



Stability Analysis of a Vaccination Model of Tuberculosis Transmission

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Abstract We present a mathematical model of tuberculosis (TB) disease incorporating vaccination. The equilibrium points are obtained while we derive basic reproduction number (R_0) by next generation matrix method using reliable Jacobian matrices. It is shown that the disease-free equilibrium is locally asymptotically stable when $R_0 < 1$ while the endemic equilibrium is unstable if $R_0 > 1$. The instability of endemic equilibrium suggests a wiping out of the susceptible population. Hence, vaccination coverage must be large enough to promote treatment and reduce the number of infected individuals. This would in turn decrease the basic reproduction number of TB disease so that a stable disease-free equilibrium would always be achieved in the host population.

Keywords tuberculosis, mathematical model, equilibrium points, stability, basic reproduction number

1. Introduction

Infectious diseases like tuberculosis (TB), human immunodeficiency virus (HIV), measles and chicken pox are important public health problem [1]. Since vaccination is considered to be an efficient strategy against TB, the development of a mathematical framework that could predict optimal vaccination coverage level is necessary. As a first step, the World Health Organization (WHO) through Directly Observed Strategy, Short course (DOTS) have developed BCG vaccines and other new vaccines which aim at preventing infection and improving TB treatment [2]. At the population level, deterministic TB mathematical models incorporating vaccination have been proposed and analyzed to evaluate the overall effect of vaccination on the dynamics of TB disease [3-9].

In the present study, we formulate a mathematical model in which the population is split into four compartments: a susceptible group (S), a vaccinated group (V), an infected group (I) and a removed recovered group (R). The model assumes that the natural death rate is not equal to birth rate so that we have a varying population size. Furthermore, a susceptible individual will move into the infected group upon contact with an infected individual. The removed group also contains people who are vaccinated. With all these considerations, the differential equations for the SVIR model are:

$$S' = \pi - \beta IS - (\mu + \theta)S \quad (1)$$

$$V' = \theta S - (1-f)\beta IV - (\mu + q)V \quad (2)$$

$$I' = \beta IS - (\mu + \mu_r)I \quad (3)$$

$$R' = qV - \mu R \quad (4)$$

The description of parameters of the model is given in Table 1.



Table 1: Description of Parameters of the model

Parameters	Definitions
π	recruitment rate
β	transmission rate
μ	natural rate
μ_T	death rate due to TB
θ	vaccination rate
f	efficacy rate of vaccine
q	waning rate of vaccine

2. Mathematical Analysis

2.1. Equilibrium points

If a population is free of TB (DFE), $I = 0$, then the system reduces to

$$S' = \pi - (\mu + \theta)S \quad (5)$$

$$V' = \theta S - (\mu + q)V \quad (6)$$

$$R' = qV - \mu R \quad (7)$$

Recalling that $S' = V' = R' = 0$ is necessary for an equilibrium, we have the disease-free equilibrium (DFE) A_0 given by

$$A_0 = (S_0, V_0, I_0, R_0) = \left(\frac{\pi}{\mu + \theta}, \frac{\theta\pi}{(\mu + \theta)(\mu + q)}, 0, \frac{q}{\mu} \left\{ \frac{\theta\pi}{(\mu + \theta)(\mu + q)} \right\} \right) \quad (8)$$

At the endemic equilibrium, the disease persists in the population and consequently $I \neq 0$. Hence, there exists an endemic equilibrium $A^* = (S^*, V^*, I^*, R^*)$ where

$$S^* = \frac{\mu + \mu_T}{\beta} \quad (9)$$

$$I^* = \pi\beta - \frac{(\mu + \theta)(\mu + \mu_T)}{\beta(\mu + \mu_T)} \quad (10)$$

$$V^* = \frac{\theta\pi[\pi\beta - (\mu + \theta)(\mu + \mu_T)]}{(\mu + \theta)[(1 - f)(\mu + \mu_T) - (\mu + q)\{\pi\beta - (\mu + \theta)(\mu + \mu_T)\}]} \quad (11)$$

$$R^* = \frac{q\theta\pi[\pi\beta - (\mu + \theta)(\mu + \mu_T)](\mu + \theta)(\mu + \mu_T)}{\mu(\mu + \theta)[(1 - f)(\mu + \mu_T) - (\mu + q)\{\pi\beta - (\mu + \theta)(\mu + \mu_T)\}]} \quad (12)$$

The threshold parameter, R_0 , that determines the stability of TB model equilibria is calculated using next generation matrix method formulated by van den Driessche and Watmough [10] and is obtained as

$$R_0 = \frac{\beta}{(\mu + \theta)(\mu + \mu_T)} \quad (13)$$

2.2. Stability analysis of DFE

We shall need the following theorem in the stability analysis of the DFE of model (1) - (4).

Theorem 1 [14]

$$\text{Let } \frac{dx}{dy} = P(x, y), \quad \frac{dy}{dt} = Q(x, y) \quad \text{and} \quad X = \begin{pmatrix} x \\ y \end{pmatrix}$$

Let $X_1 = \begin{pmatrix} x_1 \\ y_1 \end{pmatrix}$ be a critical point of the plane autonomous system.



$$X_1 = g(x) = X_1 = g(x) \begin{pmatrix} p(x, y) \\ Q(x, y) \end{pmatrix},$$

Where $p(x, y)$, $Q(x, y)$ have continuous first partial derivatives in a neighbourhood of X_1

- (a) If all the eigenvalues of $A = g^1(X_1)$ have negative real parts, then X_1 is locally asymptotically stable critical point
- (b) If $A = g^1(X_1)$ has at least one eigenvalue with positive real part, then X_1 is an unstable critical point.

The Jacobian matrix of DFE is

$$J = \begin{pmatrix} -(\mu + \theta) - \lambda & 0 & 0 & 0 \\ 0 & -(\mu + q) - \lambda & 0 & 0 \\ 0 & 0 & -(\mu + \mu_T) - \lambda & 0 \\ 0 & q & 0 & -\mu - \lambda \end{pmatrix} \quad (14)$$

The eigenvalues of the DFE is obtained by solving

$$|J - \lambda I| = 0 \quad (15)$$

Solving (15), the eigenvalues are

$$\begin{aligned} \lambda_1 &= -(\mu + \theta) \\ \lambda_2 &= -(\mu + q) \\ \lambda_3 &= -(\mu + \mu_T) \\ \lambda_4 &= -\mu \end{aligned}$$

Clearly, all the eigenvalues λ_i , $i = 1(1)4$ are negative. Hence, by Theorem 1, the DFE is locally asymptotically stable. Furthermore, the local stability of DFE with respect to basic reproduction number (R_0) is demonstrated in Theorem 2 below.

Theorem 2: If $R_0 < 1$, then the DFE of model system (1) - (4) is locally asymptotically stable.

Proof

Using realistic parameter values of the model, let $\beta = 0.5$, $\pi = 0.1$, $\theta = 0.7$, $\mu = 0.1$, $\mu_T = 0.01$. Then, $R_0 = 0.5681 < 1$. Hence, the DFE A_0 is asymptotically stable. This suggests that infection is temporal and the disease will eventually die out.

2.3. Stability analysis of endemic equilibrium

By using a reliable Jacobian matrix of the endemic equilibrium point, the eigenvalues of the matrix can be analyzed to find its local stability. If at least one eigenvalue has a positive real part, then the endemic equilibrium is unstable. However, using the Theorem below, we can demonstrate the instability of endemic equilibrium for $R_0 > 1$. Under this scenario, the infection is persistent in the population and may lead to eventual wiping out of the entire susceptible population. Hence, appropriate intervention strategy for controlling the spread of the disease must be taken.

Theorem 3: If $R_0 > 1$, the endemic equilibrium is unstable.

Proof: Let $\beta = 1.3$, $\pi = 0.6$, $\mu = 0.1$, $\mu_T = 0.04$, $\theta = 0.02$. We obtain $R_0 = 46.9286 > 1$. This shows that A^* is unstable. Hence, the proof.

3. Discussion of results and conclusion

A vaccination model for the dynamics of TB has been analyzed for stability. The results show that if $R_0 < 1$, the DFE is locally stable while the endemic equilibrium is unstable when



$R_0 > 1$. These results provide useful insights about the critical vaccination level necessary to ensure a locally stable DFE for eradication of disease or prevention of TB infection. The vaccination coverage must lie below a critical level ($R_0 < 1$) to reduce the number of infectious individuals. Therefore, an efficient vaccination campaign is required to decrease the proportion of contacts of susceptible population with infected individuals.

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