

十一、研究計畫中英文摘要：請就本計畫要點作一概述，並依本計畫性質自訂關鍵詞。

(一) 計畫英文摘要。(五百字以內)

Keywords : Influenza, Hemagglutinin, amino acid, molecular evolution, physiochemical property

Hemagglutinin (HA) protein is very important in the event of influenza (flu) infection, because it binds to the receptor on the cellular surface of human lung specifically, and bring about membrane fusion by the change of protein conformation. All of the processes are physiochemical interactions in the molecular level. There are two significant physiochemical features for the Influenza infection which broke out in 1918 may responsible to the high infection and mortality: (1) In general, the size of HA binding position is narrow, but becoming larger by one amino acid change on the binding position in the flu of 1918, that apt to promote the infection to human. (2) Two histidine-rich segments in the HA protein with basicity may promote the membrane fusion in the infection process. One of the two segments found only in avian flu.

According to these clues, we inferred that the infection host and the probability of cross-species infection could be determined by the physiochemical properties of residues in the HA protein sequence.

In this project, we will study the correlation regarding the properties of the HA protein of influenza A viruses that affecting the probability of cross-species infection, the infective host and the infection ability. Clustering analysis will be used for molecular evolution of the HA protein, at first. Secondly, we will define and quantify the HA protein sequences by physiochemical properties of residues, clustering analysis will apply. We also will utilize the method of data mining to discover the significant residues among the HA protein sequences that infecting different species. Finally, we will study the structural effects of residue change of the HA sequence that binding to the receptor about these significant residues. All the HA protein sequences was collected from public database.