Applied Mathematical Modelling 34 (2010) 1511–1523

Contents lists available at ScienceDirect

Applied Mathematical Modelling

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

Properties of stability and Hopf bifurcation for a HIV infection model with time delay ☆

Xinyu Song *, Xueyong Zhou, Xiang Zhao

Department of Mathematics, Xinyang Normal University Xinyang 464000, Henan, PR China

ARTICLE INFO

Article history:
Received 26 October 2008
Received in revised form 25 August 2009
Accepted 1 September 2009
Available online 15 September 2009

Keywords:
Time delay
HIV infection
Hopf bifurcation
Global stability

ABSTRACT

In this paper, we consider the classical mathematical model with saturation response of the infection rate and time delay. By stability analysis we obtain sufficient conditions for the global stability of the infection-free steady state and the permanence of the infected steady state. Numerical simulations are carried out to explain the mathematical conclusions.

1. Introduction

It is known that HIV (human immunodeficiency virus) has become a global problem. The human is suffering enormously due to HIV and AIDS (acquired immunodeficiency syndrome). For example, AIDS is now the leading cause of death in Sub-Saharan Africa. Many countries in this region have failed to bring the epidemic under control. It is said that nearly two-thirds of the world's HIV positive people live in Sub-Saharan Africa. So, in the last decades the infection by HIV, which caused AIDS, has been the subject of most intense studies that encompass diverse fields of scientific research. Although major progress has been achieved by medical and biological researchers in understanding different aspects of the virus–host interaction, the mechanisms by which HIV causes AIDS still remain unexplained.

Mathematical models have been proven to be valuable in understanding the dynamics of HIV infection. Most of them use ordinary (or partial) differential equations to describe different aspects of the dynamics of the host–parasite interaction [1–5]. And these models typically consider the dynamics of the $CD4^+$ and virus populations as well as the effects of drug therapy [6]. There are also some models which include an intracellular delay [7–10]. Models that included delays have been introduced to account for the time between viral entry into a target cell and the production of new virus particles. Recently, Song et al. [11] have investigated the following viral model with delay:

$$\begin{cases} \dot{T} = s - dT + aT\left(1 - \frac{T}{T_{max}}\right) - \beta TV, \\ \dot{I} = \beta e^{-m\tau} T(t-\tau)V(t-\tau) - \delta I, \\ \dot{V} = pI - cV, \end{cases} \tag{1.1}$$

☆ This work is supported by the National Natural Science Foundation of China (No. 10771179) and Program for Innovative Research Team (in Science and Technology) in University of Henan Province (2010IRTSTHN006)

* Corresponding author.
E-mail address: xysong88@163.com (X. Song).

0307-904X/$ - see front matter © 2009 Elsevier Inc. All rights reserved.
doi:10.1016/j.apm.2009.09.006

where T is the number of target cells, I is the number of infected cells, V is the viral load of the virous, s represents the rate at which new T cells are created from sources, a is the maximum proliferation rate of target cells. T_{max} is the T population density at which proliferation shuts off. In model (1.1), d is death rate of the T cells, β is the infection rate constant, the term $e^{-m\tau}$ accounts for cells that are infected at time t but die before becoming productively infected τ time units later. δ is the death rate of the infective cells, p is the reproductively rate of the infected cells, and $\frac{p}{\delta}$ is the total number of virion produced by a productively infected cell during its lifetime, c is the clearance rate constant of virions.

Song et al. studied the effect of time delay on the stability of the endemically infected equilibrium, criteria were given to ensure that the infected equilibrium was asymptotically stable for all delays. The conditions for the existence of orbitally asymptotically stable periodic solutions was also established. All the results were under the case $m = 0$ in system (1.1).

Although the rate of infection in most HIV models is bilinear in the virus V and the uninfected target cells T, actual incidence rates are probably not strictly linear in each variable over the entire range of V and T. For example, a less than linear response in V could occur due to saturation at high virus concentration, where the infectious fraction is high so that exposure is very likely. Thus, it is reasonable for us to assume that the infection rate of modelling HIV, HBV and HCV infection in saturated mass action, $\beta TV^l/(1+\alpha V^q)$, where, $l, q, \alpha > 0$ are constants. In this paper, we shall investigate the viral model with saturation response of the infection rate ($l = q = 1$). The model can be written as the following form:

$$\begin{cases} \dot{T} = s - dT + aT\left(1 - \frac{T}{T_{max}}\right) - \frac{\beta TV}{1+\alpha V}, \\ \dot{I} = \frac{\beta e^{-m\tau} T(t-\tau)V(t-\tau)}{1+\alpha V(t-\tau)} - \delta I, \\ \dot{V} = pI - cV. \end{cases} \tag{1.2}$$

The meaning of the parameters is the same as above. We will analyze the stability of equilibria and Hopf bifurcation. And we will show that when delay τ passes through a critical value, the endemic equilibrium loses its stability and Hopf bifurcation occurs. Since the coefficients of the corresponding characteristic equation depend on delay τ, there are stability switches, and all roots of the characteristic equation have negative real parts when τ is large enough.

This paper is organized as follows. In the next section, the local and global stability of the viral-free equilibrium are studied. In Section 3, we will give the conditions for existence of the permanence at the endemic equilibrium. In Section 4, the Hopf bifurcation at the infected equilibrium is determined. In Section 5, some numerical simulations are performed to illustrate the analytical results.

2. Stability of the viral-free equilibrium E_1 and the infected equilibrium E_2

We denote the Banach space of continuous functions $\varphi : [-\tau, 0] \to \mathbb{R}^3$ with norm

$$\|\varphi\| = \sup_{-\tau \leqslant \theta \leqslant 0} \{|\varphi_1(\theta)|, |\varphi_2(\theta)|, |\varphi_3(\theta)|\}$$

by C, where $\varphi = (\varphi_1, \varphi_2, \varphi_3)$. Further, let

$$C_+ = \{\varphi = (\varphi_1, \varphi_2, \varphi_3) \in C : \varphi_i \geqslant 0 \text{ for all } \theta \in [-\tau, 0],\ i = 1, 2, 3\}.$$

The initial condition for system (1.2) is given as

$$T(\theta) = \varphi_1(\theta), \quad I(\theta) = \varphi_2(\theta), \quad V(\theta) = \varphi_3(\theta), \quad -\tau \leqslant \theta \leqslant 0,$$

where $\varphi = (\varphi_1, \varphi_2, \varphi_3)$.

First, we know that the possible non-negative equilibria of system (1.2) are $E_1(\widehat{T}, 0, 0)$ and $E_2(\overline{T}, \overline{I}, \overline{V})$, where

$$\widehat{T} = \frac{T_{max}}{2a}\left[a - d + \sqrt{(a-d)^2 + \frac{4as}{T_{max}}}\right],$$

$$\overline{T} = \frac{T_{max}}{2a}\left[\left(a - d - \frac{\beta}{\alpha}\right) + \sqrt{\left(a - d - \frac{\beta}{\alpha}\right)^2 + \frac{4as}{T_{max}} + \frac{4ac\delta}{\alpha p T_{max} e^{-m\tau}}}\right],$$

$$\overline{I} = \frac{c\overline{V}}{p},$$

$$\overline{V} = \frac{p\beta e^{-m\tau}\overline{T} - c\delta}{\alpha c\delta}.$$

The basic reproductive number is given by

$$R_0 = \frac{p\beta e^{-m\tau}\overline{T}}{c\delta}.$$

In the following, we consider the locally asymptotic stability of the viral-free equilibrium E_1 and the infected equilibrium E_2.

Theorem 2.1. (1) *If $R_0 < 1$, then E_1 is locally asymptotically stable for any time delay $\tau \geqslant 0$.*