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Competitive exclusion in a multi-strain virus model with spatial diffusion and age of infection $\stackrel{\bigstar}{=}$

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ABSTRACT

In this paper, a multi-strain virus dynamic model with spatial diffusion, age of infection and general incidence function is formulated. The well-posedness of the initial-boundary value problem of the model in the bounded domain $\Omega \subset \mathbb{R}^n$ is analyzed. By constructing a suitable Lyapunov functional, the global stability of the uninfected steady state is established if all reproduction numbers are smaller or equal to one. It is shown that if \mathcal{R}_i , the reproduction number corresponding to strain *i* is larger than one, the steady state corresponding to strain *i* exists, if $\mathcal{R}_1 > 1$ is the maximal reproduction number, the steady state E_1 corresponding strain one is globally stable. That is, competitive exclusion occurs and strain one eliminates all other strains.

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1. Introduction

Since the time of Gause [8], scientists have been fascinated by the principles that govern species coexistence and competitive exclusion. Coexistence and competitive exclusion has been studied in the context of ecological models, epidemiological models, within-host models and other settings. The first rigorous proof of the competitive exclusion principle was given by Bremermann and Thieme [1] in epidemiological setting. Bremermann and Thieme showed that in the most basic multi-strain SIR model the strain with the largest reproduction number outcompetes the remaining strains and persists in the population. This principle was

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extended to age-since-infection structured epidemic models with environmental transmission by Martcheva and Li [13]. Regarding epidemic models with diffusion, Martcheva and Tuncer [20] showed that in a twostrain SIS model with diffusion and spatially non-homogeneous coefficients coexistence may occur. Wu *et al.* [22] investigated the topic further and showed competitive exclusion in some special cases with constants coefficients.

Within-host models have also received significant attention. De Leenheer and Smith [5] first established the global stability of the infection equilibrium in the most widely used HIV/HCV mathematical model using the so-called "sector condition". Global competitive exclusion was then proved in a multi-strain ODE version by De Leenheer and Pilyugin [4]. This result was also extended to a multi-strain age-since-infection structured model by Browne [2]. Variations of the within-host HIV model with diffusion have also been considered. Stancevic *et al.* [17] consider a version with simple recruitment but reaction and diffusion terms in all classes. They find Turing instability in the model. More recently, a spatial version of the classical within-host HIV model with diffusion and spatially heterogeneous coefficients was more thoroughly analyzed and global asymptotic behavior of the solutions was established [16]. To our knowledge, spatial multi-strain versions of the model have not been considered.

Versions of the basic within-host HIV ODE model with general incidence have also been considered. Tian and Liu [19] consider the model with simple recruitment and general incidence. They find that the infection equilibrium is globally stable whenever it exists. The global stability of a diffusion version of the within-host model with general incidence was recently studied by McCluskey and Yang [15].

In this paper we consider a multi-strain version of the basic within-host HIV model with general incidence, age-since-infection structure of infected T cells, and diffusion of the virus. We aim to show global competitive exclusion under these conditions, thus extending prior results. In the next section, we introduce the multi-strain model with age-since-infection structure, diffusion and general incidence. In section 3 we derive some preliminary results related to the properties of the flow. In section 4 we show the global stability of the infection-free state. In section 5 we consider the uniform persistence of the system and we prove the competitive exclusion principle. Section 6 discusses some applications and section 7 summarizes our results.

2. The multi-strain model

In this section we introduce our multi-strain model with age-since-infection structure, diffusion and general incidence. The model is given below.

$$\begin{cases} \frac{\partial u}{\partial t} = r - mu(x,t) - \sum_{i=1}^{n} f_i(u(x,t), V_i(x,t)), \\ \frac{\partial w_i(x,\theta,t)}{\partial \theta} + \frac{\partial w_i(x,\theta,t)}{\partial t} = -\delta_i(\theta)w_i(x,\theta,t), \quad i = 1, \cdots, n, \\ \frac{\partial V_i}{\partial t} = D_i\Delta V_i + \int_0^\infty p_i(\theta)w_i(x,\theta,t)d\theta - c_iV_i(x,t), \end{cases}$$
(2.1)

for $t > 0, x \in \Omega$, with homogeneous Neumann boundary conditions

$$\frac{\partial V_i}{\partial \nu} = 0, \ t > 0, \ x \in \partial \Omega, \quad i = 1, \cdots, n,$$
(2.2)

and the initial and boundary conditions:

$$\begin{cases} w_i(x,0,t) = f_i(u(x,t), V_i(x,t)), & x \in \bar{\Omega}, \quad i = 1, \cdots, n, \\ u_i(x,0) = u_{i0}(x), \quad w_i(x,\theta,0) = w_{i0}(x,\theta), \quad V_i(x,0) = V_{i0}(x), \quad x \in \bar{\Omega}. \end{cases}$$
(2.3)

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