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Traveling waves in a nonlocal dispersal SIRH model with relapse

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ABSTRACT

This paper is concerned with traveling wave solutions of a nonlocal dispersal Susceptible–Infective–Removal–Healing (for short SIRH) model with relapse. It is found that the existence and nonexistence of traveling waves of the system are not only determined by the critical wave speed c^*, but also by the basic reproduction number $\mathcal{R}_0$ of the corresponding system of ordinary differential equations. More precisely, we use Schauder's fixed-point theorem to obtain the existence of traveling waves for $\mathcal{R}_0 > 1$ and $c > c^*$, and the nonexistence of traveling waves for $\mathcal{R}_0 > 1$ and $0 < c < c^*$. Some numerical simulations and discussions are also provided to illustrate our analytical results.

1. Introduction

As we know, several epidemic infectious brought big disasters in history. At the end of the fifteenth century, smallpox attacked the American continent and Amerindian are nearly extinct. In 1937, the black death broke out in Sicily and then swept the whole of Europe in three years. In 2002, SARS broke out in east Asia and quickly spread to southeast Asia and North America. It is interesting to study how such infectious diseases spread from one location to other areas [1]. In 2012, Wang et al. [2] have considered the following SIR disease outbreak model with the standard incidence

$$\begin{cases} \dfrac{\partial S}{\partial t} = d_1 \Delta S - \dfrac{\beta SI}{S+I}, \\ \dfrac{\partial I}{\partial t} = d_2 \Delta I + \dfrac{\beta SI}{S+I} - \gamma I, \\ \dfrac{\partial R}{\partial t} = d_3 \Delta R + \gamma I. \end{cases} \tag{1.1}$$

Based on that of Wang and Wu [3] and several earlier studies [4–6], they showed a threshold condition for the existence and nonexistence of traveling waves. Then, Wang et al. [7] have extended their results and methods to the following

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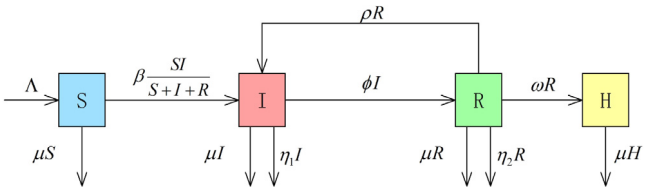

Fig. 1. Transfer diagram for the SIRH model.

three-dimensional diffusive disease model

$$\begin{cases} \dfrac{\partial S}{\partial t} = d_1 \Delta S - \dfrac{\beta SI}{S+I+R}, \\ \dfrac{\partial I}{\partial t} = d_2 \Delta I + \dfrac{\beta SI}{S+I+R} - (\gamma + \delta) I, \\ \dfrac{\partial R}{\partial t} = d_3 \Delta R + \gamma I. \end{cases} \tag{1.2}$$

As we know that reaction–diffusion equations have been used to describe a variety of phenomena in epidemiology and spatial ecology. However, nonlocal dispersal is better to describe the long range process than the random diffusion in many areas, such as materials science, phase transition, ecology, genetics, neurology and epidemiology. The study of traveling waves of nonlocal dispersal epidemic models have attracted much attention. Li et al. [8] and Yang et al. [9] considered traveling waves of nonlocal dispersal SIR models without the vital dynamics, which have rapid outbreak patterns and can only be used to model the fast diseases. Li et al. [10] studied the existence, nonexistence and minimal wave speed of traveling waves of a nonlocal dispersal delayed SIR model with constant external supplies and Holling-II incidence rate. Yang et al. [11] considered traveling wave solutions of a nonlocal dispersal SIR epidemic model. One also can see [12–22] for traveling waves of nonlocal dispersal equations and [23,24] for other development of epidemic models.

Note that the known results for traveling waves of the epidemic model do not consider the relapse to the disease. The current paper is concerned with the following nonlocal dispersal SIRH model:

$$\begin{cases} \dfrac{\partial S(x,t)}{\partial t} = d[(J*S)(x,t) - S(x,t)] + \Lambda - \mu S(x,t) - \dfrac{\beta S(x,t) I(x,t)}{S(x,t)+I(x,t)+R(x,t)}, \\ \dfrac{\partial I(x,t)}{\partial t} = d[(J*I)(x,t) - I(x,t)] + \dfrac{\beta S(x,t) I(x,t)}{S(x,t)+I(x,t)+R(x,t)} + \rho R(x,t) - (\mu + \eta_1 + \phi) I(x,t), \\ \dfrac{\partial R(x,t)}{\partial t} = d[(J*R)(x,t) - R(x,t)] + \phi I(x,t) - \rho R(x,t) - (\mu + \eta_2 + \omega) R(x,t), \\ \dfrac{\partial H(x,t)}{\partial t} = \omega R(x,t) - \mu H(x,t). \end{cases} \tag{1.3}$$

The transfer diagram is shown in Fig. 1.

Here, S, I and R denote the sizes of the susceptible, infected and removed individuals respectively, while H denotes the healing individuals who will not be infected again. β denotes the per-capita effective contact rate (transmission rate), that is, $\frac{\beta SI}{S+I+R}$ denotes the rate of transitions from S to I, the result of the frequency-dependent interactions between individuals in the classes S and I, μ denotes the natural mortality rate, ρ denotes the rate of relapse, ϕ denotes the per-capita recovery (treatment) rate, ω denotes the permanent cure rate and Λ denotes the total recruitment rate into this homogeneous social mixing community. From the last equation of the system (1.3), we can see that H is only related to R. Hence, we only need to study the following system:

$$\begin{cases} \dfrac{\partial S(x,t)}{\partial t} = d[(J*S)(x,t) - S(x,t)] + \Lambda - \mu S(x,t) - \dfrac{\beta S(x,t) I(x,t)}{S(x,t)+I(x,t)+R(x,t)}, \\ \dfrac{\partial I(x,t)}{\partial t} = d[(J*I)(x,t) - I(x,t)] + \dfrac{\beta S(x,t) I(x,t)}{S(x,t)+I(x,t)+R(x,t)} + \rho R(x,t) - (\mu + \eta_1 + \phi) I(x,t), \\ \dfrac{\partial R(x,t)}{\partial t} = d[(J*R)(x,t) - R(x,t)] + \phi I(x,t) - \rho R(x,t) - (\mu + \eta_2 + \omega) R(x,t). \end{cases} \tag{1.4}$$

where $J*S(x,t) = \int_{\mathbb{R}} J(x-y) S(y,t) dy$ is the rate at which the susceptible individuals are arriving at position x from all other places, and $-S(x,t) = -\int_{\mathbb{R}} J(x-y) S(x,t) dy$ is the rate at which they are leaving location x to travel to all other sites, where $J(x-y)$ is thought of as the probability distribution of jumping from location y to location x. Thus, $J*S(x,t) - S(x,t)$ describes that the rate of susceptible individuals at position x at time t depends on the influence of neighboring $S(x,t)$ at all other positions y. Simultaneously, $J*I(x,t) - I(x,t)$ and $J*R(x,t) - R(x,t)$ describe that the rate of infected and