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Mapping the antigenic evolution of seasonal influenza H3N2 virus in China

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China has been long recognized to play a pivotal role in global influenza transmission. However, due to a lack of sufficient viral data, the antigenic evolution of seasonal influenza virus in China and its impact on global influenza epidemics are not adequately understood. We have carried out a large-scale determination of hemagglutinin (HA) sequences of over 1000 human A (H3N2) viruses isolated between 1968 and 2010 from diverse regions of mainland China. To systematically characterize the antigenic evolution of human A(H3N2) viruses in China, we have further developed a computational method that can predict antigenic clusters of influenza A (H3N2) viruses with high accuracy from viral HA sequences, which is denoted as PREDAC. Application of PREDAC to the large-scale HA sequence data have identified 17 antigenic clusters that have dominated for at least one season between 1968 and 2010. By tracking the dynamics of the dominant antigenic clusters, we found that the antigenic evolution of influenza virus in China is more complicated than that in USA and Europe: dominant antigenic clusters change more frequently in China.