1***, we shall prove that $\lambda_4\ and\ \lambda_5$ are both negative or otherwise.

Let A$= \begin{pmatrix} -(c+m+\varepsilon) & ks^o \\ m & -(c+\psi e+\mu_\tau) \end{pmatrix}$

$$Trace(A) = -(c+m+\varepsilon) - (c+\psi e+\mu_\tau) \quad (23)$$

$$Det(A) = (c+m+\varepsilon)(c+\psi e+\mu_\tau) - kms^o \quad (24)$$

If $\lambda_4\ and\ \lambda_5$ are both negative, then we have

$\lambda_4 + \lambda_5 < 0$, it implies that $Trace(A) < 0$

i.e.$-(c+m+\varepsilon) - (c+\psi e+\mu_\tau) < 0$

It is clear that$Trace(A) < 0$ since all the parameters are positive constant.

Also, $\lambda_4.\lambda_5 > 0$, it implies that $Det(A) > 0$

i.e.$(c+m+\varepsilon)(c+\psi e+\mu_\tau) - kms^o > 0$

$$\Rightarrow \quad kms^o < (c+m+\varepsilon)(c+\psi e+\mu_\tau) \quad (**)$$

Dividing both sides of inequality (**) by $(c+m+\varepsilon)(c+\psi e+\mu\tau$ yields:

$$\frac{kms^o}{(c+m+\varepsilon)(c+\psi e+\mu_\tau)} < 1, \quad \text{where } c = \alpha + \mu \quad (25)$$

The inequality (25) determines the threshold under which the disease can be eliminated or brought under control. It is the necessary and sufficient condition for the disease free equilibrium of the model to be stable.

3.3 The Effective Reproduction Number, R_e

We determine the basic reproduction number, R_e for the model equations (10) to (14). This will be calculated using the next generation matrix method as described by [15].

Consider the next generation matrix G, which is made up of two parts: F and V^{-1}, where

$$F = \left[\frac{\partial F_i(E^o)}{\partial x_j}\right]$$

And

$$V = \left[\frac{\partial V_i(E^o)}{\partial x_j}\right]$$

The F_i's are the new infections while the V_i's shows the transfer of infections from one compartment to another. Here E^o is the disease-free equilibrium state. The basic reproduction number is the dominant Eigen value of the matrix G.

In this model, there are two disease states i.e. the latent class, L and the infectious class, I.

Recall that

$$\frac{dL}{dt} = kS\frac{I}{N} - (\alpha + \mu + m + \varepsilon)L$$

$$\frac{dI}{dt} = mL - (\alpha + \psi e + \mu + \mu_\tau)I$$

The vector F_x, of the rates of new infections in compartments L and I is given by

$$F_x = \begin{bmatrix} kS\dfrac{I}{N} \\ 0 \end{bmatrix}$$

Also the remaining transfer terms in compartments L and I is given by

$$V_x = \begin{bmatrix} ((\alpha + \mu + m + \varepsilon)L \\ (\alpha + \psi e + \mu + \mu_\tau)I - mL \end{bmatrix}$$

Now we compute the matrix of partial derivatives of F_x at the disease-free equilibrium state $E^o = (V^o, S^o, 0,0,0,)$. Thus,

$$F_x(E^o) = \begin{pmatrix} 0 & kS^o \\ 0 & 0 \end{pmatrix} \text{Where} s^o = \frac{q(\beta+\Upsilon)+(\alpha+\mu)\{(1-f)\beta+(1-\eta)\Upsilon\}}{(\alpha+\mu)(\alpha+\mu+q)}$$

And the matrix of the partial derivatives of V_x at the disease-free equilibrium state $E^o = (V^o, S^o, 0,0,0,)$ is:

$$V_x(E^o) = \begin{pmatrix} \alpha + \mu + m + \varepsilon & 0 \\ -m & \alpha + \psi e + \mu + \mu_\tau \end{pmatrix}$$

R_0 is the dominant Eigen value of the next generation matrix G.

$G = F_x(E^o)V_x^{-1}$.

Using the software, Mapple, we have:

$$V_x^{-1} = \begin{pmatrix} \dfrac{1}{\alpha + \mu + m + \varepsilon} & 0 \\ \dfrac{m}{(\alpha + \mu + m + \varepsilon)(\alpha + \psi e + \mu + \mu_\tau)} & \dfrac{1}{\alpha + \psi e + \mu + \mu_\tau} \end{pmatrix}$$

So that

$$G = \begin{pmatrix} 0 & kS^o \\ 0 & 0 \end{pmatrix} \times \begin{pmatrix} \dfrac{1}{\alpha + \mu + m + \varepsilon} & 0 \\ \dfrac{m}{(\alpha + \mu + m + \varepsilon)(\alpha + \psi e + \mu + \mu_\tau)} & \dfrac{1}{\alpha + \psi e + \mu + \mu_\tau} \end{pmatrix}$$

$$G = \begin{pmatrix} \dfrac{kmS^o}{(\alpha + \mu + m + \varepsilon)(\alpha + \psi e + \mu + \mu_\tau)} & \dfrac{kS^o}{\alpha + \psi e + \mu + \mu_\tau} \\ 0 & 0 \end{pmatrix}$$

By definition, R_o is the dominant or the leading Eigen value of G. So,

$$R_e = \frac{kmS^o}{(\alpha + \mu + m + \varepsilon)(\alpha + \psi e + \mu + \mu_\tau)}$$

But $S^o = \frac{q(\beta+\Upsilon)+(\alpha+\mu)\{(1-f)\beta+(1-\eta)\Upsilon\}}{(\alpha+\mu)(\alpha+\mu+q)}$

Therefore,

$$R_e = \frac{kmq(\beta + \Upsilon) + km(\alpha + \mu)\{(1 - f)\beta + (1 - \eta)\Upsilon\}}{(\alpha + \mu + m + \varepsilon)(\alpha + \psi e + \mu + \mu_\tau)(\alpha + \mu)(\alpha + \mu + q)}$$

We now use the parameter values presented in **Table 1** to find the numerical value of R_e which determines whether the disease can be eliminated or not.

Let $R_e = \frac{Num}{Den}$

Where $Num = kmq(\beta + \Upsilon) + km(\alpha + \mu)\{(1 - f)\beta + (1 - \eta)\Upsilon\}$

And $Den = (\alpha + \mu + m + \varepsilon)(\alpha + \psi e + \mu + \mu_\tau)(\alpha + \mu)(\alpha + \mu + q)$

So that,

$$Num = \{0.238 * 0.13 * 0.37 * (0.0369 + 0.0049)\} + \{0.238 * 0.13 * (0.0051 + 0.0124) * \big((0.05 * 0.0369) + (0.86 * 0.0049)\big)\}$$

$$= 4.817986856 \times 10^{-4}$$

$$Den = \{0.0049 + 0.0124 + 0.13 + (0.7 * 0.8)\} * \{0.0049 + 00124 + (0.55 * 0.8) + 0.024\} * \{0.0049 + 0.0124\} * \{0.0049 + 0.0124 + 0.37\}$$

$$= 2.280536106 \times 10^{-3}$$

$$\therefore R_e = \frac{4.817986856 \times 10^{-4}}{2.280536106 \times 10^{-3}}$$

$$= 0.2112.$$

The table below gives the values of R_e under different conditions.

Table 1: Computed Effective Reproductive Number, (R_e) and Basic Reproductive Number, (R_0) of the modified model.

Population	R_e: Treatment and vaccination	R_e: Treatment but No Vaccination	R_e: Vaccination but No Treatment	R_0: Without Vaccination and without Treatment
Without Migrant	0.22235	0.22942	17.2160	17.763

3.4 Graphical Simulation

In this section, the numerical simulations for the model systems under different conditions are presented. This we shall achieve by using the parameter values given in **Table 1 and 2.**

Table 2: Model parameters and their interpretations

S/N	PARAMETER	SYMBOL	VALUE(per year)	SOURCE
01	The rate of new births	β	0.0369	[13]
02	The rate of Latent infection	k	0.2380	[12]
03	The rate of Expiration of vaccine	q	0.3700	[12]
04	Treatment rate for active TB	ψ	0.5500	[14]
05	Treatment rate of latent TB	ε	0.7000	[13]
06	The rate at which latent becomes infectious	m	0.1300	[14]
07	The natural mortality rate	μ	0.0124	[13]
08	TB induced death	μ_τ	0.0240	[14]
09	Efficacy of vaccine	f	0.9500	[12]
10	Efficacy of treatment	e	0.8000	Assumed
11	The rate at which recovered become Susceptible	π	0.0001	[14]

Initial conditions are given as follows: S(0)=11 000, L(0)=3 500, I(0)=500, R(0)=0 (Nadhirah,2013).

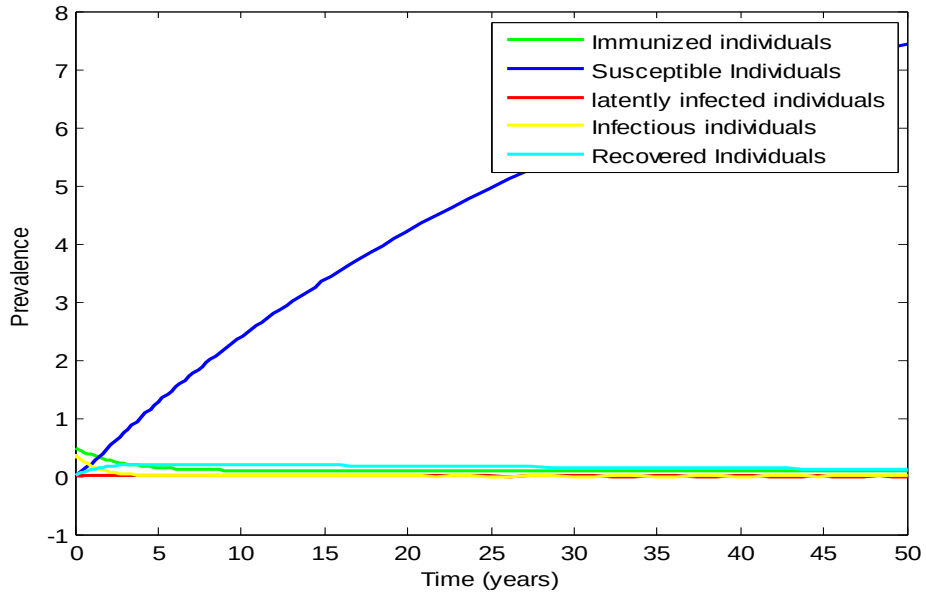

Figure 1: Graph showing the prevalence of each class in the presence of vaccination and treatment.

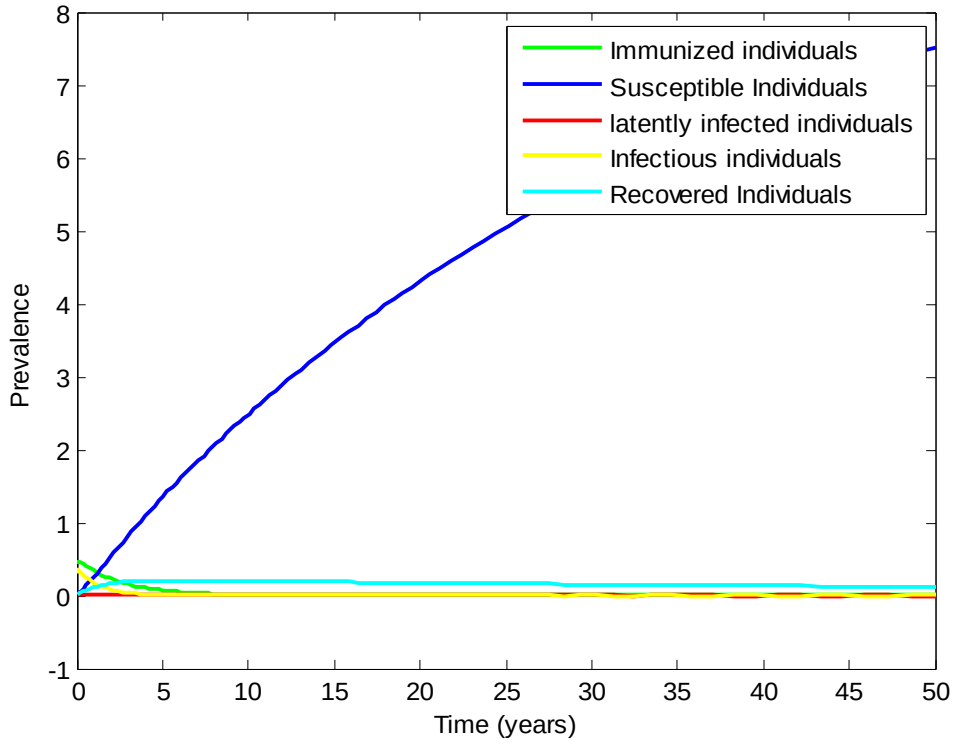

Figure 2: Graph showing the prevalence of each class in the presence of treatment and absence of vaccination.

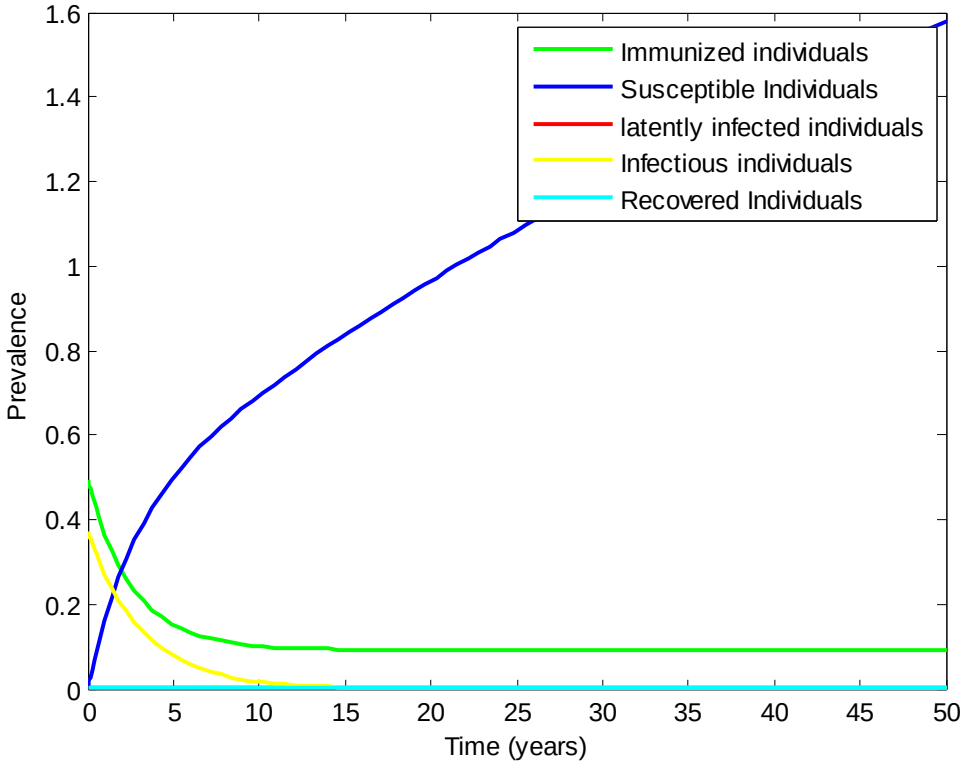

Figure 3: Graph showing the prevalence of each class in the presence of vaccination and absence of treatment.

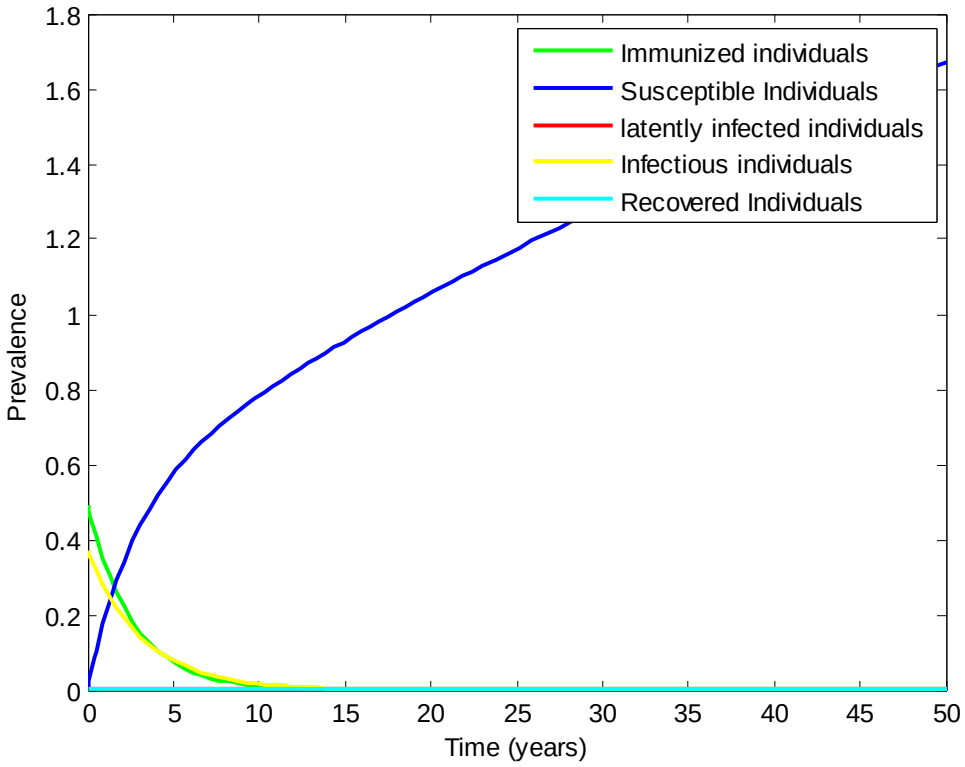

Figure 4: Graph showing the prevalence of each class in the absence of vaccination and treatment.

IV. DISCUSSION AND CONCLUSION

We put forward a mathematical model for predicting the eradication of tuberculosis in the course of vaccination treatment strategy with not present of migration effect. It was assumed that the participants into population are new-births. We examine the existence and uniqueness of the solution of the model and it was establish that the solution exist and unique. Stability analysis was carried out and it was found that the modified model is stable since term β (rate of new births) cannot be zero. Also, the disease free equilibrium is locally asymptotically stable since DFE<1. Furthermore, effective reproduction number (R_e) was found to be 0.22235 when there is treatment and vaccination, 0.22942 when there is treatment and no vaccination and 17.2160 when there is vaccination and no treatment while basic reproduction number (R_0) was found to be 17.763 as shown in Table 1.In figure 1,2, and 4 as infected individual are leaving the infected compartment, the susceptible individual are increasing which implies that, TB eradicate faster in the absence of migration. Therefore, migrant that are infected should be strongly be discouraged from leaving his/her resident country before treatment.

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