台灣 2013 年野鳥分離之禽流感病毒 H10 亞型毒株基因分析

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摘要

禽流感病毒偶爾會發生跨越物種障礙感染禽類以外的物種，近年來感染人類的 H5N1 以及 H7N9 流感病毒就是由禽傳播到人的例子。到目前的高病原性家禽流行性感冒多落在 H5 與 H7 亞型，其引起家禽的高死亡率且病毒快速傳播的能力可造成養殖業重大損失。而 H10 亞型則被認為是除了 H5 與 H7 亞型外，很有可能對家禽或人類造成威脅的亞型之一。H10 亞型病毒即有多次感染禽類與哺乳類的記錄，甚至引起重大損失及人員死亡的案例。本組執行野鳥禽流感病毒監測工作項目中，於 2013 年 11 月間分離到的二株 H10 亞型禽流感病毒，以核酸進行亞型分型時 HA 部分訊號極弱，進行全長定序及基因演化分析後，發現其 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。

Genetic analysis of H10 subtype avian influenza viruses isolated from wild birds in Taiwan 2013

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Abstract

Avian influenza A viruses occasionally cross the barrier to infect species other than birds. The novel H5N1 and H7N9 influenza viruses causing endemics in human are the examples of bird-to-human transmission . To date, highly pathogenic avian influenza (HPAI) viruses belong to H5 or H7 subtypes. HPAI viruses can cause high mortality in poultry, and the viruses spread rapidly and result in huge economic losses. Besides H5 and H7 subtypes, H10 is one of the subtypes to have the potential of threatening poultry or human. There are many records of the H10 subtype viruses infecting poultry or mammalian, and some of the infection cause serious damage or human death. In our surveillance on avian influenza viruses in wild birds, we isolated two strains of H10 subtype virus in 2013. The viruses showed very weak HA genome signal in PCR subtyping system. Genomic sequences of both strains suggested that the strains derived from reassortment of Eurasian and North American lineages.