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

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DEPARTMENT OF DEFENSE (AFHSB)
Avian Influenza A (H7N9) Surveillance Summary #76
24 MAY 2017 (next Summary 7 JUN 2017)

CASE REPORT: As of 24 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 869 (+40) cases with at least 238 (+12) deaths. The number of human cases identified this season accounts for approximately 50% (+1%) of all human cases of H7N9 reported since 2013. The total case count since the disease was first identified in APR 2013 is 1,731 cases with at least 571 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 447 (-14) (26%) of the cases reported have been female. AFHSB’s total number of female cases decreased this week due to the case-specific demographic information provided in WHO’s release of its monthly report on influenza at the human-animal interface on 16 MAY. The most recent known date of onset was 13 MAY. Since 2013, China has reported cases in 22 (+1) provinces and autonomous regions: Anhui, Fujian, Gansu, Guangdong, Guangxi, Guizhou, Hebei, Hubei, Henan, Hunan, Jiangsu, Jiangxi, Jilin, Liaoning, Shaanxi, Shandong, Shanxi, Sichuan, Tibet, Yunnan, Zhejiang, and Xinjiang; and four municipalities: Beijing, Chongqing, Shanghai, and Tianjin. Since OCT 2016, cases have been reported from 21 (+1, Shanxi) 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 seasonal epidemic, 153 (18%) of 869 cases.

On 16 MAY, Shanxi Province reported its first human case of H7N9 in a 66-year-old female from Datong City. Shanxi Province borders Shaanxi, Henan, and Hebei Provinces in northwestern China. On 23 MAY, Shanxi reported its second human case in a 57-year-old male farmer who was hospitalized with fever, cough, and fatigue on 7 MAY but was not diagnosed with H7N9 for more than two weeks.

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 24 MAY, AFHSB has identified 11 (+2) spatial clusters during this season of H7N9. One new cluster occurred in Shaanxi Province and involved two cases; the presumed index case was a 62-year-old male who had symptom onset on 18 APR and was visited in the hospital by the second case, who had symptom onset on 29 APR. The other new cluster occurred in Hebei Province and also involved two cases; the presumed index case was a 62-year-old female who had symptom onset on 16 APR and was the mother of the second case, who had symptom onset on 2 MAY.

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. A recent Eurosorveillance study reported HPAI H7N9 can mutate to include antiviral resistance during prophylaxis or treatment.

A recent study in BMC Public Health found that despite evidence poultry farmers are at high risk for H7N9 infection due to sustained occupational exposure, interviews with 297 Jiangsu poultry farmers revealed they generally perceived the severity of H7N9 to be high but viewed their personal vulnerability to infection as low. The authors reported that interventions designed to enhance the perceived effectiveness of key personal protective measures such as hand-washing and wearing PPE, particularly among lower-educated respondents, may effectively motivate adoption of these behaviors.

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.

(+)xx) represents the change in number from the previous AFHSB Summary 10 MAY 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 seasonal epidemic of H7N9 (SEP 2015-AUG 2016) with the previous three seasons and reported that the most recent epidemic “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 4,228 virus-positive samples from the environment and chickens, pigeons, ducks, and wild birds since the beginning of the outbreak in 2013. On 17 MAY, China’s Inner Mongolia Autonomous Region reported its first identification of H7N9 in poultry and environmental samples collected from live poultry markets (LPMs) in three cities: Hinggan League/Xing’an, Tongliao City, and Xilingol League. To date, there have been no human cases of H7N9 reported in Inner Mongolia, which borders Mongolia in the north. Hinggan League, Tongliao City, and Xilingol League are 650km, 300km, and 550km from the closest border crossing with Mongolia, respectively.

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 Province 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 LPMs in Guangdong showed changes consistent with highly pathogenic avian influenza virus. As of 24 MAY, FAO and OIE have reported the highly pathogenic form of H7N9 in LPMs from Fujian, Guangdong, Guangxi, and Hunan provinces, and from farms and backyard flocks in Guangxi, Hebei, Henan, and Hunan provinces. Additionally, on 24 MAY, China’s MOA announced an outbreak of H7N9 on a farm in Wuqing District, Tianjin Municipality, in which there was a die-off of 6,000 (out of 10,000) domestic poultry. While pathogenicity was not mentioned in this initial announcement, the level of bird mortality likely indicates the outbreak was highly pathogenic; confirmation from China MOA is pending. WHO 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.

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.

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. A recent case report in BMC Pulmonary Medicine described the successful use of extracorporeal membrane oxygenation (ECMO) for a patient with H7N9-associated acute respiratory distress syndrome.
Avian Influenza A (H7N9) Human Cases by Estimated Week of Onset
As of 24 MAY 2017 (N = 1,731)
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 24 human cases in Anhui (2), Beijing (2), Guangdong (1), Guangxi (1), Hebei (3), 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.

Source: FAO H7N9 Situation Update 17 MAY 2017

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Cumulative Human Cases of Avian Influenza A (H7N9)
1 APR 2013 - 24 MAY 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.