RAPID RISK ASSESSMENT

Human infection with avian influenza A(H7N9) virus

Fourth update 2 February 2015

Main conclusions

On 26 January 2015, the Public Health Agency of Canada announced the detection of influenza A(H7N9) infection in a resident of British Columbia upon return from travelling to China. This is the first documented case in North America. The case was diagnosed through routine testing while attending a general practice with mild flu symptoms. On the 29 January 2015, a second case, with the same travel history and close contact to the first case, tested positive for influenza A(H7N9). This individual presented with more severe flu symptoms. Neither case required hospitalisation and both are recovering at home.

Since the notification of a novel reassortant influenza A(H7N9) virus on 31 March 2013, a total of 488 laboratory-confirmed cases of human infection with avian influenza A(H7N9) virus, including 185 deaths, have been reported to the World Health Organization (WHO): 469 cases by the China National Health and Family Planning Commission, four cases by the Taipei Centers for Disease Control (Taipei CDC), 12 cases by the Centre for Health Protection, China, Hong Kong SAR, one case in a Chinese traveller, reported from Malaysia and two cases reported in Canada.

The majority of recently reported human cases are associated with exposure to infected live poultry or contaminated environments, including markets where live poultry are sold. Influenza A(H7N9) viruses continue to be detected in poultry and their environments in the areas where human cases are occurring. Information to date suggests that these viruses do not transmit easily from human to human and the information does not support sustained human-to-human transmission.

At present, the most immediate threat to EU citizens is to those living or visiting influenza A(H7N9)-affected areas in China . It is advisable to avoid live bird markets and contact with live poultry and avoid consuming raw or incompletely cooked meat products and eggs in those same areas in China. The previous report by Malaysia of one human case with avian influenza A(H7N9) virus infection in February 2014, and the recent importation of A(H7N9) from China to Canada in travellers, highlights the possibility of travel-related cases also being detected in Europe, especially during the period December to February when a marked increase in human cases is generally recorded in China. Community-level spread in following importation into Europe is unlikely as the virus does not transmit easily among people. Nonetheless, travellers developing severe respiratory or flu-like symptoms within ten days after travel to affected areas and exposure to poultry or untreated poultry products in China should be rapidly managed and appropriately sampled for influenza testing.

Sporadic cases imported from China do not alter ECDC's risk assessment from February 2014.

Erratum: 4 February 2015 – number 50 in the Reference list was amended.

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Source and date of request

By the request of the European Commission, on 27 January 2015.

Public health issue

This document aims to:

- summarise the epidemiological and virological information about human infections with avian influenza A(H7N9)viruses in China and Canada
- assess the risk to public health in the EU/EEA and to EU/EEA citizens.

This rapid risk assessment builds on earlier ECDC rapid risk assessments on avian influenza.

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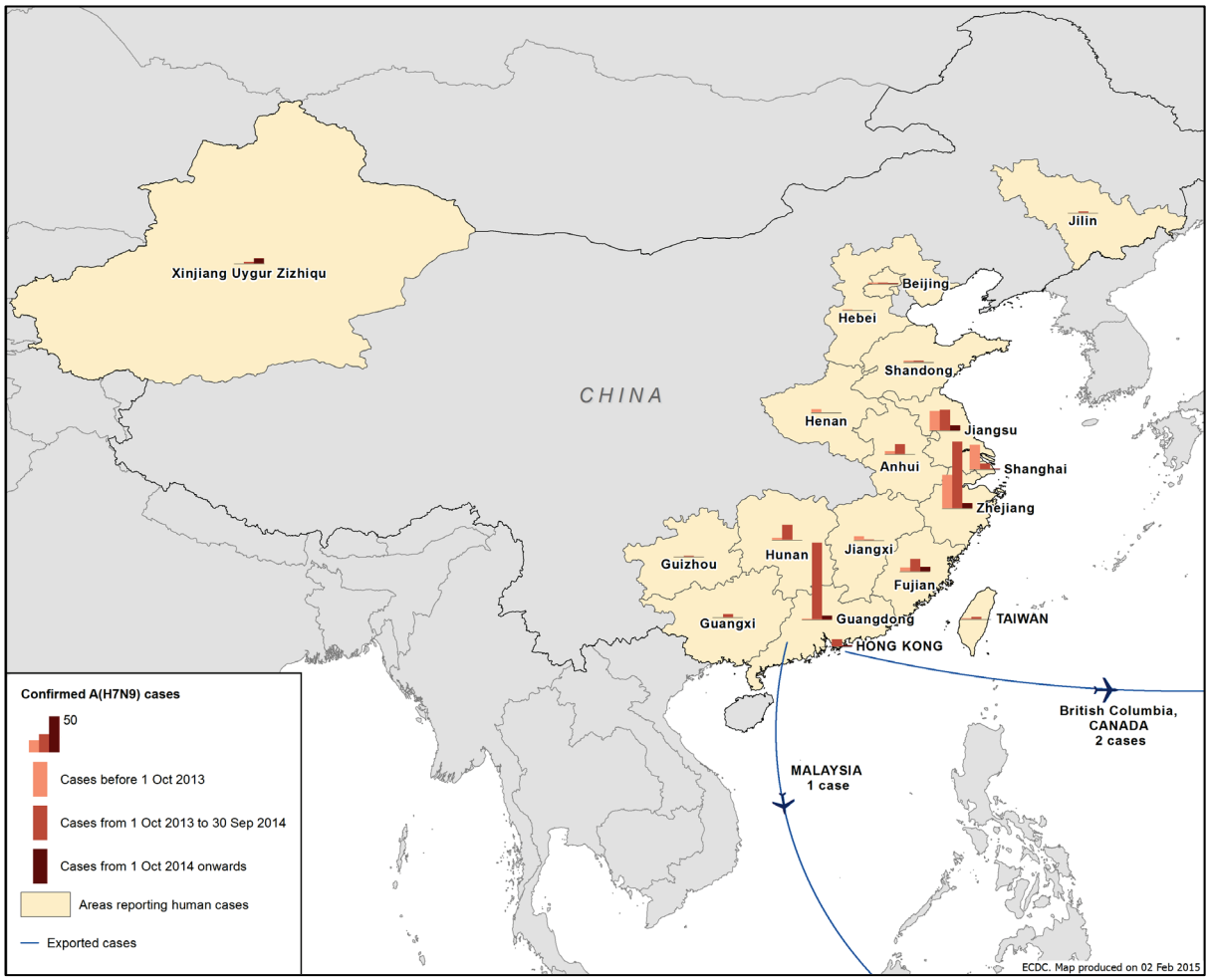
ECDC acknowledges the valuable contributions of all experts. All experts have submitted Declarations of Interest. ECDC has reviewed these and finds that none of them represent conflicts of interest with the comments and suggestions the experts have made. It should be noted that opinions expressed by individual experts do not necessarily represent the opinion of their institutions.

Event information

China

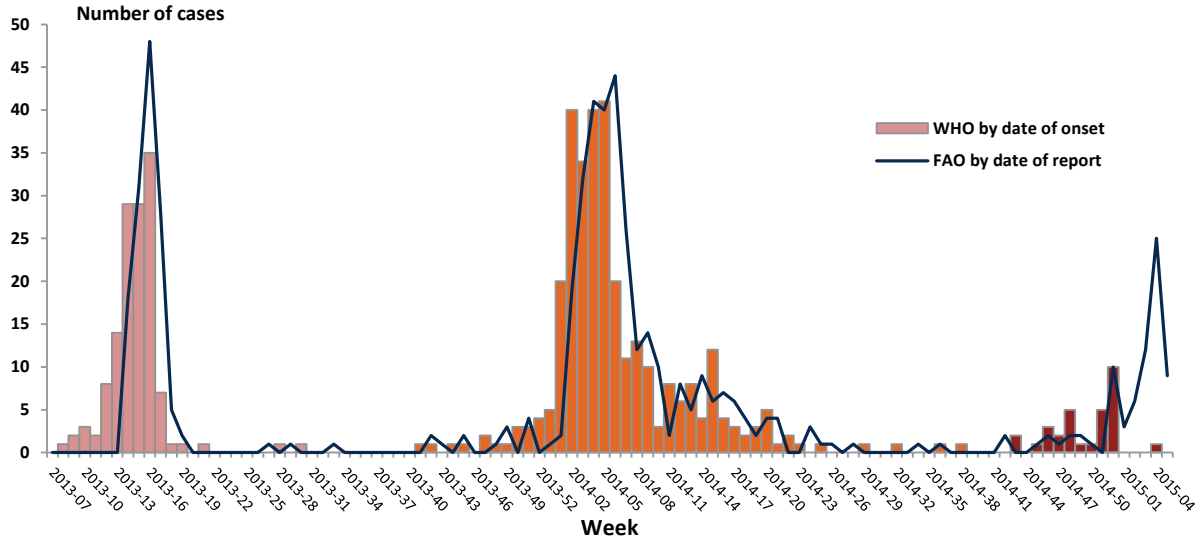
In March 2013, Chinese authorities announced the identification of a novel reassortant A(H7N9) influenza virus in patients in eastern China. As of 29 January 2015, 485 laboratory-confirmed cases have been reported in China: Zhejiang (145), Guangdong (112), Shanghai (43), Jiangsu (63), Fujian (28), Hunan (24), Jiangxi (6), Henan (4), Anhui (18), Beijing (5), Xinjiang Uyghur (9), Shandong (4), Jilin (2), Hebei (1), Guangxi (4), Guizhou (1), Hong Kong (12) and Taiwan (4) (Figure 1).

Figure 1. Distribution of confirmed A(H7N9) human cases by place of reporting, week 07/2013 to 04/2015, in China (n=485)



The outbreak shows a seasonal pattern peaking in the winter months and sporadic cases during the summer (Figure 2). The first wave in spring 2013 (week 07/2013 to week 40/2013) included 135 cases, the second wave 319 cases between week 41/2013 to week 40/2014, and a third wave started in October 2014 (week 41/2015) with 31 cases as of 29 January 2015. The three waves occurred during the cold season in China with only a few cases during the summer months.

Figure 2. Distribution of confirmed A(H7N9) cases by week*, week 07/2013 to 05/2015, China



**WHO data shows cases by the week of onset (n=485) and FAO data shows cases by the week of reporting (n=530).*
Sources for the data: WHO Disease Outbreak News (DONs), Food and Agriculture Organization of the United Nations (FAO)

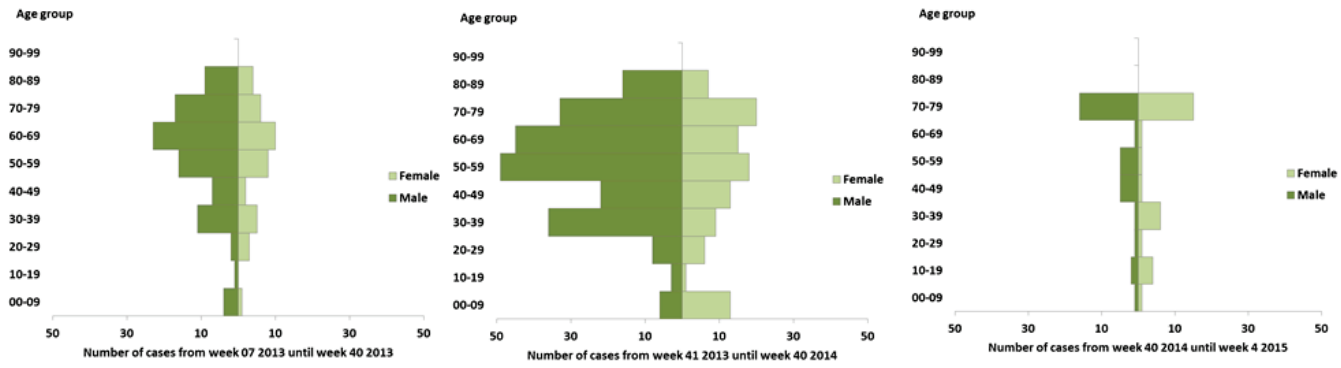
Overall, 185 of the 485 cases notified in China have died (case-fatality ratio-CFR=38%) [1]. In the first wave period, 43 of 135 cases died (CFR 32%) and 134 of 319 cases died (CFR 42%) in the second wave. These estimates are based on the information available at the time of notification. Therefore, CFR may be affected by completeness of information about outcome at time of notification. Seventy-percent of cases (n=337) have developed severe respiratory disease.

While the data are scarce for the first wave regarding the date of hospitalisation and severity, during the second wave, 317 of 319 patients were hospitalised and, of these, 274 were reported to have been in severe or critical condition at the time of notification. During the third wave and as of week 05/2015, 29 of the 31 cases have been hospitalised and 27 of the cases were reported as being in a severe or critical condition. Only a few mild A(H7N9) cases have been detected.

The average age for all reported cases is 55 years, ranging from one to 91 years. Among 480 patients with documented gender, 325 (68%) are male. In the first wave, of the 130 cases with known age and gender, 70% (91) were male while during the second wave, 69% (218) of the 318 cases with known age and gender were male. During the third wave, 16 (50%) of the 31 cases were male (Figure 3).

There was no significant change in gender ($chi^2_{(1)}$=0.21, p=0.65) and median age ($chi^2_{(1)}$=2.26, p=0.13) distributions between the first two waves.

Figure 3. Distribution of confirmed A(H7N9) human cases by age and gender, illustrated by the three waves , China (n=479*)



**Source for the data: WHO Disease Outbreak News (DONs)*

Malaysia

A Chinese tourist travelling to Sabah (Malaysia) was the first case of influenza A(H7N9) diagnosed and reported outside China and Taiwan on 12 February 2014. The patient, a 67-year-old woman from Guangzhou, Guangdong Province, reported relevant exposure to a live bird market (LBM) in China before travelling. She developed acute respiratory distress symptoms and sought hospital care one week later, on 7 February, while on holiday in Malaysia. After receiving intensive care therapy in a specialised hospital in Kota Kinabalu, Sabah, she recovered and was discharged on 13 March. Of the 191 identified contacts, six were symptomatic, but nasopharyngeal specimens tested negative for influenza [2].

Canada

On 26 January 2015, the Public Health Agency of Canada confirmed the detection of an influenza A(H7N9) infection in a woman that developed influenza-like symptoms on 14 January 2015, two days after returning from a two week travel to China together with her husband. She attended a primary care facility where nasopharyngeal swabs were collected for influenza diagnosis. A five-day course of antiviral therapy was provided and self-isolation and self-monitoring at home was recommended. Laboratory testing confirmed A(H7N9) infection on 26 January.

The husband reported influenza-like symptoms with onset a day prior to his wife. He became ill one day after returning from China and presented with moderate symptoms not requiring hospitalisation. On January 29, 2015 laboratory results were confirmed positive for A(H7N9) [3]. The isolate was sensitive to neuraminidase inhibitors. A five day course of antiviral therapy was also provided along with a recommendation to self-isolate and self-monitor at home. Both persons were asymptomatic while travelling back together from China to Canada, on 12 January. Both have recovered.

The travel history of the two individuals did not reveal any direct contact with live or dead poultry while in China. They indicated a possible exposure to live poultry and large amount of chicken faeces in a tourist site they visited during the week before onset of symptoms. All the close contacts have been identified and their health is being monitored by provincial health authorities. Follow-up of passengers on the plane was not initiated as the persons were not symptomatic during the flight.

These are the first cases of human infection with avian influenza A(H7N9) virus reported in Canada and the first two confirmed human cases in the Americas [4].

Disease background

Clinical aspects, spectrum of disease and treatment

The median incubation period has been estimated to be six days (range of 1–10 days) [5]. Fever and cough have been the most common symptoms, with vomiting and diarrhoea have appeared in a smaller proportion of cases [6]. Pneumonia and respiratory failure were reported in the majority (90%) of cases identified in China between 25 March and 1 December 2013, resulting in high rates of hospitalisation (99%) and further referral to intensive care units because of severe lower respiratory tract disease (63%). High frequency of underlying medical comorbidities (73%) was also reported [5]. Some milder cases have been identified through extended testing of outpatients with influenza-like illness [7], suggesting that A(H7N9) presents with a broad clinical spectrum. In particular, paediatric H7N9 patients tend to present with clinically milder disease [8].

The symptomatic case-fatality risk was estimated between 160 (63–460) and 2 800 (1 000–9 400) per 100 000 symptomatic cases [9], suggesting that A(H7N9) is not as severe as A(H5N1) [10], but is more severe than pandemic A(H1N1)-2009 [11].

Contacts of H7N9 cases are monitored to identify case clustering and potential human-to-human transmission. A few small family clusters were detected, showing high genomic sequence similarities and reported common exposure to risk sources (LBM or dead poultry) prior to onset of symptoms [8,12,13]. While occasional human-to-human transmission in the clusters cannot be ruled out, sustained human-to-human transmission has not been observed [5]. Recent studies identified seroconversion in up to 10% of asymptomatic close contacts of symptomatic H7N9 cases [14]. Serological studies in China found poultry workers being seropositive for antibodies against A(H7N9) [15-17].

A co-infection of H7N9 and a seasonal H3N2 influenza virus has already been described in China in 2013 [18]. With the seasonal influenza virus circulation in humans, there is an increased risk for reassortment of the seasonal influenza viruses with the A(H7N9) viruses in co-infected humans as well as a reassortment with other circulating avian influenza viruses of the H5 type.

Studies of H7N9 viruses isolated from humans suggest that they are resistant to adamantane antiviral agents but susceptible to neuraminidase inhibitors oseltamivir and zanamivir [19-21]. However, Arg292Lys substitutions in the viral neuraminidase associated with reduced susceptibility to neuraminidase inhibitors have been documented in several cases after the start of oseltamivir treatment [22]. A recent study, describing a family cluster with probable human-to-human transmission, detected one amino acid substitution in the PB2 gene, two new mutations in the NA and six in the PB2 gene, which were not present in isolates from the first wave in 2013. These new isolates showed drug resistance to oseltamivir but were sensitive to peramivir [23].

WHO recommends antiviral treatment with a neuraminidase inhibitor as soon as possible for patients with suspected or confirmed A(H7N9) infection, but does not recommend routine post-exposure antiviral chemoprophylaxis for close contacts of confirmed influenza A(H7N9) cases, although the initiation of empiric post-exposure antiviral treatment may be considered in certain circumstances, mainly in people with underlying medical conditions [24].

The US CDC has also published interim guidance on the use of antivirals for treatment of A(H7N9) infection [25] and for chemoprophylaxis of close contacts [26]. They recommend oseltamivir or inhaled zanamivir to close contacts of a confirmed or probable influenza A (H7N9) case according to risk of exposure. For high risk exposure (household or close family member) chemoprophylaxis should be administered, while for moderate risk exposure (healthcare worker with higher risk-contact to case), chemoprophylaxis could be considered.

Virological information

The novel influenza A(H7N9) viruses are the first low pathogenicity avian viruses that have been documented to cause severe human disease. The virus is a reassortant avian influenza A virus in which the six RNA segments encoding the internal proteins are closely related to avian A(H9N2) viruses that emerged in the chicken population in China [27-30]. The gene encoding haemagglutinin (HA) belongs to the Eurasian A(H7) avian influenza virus lineage, and the segment for neuraminidase (NA) is most similar to avian H11N9 and H7N9 viruses. The reservoir for this novel virus remains unknown, although a continuous co-circulation of multiple H9N2 genotypes in farmed poultry over a longer time might be responsible for antigenic changes and adaptation to chickens [30]. Evolution processes of H7N9 viruses in the poultry population are ongoing since 2013 resulting in a genetic heterogeneity across different regions in China [31].

Genetic characteristics of H7N9 viruses are of concern for their pandemic potential e.g. sustained human-to-human transmission due to their potential to recognise human and avian influenza virus receptors, α-2,6- and α-2,3-linked sialic acid residues, respectively or the ability to replicate in the human host [32].

Animal infections and environment detection

Active surveillance among animals for A(H7N9) is ongoing in China, where public health authorities sample chickens, waterfowls, captive-bred pigeons, quails and wild birds. Additionally, environmental samples are collected at wholesale live bird markets, live bird trading areas (stalls) at farmers' markets, large-scale poultry farms, village/backyard poultry holdings, poultry slaughterhouses, wild migrating bird habitats, and other locations. The Chinese Ministry of Agriculture has notified the World Organization for Animal Health (OIE) about the detection of some genetically similar influenza A(H7N9) isolates from birds [33].

Influenza A(H7N9) has been detected in animal and environmental samples in China. The virus has been detected in chicken, in particular in the yellow and silkie chicken breeds, ducks, pigeons, a goose and a tree sparrow, but not in pigs. Judging from surveillance results, chickens appear the poultry species most affected [34] [35]. In April 2013, 88 samples tested positive from approximately 900 000 samples collected from different surveillance sites around the country and were analysed by national and provincial avian influenza reference laboratories in China [36]. In December 2013, results from the national monitoring of influenza A(H7N9)conducted by the Chinese Ministry of Agriculture included 18 positive samples (virus genome) out of 200 tested (9.0%) from four sampling sites in Zhejiang, and two positive samples (genomic) out of 2 521 tested (0.08%) from 151 sampling sites in Guangdong. [37,38] In December 2014, 60 574 virological and 120 710 serological samples were collected from 7 379 sites in 24 provinces. Fourteen virological samples tested positive for A(H7N9): Jiangsu (1 chicken, 1 environmental), Zhejiang (6 chickens, 1 duck), Fujian (1 environmental) and Xinjiang Uygur Autonomous Region (2 chicken, 2 environmental). Sites with positive samples include eight different live poultry markets and one backyard farm [39].

Samples from the environment, particularly from live poultry markets but also some backyard farms, a kitchen and a slaughterhouse, tested positive for influenza A(H7N9) during 2013–2015 [40,41].

Since March 2013 and up to January 2015, FAO has collected reports of positive virological samples from birds and the environment, from the Chinese Ministry of Agriculture and Ministry of Health and the Chinese Centre for Disease Control and Prevention (CDC China) from: Anhui, Fujian, Guangdong, Guangxi, Hebei, Henan, Hong Kong, Hunan, Jiangsu, Jianxi, Macao, Ningxia Hui, Quinghai, Shandong, Shanghai, Xinjiang and Zhejiang.

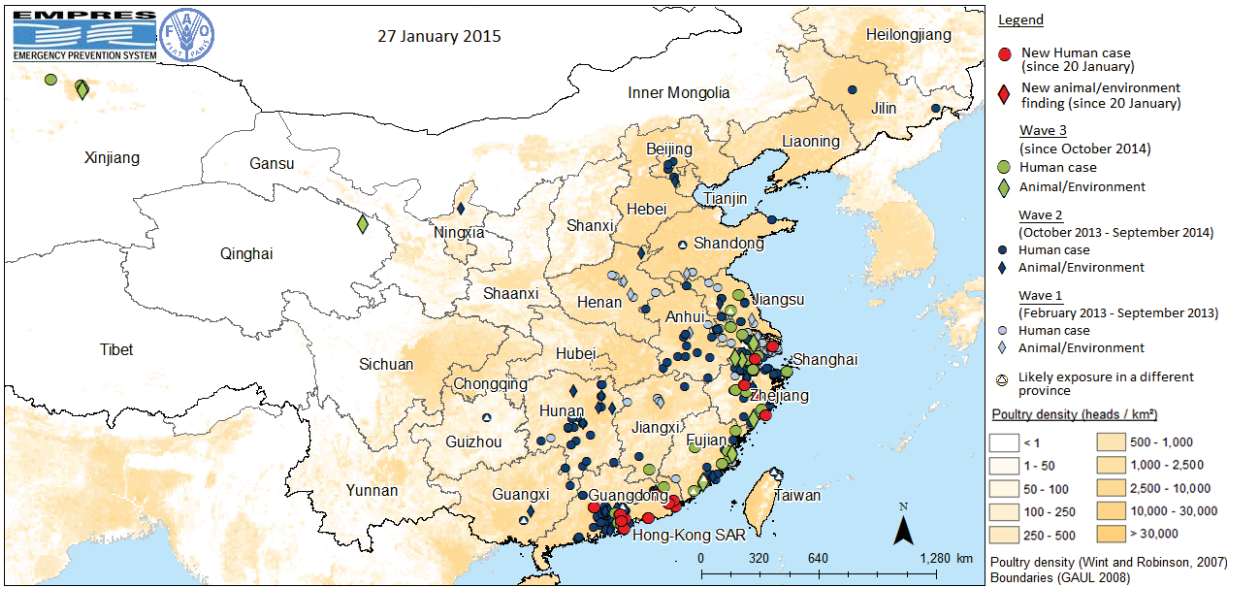
The major source of infection with influenza A(H7N9)for humans is likely to be poultry or birds handled in the live bird markets or slaughtered at home. While wild birds are the reservoir for H7 and N9 genes of influenza viruses, [42,43] live bird markets seem to serve as amplifiers [44]. In 2013, the Ministry of Agriculture reported that 'stamping-out' control measures were implemented in poultry markets and some markets were temporarily closed. These closures were associated with a decrease in the number of human cases of A(H7N9) in those localities [44]. The closure of live poultry markets in the most affected cities was effective in reducing the risk for A(H7N9)infection in humans. Following the occurrence of new cases, the main cities in Guangdong and Zhejiang but also in other provinces closed live poultry markets in 2014, following the model applied in Shanghai and Hong Kong. It is unclear to what degree the authorities in China are able to implement such measures, and it remains possible that unauthorised and informal trade will continue to take place [35]. In response to the recent (January 2015) human cases in Guangdong, local authorities of Shenzhen City implemented a 10-day closure of live bird markets from 21 to 30 January [4].

Recent data from the epidemiological investigation of the case reported in Canada after travel to China suggests that other type of exposures (i.e. recreation farms and tourist sites that hold birds) could play a role in the transmission of the virus.

Human cases and positive findings in birds or the environment

In the map bellow (Figure 4), human cases are depicted in the geographic location of their report. For some cases, exposure may have occurred in a different geographic area. Precise location of six human cases in Fujian province is not known and cases are not shown on the map. Imported cases in Sabah, Malaysia (1) and Canada (2) are also not represented.

Figure 4. Human cases of influenza A(H7N9) and positive findings in birds or the environment



Source: Food and Agriculture Organization of the United Nations (FAO), Emergency Prevention System for Transboundary Animal Diseases (EMPRES), Rome, Italy

Vaccines against avian influenza A(H7N9) infections in humans

The most important intervention in preparing for the pandemic potential of influenza A(H7N9) is the development and use of human vaccines. In May 2013, WHO published its first summary of development and release of candidate vaccine viruses for clinical trials [45]. Subsequently, nine candidate vaccine viruses have passed relevant safety testing and two-way haemagglutinin inhibition (HI) tests that allow them to be handled under BSL-2 enhanced containment [46].

Following testing and promising results of vaccine candidates in mice, chickens, ferrets and non-human primate models, several phase 1 clinical trials in healthy adults >18 years have been conducted. The vaccine candidates tested in a 2-dose schedule (day 0 and 21) in humans are based on either influenza A H7N9 recombinant virus-like particles [47] with an ISCOMATRIX adjuvant or inactivated influenza A/Shanghai/2/13 (H7N9) recombinant virus adjuvanted with MF59 [48,49]. Candidates tested so far have been shown to be immunogenic and safe, although for both candidates, local and systemic reactions were observed more often in the adjuvanted groups. However, no body temperatures reported exceeded 38.5º C. Further testing is needed before authorisation of influenza A H7N9 can be granted.

The EU Vaccine Task Force on Influenza (European Commission, European Medicines Agency, European Food Standards Authority and ECDC) has been meeting regularly since the onset of the H7N9 outbreak to consider the issues and discuss briefings from WHO and the National Institute for Biological Standards and Control.

Infection control measures in healthcare

WHO has produced guidance on laboratory biorisk management for A(H7N9) [50,51]. These guidelines are broadly applicable to management of all human cases of avian influenza and related samples. Healthcare workers often come into contact with patients with infectious diseases. Therefore, WHO recommends that basic appropriate infection prevention and control measures (standard precautions) be consistently applied in all healthcare settings at all times, and that the health status of healthcare workers be closely monitored. Together with standard precautions, healthcare workers caring for those suspected or confirmed to have H7N9 infection should use additional precautions.

Human surveillance in Europe

Surveillance for respiratory infections in humans

All novel influenza strains are notifiable diseases in the EU according to commission decisions and the International Health Regulations (IHR) through the Early Warning and Response System and IHR, respectively [52]. ECDC has developed an interim case-finding algorithm and a case definition for disease surveillance and the reporting of patients infected by the avian influenza A(H7N9) virus in EU/EEA Member States [53]. Infectious disease protocols for case investigations are available from the Consortium for the Standardization of Influenza Seroepidemiology (CONSISE) [54] and national authorities. Agreed protocols for clinical investigations have been prepared by the International Severe Acute Respiratory and Emerging Infections Consortium (ISARIC) [55].

Evidence of the effectiveness of contact tracing on board airlines in limiting spread of infection is limited and should only be considered upon a risk assessment on a case-by-case basis [56].

Diagnostics of avian influenza infections in humans

With routine diagnostic laboratory assays, the novel A(H7N9) viruses should be detected as positive for influenza A virus, and negative for influenza B, A(H1), A(H1)pdm09, A(H3) and A(H5) viruses. Hence, influenza A(H7N9) viruses are expected to be classified as un-subtypeable influenza A if no specific A(H7) diagnostic test is performed. It is standard procedure in diagnostic laboratories to send influenza A virus isolates or clinical samples that cannot be subtyped to the national reference laboratory (National Influenza Centres; NICs), and further to a WHO Collaborating Centre for characterisation, as was done in China for the first influenza A(H7N9) isolates.

European Reference Laboratory Network for Human Influenza (ERLI-Net) laboratories have rapidly developed and verified their capabilities for detecting the novel influenza A(H7N9) influenza virus [57]. In an external quality assessment RT-PCR detection panel which included an influenza A(H7N9) sample, 33 of the 36 participating EU/EEA laboratories from 29 countries detected the virus correctly as influenza A(H7) [58].

To assist European laboratories in verifying and ensuring their diagnostic capabilities with regard to avian influenza A(H7N9) virus, ECDC, ERLI-Net and the WHO Regional Office for Europe have released a technical briefing note on diagnostic preparedness in Europe for detection of avian influenza A(H7N9) viruses [59].

Discussion

Avian influenza A(H7N9) remains a widespread zoonotic disease in China and the virus is transmitted sporadically to humans in close contact with the animal reservoir (mainly chickens, in particular of the yellow and silkie chicken breeds). However, with the regular influenza season now ongoing in China and elsewhere in the northern hemisphere, there is a potential risk for co-infections with other influenza viruses, especially of mammalian origin and the development of new reassortant viruses with the possibility of increased capacity for transmission in the human population.

During 2013–2014, notification of human cases of influenza A(H7N9) in China followed a seasonal pattern with peaks in winter months and sporadic cases in the summer. The second wave, in 2014, had significantly larger amplitude, both in terms of number of cases and geographically, suggesting that the virus became more widespread in its domestic bird reservoir, providing increased opportunity for individuals to be exposed. Increased awareness and surveillance may have contributed to the increase in number of reported cases. The age and sex distribution remained the same during the first two waves. There is no clear evidence of a trend for the severity of cases, either as hospitalisation or case-fatality ratios, between successive waves seen in China, although potential data limitations mean that caution must be exercised in interpreting these data.

Intervention strategies, e.g. temporary closures of live poultry markets, seemed to have had an impact on the number of infections in the spring of 2013 and 2014. However, alternative and safer poultry processing may not be feasible in many parts of China. Furthermore, it is not always possible to identify the risk factors: a case-control study in China in 2013 suggested the association with live birds markets but found that for an important number of cases' exposure to LBMs or poultry had not been reported [60,61].

The celebration of the Chinese New Year on 19 February 2015 might increase the potential for human exposure to both A(H7N9) and seasonal influenza viruses, thereby increasing the risk of reassortment in humans. Two hundred and twenty-five million Chinese are expected to travel over the festive season, with 40% travelling abroad, in what is believed to be the world's largest annual human migration [62]. However, during and after the 2014 Chinese New Year celebrations (around 31 January), no increase in human cases was observed. Instead, human cases decreased after the first week of February. This may have been, at least in part, influenced by the measures taken, such as closure of live bird markets in main cities.

Rigorous epidemiological investigations are currently conducted in China in order to identify risk behaviours, other risks, and predisposing factors for avian influenza A(H7N9) infection.

The current influenza A(H7N9) viruses are considered to have pandemic potential [32].

Considering the spread of other avian influenza viruses over national and geographic borders in and outside Asia, it is noteworthy that neighbouring Asian countries have not reported cases of influenza A(H7N9).

Two human cases infected with influenza A(H7N9) were detected by Canadian health authorities even though symptoms were moderate and required no hospital admission.

Considering the severity of the disease, the fact that limited human-to-human transmission cannot be excluded in some clusters, that no vaccine is available against A(H7N9), and the favourable safety profile of the anti-viral drugs of choice, it is likely that the benefits of post-exposure chemoprophylaxis of close contacts with neuraminidase inhibitors outweigh the risks. Evidence of benefits and effectiveness of treatment remain very limited.

ECDC threat assessment for the EU

The A(H7N9) transmission pattern indicates a persistent zoonotic reservoir, and the continued transmission of this novel reassortant avian influenza virus capable of causing severe disease in humans in one of the most densely populated areas in the world remains a cause for concern due to the potential for a pandemic virus to develop. However, the most likely current scenario for China is that these outbreaks remain local zoonotic outbreaks in which the virus is transmitted sporadically to humans in close contact with the animal reservoir, similar to the influenza A(H5N1) situation. A seasonal pattern in human infections, similar to seasonal influenza, appears to be emerging; however it is premature to draw any firm conclusion on the pattern based on less than three seasons.

The recent introduction of influenza A(H7N9) to Canada as imported human cases provides support to the notion that sporadic imported cases of avian influenzas might also be seen in Europe. However, the risk of the disease spreading within Europe via humans is still considered low, as the virus does not transmit easily among people. The assessment of the risk for public health, by WHO on 26 January 2015, concluded that the risk has not changed after the detection of Canadian case [63].

People in the EU presenting with severe respiratory or influenza-like infection and a history of travel to the affected areas in China with potential exposure to poultry or birds will require careful investigation, management and infection control. Adequate samples for influenza tests should be rapidly taken and processed from patients with relevant exposure history within 10 days preceding symptom onset. Early or presumptive treatment with neuraminidase inhibitors should always be considered for suspect or confirmed cases. Contacts of confirmed cases should be offered post-exposure prophylaxis.

The risk of avian influenza viruses being transported to Europe in poultry through legal trade is negligible. EU regulations do not permit importation of live poultry, day-old chicks and hatching eggs and other birds (captive birds such as parrots, finches and ornamental birds) from China. The only poultry commodities authorised for import from China into the EU are sterilised meat products, heat-treated poultry meat from Shandong, and heat-treated egg products. Given the very heat-labile nature of all influenza viruses, these commodities are not considered to pose a risk of influenza virus transmission to consumers. Legal and illegal export of poultry products to several African countries appears to take place.

The risk of the avian influenza viruses arriving in Europe with migratory birds cannot be quantified. ECDC and the European Food Safety Authority (EFSA) have performed multiple independent risk assessments in the past regarding avian influenza that also cover pathways for avian influenza A(H7N9) [64-66]. The hypothesis that poultry in the affected area has been infected by wild birds has not been confirmed but neither can it be excluded. During extensive wild bird surveillance performed in China only one tree sparrow tested positive in Shanghai in April/May 2013 [67].

In order to decrease their risk of infection, EU citizens travelling or living in China should minimise their exposure to live poultry markets, avoid contact with live or dead poultry or their products, and practice good hand hygiene when visiting recreation farms or sites with wild birds [68].

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