

http://www.aimspress.com/journal/MBE

MBE, 17(5): 4527–4543. DOI: 10.3934/mbe.2020250 Received: 03 March 2020 Accepted: 16 June 2020 Published: 29 June 2020

## Research article

# Global stability for a class of HIV virus-to-cell dynamical model with Beddington-DeAngelis functional response and distributed time delay

# Xinran Zhou, Long Zhang\*, Tao Zheng, Hong-li Li and Zhidong Teng

College of Mathematics and System Sciences, Xinjiang University, Urumqi 830046, China

\* Correspondence: Email:longzhang\_xj@sohu.com.

**Abstract:** A HIV virus-to-cell dynamical model with distributed delay and Beddington-DeAngelis functional response is proposed in this paper. Using the characteristic equations and analytical means, the principle reproduction number  $R_0$  on the local stability of infection-free and chronic-infection equilibria is established. Furthermore, by constructing suitable Lyapunov functionals and using LaSalle invariance principle, we show that if  $R_0 \le 1$  the infection-free equilibrium is globally asymptotically stable, while if  $R_0 > 1$  the chronic-infection equilibrium is globally asymptotically stable. Numerical simulations are presented to illustrate the theoretical results. Comparing the effects between discrete and distributed delays on the stability of HIV virus-to-cell dynamical models, we can see that they could be same and different even opposite.

**Keywords:** distributed delay; principle reproduction number; Beddington-DeAngelis functional response; Lyapunov functional; globally asymptotical stability

## 1. Introduction

In the past decades, the research on virus dynamical models has attracted great many medical scientists and bio-mathematicians for its important potential applications on prediction and prevention and control of many fatal diseases, e.g., Ebola, Zika, measles, schistosomiasis (see, e.g., [1–7]) etc. As well known, AIDS is a serious infectious disease caused by HIV viruses which choose the CD4<sup>+</sup>T lymphocytes in the human immune system as the mainly attacking target. HIV viruses increasingly destroy the CD4<sup>+</sup>T lymphocytes in large quantities till depriving of efficacy of immune system in human body, at the same time, turn the infected CD4<sup>+</sup>T lymphocytes into HIV viruses. Nowak and Bangham [8] initiatively applied a parasite model proposed by Anderson and May [9] to investigate

the virus-to-cell dynamics as follows:

$$\begin{cases}
\frac{dx}{dt} = s - dx(t) - \beta x(t)v(t), \\
\frac{dy}{dt} = \beta x(t)v(t) - py(t), \\
\frac{dz}{dt} = ky(t) - uv(t).
\end{cases}$$
(1.1)

Here *x*, *y*, *v* represent the concentration of uninfected CD4<sup>+</sup>T cells, infected CD4<sup>+</sup>T cells and HIV viruses at time *t*, respectively. *s* (*s* > 0) is the rate of newborn CD4<sup>+</sup>T cells, *d*, *p*, *u* are the death rates of uninfected CD4<sup>+</sup>T cells, infected CD4<sup>+</sup>T cells and removed rate of HIV virus particles from the system respectively. The constant  $\beta$  is the infection (or contact) rate between uninfected CD4<sup>+</sup>T cells and HIV viruses. Criteria on the globally asymptotical stability of infection-free and chronic-infection equilibria were established. Recently, a lots of significant works on the HIV dynamical models were achieved based on model (1.1). The primary issues are: computation of the principle reproduction number *R*<sub>0</sub> under different incidence functions (e.g., bilinear, saturation, Beddington-DeAngelis, nonlinear incidence, etc.) with cell-to-cell transmission and virus-to-cell transmission (or mixed transmission), stability of infection-free equilibrium, extinction of infection, existence and stability of chronic-infection equilibrium, persistence of infection (see, e.g., [10–15] and references cited therein) etc.

However, as we know that the conversion of uninfected (or infected) CD4<sup>+</sup>T cells into infected CD4<sup>+</sup>T cells (or HIV viruses) will often not respond immediately to change, but rather will do so after a time lag. Therefore, many authors introduced the time delays into HIV dynamic models (see, e.g., [16–18]). Meanwhile, Beddington-DeAngelis functional response is more realistic to characterize the dynamic evolution process of susceptible cells and viruses (e.g., [19–22]). Huang et al. [20], Nakata [21] introduced Beddington-DeAngelis functional response and discrete delay into the above model (1) as follows

$$\begin{pmatrix}
\frac{dx}{dt} = s - dx(t) - \frac{\beta x(t)v(t)}{1 + ax(t) + bv(t)}, \\
\frac{dy}{dt} = \frac{e^{-p\tau}\beta x(t-\tau)v(t-\tau)}{1 + ax(t-\tau) + bv(t-\tau)} - py(t), \\
\frac{dz}{dt} = ky(t) - uv(t).
\end{cases}$$
(1.2)

Here function  $\frac{\beta x(t)v(t)}{1+ax(t)+bv(t)}$  denotes the Beddington-DeAngelis infection rate between uninfected CD4<sup>+</sup>T cells *x* and HIV viruses *v*, *a*, *b* are positive constants,  $\tau > 0$  represents the requisite time for conversion of uninfected CD4<sup>+</sup>T cells *x* into infected CD4<sup>+</sup>T cells *y*. Many important results about the globally asymptotical stability of infection-free and chronic-infection equilibria were obtained. Furthermore, it has been proven that distributed delay is more proper to model the long-term infectious process than

discrete delay (e.g., [23-25]). Xu [23] introduced distributed delay into model (1.1) as follows

$$\begin{cases} \frac{dx}{dt} = s - dx(t) - \beta x(t)v(t), \\ \frac{dy}{dt} = \beta \int_0^\infty f_1(\tau) e^{-m_1 \tau} x(t - \tau)v(t - \tau)d\tau - ay(t), \\ \frac{dz}{dt} = k \int_0^\infty f_2(\tau) e^{-m_2 \tau} y(t - \tau)d\tau - uv(t). \end{cases}$$
(1.3)

Criteria based on principle reproduction number  $R_0$  were obtained on the globally asymptotical stability of infection-free and chronic-infection equilibria. Motivated by the above considerations, in this paper, we incorporate Beddington-DeAngelis functional response and distributed delay into model (1.2) as follows

$$\begin{cases} \frac{dx}{dt} = s - dx(t) - \frac{\beta x(t)v(t)}{1 + ax(t) + bv(t)}, \\ \frac{dy}{dt} = \int_0^\tau f(\sigma) \frac{e^{-d\sigma}\beta x(t - \sigma)v(t - \sigma)}{1 + ax(t - \sigma) + bv(t - \sigma)} d\sigma - py(t), \\ \frac{dz}{dt} = ky(t) - uv(t). \end{cases}$$
(1.4)

The integral term  $\int_0^{\tau} f(\sigma) \frac{e^{-d\sigma}\beta x(t-\sigma)v(t-\sigma)}{1+ax(t-\sigma)+bv(t-\sigma)} d\sigma$  represents the total quantity of target CD4<sup>+</sup>T cells *x* exposed to the HIV viruses *v* and still survive and convert into infected CD4<sup>+</sup>T cells *y* within time intervals  $[0, \tau]$ . Here,  $f(\sigma) : [0, \tau] \to [0, \infty)$  is the distribution function which accounts for the variance of infected cells to become productively infected from individual to individual, assumed to be compact support,  $f(\sigma) \ge 0$  and  $\int_0^{\tau} f(\sigma) d\sigma = 1$  (refer to [11]).

The main purpose of this paper is to explore the effect of distributed delay and Beddington-DeAngelis functional response on the dynamical behavior of HIV virus-to-cell dynamical model (1.4). Furthermore, by introducing the principle reproduction number  $R_0$  to discuss the locally and globally asymptotical stability of free-infection equilibrium  $E_0$  and chronic-infection equilibrium  $E^*$  by constructing proper Lyapunov functionals and LaSalle invariance principle.

The organization of this paper is as follows. In the second section, we discuss the positivity and boundedness of solutions of system (1.4). In the section 3, criteria are obtained on the local stability of infection-free equilibrium  $E_0$  if principle reproduction number  $R_0 < 1$ , and chronic-infection equilibrium  $E^*$  if  $R_0 > 1$ . In the section 4, we further establish criteria on the globally asymptotical stability of infection-free equilibrium  $E_0$  if  $R_0 \le 1$ , and chronic-infection equilibrium  $E^*$  if  $R_0 > 1$ . In the section 5, the theoretical results are illustrated by numerical simulations and discussion. Comparing of effects between discrete delay and distributed delay on the stability with models (1.2) and (1.4), we can see that they would be complete different even opposite if the same values of delay is taken within a proper interval. In the last section, a brief conclusion is presented.

#### 2. Positivity and boundedness of solutions

The initial conditions of model (1.4) are given as

$$x(\theta) = \varphi_1(\theta), \quad y(\theta) = \varphi_2(\theta), \quad v(\theta) = \varphi_3(\theta), \quad \theta \in [-\tau, 0].$$
 (2.1)

Where  $\varphi = (\varphi_1, \varphi_2, \varphi_3)^T \in C([-\tau, 0], R^3_+)$  such that  $\varphi_i(\theta) \ge 0(\tau \le \theta \le 0, i = 1, 2, 3)$ , and *C* be the Banach space of continuous functions from  $[-\tau, 0]$  to  $R^3$  equipped with the sup-norm.

With respect to the positivity and boundedness of solutions for models (1.4), we have the following result.

**Theorem 2.1.** Let  $(x(t), y(t), v(t))^T$  be any solution of model (1.4) with initial conditions (2.1), we have that all solutions  $(x(t), y(t), v(t))^T$  of model (1.4) are non-negative on  $[0, +\infty)$  and ultimately bounded. **Proof.** Assume x(t) is not positive on the maximum existing interval [0, T), then there exists a  $t_1 \in [0, T)$  such that  $x(t_1) = 0$  and x(t) > 0 for all  $t \in [0, t_1)$ , therefore, we can easily see that  $\dot{x}(t_1) \leq 0$ . On the other hand, from the first equation of model (1.4), we can see  $\dot{x}(t_1) = s > 0$ . This leads to a contradiction. Therefore, x(t) is always nonnegative for all  $t \in [0, T)$ . From the other two equations of model (1.4), we have

$$\begin{split} y(t) = y(0)e^{-dt} &+ \int_0^t \int_0^\tau f(\sigma) \frac{e^{-d\sigma}\beta x(\theta - \sigma)v(\theta - \sigma)}{1 + ax(\theta - \sigma) + bv(\theta - \sigma)} d\sigma e^{-d(t-\theta)} d\theta \\ v(t) = v(0)e^{-ut} + \int_0^t ky(\theta)e^{-u(t-\theta)}d\theta. \end{split}$$

Therefore, it is easy to see that y(t) and v(t) are all non-negative for all  $t \in [0, T)$ .

Next, we prove the boundedness of the system, from the first equation of system (1.4) we can obtain

$$\dot{x}(t) = s - dx(t) - \frac{\beta x(t)v(t)}{1 + ax(t) + bv(t)} \le s - dx(t).$$

By comparison theorem, we obtain  $\lim_{t\to+\infty} \sup x(t) \le \frac{s}{d}$ , so x(t) is bounded on [0, T). Define

$$F(t) = \int_0^\tau f(\sigma) e^{-d\sigma} x(t-\sigma) d\sigma + y(t),$$

and  $\delta = \min\{d, p\}$ . We have

$$\frac{dF(t)}{dt} = \int_{0}^{\tau} f(\sigma)e^{-d\sigma}[s - dx(t - \sigma) - \frac{\beta x(t - \sigma)v(t - \sigma)}{1 + ax(t - \sigma) + bv(t - \sigma)}]d\sigma 
+ \int_{0}^{\tau} f(\sigma)\frac{e^{-d\sigma}\beta x(t - \sigma)v(t - \sigma)}{1 + ax(t - \sigma) + bv(t - \sigma)} - py(t) 
= s \int_{0}^{\tau} f(\sigma)e^{-d\sigma}d\sigma - d \int_{0}^{\tau} f(\sigma)e^{-d\sigma}x(t - \sigma)d\sigma - py(t) 
\leq s \int_{0}^{\tau} f(\sigma)e^{-d\sigma}d\sigma - \delta F(t).$$
(2.2)

This implies that F(t) is bounded, therefore y(t) is bounded too. By the third equation of system (1.4), v(t) is also bounded. Because all solution (x(t), y(t), v(t)) of model (1.4) is bounded on [0, T), therefore, we can see that  $T = +\infty$ . This completes the proof of Theorem 2.1.

### 3. Local stability of equilibria

In this part, we discuss the local stability of the equilibria of model (1.4). Obviously, there is always a infection-free equilibrium  $E_0(s/d, 0, 0)$  for model (1.4). Next, we will analyze the positive chronic-

4531

infection equilibrium  $E^* = (x^*, y^*, v^*)$  of model (1.4). Consider the following equations

$$\begin{cases} s - dx^* - \frac{\beta x^* v^*}{1 + ax^* + bv^*} = 0, \\ \int_0^\tau f(\sigma) e^{-d\sigma} d\sigma \frac{\beta x^* v^*}{1 + ax^* + bv^*} - py^* = 0, \\ ky^* - uv^* = 0. \end{cases}$$
(3.1)

We have

$$x^* = \frac{pu + kbs \int_0^\tau f(\sigma)e^{-d\sigma}d\sigma}{(bkd + \beta k) \int_0^\tau f(\sigma)e^{-d\sigma}d\sigma - apu}, \quad v^* = \frac{k}{pu}(s - dx^*) \int_0^\tau f(\sigma)e^{-d\sigma}d\sigma, \quad y^* = \frac{u}{k}v^*.$$
(3.2)

For the positivity of the chronic-infection equilibrium  $E^* = (x^*, y^*, v^*)$ , we need  $x^* > 0$ , which means

$$(bkd + \beta k) \int_0^\tau f(\sigma) e^{-d\sigma} d\sigma - apu > 0.$$
(3.3)

Denote

$$R_0 = \frac{k\beta s \int_0^\tau f(\sigma) e^{-d\sigma} d\sigma}{pu(d+as)}.$$

when  $R_0 > 1$ , Eq (3.3) is always true, meanwhile  $v^* > 0$  also holds.

First, about the local stability (or un-stability) for infection-free equilibrium  $E_0$  of model (1.4), we have the following result.

**Theorem 3.1.** The infection-free equilibrium  $E_0$  of model (1.4) is locally asymptotically stable (or unstable) if  $R_0 < 1$  (or  $R_0 > 1$ ).

**Proof.** For the infection-free equilibrium  $E_0$ , we can obtain the characteristic equation of system (1.4) as follows:

$$(\lambda+d)[(\lambda+p)(\lambda+u) - \int_0^\tau f(\sigma)e^{-d\sigma}d\sigma \frac{k\beta s}{d+as}e^{-\lambda\tau}] = 0.$$

Because of  $\lambda = -d < 0$ , so the stability of  $E_0$  depends on

$$h(\lambda) = (\lambda + p)(\lambda + u) - \int_0^\tau f(\sigma)e^{-d\sigma}d\sigma \frac{k\beta s}{d + as}e^{-\lambda\tau}.$$

Case 1:  $R_0 < 1$ , from

$$h(\lambda) = (\lambda + p)(\lambda + u) - \int_0^\tau f(\sigma)e^{-d\sigma}d\sigma \frac{k\beta s}{d + as}e^{-\lambda\tau} = 0,$$

it follows that

$$G(\lambda) = \frac{\int_0^{\tau} f(\sigma) e^{-d\sigma} d\sigma \frac{k\beta s}{d+as} e^{-\lambda \tau}}{(\lambda+p)(\lambda+u)} = 1.$$

Mathematical Biosciences and Engineering

Let  $\lambda = x + iy$  ( $x, y \in R$ ), if  $x \ge 0$ , we obtain

$$1 = |G(\lambda)| = \frac{\left|\int_{0}^{\tau} f(\sigma)e^{-d\sigma}d\sigma\frac{k\beta s}{d+as}e^{-\lambda\tau}\right|}{|(\lambda+p)(\lambda+u)|}$$

$$\leq \frac{\left|\int_{0}^{\tau} f(\sigma)e^{-d\sigma}d\sigma\frac{k\beta s}{d+as}e^{-x\tau}\right|}{|(x+p)(x+u)|}$$

$$\leq \frac{\left|\int_{0}^{\tau} f(\sigma)e^{-d\sigma}d\sigma\frac{k\beta s}{d+as}\right|}{|pu|}$$

$$= \frac{k\beta s\int_{0}^{\tau} f(\sigma)e^{-d\sigma}d\sigma}{pu(d+as)} = R_{0} < 1,$$
(3.4)

which is a contradiction. Thus, if  $R_0 < 1$ , then x < 0, and hence  $E_0$  is locally asymptotically stable. Case 2: If  $R_0 > 1$ , we obtain

$$h(0) = pu - \int_0^\tau f(\sigma) e^{-d\sigma} d\sigma \frac{k\beta s}{d+as} < 0,$$

and  $\lim_{\lambda\to\infty} h(\lambda) = +\infty$ . Therefore,  $h(\lambda) = 0$  has at least one non-negative root. Hence, if  $R_0 > 1$ , then  $E_0$  is unstable. This completes the proof of Theorem (3.1).

Next, about the local stability for chronic-infection equilibrium  $E^*$  of model (1.4), we have the following result.

**Theorem 3.2.** If  $R_0 > 1$ , then the chronic-infection equilibrium  $E^*$  of model (1.4) is locally asymptotically stable.

**Proof.** We can obtain that the characteristic equation at the chronic-infection equilibrium  $E^*$  as follow:

$$\begin{aligned} &(\lambda + d + \frac{\beta v^* (1 + bv^*)}{(1 + ax^* + bv^*)^2})[(\lambda + p)(\lambda + u) - \int_0^\tau f(\sigma)e^{-d\sigma}d\sigma \frac{k\beta x^* (1 + ax^*)}{(1 + ax^* + bv^*)^2}e^{-\lambda\tau}] \\ &+ \int_0^\tau f(\sigma)e^{-d\sigma}d\sigma \frac{\beta v^* (1 + bv^*)}{(1 + ax^* + bv^*)^2} \frac{k\beta x^* (1 + ax^*)}{(1 + ax^* + bv^*)^2}e^{-\lambda\tau} = 0. \end{aligned}$$
(3.5)

That is

$$(\lambda + p)(\lambda + u) = \frac{(\lambda + d) \int_0^\tau f(\sigma) e^{-d\sigma} d\sigma \frac{k\beta x^* (1 + ax^*)}{(1 + ax^* + bv^*)^2} e^{-\lambda \tau}}{\lambda + d + \frac{\beta v^* (1 + bv^*)}{(1 + ax^* + bv^*)^2}}.$$
(3.6)

Let

$$L = (\lambda + p)(\lambda + u), \quad R = \frac{(\lambda + d) \int_0^\tau f(\sigma) e^{-d\sigma} d\sigma \frac{k\beta x^*(1 + ax^*)}{(1 + ax^* + bv^*)^2} e^{-\lambda \tau}}{\lambda + d + \frac{\beta v^*(1 + bv^*)}{(1 + ax^* + bv^*)^2}},$$

If  $\lambda$  is a root of (3.2) with nonnegative real part, it follows

$$|L| = |(\lambda + p)(\lambda + u)| \ge pu.$$

Mathematical Biosciences and Engineering

Furthermore, from (3.1), we can have

$$|R| = \left| \frac{(\lambda + d) \int_{0}^{\tau} f(\sigma) e^{-d\sigma} d\sigma \frac{k\beta x^{*}(1+ax^{*})}{(1+ax^{*}+bv^{*})^{2}} e^{-\lambda\tau}}{\lambda + d + \frac{\beta v^{*}(1+bv^{*})}{(1+ax^{*}+bv^{*})^{2}}} \right|$$

$$= \left| \frac{(\lambda + d) \int_{0}^{\tau} f(\sigma) e^{-d\sigma} d\sigma k\beta x^{*}(1+ax^{*}) e^{-\lambda\tau}}{(\lambda + d)(1+ax^{*}+bv^{*})^{2} + \beta v^{*}(1+bv^{*})}} \right|$$

$$< \left| \frac{\int_{0}^{\tau} f(\sigma) e^{-d\sigma} d\sigma k\beta x^{*}(1+ax^{*}) e^{-\lambda\tau}}{(1+ax^{*}+bv^{*})^{2}} \right|$$

$$= pu \left| \frac{\beta x^{*}v^{*}(1+ax^{*}) e^{-\lambda\tau}}{(s-dx^{*})(1+ax^{*}+bv^{*})^{2}} \right|$$

$$< pu \left| \frac{1+ax^{*}}{1+ax^{*}+bv^{*}} \right|$$

$$< pu.$$
(3.7)

Consequently, we obtain |L| > |R|, which leads to a contradiction. Therefore, we can get that (3.5) cannot have any root with positive real part. Hence, the chronic-infection equilibrium  $E^*$  is locally asymptotic stable as  $R_0 > 1$ . This completes the proof of Theorem 3.2.

## 4. Global stability of equilibria

In this section, we will prove the globally asymptotical stability of infection-free equilibrium  $E_0$  and chronic-infection equilibrium  $E^*$  for model (1.4). First for the globally asymptotical stability of  $E_0$ , we have the following result.

**Theorem 4.1.** The infection-free equilibrium  $E_0$  of model (1.4) is globally asymptotically stable if  $R_0 \le 1$ .

**Proof.** Define a Lyapunov functional  $V_1$  as follows:

$$V_1(x, y, v) = \int_0^\tau f(\sigma) e^{-d\sigma} d\sigma \frac{x_0}{1 + ax_0} (\frac{x(t)}{x_0} - 1 - \ln \frac{x(t)}{x_0}) + y(t) + \frac{p}{k} v(t) + U^-(t).$$

Where  $x_0 = \frac{s}{d}$ , and

$$U^{-}(t) = \int_0^{\tau} \int_{t-\sigma}^t f(\sigma) \frac{e^{-d\sigma} \beta x(\xi) v(\xi)}{1 + ax(\xi) + bv(\xi)} d\xi d\sigma.$$

Derivative  $U^{-}(t)$  on both sides, we have:

$$\frac{dU^{-}(t)}{dt} = \int_{0}^{\tau} f(\sigma) \frac{e^{-d\sigma} \beta x(t)v(t)}{1 + ax(t) + bv(t)} d\sigma - \int_{0}^{\tau} f(\sigma) \frac{e^{-d\sigma} \beta x(t - \sigma)v(t - \sigma)}{1 + ax(t - \sigma) + bv(t - \sigma)} d\sigma$$

$$= \int_{0}^{\tau} f(\sigma) e^{-d\sigma} d\sigma \frac{\beta x(t)v(t)}{1 + ax(t) + bv(t)} - \int_{0}^{\tau} f(\sigma) \frac{e^{-d\sigma} \beta x(t - \sigma)v(t - \sigma)}{1 + ax(t - \sigma) + bv(t - \sigma)} d\sigma.$$
(4.1)

Mathematical Biosciences and Engineering

Therefore, we obtain that

$$\begin{aligned} \frac{dV_1}{dt} &= \int_0^\tau f(\sigma) e^{-d\sigma} d\sigma \frac{1}{1+ax_0} (1-\frac{x_0}{x}) \dot{x}(t) + \dot{y}(t) + \frac{p}{k} \dot{v}(t) + \frac{dU^-(t)}{dt} \\ &= \int_0^\tau f(\sigma) e^{-d\sigma} d\sigma \frac{1}{1+ax_0} (1-\frac{x_0}{x}) \left[ s - dx(t) - \frac{\beta x(t)v(t)}{1+ax(t)+bv(t)} \right] \\ &+ \int_0^\tau f(\sigma) \frac{e^{-d\sigma} \beta x(t-\sigma)v(t-\sigma)}{1+ax(t-\sigma)+bv(t-\sigma)} d\sigma - py(t) \\ &+ \frac{p}{k} (ky(t) - uv(t)) + \int_0^\tau f(\sigma) e^{-d\sigma} d\sigma \frac{\beta x(t)v(t)}{1+ax(t)+bv(t)} \\ &- \int_0^\tau f(\sigma) \frac{e^{-d\sigma} \beta x(t-\sigma)v(t-\sigma)}{1+ax(t-\sigma)+bv(t-\sigma)} d\sigma \\ &= \int_0^\tau f(\sigma) e^{-d\sigma} d\sigma \frac{1}{1+ax_0} (1-\frac{x_0}{x(t)}) \left[ dx_0 - dx(t) - \frac{\beta x(t)v(t)}{1+ax(t)+bv(t)} \right] \\ &- \frac{pu}{k} v(t) + \int_0^\tau f(\sigma) e^{-d\sigma} d\sigma \frac{\beta x(t)v(t)}{1+ax(t)+bv(t)} \\ &= -\frac{d\int_0^\tau f(\sigma) e^{-d\sigma} d\sigma}{1+ax_0} (x(t) - x_0)^2 \\ &+ \int_0^\tau f(\sigma) e^{-d\sigma} d\sigma \frac{1+ax(t)}{1+ax_0} \times \frac{\beta x_0v(t)}{1+ax(t)+bv(t)} - \frac{pu}{k} \\ &= -\frac{d\int_0^\tau f(\sigma) e^{-d\sigma} d\sigma}{x(t)(1+ax_0)} (x(t) - x_0)^2 + \frac{puv(t)}{k} \times \frac{1+ax(t)}{1+ax(t)+bv(t)} (R_0 - 1) \\ &- \frac{pub}{k(1+ax(t)+bv(t))} v^2(t). \end{aligned}$$

Therefore, when  $R_0 \leq 1$  we have  $\frac{dV_1}{dt} \leq 0$ . And  $\frac{dV_1}{dt} = 0$  if and only if  $x = x_0, v = 0$ . Let M be the largest invariant set  $\{(\phi_1, \phi_2, \phi_3)^T \in R^3_+, \dot{V}_1 = 0\}$ , we have  $M = \{E_0\}$ . It follows from LaSalle invariance principle, when  $R_0 \leq 1$ , then  $E_0$  is globally asymptotically stable. This completes the proof of Theorem 4.1.

Next, about the globally asymptotical stability of  $E^* = (x^*, y^*, v^*)$  of system (1.4), we have the following result:

**Theorem 4.2.** If  $R_0 > 1$ , the chronic-infection  $E^*$  of model (1.4) is globally asymptotically stable. **Proof.** We define Lyapunov functional  $V_2$  as follows:

$$V_2(x, y, v) = U(t) + py^* U^+(t),$$
(4.3)

$$\begin{split} U(t) = &(\int_{0}^{\tau} f(\sigma) e^{-d\sigma} d\sigma)^{2} \bigg[ x(t) - x^{*} - \int_{x^{*}}^{x(t)} \frac{1 + a\theta + bv^{*}}{1 + ax^{*} + bv^{*}} \times \frac{x^{*}}{\theta} d\theta \bigg] \\ &+ \bigg[ (\int_{0}^{\tau} f(\sigma) e^{-d\sigma} d\sigma) (y(t) - y^{*} - y^{*} \ln \frac{y(t)}{y^{*}}) \bigg] \\ &+ \bigg[ (\int_{0}^{\tau} f(\sigma) e^{-d\sigma} d\sigma) \frac{p}{k} (v(t) - v^{*} - v^{*} \ln \frac{v(t)}{v^{*}}) \bigg], \end{split}$$
(4.4)

Mathematical Biosciences and Engineering

and

$$U^{+}(t) = \int_{0}^{\tau} \int_{t-\sigma}^{t} f(\sigma) e^{-d\sigma} \left[ \left( \int_{0}^{\tau} f(\sigma) e^{-d\sigma} d\sigma \right) \frac{\beta x(\xi) v(\xi)}{p y^{*} (1 + a x(\xi) + b v(\xi))} - 1 - \ln \left( \int_{0}^{\tau} f(\sigma) e^{-d\sigma} d\sigma \right) \frac{\beta x(\xi) v(\xi)}{p y^{*} (1 + a x(\xi) + b v(\xi))} \right] d\xi d\sigma.$$

$$(4.5)$$

We can find that

$$\frac{dU^{+}(t)}{dt} = \int_{0}^{\tau} \left(\int_{0}^{\tau} f(\sigma)e^{-d\sigma}d\sigma\right) \frac{f(\sigma)e^{-d\sigma}\beta x(t)v(t)}{py^{*}(1+ax(t)+bv(t))} d\sigma 
- \int_{0}^{\tau} \left(\int_{0}^{\tau} f(\sigma)e^{-d\sigma}d\sigma\right) \frac{f(\sigma)e^{-d\sigma}\beta x(t-\sigma)v(t-\sigma)}{py^{*}(1+ax(t-\sigma)+bv(t-\sigma))} d\sigma 
+ \int_{0}^{\tau} e^{-d\sigma} \ln\left(\frac{x(t-\sigma)v(t-\sigma)}{1+ax(t-\sigma)+bv(t-\sigma)} \times \frac{1+ax(t)+bv(t)}{x(t)v(t)}\right) d\sigma 
= \frac{1}{py^{*}} \left(\int_{0}^{\tau} f(\sigma)e^{-d\sigma}d\sigma\right)^{2} \frac{\beta x(t)v(t)}{1+ax(t)+bv(t)} 
- \frac{1}{py^{*}} \left(\int_{0}^{\tau} f(\sigma)e^{-d\sigma}d\sigma\right) \int_{0}^{\tau} f(\sigma)\frac{e^{-d\sigma}\beta x(t-\sigma)v(t-\sigma)}{1+ax(t-\sigma)+bv(t-\sigma)} d\sigma 
+ \int_{0}^{\tau} f(\sigma)e^{-d\sigma} \ln\left(\frac{x(t-\sigma)v(t-\sigma)}{1+ax(t-\sigma)+bv(t-\sigma)} \times \frac{1+ax(t)+bv(t)}{x(t)v(t)}\right) d\sigma.$$
(4.6)

Therefore, we can obtain

$$\begin{split} \frac{dV_2}{dt} =& (\int_0^\tau f(\sigma)e^{-d\sigma}d\sigma)^2 (1 - \frac{1 + ax(t) + bv^*}{1 + ax^* + bv^*} \times \frac{x^*}{x})\dot{x}(t) \\ &+ (\int_0^\tau f(\sigma)e^{-d\sigma}d\sigma)(1 - \frac{y^*}{y})\dot{y}(t) \\ &+ (\int_0^\tau f(\sigma)e^{-d\sigma}d\sigma)\frac{p}{k}(1 - \frac{v^*}{v(t)})\dot{v}(t) + py^*\frac{dU^+(t)}{dt} \\ =& (\int_0^\tau f(\sigma)e^{-d\sigma}d\sigma)^2(1 - \frac{1 + ax(t) + bv^*}{1 + ax^* + bv^*} \times \frac{x^*}{x}) \Big[ dx^* - dx(t) \\ &+ \frac{\beta x^*v^*}{1 + ax^* + bv^*} - \frac{\beta x(t)v(t)}{1 + ax(t) + bv(t)} \Big] \\ &+ (\int_0^\tau f(\sigma)e^{-d\sigma}d\sigma)(1 - \frac{y^*}{y}) \Big[ \int_0^\tau f(\sigma)\frac{e^{-d\sigma}\beta x(t - \sigma)v(t - \sigma)}{1 + ax(t - \sigma) + bv(t - \sigma)} d\sigma \\ &- py(t) \Big] + (\int_0^\tau f(\sigma)e^{-d\sigma}d\sigma)\frac{p}{k}(1 - \frac{v^*}{v})[ky(t) - uv(t)] + py^*\frac{dU^+(t)}{dt} \\ =& (\int_0^\tau f(\sigma)e^{-d\sigma}d\sigma)^2(1 - \frac{1 + ax(t) + bv^*}{1 + ax^* + bv^*} \times \frac{x^*}{x}) \Big[ - d(x(t) - x^*) \\ &+ \frac{\beta x^*v^*}{1 + ax^* + bv^*} - \frac{\beta x(t)v(t)}{1 + ax(t) + bv(t)} \Big] \end{split}$$

Mathematical Biosciences and Engineering

$$\begin{aligned} &+ (\int_{0}^{\tau} f(\sigma)e^{-d\sigma}d\sigma)(1 - \frac{y^{*}}{y(t)}) \Big[ \int_{0}^{\tau} f(\sigma) \frac{e^{-d\sigma}\beta x(t-\sigma)v(t-\sigma)}{1+ax(t-\sigma)+bv(t-\sigma)} d\sigma - py(t) \Big] \\ &+ (\int_{0}^{\tau} f(\sigma)e^{-d\sigma}d\sigma) \frac{p}{k}(1 - \frac{v^{*}}{v(t)}) [ky(t) - uv(t)] + py^{*} \frac{dU^{+}(t)}{dt} \\ &= - (\int_{0}^{\tau} f(\sigma)e^{-d\sigma}d\sigma)^{2} \frac{d(1+bv^{*})}{x(t)(1+ax^{*}+bv^{*})} (x(t) - x^{*})^{2} + (\int_{0}^{\tau} f(\sigma)e^{-d\sigma}d\sigma)py^{*} \\ &- (\int_{0}^{\tau} f(\sigma)e^{-d\sigma}d\sigma)py^{*} \frac{1+ax(t)+bv^{*}}{1+ax^{*}+bv^{*}} \frac{x^{*}}{x(t)} + (\int_{0}^{\tau} f(\sigma)e^{-d\sigma}d\sigma)py^{*} \frac{1+ax(t)+bv^{*}}{1+ax^{*}+bv^{*}} \frac{v(t)}{v^{*}} \\ &- py^{*} \frac{y^{*}(1+ax^{*}+bv^{*})}{y(t)x^{*}v^{*}} \int_{0}^{\tau} f(\sigma) \frac{e^{-d\sigma}x(t-\sigma)v(t-\sigma)}{1+ax(t-\sigma)+bv(t-\sigma)} d\sigma + (\int_{0}^{\tau} f(\sigma)e^{-d\sigma}d\sigma)py^{*} \\ &- (\int_{0}^{\tau} f(\sigma)e^{-d\sigma}d\sigma)py^{*} \frac{v(t)}{v^{*}} - (\int_{0}^{\tau} f(\sigma)e^{-d\sigma}d\sigma)py^{*} \frac{y(t)v^{*}}{y^{*}v(t)} + (\int_{0}^{\tau} f(\sigma)e^{-d\sigma}d\sigma)py^{*} \\ &+ py^{*} \int_{0}^{\tau} f(\sigma)e^{-d\sigma}d\sigma)^{2} \frac{d(1+bv^{*})}{x(t)(1+ax^{*}+bv^{*})} (x(t) - x^{*})^{2} \\ &+ py^{*} \left[ 3(\int_{0}^{\tau} f(\sigma)e^{-d\sigma}d\sigma) - (\int_{0}^{\tau} f(\sigma)e^{-d\sigma}d\sigma) \frac{1+ax(t)+bv^{*}}{1+ax^{*}+bv^{*}} \frac{x^{*}}{x(t)} \\ &- (\int_{0}^{\tau} f(\sigma)e^{-d\sigma}d\sigma) \times \frac{y(t)v^{*}}{y^{*}v(t)} - \frac{y^{*}(1+ax^{*}+bv^{*})}{y(t)x^{*}v^{*}} \int_{0}^{\tau} f(\sigma) \frac{e^{-d\sigma}x(t-\sigma)v(t-\sigma)}{1+ax(t-\sigma)+bv(t-\sigma)} d\sigma \right] \end{aligned}$$

$$= -\left(\int_{0}^{\tau} f(\sigma)e^{-d\sigma}d\sigma\right)^{2} \frac{d(1+bv^{*})}{x(t)(1+ax^{*}+bv^{*})}(x(t)-x^{*})^{2} + py^{*}\left[3\left(\int_{0}^{\tau} f(\sigma)e^{-d\sigma}d\sigma\right) - \left(\int_{0}^{\tau} f(\sigma)e^{-d\sigma}d\sigma\right)\frac{1+ax(t)+bv^{*}}{1+ax^{*}+bv^{*}}\frac{x^{*}}{x(t)} \right) \right.$$

$$+ py^{*}\left[3\left(\int_{0}^{\tau} f(\sigma)e^{-d\sigma}d\sigma\right) \times \frac{y(t)v^{*}}{y^{*}v(t)} - \frac{y^{*}(1+ax^{*}+bv^{*})}{y(t)x^{*}v^{*}} \int_{0}^{\tau} f(\sigma)\frac{e^{-d\sigma}x(t-\sigma)v(t-\sigma)}{1+ax(t-\sigma)+bv(t-\sigma)}d\sigma\right]$$

$$+ py^{*}\left(\int_{0}^{\tau} f(\sigma)e^{-d\sigma}d\sigma\right) \left(-\frac{v(t)}{v^{*}} + \frac{v(t)}{v^{*}}\frac{1+ax(t)+bv^{*}}{1+ax(t)+bv(t)}\right) + py^{*}\int_{0}^{\tau} f(\sigma)e^{-d\sigma}d\sigma\right)^{2}\frac{d(1+bv^{*})}{x(t)(1+ax^{*}+bv^{*})}(x(t)-x^{*})^{2}$$

$$+ py^{*}\int_{0}^{\tau} f(\sigma)e^{-d\sigma}d\sigma\right)^{2}\frac{d(1+bv^{*})}{x(t)(1+ax^{*}+bv^{*})}(x(t)-x^{*})^{2} + py^{*}\int_{0}^{\tau} f(\sigma)e^{-d\sigma}\left[1-\frac{1+ax(t)+bv^{*}}{1+ax^{*}+bv^{*}}\frac{x^{*}}{x(t)} + \ln\left(\frac{1+ax(t)+bv^{*}}{1+ax(t-\sigma)+bv(t-\sigma)}\right)\right]d\sigma$$

$$+ py^{*}\int_{0}^{\tau} f(\sigma)e^{-d\sigma}\left[1-\frac{y^{*}(1+ax^{*}+bv^{*})}{y(t)x^{*}v^{*}} \times \frac{x(t-\sigma)v(t-\sigma)}{1+ax(t-\sigma)+bv(t-\sigma)} + \ln\left(\frac{y^{*}(1+ax^{*}+bv^{*})}{y(t)x^{*}v^{*}} \times \frac{x(t-\sigma)v(t-\sigma)}{1+ax(t-\sigma)+bv(t-\sigma)}\right]d\sigma$$

$$+ py^{*}\int_{0}^{\tau} f(\sigma)e^{-d\sigma}\left[1-\frac{y^{*}(1+ax(t)+bv(t)}{1+ax(t)+bv^{*}} + \ln\frac{1+ax(t)+bv(t)}{1+ax(t)+bv^{*}}\right]d\sigma$$

$$+ py^{*}\int_{0}^{\tau} f(\sigma)e^{-d\sigma}\left(1-\frac{1+ax(t)+bv(t)}{1+ax(t)+bv^{*}} + \ln\frac{1+ax(t)+bv(t)}{1+ax(t)+bv^{*}}\right)d\sigma$$

$$+ py^{*}\int_{0}^{\tau} f(\sigma)e^{-d\sigma}d\sigma\left(1-\frac{1+ax(t)+bv(t)}{1+ax(t)+bv^{*}} + \frac{v(t)}{1+ax(t)+bv^{*}}\right)d\sigma$$

$$+ py^{*}\int_{0}^{\tau} f(\sigma)e^{-d\sigma}d\sigma\left(1-\frac{1+ax(t)+bv(t)}{1+ax(t)+bv^{*}} + \frac{v(t)}{1+ax(t)+bv(t)}\right)d\sigma$$

$$+ py^{*}\int_{0}^{\tau} f(\sigma)e^{-d\sigma}d\sigma\left(1-\frac{1+ax(t)+bv(t)}{1+ax(t)+bv^{*}}\right)d\sigma$$

For any  $\eta(t) > 0$ , the function

$$H(t) = 1 - \eta(t) + \ln \eta(t)$$

Mathematical Biosciences and Engineering

is always non-positive, and H(t) = 0 if and only if  $\eta(t) = 1$ .

Furthermore, we have

$$-1 - \frac{v(t)}{v^*} + \frac{1 + ax(t) + bv(t)}{1 + ax(t) + bv^*} + \frac{v(t)}{v^*} \frac{1 + ax(t) + bv^*}{1 + ax(t) + bv(t)}$$

$$= \frac{-b(1 + ax)(v(t) - v^*)^2}{v^*(1 + ax + bv)(1 + ax + bv^*)} \le 0.$$
(4.9)

Hence, we can see that  $\frac{dV_2}{dt} \le 0$ . And  $\frac{dV_2}{dt} = 0$  if and only if  $x(t) = x^*, y(t) = y^*, v(t) = v^*$ . From the Lyapunov-LaSalle invariance principle, it indicates that when  $R_0 > 1$ , the chronic-infection equilibrium  $E^*$  is globally asymptotically stable. This completes the proof of Theorem 4.2.

### 5. Numerical simulations and discussion

In this paper, we studied a class of HIV virus-to-cell dynamic model with distributed delay and Beddington-DeAngelis functional response, by analysis methods and constructing proper Lyapunov functionals, threshold criteria of principle reproduction number  $R_0$  for model (1.4) were established. We see that if  $R_0 \le 1$  the infection-free equilibrium  $E_0 = (s/d, 0, 0)$  is globally asymptotically stable, while if  $R_0 > 1$  the chronic-infection equilibrium  $E^* = (x^*, y^*, v^*)$  is globally asymptotically stable. Now, we will use numerical simulations to illustrate our results, for convenience, we take

$$f(\sigma) = \frac{1}{\tau}, \quad 0 \le \sigma \le \tau.$$
 (5.1)

Obviously, we have

$$\int_0^\tau f(\sigma)d\sigma = \int_0^\tau \frac{1}{\tau}d\sigma = 1.$$

We take the values of parameters in both model (1.2) and (1.4) as in the following Table 1.

rable 1. values of parameters.										
models	а	b	d	S	β	р	k	и		
(1.2) and (1.4)	0.6	0.8	0.1	0.8	0.8	0.5	0.3	0.2		

Table 1. Values of parameters.

We have the following results for model (1.4):

Case 1, we take  $\tau = 40$  with other values of parameters in Table 1, we can easily get  $R_0 = 0.8124 < 1$ . From the Theorem 4.1, we can see that the infection-free equilibrium  $E_0 = (8, 0, 0)$  of model (1.4) is globally asymptotically stable (see Figure 1(a) and (b)).

Case 2, we take  $\tau = 0.2$  with other values of parameters in Table 1, we can easily obtain  $R_0 = 3.2775 > 1$ . From the Theorem 4.2 we, can see that the chronic-infection equilibrium  $E^* = (1.4405, 1.2989, 1.9483)$  of model (1.4) is globally asymptotically stable (see Figure 1(c) and (d)).

Furthermore, we will compare the effects between discrete delay and distributed delay on the stability of the virus-to-cell dynamical models, i.e., models (1.2) and (1.4). According to [20], the

principle reproduction number of model (1.2) is

$$R_0^* = \frac{k\beta s e^{-p\tau}}{pu(d+as)}$$

The principle reproduction number of model (1.4) is

$$R_0 = \frac{k\beta s(1 - e^{-d\tau})}{\tau dpu(d + as)}.$$

In the case of values of parameters in Table 1, we have the following conclusions:

$$\begin{cases} R_0^* \ge 1, R_0 > 1, if \quad 0 < \tau \le 2.3941. \\ R_0^* < 1, R_0 \ge 1, if \quad 2.3942 < \tau \le 31.715. \\ R_0^* < 1, R_0 < 1, if \quad \tau > 31.716. \end{cases}$$
(5.2)

By calculation, we can see that the two equilibria of model (1.2) are

$$E_{0}^{*} = (s/d, 0, 0), \bar{E}^{*} = \left(\frac{sbk + pue^{p\tau}}{k\beta + bdk - apue^{p\tau}}, \frac{s\beta ke^{-p\tau}(1 - \frac{1}{R_{0}^{*}})}{p(k\beta + bdk - apue^{p\tau})}, \frac{s\beta k^{2}e^{-p\tau}(1 - \frac{1}{R_{0}^{*}})}{pu(k\beta + bdk - apue^{p\tau})}\right)$$

And

$$E_0 = (s/d, 0, 0), E^* = (x^* = \frac{dpu + (1 - e^{-d\tau})kbs}{\tau(1 - e^{-d\tau})(bkd + \beta k) - a\tau dpu}, y^* = \frac{u}{k}v^*, v^* = \frac{k}{\tau dpu}(s - dx^*)(1 - e^{-d\tau})(bkd + \beta k) - a\tau dpu}$$

are the infection-free and chronic-infection equilibria of system (1.4), respectively.

We take the values of parameters as in the Table 1 for both models (1.2) and (1.4). If the delay  $\tau = 0.2$  is taken for both models (1.2) and (1.4), we can see  $R_0^* = 2.9953 > 1$ , by [20], the chronic-infection equilibrium  $\bar{E}^* = (1.5303, 1.1708, 1.7562)$  of model (1.2) is globally asymptotically stable (see Figure 2(a),(b)). And  $R_0 = 3.2775 > 1$ , the chronic-infection equilibrium  $\overline{E}^* = (1.4405, 1.2989, 1.9483)$  of model (1.4) is globally asymptotically stable (see Figure 1(c),(d)). If delay  $\tau = 2.8$  is taken for both models (1.2) and (1.4), we can see  $R_0^* = 0.8163 < 1$ , by [20] the infection-free equilibrium  $E_0^* = (8, 0, 0)$  of model (1.2) is globally asymptotically stable (see Figure 2(e) and (f). While  $R_0$ = 2.8873 > 1, the chronic-infection equilibrium  $E^* = (1.5709, 1.1215, 1.6822)$  of model (1.4) is globally asymptotically stable (see Figure 1(e),(f)). If delay  $\tau = 40$  is taken for both models (1.2) and (1.4), we can see  $R_0^* = 6.8231 \times 10^{-9} < 1$ , by [20] the infection-free equilibrium  $E_0^* = (8, 0, 0)$  of model (1.2) is globally asymptotically stable (see Figure 2(c) and (d)). While  $R_0 = 0.8124 > 1$ , the infection-free equilibrium  $E_0^* = (8, 0, 0)$  of model (1.2) is globally asymptotically stable (see Figure 1(a),(b)).

The details of above numerical simulations for both models (1.2) and (1.4) are as follows:

τ	$R_0^*$	$E_0^*$	$ar{E}^*$	$R_0$	$E_0$	$E^*$
0.2	2.9953	_	GAS (Figure 2(a), (b))	3.2775	_	GAS (Figure 1(c), (d))
2.8	0.8163	GAS (Figure 2(e), (f))	_	2.8873	_	GAS (Figure 1(e), (f))
40	$6.231 \times 10^{-9}$	GAS (Figure 2(c), (d))	-	0.8124	GAS (Figure 1(a), (b))	_

Table 2. Numerical simulations of the models (1.2) and (1.4).

<sup>1</sup> Here, GAS=globally asymptotically stable.

Mathematical Biosciences and Engineering



**Figure 1.** (a), (b): Time series and 3-dimension phases of solutions (x(t), y(t), v(t)) of system (1.4) in case 1 with initial functions:  $(x(\theta), y(\theta), v(\theta)) = (0.3 + 0.1 * sin(\theta) + 0.4 * k, 0.3 + 0.2 * sin(\theta) + 0.3 * k, 0.1 + 0.3 * sin(\theta) + 0.35 * k), k = 1, 2, \dots, 20$ , for all  $\theta \in [-40, 0]$ , respectively. (c), (d): Time series and 3-dimension phases of solutions (x(t), y(t), v(t)) of system (1.4) in case 2 with initial functions:  $(x(\theta), y(\theta), v(\theta)) = (0.3 + 0.1 * sin(\theta) + 0.4 * k, 0.3 + 0.2 * sin(\theta) + 0.3 * k, 0.1 + 0.3 * sin(\theta) + 0.3 * k), k = 1, 2, \dots, 20$ , for all  $\theta \in [-0.2, 0]$ , respectively. (e), (f): Time series and 3-dimension phases of solutions phases of solutions (x(t), y(t), v(t)) of system (1.4) with initial functions:  $(x(\theta), y(\theta), v(\theta)) = (0.3 + 0.1 * sin(\theta) + 0.2 * k, 0.3 + 0.2 * sin(\theta) + 0.2 * k, 0.3 + 0.2 * sin(\theta) + 0.2 * k, 0.3 + 0.2 * sin(\theta) + 0.2 * k, 0.1 + 0.3 * sin(\theta) + 0.2 * k), k = 1, 2, \dots, 20$ , for all  $\theta \in [-2.8, 0]$ , respectively.

Mathematical Biosciences and Engineering



**Figure 2.** (a), (b): Time series and 3-dimension phases of solutions (x(t), y(t), v(t)) of system (1.2) when delay  $\tau = 0.2$  and with initial functions:  $(x(\theta), y(\theta), v(\theta)) = (0.2 + 0.2 * k, 0.2 + 0.2 * k, 0.2 + 0.01 * k)$ ,  $k = 1, 2, \dots, 20$ , for all  $\theta \in [-0.2, 0]$ , respectively.(c), (d): Time series and 3-dimension phases of solutions (x(t), y(t), v(t)) of system (1.2) when delay  $\tau = 40$  and with initial functions:  $(x(\theta), y(\theta), v(\theta)) = (0.2 + 0.2 * k, 0.2 + 0.2 * k, 0.2 + 0.01 * k)$ ,  $k = 1, 2, \dots, 20$ , for all  $\theta \in [-40, 0]$ , respectively. (e), (f): Time series and 3-dimension phases of solutions (x(t), y(t), v(t)) of system (1.2) when delay  $\tau = 2.8$  and with initial functions:  $(x(\theta), y(\theta), v(\theta)) = (2.2 + 0.2 * k, 0.2 + 0.2 * k, 0.2 + 0.01 * k)$ ,  $k = 1, 2, \dots, 20$ , for all  $\theta \in [-2.8, 0]$ , respectively.

Mathematical Biosciences and Engineering

Based on the above comparison, we can draw a conclusion: for HIV virus-to-cell dynamical models (1.2) and (1.4), the effects of discrete and distributed delays on stability could be similar and different even opposite. If  $0 < \tau \le 2.3941$  and with the same values of parameters in Table 1, the basic reproduction number  $R_0^* > 1$  and  $R_0 > 1$  both hold corresponding to models (1.2) and (1.4), both  $\bar{E}^*$ and  $E^*$  are globally asymptotically stable. However, if  $2.3942 < \tau \le 31.715$  and with the same values of parameters, the basic reproduction number  $R_0^* < 1$  holds for model (1.2), while  $R_0 > 1$  holds for model (1.4). Meanwhile, the stability on the  $E_0$ ,  $E^*$  of model (1.4) and  $E_0^*$ ,  $\overline{E}^*$  of model (1.2) presents completely opposite results. Furthermore, if  $\tau > 31.716$  and with the same values of parameters, the basic reproduction number  $R_0^* < 1$  and  $R_0 < 1$  both hold corresponding to models (1.2) and (1.4), both  $E_0^*$  and  $E_0$  are globally asymptotically stable. Briefly, under the same set of parameters, when the same values are taken for both discrete and distributed delays of models (1.2) and (1.4) within a properly interval respectively, if the infection-free equilibrium of model (1.2) with discrete delay is globally asymptotically stable, then the chronic-infection equilibrium of model (1.4) with distributed delay could be globally asymptotically stable. In other word, if the virus turn to extinct with discrete time delay, it could be persistent with distributed time delay for HIV virus-to-cell infectious models. However, if the same values of parameters are taken for discrete and distributed delays in other intervals respectively, both models (1.2) and (1.4) have the same results about stability.

## 6. Conclusions

In this paper, a class of HIV virus-to-cell dynamics model with Beddington-DeAngelis functional response and distribution delay is studied. The principle reproduction number  $R_0$  is obtained, by which threshold values on the globally asymptotical stability of infection-free equilibrium  $E_0$  and chronic-infection equilibrium  $E^*$  of model (4) are established. If  $R_0 \leq 1$  the infection-free equilibrium  $E_0$  is globally asymptotically stable, while  $R_0 > 1$  the chronic-infection equilibrium  $E^*$  is globally asymptotically stable. Comparing with the effects of discrete and distributed delays on the stability of HIV virus-to-cell dynamic models, they could be same and different even opposite, the HIV virus could be more persistent in a distributed delay model than a discrete delay model.

## Acknowledgments

We are grateful to the handling editor and anonymous reviewers for their valuable comments and suggestions that greatly improved the readability of this paper. This work is supported by the National Natural Science Foundation of China (Grant Nos. 11861065, 11771373, 11702237), the Natural Science Foundation of Xinjiang Province (2019D01C076, 2017D01C082).

## **Conflict of interest**

The authors declare no conflicts of interest.

## References

1. D. D. Richman, D. M. Margolis, M. Delaney, W. C. Greene, D. Hazuda, R. J. Pomerantz, The challenge of finding a cure for HIV infection, *Science*, **323** (2009), 1304–1307.

- 2. V. Leonenko, G. Bobashev, Analyzing influenza outbreaks in Russia using an age-structured dynamic transmission model, *Epidemics*, **29** (2019), 100–358.
- 3. Y. Cai, K. Wang, W. Wang, Global transmission dynamics of a Zika virus model, *Appl. Math. Lett.*, **92** (2019), 190–195.
- 4. Y. Cai, Z. Ding, B. Yang, Z. Peng, W. Wang, Transmission dynamics of Zika virus with spatial structure-A case study in Rio de Janeiro, Brazil, *Physica A: Stat. Mech. Appl.*, **514** (2019), 729–740.
- 5. E. Grigorieva, E. Khailov, Determination of the opimal controls for an Ebola epidemic model, *Disc. Cont. Dynam. Syst. S.*, **11** (2018), 1071–1101.
- J. Huang, S. Ruan, X. Wu, X. Zhou, Seasonal transmission dynamics of measles in China, *Theor. Biosci.*, 137 (2018), 185–195.
- 7. T. Zhang, X. Zhao, Mathematical modeling for schistosomiasis with seasonal influence : A case study in Hubei, China, *SIAM J. Appl. Dyn. Syst.*, **19** (2020), 1438–1471.
- 8. M. A. Nowak, C. R. M. Bangham, Population dynamics of immune responses to persistent virus, *Science*, **272** (1996), 74–79.
- 9. R. M. Anderson, R. M. May, The population dynamics of microparasites and their invertebrate hosts, *Philos. Trans. R. Soc. Lond. Ser. B*, **291** (1981), 451–524.
- 10. A. S. Perelson, P. W. Nelson, Mathematical analysis of HIV-I: dynamics in vivo, *SIAM Rev.*, **41** (1999), 3–44.
- 11. X. Lai, X. Zou, Modeling HIV-1 virus dynamics with both virus-to-cell infection and cell-to-cell transmission, *SIAM J. Appl. Math.*, **74** (2014), 898–917.
- 12. A. L. Hill, D. I. Rosenbloom, M. A. Nowak, R. F. Siliciano, Insight into treatment of HIV infection from viral dynamics models, *Immun. Rev.*, **285** (2018), 9–25.
- 13. P. Aavani, L. S. Allen, The role of CD4 T cells in immune system activation and viral reproduction in a simple model for HIV infection, *Appl. Math. Model.*, **75** (2019), 210–222.
- 14. D. Olabode, L. Rong, X. Wang, Optimal control in HIV chemotherapy with termination viral load and latent reservoir, *Math. Biosci. Eng.*, **16** (2018), 619–635.
- 15. X. Wang, L. Rong, HIV low viral load persistence under treatment: Insights from a model of cell-to-cell viral transmission, *Appl. Math. Lett.*, **94** (2019), 44–51.
- 16. P. W. Nelson, A.S. Perelson, Mathematical analysis of delay differential equation models of HIV-1 infection, *Math. Biosci.*, **179** (2002), 73–94.
- 17. R. Xu, Global stability of an HIV-1 infection model with saturation infection and intracellular delay, *J. Math. Anal. Appl.*, **375** (2011), 75–81.
- J. Lin, R. Xu, X, Tian, Threshold dynamics of an HIV-1 virus model with both virus-to-cell and cell-to-cell transmissions, intracellular delay, and humoral immunity, *Appl. Math. Comput.*, **315** (2017), 516–530.
- 19. G. Huang, W. Ma, Y. Takeuchi, Global properties for virus dynamics model with Beddington-DeAngelis functional response, *Appl. Math. Lett.*, **22** (2009), 1690–1693.

- 20. G. Huang, W. Ma, Y. Takeuchi, Global analysis for delay virus dynamics model with Beddington-DeAngelis functional response, *Appl. Math. Lett.*, **24** (2011), 1199–1203.
- 21. Y. Nakata , Global dynamics of a viral infection model with a latent period and beddington-DeAngelis response, *Nonlinear Anal. TMA*, **74** (2011), 2929–2940.
- 22. H. Xiang, L. Feng, H. Huo, Stability of the virus dynamics model with Beddington-DeAngelis functional response and delays, *Appl. Math. Model.*, **37** (2013), 5414–5423.
- 23. R. Xu, Global dynamics of an HIV-1 infection model with distributed intracellular delays, *Comput. Math. Appl.*, **61** (2011), 2799–2805.
- J. Wang, M. Guo, X. Liu, Z. Zhao, Threshold dynamics of HIV-1 virus model with cell-to-cell transmission, cell-mediated immune responses and distributed delay, *Appl. Math. Comput.*, 291 (2016), 149–161.
- 25. Y. Nakata, Global dynamics of a cell mediated immunity in viral infection models with distributed delays, *J. Math. Anal. Appl.*, **375** (2011), 14–27.



© 2020 the Author(s), licensee AIMS Press. This is an open access article distributed under the terms of the Creative Commons Attribution License (http://creativecommons.org/licenses/by/4.0)