Armed Forces Health Surveillance Branch
H7N9 Surveillance Summary
(10 MAY 2017)

The overall classification of this document is:
APPROVED FOR PUBLIC RELEASE

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CASE REPORT: As of 10 MAY, according to WHO, FAO, China's National Health and Family Planning Commission (NHFPC), 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 829 (+46) cases with at least 226 (+13) deaths. The number of human cases identified this season accounts for approximately 49% (+1%) of all human cases of H7N9 reported since 2013. The total case count since the disease was first identified in APR 2013 is 1,691 cases with at least 551 deaths, 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 33%; the average age of those affected is 55 years; and at least 461 (+17) of the cases reported have been female. The most recent known date of onset was 2 MAY. Since 2013, China has reported cases in 21 (+1) provinces and autonomous regions: Anhui, Fujian, Gansu, Guangdong, Guangxi, Guizhou, Hebei, Hubei, Henan, Hunan, Jiangsu, Jiangxi, Jilin, Liaoning, Shaanxi, Shandong, Sichuan, Tibet, Yunnan, Zhejiang, and Xinjiang; and four municipalities: Beijing, Chongqing, Shanghai, and Tianjin. Since OCT 2016, cases have been reported from 20 (+1, Shaanxi) different provinces and autonomous regions, and all four municipalities of China. Jiangsu Province has reported the most cases of any single province during the fifth wave, 150 (18%) of 829 cases.

On 3 MAY, Shaanxi Province reported its first human case of H7N9 in a 62-year-old male who developed symptoms on 23 APR and died on 1 MAY. During the same week, the province reported three additional cases, including one death. Shaanxi has not reported H7N9 positive samples in poultry or in the environment. On 5 MAY, the Shaanxi Provincial Health Committee announced the closure of live poultry markets (LPMs) in Xi’an and Xianyang, effective immediately.

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 reports that at the conclusion of the fourth wave of H7N9, there had been 26 known disease clusters since the beginning of the outbreak in 2013, and that cluster-associated cases accounted for 7% of total reported cases. As of 10 MAY, AFHSB has identified nine spatial clusters during this season of H7N9.

A new study in the Chinese Medical Journal reported an instance of likely human-to-human transmission of H7N9 that involved two cases and occurred in DEC 2016 in a hospital nephrology unit. The index case reported visiting a LPM within 10 days of symptom onset; the secondary case had no history of exposure to live poultry or to LPMs and developed respiratory symptoms on 21 DEC after sharing a room and having brief physical contact with the index case for 2 hours. This cluster is already included in the total number of clusters during the fifth seasonal epidemic above. A new study in Nature described the epidemiological, clinical, and virologic features of two separate family clusters, each involving two cases, that occurred in Fujian Province in DEC 2015. The authors determined that one cluster resulted from common exposure to live poultry or contaminated environments and the other cluster likely resulted from human-to-human transmission. The authors also found that the genome sequence of the viruses isolated within each family cluster were highly homologous.

In a recent 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 its 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. On 28 APR, Macao Special Administrative Region (SAR) announced it would be imposing a ban on the import and sale of all live poultry in the region beginning 1 MAY. Additionally, Macao SAR announced that it would be providing subsidies to those in the poultry industry affected by three outbreaks of H7N9 that occurred between DEC 2016 and FEB 2017, including a daily allowance of 200 MOP (~25 USD) for the period during which sales were suspended.

(+xx) represents the change in number from the previous AFHSB Summary of 26 APR 2017.
All information has been verified unless noted otherwise.
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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. A recent MMWR study compared the “fourth wave” of H7N9 (SEP 2015-AUG 2016) with the previous three waves and reported that the most recent wave “demonstrated a greater proportion of infected persons living in rural areas, a continued spread of the virus to new areas, and a longer epidemic period.” 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 over 4,000 virus-positive samples from the environment and chickens, pigeons, ducks, and wild birds since the beginning of the outbreak in 2013.

A recent 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 of these samples were of the 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 27 FEB, WHO reported a change in the genetic sequence of two isolates from confirmed H7N9 cases in Guangdong Province indicating the virus is evolving from a low pathogenic to a highly pathogenic avian virus. Similar changes were also found in genetic sequence data from another recent case with travel history to Guangdong that was reported by Taiwan to WHO on 4 FEB. Additionally, the Ministry of Agriculture (MOA) of China notified OIE on 21 FEB that genetic sequences of virus samples from live poultry markets in Guangdong showed changes consistent with highly pathogenic avian influenza virus. As of 9 MAY, FAO and OIE have reported the highly pathogenic form of H7N9 in LPMs from four provinces: Fujian, Guangdong, Guangxi, and Hunan provinces, and from farms and backyard flocks in Guangxi, Hebei, and Hunan provinces. WHO reports that there is no evidence this change from a low pathogenic to highly pathogenic avian influenza virus has had any impact on the pathogenicity or transmissibility of H7N9 in humans.

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. On 4 MAY, China’s NHFPC held a joint meeting on H7N9 epidemic prevention and control with the country’s Department of Agriculture, Administration of Industry and Commerce, and Food and Drug Administration. Over 3,000 state and regional officials participated in the meeting.

MEDICAL COUNTERMEASURES & RESEARCH: On 27 APR, the clinical stage biotechnology company Moderna Therapeutics published preclinical data demonstrating that its mRNA vaccine against H7N9, mRNA-1851, generates strong protective immunity in mice, ferrets, and non-human primates. A Phase I study of healthy volunteers is underway in the U.S. with 156 participants.

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.
Avian Influenza A (H7N9) Human Cases by Estimated Week of Onset
As of 10 MAY 2017 (N = 1,691)
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 23 human cases in Anhui (2), Beijing (2), Guangdong (1), Guangxi (1), Hebei (2), Hunan (1), Hubei (2), Jiangsu (1), Jiangxi (6), Sichuan (2) and Zhejiang (3) provinces are currently not known; these cases are therefore not shown on the map.
Cumulative Human Cases of Avian Influenza A (H7N9)
1 APR 2013 - 10 MAY 2017

Cumulative Cases (N=1691*)
- 0
- 1 - 9
- 10 - 29
- 30 - 62
- 63 - 319
- Imported Cases

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

Wave 1
APR 2013-SEP 2013

Wave 2
OCT 2013-SEP 2014

Wave 3
OCT 2014-SEP 2015

Wave 4
OCT 2015-SEP 2016

Wave 5
OCT 2016-MAY 2017

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

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