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A Compartmental Model on the Effect of Quarantine on MDR-TB

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Abstract

This paper presents a five compartmental deterministic model to study the effect of quarantine in managing multidrug-resistant tuberculosis (MDR-TB). We established that the model exhibits two equilibria; disease free equilibrium (DFE) and endemic equilibrium point (EEP). The DFE was shown to be locally asymptotically stable when the basic reproduction number, R_0 is less than unity ($R_0 < 1$). The global stability of both the DFE and EEP were established with the aid of constructed Lyapunov functions. We proved that the model undergoes backward bifurcation, which gives direction to the medical experts that keeping the basic reproduction number less than unity ($R_0 < 1$) is not enough to curtail the spread of the infection but rather think of other measures. The numerical simulation done gives a pictorial representation of the impact of quarantine in managing MDR-TB as it helps in reducing the disease incidence.

1 Introduction

In the 2018 global tuberculosis report of WHO, it was reported that a quarter of the world is infected with tuberculosis (TB) which is inclusive of dif-

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ferent TB strains like; drug susceptible TB, multidrug-resistant TB, extensively drug-resistant TB (XDR-TB) and totally drug-resistant TB (TDR-TB). MDR-TB was discovered in Great Britain in the year 1956 [1] but only gained attention as a public health threat in the 90's. MDR-TB is the strain of TB that gives resistance to at least isoniazid and rifampicin, which are the two most powerful anti-TB drugs. This is an infection that emerges usually when the anti-TB drugs are mismanaged (incomplete course of treatment) or misused (wrong dose or time length to complete the drugs) [3]. It can as well be transmitted from a carrier to a susceptible person.

The reported data of Matteo Zignol et al. (2016) [8] show the percentages of those diagnosed of MDR-TB as 62% in 2011 (Uzbekistan), 62.3% in 2012 (Moldova), 57.8% in 2013 (Kazakhstan), 55.1% in 2013 (Krygyzstan), 69.1% in 2014 (Belarus), 62.1% in 2014 (Estonia) and 52.2% in 2014 (Tajikistan). In the year 2017, there are 457,000 cases of MDR-TB reported globally with the most concentrations in India, China and Russian Federation constituting 47% of the total reported cases. With this figure of reported cases, there is still a wide gap between the detection and treatment rates of MDR-TB patients as just a paltry 25% of the reported cases got enrolled for treatment in the year 2017 [10]. Presently, there are two treatment regimens, varying based on the time length for the drugs administration; the shorter treatment regimen (with 7 drugs) [11] which is for the period of 9 months and longer treatment regimen (with 9 drugs) which is for the period of 18 months [12]. However, the efficacy of the 18 months regimen over that of the 9 months has been established. The treatment of multidrug-resistant TB (MDR-TB) and extensively drug resistant TB (XDR-TB) must be merged with measures to prevent drug susceptible TB, vis-á-vis early detection, completion of treatment and the administration of correct drugs combination among other measures, as a wider treatment coverage for MDR-TB will decrease MDR-TB incident [2]. The research of Ronoh et al. (2016) [7] further stress the importance of compliance with treatment instructions as doing otherwise would support the persistence of the infection.

In this work, we formulate a compartmental model with quarantine class to address the growing issues of multidrug-resistant TB. This is imperative as the tuberculosis menace is now multi-facetted, ranging from; drug susceptible TB, multidrug-resistant TB, extensively drug-resistant TB (XDR) and totally drug-resistant TB (TDR). The quarantine compartment is designed to monitor drug susceptible patients who may develop multidrug-resistant TB due to drugs maladministration. Adopting this method is mainly to prevent losing patients due to the absence of follow up, as it is in consonance

with the discussion in [5].
There are four (4) sections inclusive of this, which is followed by the model formulation section. The stability analysis is done in section 3 and the fourth section concludes it.

2 Model Formulation

2.1 Introduction

Human population is divided into five groups; susceptible S, infected asymptomatic individuals E (exposed), infected with symptoms I (infectious), individuals with multidrug-resistant TB Q and the recovered individuals R. The growth rate of the population is Π and the total population $N(t)$ at any time t is

$$N(t) = S(t) + E(t) + I(t) + Q(t) + R(t).$$

We assume the homogeneous mixing of susceptible individuals with the infectious ones as it is the contacts that lead to TB infection spread. The rate of infection is expressed as

$$\lambda_1 = \beta c I = \lambda N \tag{1}$$

where β is the probability of a susceptible individual getting infected and c is the per capita contact rate. Susceptible individuals can progress to the exposed state E at the rate $f\lambda_1$ or the infectious state I at the rate $(1-f)\lambda_1$. Exposed individuals progress to the I class either through endogenous reactivation k or exogenous reinfection $\delta\lambda_1$. Individuals infected of TB develop multidrug-resistant TB at the rate ω while treatment relapse to the quarantine class occur at the rate γ. The treatment success rate for both drug susceptible and multidrug-resistant TB infected individuals are σ and α respectively, while the death due to both drug susceptible TB and multidrug-resistant TB are ε_1 and ε_2 respectively. It is as well assumed that people die naturally at the rate μ and all parameter values declared are in the interval $[0, 1]$. The model is diagrammatically presented in Figure 1. The mathematical system describing the model is

$$\frac{dS}{dt} = \Pi - (\lambda_1 + \mu)S \tag{2}$$

$$\frac{dE}{dt} = f\lambda_1 S - (\delta\lambda_1 + k + \mu)E \tag{3}$$

$$\frac{dI}{dt} = (1-f)\lambda_1 S + (\delta\lambda_1 + k)E - (\sigma + \omega + \varepsilon_1 + \mu)I \tag{4}$$

$$\frac{dQ}{dt} = \omega I + \gamma R - (\alpha + \varepsilon_2 + \mu)Q \tag{5}$$

$$\frac{dR}{dt} = \sigma I + \alpha Q - (\gamma + \mu)R, \tag{6}$$

with the initial conditions

$$S(0) \geq 0, E(0) \geq 0, I(0) \geq 0, Q(0) \geq 0, R(0) \geq 0. \tag{7}$$

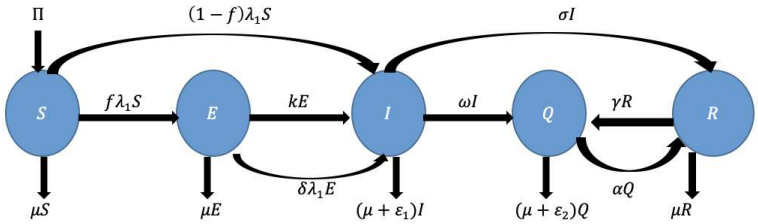

Figure 1: A quarantine model for tuberculosis

2.2 Positivity of the Solution and Invariant Region

The formulated model (nonlinear system (2)-(6)) above shall only be epidemiologically meaningful if all the variables are non-negative at any time t. Hence, the positivity of the model as well as its invariant region are thus established.

Lemma 1: Given that the initial conditions of (nonlinear system (2)-(6)) are as given in (7), then the solutions $S(t)$, $E(t)$, $I(t)$, $Q(t)$ and $R(t)$ are positive for all $t > 0$.

Proof: Suppose that $t^* = \sup\{t > 0 : S(t) > 0, E(t) > 0, I(t) > 0, Q(t) > 0, R(t) > 0\} \in [0, t]$, then $t^* > 0$. From the first equation of system (2)-(6),

$$\frac{dS}{dt} = \Pi - (\lambda_1 + \mu)S,$$

then we have

$$\frac{d}{dt}\left[S(t)e^{\left(\mu t + \int_0^t \lambda_1(\xi)d\xi\right)}\right] = \Pi e^{\left(\mu t + \int_0^t \lambda_1(\xi)d\xi\right)}$$

$$\Rightarrow S(t_1)e^{\left(\mu t_1+\int_0^{t_1}\lambda_1(\xi)d\xi\right)}-S(0)=\int_0^{t_1}\Pi e^{\left(\mu y+\int_0^{y}\lambda_1(\xi)d\xi\right)}dy$$

$$\Rightarrow S(t_1)=e^{-\left(\mu t_1+\int_0^{t_1}\lambda_1(\xi)d\xi\right)}\left[S(0)+\int_0^{t_1}\Pi e^{\left(\mu t_1+\int_0^{t_1}\lambda_1(\xi)d\xi\right)}dy\right]>0.$$

$E(t), I(t), Q(t)$ and $R(t)$ can similarly be shown to be positive.

Lemma 2: The biologically feasible region

$$\Omega=\left\{S(t),E(t),I(t),Q(t),R(t)\in\mathbb{R}_+^5 : S(t)+E(t)+I(t)+Q(t)+R(t)\leq\frac{\Pi}{\mu}\right\}$$

is positively invariant.

$$\frac{dN(t)}{dt}=\Pi-\mu N(t)-(\varepsilon_1 I+\varepsilon_2 Q),$$

so that

$$\frac{dN(t)}{dt}\leq\Pi-\mu N(t).$$

Hence, standard comparison theorem [9] can be used to show that $N(t)\leq N(0)e^{-\mu t}+\frac{\Pi}{\mu}(1-e^{-\mu t})$.

3 Stability Analysis

3.1 Local Stability of Disease-Free Equilibrium (DFE)

The DFE of the Model (nonlinear system (2)-(6)) is given by $E_0=\left(\frac{\Pi}{\mu},0,0,0,0\right)$. The linear stability of E_0 shall be established using the next generation operator method on the system. The matrices F (the new infection terms) and V (the transition terms) are respectively by

$$F=\begin{pmatrix}0 & f\beta S & 0\\ 0 & (1-f)\beta S & 0\\ 0 & 0 & 0\end{pmatrix} \tag{8}$$

and

$$V=\begin{pmatrix}k+\mu+\delta\lambda_1 & 0 & 0\\ -(k+\delta\lambda_1) & (\sigma+\omega+\varepsilon_1+\mu) & 0\\ 0 & \omega & (\alpha+\varepsilon_2+\mu)\end{pmatrix} \tag{9}$$

Evaluating (8) and (9) at the DFE and calculating for the spectral radius ρ of $FV^{-\prime}$ i.e. $\rho(FV^{-\prime})$ gives

$$\rho(FV^{-\prime}) = R_0 = \frac{\beta c\Pi[k+\mu(1-f)]}{\mu(k+\mu)(\sigma+\omega+\varepsilon_1+\mu)}. \tag{10}$$

Basic reproduction number (R_0) is the number of secondary infections from a single recorded one.

Theorem 1: The DFE, (E_0), of the model (1) is locally asymptotically stable in Ω if $R_0 < 1$, and unstable otherwise.

Proof: The Jacobian matrix (J_0) of the nonlinear system (2)-(6) at the DFE $\left(\frac{\Pi}{\mu}, 0, 0, 0, 0\right)$ is given by

$$J_0 = \begin{pmatrix} -\mu & 0 & -\frac{\beta c\Pi}{\mu} & 0 & 0 \\ 0 & -(k+\mu) & \frac{f\beta c\Pi}{\mu} & 0 & 0 \\ 0 & k & \frac{(1-f)\beta c\Pi}{\mu} - (\sigma+\omega+\varepsilon_1+\mu) & 0 & 0 \\ 0 & 0 & \omega & -(\alpha+\varepsilon_2+\mu) & \gamma \\ 0 & 0 & \sigma & \alpha & -(\gamma+\mu) \end{pmatrix}. \tag{11}$$

If the eigenvalue is denoted as η, then the eigenvalues of (11) shall be obtained from $|J_0 - I| = 0$,

$$\Rightarrow \begin{vmatrix} -(\mu+\eta) & 0 & -\frac{\beta c\Pi}{\mu} & 0 & 0 \\ 0 & -(k+\mu+\eta) & \frac{f\beta c\Pi}{\mu} & 0 & 0 \\ 0 & k & \frac{(1-f)\beta c\Pi}{\mu} - (\sigma+\omega+\varepsilon_1+\mu+\eta) & 0 & 0 \\ 0 & 0 & \omega & -(\alpha+\varepsilon_2+\mu+\eta) & \gamma \\ 0 & 0 & \sigma & \alpha & -(\gamma+\mu+\eta) \end{vmatrix} = 0. \tag{12}$$

Obviously, the first eigenvalue of the above equation is $-\mu$, while the remaining eigenvalues are as expressed below.

$$\eta_{2,3} = \frac{1}{4}\left(-(\alpha+2\varepsilon_2+3\mu) \pm \sqrt{\alpha^2+\alpha(4\varepsilon_2-2\mu)+(2\varepsilon_2+\mu)^2}\right) \tag{13}$$

and

$$\eta_{4,5} = \frac{1}{2\mu}\left(-b \pm \sqrt{b^2 - 4\mu^2(k+\mu)(\sigma+\omega+\varepsilon+\mu)\left\{1 - \frac{\beta c\Pi[k+\mu(1-f)]}{\mu(k+\mu)(\sigma+\omega+\varepsilon+\mu)}\right\}}\right), \tag{14}$$

where
$b = \mu[(k+\mu)+(\sigma+\omega+\varepsilon+\mu)] - \beta c\Pi(1-f)$.

For $\eta_{2,3}$ to be negative, it is required that

$$(\alpha + 2\theta + 3\mu) > \sqrt{\alpha^2 + \alpha(4\varepsilon_2 - 2\mu) + (2\varepsilon_2 + \mu)^2} \tag{15}$$

Squaring both sides of (15) and subsequently simplifying it gives

$$\alpha + \varepsilon_2 + \mu > 0,$$

which is always true, and as such, $\eta_{2,3} < 0$.
Also, since

$$R_0 = \frac{\beta c \Pi[k + \mu(1-f)]}{\mu(k+\mu)(\sigma + \omega + \varepsilon_1 + \mu)},$$

then (14) implies

$$\frac{-b \pm \sqrt{b^2 - 4\mu^2(k+\mu)(\sigma + \omega + \varepsilon + \mu)\{1 - R_0\}}}{2\mu}. \tag{16}$$

Since the eigenvalues of (16) depend on R_0, $R_0 < 1 \Rightarrow \eta_{4,5} < 0$ while $R_0 > 1 \Rightarrow \eta_4 > 0$ and $\eta_5 < 0$. Hence, $R_0 < 1$ guarantees the stability and as such completes the proof.

3.2 Global Stability of Disease-Free Equilibrium (DFE)

Theorem 2: The disease free equilibrium (DFE), E_0 of the model is globally asymptotically stable.

Proof: Consider the Lyapunov function

$$V_1 = (S - S^* - S^* \ln \frac{S}{S^*}) + E + I + Q + R, \tag{17}$$

$$V_1' = \frac{(S - S^*)}{S} S' + E' + I' + Q' + R' \tag{18}$$

$$\begin{aligned} \Rightarrow V_1' = \frac{(S - S^*)}{S}[\Pi - (\lambda_1 + \mu)S] + f\lambda_1 S - (\delta\lambda_1 + k + \mu)E + \\ (1-f)\lambda_1 S + (\delta\lambda_1 + k)E - (\sigma + \omega + \varepsilon_1 + \mu)I + \omega I \\ + \gamma R - (\alpha + \varepsilon_2 + \mu)Q + \sigma I + \alpha Q - (\gamma + \mu)R. \end{aligned} \tag{19}$$

$\lambda_1 = 0$

$$\Rightarrow V_1' = \frac{(S - S^*)}{S}[\Pi - \mu S] - \mu E - (\varepsilon_1 + \mu)I - (\varepsilon_2 + \mu)Q - \mu R \tag{20}$$

$$\Rightarrow V_1' = \frac{(S - S^*)}{S}\left[\mu S^* - \mu S\right] - \mu E - (\varepsilon_1 + \mu)I - (\varepsilon_2 + \mu)Q - \mu R \quad (21)$$

$$\Rightarrow V_1' = \frac{-\mu(S - S^*)^2}{S} - \mu E - (\varepsilon_1 + \mu)I - (\varepsilon_2 + \mu)Q - \mu R. \quad (22)$$

It is obvious from (22) that $V_1' \leq 0$ and the equality holds only when $S = S^*$. From the LaSalle's invariance principle [4], the DFE, E_0 of the model is globally asymptotically stable.

3.3 Bifurcation Analysis and Global Stability of Endemic Equilibrium Point (EEP)

3.3.1 Bifurcation Analysis

At equilibrium, then we have from (1),

$$\lambda_1^* = \beta c I^*, \quad (23)$$

as well as

$$S^* = \frac{\Pi}{\lambda_1^* + \mu},\ E^* = \frac{f\lambda_1^*\Pi}{(\lambda_1^* + \mu)(\delta\lambda_1^* + k + \mu)},\ I^* = \frac{(1-f)(\delta\lambda_1^* + k + \mu)\lambda_1^*\Pi + f\lambda_1^*\Pi(\delta\lambda_1^* + k)}{(\lambda_1^* + \mu)(\delta\lambda_1^* + k + \mu)(\sigma + \omega + \varepsilon_1 + \mu)}$$

$$Q^* = \frac{[\omega(\gamma + \mu) + \gamma\sigma][(1-f)(\delta\lambda_1^* + k + \mu) + f(\delta\lambda_1^* + k)]\lambda_1^*\Pi}{(\lambda_1^* + \mu)(\delta\lambda_1^* + k + \mu)(\sigma + \omega + \varepsilon_1 + \mu)[(\gamma + \mu)(\alpha + \varepsilon_2 + \mu) - \gamma\alpha]}$$

$$R^* = \frac{[\alpha(\sigma + \omega) + \sigma(\varepsilon_2 + \mu)][(1-f)(\delta\lambda_1^* + k + \mu) + f(\delta\lambda_1^* + k)]\lambda_1^*\Pi}{(\lambda_1^* + \mu)(\delta\lambda_1^* + k + \mu)(\sigma + \omega + \varepsilon_1 + \mu)[(\gamma + \mu)(\alpha + \varepsilon_2 + \mu) - \gamma\alpha]} \quad (24)$$

Substituting I^* into (23), it can be shown that the endemic equilibrium of the model satisfy the following quadratic equation

$$A(\lambda_1^*)^2 + B\lambda_1^* + C = 0, \quad (25)$$

where

$$A = \delta(\sigma + \omega + \varepsilon_1 + \mu)$$

$$B = (k + \mu + \mu\delta)(\sigma + \omega + \varepsilon_1 + \mu) - \beta c\delta\Pi$$

$$C = \mu(k + \mu)(\sigma + \omega + \varepsilon_1 + \mu) - \beta c\Pi[k + \mu(1 - f)].$$

As such, the positive EEP of nonlinear system (2)-(7) are obtained when (25) is solved for the values of λ_1 and subsequently substituted in (23) to obtain

I^*. The coefficient A is always positive and also, C is always positive when $R_0 < 1$ and negative when $R_0 > 1$. Hence, the following is established.

Theorem 3: The tuberculosis model has

1. a unique endemic equilibrium if $C < 0 \Leftrightarrow R_0 > 1$,
2. a unique endemic equilibrium if $B < 0$ and $C = 0$ or $B^2 - 4AC = 0$,
3. two endemic equilibria if $C > 0, B < 0$ and $B^2 - 4AC > 0$,
4. no endemic equilibrium otherwise.

Clearly, case 1 above indicates that the model has a unique endemic equilibrium point. On the other hand, case 3 is an indication of the possibility of backward bifurcation. Backward bifurcation is the scenario when locally asymptotically stable DFE coexists with a locally asymptotically EEP when $R_0 < 1$. The indication of this bifurcation is that keeping $R_0 < 1$ is no longer sufficient although required to tame TB spread. To check this, let the discriminant $B^2 - 4AC$ be zero, then solving for the critical value of R_0 (R_c) gives

$$R_c = 1 - \frac{B^2}{4A\mu(k+\mu)(\sigma+\omega+\varepsilon_1+\mu)}.$$

Lemma 3: The model undergoes backward bifurcation when case (3) of Theorem 3 holds and $R_c < R_0 < 1$. It is important to remark that the global asymptotic stability property of the DFE established earlier is only feasible outside the region of the backward bifurcation.

3.3.2 Global Stability of EEP

Theorem 4: The endemic equilibrium point $E_1 = \{S^*, E^*, I^*, Q^*, R^*\} \in \Omega$ of the nonlinear system (2)-(6) is globally asymptotically stable.

Proof: Using the method as discussed in [15] and [16], consider the Lyapunov function

$$V_2 = K_1(S - S^* - S^* \ln \frac{S}{S^*}) + K_2(E - E^* - E^* \ln \frac{E}{E^*}) + K_3(I - I^* - I^* \ln \frac{I}{I^*}), \tag{26}$$

then the time derivative of V is

$$V_2' = K_1 \left(\frac{S - S^*}{S}\right) \frac{dS}{dt} + K_2 \left(\frac{E - E^*}{E}\right) \frac{dE}{dt} + K_3 \left(\frac{I - I^*}{I}\right) \frac{dI}{dt}. \tag{27}$$

Substituting $\frac{dS}{dt}$, $\frac{dE}{dt}$ and $\frac{dI}{dt}$ as expressed in (2)-(4) in (27),

$$V_2' = K_1\left(\frac{S-S^*}{S}\right)[\Pi-(\lambda_1+\mu)S]+K_2\left(\frac{E-E^*}{E}\right)[f\lambda_1 S-\delta\lambda_1 E-(k+\mu)E]$$

$$+K_3\left(\frac{I-I^*}{I}\right)[(1-f)\lambda_1 S+(\delta\lambda_1+k)E-(\sigma+\omega+\varepsilon_1+\mu)I]. \tag{28}$$

At equilibrium, $\Pi = \beta c I^* S^* + \mu S^*$, $(k+\mu) = \frac{f\beta c I^* S^* - \delta\beta c I^* E^*}{E^*}$ and $(\sigma+\omega+\varepsilon_1+\mu) = \frac{(1-f)\beta c I^* S^* + \delta\beta c I^* E^* + kE^*}{I^*}$ which upon substitution into (28) gives

$$V_2' = K_1\left(\frac{S-S^*}{S}\right)[\beta c I^* S^* + \mu S^* - (\lambda_1+\mu)S]$$

$$+K_2\left(\frac{E-E^*}{E}\right)\left(f\lambda_1 S-\delta\lambda_1 E-\left[\frac{f\beta c I^* S^* - \delta\beta c I^* E^*}{E^*}\right]E\right)$$

$$+K_3\left(\frac{I-I^*}{I}\right)\left((1-f)\lambda_1 S+(\delta\lambda_1+k)E-\left[\frac{(1-f)\beta c I^* S^* + \delta\beta c I^* E^* + kE^*}{I^*}\right]I\right). \tag{29}$$

$$\Rightarrow V_2' = -K_1\mu\frac{(S-S^*)^2}{S} + K_1\left(1-\frac{S^*}{S}\right)[\beta c I^* S^* - \beta c I S]$$

$$+K_2\left(1-\frac{E^*}{E}\right)\left(f\lambda_1 S-\delta\lambda_1 E-\left[\frac{f\beta c I^* S^* - \delta\beta c I^* E^*}{E^*}\right]E\right)$$

$$+K_3\left(1-\frac{I^*}{I}\right)\left((1-f)\lambda_1 S+(\delta\lambda_1+k)E-\left[\frac{(1-f)\beta c I^* S^* + \delta\beta c I^* E^* + kE^*}{I^*}\right]I\right). \tag{30}$$

Let $\frac{S}{S^*} = x_1$, $\frac{E}{E^*} = x_2$, $\frac{I}{I^*} = x_3$, $I^*S^* = a$, $I^*E^* = b$ and $kE^* = g$. Then simplifying (30) gives

$$-K_1\mu\frac{(S-S^*)^2}{S} + K_1\beta ca + [-K_1\beta ca + K_2 f\beta ca + K_3(1-f)\beta ca]\,x_1x_3 +$$

$$[-K_2\delta\beta cb + K_3\delta\beta cb]x_2x_3$$

$$+[K_2\delta\beta cb - K_3(1-f)\beta ca - K_3\delta\beta cb - K_3 g + K_1\beta ca]x_3$$

$$+[-K_2 f\beta ca - K_3\delta\beta cb + K_3 g - K_2\delta\beta cb]x_2$$

$$-(1-f)\beta ca x_1 - K_1\frac{1}{x_1} - K_2 f\beta ca\frac{x_1x_3}{x_2} - g\frac{x_2}{x_3}$$

$$+f\beta ca + (1-f)\beta ca + 2\delta\beta cb + g. \tag{31}$$

The values of K_1, K_2, K_3, g and δ are gotten by equating the coefficients of x_1x_3, x_2x_3, x_3, x_2 and x_1 to 0. This gives $K_1 = K_2 = K_3$; $f = 1$; $g = \beta ca$; $\delta = 0$.

Choosing the value of $K_1 = K_2 = K_3 = 1$ and substituting the values of f, g and δ gives

$$V_2' = \frac{-\mu(S-S^*)^2}{S} + \beta ca\left[3 - \frac{1}{x_1} - \frac{x_1x_3}{x_2} - \frac{x_2}{x_3}\right]. \tag{32}$$

Since arithmetic mean (AM) is greater than or equal to geometric mean (GM)
$[AM \geq GM]$, then

$$\frac{1}{x_1} + \frac{x_1x_3}{x_2} + \frac{x_2}{x_3} \geq 3.$$

It can be seen from (32) that $V_2' \leq 0$ for which the equality holds when $x_1 = x_2 = x_3 = 1$ (which implies $S = S^*$, $E = E^*$ and $I = I^*$). From the LaSalle's invariance principle [4], the endemic equilibrium point EEP is globally asymptotically stable.

3.4 Sensitivity Analysis and Numerical Simulation

3.4.1 Sensitivity Analysis

The measure of the behavior of an infection is basically through the basic reproduction number (R_0). The R_0 of the model is partially differentiated with respect to its parameters so as to understand the effect of each in the incident of the infection. The parameters involved are $\Pi, \beta, c, k, f, \mu, \sigma, \omega$ and ε_1. Positive results indicate the parameter helps in increasing the incident of the disease while negative results do the opposite.

$$\frac{\partial R_0}{\partial \Pi} = \frac{\pi\beta c((1-f)\mu + k)}{\mu(k+\mu)(\sigma+\omega+\varepsilon_1+\mu)},$$

$$\frac{\partial R_0}{\partial \beta} = \frac{\pi c((1-f)\mu + k)}{\mu(k+\mu)(\sigma+\omega+\varepsilon_1+\mu)},$$

$$\frac{\partial R_0}{\partial c} = \frac{\pi\beta((1-f)\mu + k)}{\mu(k+\mu)(\sigma+\omega+\varepsilon_1+\mu)}$$

$$\frac{\partial R_0}{\partial k} = \frac{\pi\beta cf}{(k+\mu)^2(\sigma+\omega+\varepsilon_1+\mu)},$$

$$\frac{\partial R_0}{\partial f} = -\frac{\pi\beta c}{(k+\mu)(\sigma+\omega+\varepsilon_1+\mu)}$$
$$\frac{\partial R_0}{\partial \sigma} = -\frac{\pi\beta c((1-f)\mu+k)}{\mu(k+\mu)(\sigma+\omega+\varepsilon_1+\mu)^2}$$

$$\frac{\partial R_0}{\partial \omega} = -\frac{\pi\beta c((1-f)\mu+k)}{\mu(k+\mu)(\sigma+\omega+\varepsilon_1+\mu)^2}, \frac{\partial R_0}{\partial \varepsilon_1} = -\frac{\pi\beta c((1-f)\mu+k)}{\mu(k+\mu)(\sigma+\omega+\varepsilon_1+\mu)^2}$$

3.4.2 Numerical Simulation

This section presents the numerical results gotten after simulating the model. Impacts of some of the key parameters that are sensitive to change (as shown in the sensitivity analysis) are tested and the resulting graphs are presented below. The hypothetical values of the variables and parameters are $S = 8000, E = 1000, I = 500, Q = 300, R = 200, \alpha = 0.5, \beta = 0.35, c = 80, \delta = 0.7, \varepsilon_1 = 0.3, \varepsilon_2 = 0.1, f = 0.99, \gamma = 0.1, k = 0.00013, \Pi = 0.03, \sigma = 0.85, \omega = 0.8, \mu = 0.01$.

Figures 2-5 are further corroborating the results gotten in section 3.4.1. The rate of change of R_0 with respect to Π, β, c and k is positive while it is negative with respect to f, σ, ω and ε_1. The positive results indicate the wilder spread of the infection while the negative ones give hints on the possible control of the infection.

Figure 2 explains that the more people get recruited into the population, the more the possible spread of MDR-TB. The case is the same for β (infectivity probability) i.e., the higher the probability, the higher the recorded cases of the infection as displayed in Figure 3. It should be further noted that lower β value leads to sharp reduction in the quarantine compartment where the MDR-TB patients are housed.

f (direct progression from S to E) on the other hand does the opposite. If all the infected individuals are to pass through the exposed class E without direct progression to I, the infection is liable to be kept under control as explained in Figure 4. The same trend is maintained when ω (probability of developing MDR-TB) is varied. Although, it would be expected that higher values of ω keep the infection out of control, but it is actually explaining the role of quarantine in curbing the spread of the infection as displayed in Figure 5. When patients that develop MDR-TB are left to mingle freely with the general public, there shall be higher probability of the spread of MDR-TB. However, keeping them in quarantine class do two things; keeping the general public safe from contracting MDR-TB and also, keeping the MDR-TB

patients under watch in taking their drugs as instructed due to the long drug administration period.

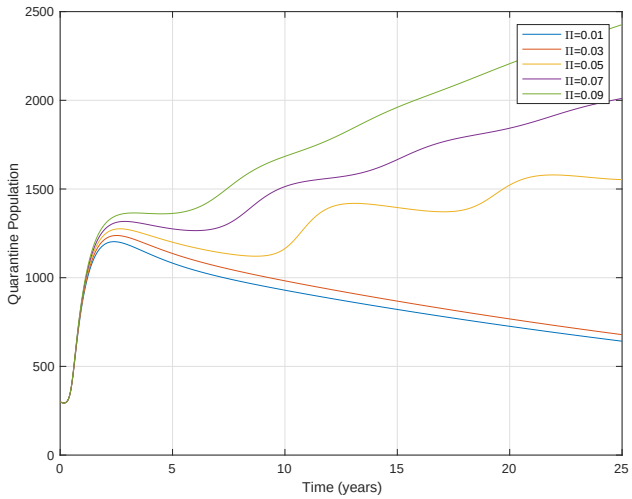

Figure 2: Effect of Π (recruitment rate) on Q

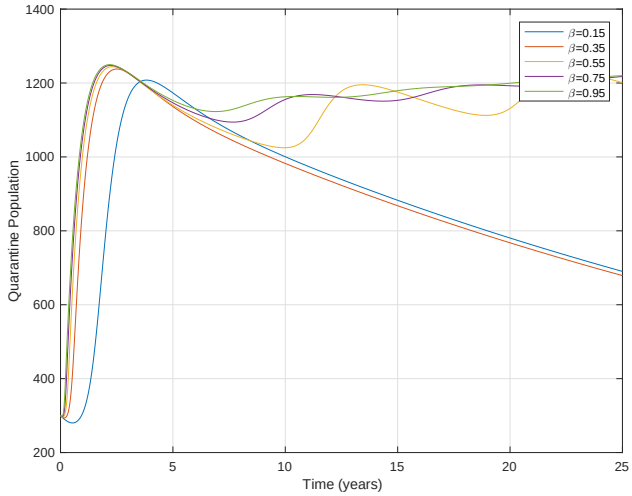

Figure 3: Effect of β (probability of infectivity) on Q

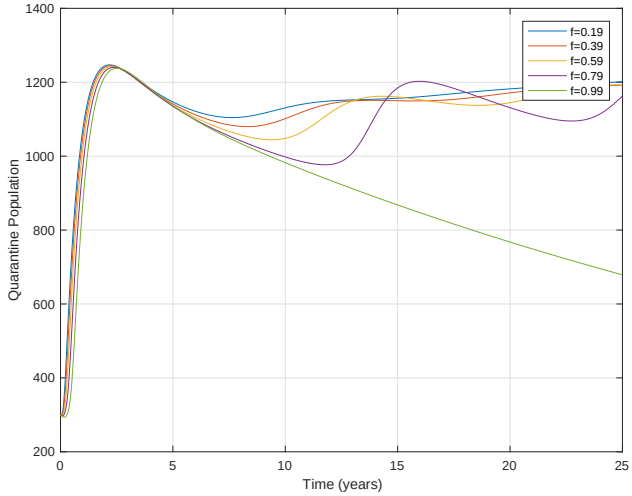

Figure 4: Effect of f (progression from S to E) on Q

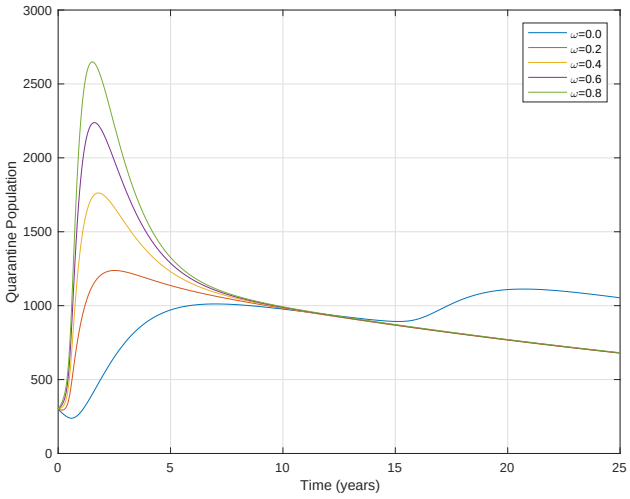

Figure 5: Effect of ω (progression from I to Q) on Q

4 Summary

This paper presents a five compartment model (susceptible, exposed, infectious, quarantine and recovered) to discuss the effect of quarantine on addressing the spread of multidrug-resistant TB, as there are not much researches regarding the use of quarantine in addressing the disease incidence presently. We established the local and global stabilities of both the disease free equilibrium (DFE) points and endemic equilibrium points (EEP) and further proved that the model undergoes backward bifurcation. This means that more is needed to be done to address the disease incidence as keeping the basic reproduction number, $R_0 < 1$ is not sufficient to curb the wild spread of MDR-TB. The numerical simulation done shows that quarantine has quite an impact in curbing the spread of disease as the results show reasonable reduction in the MDR-TB cases.
Generally, tuberculin skin test should be encouraged in communities that are prone to TB infection so as to ascertain the medical fitness of any individual residing in such community as discussed in [14].

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