The stability analysis for HIV virus-antibody model

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Abstract

Stilianakis et al.[1] used numerical simulations to explore the details of the stochastic dynamical behaviour associated with the appearance of mutant strains of HIV. They stress on several findings:

(1) the model dynamics depend crucially on the HIV mutation rate.

(2) the model dynamics equally strongly depend on the initial size of the virus population and the initial virus density.

(3) the detailed time scales, and the proportion of those infacted who progress to AIDS within 50 years, depend on the parameters characterizing the system dynamics. [2]

The aim of this study is to prove local and global stability of the equilibrium point where the HIV virus and antibody can co-exist.

The model is

$$\frac{dv}{dt} = v(r - px) \tag{1}$$

$$\frac{dx}{dt} = kv - bx - uvx \tag{2}$$

v is the population size of virus,x is an immune response which acts only against viral strain. Strain reproduces at rate r and virus is removed by an immune response at rate p .The immune response is activated at rate k and the immune response decays at rate b and uvx is the impairment of the immune response.

The equilibrium point $(0,0)$ is unstable and $(\frac{br}{pk-ru}, \frac{r}{p})$ is locally stable if it exists.By applying Bendixson-Dulac theorem and Poincare-Bendixson theorem,under the condition $pk > ru$,the equilibrium point is shown to be globally stable.

Conversely, in the case of that virus is difficult to remove by the antibody,that is in the case of $pk < ru$, the amount of the virus will increase in all conditions. So, to create an active antibody condition is the best way to get rid of virus's control.

At the next step, the cross-reactive immune response and the new group such as (x_2, v_2) will be introduced to the model and base on the new model, local stability and global stability will be analysed.

References

[1]N.I.Stilianakis,D.Schenzle,and K.Dietz,On the antigenic diversity threshold model for AIDS. *Matha.Biosci.*123:235-247(1994).

[2]ROBERT M. MAY,DOV J. STEKEL and MARTIN A. NOWAK,Antigenic Diversity Thresholds and Hazard Functions. *MATHEMATICALBIOSCIENCES* 139:59-68(1997)