Modeling the spread of an infectious disease with bacteria and carriers in the environment

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ABSTRACT

An SIS model with immigration for the spread of an infectious disease with bacteria and carriers in the environment is proposed and analyzed. It is assumed that susceptibles get infected directly by infectives as well as by their contacts with bacteria discharged by infectives in the environment. The growth rate of density of bacteria is assumed to be proportional to the density of infectives and decreases naturally as well as by bacterial interactions with susceptibles and carriers. The carrier population density is considered to follow the logistic model and grows due to conducive human population density related factors. It is assumed further that the number of bacteria transported by carriers to susceptibles is proportional to densities of both bacteria and carriers. The model study shows that the spread of the infectious disease increases due to growth of bacteria and carriers in the environment and disease becomes more endemic due to immigration.

1. Introduction

In past several decades, the spread of various infectious diseases has been modeled and analyzed by considering direct contacts between susceptibles and infectives [1–3] ignoring the role of bacteria present in the environment. But there are some infectious diseases such as typhoid which spread indirectly by bacteria discharged by infectives in the environment [4]. The third world countries are most affected by such diseases due to lack of sanitation and wide presence of carriers such as flies, ticks, mites, etc., in the environment. They transport bacteria of infectious diseases such as typhoid fever, leprosy, cholera, conjunctivitis, tuberculosis, dysentery, diarrhea etc., from the environment to susceptibles and thus spread such diseases in human population. Some of these diseases like dysentery, cholera, typhoid fever etc., are known as food or water borne diseases and are transmitted in human population by flies which carry bacteria of these diseases and transport them into the food and water of susceptible population [5]. Thus the density of carrier population, which may grow with human population density related factors such as household discharges in the environment, plays an important role in the spread of infectious diseases and must be considered in any study.

As mentioned above, though the modeling and analysis of infectious diseases have been conducted by several researchers [1–3], the effects of presence of bacteria and carriers in the environment on the spread of infectious disease have not been studied using mathematical models [4]. Hethcote [6] discussed an epidemic model in which carrier population is assumed to be a constant. But, in general, the size of the carrier population is not constant and depends on the environmental conditions in the habitat. Singh et al. [7], Ghosh et al. [8] and Das et al. [9] have considered variable growth of carrier population which depends on household emissions and other population density related factors in their models. They have

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shown that the spread of infectious disease increases due to transport of bacteria by carriers but they have ignored the interactions of susceptibles with bacteria as well as bacteria with carriers in the environment. Although, Ghosh et al. [10,11] have studied the spread of infectious diseases with bacteria in the environment but they have ignored the role of carriers present in the environment. It is pointed out here that the number of bacteria transported by carriers depends upon the densities of carriers and bacteria in the environment and this aspects must be taken into account in the modeling process.

In this paper, therefore, an SIS model with immigration for the spread of an infectious disease is proposed and analyzed by considering that the number of bacteria transported by carriers is proportional to density of carriers and density of bacteria in the environment. The direct interactions of susceptibles with bacteria in the environment are also taken into account.

2. Mathematical model

Let $N(t)$ be the total human population density in the region under consideration at any time t, which is divided into two subclasses namely, susceptible class with density $X(t)$ and infective class with density $Y(t)$. Let $B(t)$ be the density of bacteria population present in the environment at time t, which are emitted by infectives. Let $B_1(t)$ be the density of that subpopulation of bacteria which are transported to the susceptibles by the carrier population. Let $C(t)$ be the density of carriers present in the environment at time t. Then the density of bacteria B_1 transported by carriers is proportional to densities of bacteria and carriers, (i.e. BC).

It is considered that susceptibles are infected by direct contacts with infectives with the contact rate β, (i.e. βXY) and also by carriers indirectly with the rate λ_1, (i.e. $\lambda_1 XB_1$). It is also considered that susceptibles get infected by direct contact with bacteria due to movement in the bacteria-filled environment with the rate λ, (i.e. λXB). The natural death rate d of human population is assumed to be proportional to its density. It is further assumed that some of the infectives will recover and join the susceptible class. The recovery rate ν is assumed to be proportional to its density, (i.e. νY). The disease related death rate α is considered to be proportional to the density of infective population (i.e. αY). The natural death rate μ_0 of bacteria is assumed to be proportional to the density of the bacterial population (i.e. $\mu_0 B$). The decay rate μ_1 of bacteria in the environment due to transport by carriers is assumed to be proportional to the density of the carrier population as well as the density of the bacteria population, (i.e. $\mu_1 BC$). Since susceptibles may move in the bacteria-filled environment, the decay rate π of bacteria due to their uptake by susceptible individuals is assumed to be proportional to the density of susceptible individuals as well as the density of bacterial population, (i.e. πXB). It is also assumed that the density of carriers follows the logistic model with intrinsic growth rate s and carrying capacity L and its growth rate increases further due to conducive human density related factors, (i.e. $s_1 NC$).

In view of the above assumptions and considerations, the governing equations of the problem are written as follows:

$$\frac{dX}{dt} = A - \beta XY - \lambda XB - \lambda_1 XB_1 - dX + \nu Y,$$

$$\frac{dY}{dt} = \beta XY + \lambda XB + \lambda_1 XB_1 - (\nu + \alpha + d)Y,$$

$$\frac{dB}{dt} = \mu Y - \mu_0 B - \mu_1 BC - \pi XB, \tag{1}$$

$$\frac{dB_1}{dt} = \theta BC - \theta_0 B_1,$$

$$\frac{dC}{dt} = sC\left(1 - \frac{C}{L}\right) - s_0 C + s_1 NC,$$

where $X(0) > 0, Y(0) \geq 0, B(0) \geq 0, B_1(0) \geq 0, C(0) \geq 0$.

In the model system (1), the constant A is the rate of immigration of susceptibles, constant θ is the rate of bacteria carried by carriers to susceptibles and constants μ_0 and θ_0 are depletion rates of B and B_1 respectively in the environment due to control measures. The constant s_0 is the decay rate of carriers C due to control measures. It is noted here that $s - s_0 > 0$.

Using the fact that $X + Y = N$, the above system reduces to the following system:

$$\frac{dY}{dt} = \beta(N - Y)Y + \lambda(N - Y)B + \lambda_1(N - Y)B_1 - (\nu + \alpha + d)Y,$$

$$\frac{dN}{dt} = A - dN - \alpha Y,$$

$$\frac{dB}{dt} = \mu Y - \mu_0 B - \mu_1 BC - \pi(N - Y)B, \tag{2}$$

$$\frac{dB_1}{dt} = \theta BC - \theta_0 B_1,$$

$$\frac{dC}{dt} = sC\left(1 - \frac{C}{L}\right) - s_0 C + s_1 NC.$$

It suffices to study model system (2).