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Project Title:
Project Number: DOH95-DC-1401
Executing Institute: Academia Sinica
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P.I. Institute: Institute of Biomedical Sciences

Abstract

Background & **Aims** — In order to provide adequate information at the timely basis for influenza vaccine strain selection in Taiwan, this study aims to evaluate the currant surveillance system and to improve the infrastructure for adequate data collection and analysis when influenza vaccine production capacity is established locally to serve the need of the people in Taiwan. We also develop tools to analyze the dynamics of the HA1 gene of influenza A (H1N1 & H3N2) and influenza B viruses, as well as analyzing whole genome of influenza viruses.

Methods – This project applying the antigenic predict model to analyze HA1 gene of influenza A (H1N1 & H3N2) combining genotypes and HI data, including method to computerize HI data. And using influenza B viruses prediction method to analyze two lineages Yamagata and Victoria molecule evolution.

Results –Two lineages of B viruses, Yamagata and Victoria, have co-circulated globally, and both lineages underwent continuing re-assortment of gene segments. While the HA remains distinct for each lineage, other gene segments are shared however. The Multidimensional scaling (MDS) method has also been established for use.

Suggestions – Whole genome analysis is helpful at time for understanding the dynamics of virus evolution, especially for influenza B. It might be important to establish the reagents for typing influenza B with HI methods. It is important to document all the methods in writing and to standardize the application for routine use in the future.

Key words: Influenza virus, Molecule evolution, Antigenic predict model &Vaccine strain selection