Journal of the Nigerian Society for Mathematical Biology
Volume 1 (2018), pp. 11 - 18

A note on the backward bifurcation phenomenon in a tuberculosis mathematical model for highly endemic regions

A. Nwankwo*and D. Okuonghae†

Abstract

This work investigates the existence of the backward bifurcation phenomenon in a mathematical model designed to simulate hyperendemic TB in the Asia-Pacific (James et al [7]). It is shown that the possibility of the backward bifurcation is determined by the loss of partial immunity to TB, immunity conferred due to the administration of the BCG vaccine and recovery from a previous infection due to treatment. The existence of the backward bifurcation in the system has a very strong implication for disease control as the likelihood of a stable high endemic level is possible even when the epidemiological parameters are indicative of feasible control strategies that normally should lead to disease eradication when the control reproduction number of the model is used as a tool for designing public health control policies.

Keywords: Backward Bifurcation; tuberculosis; reproduction number; partial immunity.

1 Introduction

A classical requirement for the eradication of a disease in a population is for the basic (control) reproduction number (a threshold quantity which measures the average number of new cases generated by a typically infected individual in a wholly susceptible population) of an epidemic mathematical model, describing the transmission dynamics of the disease, to be less than unity. On the other hand, the disease will persist if the basic (control) reproduction number exceeds unity, where a stable endemic equilibrium exists. This phenomenon, where the disease-free equilibrium loses its stability and a stable endemic equilibrium appears as the basic (control) reproduction number increases through one is known as forward bifurcation. A schematic diagram of forward bifurcation is given in Figure 1. Some of the main characteristics of this phenomenon are [3]:

(i) the absence of positive (endemic) equilibria near the DFE when the associated reproduction number is less than unity where in this case, the DFE is often the only equilibrium;

(ii) a low endemic level when the associated reproduction number is slightly above unity.

Generally, the disease-free equilibrium (DFE) can be globally asymptotically stable (GAS), in this case.

However, several researchers have demonstrated that it is possible for the DFE to co-exist with two endemic equilibria, giving rise to the occurrence of a backward bifurcation, when the associated reproduction number of the model is less than unity (one). In recent years, the backward bifurcation phenomenon has been of interest to several researchers [4, 5, 6, 8, 9, 10, 11, 12, 13, 14]. For example, the works in [9, 10], amongst several others, showed that exogenous re-infection is a cause of backward bifurcation in tuberculosis models that includes exogenous

*Graduate Student, Department of Mathematics, University of Benin, Benin City, Nigeria.

†Corresponding author: Department of Mathematics, University of Benin, Benin City, Nigeria; daniel.okuonghae@uniben.edu; danny.okuonghae@corpus-christi.oxon.org

re-infection in the disease transmission process. When it is evident that there is the possibility of a backward bifurcation in a system, then the requirement of having the basic reproduction number to be less than unity becomes only a necessary, but not sufficient condition, for disease eradication, even when the reproduction number is sustained at a value less than one.

Hence, the presence of backward bifurcation is important in a practical sense because control programs are aimed at reducing the basic (control) reproduction number of the model below unity (and sustaining it at this value) in order to achieve disease eradication; this means that the occurrence of a backward bifurcation in the system may have important public health implications. More importantly, in a backward bifurcation setting, once the associated reproduction number crosses unity, the disease can invade to a relatively high endemic level so that even when the reproduction number is reduced to a slightly lower level, it will not necessarily make the disease disappear. A schematic diagram of backward bifurcation is given in Figure 2.

The work by James et al [7] includes a formulated mathematical model for simulating the dynamics of tuberculosis in the highly endemic regions of the Asia-pacific. However, in this short work, we want to show that high endemic levels can still be achieved even when the assumed reproduction number of the model is less than one. Therefore, examining the cause of the backward bifurcation in such a setting is very important especially with regards to measuring the disease endemic level when condition(s) for the backward bifurcation exists and comparing this to the calculated value of the reproduction number of the model, in this case.

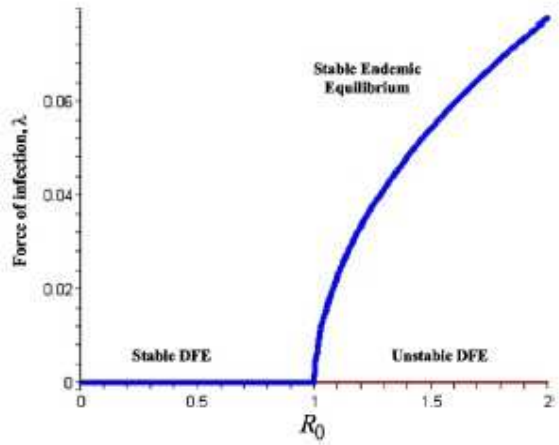

Figure 1: Forward bifurcation diagram. Source: Gumel A.B. [5].

2 Tuberculosis Mathematical Model (James et al [7])

The model for the transmission dynamics of TB designed for simulating the highly endemic regions of the Asia-pacific is as given in [7] and presented in (1) (the associated variables and

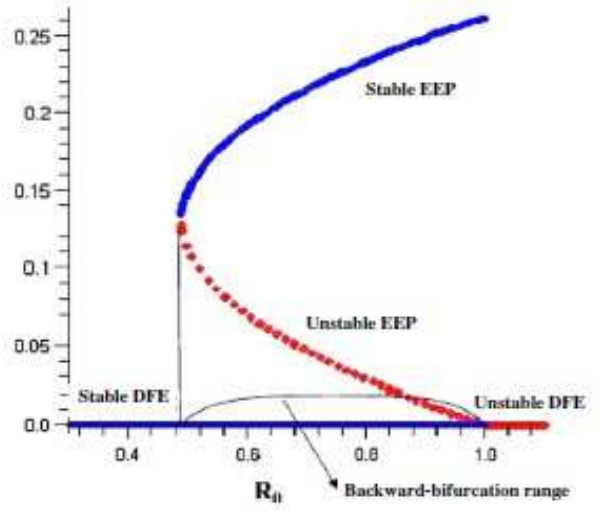

Figure 2: Backward bifurcation diagram. Source: Gumel A.B. [5].

parameters of the model are described in Table 1).

$$\begin{aligned}
\frac{dS_A}{dt} &= (1-l)\pi N - (\lambda + \lambda_m + \mu)S_A,\\
\frac{dS_B}{dt} &= l\pi N + \varphi T + \varphi_m T_m - (\lambda_d + \lambda_{dm} + \mu)S_B,\\
\frac{dL_A}{dt} &= \lambda S_A + \lambda_d(S_B + L_B + L_{Bm}) - (\varepsilon + \kappa + \mu)L_A,\\
\frac{dL_{Am}}{dt} &= \lambda_m S_A + \lambda_{dm}(S_B + L_B + L_{Bm}) - (\varepsilon + \kappa + \mu)L_{Am},\\
\frac{dL_B}{dt} &= \kappa L_A + \gamma I - (\lambda_d + \lambda_{dm} + \nu + \mu)L_B,\\
\frac{dL_{Bm}}{dt} &= \kappa L_{Am} + \gamma I_m - (\lambda_d + \lambda_{dm} + \nu + \mu)L_{Bm},\\
\frac{dI}{dt} &= \varepsilon L_A + \nu L_B + (1-\eta)\omega T - (\gamma + \delta + \mu_i)I,\\
\frac{dI_m}{dt} &= \varepsilon L_{Am} + \nu L_{Bm} + \eta\omega T + \omega T_m - (\gamma + \delta_m + \mu_i)I_m,\\
\frac{dT}{dt} &= \delta I - (\varphi + \omega + \mu_t)T,\\
\frac{dT_m}{dt} &= \delta_m I_m - (\varphi_m + \omega + \mu_t)T_m,
\end{aligned} \tag{1}$$

where $N = S_A + S_B + L_A + L_{Am} + L_B + L_{Bm} + I + I_m + T + T_m$ is the total population.

The forces of infection were given as

$$\lambda = \frac{\beta\rho(I + oT)}{N}, \quad \lambda_d = \frac{\chi\beta\rho(I + oT)}{N}, \quad \lambda_m = \frac{\beta_m\rho(I_m + oT_m)}{N} \quad and$$
$$\lambda_{dm} = \frac{\chi\beta_m\rho(I_m + oT_m)}{N}.$$

The system (1) has a disease free equilibrium (DFE) given by

$$\xi_0 = (S_A^*, S_B^*, L_A^*, L_{Am}^*, L_B^*, L_{Bm}^*, I^*, I_m^*, T^*, T_m^*) = \left(\frac{(1-l)\pi N}{\mu}, \frac{l\pi N}{\mu}, 0, 0, 0, 0, 0, 0, 0, 0\right)$$

The local stability of the DFE (ξ_0), can be established using the next generation method approach in [2] and the effective reproduction number, denoted by $\mathcal{R}_{eff}$, can be computed and

Variable	Interpretation
S_A	Population of susceptible individuals
S_B	Population of susceptible individuals with improved immunity due to previous infection and vaccination
$L_A(L_{Am})$	Population of infected individuals with early latent DS-TB (MDR-TB)
$L_B(L_{Bm})$	Population of infected individuals with late latent DS-TB (MDR-TB)
$I(I_m)$	Population of infectious individuals with DS-TB (MDR-TB)
$T(T_m)$	Population of individuals treated of DS-TB (MDR-TB)
Parameter	**Interpretation**
μ	TB-free mortality rate
μ_i	TB-specific mortality rate
μ_t	Treated TB-specific mortality rate
π	Birth-rate
l	BCG vaccination rate
β (β_m)	Effective contact rate for DS-TB (MDR-TB)
ε	Early progression
κ	Transition to late latency
ρ	Infectious proportion
γ	Spontaneous recovery
η	Amplification
o	Treatment modification of infectiousness
χ	Partial immunity
$\varphi(\varphi_m)$	Treatment rate for DS-TB (MDR-TB)
$\delta(\delta_m)$	Detection rate for DS-TB (MDR-TB)
ω	Default rate
ν	Reactivation

Table 1: Description of variables and parameters in the model (1) [7].

is

$$\mathcal{R}_{eff} = max(\mathcal{R}_d, \mathcal{R}_m),$$

where $\mathcal{R}_d$ and $\mathcal{R}_m$ are the control reproduction numbers for the drug susceptible strain and the multi-drug resistant strain, respectively, and are given as

$$\begin{aligned} \mathcal{R}_d &= \frac{-\beta\rho(1-l+\chi l)(\kappa\nu+\varepsilon g_2)(\delta o+g_5)}{g_1(\gamma\nu g_5+g_2\delta\omega(\eta-1)-g_2g_3g_5)} > 0 \quad \text{and} \\ \mathcal{R}_m &= \frac{-\beta_m\rho(1-l+\chi l)(\kappa\nu+\varepsilon g_2)(\delta_m o+g_6)}{g_1(\gamma\nu g_6+g_2\delta_m\omega-g_2g_4g_6)} > 0. \end{aligned} \tag{2}$$

The result below follows from Theorem 2 in [2].

Lemma 2.1 *The DFE* (ξ_0) *of the model* (1) *is locally-asymptotically stable (LAS) if* $\mathcal{R}_{eff} < 1$, *and unstable if* $\mathcal{R}_{eff} > 1$.

3 Backward Bifurcation Analysis

We claim the following.

Theorem 3.1 *The model* (1) *exhibits backward bifurcation at* $\mathcal{R}_{eff} = 1$ *whenever a bifurcation coefficient, denoted by a (and given by* (6)*), is positive.*

Proof. Suppose

$$\xi_1 = (S_A^{**}, S_B^{**}, L_A^{**}, L_{Am}^{**}, L_B^{**}, L_{Bm}^{**}, I^{**}, I_m^{**}, T^{**}, T_m^{**})$$

represents any arbitrary endemic equilibrium of the model (1) (that is, an equilibrium of the model in which at least one of the infected compartments is non-zero). The existence of the backward bifurcation will be explored using the Centre Manifold theory [1]. Let

$$S_A = x_1, \quad S_B = x_2, \quad L_A = x_3, \quad L_{Am} = x_4, \quad L_B = x_5, \quad L_{Bm} = x_6, \quad I = x_7,$$
$$I_m = x_8, \quad T = x_9 \quad \text{and} \quad T_m = x_{10}, \quad \text{where} \quad N = \sum_{i=1}^{i=10} x_i.$$

Let $F(x) = (x_1, x_2, ..., x_{10})$. Hence, the model (1) can be written as

$$\begin{aligned} \dot{x}_1 &\equiv f_1 = (1-l)\pi N - (\lambda+\lambda_m+\mu)x_1, \\ \dot{x}_2 &\equiv f_2 = l\pi N + \varphi x_9 + \varphi_m x_{10} - (\lambda_d+\lambda_{dm}+\mu)x_2, \\ \dot{x}_3 &\equiv f_3 = \lambda x_1 + \lambda_d(x_2+x_5+x_6) - (\varepsilon+\kappa+\mu)x_3, \\ \dot{x}_4 &\equiv f_4 = \lambda_m x_1 + \lambda_{dm}(x_2+x_5+x_6) - (\varepsilon+\kappa+\mu)x_4, \\ \dot{x}_5 &\equiv f_5 = \kappa x_3 + \gamma x_7 - (\lambda_d+\lambda_{dm}+\nu+\mu)x_5, \\ \dot{x}_6 &\equiv f_6 = \kappa x_4 + \gamma x_8 - (\lambda_d+\lambda_{dm}+\nu+\mu)x_6, \\ \dot{x}_7 &\equiv f_7 = \varepsilon x_3 + \nu x_5 + (1-\eta)\omega x_9 - (\gamma+\delta+\mu_i)x_7, \\ \dot{x}_8 &\equiv f_8 = \varepsilon x_4 + \nu x_6 + \eta\omega x_9 + \omega x_{10} - (\gamma+\delta_m+\mu_i)x_8, \\ \dot{x}_9 &\equiv f_9 = \delta x_7 - (\varphi+\omega+\mu_t)x_9, \\ \dot{x}_{10} &\equiv f_{10} = \delta_m x_8 - (\varphi_m+\omega+\mu_t)x_{10}, \end{aligned} \tag{3}$$

with

$$\lambda = \frac{\beta\rho(x_7+ox_9)}{\sum_{i=1}^{i=10} x_i}, \quad \lambda_d = \frac{\chi\beta\rho(x_7+ox_9)}{\sum_{i=1}^{i=10} x_i}, \quad \lambda_m = \frac{\beta_m\rho(x_8+ox_{10})}{\sum_{i=1}^{i=10} x_i}, \quad and$$
$$\lambda_{dm} = \frac{\chi\beta_m\rho(x_8+ox_{10})}{\sum_{i=1}^{i=10} x_i}.$$

Without loss of generality, consider the case when $\mathcal{R}_{eff} = 1$. Furthermore, let $\beta = \beta^*$, be a bifurcation parameter. Solving for $\beta = \beta^*$ from $\mathcal{R}_d = 1$ gives

$$\beta = \beta^* = \frac{g_1(\gamma\nu g_5 + g_2\delta\omega(\eta - 1) - g_2g_3g_5)}{-\rho(1 - l + \chi l)(\kappa\nu + \varepsilon g_2)(\delta o + g_5)} > 0.$$

The Jacobian of the transformed system (3), evaluated at the DFE (ξ_0) with $\beta = \beta^*$, is given by

$$J(\xi_0)|_{\beta=\beta^*} = \begin{pmatrix} -\mu & 0 & 0 & 0 & 0 & 0 & -A_1 & -A_2 & -oA_1 & -oA_2 \\ 0 & -\mu & 0 & 0 & 0 & 0 & -A_3 & -A_4 & \varphi - oA_3 & \varphi_m - oA_4 \\ 0 & 0 & -g_1 & 0 & 0 & 0 & A_1 + A_3 & 0 & o(A_1 + A_3) & 0 \\ 0 & 0 & 0 & -g_1 & 0 & 0 & 0 & A_2 + A_4 & 0 & o(A_2 + A_4) \\ 0 & 0 & \kappa & 0 & -g_2 & 0 & \gamma & 0 & 0 & 0 \\ 0 & 0 & 0 & \kappa & 0 & -g_2 & 0 & \gamma & 0 & 0 \\ 0 & 0 & \varepsilon & 0 & \nu & 0 & -g_3 & 0 & (1-\eta)\omega & 0 \\ 0 & 0 & 0 & \varepsilon & 0 & \nu & 0 & -g_4 & \eta\omega & \omega \\ 0 & 0 & 0 & 0 & 0 & 0 & \delta & 0 & -g_5 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & \delta_m & 0 & -g_6 \end{pmatrix},$$

where

$$A_1 = \beta^*\rho(1-l), \quad A_2 = \beta_m\rho(1-l), \quad A_3 = \chi\beta^*\rho l, \quad A_4 = \chi\beta_m\rho l, \quad g_1 = \varepsilon + \kappa + \mu,$$
$$g_2 = \nu + \mu, \quad g_3 = \gamma + \delta + \mu_i, \quad g_4 = \gamma + \delta_m + \mu_i, \quad g_5 = \varphi + \omega + \mu_t \quad \text{and} \quad g_6 = \varphi_m + \omega + \mu_t.$$

We obtain the components of the right eigenvectors of $J(\xi_0)|_{\beta=\beta^*}$, associated with the zero eigenvalue, which is given as $\mathbf{w} = (\omega_1, \omega_2, ..., \omega_{10})^T$, to be

$$\begin{aligned}
\omega_1 &= -\frac{\omega_7}{\mu g_5 X(1-\mathcal{R}_m)}\left(A_1g_5X(1-\mathcal{R}_m) + A_2g_1g_2g_6\omega\eta\delta + oA_1\delta X(1-\mathcal{R}_m) + oA_2\delta_m g_1g_2\omega\eta\delta\right), \\
\omega_2 &= \omega_7\left(\frac{\varphi\delta}{\mu g_5} + \frac{\varphi_m\delta_m g_1g_2\omega\eta\delta}{\mu g_5X(1-\mathcal{R}_m)} - \frac{A_3}{\mu} - \frac{A_4g_1g_2g_6\omega\eta\delta}{\mu g_5X(1-\mathcal{R}_m)} - \frac{oA_3\delta}{\mu g_5} - \frac{oA_4\delta_m g_1g_2\omega\eta\delta}{\mu g_5X(1-\mathcal{R}_m)}\right), \\
\omega_3 &= (A_1+A_3)\omega_7\frac{(g_5+o\delta)}{g_1g_5} > 0, \quad \omega_4 = \frac{(A_2+A_4)(o\delta_m+g_6)g_2\omega\eta\delta\omega_7}{g_5X(1-\mathcal{R}_m)}, \\
\omega_5 &= \frac{\omega_7}{g_2}\left(\gamma + \frac{\kappa(A_1+A_3)(g_5+o\delta)}{g_1g_5}\right) > 0, \quad \omega_6 = \frac{(g_1g_6\gamma + \kappa(A_2+A_4)(o\delta_m+g_6)\omega\eta\delta\omega_7}{g_5X(1-\mathcal{R}_m)}, \\
\omega_7 &= \omega_7 > 0, \quad \omega_8 = \frac{g_1g_2g_6\omega\eta\delta\omega_7}{g_5X(1-\mathcal{R}_m)}, \quad \omega_9 = \frac{\delta\omega_7}{g_5} > 0 \quad \text{and} \quad \omega_{10} = \frac{g_1g_2\delta_m\omega\eta\delta\omega_7}{g_5X(1-\mathcal{R}_m)},
\end{aligned} \tag{4}$$

where $X = [g_1g_2g_4g_6 - g_1g_2\omega\delta_m - \nu\gamma g_1g_6]$.

Also,the components of the left eigenvector of $J(\xi_0)|_{\beta=\beta^*}$, denoted by $\mathbf{v} = (\nu_1, \nu_2, ..., \nu_{10})^T$, satisfying $\mathbf{v}.\mathbf{w} = 1$, are given by

$$\begin{aligned}
&\nu_1 = \nu_2 = \nu_4 = \nu_6 = \nu_8 = \nu_{10} = 0, \quad \nu_3 = \nu_7\frac{(\kappa\nu + \varepsilon g_2)}{g_1g_2}, \quad \nu_5 = \frac{\nu\nu_7}{g_2}, \\
&\nu_7 = \nu_7 > 0 \quad \text{and} \quad \nu_9 = \frac{(oA_1 + oA_3)(\kappa\nu + \varepsilon g_2)\nu_7}{g_1g_2g_5} + \frac{(1-\eta)\omega\nu_7}{g_5}.
\end{aligned} \tag{5}$$

It follows from Theorem 4.1 in [1], by computing the associated non-zero partial derivatives of $F(x)$ of the system (3) (evaluated at the DFE (ξ_0), that the associated bifurcation coefficients , a and b, are given by

$$a = \sum_{k,i,j=1}^{n}\nu_k\omega_i\omega_j\frac{\partial^2 f_k}{\partial x_i\partial x_j}(0,0), \quad \text{and} \quad b = \sum_{k,i=1}^{n}\nu_k\omega_i\frac{\partial^2 f_k}{\partial x_i\partial\beta_v^*}(0,0),$$

which, after several algebraic calculations lead to

$$\begin{aligned} a = \Big\{ & -(G_1+\chi G_2)[g_1g_2X(1-\mathcal{R}_m)\varphi\delta + g_1^2g_2^2\varphi_m\delta_m\omega\eta\delta \\ & + [2g_1g_2g_5 + 2g_1g_2\delta + g_1g_5\gamma + \rho\beta^*(1-l+\chi)(g_5+o\delta)(g_2+\kappa)]\mu X(1-\mathcal{R}_m) \\ & + g_1g_2\omega\eta\delta[g_1g_2g_6 + g_1g_2\delta_m + g_1g_6\gamma + (g_6+o\delta_m)(g_2+\kappa)\rho\beta_m(1-l+\chi)]] \\ & - G_3[\rho\beta_m(1-l)g_1^2g_2^2\omega\eta\delta(g_6+o\delta_m) + \rho\beta^*(1-l)g_1g_2X(1-\mathcal{R}_m)(g_5+o\delta) \\ & + \chi^2\rho\beta_m l g_1^2g_2^2\omega\eta\delta(g_6+o\delta_m) + \chi^2\rho\beta^* l g_1g_2X(1-\mathcal{R}_m)(g_5+o\delta)] \\ & + (G_1+\chi G_2)[\rho\beta_m(1-l)g_1^2g_2^2\omega\eta\delta(g_6+o\delta_m) + \rho\beta^*(1-l)g_1g_2X(1-\mathcal{R}_m)(g_5+o\delta) \\ & + \chi\rho\beta_m l g_1^2g_2^2\omega\eta\delta(g_6+o\delta_m) + \chi\rho\beta^* l(g_5+o\delta)] + G_3(\chi g_1g_2X(1-\mathcal{R}_m)\varphi\delta \\ & + \chi g_1^2g_2^2\varphi_m\delta_m\omega\eta\delta + \chi\mu X(1-\mathcal{R}_m)[g_1g_5\gamma + \kappa\rho\beta^*(1-l+\chi)(g_5+o\delta)] \\ & + \chi g_1g_2\omega\eta\delta[g_1g_6\gamma + \kappa\rho\beta_m(1-l+\chi)(g_6+o\delta_m)\Big\} \times \nu_7\frac{(\kappa\nu+\varepsilon g_2)}{g_1g_2}\frac{\rho\beta^*\omega_7^2(1+\frac{\delta}{g_5})}{g_1g_2g_5\mu X(1-\mathcal{R}_m)}, \end{aligned} \tag{6}$$

where $G_1 = \frac{(1-l)\mu}{\pi N}$, $G_2 = \frac{l\mu}{\pi N}$, $G_3 = \frac{\mu}{\pi N}$ and

$$b = \nu_7\frac{(\kappa\nu+\varepsilon g_2)}{g_1g_2}\omega_7\rho(1-l+\chi l)\left(1+\frac{o\delta}{g_5}\right) > 0. \tag{7}$$

Since the bifurcation parameter b is positive, the system (1) or the transformed system (3) will undergo a backward bifurcation if the bifurcation coefficient a given by (6) is positive. Consider the case of the model (1) with $\chi = 0$. It is easy to show that, for this case, the expression of the backward bifurcation coefficient, a, given in (6) (and noting that all parameters of the model (1) are positive and $\beta^* > 0$), reduces to

$$\begin{aligned} a = \Big\{ & -(G_1[g_1g_2X(1-\mathcal{R}_m)\varphi\delta + g_1^2g_2^2\varphi_m\delta_m\omega\eta\delta + [2g_1g_2g_5 + 2g_1g_2\delta \\ & + g_1g_5\gamma + \rho\beta^*(1-l)(g_5+o\delta)(g_2+\kappa)]\mu X(1-\mathcal{R}_m) \\ & + g_1g_2\omega\eta\delta(g_1g_2g_6 + g_1g_2\delta_m + g_1g_6\gamma + (g_6+o\delta_m)(g_2+\kappa)\rho\beta_m(1-l))] \\ & - [\rho\beta_m(1-l)g_1^2g_2^2\omega\eta\delta(g_6+o\delta_m) + \rho\beta^*(1-l)g_1g_2(g_5+o\delta)X(1-\mathcal{R}_m)][G_3-G_1]\Big\} \\ & \times \nu_7\frac{(\kappa\nu+\varepsilon g_2)}{g_1g_2}\frac{\rho\beta^*\omega_7^2(1+\frac{\delta}{g_5})}{g_1g_2g_5\mu X(1-\mathcal{R}_m)} < 0, \end{aligned} \tag{8}$$

since $G_3 - G_1 > 0$.

This result remains the same whether $\mathcal{R}_m$ is less than unity or not. Thus, it follows from Theorem 4.1 in [1] that the model (1) does not undergo backward bifurcation in the case when $\chi = 0$. Hence, it is clear from Theorem 3.1 that the backward bifurcation phenomenon will not occur if immunity due to recovery from a previous infection via treatment and vaccination with BCG is life-long.

This work identifies the fact that there could be high endemic levels of tuberculosis infection in a population even when the associated reproduction number of the model in (1) is less than unity, hereby rendering the requirement that the reproduction number being less than unity, is only a necessary, but not sufficient, condition for disease eradication. The analysis above show that the presence of partial immunity in the model (1) in [7] (designed for simulating the highly endemic regions of the Asia-pacific) can trigger the occurrence of the backward bifurcation phenomenon, leading to the possibility of a stable, high endemic levels, even when model parameter values are indicative of the possibility of disease eradication. Hence, this study is suggesting that, in places where effort is being geared towards effective tuberculosis control and it seems that endemic levels are high, it is imperative to look out for factors that can allow for the possibility of a backward bifurcation in a model used to simulate the dynamics of the disease in such populations.

References

[1] Castillo-Chavez C. and Song B. (2004) *Dynamical models of tuberculosis and their application.* Mathematical Biosciences and Engineering, 2:361-404.

[2] Driessche van den P. and Watmough J. (2002) *Reproduction number and sub-threshold endemic equilibria for compartmental models of disease transmission.* Mathematical Biosciences, 180:29-48.

[3] Dushoff J., Wenzhang H. and Castillo-Chavez C. (1998) *Backwards bifurcations and catastroph in simple models of fatal diseases.* Journal of Mathematical Biology, 36:227-248.

[4] Gao J. and Zhao M.(2011) *Stability and bifurcation of an epidemic model with saturated treatment function.* Computing and Intelligent System, 234:306-315.

[5] Gumel A.B. (2012)*Causes of backward bifurcation in some epidemiological models.* Journal of Mathematical Anal Appl, 395:355-365.

[6] Hadeler K. and van den Driessche P. (1997) Backward bifurcation in epidemic models. Mathematical Biology, 146:15-35.

[7] James M.T. Justin T.D. and Emma S.M. (2014) *Construction of a mathematical model for tuberculosis transmission in highly endemic regions of the Asia-pacific.* Journal of Theoretical Biology, 358:74-84.

[8] Nazari F., Gumel A.B. and Elbasha E.H. (2015) *Differential characteristics of of primary-infection and re-infection can cause backward bifurcation in HCV transmission dynamics.* Mathematical Biosciences,263:51-69.

[9] Okuonghae D. and Omosigho S.E. (2011) *Analysis of a mathematical model for tuberculosis: what could be done to increase case detection.* Journal of Theoretical Biology, 269:31-45.

[10] Okuonghae D. and Ikhimwin B.O. (2016)*Dynamics of a mathematical model for tuberculosis with variability in susceptibility and disease progressions due to diffference in awareness level.* Frontiers in Microbiology, 6:1530. doi:10.3389/fmicb.2015.01530.

[11] Okuonghae D. and Aihie V. (2008). *Case detection and rirect observation therapy strategy (DOTS) in Nigeria: its effect on TB dynamics.* Journal of Biological Systems, 16(1): 1 - 31.

[12] Roumen A., Salisu M.G. and Salisu U. (2004) *Backward bifurcation analysis of epidemic model with partial immunity.* Computers and Mathematics with Application, 68(9):931-940.

[13] Wang W. (2006) *Backward bifurcation of an epidemic model with treatment.* Mathematical Biosciences, 201(1):58-71.

[14] Xue Y. and Wang J. *Backward bifurcation of an epidemic model with infectious force in the infected and immune period.* Abstract and Applied Analysis,doi:10.1155/2012/647853.