

# 臺灣家禽流行性感冒演化分析暨赴美國東南家禽實驗室研

## 習出國報告

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### 摘要

2015 (104) 年臺灣爆發 2.3.4.4 亞群 H5 HPAIV，依基因之組成分成五大群：H5N2、H5N3、H5N8/TW GO、H5N8/TW G1 及 H5N8/TW G2。今(106)年選取了不同亞型、動物來源及地理分布，共計 21 株 H5 亞型病毒之 HA 基因完成定序，並持續檢出其中新型 H5N2、H5N8/TWG1 及 H5N8/TW G2 三群病毒，其 HA 基因已呈現隨時間演化變異的現象，由此可知 106 年這三群病毒仍存在於臺灣之家禽場。其中二株病毒隸屬於新型 H5N2 及 H5N8/TW G1 分群，分別有 NP 基因及 NS 基因可於基因庫上比對到更相近之野鳥基因。

本次出國由林育如副研究員及陳麗璇助理研究員赴美國農業部農業研究局東南家禽實驗室（Southeast Poultry Research Laboratory, SEPRL; Agricultural Research Service, ARS; U.S. Department of Agriculture, USDA）研習有關禽流感分子流行病學軟體分析及高生物安全禽流感動物試驗設施研究與操作實務訓練，進行雙方合作研究，以提升實驗室診斷及研究能力，進而協助防疫需求，並持續建立雙方交流合作關係。

**Phylogenic analysis of avian influenza viruses in Taiwan and  
a report on studying in Southeast Poultry Research  
Laboratory in USA.**

Li-Hsuan Chen

**Abstract**

Five groups of H5Nx according to composition of 8 segments were identified since outbreak in early 2015 in Taiwan. Twenty-one strains of novel H5 avian influenza viruses (AIVs) were selected for HA gene analysis based on different subtypes, species and distribution in 2017. At least 3 subgroups (H5N2, H5N8/TW G1 and H5N8/TW G2) can be detected in poultry farms in 2017, and the HA genes showed diversity over time. Two reassortants of H5N2 and H5N8/TW G1 subgroups viruses containing 2 Eurasian LPAI segments nucleoprotein (NP) and NS were identified, respectively.

Two of our staff members from the Division of Epidemiology visited Southeast Poultry Research Laboratory of U.S. Department of Agriculture in USA in December, 2017. The purpose of the technical visit was to share experiences in the molecular epidemiology analysis for avian influenza virus and the biocontainment facilities of poultry. The final aims of this project are to guide and share the experience for further learning of avian influenza diagnosis and establishing cooperation between Taiwan and USDA.