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Forced Epidemic Waves in a Nonlocal Dispersal SIR Model with Shifting Transmission and Time Delay*

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Abstract This paper is concerned with the forced epidemic waves of a nonlocal dispersal SIR model with shifting transmission and time delay. We first demonstrate that the existence of forced waves can be reduced to a fixed point problem. Then by constructing different pairs of upper and lower solutions and using Schauder's fixed point theorem, we establish two types of forced epidemic waves that reveal different state conversions of the disease. Moreover, we prove the nonexistence of forced epidemic waves when the basic reproduction number is less than unity. Finally, some biological explanations for the theoretical results are given in the discussion.

Keywords Forced waves, shifting transmission, nonlocal dispersal, SIR model, time delay

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1. Introduction

Since the pioneering work of Kermack and McKendrick [21], compartmental models have played an important role in mathematical epidemiology, serving as powerful tools for analyzing and predicting disease spread. However, traditional compartmental models of ordinary differential equations (i.e., ODEs) cannot capture the spatial effects in disease transmission. Consequently, it is essential to consider reaction-diffusion systems in mathematical modeling. Compared to classical diffusion models, nonlocal dispersal models can accurately describe both the long-

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distance transmission of infectious diseases and the large-scale movement of host populations. Furthermore, for diseases with incubation periods, incorporating time delay into the model is a common approach. In particular, Li et al. [25] proposed the following nonlocal dispersal SIR model with time delay:

$$\begin{cases} \dfrac{\partial S(x,t)}{\partial t} = d_1[(J*S)(x,t) - S(x,t)] + B - \sigma S(x,t) - \dfrac{\beta S(x,t) I(x,t-\tau)}{1+\alpha I(x,t-\tau)}, \\ \dfrac{\partial I(x,t)}{\partial t} = d_2[(J*I)(x,t) - I(x,t)] + \dfrac{\beta S(x,t) I(x,t-\tau)}{1+\alpha I(x,t-\tau)} - (\mu+\gamma) I(x,t), \\ \dfrac{\partial R(x,t)}{\partial t} = d_3[(J*R)(x,t) - R(x,t)] + \gamma I(x,t) - \mu_1 R(x,t), \end{cases} \tag{1.1}$$

where $S(x,t)$, $I(x,t)$ and $R(x,t)$ represent the population sizes of susceptible, infective and removed class at location x and time t, respectively. $d_i > 0$ $(i = 1,2,3)$ are diffusion coefficients. $B > 0$ is the recruitment rate of the susceptible population. σ, μ and μ_1 are all positive constants and denote the death rates of each class. $\gamma > 0$ is the recovery rate while $\beta > 0$ is the infection rate. $\alpha > 0$ is the saturation parameter [8]. $\tau > 0$ is the time delay representing the incubation period of the disease. Furthermore, the nonlocal diffusion is characterized by the convolution operator $J * u(x,t) - u(x,t) := \int_{-\infty}^{+\infty} J(x-y)u(y,t)\mathrm{d}y - u(x,t)$, where J is the probability density function [3]. In recent years, the convolution operator above has been widely used to describe large-scale free movement of individuals in either ecological models [2, 5, 14, 19, 23, 32, 37] or epidemic models [13, 20, 25, 26, 34].

Since the third equation in (1.1) is decoupled from others, we only need to consider the first two equations. Introduce the following substitutions as

$$\widetilde{S}(x,t) = \frac{\sigma}{B} S\left(x, \frac{t}{d_2}\right), \quad \widetilde{I}(x,t) = \frac{\sigma}{B} I\left(x, \frac{t}{d_2}\right),$$
$$\widetilde{\sigma} = \frac{\sigma}{d_2}, \quad \widetilde{d} = \frac{d_1}{d_2}, \quad \widetilde{\beta} = \frac{\beta B}{\sigma d_2}, \quad \widetilde{\tau} = d_2\tau, \quad \widetilde{\alpha} = \frac{\alpha B}{\sigma}, \quad \widetilde{\mu} = \frac{\mu}{d_2}, \quad \widetilde{\gamma} = \frac{\gamma}{d_2}$$

and drop the tilde for convenience, then the first two equations of (1.1) reduce to

$$\begin{cases} \dfrac{\partial S(x,t)}{\partial t} = d[(J*S)(x,t) - S(x,t)] + \sigma - \sigma S(x,t) - \dfrac{\beta S(x,t) I(x,t-\tau)}{1+\alpha I(x,t-\tau)}, \\ \dfrac{\partial I(x,t)}{\partial t} = (J*I)(x,t) - I(x,t) + \dfrac{\beta S(x,t) I(x,t-\tau)}{1+\alpha I(x,t-\tau)} - (\mu+\gamma) I(x,t). \end{cases} \tag{1.2}$$

For model (1.2), Li et al. [25] established the existence, nonexistence and minimal wave speed of traveling waves connecting the disease free equilibrium $(1,0)$ to the endemic equilibrium $\left(\frac{\mu+\gamma+\alpha\sigma}{\alpha\sigma+\beta}, \frac{\sigma[\beta-(\mu+\gamma)]}{(\mu+\gamma)(\alpha\sigma+\beta)}\right)$, and further illustrated how the latency of infection and the spatial movement of the infective individuals affect the minimal wave speed.

As we all know, climate change is one of the major challenges of the world today and has attracted global attention. In fact, climate change is an important factor in triggering diseases. For example, climate change affects the emergence of vector-borne diseases such as malaria, dengue and West Nile virus by altering their ranges, distribution or seasonality [27]. On the other hand, climate change also affects the transmission capacity of diseases. For instance, elevated temperatures