Projecting evolutionary trajectory of influenza A virus: Multidimensional scaling and individual based antigenic drift model

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Antigenicity of influenza A viruses is known to evolve rapidly by changing variable amino acid sites of hemagglutinin, which enable them to escape host immune response and to spread every year in the host population. Predicting the evolutionary direction of the viral antigenicity is very difficult particularly because of high dimensionality of its phenotypic space (antigen space) due to combinational diversity of variable amino acid sites. Recently a technique called multidimensional scaling (MDS) is focusing attention in the evolutionary studies of influenza, which translate the genetic and immunological distances between viral strains into distance in a low dimensional model space. Application of MDS to over 30 years evolution of A Hong Kong influenza viruses (H3N2 subtype) has revealed a linear trend in their evolutionary trajectory. In this paper, I study possible factors that are responsible for an extracted linear trend in MDS map in the phylodynamical trajectory of influenza virus evolution, by using extensive simulations of individual-based model (IBM) for the coupled dynamics of viral antigenic drift and specific immune defense of hosts. Analyses revealed that if phylogenetical tree shape of IBM simulation is "cactus like" as is observed in influenza A Hong Kong virus phylogeny, a linear trend is realized if MDS is applied to the Hamming distance relationship between strains. We also discuss how big turns between linear trends, observed both in real data and simulation data, are related to the phylogenetical changes of virus population.