2015年台灣新興家禽流行性感冒H5Nx亞型病毒之序列分析

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摘要

2014年1月，分類於H5N1高病原性家禽流行性感冒2.3.4.4亞群之新型重組H5N8病毒在韓國的家禽及野鳥造成嚴重疫情，同年9月開始陸續擴散至日本、俄羅斯、歐洲及北美等地區。台灣於2015年1月開始在禽場檢體中檢測出三種亞型之H5Nx病毒。為明瞭此病毒群之演化，本研究進行24株病毒全8段基因之全長定序及分析。依據基因序列親緣樹分析，發現共有四種基因型存在於台灣家禽場中，包括1型H5N2、1型H5N3及2型H5N8亞型病毒。四種台灣H5Nx病毒均演化自2.3.4.4亞群前期之病毒，重組成至少含有2段野鳥病毒基因的新型病毒。此種新亞型之抗原移變（antigenic shift）在過往H5N1演化過程中較為少見，因此未來在病毒基因重組及演化之監測值得重視。

Genetic analysis of novel avian influenza H5Nx viruses in TAIWAN, 2015

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Abstract

Beginning in January 2014, a distinct group of highly pathogenic avian influenza (HPAI) H5 reassortant viruses (H5N8, clade 2.3.4.4) has caused outbreaks in South Korea, and by late 2014, it had spread to Japan, the Russian Federation, Europe, and North America. In January 2015, H5Nx clade 2.3.4.4 AIVs were detected in Taiwan and caused outbreaks in poultry. To better understand genetic relatedness between these viruses in different regions, we sequenced all gene segments of 24 Taiwan H5Nx viruses and compared them with AIV sequences in GenBank. There were four novel HPAI H5Nx reassortant pattern viruses (1 H5N2, 1 H5N3, and 2 H5N8) emerging into Taiwan. All the four novel H5Nx reasortants evolved from early members of H5N1 clade 2.3.4.4, and contain at least two wild-bird-origin AIV RNA segments. This rapid emergence of new H5Nx combinations is unprecedented in the H5N1 evolutionary history. Further work to monitor for such reassortments and an evaluation of these viruses are warranted.