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Backward Bifurcation Analysis of a Tuberculosis Model with Vaccination as a Control Strategy

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***Abstract*— It is well known that backward bifurcation plays a critical role in the transmission of infectious that can be prevented by vaccination. In this paper, we investigate the occurrence of backward bifurcation in a tuberculosis vaccination model. The method of analysis is based on the use of center manifold theory. Threshold values are determined while we derive sufficient conditions for the possibility of backward bifurcation. The result revealed the existence of a backward bifurcation in the model for the basic reproduction number R0 < 1. The implication of this result is that it is now possible for the disease to persist endemically under a condition which otherwise prevents establishment of disease.**

***Index Terms*— tuberculosis, model, vaccination, center, manifold theory, basic reproduction number, backward bifurcation.**

I. INTRODUCTION

Bifurcation in mathematical modeling is a phenomenon showing how the disease-free equilibrium (DFE) of a disease model divides into a branch representing an endemic equilibrium and a further branch of the disease-free equilibrium resulting into a change in its stability properties and dynamic behavior [1]. Backward bifurcation which is characterized by multiple co-existing equilibra allows a disease to persist even though $R_0<1$ (see ref.[2]). More specifically, at $R_0<1$, a stable DFE co-exists with two endemic equilibra, one being a small equilibrium with a smaller number of infectious individuals which is unstable and the other a large endemic equilibrium with a larger number of infected individuals which is stable. Due to this, the disease suddenly establishes a large endemic state which can only be eradicated by reducing R_0 well below a critical value less than one [3]. Therefore, the study of backward bifurcation in epidemic models is very vital because control programmes must reduce R_0 further below unity (one) to eliminate a disease.

In this paper, we investigate the possibility of backward bifurcation in a tuberculosis (TB) model with vaccination. To do this, the center manifold theory of bifurcation analysis proposed by Castillo-Chavez and Song [4] and which has been applied in some epidemic models [5], [6], [7] shall be used.

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II. MATHEMATICAL FORMULATION

The model is [8]

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

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

$$I' = \beta IS - (\mu + \mu T)I \quad (3)$$

The description of the variables and the model parameters are shown in the following table:

Table 1: Model Variables and Parameters

Variable /Parameter	Description
S	Susceptible class
V	Vaccinated class
I	Infected class
π	Recruitment rate of susceptible class
β	Transmission rate
μ	Natural death rate
μ_T	Death rate due to TB
q	Waning rate of vaccine
f	Efficacy rate of vaccine
θ	Vaccination rate

Model equations (1) – (3) has a disease free equilibrium A_o given by

$$A_0 = \left(\frac{\pi}{\mu + \theta}, \frac{\theta\pi}{(\mu + \theta)(\mu + q)}, 0 \right) \quad (4)$$

The basic reproduction number of the model is determined by using next generation matrix method proposed by van den Driessche and Watmough [9] and is obtained as

$$R_o = \frac{\beta\pi}{(\mu + \theta)(\mu + \mu_T)} \quad (5)$$

III. BIFURCATION ANALYSIS

Existence of Backward Bifurcation in the Model

Here, we look for conditions on the parameter values that can cause a backward bifurcation to occur in the model. In order to do that, we will make use of the general center manifold theory of Castillo –Chavez and Song [4]. The theorem prescribes the role of coefficients a and b for the occurrence of backward bifurcation. More precisely, if a > 0 and b > 0, a backward bifurcation occurs. Let the bifurcation parameters β^* be chosen so that at R_o =1 in equation (5),

we have

$$\beta^* = \frac{(\mu+\theta)(\mu+\mu_T)}{\pi} \qquad (6)$$

The linearized matrix of the model around disease-free equilibrium A_o and evaluated at β^* is obtained as

$$J(A_o, \beta^*) = \begin{pmatrix} -\mu-\theta & 0 & \frac{\beta\pi}{\mu+\theta} \\ 0 & -\mu-q & \frac{-(1-f)\theta\pi\beta}{(\mu+\theta)(\mu+q)} \\ 0 & q & \frac{\beta\pi}{\mu+\theta} - (\mu+\mu_T) \end{pmatrix}$$

Let $w = (w_1, \quad w_2, \quad w_3)^T$ denote a right eigenvector associated with the zero eigenvalues. Taking into consideration the Jacobian $J(A_0, \beta^*)$ of the transformed equations at $\beta = \beta^*$, around the disease-free equilibrium A_0, we evaluate the linearized matrix

$$\begin{pmatrix} -\mu-\theta & 0 & \mu+\mu_T \\ 0 & -\mu-q & -(1-f)\theta \\ 0 & q & \frac{\mu+\mu_T}{\mu+\theta} - (\mu+\mu_T) \end{pmatrix} \begin{pmatrix} w_1 \\ w_2 \\ w_3 \end{pmatrix} = \begin{pmatrix} 0 \\ 0 \\ 0 \end{pmatrix}$$

Thus, we get

$$-(\mu-\theta)w_1 + (\mu+\mu_T)w_3 = 0$$

$$(-\mu-q)w_2 - (1-f)\theta w_3 = 0$$

$$qw_2 + \left[\frac{\mu+\mu_T}{\mu+\theta} - (\mu+\mu_T)\right]w_3 = 0$$

This implies that

$$w_1 = \frac{-(\mu+\mu_T)[(\mu+q)+(1-f)\theta]}{\mu+\theta}$$

$$w_2 = q - \mu - \mu_T - \frac{(\mu+\mu_T)}{\mu+\theta}$$

$$w_3 = -\mu - q - (1-f)\theta$$

In a similar way, the left eigenvector $v = (v_1, v_2, v_3)^T$ corresponding to the zero eigenvalue of $J(A_0, \beta^*)$ satisfying $v \cdot w = 1$ is computed as

$$v_1 = 0, v_2 = q - \frac{(\mu+\mu_T)}{\mu+\theta} - (\mu+\mu_T),$$

$$v_3 = -2\mu - \mu_T \frac{(\mu+\mu_T)}{\mu+\theta}$$

Derivation of bifurcation coefficients a and b

Taking into account equation (1) - (3) and using the following expressions from [4], we obtain

$$\left.\begin{aligned} a &= \sum_{kij=1}^{n} v_k w_i w_j \frac{\partial^2 f_k(0,0)}{\partial x_i \partial x_j}, \\ b &= \sum_{kj=1}^{n} v_k w_i \frac{\partial^2 f_k(0,0)}{\partial x_j \partial \phi} \end{aligned}\right\}$$

It follows then that

$$a = 2v_1w_1w_3\frac{\partial^2 f_1}{\partial S\partial I}(E_0,\beta^*) + 2v_2w_1w_2\frac{\partial^2 f_3}{\partial S\partial I}(E_0,\beta^*) \quad (9)$$

$$b = 2v_1w_2\frac{\partial^2 f_3}{\partial S\partial I}(E_0,\beta^*) \quad (10)$$

where $f_i i$ = 1, 2, 3 denotes the right side of equations (1) – (3).

The partial derivatives of f_i at the disease-free equilibrium are given by

$$\left.\begin{aligned}
\frac{\partial^2 f_i}{\partial S\partial I}(A_o,\beta^*) &= -\beta^* = \frac{-(\mu+\theta)(\mu+\mu_T)}{\pi}\\
\frac{\partial^2 f_i}{\partial I\partial S}(A_o,\beta^*) &= -\beta^* = \frac{-(\mu+\theta)(\mu+\mu_T)}{\pi}\\
\frac{\partial^2 f_3}{\partial S\partial I}(A_o,\beta^*) &= \beta^* = \frac{(\mu+\theta)(\mu+\mu_T)}{\pi}\\
\frac{\partial^2 f_3}{\partial I\partial S}(A_o,\beta^*) &= \beta^* = \frac{(\mu+\theta)(\mu+\mu_T)}{\pi}\\
\frac{\partial^2 f_3}{\partial \beta}\partial I(A_o,\beta^*) &= S_0 = \frac{\pi}{\mu+\theta}\\
\frac{\partial^2 f_3}{\partial I\partial \beta}\partial I(A_o,\beta^*) &= S_0 = \frac{\pi}{\mu+\theta}
\end{aligned}\right\}$$

where f_i, i = 1,2,3, are the right hand side of equation (1) – (3) and all other second order partial derivatives are equal to zero. By substituting equation (11) together with the right and left eigenvectors w and v into equation (9) – (10) gives

$$a = 2\left\{\frac{(\mu+\mu_T)[(\mu+q)(1-f)\theta]}{\mu+\theta}(\mu+q)\left(\frac{(\mu+\theta)(\mu+\mu_T)}{\pi}\right)\times\left(2\mu+\mu_T+\frac{(\mu+\mu_T)}{\mu+\theta}\right)\right\}>0 \quad (12)$$

(μ,π,μ_T,q *and* θ are all positive constants since the model monitors human population)

$$b = \left(2\mu+\mu_T+\frac{(\mu+\mu_T)}{\mu+\theta}\right)[(\mu+q)+(1-f)\theta]\frac{\mu}{\mu+\theta}>0 \quad (13)$$

by the same argument in equation (12).

IV. Conclusion

The result of the bifurcation analysis showed the possibility of a backward bifurcation in the model due to temporary immunity offered by the vaccine. The physical interpretation of this result is that it is possible for TB to become endemic under this condition. This information would assist public health officials and all TB stakeholders to evolve effective treatment strategies aimed at controlling the basic reproduction number of the disease in order to prevent epidemic outbreak and achieve a tuberculosis-free environment.

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