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The Dynamics of Natural Mortality, Life Expectancy and TB in an Age-Structured Population

Umar Mallam Abdulkarim
Department of Mathematical Sciences, Nasarawa State University Keffi, Nigeria

Abstract: We have extended the classical Mckendrick-Foerster age structured population model to study the effect of population area size on the transmission dynamics of tuberculosis in an age-structured population, in which infective recovers, after treatment and become susceptible again when in contact with the disease. The natural mortality rate is assumed density and area size depended, with the population assumed to be in proportionate mixing. We defined a model in which the area sizes and the total population influences the rate at which death by nature occurs in the population. This model is extended to study the influence the area size of the population has on the natural mortality rate, life expectancy of the population and the transmission dynamics of the infection. The analytical solutions of the governing equations are obtained. The existence of the non trivial steady states is examined with their local and global stability.

Key words: Life expectancy, population areas size, proportionate mixing, stability, steady state, mortality rate

INTRODUCTION

Tuberculosis, TB is a disease that affects animals and human population. It is coursed by the bacteria, Tubercle bacillus, which lives in the lungs of infected host. The virus is spread in the air when infected individual cough, sneeze and sing (Castillo-Chavez, 2004). Most infected individual often remain in the latency stage of the infection for their entire life. The risk of progression to active TB increases in the presence of co-infections that debilitate the immune system as in the case of HIV and AIDS. The earliest mathematical models on dynamics of TB concentrate on the prediction and control strategies using simulation approaches. However, recent models examines TB control strategies as in Castillo-Chavez (2004), Hethcote (2002) and Umar (2007) optimal vaccination policy, TB co-infection with HIV/AIDS, drug resistant TB, response of immune system, impact of demography, the role of public transportation system and the impact of contact pattern as in Song *et al.* (2002) are some of the direction recent TB models are focused. In this work, we examine the effect of area size on the natural mortality rate life expectancy of population. The population area size is used as control strategy towards the eradication of TB transmission.

MODEL EQUATION

Assume that infective recover after treatment and those not treated who progress to active infection are removed and treated to stop further transmission. All treated are returned to the susceptible compartment. Suppose the infection does not affect individual fertility and natural mortality and that the disease is not vertically transmitted to the new born. Then we can extend the S-I-R compartmental epidemic model to study the transmission dynamics of the disease. The diseases incidence is obtained in line with proportionate mixing assumption as,

$$S(t,a)k_1(a)\int_0^{\infty}\frac{I(t,\bar{a})}{A(a,\bar{a})}k_2(\bar{a})d\bar{a}$$

Where, $A(a,\bar{a})$ is the population area size occupied by susceptible and infective of ages a and $\bar{a}$. We define,

$$k(a,\bar{a})=\frac{c(\bar{a})A(a,\bar{a})}{\int_0^{\infty}c(\bar{a})A(a,\bar{a})d\bar{a}}$$

Where $k(a,\bar{a})$, is the age specific (average) probability of becoming infected through contact with infectious individual, as an extension of Castillo-Chavez representation, where the contact rate is expressed in terms of the total population size, n(t, a) c(a) is the age specific contact/activity rate. The per capital force of infection in line with Castillo-Chavez (2004), Doma (2004) and Inaba (1990) is:

$$k_1(a)\int_0^{\infty}\frac{I(t,\bar{a})}{A(t,\bar{a})}k_2(\bar{a})d\bar{a}$$

Where, $k_1(a)$, is the age specific infectiousness, $k_2(a)$ is the age specific contagious rate. The total area occupied by the population is:

$$A = \int_0^{\infty} A(a,\bar{a})d\bar{a}$$

All new born from all compartments per unit of time are susceptible obtained as:

$$\begin{aligned}
&S(t,0) = \int_0^{\infty} \alpha(a,P(t))n(t,a)da\\
&I(t,0) = 0\\
&P(t) = \int_0^{\infty} n(t,a)da,\\
&n(t,a) = S(t,a) + I(t,a). + R(t,a)\\
&S(0,a) = S_0(a)\\
&I(0,a) = I_0(a)\\
&R(0,a) = R_0(a)
\end{aligned}$$

Where $\alpha(a, P(t))$ is the fertility function (Inaba, 1990; Castillo-Chavez, 2004; Doma, 2004).

Using these assumptions we obtained the governing equations for transmission dynamics of the disease in the population:

$$\begin{aligned}
&(\partial_t + \partial_a)S(t,a) = -\mu(B,A)S(t,a)\\
&-c(a)ak_1(a)\lambda(t)S(t,a) + \gamma I(t,a)
\end{aligned} \quad (1)$$

$$\begin{aligned}
&(\partial_t + \partial_a)I(t,a) = c(a)k_1(a)\lambda(t)S(t,a)\\
&-\mu(B,A)I(t,a) - rI(t,a)
\end{aligned} \quad (2)$$

$$(\partial_t + \partial_a)R(t,a) = rI(t,a) - \mu(B,A)R(t,a) \quad (3)$$

Where, $\mu(B, A)$, is the population and area size depended mortality rate, γ is the recovery rate and r is the proportion of the infective removed. Using proportionate mixing assumption, the per capital force of infection is reduced to,

$$\lambda(t) = k_1(a)\int_0^{\infty} \frac{I(t,\bar{a})}{A(t,\bar{a})}k_2(\bar{a})d\bar{a} \quad (4)$$

New incidence of TB can be described as,

$$S(t)c(a)k_1(a)\int_0^{\infty} \frac{I(t,\bar{a})}{A(t,\bar{a})}k_2(\bar{a})d\bar{a} \quad (5)$$

same as in Castillo-Chavez (2004) where the population area size is replaced by the total population. The number of susceptible recruited per unit of time is defined in line with Gurtin-McCamy representation as:

$$S(t,0) = \int_0^{\infty} \alpha(a,P(t))n(t,a)da$$

Unlike, Castillo-Chavez (2004) who assumed constant recruitment into the susceptible population, as Δ, We assume the following initial conditions,

$$\begin{aligned}
&S(0,a) = S_0(a)\\
&I(0,a) = I_0(a)\\
&R(0,a) = R_0(a)\\
&I(t,0) = 0\\
&B(t) = \int_0^{\infty} n(t,a)da,
\end{aligned}$$

$n(t, a) = S(t, a) + I(t, a) + R(t, a)$, is the total population density. Adding Eq. 1-2 gives the Mckendrick-Foerster and Gurtin-McCamy type age-structured population model:

$$(\partial_t + \partial_a)n(t,a) = -\mu(a,A)n(t,a) \quad (5)$$

$$n(t,0) = \int_0^{\infty} \alpha(a,A)n(t,a)da \quad (6)$$

$$n(0,a) = S_0(a) + I_0(a) + R_0(t,a) \quad (7)$$

Suppose at the start of the epidemic the population is at steady age distribution, with exponential growth, as:

$$N(t,a) = n(a) = e^{r_0 t}\beta(a)$$

Where, r_0 is the intrinsic rate of natural growth or increase and $\beta(a)$ is the total population at age a. Eq. 1-4 are same as 5-7. The solution to the Eq. 1-4 can be obtained through characteristics lines:

$$\frac{da}{dt} = 1, \quad \text{on} \quad \frac{dS}{dt} = -(\mu(B,A) + c(a)k_1(a)\lambda(t))S(t,a) + \gamma I(t,a)$$

The density of the susceptible and infected population compartments are:

$$S(t,a) = S_0(a)e^{-\int_{a_0}^{a}\omega(t,a)da} = S_0(a-t)e^{-\int_{a-t}^{a}\omega(t,a)da}, \; a > t$$

Where, $\omega(t, a) = \mu(B, A) + c(a)\, k_1(a)\lambda(t)$ and for $a < t$, we get

$$S(t,a) = S_0(t,a) = S(t_0,0)e^{-\int_0^{a}\omega(t,a)da} = S(t-a,0)e^{-\int_0^{a}\omega(t,a)da}$$

$$I(t,a) = I_0(a-t) + \int_{a-t}^{a} \omega(t,a)S(t,a)da \quad a > t$$

Also, I (t, a) = {

$$I(t,a) = I_0(t-a),0) + \int_{0}^{a} \omega(t,a)S(t,a)da, \quad a < t$$

a_0, and t_0 are the initial age of an individual at time t = 0 in the original population and time of birth of an individual. The renewal equation is:

$$S(t,0) = \int_0^t \alpha(a,P(t))\rho(t,a)da + \int_t^{\infty} \alpha(a,P(t))\eta(t,a)da$$

Where:

$$\rho(t,a) = S_0(t-a)e^{-\int_0^a \omega(t,a)da} + I(t-a) + e^{-\int_0^a \omega(t,a)S(t,a)da}$$

$$\eta(t,a) = S(a-t)e^{-\int_0^a \omega(t,a)da} + I(t,a) + e^{-\int_{a-t}^a \omega(t,a)S(t,a)da}$$

In real terms, we consider, the population density of the compartments for a < t.

The density of the population compartment are then obtained as:

$$S(t,a) = S_0(t_0,0)e^{-\int_0^a \omega(t,a)da} = S(t-a,0)e^{-\int_0^a \omega(t,a)da}$$

$$I(t,a) = I_0(t_0,0) + \int_0^a \omega(t,a)S(t,a)da$$

We assume that,

$$\int_0^{\infty} A(a,\bar{a})d\bar{a} > B,$$

in line with the slow transmission pattern of TB and

$$\mu(B,A) = \varepsilon + \frac{1}{A}B,$$

Where, B is the total stationary population size, ε is a small quantity greater than zero. If the area size tends to,∞ with a fixed B, then the population natural mortality rate is reduces to, μ(B, A)→ε and the function,
ω(t, a) = ε + c(a)k_1(a)λ(t),

$$S(t,a) = S(t_0,0)e^{-\int_0^a \chi(r)dr}, \quad \chi(a) = \varepsilon + c(a)k_1(a)\lambda(t)$$

$$I(t,a) = I_0(t_0,0) + \int_0^a (m + c(r)k_1(r)\lambda(t))S(t,r)dr.$$

The limiting population sizes for both compartments with increase in area size, given the total population B, are, simply obtained as above. However, if the area size deceases, then the death rate will surely increase to the form μ(B, A) = ε + ∂, where,

$$\text{Lim}\frac{B}{A} \to \delta > 0,\ 0 < \delta < \infty,$$

as A tends to 0, with the limiting population size as:

$$S(t,a) = S(t_0,0)e^{-\int_0^a \xi(r)dr}, \quad \xi(a) = m + c(a)k_1(a)\lambda(t), \quad m = \varepsilon + \delta,$$

$$I(t,a) = I_0(t_0,0) + \int_0^a (m + c(r)k_1(r)\lambda(t))S(t,r)dr.$$

As the area size decreases, we would have more incidences of the diseases and thus, decrease in the number of susceptible population, alternatively as the area size increase, we would have more number of susceptible and less infected individuals. Thus, our function μ(B, A) is well defined. Using the representation of the natural mortality rate, we define the life expectancy of the population in absence of the infection, as,

$$\int_0^{\infty} \pi(a)da,$$

Where,

$$\pi(a) = De^{-\frac{B}{A}a}, \quad D = e^{-\varepsilon}$$

is the proportion of individuals who survive to age a, given the area size A (Castillo-Chavez, 2004; Inaba, 1990). Thus average life expectancy of the population is,

$$\frac{A}{B}e^{-\varepsilon}$$

holding fixed and varying population area size. The average life expectancy depends on the population area size. The larger the value of A the smaller the natural mortality rate and the larger the average life expectancy of the population. Since n(t, a) = S(t, a) + I(t, a) + R(t, a), we would limit our discussions of the disease dynamics to the Susceptible and infective compartments.

EXISTENCE AND LOCAL STABILITY OF ENDEMIC AND DISEASE-FREE STATE

Let (S*(a), I*(a)) be the endemic steady state solution for the governing equations and λ*, be the force of infection at the steady state, then we get the following equations:

$$\frac{dS^*(a)}{da} = \mu(a,A)S^*(a) - k_1(a)S^*(a)\lambda^* + \gamma I^*(a)$$

$$\frac{dI^*(a)}{da} = k_1(a)\lambda^* S^*(a) - (\mu(a,A) - r)I^*(a)$$

$$S^*(0) = e^{r_0}\int_0^\infty \alpha(a, n^*(a))\beta(a)da$$

$$n^*(a) = e^{r_0}\int_0^\infty \beta(a)da$$

Solving these equations gives,

$$S^*(a) = \{S^*(0) + \gamma\int_0^a I(p)e^{M(p,A)}dp\}e^{-M(a,A)},$$

$$M(a,A) = \int_0^a (\mu(B,A) - k_1(p)\lambda^*)dp$$

$$I^*(a) = \{I^*(0) + \lambda^*\int_0^a k_1(p)(S^*(0) + \phi(a))e^{\eta(p,A)}dp\}e^{-\eta(a,A)}$$

$$\eta(a,A) = \int_0^a (\mu(M,A) - r)dp$$

We assume that

$$\mu(B, A) - r \geq 0, \text{ or}$$

$$r - \varepsilon \leq \frac{B}{A}$$

and

$$\mu(B, A) - c(a)k_1(a)\lambda^* \leq 0,$$

$$\eta(a,A) = -(r-\varepsilon)a \leq -\frac{B}{A}a, M(a,A)$$

$$= ra - \lambda^*\int_0^a c(a)k_1(a)da \leq 0$$

for large area size and fixed age a,

$$e^{-\eta(a,A)} = e^{\frac{B}{A}a}, e^{-M(a,A)} = e^{-(\frac{B}{A}a - \lambda^*\int_0^a k_1(a))da} = e^{-(\frac{B}{A} - r)a}$$

In accordance with these assumptions, the endemic steady state exists and has the form,

$$S^*(a) = \{S^*(0) + \gamma\int_0^a I(p)e^{(\frac{B}{A} - r)a}dp\}e^{-(\frac{B}{A} - r)a},$$

$$I^*(a) = \{I^*(0) + \lambda^*\int_0^a k_1(p)(S^*(0) + \phi(a))e^{\frac{B}{A}a}dp\}e^{-\frac{B}{A}a}$$

$$\phi(a) = \gamma\int_0^a I^*(a)e^{(\frac{B}{A} - r)a}da$$

The endemic steady state exists if increases. However, if A decrease we would a trivial steady state, which is not the focus of our studies. We assume that A increases and examine the stability. The local stability of the endemic steady state is determined by linearization of the system in the neighborhood of the steady state, using perturbation about the steady state solution. Thus

$$S(t,a) = \bar{s}(a) + s^*(a)$$

$$I(t,a) = I(a) + I^*(a)$$

$$\lambda^* = \lambda_0 = \frac{k_1(a)c(a)\int_0^\infty k_2(\bar{a})\bar{I}(\bar{a})d\bar{a}}{\int_0^\infty (A(a,\bar{a})d\bar{a}}$$

Substitution into the governing equations gives the followings linear systems,

$$\frac{d\bar{s}(a)}{da} = ((\mu(B,A) - c(a)k_1(a)\lambda^*)\bar{s}(a)$$

$$\frac{d\bar{I}(a)}{da} + r\bar{I}(a) = c(a)k_1(a)\lambda^*\bar{S}(a)$$

Using the initial conditions and the model assumptions we obtained the solutions,

$$\bar{S}(0) = S(0) - S^*(0), \bar{I}(0) = I(0) - I^*(0)$$

$$\bar{S}(a) = \bar{S}(0)p(a)e^{-ra}, \quad p(a) = e^{\mu(B,A)a} = \bar{c}e^{\frac{B}{A}a}, \quad \bar{c} = e^{\varepsilon}$$

$$\bar{I}(a) = \{\bar{I}(0) + \bar{S}(0)\bar{c}e^{\frac{B}{A}a}ra\}e^{-ra}.$$

$$\lambda^* = \frac{c(a)k_1(a)}{A}e^{-ra}\int_0^\infty k_2(p)\Omega(p)dp, \ \Omega(a) = (\bar{I}(0) + \bar{S}(0)\bar{c}e^{\frac{B}{A}p}rp)$$

The solution of these equations in terms of the small perturbations about the steady state tends to zero as a approaches the maximum age, ψ for fixed rate of progression to active TB, independent of the value of A. Thus the endemic steady state (S*(a), I*(a)) is globally asymptotically stable and any infection in the population will not die out but will persist. Let (S*(a),0) be the disease-free steady state, then using the perturbation,

$$S(t,a) = S^*(a) + \bar{S}(a), I(t,a) = \bar{I}(a)$$

We get the following linearization problem about the steady state:

$$\frac{d\bar{S}(a)}{da} = (\mu(B,A) + c(a)k_1(a)\lambda^*)\bar{S}(a)$$

$$\bar{S}(a) = \bar{S}(0)p(a)e^{-ra}, \quad p(a) = e^{\mu(B,A)a} = \bar{c}e^{\frac{B}{A}a}, \quad \bar{c} = e^{\varepsilon}$$

$$\bar{I}(a) = \{\bar{I}(0) + G(a)\lambda^*\}\bar{c}e^{-\frac{B}{A}a},$$

$$G(a) = \int_0^a c(p)k_1(p)(F(a) + Q(a))\bar{c}e^{\frac{B}{A}p}dp$$

$$\lambda^* = \frac{c(a)k_1(a)}{A}\bar{c}e^{-\frac{B}{A}a}H(a), H(a) = \int_0^\infty k_2(p)(\bar{I}(0) + G(p)\lambda^*)dp$$

However, using our assumptions, we get the analytical expression for the susceptible and infectious population compartments of age a,

$$S(a) = \frac{A}{B} r a e^{(\varepsilon+\frac{B}{A})a} S(t_0, 0)$$

$$I(a) = I(t_0, 0) + \frac{rA}{B(\varepsilon + B/A)} e^{(\varepsilon+B/A)a}$$

$$\{(1 - \frac{1}{\varepsilon + B/A})\varepsilon + \frac{B}{A}(a^2 - \frac{1}{\varepsilon + B/A})\}$$

Thus, if the stationary population is increased, with fixed area size, then the susceptible population compartment decreases while the infectious population compartment tends to the initial infectious population size for any given value of a,. However, increasing the population area size, leads to negative infected population compartment. This may be due to the fact that, at such value of A, the infectious population compartment disappears, they don't exist. The susceptible population compartment increases. This further explains the fact that for large area size and fixed stationary population size, transmission of the infection is minimized. In fact the infection may simply die out, if the few infectious individuals are treated as assumed in the model.

CONCLUSION

This studies clearly shows that population area size plays an important in transmission of dynamic of TB. Increasing the area size of the population helps to reduces rate of transmission of TB especially when treatment is practiced and possible eliminate the virus. It also reduces the natural mortality rate and increases life expectancy of the population.

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