Understanding Original Antigenic Sin in Influenza with a Dynamical System

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Appendix

A Review of the Influenza A Genome

In this paper, I model the influenza A virus infection to study the mechanism of original antigenic sin. Influenza A virus is an RNA virus in the family Orthomyxoviridae. A functional influenza A virus particle consists of a spherical lipid bilayer shell and eight distinct RNA molecules which encode 11 proteins. Two glycoproteins, hemagglutinin (HA) and neuraminidase (NA), are on the surface of the virus particle. HA contributes to the binding of the virus to the sialic acid on the surface of the target upper respiratory tract epithelial cells and facilitates subsequent virus fusion and entry into the cells [1–3]. NA is the key component that facilitates virus release from the surface membrane of infected cells [4]. Nucleocapsid protein (NP), a nucleoprotein, encapsulates and transports viral RNA in the host cells [5]. The matrix protein, M1, binds to the inner side of the viral lipid bilayer membrane, helps assemble virus particles in the host cells, and is the central component in virus budding [4]. M2, a glycoprotein inside the lipid bilayer, serves as the ion channel adjusting the pH value in the virus particle, uncoats the virus particle, and contributes to efficient virus replication [6]. Additionally, there are two non-structural proteins, namely NS1 and nuclear export protein (NEP, formerly named NS2), as well as four RNA polymerases, namely PA, PB1, recently discovered PB1-F2 [7], and PB2. NS1 interferes with the cellular antivirus defense system [8]. NEP exports newly synthesized viral ribonucleoprotein (RNP) complexes comprising viral RNA, NP, and PB1 from the nucleus [9]. PA, PB1, PB1-F2, and PB2 replicate the viral RNAs in the nucleus of the infected cell.

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