Influenza Program Project : Virology, Immunopathogenesis, Immunological platform

Abstract:

In this project we would like to establish standard immunological and infection platform in order to investigate the effects of influenza viral genome variations on host immune response. These technologies would be helpful in selection of potential influenza vaccine candidate in the future. In previous study, influenza viral NS1 protein has been reported to be associated with the resistance to the antiviral effects of host immune response and play an important role in viral virulence. Thus, we first focus on the analysis of NS gene. The results showed influenza A H1N1 clinical isolates from 2000 had a isoleucine to valine mutation at position 226 in poly(A)-binding protein II binding domin, and isolates from 2006 had a glutamine to lysine substitution at position 25 in RNA binding domain of NS1. These changes might result in epidemics of influenza A H1N1 in 2000 and 2006. Hemagglutinin (HA) and neuraminidase (NA) of influenza envelope proteins are the major antigens which trigger host immune response. Secondly, we would like to set up an immunological analysis platform for rapid detection of antibody for influenza viral infection. The method we recently built up could detect viral infected cells by anti-M and anti-NP antibody and neutralizing antibody could also be evaluated by flow cytometry. In addition, serum antibody could be measured by ELISA with high sensitivity. Thirdly, cellular and humoral immunity are important in controlling influenza viral infection. In this part we would like to study the immune response of both influenza nature infection and vaccinated individuals. The preliminary data showed the absolute cell numbers of CD3, CD4, CD8 and CD16CD56 from influenza virus infected patients were lower when compared with adenovirus infected ones. In addition, the expression level of TLR-3, TLR-4 and CD4CD25 were increased after influenza vaccination. The significance of those findings will be further investigated. Fourthly, we aim to establish a phage display system of hemagglutinin surface molecule to identify immunodominant determinants located within the circulating influenza A viruses in Taiwan. These platforms will be contributed to evaluate the immune response resulting from viral genome variations, nature infection, vaccination, and aid in the selection of vaccine strain candidate.

Keyword: Influenza virus, sequence analysis, vaccine, immunological platform, phage display