

2015 年及 2016 年於台灣分離之野鳥 H10 亞型禽流感病毒序列分析

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摘要

家禽流行性感冒可依其基因體差異性區分為美洲分支歐亞分支。2013 年 11 月於溼地野鳥糞便檢體分離到二株 H10 亞型禽流感病毒，其 8 段基因體分別由歐亞分支與美洲分支的禽流感病毒基因重組而成。與此同時，2013 年 11 月至 2014 年 2 月間，中國江西省南昌市傳出 3 例民眾於接觸活禽市場禽鳥後感染 H10N8 引發重症死亡病例。且自此之後南昌市活禽市場的場雞隻被分離到 H10 亞型病毒的數量明顯增加。H10 亞型病毒與在家禽流行的 H9N2 重組並適應於家禽後可能提高對於人類的風險。本報告收集 2015 年 11 月至 2016 年 3 月本組於野鳥禽流感監測檢體中分離到之 10 株 H10 亞型禽流感病毒。將上述 10 株病毒及以往近年來在野鳥分離到的 H10 亞型病毒株進行近析基因體定序，並進行親緣性分析。於野鳥分離到的病毒基因大多屬於歐亞分支，只有數次有出現過混有美洲分支的基因病毒株，然而此種情況為偶然發生，目前尚未在這些檢體有發現美洲分支的基因體持續存在的證據。本次分析的結果可提供在台灣候鳥飛行路線上的禽流感病毒可能的變異情形。其內部六段基因序列資料也可作為研究其他亞型毒株之參考。

Genetic analysis of H10 subtype avian influenza viruses isolated from wild birds in Taiwan 2015/2016.

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Abstract

According to genetic diversity, avian influenza viruses can be divided into American lineage and Eurasian lineage. Most of avian influenza viruses isolated from wild birds in Taiwan belong to Eurasian lineage. We found two intercontinental reassortant H10N7 subtype strains from wild birds surveillance in 2013. At the same time, three cases were reported that patients were infected by H10N8 and led to death in Jiangxi, China, between November 2013 and February 2014. All patients infected by H10N8 viruses had history of visiting live-poultry market. After August 2013, the prevalence of H10 subtype viruses got higher in chicken in Nanchang live poultry market. According to phylogenetic analysis, human cases were suspected to be infected by viruses of chicken origin. Although H10 subtype influenza viruses are usually low pathogenic to avian, the viruses reassortant with poultry viruses such as H9N2 may increase the risk to human. From November 2015 to March 2016, we isolated 10 strains H10 subtype viruses. We had sequenced the genomes of H10 subtype viruses since 1998, and then analyzed the sequence phylogenicity. Most viral genomes belong to Eurasian lineage. A few of viruses with mixed American lineage genes appeared occasionally, and the viruses usually existed only a season in the wild birds in Taiwan. The genome phylogenicity data can provide the clues of avian Influenza viruses evolutionary dynamic in migratory wild birds which fly through Taiwan. The six internal genes of H10 avian Influenza viruses can not only be used in H10 genetic analysis, but also be the reference gene pool for other studies.