

Armed Forces Health Surveillance Branch H7N9 Surveillance Summary (30 AUG 2017)



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DEPARTMENT OF DEFENSE (AFHSB)

Avian Influenza A (H7N9) Surveillance Summary #81

30 AUG 2017 (next Summary as needed)



CASE REPORT: As of 30 AUG, according to WHO, FAO, China's National Health and Family Planning Commission (National HFPC) and provincial governments within China, the total influenza A (H7N9) human case count since the fifth seasonal epidemic of H7N9 began on 1 OCT 2016 is 926 (+4) cases with at least 282 deaths. The four new cases were reported in Fujian (1), Hunan (1), and Xinjiang (2). The number of human cases identified this season accounts for approximately 52% of all human cases of H7N9 reported since 2013. The total case count since the disease was first identified in APR 2013 is 1,788 cases with at least 420 deaths (CDC reports at least 610 (+18) deaths as of 25 AUG) in China, Hong Kong, Macao, Taiwan, Malaysia, and Canada. All cases in Taiwan (6), Hong Kong (21), Macao (2), Malaysia (1), and Canada (2) are believed to have been imported from Mainland China. The overall case-fatality proportion among known cases is 34% (+1%); the average age of those affected is 55 years; and at least 459 (26%) of the cases reported have been female. The most recent known date of onset was 9 AUG. Since 2013, China has reported cases in 24 provinces and autonomous regions: Anhui, Fujian, Gansu, Guangdong, Guangxi, Guizhou, Hebei, Hubei, Henan, Hunan, Inner Mongolia, Jiangsu, Jiangxi, Jilin, Liaoning, Shaanxi, Shandong, Shaanxi, Shanxi, Sichuan, Tibet, Yunnan, Zhejiang, and Xinjiang; and four municipalities: Beijing, Chongqing, Shanghai, and Tianjin. The fifth seasonal epidemic of H7N9 has been more geographically widespread than any of the preceding four seasonal epidemics; in the current season, cases have been reported from all the areas listed above. Seven of these provinces and autonomous regions reported their first cases of H7N9 during the fifth seasonal epidemic (Gansu, Inner Mongolia, Shaanxi, Shanxi, Sichuan, Tibet, and Yunnan). Jiangsu has reported the most cases of any single province during this time period, 158 (17%) of 926 cases.

On 10 JUL, China's Ministry of Agriculture (MOA) issued a notice announcing that a comprehensive national highly pathogenic avian influenza vaccination program for poultry would begin in Fall 2017. On 14 JUN, China released the vaccine evaluation and technical standards for the H5/H7 bivalent inactivated vaccine that will be used for the program. FAO reports that Anhui, Henan, and Zhejiang provinces and Ningxia Hui Autonomous Region have released poultry immunization plans for Fall 2017 that also include the immunization of poultry against H7N9 specifically.

TRANSMISSION: In a CDC [study](#) published in APR 2015, H7N9 antibodies were found among 6.7% of case contacts identified between MAR 2013 and MAY 2014 in China, suggesting that human-to-human transmission does occur and could cause mild or asymptomatic infections. Since much of the reporting out of China occurs in monthly batches, with limited information on age, gender, and location, it is possible that only the most severe cases and fatalities are being reported by China. It is unknown how many mild or asymptomatic cases have occurred and how many cases have occurred without laboratory testing. This lack of information coupled with the infrequent reporting makes spatial and temporal cluster analysis difficult. CDC reported that at the conclusion of the fourth seasonal epidemic of H7N9, there had been a total of 26 known disease clusters since 2013. As of 30 AUG, AFHSB has identified 14 spatial clusters during the fifth seasonal epidemic.

In a 21 MAR study in Nature Communications, researchers from Hong Kong University identified a mutation in the viral genome of H7N9—a unique nucleotide substitution (NS-G540A) acquired through prior reassortment with low pathogenic H9N2—which is responsible for the virus's unique ability to circulate efficiently in avian hosts as well as replicate in mammalian cells. This particular mutation is also present in human infections with avian influenza subtypes H10N8 and H5N6. An 11 MAY Eurosurveillance study reported highly pathogenic H7N9 can mutate to include antiviral resistance during prophylaxis or treatment. A 15 JUN study in PLOS Pathogens identified three mutations that could occur in the H7 hemagglutinin protein and would make the virus more likely to bind to human rather than avian airway receptors.

SURVEILLANCE: Reagents for surveillance testing purposes are available via the [CDC website](#). NMRC has produced amplicon H7N9 positive testing control material using the published WHO primers/probes. Kits were sent to AFRIMS, NAMRU-3, NAMRU-6, NAMRU-2, Phnom Penh, NMRC-A, and NHRC for surveillance. Nineteen DoD laboratories were sent diagnostic kits, as have all 50 states, the District of Columbia, Puerto Rico, and more than 60 international labs.

INTERAGENCY/GLOBAL ACTIONS: On 26 JAN, the U.S. CDC [announced](#) a Level 1: Practice Usual Precautions travel advisory for China. U.S. CDC and WHO advise no special screenings at points of entry and no trade or travel restrictions at this time.

(+xx) represents the change in number from the previous AFHSB Summary of 2 AUG 2017.

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BACKGROUND: On 1 APR 2013, WHO reported three human cases of infection with a novel influenza A (H7N9) virus in China. This was the first time human infection with H7N9 had been detected. CDC believes the H7N9 virus is likely a reassortant of H7N3 viruses from domestic ducks and H9N2 viruses from other domestic poultry. Seasonality has been observed since the beginning of this outbreak with a consistent pattern of declining incidence through the summer months followed by a spike in cases in the winter months. Confirmed avian H7N9 has been rare and subclinical but has been previously identified. H7N9 is usually asymptomatic in birds and many bird owners are likely unaware of infections and the risk of transmission. Detection in birds requires routine active surveillance, which FAO reports has resulted in at least 4,246 virus-positive samples from the environment and chickens, pigeons, ducks, and wild birds since the beginning of the outbreak in 2013.

A 10 MAR CDC [MMWR](#) study reported that genetic sequences of 74 virus samples collected from infected persons or live bird markets during the fifth epidemic indicate H7N9 viruses have diverged into two distinct genetic lineages, the Pearl River Delta lineage and the Yangtze River Delta lineage; 69 (93%) of these samples were of the newer Yangtze River Delta lineage. CDC's preliminary data suggests the Yangtze River Delta viruses are antigenically distinct from earlier H7N9 viruses and from existing candidate vaccine viruses (CVVs). On 2 MAR, experts from the WHO Global Influenza Surveillance and Response System [recommended](#) two new CVVs for development: 1) an A/Guangdong/17SF003/2016-like virus, which is a highly pathogenic virus from the Yangtze River Delta lineage; and 2) an A/Hunan/2650/2016-like virus, which is a low pathogenic virus also from the Yangtze River Delta lineage. On 23 MAY, CDC [reported](#) that development of the second of these two CVVs, which is matched to the H7N9 virus lineage that has predominated during the fifth seasonal epidemic, had been completed and was being shipped to various manufacturers in China. [WHO](#) posted information about the availability of this CVV on 18 MAY.

RESEARCH & MEDICAL COUNTERMEASURES: In JUL, FAO published a risk analysis regarding the spread of Chinese-origin highly pathogenic H7N9 in poultry, as well as human exposure to highly pathogenic H7N9, during the period MAY–SEPT 2017. Key factors in the risk analysis included: likelihood of virus spread from known affected areas to currently unaffected areas of China; likelihood of spread to unaffected countries in the South and Southeast Asia regions; likelihood of spread to unaffected countries beyond the Southeast Asia region; and likelihood of human exposure within affected areas of China. FAO addressed each of these questions in a separate table of probabilities. The likelihood of human exposure through contact with infected birds, live poultry market (LPM) visits, or upon consumption of poultry products was evaluated as “low to moderate, with low uncertainty, and moderate for occupational exposure.” The likelihood of highly pathogenic H7N9 spreading to unaffected countries in the South and Southeast Asia regions during the specified time period ranged from “negligible” to “moderate” depending on formal and informal trade practices, biosecurity measures, and movement of wild birds. The likelihood of virus spread to unaffected countries beyond the Southeast Asia region was assessed as “negligible” for all countries.

On 27 FEB, WHO [reported](#) a change in the genetic sequence of isolates from two confirmed human H7N9 cases in Guangdong Province indicating the virus is evolving from a low pathogenic to a highly pathogenic avian influenza virus. Similar changes were also found in genetic sequence data from a case with travel history to Guangdong that was reported by Taiwan on 4 FEB. China's MOA notified [OIE](#) on 21 FEB that genetic sequences of virus samples from LPMs in Guangdong showed changes consistent with highly pathogenic avian influenza virus. As of 30 AUG, FAO and OIE have reported the highly pathogenic form of H7N9 in poultry and environmental samples from LPMs in Fujian, Guangdong, Guangxi, and Hunan, and from farms and backyard flocks in Guangxi, Hebei, Heilongjiang, Henan, Hunan, Inner Mongolia, Shaanxi, and Tianjin.

Following the identification of the first two human infections with highly pathogenic H7N9, provincial China CDC labs have reportedly been conducting genetic analyses of respiratory specimens from all confirmed human cases of H7N9 in the country. According to the Chinese National Influenza Center (CNIC) as of 30 JUN, H7N9 virus isolates from 25 human cases had been found to be highly pathogenic for birds; the isolates were from Taiwan (in a case exported from Guangdong), Guangdong, Guangxi, and Hunan provinces. As of 30 JUN, CNIC reported there has been no evidence of increased disease severity or transmissibility to or among humans related to this change in the virus. WHO has also noted that there is no evidence this change from a low pathogenic to a highly pathogenic avian influenza virus has had any impact on the pathogenicity or transmissibility of H7N9 in humans. “Highly pathogenic” and “low pathogenic” refer only to the ability of influenza A viruses to cause disease in avian populations and do not describe disease severity, transmissibility, or pathogenicity of influenza A infections in human populations. However, the recent identification of a highly pathogenic form of H7N9 indicates yet another genetic change in the virus not observed in the previous four seasons and with unknown implications for human populations.

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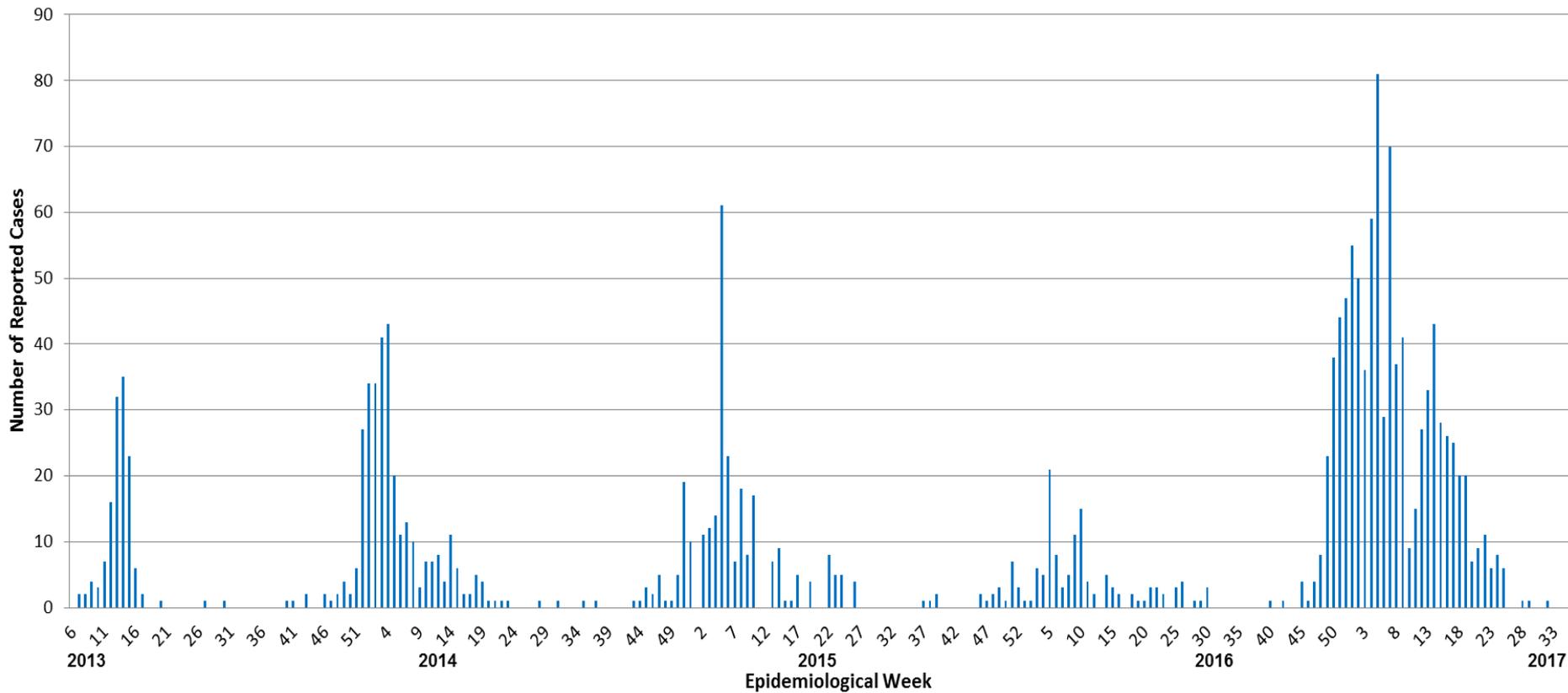
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Avian Influenza A (H7N9) Human Cases by Estimated Week of Onset

As of 30 AUG 2017 (N = 1,788)



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Source: [FAO H7N9 Situation Update 23 AUG 2017](#)

This map illustrates the geographic distribution of human H7N9 cases and H7N9-positive samples in birds or the environment in China since OCT 2015. Human cases are depicted in the geographic location where they were reported; for some cases, exposure may have occurred in a different geographic location. Precise location of 30 human cases in Anhui (2), Beijing (2), Guangdong (1), Guangxi (1), Hebei (3), Hunan (1), Hubei (2), Jiangsu (2), Jiangxi (6), Sichuan (2), Zhejiang (3) and unknown (5) provinces are currently not known; these cases are therefore not shown on the map.

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Cumulative Human Cases of Avian Influenza A (H7N9)

1 APR 2013 - 30 AUG 2017



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*47 cases from China were reported without location information in 2015 – 2017



Since the beginning of the avian influenza A (H7N9) outbreak, spikes in cases have been associated with seasonality. These seasonal epidemics typically span 1 OCT to 30 SEP of the following year (see the above maps). These maps only illustrate autochthonous cases in China, not imported cases.

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