CASE REPORT: As of 26 APR, 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 783 (+53) cases with at least 213 (+5) deaths. The number of human cases identified this season accounts for approximately 48% (+2%) of all human cases of H7N9 reported since 2013. The total case count since the disease was first identified in APR 2013 is 1,645 cases with at least 545 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% (+2%); the average age of those affected is 55 years; and at least 444 (+15) of the cases reported have been female. The most recent known date of onset was 11 APR. Since 2013, China has reported cases in 20 provinces and autonomous regions: Anhui, Fujian, Gansu, Guangdong, Guangxi, Guizhou, Hebei, Hubei, Henan, Hunan, Jiangsu, Jiangxi, Jilin, Liaoning, Shandong, Sichuan, Tibet, Yunnan, Zhejiang, and Xinjiang; and four municipalities: Beijing, Chongqing, Shanghai, and Tianjin. Since OCT 2016, cases have been reported from 19 (+1, Jilin) different provinces and autonomous regions, and four (+1, Tianjin) municipalities of China. Jiangsu Province has reported the most cases of any single province during the fifth wave, 148 (19%) of 783 cases.

On 26 APR, Tianjin municipality reported its first case of H7N9 in the current seasonal epidemic in a 58-year-old woman from Wuqing District; the region has reported a total of three human cases since 2013. On 18 APR, the Hong Kong Center for Health Protection (CHP) reported two new human cases of H7N9 in Tibet Autonomous Region soon after Tibet's first report of a human case on 8 APR. As of 26 APR, Gansu Province has reported two additional human cases of H7N9 since reporting its first human case on 8 APR in an 82-year-old woman who had symptom onset on 3 APR and has since recovered. All three cases reported contact with live poultry. The first case was reported soon after the province’s first positive sample of H7N9, taken from a live poultry market (LPM) near Suzhou market.

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 27 APR, AFHSB has identified nine (+1) spatial clusters during this season of H7N9. On 20 APR, WHO reported a new cluster in Tibet that involved two male poultry workers, aged 41 and 39, who worked at the same poultry stall in Lhasa City and had symptom onset on 27 MAR and 28 MAR, respectively.

A new Eurosurveillance study on the elevated number of human H7N9 infections reported in Jiangsu Province from OCT 2016–JAN 2017, concluded that visiting LPMs was the main risk factor for H7N9 infection for the public due to contact with poultry and potential environmental contamination. In a recent study in Nature Communications, researchers from Hong Kong University (HKU) identified a mutation in the viral genome of H7N9—a unique nucleotide substitution (NS-G540A) acquired through early 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. In a press release on 22 MAR, HKU reported that these findings have significant implications for drug development and for monitoring novel avian influenza viruses in birds; they discuss a novel target for anti-influenza drug development and an important biomarker for monitoring the emergence and transmission of avian influenza viruses in humans and preventing human-to-human infection of the viruses.

(+xx) represents the change in number from the previous AFHSB Summary of 12 APR 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. 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 2,000 virus-positives 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. According to FAO on 26 APR, the highly pathogenic form of H7N9 has now been confirmed in chicken and environmental samples from 23 LPMs in Fujian, Guangdong, Guangxi, and Hunan provinces, and from three farms in Guangxi (1) and Hunan (2) provinces. OIE reported the first identification of highly pathogenic H7N9 in birds on 21 MAR in samples from a LPM in Guangdong Province and on 24 MAR on a farm in Hunan Province. 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 1 MAR, WHO held a virtual press briefing addressing the fifth season of H7N9 in China as well as other current outbreaks of avian influenza globally. A panel of experts reported that the risk of sustained human-to-human transmission remains low, and that H7N9 is now past its peak for the current season. On 21 APR, China's MOA issued a notice on the strengthening of inter-province poultry movement control to be implemented beginning 14 APR; the measures include quarantine certification, sample collection before poultry movement (a minimum of 30 samples per flock), requirements for testing and culling, the role of farmers and veterinary authorities during active and passive surveillance, and the illegal use of vaccines.

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 of 12 APR 2017. All information has been verified unless noted otherwise. For questions or comments, please contact: dha.ncr.health-surv_list.afhs-jb-alert-response@mail.mil

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Avian Influenza A (H7N9) Human Cases by Estimated Week of Onset
As of 26 APR 2017 (N = 1,645)

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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 22 human cases in Anhui (2), Beijing (1), 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.

Source: FAO H7N9 Situation Update 26 APR 2017
Cumulative Human Cases of Avian Influenza A (H7N9)
1 APR 2013 - 26 APR 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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