

# 動物流行性感冒病毒的威脅

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## 摘要

在人類，感染 A 型或 B 型流感病毒時通常是出現以發熱，咳嗽，喉嚨痛和不適為特徵的急性、有限度的上呼吸道疾病。然而，流行性感冒也可以是從亞臨床甚至無症狀感染到嚴重原發性病毒性肺炎，呈現廣泛病徵的疾病。A 型流感病毒（IAVs）被認為是下一次全球性大流行病之一，最大的威脅是因為動物儲主保有大量的病毒偶爾會波及人類。大流行性流感病毒是通過從人和/或動物流感病毒“混合和匹配”病毒基因重新分配，產生在基因和抗原性的新病毒。這些“抗原性漂移”導致產生免疫學上新穎的流感病毒而引入尚未有新病毒免疫力的人群中。而野生水禽類被認為是 A 型流感病毒多樣性的儲庫宿主，存在 16 種抗原性不同的 HA 和 9 種 NA 亞型；目前只有少數亞型已經成功地跨越宿主性到其他禽類和哺乳動物宿主。1997 年，在香港首次爆發人類感染 H5N1 禽流感病毒。2013 年，台灣曾報告第一例感染 A 型（H6N1）型病毒的人類病例。自 2013 年以來，禽流感 H7N9 病毒在中國引起人類感染。2016-17 年度大流行病引發了人們擔心病毒流行病學可能發生變化，增加了大流行病的威脅。

# **The threat of animal influenza viruses**

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## **Abstract**

In humans, the infection of influenza A or B viruses manifests typically as an acute and self-limited upper respiratory tract illness characterized by fever, cough, sore throat, and malaise. However, influenza can present different clinical signs, ranging from sub-clinical or even asymptomatic infection, to a severe primary viral pneumonia. Influenza A viruses (IAVs) are considered to have high global pandemic potential due to the abundance of permanent animal reservoirs harboring viruses that occasionally spill over into human populations. Pandemic influenza viruses arise from genomic reassortment whereby genetically and antigenically new virus strains (or subtypes?) are created by the “mixing-and-matching” of viral genes with human and/or animal influenza viruses. These “antigenic shift” events introduce an immunologically novel influenza virus into the human population, which has no pre-existing immunity to it. Sixteen antigenically distinct HA (hemagglutinin) and nine NA (neuraminidase) subtypes exist in wild aquatic birds, which are considered to be the primary reservoir hosts for IAV and host the highest diversity of IAVs. Only a few of these subtypes have successfully crossed into other avian and mammalian hosts. The first outbreak of avian influenza A(H5N1) virus in humans occurred in Hong Kong in 1997 and in 2013, the first human case of avian influenza A (H6N1) infection was reported in Taiwan. Since 2013, cases of human avian influenza A H7N9 infections have been documented in China and a large

epidemic in 2016-2017 in China raised further concerns that the epidemiology of the virus may have changed, thus increasing the threat of a pandemic.