Estimate of viral productivity and infectivity *in vitro*

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The availability of potent antiviral drug and mathematical models have reveal important viral properties such as half-life of HIV virion, short and long lived productively infected cells for the last two decade. These findings really improved our understanding of HIV infection and the strategy of drug therapy. However, even now, we do not have any analytical methods to estimate viral productivity (virus burst size) and infectivity (infection rate). In this talk, I am going to show our mathematical and experimental approach for the estimation.

Our conceptual idea is that very simple viral experiment can be explained by a mathematical model. We use the following mathematical model to describe *in vitro* viral replication experiment:

$$x' = -dx - \beta xv, \quad y' = \beta xv - ay, \quad v' = ky - rv \quad (1).$$

Here x, y, v are the number of target cells, infected cells, and virions, respectively. If we can completely inhibit *de novo* replications (i.e., $\beta = 0$), then model (1) is reduced to

$$y' = -ay, \quad v' = ky - rv \quad (2).$$

Because model (2) is linear differential equations, we can obtain the explicit solution and then the viral productivity (k) is

$$k = \frac{\left(v(t_2) - v(t_1)e^{-r(t_2-t_1)}\right)(r-a)}{y(t_1)\left(e^{-a(t_2-t_1)} - e^{-r(t_2-t_1)}\right)} \quad (3).$$

On the other hand, for example, if the time-scale of virion is sufficiently faster than that of the infected cells, then we can find a constant of motion for model (1) and therefore can derive the viral infectivity (β) as follows:

$$\beta = \frac{a \log x(t_2)/x(t_1) + d \log v(t_1)/v(t_2)}{k/r\left(x(t_2) - x(t_1)\right) + v(t_1) - v(t_2)} \quad (4).$$

Here t_1 and t_2 are arbitrary times during the experiment.

Based on the theory of the formulations (3) and (4), we have designed and developed *in vitro* viral replication system and are trying to estimate the viral productivity and infectivity.