

Project Title: Molecular Evolution of Influenza viruses in Taiwan and the Roles of Genes in the Antigenicity

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Executing Institute: Center for Diseases Control , center of laboratory research and development

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Abstract:

Influenza A virus has the ability to overcome immunity from previous infections through acquisition of genetic changes. Thus, understanding the evolution of the viruses in humans is important for surveillance and the selection of vaccine strains. The segmented genome of influenza virus allows exchange of gene segments between cocirculating strains. Not only surface protein Hemagglutinin, but also Neuraminidase and internal proteins probably may influence virus antigenicity. Preparation for an influenza pandemic is presently a high priority in Taiwan. Laboratory-based surveillance systems must be timely in order to be effective. The data presented here highlights the need of characterize the circulating strains both antigenically and genetically during regular surveillance. Any contribution of individual genes or gene combinations to usual or unusual epidemic characteristics might thus be identified ensuring that virus strains can be selected for vaccine formulation that will most closely match the circulating viruses.

Keyword: Influenza Virus, Reassortment, Antigenicity, Phylogenetic analysis, Taiwan