# A Tuberculosis Mathematical Model with Infected Population and Vaccination

**Research Article**

**Lakhan Nagar[1]\*, Pradeep Porwal[1], V.K. Gupta[2] and S.K. Tiwari[1]**

1 School of Studies in Mathematics, Vikram University, Ujjain, Madhya Pradesh, India.

2 Department of Mathematics, Government Madhav Science P.G. College, Ujjain, Madhya Pradesh, India.

**Abstract:** Tuberculosis is an infectious disease that usually affects the lungs. World Health Organization has declared that tuberculosis Disease can cause global warming. So, TB must be solved especially in prediction and vaccination. In this model the infected population is divided into two groups, namely infectious infected and noninfectious infected population. This paper explains about the equilibrium point, and analyzing the stability model.

**Keywords:** Basic reproduction number, vaccination, tuberculosis, stability.

© JS Publication.

## 1. Introduction

Tuberculosis is an infectious disease caused by bacteria called Mycobacterium tuberculosis. The bacteria usually attacks the lungs, but it can also affect organs in the central nervous system, lymphatic system, and circulatory system among others [4]. World Health Organization declared TB as global epidemic in 1993. TB is a contagious disease that spread like the common cold [8]. If a person got the tuberculosis, then it couldn't only seen by the main caution of factors which is causing tuberculosis disease, but also the possibility of exogenous re-infection happening [9].

This paper will discuss about the forming and analyzing mathematical model of to Tuberculosis virus infection. We modify and analyze a tuberculosis spread model with two groups of infected population that was introduced by Blower et al. [10]. And has been developed by Ozcaglar et al. [3]. Modifications are done by considering the assumption that exposed individual can move naturally into recovered population and it is assumed that individual who has been recovered cannot be re-infected by tuberculosis. Modifications of the model are also done by adding V compartment [1], namely vaccinated population. The way of model forming takes a focus about the infection by exogenous re-infection or there are more contact to active tuberculosis one. From the model forming, will be analyzed the behavior of solution around equilibrium point, so that it can analyze the equilibrium point is stable or not. Finally we will know how to solve this tuberculosis disease, and then it would give back. Susilo Nugroho in his essay discussed about the modeling of disease spread by the vaccination influences using SIR model [6]. This essay decrease back SIR model by taking care the birth and death factors. Mathematical modeling is a powerful tool extensively used by researchers in epidemiology to have a better understanding of the transmission dynamics of the infectious diseases. Several authors in [2, 5, 6, 10] have studied the dynamics of TB using mathematical modeling

---

\* E-mail: lakhannagar988@gmail.com

approach with the view to investigate the role played by one or more control measure in curtailing the prevalence in both developing and developed countries.

## 2.   Model Formulation

We introduced the modification of tuberculosis spread model with two groups of infected population. Total population is divided into six compartments: the vaccinated population $(V)$, the exposed population $(E)$, the infectious infected population $(I_1)$, the noninfectious infected population $(I_n)$, the threaded population (T), and the recovered population $(R)$ it is assumed that the rate of incoming individuals into vaccinated population is constant $n\alpha$. Vaccinated individual can move into exposed population with fraction $(1-f)$, $0 < f < 1$, exposed individual can moved into infectious infected population with rate $\nu$. A fraction q, $0 < q < 1$, of exposed population progresses to infectious infected population, and the remaining $(1-q)$ fraction progresses to non infectious infected population. The natural mortality rate for the six compartments is  and the mortality rare due to tuberculosis for infectious and non infectious infected population is $\mu_T$. The dynamical transfer among the six compartments is depicted in the following transfer diagram.
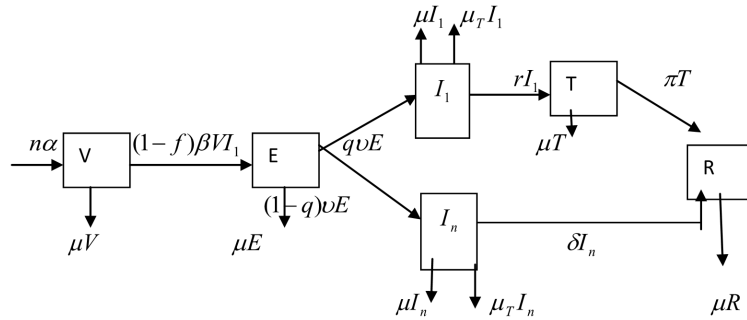


Based on our assumption and the transfer diagram, the model can be described by six ordinary differential equations as follow

$$\frac{dV}{dt} = n\alpha - (1-f)\beta V I_1 - \mu V$$

$$\frac{dE}{dt} = (1-f)\beta V I_1 - \upsilon E - \mu E$$

$$\frac{dI_1}{dt} = q\upsilon E - r I_1 - \mu I_1 - \mu_T I_1$$

$$\frac{dI_n}{dt} = (1-q)\upsilon E - (\mu + \mu_T + \delta) I_n$$

$$\frac{dT}{dt} = r I_1 - (\mu + \pi) T$$

$$\frac{dR}{dt} = \pi T + \delta I_n - \mu R$$

## 3.   The Basic Reproduction Number

System has the disease free equilibrium $E = \left(\frac{n\alpha}{\mu}, 0, 0, 0, 0, 0\right)$. And the endemic equilibrium $E^* = (V^*, E^*, I_1^*, I_n^*, T^*, R^*)$. Where

$$V^* = \frac{n\alpha}{(1-f)\beta I_1 - \mu}$$

$$E^* = \frac{(1-f)\beta V I_1}{(\upsilon + \mu)}$$

$$I_1^* = \frac{q\upsilon E}{r + \mu + \mu_T}$$

$$I_n^* = \frac{(1-q)\upsilon E}{\mu + \mu_T + \delta}$$

$$T^* = \frac{rI_1}{\mu + \pi}$$

$$R^* = \frac{\pi T + \delta I_n}{\mu}$$

From the system, the matrices of F and V at the diseases free equilibrium are

$$F = \begin{pmatrix} 0 & (1-f)\frac{\beta n\alpha}{\mu} & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}$$

$$V = \begin{pmatrix} \upsilon + \mu & 0 & 0 \\ -q\upsilon & r + \mu + \mu_T & 0 \\ -(1-q)\upsilon & 0 & \mu + \mu_T + \delta \end{pmatrix}$$

$$|V| = (\upsilon + \mu)(r + \mu + \mu_T)(\mu + \mu_T + \delta)$$

$$adj\ v = \begin{pmatrix} (r + \mu + \mu_T)(\mu + \mu_T + \delta) & 0 & 0 \\ q\upsilon(\mu + \mu_T + \delta) & (\upsilon + \mu)(\mu + \mu_T + \delta) & 0 \\ (1-q)\upsilon(r + \mu + \mu_T) & 0 & (\upsilon + \mu)(r + \mu + \mu_T) \end{pmatrix}$$

$$V^{-1} = \begin{pmatrix} \frac{1}{\upsilon+\mu} & 0 & 0 \\ \frac{q\upsilon}{(\upsilon+\mu)(r+\mu+\mu_T)} & \frac{1}{(r+\mu+\mu_T)} & 0 \\ \frac{(1-q)\upsilon}{(\upsilon+\mu)(\mu+\mu_T+\delta)} & 0 & \frac{1}{(\mu+\mu_T+\delta)} \end{pmatrix}$$

$$FV^{-1} = \begin{pmatrix} 0 & \frac{(1-f)\beta n\alpha}{\mu} & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \begin{pmatrix} \frac{1}{(\upsilon+\mu)} & 0 & 0 \\ \frac{q\upsilon}{(\upsilon+\mu)(r+\mu+\mu_T)} & \frac{1}{(r+\mu+\mu_T)} & 0 \\ \frac{(1-q)\upsilon}{(\upsilon+\mu)(\mu+\mu_T+\delta)} & 0 & \frac{1}{\mu+\mu_T+\delta} \end{pmatrix}$$

$$= \begin{pmatrix} \frac{(1-f)\beta n\alpha}{\mu} \frac{q\upsilon}{(\upsilon+\mu)(r+\mu+\mu_T)} & \frac{(1-f)\beta n\alpha}{\mu} \frac{1}{(r+\mu+\mu_T)} & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}$$

$$R_O = \rho(FV^{-1}) = \frac{(1-f)\beta n\alpha q\upsilon}{\mu(\upsilon + \mu)(r + \mu + \mu_T)}$$

# 4.   Stability Analysis

## 4.1.   Local stability for disease free equilibrium point

$$J = \begin{pmatrix} -\mu & 0 & -\frac{(1-f)\beta n\alpha}{\mu} & 0 & 0 & 0 \\ 0 & -(\upsilon + \mu) & (1-f)\frac{\beta n\alpha}{\mu} & 0 & 0 & 0 \\ 0 & q\upsilon & -(r + \mu + \mu_T) & 0 & 0 & 0 \\ 0 & (1-q)\upsilon & 0 & -(\mu + \mu_T + \delta) & 0 & 0 \\ 0 & 0 & r & 0 & -(\mu + \pi) & 0 \\ 0 & 0 & o & \delta & \pi & -\mu \end{pmatrix}$$

$$\lambda_1 = -\mu$$

$$\lambda 2 = -(\mu + \mu_T + \delta)$$

$$\lambda 3 = -(\mu + \pi)$$

$$\lambda 4 = -\mu$$

And $\lambda_5$, $\lambda_6$ given by

$$\lambda^2 + (v + \mu + r + \mu + \mu_T)\lambda + (v + \mu)(r + \mu + \mu_T) - qv(1-f)\frac{\beta n\alpha}{\mu} = 0$$

So that all the eigen values are negative if and only if

$$(v + \mu)(r + \mu + \mu_T) - qv(1-f)\frac{\beta n\alpha}{\mu} > 0$$

$$(v + \mu)(r + \mu + \mu_T) > qv(1-f)\frac{\beta n\alpha}{\mu}$$

$$1 > \frac{(1-f)\beta n\alpha qv}{\mu(v + \mu)(r + \mu + \mu_T)}$$

$$1 > R_0$$

$$R_0 < 1$$

So the system is locally asymptotically stable if $R_0 < 1$.

## 4.2. Local stability for endemic

$$\begin{pmatrix} -(1-f)\beta I_1^* - \mu & 0 & -(1-f)\beta V^* & 0 & 0 & 0 \\ (1-f)\beta I_1^* & -(v+\mu) & (1-f)\beta V^* & 0 & 0 & 0 \\ 0 & qv & -(r+\mu+\mu_T) & 0 & 0 & 0 \\ 0 & (1-q)v & 0 & -(\mu+\mu_T+\delta) & 0 & 0 \\ 0 & 0 & r & 0 & -(\mu+\pi) & 0 \\ 0 & 0 & 0 & \delta & \pi & -\mu \end{pmatrix}$$

The Eigen values are

$$\lambda_1 = -\mu$$

$$\lambda_2 = -(\mu + \pi)$$

$$\lambda_3 = -(\mu + \mu_T + \delta)$$

And other Eigen values are given by

$$\lambda^3 + a2\lambda^2 + a_1\lambda + a_0 = 0$$

So by Routh Hurwitz criteria the system is asymptotically stable if $a_0 > 0$, $a_2 > 0$ and $a_2 a_1 > a_0$. Where

$$a_0 = ((1-f)\beta I_1^* + \mu))(r+\mu)(r+\mu+\mu_T) - qv(1-f)\beta V^*((1-f)\beta I_1^* + \mu)) + (1-f)\beta V^*(1-f)\beta I_1^* qv$$

$$a_1 = ((1-f)\beta I_1^* + \mu))(v+\mu) + ((1-f)\beta I_1^* + \mu))(r+\mu+\mu_T) + (v+\mu)(r+\mu+\mu_T) - qv(1-f)\beta V^* + (1-f)\beta I_1^* qv$$

$$a_2 = ((1-f)\beta I_1^* + \mu) + (\mu+v) + (r+\mu+\mu_T)$$

# 5.   Conclusion

In this paper, we propose an Model of vaccinated tuberculosis spread within two groups of infected population .The local stability of the model was determined by considering the basic reproduction number. We prove that if $R_0 < 1$ then the disease free equilibrium is asymptotically stable and a unique endemic equilibrium exists and asymptotically stable under some conditions.

## References

[1] A.B.Gumel, C.C.Mccluskey and J.Watmough, *An SVEIR model for assessing potential impact of an imperfect anti-SARS vaccine*, Mathematical Bioscience and Engineering , 3(2006), 485-512.

[2] A.U.Kalu and S.C.Inyama, *Mathematical model of the role of Vaccination and treatment on the transmission Dynamics of Tuberculosis*, Math Notes, 11(2012), 10-23.

[3] C.Ozcaglar, A.Shabbeer, S.L.Vandenberg and B.Yenger and K.Bennett, *Epidemiological models of Mycobacterium tuberculosis complex infections*, Mathematical Bioscience, 236(2012), 77-96.

[4] Imane Abouelkheir et al., *Optimal control strategy of a tuberculosis epidemic model with drug resistant TB*, International Journal of science and research, (2013), 2319-7064.

[5] J.Nainggolan, S.Supian, A.K.Supriatna and N.Anggriant, *Mathematical model of Tuberculosis Transmission with Recurrent infection and vaccination*, Journal of physics conference series, (2013), 423.

[6] N.H.Shah and J.Gupta, *Mathematical modelling of pulmonary and Ex-pulmonary Tuberculosis*, International Journal of Mathematics Treands and Technology, 4(2013), 158-162.

[7] N.Susilo, *Vaccination influence to disease epidemic with SIR endemic model*, Thesis, Surakarta university, Indonesia, (2009).

[8] P.Chaulet, *Treatment of tuberculosis : case holding until cure, WHO/TB/83*, World Health Organization, Geneva, (1983), 141.

[9] S.A.Egbetade et al., *On existence of a vaccination model of Tuberculosis disease pandemic*, International Journal of Engineering and Science, 5(2013), 41-44.

[10] S.Bowong, J.J.Tewa and J.C.Kamgang, *Stability Analysis of the Transmission Dynamics of Tuberculosis Models*, World Journal of Mathematical Modeling and Simulation, 2(2011), 83-100.

[11] S.M.Blower, A.R.Mclean, T.C.Porco, P.M.Small, M.A.Sanchez, A.R.Mose and P.C.Hopewell, *The intrinsic transmission dynamics of tuberculosis epidemics*, Nature Medicine, 1(1995), 815-821.