

ANALYZING THE TRANSMISSION DYNAMICS OF TUBERCULOSIS IN KADUNA METROPOLIS, NIGERIA

M. K. Dauda^{1*}, A. S. Magaji¹, P.N. Okolo¹, J. Bulus¹, U. S. Shehu²

¹Department of Mathematical Sciences, Kaduna State University, Kaduna, Nigeria.

²Department of Mathematics and Statistics, Kaduna Polytechnic, Kaduna, Nigeria.

*Corresponding Author's Email Address: mkdika@kasu.edu.ng

ABSTRACT

A mathematical model for the transmission dynamics of tuberculosis in Kaduna metropolis, is formulated and analysed. For the prevalence of the disease, the model was considered in proportions of susceptible, exposed, infectious and recovered compartments. The disease-free equilibrium (DFE) and Endemic Equilibrium (EE) states of the model in proportions were obtained and DFE state was used to compute the basic reproduction number R_0 , as important threshold whose values allow to establish whether an infection will spread in a population or not. The stability analysis shows that the disease-free equilibrium is locally and globally asymptotically stable whenever the basic reproduction number is less than unity using Routh – Hurwitz stability criterion and Lyapunov function respectively. It is further proved using Routh-Hurwitz that the endemic equilibrium state is locally asymptotically stable whenever the basic reproduction number is greater than unity. The computed results of the basic reproduction number R_0 estimated to be 1.0623, as well as the stability analysis revealed that tuberculosis infection will remain endemic (persist) in Kaduna metropolis. Furthermore, effective control measures such as expanded and regular immunization campaign will decrease the infection burden.

Keywords: Tuberculosis, Equilibria, Reproduction Number, Stability, Routh-Hurwitz Criterion, Lyapunov Function

1. INTRODUCTION

Tuberculosis (TB) has recently re-emerged as a major global health concern. However, TB has been plaguing humanity for centuries before this, with the earliest documentation of TB occurring in Egypt as early as 5000 years ago, based on the isolation of *Mycobacterium tuberculosis* DNA from mummies (Daniel, 2006; Methema et al., 2006). TB has remained one of the most challenging infectious diseases that humankind faces (Adepoju, 2020).

Tuberculosis (TB) is caused by bacteria (*Mycobacterium tuberculosis*) that most often affect the lungs but TB bacteria can affect any part of the body such as kidney, spine, and brain (CDC, 2019; WHO, 2020). TB is spread from person to person through the air. When people with TB disease of the lungs or throat cough, speak, sing, sneeze or spit, they propel the TB germs into the air. A person needs to inhale only a few of these germs to become infected. General signs and symptoms include fever, chills, night sweats, loss of appetite, weight loss, and fatigue, and significant finger clubbing may also occur (CDC, 2019; Dye, 2006). About one-quarter of the world population has a TB infection, which means people have been infected by TB bacteria but not (yet) ill with the disease and cannot transmit it. People infected with TB bacteria have a 5 – 15% lifetime risk of falling ill with TB. Those with

compromised immune system such as people living with HIV, malnutrition or diabetes, or people who use tobacco, have a higher risk of falling ill (WHO, 2019). People with active TB can infect 5 – 15 other people through close contact over the course of a year.

In 2017, about 1.7 million people including over 250,000 children globally, died of TB-related causes. Over 95% of TB deaths occur in low and middle-income countries especially in Africa (CDC, 2019). TB occurs in every part of the world. In 2019, the largest number of new TB cases occurred in the WHO South-East region, with 44% of new cases, followed by the WHO African region, with 25% of the new cases and the WHO Western Pacific with 18% (CDC, 2019).

According to the 2017 Global TB Report (WHO, 2017), Nigeria is among the 14 high burden countries for TB, TB/HIV and MDR-TB, ranking 7th among the 30 high TB burden countries and 2nd in Africa. TB kills 18 Nigerians every hour. Forty-seven Nigerians develop active TB, seven of which are children, every hour. One of the major challenges of TB response in Nigeria is attributed to low TB case finding both in adult and children. This is partly attributed to poor knowledge about TB and it influenced the health seeking behaviour of people and low TB treatment coverage.

Nigeria is struggling with increasing incidence of tuberculosis cases and suboptimal coverage of diagnosis services (Adepoju, 2020). Nigeria has the highest tuberculosis burden in Africa and one of the world's widest gap between estimated and reported cases according to the recently released Global TB Report 2019 (WHO, 2019).

A comparison of the reports for 2018 and 2019 showed the disease burden is increasing in Nigeria in sharp contrast with the improving global outlook. Tuberculosis incidences rose in Nigeria from 418000 in 2017 to 429000 cases in 2018, and deaths also rose from 155000 to 157000 within the same period, with tuberculosis treatment coverage stagnant at 24% (NTLCP, 2019).

A number of mathematical modelling studies have been carried out in recent time to quantify Tuberculosis (TB) infection burden. For instance, Koriko and Yusuf (2008) considered the dynamics of the tuberculosis disease population using SIRS model. Results from their study showed that the population dynamics depends more on the number of actively infected people in the population at the initial time and also on the disease incidence transmission rate at a given time. Okuonghae (2013) presented a novel and realistic mathematical model that incorporate genetic heterogeneity into the tuberculosis epidemiology. From the result, it was shown that if a large fraction of susceptible individuals that have no or partial resistance to TB gets infected and move into the class of normal progressors, then the disease can be managed with effective and complete treatment and little incidence of self-cure. Jerubet et al., (2019) developed a mathematical model that explains the transmission of Tuberculosis. The result of model which consists of

four compartments showed that as more people come into contact with infectious individuals, the spread of the TB would increase. Nayeem and Sultana (2019) developed a dynamical model to understand the underlying dynamics of Tuberculosis infection at the population level. The mathematical analysis reveals that the model exhibits a backward bifurcation when TB treatment remains in the infected class. Mettle *et al*, (2020) employed a SEIR epidemics model with demography for both deterministic and stochastic terms to model tuberculosis dynamics among high-burden districts. The deterministic model showed success in modelling TB infection in the region to the transmission dynamics of the stochastic SEIR model over time.

Nonetheless, only few studies have been carried out in Nigeria to explore tuberculosis infection using SEIR models. Enagi *et al*, (2017) modelled the effect of combining immunization with latent tuberculosis treatment in controlling the spread of Tuberculosis in Nigeria. Their results show that the disease-free equilibrium state will be stable if effort is intensified in bringing down both the contraction rate and the rate of break down to infectious Tuberculosis. Ahmad *et al*, (2018) proposes a mathematical model to evaluate TB burden in Nigeria by using data obtained from the local TB control program in the community. The results show that effort should be oriented to move active case finding rather than increasing the treatment effectiveness only. It also reveals that the persistence of the disease is related to a large number of latently infected individuals and quantifies the lives that could be saved by increasing notification rate using active finding strategy. Akinrafon and Adejumo (2019) formulated a continuous two Markov process model for TB dynamics with the introduction impact in the susceptible and the exposed classes. Their results on the sensitivity analysis on the impact of key parameters, showed that intervention efforts at 50% - 85% effectively reduce TB incidence despite reinfection of recovered individuals. However, in Kaduna State of Nigeria, no mathematical modelling study employing the SEIR model with demography to determine whether or not TB will become endemic or not in the population.

Consequently, this current study employs SEIR compartmental model in investigating Tuberculosis (TB) infection transmission dynamics in Kaduna Metropolis, incorporating basic demography. Moreover, computation of the basic reproduction number was established using the next generation matrix operator. Stability of the equilibrium points was established using Routh-Hurwitz stability criterion. Numerical results for the basic reproduction number and herd immunity threshold were investigated using data obtained from the Tuberculosis Medical Centre, Kaduna.

2. MATERIALS AND METHODS

In this section, a mathematical model for tuberculosis transmission is described in respect of the epidemiological dynamics of the disease in the Kaduna Metropolis of Kaduna State. This model will help in predicting the transmission of the disease and to determine effective ways of controlling it in the Kaduna metropolis. Since we are dealing with a large population, a deterministic or compartmental mathematical model is used. In the deterministic model, individuals in the population are assigned to different subgroups or compartments, each representing a specific stage of the epidemic. The standard Susceptible-Exposed-Infected-Removed (SEIR) epidemiological models are utilized to study and analyze the disease. Thus, the simple SEIR model is used to explain the spread of tuberculosis in Kaduna Metropolis of Kaduna State.

Model Assumptions and Definition of Variables and Parameters

The following assumptions are considered while building the model;

- Age, sex, social status, race coupled with climatic conditions in the metropolis does not affect the probability of an individual being infected.
- The birth and deaths occur at equal rates.
- We assume that once an individual is infected, the person becomes exposed to the disease before becoming infectious.
- The disease is transmitted in a closed environment and there is no emigration or immigration. Thus, the total population, N of individuals in the metropolis remains constant.
- Individuals are likely to be infected by the infectious individuals in case of contact except those who are immune.
- Those that recovered become immune and are educated about the transmission of the disease. The transmission of the disease within the sanatorium is neglected.

The variables and parameters used in the model are defined in Table 1.

Table 1: Variables and Parameters used in the model and their description

Variable/Parameter	Description
$S(t)$	The number of susceptible individuals in the population at time t
$E(t)$	The number of exposed individuals in the population at time t
$I(t)$	The number of infectious individuals in the population at time t
$R(t)$	The number of recovered individuals in the population at time t
β	Infection transmission rate
τ	Loss of latency rate
ρ	Recovery rate
μ	Recruitment/Natural death rate

From the above assumptions, definition of variables and parameters, the interactions and flow in the different compartments are as depicted in the schematic flow diagram below.

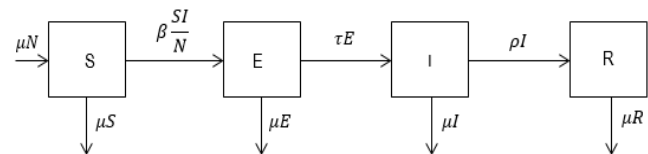


Figure 1: Flow chart showing the SEIR model

The susceptible population $S(t)$, is generated by birth of individuals into the population at the rate μ , and it is reduced by infection rate β . The susceptible population is further reduced by natural death at the rate μ . Putting all these assumptions and definition together gives the rate of change of the susceptible population as

$$\frac{dS}{dt} = \mu N - \beta \frac{IS}{N} - \mu S.$$

The population of exposed (latent) humans $E(t)$ is generated following infection (at the rates β . They are decreased as a result of progression into the infectious class (loss of latency) at the rate τ , and natural death at the rate μ , so that

$$\frac{dE}{dt} = \beta \frac{IS}{N} - (\tau + \mu)E.$$

Infectious humans I are generated as a result of progression into

the infected class from the exposed class at the rate τ . It is diminished by recovery at the rate ρ , and natural death at the rate μ . Hence,

$$\frac{dI}{dt} = \tau E - (\rho + \mu)I.$$

The population of recovered individuals $R(t)$ are generated as a result of recovery of infectious individuals at the rate ρ , they are decreased by natural death rate μ . Hence,

$$\frac{dR}{dt} = \rho I - \mu R.$$

The Model Equations

The above assumptions and formulations lead to the following system of ordinary differential equations:

$$\frac{dS}{dt} = \mu N - \beta \frac{IS}{N} - \mu S. \quad (1)$$

$$\frac{dE}{dt} = \beta \frac{IS}{N} - (\tau + \mu)E. \quad (2)$$

$$\frac{dI}{dt} = \tau E - (\rho + \mu)I. \quad (3)$$

$$\frac{dR}{dt} = \rho I - \mu R. \quad (4)$$

$$S(0) = S_0 > 0, E(0) = E_0 > 0, I(0) = I_0 > 0 \text{ and } R(0) = R_0 > 0 \quad (5)$$

The Model Equations in terms of proportions

For prevalence of the disease, it is necessary to consider the model in terms of proportions of susceptible, exposed, infectious and recovered compartments.

Adding equations (1) – (4) gives the rate of change of the total population as

$$\frac{dN}{dt} = \mu N - \mu N = 0 \quad (6)$$

the proportion for each class are defined as follows:

$$s = \frac{S}{N}, e = \frac{E}{N}, i = \frac{I}{N}, r = \frac{R}{N}$$

Using equation (1) and equation (6) yields

$$\begin{aligned} \frac{ds}{dt} &= \frac{d\left(\frac{S}{N}\right)}{dt} = \frac{1}{N} \frac{dS}{dt} - \frac{S}{N^2} \frac{dN}{dt} \\ &= \frac{1}{N} \left(\mu N - \beta \frac{IS}{N} - \mu S \right) - \frac{S}{N^2} (0) \\ &= \mu - (\mu + \beta i)s \end{aligned} \quad (7)$$

Using equation (2) and equation (6) gives

$$\begin{aligned} \frac{de}{dt} &= \frac{d\left(\frac{E}{N}\right)}{dt} = \frac{1}{N} \frac{dE}{dt} - \frac{E}{N^2} \frac{dN}{dt} \\ &= \frac{1}{N} \left(\beta \frac{IS}{N} - (\tau + \mu)E \right) - \frac{E}{N^2} (0) \\ &= \beta si - (\mu + \epsilon)e \end{aligned} \quad (8)$$

Using equation (3) and equation (6) gives

$$\begin{aligned} \frac{di}{dt} &= \frac{d\left(\frac{I}{N}\right)}{dt} = \frac{1}{N} \frac{dI}{dt} - \frac{I}{N^2} \frac{dN}{dt} \\ &= \frac{1}{N} (\tau E - (\rho + \mu)I) - \frac{I}{N^2} (0) \\ &= \tau e - (\mu + \rho)i \end{aligned} \quad (9)$$

Using equation (4) and equation (6) yields

$$\begin{aligned} \frac{dr}{dt} &= \frac{d\left(\frac{R}{N}\right)}{dt} = \frac{1}{N} \frac{dR}{dt} - \frac{R}{N^2} \frac{dN}{dt} \\ &= \frac{1}{N} (\rho I - \mu R) - \frac{R}{N^2} (0) \\ &= \gamma i - \mu r \end{aligned} \quad (10)$$

Thus the system (1) – (4) expressed in proportion is given below:

$$\frac{ds}{dt} = \mu - (\mu + \beta i)s \quad (7)$$

$$\frac{de}{dt} = \beta si - (\mu + \tau)e \quad (8)$$

$$\frac{di}{dt} = \tau e - (\mu + \rho)i \quad (9)$$

$$\frac{dr}{dt} = \gamma i - \mu r \quad (10)$$

We have $0 \leq s, 0 \leq e, 0 \leq i, 0 \leq r$ and $s + e + i + r \leq 1$. Since $r = 1 - s - e - i$, it is enough to consider the first three equations of the system (1) – (4), and the new system becomes

$$\frac{ds}{dt} = \mu - (\mu + \beta i)s \quad (11)$$

$$\frac{de}{dt} = \beta si - (\mu + \tau)e \quad (12)$$

$$\frac{di}{dt} = \tau e - (\mu + \rho)i \quad (13)$$

The set $\Omega = \{(s, e, i) : s \geq 0, e \geq 0, i \geq 0, s + e + i \leq 1\}$ is a positively compact set for the system (11) – (13). The system is well posed.

Equilibrium states

We consider the equilibrium states in absence of infection as well as in the presence of infection namely, the disease-free equilibrium (DFE) state and the endemic equilibrium (EE) state.

This is achieved by setting the right hand sides of equations (11) – (13) to zero and solving the resulting nonlinear systems.

Thus

$$\mu - (\mu + \beta i)s = 0 \quad (14)$$

$$\beta si - (\mu + \tau)e = 0 \quad (15)$$

$$\tau e - (\mu + \rho)i = 0 \quad (16)$$

Equations (16) implies that

$$e^* = \frac{(\mu + \rho)i}{\tau} \quad (17)$$

Substituting the value of e^* , into equation (15) yields

$$\begin{aligned} \beta si - \frac{(\mu + \tau)(\mu + \rho)i}{\tau} &= 0 \\ i \left(\beta s - \frac{(\mu + \tau)(\mu + \rho)}{\tau} \right) &= 0 \\ \Rightarrow i^* = 0 \text{ or } s &= \frac{(\mu + \tau)(\mu + \rho)}{\tau \beta} \end{aligned}$$

For $i^* = 0$

Substituting the value $i^* = 0$ into equations (17) and (14) gives $e^* = 0$ and $s^* = 1$

Thus the disease free equilibrium state is given by

$$\mathcal{E}_0 = (s^*, e^*, i^*, r^*) = (1, 0, 0, 0) \quad (18)$$

$$\text{For } i^* \neq 0 \Rightarrow s^{**} = \frac{(\mu + \tau)(\mu + \rho)}{\tau \beta} \quad (19)$$

Substituting the value of s^{**} into equation (14) gives

$$\begin{aligned} \mu - (\mu + \beta i) \frac{(\mu + \tau)(\mu + \rho)}{\tau \beta} &= 0 \\ \mu \tau \beta - \mu(\mu + \tau)(\mu + \rho) - \beta i^{**}(\mu + \tau)(\mu + \rho) &= 0 \\ \beta i^{**}(\mu + \tau)(\mu + \rho) &= \mu \tau \beta - \mu(\mu + \tau)(\mu + \rho) \\ i^{**} &= \frac{\mu \tau}{(\mu + \tau)(\mu + \rho)} - \frac{\mu}{\beta} \\ i^{**} &= \frac{\mu}{\beta} \left(\frac{\tau \beta}{(\mu + \tau)(\mu + \rho)} - 1 \right) \end{aligned} \quad (20)$$

Substituting the value of i^{**} into equations (17) gives

$$\begin{aligned} e^{**} &= \frac{\mu(\mu + \rho)}{\tau \beta} \left(\frac{\tau \beta}{(\mu + \tau)(\mu + \rho)} - 1 \right) \\ (21) \end{aligned}$$

The endemic equilibrium (EE) state is given by

$$\mathcal{E}_1 = (s^{**}, e^{**}, i^{**}, r^{**}) =$$

$$\left(\frac{(\mu+\tau)(\mu+\rho)}{\tau\beta}, \frac{\mu(\mu+\rho)}{\tau\beta} \left(\frac{\tau\beta}{(\mu+\tau)(\mu+\rho)} - 1 \right), \frac{\mu}{\beta} \left(\frac{\tau\beta}{(\mu+\tau)(\mu+\rho)} - 1 \right) \right) \quad (22)$$

Basic Reproduction Number R_0

The basic reproduction number or reproductive number of an infectious disease is the average number of secondary infections when one infected individual is introduced into a host population where everyone is susceptible (Diekmann et al., 1990; Diekmann et al., 2010). We use the next generation matrix approach to compute the Basic Reproduction Number R_0 .

The associated non-negative matrix F , for the new infective terms and the non-singular M -matrix, V , for the remaining transfer terms at the DFE are respectively given by

$$F = \begin{pmatrix} 0 & \beta \\ 0 & 0 \end{pmatrix}$$

and

$$V = \begin{pmatrix} (\mu + \tau) & 0 \\ -\tau & (\mu + \rho) \end{pmatrix}$$

Now

$$V^{-1} = \begin{pmatrix} \frac{1}{(\mu+\tau)} & 0 \\ \frac{\tau}{(\mu+\tau)(\mu+\rho)} & \frac{1}{(\mu+\rho)} \end{pmatrix}$$

So that

$$FV^{-1} = \begin{pmatrix} \frac{\tau\beta}{(\mu+\tau)(\mu+\rho)} & \frac{\beta}{(\mu+\rho)} \\ 0 & 0 \end{pmatrix}$$

It follows that the basic reproduction number, which is the leading eigenvalue of the matrix FV^{-1} , denoted by R_0 , is given by (where ρ denotes the spectral radius)

$$R_0 = \rho(FV^{-1}) = \frac{\tau\beta}{(\mu+\tau)(\mu+\rho)} \quad (23)$$

Local Stability of Disease Free Equilibrium (DFE) State

We investigate the local stability of the disease free (DFE) state by evaluating the associated Jacobian of equations (11) – (14) at the DFE state. The Jacobian matrix J for the system (14) – (16), evaluated at the disease-free equilibrium, \mathcal{E}_0 , is given by

$$J(\mathcal{E}_0) = \begin{pmatrix} -\mu & 0 & -\beta \\ 0 & -(\mu + \tau) & \beta \\ 0 & \tau & -(\mu + \rho) \end{pmatrix} \quad (24)$$

Theorem 1: The DFEs of the model (14) – (16), given by \mathcal{E}_0 , is locally asymptotically stable (LAS) if $R_0 < 1$ and \mathcal{E}_0 is unstable if $R_0 > 1$.

Proof

It suffices to show that all the eigenvalues of the characteristic equation of the Jacobian matrix $J(\mathcal{E}_0)$, have negative real parts. The Routh-Hurwitz stability criterion (Hurwitz, 1964) will be used to determine the sign of the eigenvalues.

The characteristic polynomial of $J(\mathcal{E}_0)$ is given by

$$P(\lambda) = (-\mu - \lambda)[(-\tau + \mu) - \lambda][(-\rho + \mu) - \lambda] - \tau\beta \\ = (-\mu - \lambda)[(\tau + \mu)(\rho + \mu) + \lambda(\tau + \mu) + \lambda(\rho + \mu) + \lambda^2 - \tau\beta]$$

that is

$$P(\lambda) = (-\mu - \lambda)[\lambda^2 + \lambda(\tau + \rho + 2\mu) + (\tau + \mu)(\rho + \mu) - \tau\beta] \quad (25)$$

Then the eigenvalue of the matrix $J(\mathcal{E}_0)$ is

$$\lambda = -\mu$$

And the root of the polynomial

$$q(\lambda) = \lambda^2 + A\lambda + B \quad (26)$$

Where

$$A = (\tau + \rho + 2\mu)$$

$$B = (\tau + \mu)(\rho + \mu) - \tau\beta$$

$$= (\tau + \mu)(\rho + \mu) \left(1 - \frac{\tau\beta}{(\tau + \mu)(\rho + \mu)} \right)$$

$$= (\tau + \mu)(\rho + \mu)(1 - R_0) \quad (27)$$

For $R_0 < 1$, we have $A > 0$ and $B > 0$, and thus following Routh-Hurwitz stability criterion (Hurwitz, 1964) for the polynomial $P(\lambda)$, the state \mathcal{E}_0 is locally asymptotically stable whenever $R_0 < 1$.

Global Asymptotic Stability (GAS) of Disease Free Equilibrium (DFE) State

To ensure that the tuberculosis infection eradication is independent of initial sizes of the population of the model, it is imperative to show that the DFE of the model (14) – (16), given by \mathcal{E}_0 , is globally asymptotically stable (GAS). This is done now.

Theorem 2: The DFE of model (14) – (16), given by Ω_0 is GAS whenever $R_0 \leq 1$.

Proof

Consider the Lyapunov function

$$F = \tau e + (\tau + \mu)i, \quad (28)$$

with Lyapunov derivative (where a prime represents differentiation with respect to t)

$$F' = \tau[\beta si - (\mu + \tau)e] + (\tau + \mu)[\tau e - (\mu + \rho)i] \\ = \tau\beta s^*i - (\tau + \mu)(\rho + \mu)i$$

$$= [\tau\beta s^* - (\tau + \mu)(\rho + \mu)]i$$

$$= (\tau + \mu)(\rho + \mu) \left[\left(\frac{\tau\beta}{(\tau + \mu)(\rho + \mu)} - 1 \right) \right] i$$

$$= (\tau + \mu)(\rho + \mu)i [(R_0 - 1)] \quad (29)$$

$$\leq 0 \text{ for } R_0 \leq 1 \quad (30)$$

It follows from the LaSalle invariance principle (LaSalle, 1976) that every solution to the equations (14) – (16) with initial conditions in \mathbb{R}^3 , approaches \mathcal{E}_0 , as $t \rightarrow \infty$, for $R_0 \leq 1$.

Local Stability of the Endemic Equilibrium (EE) State

Substituting the value of R_0 , in equation (23) into Equation (22), the Endemic Equilibrium (EE) state can be expressed as

$$\mathcal{E}_1 = (s^{**}, e^{**}, i^{**}) = \left(\frac{1}{R_0}, \frac{\mu(\mu+\rho)}{\tau\beta} (R_0 - 1), \frac{\mu}{\beta} (R_0 - 1) \right) \quad (31)$$

Theorem 3: The unique endemic equilibrium of the model (14) – (16) given by \mathcal{E}_1 is locally asymptotically stable (LAS) whenever $R_0 > 1$.

Proof:

To investigate the local stability of the endemic equilibrium, the associated Jacobian matrix of the system (14) – (16) is evaluated at the endemic equilibrium. Thus the Jacobian matrix at \mathcal{E}_1 is given by

$$J(\mathcal{E}_1) = \begin{pmatrix} -\mu R_0 & 0 & \frac{-\beta}{R_0} \\ \mu(R_0 - 1) & -(\mu + \tau) & \frac{\beta}{R_0} \\ 0 & \varepsilon & -(\mu + \rho) \end{pmatrix} \quad (32)$$

The characteristic polynomial of $J(\mathcal{E}_1)$ is given by
 $(-\mu R_0 - \lambda) [(-\tau + \mu) - \lambda](-\rho + \mu) - \lambda - \frac{\tau\beta}{R_0} - \frac{\mu\tau\beta}{R_0}(R_0 - 1) = 0$
 $(-\mu R_0 - \lambda) \left[\lambda^2 + \lambda(\tau + \rho + 2\mu) + (\tau + \mu)(\rho + \mu) - \frac{\tau\beta}{R_0} \right] - \frac{\mu\tau\beta}{R_0}(R_0 - 1) = 0$

By further simplifying to obtain the characteristic equation in the form

$$P(\lambda) = \lambda^3 + A\lambda^2 + B\lambda + C = 0 \quad (33)$$

The coefficients are given by

$$A = \mu R_0 + (\tau + \rho + 2\mu)$$

$$B = \mu R_0(\tau + \rho + 2\mu) + (\tau + \mu)(\rho + \mu) - \frac{\tau\beta}{R_0} = \mu R_0(\tau + \rho + 2\mu)$$

$$C = \mu R_0(\tau + \mu)(\rho + \mu) - \mu\tau\beta + \frac{\mu\tau\beta}{R_0}(R_0 - 1) = (\tau + \mu)(\rho + \mu) \left[\mu R_0 - \mu R_0 + \frac{\mu R_0}{R_0}(R_0 - 1) \right] = \mu(\tau + \mu)(\rho + \mu)(R_0 - 1)$$

The Routh-Hurwitz stability criteria can be used to determine the sign of the eigenvalues (Hurwitz, 1964).

All the three eigenvalues have negative real part if and only if $A > 0$, $C > 0$ and $AB - C > 0$.

Obviously, $A > 0$ and

$$C = \mu(\tau + \mu)(\rho + \mu)(R_0 - 1) > 0 \text{ for } R_0 > 1$$

Next, consider $AB - C$

$$\begin{aligned} AB - C &= [\mu R_0 + (\tau + \rho + 2\mu)][\mu R_0(\tau + \rho + 2\mu) - \mu(\tau + \mu)(\rho + \mu)(R_0 - 1)] \\ &= \mu R_0[\mu R_0(\tau + \rho + 2\mu)] + \mu R_0[(\tau + \mu) + (\rho + \mu)][(\tau + \mu) + (\rho + \mu)] - \mu R_0(\tau + \mu)(\rho + \mu) + \mu(\tau + \mu)(\rho + \mu) \\ &= \mu R_0[\mu R_0(\tau + \rho + 2\mu) + \mu R_0[(\tau + \mu)^2 + 2(\tau + \mu)(\rho + \mu) + (\rho + \mu)^2] - \mu R_0(\tau + \mu)(\rho + \mu) + \mu(\tau + \mu)(\rho + \mu)] \\ &= \mu R_0[\mu R_0(\tau + \rho + 2\mu) + \mu R_0[(\tau + \mu)^2 + (\tau + \mu)(\rho + \mu) + (\rho + \mu)^2] + \mu(\tau + \mu)(\rho + \mu)] \\ &= \mu R_0[\mu R_0(\tau + \rho + 2\mu) + \mu R_0[(\tau + \mu)^2 + (\rho + \mu)^2] + \mu(\tau + \mu)(\rho + \mu)(R_0 + 1)] > 0 \text{ for } R_0 > 1 \end{aligned}$$

Thus the endemic equilibrium state \mathcal{E}_1 is locally asymptotically stable.

4. RESULTS AND DISCUSSION

The parameters of the tuberculosis model were estimated using the data obtained from Tuberculosis Medical Centre, Kaduna and from literature. The data obtained from Tuberculosis Medical Centre, Kaduna for ten years (2009 – 2018) are as shown in Figure 2.

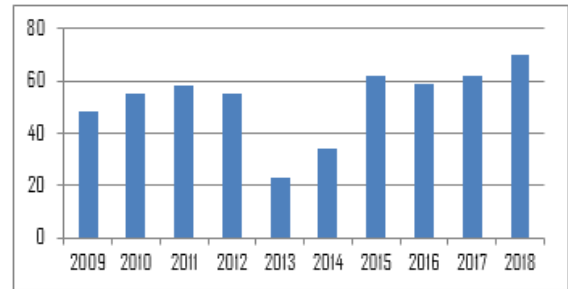


Figure 2: Histogram of Tuberculosis cases in Kaduna Metropolis of Kaduna State

The natural death rate in Nigeria is estimated to be 12.8 deaths per 1000 population or individuals (CDC, 2011; Chaisson, and Martinson, 2008). Based on the assumption of a closed population system, the natural birth and death rates are assumed to be equal, we therefore have death/birth rate, $\mu = 0.0128$.

For our model, we shall use the year 2008 as the base year. Records available at the Federal Medical Centre Kaduna, indicated that a total of 82 individuals were screened for TB infections and of this number, 48 were found to be infected with various strains of mycobacteria (mycobacterium 60 tuberculosis). Thus the infection transmission rate β , is estimated as:

$$\beta = \frac{\text{effective contact}}{\text{total contact}} = \frac{48}{82} = 0.5853$$

The incubation or latency period for tuberculosis is approximately 6 weeks. Hence the exposed rate is estimated as

$$\tau = \frac{1}{\text{latency period}} = \frac{1}{6} = 0.1666/\text{week}$$

The expected duration of infection is the inverse of the removal rate (Chaisson and Martinson, 2008). For tuberculosis, the infectious or contagious period is 2 weeks. Hence, the recovery rate,

$$\rho = \frac{1}{\text{infectious period}} = \frac{1}{2} = 0.5000/\text{week}$$

The table below shows the estimated value of the parameters used in the model.

Table 2: Parameters and their estimated values used in the model

Parameter	Symbol	Value
Death Rate	μ	0.0128
Transmission rate	β	0.5853
Infectious Rate	τ	0.1666
Recovery rate	ρ	0.5

Estimate of the Basic Reproduction Number and the Herd Immunity Threshold

Using the estimated parameter values in Table 2 and equation (23), the Basic Reproductive Number for the SEIR model is estimated as

$$R_0 = \frac{\beta\tau}{(\mu + \tau)(\mu + \rho)} = \frac{0.5853 \times 0.1666}{(0.0128 + 0.1666)(0.0128 + 0.500)} = 1.0623 > 1 \quad (34)$$

Since $R_0 > 1$, Tuberculosis infection is expected to persist in the Kaduna Metropolis resulting in endemic equilibrium state. This is due to the fact that rate of transmission is greater than the recovery rate. The number of contacts between susceptible individuals and the infective ones is given by

$$\sigma = \frac{\beta}{\rho} = \frac{0.5853}{0.5000} = 1.1706 \quad (35)$$

This shows that an average of one tuberculosis patient contacts 1.1706 susceptible individuals during an infectious period.

The herd immunity threshold shows the percentage or proportion of the population that needs to be immunized to control the transmission of the disease when there is an outbreak. The herd immunity threshold is given as

$$H_1 = 1 - \frac{1}{R_0} = 1 - \frac{1}{1.0623} = 0.0586 \quad (36)$$

The herd immunity threshold estimates of Kaduna Metropolis with a risk of endemic Tuberculosis suggests that a minimum of 5% of the proportion of the population need to be immunized to control the spread of tuberculosis infection.

Stability Analysis of the Disease-Free Equilibrium (DFE) State

The disease – free equilibrium point for the model was determined as $(\mathcal{E}_0 = s^*, e^*, i) = (1, 0, 0)$. The stability of the Disease-free equilibrium point was established based on theorem 1 using the Routh-Hurwitz stability criterion.

The basic reproduction number $R_0 = 1.0623 > 1$, and from the characteristic equation of the Jacobian matrix at \mathcal{E}_0 , one eigenvalue is negative and the other characteristic polynomial obtained as $\lambda^2 + A\lambda + B$. The values of the coefficients A and B are given as

$$A = 0.6916 \text{ and } B = -5.722 \times 10^{-3}.$$

Since $A > 0$ and $B < 0$, then the Routh – Hurwitz stability condition did not hold. Thus, the disease-free equilibrium point is not stable. This indicates that Tuberculosis infection persist in Kaduna metropolis.

Stability of the Endemic Equilibrium (EE) State

From equation (31), the endemic equilibrium point was given as $\mathcal{E}_1 = (s^{**}, e^{**}, i^{**}) = (0.94131, 1.5382 \times 10^{-3}, 5.00021 \times 10^{-4})$. The local asymptotical stability of the model at \mathcal{E}_1 was analysed based on Theorem 3 using the Routh – Hurwitz stability criterion. The basic reproduction number $R_0 = 1.0623 > 1$ indicated that the model is characterized by endemic state. The characteristic polynomial of the Jacobian matrix at \mathcal{E}_1 was obtained as

$$\lambda^3 + A\lambda^2 + B\lambda + C.$$

The values of the coefficients A , B , C and $AB - C$ of the characteristic polynomial are as summarize in Table 3.

Table 3: Coefficients of the characteristic polynomial at the endemic equilibrium state.

A	B	C	$AB - C$
0.70488	9.1840×10^{-3}	7.1528×10^{-5}	0.2368

Table 3 revealed that the Routh – Hurwitz stability criterion is satisfied since $A > 0, B > 0, C > 0$ and $AB - C > 0$. Hence, the endemic equilibrium (EE) state, \mathcal{E}_1 is locally asymptotically stable. This is consistent with theorem 3 since $R_0 > 1$.

The standard SEIR differential equation model to predict the prevalence, transmission and spread of tuberculosis in Kaduna Metropolis is presented. A threshold parameter, R_0 which is the basic reproductive number was computed using the next generation matrix operator. The disease-free equilibrium state was

analysed using the linearization method and Routh – Hurwitz stability criterion. The results obtained in Theorem 1 and Theorem 2 revealed that the disease – free equilibrium state is locally as well as globally asymptotically stable whenever the basic reproduction number (R_0) is less than unity. The implication is that tuberculosis can be eliminated from the population if $R_0 < 1$. The endemic equilibrium state was investigated using Routh-Hurwitz stability condition on the characteristic equation of the Jacobian matrix at the endemic equilibrium point. The result found in Theorem 3 shows that the endemic equilibrium state is locally asymptotically stable whenever $R_0 > 1$. This implies that tuberculosis infection will persist in the population if the initial sizes of the proportion of the population of the model are in the basin of attraction of the EE, (\mathcal{E}_1) (Theorem 3).

The parameters of the tuberculosis model were estimated using the data obtained from Tuberculosis Medical Centre, Kaduna and from literature. The values of the estimated parameters were used to obtain the value of basic reproduction number as $R_0 = 1.0623 > 1$. Since $R_0 > 1$, Tuberculosis infection is expected to persist in the Kaduna Metropolis resulting in endemic equilibrium state. This is due to the fact that rate of transmission is greater than the recovery rate. The number of contacts between susceptible individuals and the infective ones is given by $\sigma = \frac{\beta}{\gamma} = \frac{0.5853}{0.5000} = 1.1706$. This shows that an average of one tuberculosis infected patient contacts 1.1706 susceptible individuals during an infectious period.

The value of the basic reproduction number was used to estimate herd immunity threshold (H_1), which was given as $H_1 = 0.0586$. The herd immunity threshold estimates of Kaduna Metropolis with a risk of endemic Tuberculosis suggests that a minimum of 5% of the population need to be immunized on a regular basis to control the spread of tuberculosis infection in the region.

The numerical solution for the stability of the disease – free equilibrium state using the Routh – Hurwitz stability shows DFE state is locally as well as globally asymptotically unstable. This implies that tuberculosis disease cannot be eliminated from the metropolis unless the infection transmission is decreased or other measures such as effective and expanded immunization campaign is put in place. Further numerical result for the endemic equilibrium state in Table 3 using Routh – Hurwitz conditions revealed the estimated endemic equilibrium state is locally asymptotically stable which is consistent with Theorem 3. The implication is that tuberculosis infection will remain endemic within the population unless control measures are put in place.

Conclusion

In this study, the transmission dynamics of tuberculosis infection in Kaduna metropolis, using the SEIR compartmental model was formulated and analysed data obtained from Tuberculosis Medical Centre, Kaduna. The disease-free equilibrium (DFE) state of the model was determined and used to compute the basic reproduction number R_0 . Stability analysis for the disease-free equilibrium state (DFEs) and the endemic equilibrium state (EEs) was carried out and the results shows that DFEs is locally as well as globally asymptotically stable whenever the basic reproduction number $R_0 < 1$, and EEs is locally asymptotically stable whenever $R_0 > 1$. The numerical value of the basic reproduction number R_0 , as

well as the numerical stability analysis shows that tuberculosis infection will remain endemic (persist) in Kaduna metropolis unless effective control measures such as expanded and regular immunization campaign are carried out.

Acknowledgements

The authors are thankful to the anonymous reviewers for their useful comments and suggestions.

REFERENCES

- Adepoju P. (2020). Nigeria's widening tuberculosis gap. *Lancet Infectious Diseases*, 20(1), 29. [doi.org/10.1016/S1473-3099\(19\)](https://doi.org/10.1016/S1473-3099(19)3099(19))
- Ahmad N.M.R., Montanola-Sales C., Prats C., Musa M., Lopez D. and Cusanoras-Gurcia J. (2018). Analysis Policy making for tuberculosis control in Nigeria. *Complexity*, 1-13. <https://doi.org/10.1155/2018/92533846>.
- Akinrafon A. A., and Adejumo O. A. (2019). Modelling Tuberculosis in South-West Nigeria. *Annals-computer science series*. 17th Tome, 2nd Fasc-2019.
- Centers for Disease Control and Prevention (CDC). (2011). Division of Tuberculosis Elimination, "Core Curriculum on Tuberculosis: What the Clinician Should Know".
- Centre for Disease Control and Prevention. (2019). TB Fact sheets, <https://www.cdc.gov/tb/publications/reports2019.htm>
- Chaisson R.E., and N. A. Martinson N.A. (2008). "Tuberculosis in Africa-combating an HIV-driven crisis". *The New England Journal of Medicine* 358 (11) (2008), 1089-92.
- Daniel T.M. (2006). The history of tuberculosis. *Respiratory Medicine*, 100(11) 1862-1870.
- Diekmann O., Heesterbeek J.A.P., and Metz J.A.J. (1990). 'On the definition and the computation of the basic reproduction ratio R_0 in models for infectious diseases in heterogeneous populations. *Journal of mathematical Biology*, 28(1), 365-382.
- Diekmann O., Heesterbeek J.A.P., and Roberts M.G. (2010). 'The construction of next-generation matrix for compartmental epidemic models". *Journal of the Royal Society Interface*, 7(2), 873-885.
- Dye C. (2006). Global Epidemiology of Tuberculosis. *Lancet* 367(2), 938-40.
- Enagi A.I., Ibrahim M.O., Akinwade I.A., Bawa M., Wachin A. A. (2017). A Mathematical model of Tuberculosis control incorporating vaccination, latency and infectious treatments. (Case Study of Nigeria). *International Journal of Mathematics and Computer Science*, 12 (2) 97-106.
- Hurwitz A. (1964). On the conditions under which an equation has only roots with negative real parts. *Selected Papers on Mathematical Trends in Control Theory*.
- Jerubet R., Kimathi G., Wanaina M. (2019). Analysing and Modelling of Tuberculosis Dynamics. *Journal of Advances in Mathematics and Computer Science*, 32 (2), 1-14.
- Koriko O. K. and Yusuf T. T. (2008). Mathematical Model to Simulate Tuberculosis Disease Population Dynamics. *American Journal of Applied Sciences*, 5(4), 301-306.
- LaSalle J.P. (1976). The Stability of Dynamical Systems. *CBMS-NSF Regional Conference Series in Applied Mathematics*, vol., 25, SIAM, Philadelphia.
- Methema B., Kurepina N.E., Bifani P.J., Kreiswirth B.N. (2006). Molecular epidemiology of tuberculosis: current insights. *Clinical Microbiology Review*, 19(4), pp 658-685.
- Nayeem J., Sultan I. (2019). Mathematical Analysis of the Transmission Dynamics of Tuberculosis. *American Journal of Computational Mathematics*, 9, 158-173.
- Okuonghae D. (2013). A mathematical model of tuberculosis transmission with heterogeneity n disease susceptibility and progression under treatment regime for infectious cases. *Applied Mathematical Modelling*, 37, 2013, 6786-6808.
- World Health Organisation. (2017). Global tuberculosis report 2017, Geneva, <https://apps.int/iris>
- World Health Organisation. (2019). Global tuberculosis report 2019, Geneva, <https://apps.int/iris>
- World Health Organisation. (2020). Nigeria tuberculosis fact sheets, 14 Oct., 2020 <https://www.who.int/es/news-room/fact-sheets/detail/tuberculosis>