Nonlinear Analysis: Real World Applications 23 (2015) 129–147

Contents lists available at ScienceDirect

Nonlinear Analysis: Real World Applications

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

Traveling waves in a nonlocal dispersal SIR epidemic model

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ARTICLE INFO

Article history:
Received 10 August 2013
Received in revised form 22 November 2014
Accepted 4 December 2014
Available online 29 December 2014

Keywords:
SIR model
Nonlocal dispersal
Traveling waves
Schauder's fixed point theorem
Laplace transform

ABSTRACT

This paper is concerned with traveling wave solutions of a nonlocal dispersal SIR epidemic model. The existence and nonexistence of traveling wave solutions are determined by the basic reproduction number and the minimal wave speed. This threshold dynamics are proved by Schauder's fixed point theorem and the Laplace transform. The main difficulties are that the semiflow generated by the model does not have the order-preserving property and the solutions lack of regularity.

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1. Introduction

Since the pioneering work of Kermack–McKendrick (see [1] for example), the SIR epidemic model and their various extensions have been frequently used in the study of theoretical epidemiology. It is well known that in many cases the spatial variation of populations plays an important role in the disease spreading model and the time variation governs the dynamical behavior of the disease spreading, see [2–5]. Meanwhile, the disease propagation in space is relevant to the so-called traveling wave solutions. For applications to the disease control and prevention, it is important to determine whether traveling waves exist and what the propagation speed is. Thus, there are many works to use spatially dependent models to study the disease transmission, such as the reaction–diffusion, non-local response, or patch models (see [6–13]).

Recently, Wang et al. [14] have considered the following SIR disease outbreak model with the standard incidence

$$\begin{cases} \dfrac{\partial}{\partial t}S = d_1\dfrac{\partial^2 S}{\partial x^2} - \dfrac{\beta SI}{S+I}, \\ \dfrac{\partial}{\partial t}I = d_2\dfrac{\partial^2 I}{\partial x^2} + \dfrac{\beta SI}{S+I} - \gamma I, \\ \dfrac{\partial}{\partial t}R = d_3\dfrac{\partial^2 R}{\partial x^2} + \gamma I. \end{cases} \tag{1.1}$$

They gave a threshold condition for the existence and nonexistence of traveling waves. And their proof is mainly based on that of Wang and Wu [15] and several earlier studies, see [10,16–18]. Recently, Wang et al. [19] and Wang [20] have

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http://dx.doi.org/10.1016/j.nonrwa.2014.12.001
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extended their method and results to the following three-dimensional diffusive disease model

$$\begin{cases} \dfrac{\partial}{\partial t}S = d_1\dfrac{\partial^2 S}{\partial x^2} - \dfrac{\beta SI}{S+I+R}, \\ \dfrac{\partial}{\partial t}I = d_2\dfrac{\partial^2 I}{\partial x^2} + \dfrac{\beta SI}{S+I+R} - (\gamma+\delta)I, \\ \dfrac{\partial}{\partial t}R = d_3\dfrac{\partial^2 R}{\partial x^2} + \gamma I, \end{cases} \tag{1.2}$$

where S, I and R denote the sizes of the susceptible, infected and removal individuals, respectively. The infection rate β and the removal rate γ are positive numbers. $\delta > 0$ represents the death rates of infected individuals. $d_i > 0$ $(i = 1, 2, 3)$ are dispersal rates for the susceptible, infected and removal individuals, respectively. They showed that (1.2) admits a traveling wave solution of the form $(S(x+ct), I(x+ct), R(x+ct))$ such that $S(-\infty) := S_{-\infty} > S(\infty) := S_\infty$, $I(\pm\infty) = 0$, $R(-\infty) = 0$ and $R(+\infty) = \gamma(S_{-\infty} - S_\infty)/(\gamma+\delta)$ if $R_0 = \beta/(\gamma+\delta) > 1$, $c > c^* := 2\sqrt{d_2(\beta-\gamma-\delta)}$ and

$$d_3 < \frac{2d_2}{1-\sqrt{1-\left(\frac{c^*}{c}\right)^2}}. \tag{1.3}$$

Moreover, S is decreasing and R is increasing. On the other hand, if $c < c^*$ or $R_0 \le 1$, there exist no traveling waves of (1.2). Here, $R_0 = \beta/(\gamma+\delta)$, which is the so-called basic reproduction number calculated from the corresponding ordinary differential system of (1.2) at some initial disease-free equilibrium, completely determines the transmission dynamics and epidemic potential: if $R_0 > 1$, $I(t)$ increases to its maximum firstly and then decreases to zero, and hence an epidemic takes place; if $R_0 < 1$, then $I(t)$ decreases to zero, and the epidemic does not occur.

As we see that reaction–diffusion equations have been used to describe a variety of phenomena in epidemiology and spatial ecology. However, nonlocal dispersal is better described as a long range process rather than as a local one in many situations such as in population ecology. Thus, it is natural to describe diffusion process by an integral operators, such as convolution operator $J * u(x) = \int_{\mathbb{R}} J(x-y)u(y)dy$. Meanwhile, nonlocal dispersal problems have attracted much attention, see [21–37] and the references therein. For further understanding the development of nonlocal dispersal problems, one can see [38–44] and so on.

The current paper is concerned with the nonlocal counterpart of (1.2), which is the following nonlocal dispersal SIR model

$$\begin{cases} \dfrac{\partial S}{\partial t} = d_1(J*S - S) - \dfrac{\beta SI}{S+I+R}, \\ \dfrac{\partial I}{\partial t} = d_2(J*I - I) + \dfrac{\beta SI}{S+I+R} - (\gamma+\delta)I, \\ \dfrac{\partial R}{\partial t} = d_3(J*R - R) + \gamma I, \end{cases} \tag{1.4}$$

where $J*S(x,t)$, $J*I(x,t)$ and $J*R(x,t)$ are the standard convolutions with space invariable x. Throughout this paper, we assume that the nonlocal dispersal convolution kernel J is a smooth function on $\mathbb{R}$ and satisfies:

(J) $J \in C^1(\mathbb{R})$, $J(x) = J(-x) \ge 0$, $\int_{\mathbb{R}} J\,dy = 1$ and J is compactly supported.

Here, $J*S(x,t) = \int_R J(x-y)s(y,t)dy$ is the rate at which the susceptible individuals are arriving at position x from all other places, and $-S(x,t) = -\int_R J(x-y)S(x,t)dy$ 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. Meanwhile, $J*I(x,t) - I(x,t)$ and $J*R(x,t) - R(x,t)$ describe that the rate of infected and removal individuals at position x at time t depends on the influence of neighboring $I(x,t)$ and $R(x,t)$ at all other positions y. Model (1.4) with standard incidence rate describes that some of infected individuals will be removed from the population due to disease-induced death or quarantine, but the recovered individuals will return in the community, which captures the essential transmission dynamics and predicts infection propagation from the initial source of an outbreak.

In the present paper, we focus on the existence and nonexistence of traveling wave solutions of system (1.4). We shall prove that if $R_0 := \beta/(\gamma+\delta) > 1$, then there exists a critical velocity c_* such that for each $c > c_*$, system (1.4) admits nontrivial traveling wave solutions with wave speed c and no nontrivial traveling wave solutions of (1.4) for $0 < c < c_*$, and if $R_0 := \beta/(\gamma+\delta) \le 1$, there exist no nontrivial traveling wave solutions for every speed $c \ge 0$.

We point out that the method used in [14,19] will be not effective for system (1.4) due to the appearance of nonlocal dispersal operators. Moreover, in view of the deficiency of monotonicity of system (1.4), it is difficult to obtain the existence of traveling waves and the method in [45] may not be used directly any longer. Recently, inspired by the works in [15,16,46–48], we have successfully used the method to prove the existence of traveling waves of a nonlocal dispersal Kermack–McKendrick SIR epidemic model, which is to construct an invariant cone of initial functions defined in a large but bounded domain, to apply a fixed point theorem on this cone and then extend to the unbounded spatial domain $\mathbb{R}$ by a

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