Accepted Manuscript

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 PII:
 S0893-9659(17)30212-4

 DOI:
 http://dx.doi.org/10.1016/j.aml.2017.06.010

 Reference:
 AML 5285

To appear in: Applied Mathematics Letters

Received date : 9 April 2017 Revised date : 21 June 2017 Accepted date : 21 June 2017



Please cite this article as: W. Wang, W. Ma, A diffusive HIV infection model with nonlocal delayed transmission, Appl. Math. Lett. (2017), http://dx.doi.org/10.1016/j.aml.2017.06.010

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A diffusive HIV infection model with nonlocal delayed transmission $\stackrel{r}{\approx}$

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Abstract

A diffusive HIV infection model with nonlocal delayed transmission is proposed. In a bounded spatial domain, we investigate threshold dynamics in terms of basic reproduction number \Re_0 for the heterogeneous model. *Keywords:* HIV, Nonlocal, Basic reproduction number, Threshold dynamics.

1. Introduction and model derivation

Most existing virus dynamical models are based on the classic model proposed in [8], which is governed by ordinary differential equations. In recent years, the in-host viral infection dynamical models incorporating spatial dispersion have been considered (see, for example, [18, 19] and references therein).

It is widely known that the existence of time delays is inevitable in biology. In more realistic virus infection dynamical models, any time delays should be spatially inhomogeneous. This is due to the fact that any given individuals may not necessarily have been at the same spatial location at previous time [1]. Let Ω denote the spatial habitat with smooth boundary $\partial \Omega$. Let U = U(x,t), V = V(x,t) and $\omega = \omega(x,t)$ be the density of uninfected cells, infected cells, and virus at time t and habitat x, respectively. Let $\xi(x)$ be production rate of uninfected cells and infected by virus at rate $\beta(x)U(x,t)\omega(x,t)/(1 + a(x)\omega(x,t) + b(x)U(x,t))$ adopting Beddington-DeAngelis functional response. Here, a(x) is a measure of virus interference during infection, and b(x) determines how fast the infection rate approaches its saturation value. Virus is produced from infected cells at rate k(x)V(x,t). The death rates of uninfected cells, infected cells and virus are $d_U(x)$, $d_V(x)$ and $d_{\omega}(x)$, respectively. We assume that all the parameters are positive, continuous and bounded in the domain $\overline{\Omega}$.

By employing the method similar to [4], we can derive the following nonlocal delayed and diffusive virus

th The research is partly supported by the NNSF of China (11471034) and National Key R&D Program of China for W. Ma. *Corresponding author

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