

Molecular Evolution of Influenza Viruses in Taiwan and the Roles of Genes in the Antigenicity

Abstract

The segmented genome of influenza virus allows exchange of gene segments between cocirculating strains. Phylogenetic profiles of the genes coding for HA, NA, MP and PA segment proteins of influenza A viruses, isolated from 2005 to 2006 were analyzed in order to understand the evolutionary mechanisms of these viruses. Evolutionary analysis done in the present study provided further evidence for cocirculation of multiple subtypes as well as sequestering and reemergence of phylogenetic lineages of the internal genes. Results presented in this report demonstrate that antigenically and genetically distinct viruses within both A/H1N1 and A/H3N2 subtypes co-circulate and make changes to occur frequently contributing to the genetic diversity of the circulating strains.

Key words : Influenza Virus, Reassortment, Antigenicity, Phylogenetic analysis