Physica A 403 (2014) 100–109

Contents lists available at ScienceDirect

Physica A

journal homepage: www.elsevier.com/locate/physa

Pattern formation of an epidemic model with time delay

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HIGHLIGHTS

- We presented an epidemic model with spatial diffusion and time delay.
- We find two different types of instability.
- Delay can induce regular patterns.
- The interaction of diffusion and time delay may give rise to rich dynamic.

ARTICLE INFO

Article history:
Received 17 December 2013
Received in revised form 21 January 2014
Available online 22 February 2014

Keywords:
Epidemic model
Spatial diffusion
Time delay
Pattern formation

ABSTRACT

One of the central issues in epidemiology is the study of the distribution of disease. And time delay widely exists in the process of disease spread. Thus, in this paper, we presented an epidemic model with spatial diffusion and time delay. By mathematical analysis, we find two different types of instability. One is the diffusion induced instability, and the other one is delay induced instability. Moreover, we derive the corresponding patterns by performing a series of numerical simulations. The obtained results show that the interaction of diffusion and time delay may give rise to rich dynamics in epidemic systems.

1. Introduction

In recent years, with environmental pollution, ecological destruction and frequent population flow, the whole world major infectious diseases often breakout. Like the H7N9 avian flu, which take place in the year 2013 from February to July and have some bad effect [1–5]. Therefore it is rather important for us to research the infectious disease, in order to predict the development trend of the infectious disease and further control the epidemic.

There are some works on epidemic models without spatial factor [6–9]. However, many infectious diseases are affected by the spatial distribution. In the real world, human, animal, plant and other species are to survive in the spatial environment. In order to be more close to the reality, in the study of infectious disease, it is necessary for us to consider the evolution and distribution of the infected in the space. And this influence can be reflected in the determination of reaction–diffusion models. On the other hand, in the study of infectious disease, one of the most important goals is to predict the trends of disease spreading in space. In other words, the spatial distribution of infectious diseases is very important [10–15].

From the clinical and observational experiment we found, most infectious diseases are infected, and then appear some symptoms needing a period of time (namely incubation period), such as atypical pneumonia SIRS, H1N1 flu, smallpox, which requires us to consider joining the time delay in the model [16–19]. Time delay means that the changes of t moment depend

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http://dx.doi.org/10.1016/j.physa.2014.02.025
0378-4371/

not only on the state at t moment, but also are influenced by some factors before time t moment [20]. Therefore if the epidemic models consider both space and time delay, then the model is more consistent with the actual situation [21,22]. At present, some scholars have done related work on reaction–diffusion models with delay, mainly including the stability of equilibria, the descriptions of Hopf bifurcation, and the analysis of traveling wave solutions [23–25].

The structure of this paper is as follows. In Section 2, we obtain an epidemic model with spatial diffusion and time delay, and describe the biological meanings of these model parameters. In addition, we analyze the spatial model. In Section 3, we deduce the condition of Turing instability (diffusion and delay induced instabilities) by utilizing linear stability analysis. In Section 4, we obtain the patterns by performing a series of numerical simulations. Finally, some conclusions and discussion are given.

2. Mathematical modeling and analysis

2.1. Model formulation

It is well known that it may provide useful information by constructing mathematical models to explain the phenomenon observed in the real world. As a result, epidemic models have been studied by many scholars [26–28]. We assume that the total population (N) is divided into susceptible groups (S) and infectious groups (I). In the absence of the infective, the susceptible group grows according to a logistic mode. On the basis of the above assumptions, we arrive at the following equations:

$$\begin{aligned} \frac{\mathrm{d}S}{\mathrm{d}t} &= rN\left(1-\frac{N}{K}\right)-\beta\frac{SI}{N}-(\mu+m)S,\\ \frac{\mathrm{d}I}{\mathrm{d}t} &= \beta\frac{SI}{N}-(\mu+d)I, \end{aligned} \tag{1}$$

where r is the intrinsic growth rate, K is the carrying capacity of logistic equation, β denotes the contact transmission rate, μ is the natural mortality, d denotes the disease induced morality, m is the per-capital emigration rate of uninfectives. More details about this system can be found in Refs. [10,29].

The basic reproduction number is

$$R_0=\frac{\beta}{\mu+d},$$

and the basic demographic reproductive number is

$$R_d=\frac{r}{\mu+m}.$$

By incorporating the spatial effect and rescaling the above system, we have:

$$\begin{aligned} \frac{\partial S}{\partial t} &= vR_d(S+I)(1-(S+I))-R_0\frac{SI}{S+I}-vS+d_1\nabla^2S,\\ \frac{\partial I}{\partial t} &= R_0\frac{SI}{S+I}-I+d_2\nabla^2I, \end{aligned} \tag{2}$$

where $v=\frac{\mu+m}{\mu+d}$ is the ratio of the average life-span of susceptibles to that of infections.

For some diseases, they have a latent period [30,31]. For example, Rabies may take several days or months to develop to the infectious stage [32–35]. For such a disease, we need to introduce a time delay into the infected population. As a result, we have the following system:

$$\begin{aligned} \frac{\partial S}{\partial t} &= vR_d[S+I(t-\tau)][1-(S+I(t-\tau))]-R_0\frac{SI(t-\tau)}{S+I(t-\tau)}-vS+d_1\nabla^2S,\\ \frac{\partial I}{\partial t} &= R_0\frac{SI(t-\tau)}{S+I(t-\tau)}-I(t-\tau)+d_2\nabla^2I. \end{aligned} \tag{3}$$

2.2. Local stability

In this subsection, we discuss the local stability of the equilibria of the system (2):

$$\begin{aligned} \frac{\mathrm{d}S}{\mathrm{d}t} &= vR_d(S+I)(1-(S+I))-R_0\frac{SI}{S+I}-vS\triangleq f(S,I),\\ \frac{\mathrm{d}I}{\mathrm{d}t} &= R_0\frac{SI}{S+I}-I\triangleq g(S,I). \end{aligned} \tag{4}$$