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Dynamics of HIV-1 coinfection under different susceptible target cell populations during cell-free infection in cell culture

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Human Immunodeficiency Virus typeI (HIV-1) mutations are rapidly accumulated through recombination events which are largely caused by HIV-1 coinfection [1]. Therefore, HIV-1 coinfection has the potential to produce the drug-resistant viruses, which leads to the high pathologies and disease progression. Recently, it has been reported that coinfection occurs more frequently than at random both *in vitro* and *in vivo* [1,2], implying that this viral phenomenon is quite common in HIV-1 infection. Furthermore, one possible mechanism of HIV-1 coinfection is driven by the different susceptibility of target cells [2,3]. Thus, the elucidation of HIV-1 coinfection associated with different susceptible target cell populations is required to more accurately capture the general viral mechanism in HIV-1 infection. In this study, we constructed ordinary differential equations considering the heterogeneity of target cell populations during cell-free infection in cell culture, and reproduced the cell culture experiment data. Interestingly, our mathematical analyses demonstrated that 2 different susceptible target cell subpopulations could explain coinfection experiments in cell culture using the AIC model selection. In addition, our novel finding is that coinfecting cells are emerged from the most susceptible subpopulation at 98.2% on average. Taken together, our mathematical-experimental approach suggested that the most susceptible target cell population is the dominant resource of HIV-1 infection in cell-free infection.

[1] Q. Dang *et al.*, 2004

[2] J. Chen *et al.*, 2005

[3] A. Remion, *et al.*, 2016

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