在台灣鵝檢測到多個亞型高病原性 H5 禽流感病毒

製劑研究組
李敏旭 副研究員

摘　要

在 2015 年 1 月，從台灣鵝場檢驗出包含 H5N2,H5N3 及 H5N8 等三種 NA 亞型的高病原性 H5 家禽流感病毒，有 90%鵝場被確認感染並執行撲殺清場政策以避免病毒擴散；截至目前的檢驗結果，全部的病例僅僅除了一病例在台東外，所有 HPAI 病例分布在台灣西部從桃園到屏東等 12 縣市，,以雲林縣及屏東縣尤其損失嚴重。在致病性的分析，鄰近 HA 切割位胺基酸序列為 PLRERRRKR*GLF，具多個鹼性胺基酸為高病原性家禽流行性感冒病毒的特徵。親緣性分析這些病毒在 HA & MP 基因分析結果，起源自中國 2010-2013 年的 H5N8 病毒，且與日本及北美洲病毒最為相似。除此之外，這些病毒分別重新組裝了其它病毒株 2-6 段不同數目的基因，而形成有 H5N2、H5N3、H5N8 亞型的高病原性家禽流行性感冒病毒，但這些病毒所有的基因組成都為歐亞血統。這與北美洲的 H5N2、H5N8、H5N1 病毒分離株不同，它們的基因體混合了歐亞血統及美洲血統。

Multiple Subtypes of Highly Pathogenic H5 Avian Influenza Virus Detected in Geese in Taiwan.

Mim-Shinh, Lee

Abstract

In January 2015, three NA (nauraminidase) subtypes of highly pathogenic H5 avian influenza virus (HPAI), including H5N2, H5N3 and H5N8, were detected from goose farms in Taiwan. In this wave of outbreaks, 90% goose farms were confirmed as HPAI infection and the culling policy was applied to prevent further spread of the disease. To date, all the HPAI cases spread across 12 counties, from Taoyuan to Pingtung , in west coast of Taiwan except one case in east coast (Taitung). Among them, Yunlin and Pingtung County have suffered the most severe losses in particular. For pathogenicity analysis of isolated viruses in Taiwan, the results revealed that amino acid sequences near HA(hemagglutinin) cleavage site are PLRERRRKR * GLF, and containing multiple basic amino acids is a unique characteristic of HPAI viruses. Phylogenetic analysis of HA & MP genes of these viruses indicated they originated from H5N8 virus strains isolated in China during 2010-2013, were also and the most similar to the Japanese and North American virus isolates. In addition, 2 to 6 segments of Taiwan isolates were re-assorted from other strain, and formed H5N2, H5N3, H5N8 subtypes of HPAI respectively. Nevertheless, all the genes of these viruses are clustered in Eurasian lineage, but they are different from North American H5N2, H5N8, H5N1 isolates mixed with Eurasian and American lineages.