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Stability in a Multi-Stage HIV Infection Model with General Incidence Rate

Ruiwen Yang[1], Xiaofei Wei[1] and Jiemei Li[1,†]

Abstract In this paper, we propose a multi-stage HIV infection model with general incidence rate to describe the influence of raltegravir intensification on viral dynamics. The basic reproduction number R_0 is established. The infection-free equilibrium E_0 is locally asymptotically stable if $R_0 < 1$. The infection equilibrium E^* is locally asymptotically stable if $R_0 > 1$.

Keywords Multi-stage models, Lyapunov, incidence, stability

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1. Introduction

AIDS, caused by the human immunodeficiency virus (HIV), is a contagious disease that damages the immune system and can lead to severe illness and even death. In the field of AIDS treatment, the application of mathematical models has become a crucial area. Over the past few decades, many scholars have made remarkable contributions by developing different types of HIV mathematical models to better understand the development and treatment of AIDS.

In 1996, Nowak [1] proposed the earliest host-virus dynamic model

$$\begin{cases} \dfrac{dT}{dt} = s - \beta VT - dT, \\ \dfrac{dI}{dt} = \beta VT - \delta I, \\ \dfrac{dV}{dt} = N\delta I - cV, \end{cases} \tag{1.1}$$

which described the dynamic behavior and diffusion process of HIV in the human body based on differential equations.

In 2002, Callaway [2] proposed an efficient antiretroviral therapy model, which considered the impact of HIV treatment drugs on the model. Reverse Transcriptase Inhibitors (RT) can interfere with the transcription process of HIV virus, while Protease Inhibitors (PI) can disrupt HIV's ability to generate infectious viral particles, thus allowing infected cells to produce two types of viruses: one type contains infectious virus particles V_I,while the other type is a non-infectious virus V_{NI}.

In 2012, Dimitra [3] added two compartments to the existing model: one for infected cells without integrated DNA (I_1),and another for infected cells unable to

†the corresponding author.
Email address:yangruiwen2620@163.com(R.Yang),xiaofei288199@126.com(X.Wei), lijiemei81@126.com(J.Li)
[1]Department of Mathematics, Lanzhou Jiaotong University, Lanzhou, Gansu 730070, China

produce virus due to Raltegravir (I_2),providing a more accurate description of the role and effects of Raltegravir in the treatment of HIV, where a and b are the rates of 2-LTR circle formation and integration into DNA. References [4] studies the $(n+2)$dimensional nonlinear HIV dynamic model, which characterizes the interacting T cells of the HIV particle, susceptible $CD4^+T$ cells, and $n-$stages of infected $CD4^+T$ cells. References [5] investigated a randomized, multistage model to evaluate the effects of intensive therapy with the integrase inhibitor raltegravir on viral load and 2-LTR dynamics in HIV-suppressive therapy patients.

In 2017, Wang Xia [6] has established an infectious disease model with multiple infection stages and efficient antiretroviral therapy as follows:

$$\begin{cases} \dfrac{dT}{dt} = s - (1-\varepsilon_{RT})\beta V_I T - dT, \\ \dfrac{dI_1}{dt} = (1-\varepsilon_{RT})\beta V_I T - d_1 I_1 - (1-\varepsilon_{II})k_1 I_1 - k_2 I_1, \\ \dfrac{dI_2}{dt} = (1-p)(1-\varepsilon_{II})k_1 I_1 - \delta I_2 + aL, \\ \dfrac{dI_3}{dt} = k_2 I_1 - d_3 I_3, \\ \dfrac{dL}{dt} = p(1-\varepsilon_{II})k_1 I_1 - d_L L - aL, \\ \dfrac{dV_I}{dt} = (1-\varepsilon_{PI})N\delta I_2 - cV_I, \\ \dfrac{dV_{NI}}{dt} = \varepsilon_{PI} N\delta I_2 - cV_{NI}. \end{cases} \tag{1.2}$$

Detailed biological considerations of the parameters of the model (1.2) can be found in Table 1.

This model can better simulate the infection process of HIV, including multiple stages such as acute infection, chronic infection, and immune failure, and the impact of antiretroviral therapy in this model is also considered.

In 2012, Hattaf [7] proposed a general form of incidence function $f(x,y,v)v$, where $f \in C^1([0,+\infty),\mathbb{R}^3_+,\mathbb{R}_+)$ and satisfies

(i) $f(0,y,v)v = 0$, for all $y \geq 0$ and $v \geq 0$;

(ii) $\dfrac{\partial f(x,y,v)}{\partial x} > 0$, for all $x > 0$, $y \geq 0$ and $v \geq 0$;

(iii) $\dfrac{\partial f(x,y,v)}{\partial y} \leq 0$ *and* $\dfrac{\partial f(x,y,v)}{\partial v} \leq 0$, for all $x > 0$, $y \geq 0$ and $v \geq 0$.

The incidence rate can accurately describe the transmission and infection process of HIV, thus better support the research on disease treatment.References [8] employed the aforementioned general incidence rate to investigate a delayed virus infection model with Gaussian white noise disturbances.

References [9] considered the HIV model with general incidence rate, CTL immune response and intracellular delay. References [10] proposed a random HIV infection model with logical target cell growth, general nonlinear incidence rate, CTL immune response and parameter perturbation. Zhai [11] reduced the infection rate of susceptible persons by generating protection awareness on them through education and publicity, and proposed a new HIV/AIDS extinction threshold λ_0,