Influenza at the human-animal interface
Summary and assessment, from 9 May to 10 July 2020

- **New infections**: Since the previous update on 8 May 2020, two new human infections with avian influenza A(H9N2) viruses, one human infection with an influenza A(H1N1) variant virus and one human infection with an influenza A(H1N2) variant virus were reported.  
- **Risk assessment**: The overall public health risk from currently known influenza viruses at the human-animal interface has not changed, and the likelihood of sustained human-to-human transmission of these viruses remains low. Human infections with viruses of animal origin are expected at the human-animal interface wherever these viruses circulate in animals.  
- **IHR compliance**: All human infections caused by a new influenza subtype are required to be reported under the International Health Regulations (IHR, 2005). This includes any influenza A virus that has demonstrated the capacity to infect a human and its haemagglutinin gene (or protein) is not a mutated form of those, i.e. A(H1) or A(H3), circulating widely in the human population. Information from these notifications is critical to inform risk assessments for influenza at the human-animal interface.

**Avian Influenza Viruses**

**Current situation:**

**Avian influenza A(H5) viruses**
According to reports received by the World Organisation for Animal Health (OIE), various influenza A(H5) subtypes continue to be detected in birds in Africa, Europe and Asia.

**Avian influenza A(H7N9) viruses**
There have been no publicly available reports from animal health authorities in China or other countries on influenza A(H7N9) virus detections in animals in recent months.

Overall, the risk assessments have not changed.

**Avian influenza A(H9N2) viruses**
Since the last update on 8 May 2020, two new laboratory-confirmed human cases of influenza A(H9N2) virus infections were reported from China.

The first case was reported to WHO on 9 May. The infection was detected in a 6-year-old male from Shandong province, China, who had onset of illness on 28 April 2020. The patient was hospitalized on the day of illness onset, was treated with oseltamivir and was discharged on 8 May. The patient had exposure to domestic poultry at his home before onset of symptoms.

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1 For epidemiological and virological features of human infections with animal influenza viruses not reported in this assessment, see the yearly report on human cases of influenza at the human-animal interface published in the Weekly Epidemiological Record. Available at: [www.who.int/wer/en/](http://www.who.int/wer/en/)

2 Standardization of terminology for the influenza virus variants infecting humans: Update. Available at: [https://www.who.int/influenza/gisrs_laboratory/terminology_variant/en/](https://www.who.int/influenza/gisrs_laboratory/terminology_variant/en/)

3 World Health Organization. Case definitions for the four diseases requiring notification in all circumstances under the International Health Regulations (2005). Available at: [www.who.int/ihr/Case_Definitions.pdf](http://www.who.int/ihr/Case_Definitions.pdf)

The second case was reported to WHO on 13 May. The infection was detected in a 10-month-old male from Fujian province, China, who had onset of illness on 4 May 2020. The patient had mild illness, was not hospitalized and was treated with oseltamivir. The patient had exposure to a live bird market before onset of symptoms.

Both patients were sampled as part of routine influenza-like illness (ILI) surveillance, have recovered, and no further cases were detected among contacts at the time of reporting.

Avian influenza A(H9N2) viruses are enzootic in poultry in Asia and increasingly reported in poultry in Africa.

Risk Assessment:
1. What is the likelihood that additional human cases of infection with avian influenza A(H9N2) viruses will occur? Most human cases are exposed to the A(H9N2) virus through contact with infected poultry or contaminated environments. Human infection tends to result in mild clinical illness in most cases. Since the virus continues to be detected in poultry populations, further human cases can be expected.

2. What is the likelihood of human-to-human transmission of avian influenza A(H9N2) viruses? No case clusters have been reported. Current epidemiologic and virologic evidence suggests that these viruses have not acquired the ability of sustained transmission among humans, thus the likelihood is low.

3. What is the likelihood of international spread of avian influenza A(H9N2) virus by travellers? Should infected individuals from affected areas travel internationally, their infection may be detected in another country during travel or after arrival. If this were to occur, further community level spread is considered unlikely as this virus has not acquired the ability to transmit easily among humans.

Swine Influenza Viruses

Current situation:

Influenza A(H1N1) variant virus (A(H1N1)v)
Since the last risk assessment of 8 May 2020, one human case of infection with a swine influenza A(H1N1)v virus was reported to WHO from Germany on 3 July. The infection was detected in a 2-year-old male who developed an influenza-like illness on 9 June 2020. The patient received healthcare on 9 June 2020. A sample was collected as part of routine ILI surveillance and an unsubtypable influenza A virus was detected on 15 June. Whole genome sequencing characterized this virus as a Eurasian avian-like swine A(H1N1) virus (1C.2.2) on 1 July. The case recovered and no further cases were detected among contacts. The patient had visited a swine farm and had close contact with pigs two days before onset of illness.

Antigenic investigations on the virus isolated from the patient indicated some cross-reactivity with seasonal influenza A(H1N1)pdm09 viruses, indicating that immunity against infection with similar swine viruses may exist in the human population due to the circulation of A(H1N1)pdm09 viruses. Serological testing of close family contacts is planned.
Influenza A(H1N2) variant virus (A(H1N2)v)
Since the last risk assessment of 8 May 2020, one human case of infection with a swine influenza A(H1N2)v virus was reported to WHO from Brazil on 22 June. The infection was detected in a 22-year-old female, with no comorbidities, who worked in a swine slaughterhouse in Paraná state. The patient developed an influenza-like illness on 12 April 2020. On 14 April, the patient received medical care and was sampled on 16 April. An subtypeable influenza A virus was detected and on 22 June, genetic sequencing characterized this virus as an influenza A(H1N2)v virus. The patient was treated with oseltamivir, was not hospitalized and has recovered. Further genetic and phenotypic characterization of the virus from the patient is ongoing.

On 26 June 2020, local authorities started a retrospective and prospective investigation in the slaughterhouse where the patient worked as well in nearby municipalities where the slaughterhouse workers live. According to the preliminary epidemiological investigation, a second individual who also worked at the slaughterhouse developed respiratory symptoms during the same timeframe as the confirmed case, but no sample was collected from this person. No other suspected cases amongst contacts of the confirmed case have been identified.

Risk Assessment:
1. What is the likelihood that additional human cases of infection with swine influenza viruses will occur? Swine influenza viruses circulate in swine populations in many regions of the world. Depending on geographic location, the genetic characteristics of these viruses differ. Most human cases are exposed to swine influenza viruses through contact with infected swine or contaminated environments. Human infection tends to result in mild clinical illness in most cases. Since these viruses continue to be detected in swine populations, further human cases can be expected.
2. What is the likelihood of human-to-human transmission of swine influenza viruses? Current evidence suggests that these viruses have not acquired the ability of sustained transmission among humans, thus the likelihood is low.
3. What is the likelihood of international spread of swine influenza viruses by travelers? Should infected individuals from affected areas travel internationally, their infection may be detected in another country during travel or after arrival. If this were to occur, further community level spread is considered unlikely as these viruses have not acquired the ability to transmit easily among humans.

Eurasian A(H1N1) swine viruses
In June 2020, the China Institute of Microbiology, Center for Influenza Research and Early-Warning, published a report entitled "Prevalent Eurasian avian-like H1N1 swine influenza virus with 2009 pandemic viral genes facilitating human infection". The article described swine influenza viruses detected through swine surveillance from 2011 to 2018 in China – the viruses had genes from Eurasian avian-like A(H1N1) lineages and internal genes from the human, seasonal A(H1N1)pdm09 virus and swine influenza triple reassortant viruses. These swine influenza viruses were classified based on their genetic make-up and termed genotypes G1-G6. The paper focuses on the zoonotic potential of the genotype G4 (termed by the authors of the paper) which emerged in 2013 and became predominant in swine population since 2016. The paper reported a seroprevalence of approximately 10% in swine industry workers and efficient direct contact and respiratory droplet transmission of the viruses in a ferret model.

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## Risk assessment

The viruses discussed in paper are not new. Viruses with similar gene combinations including the G4 genotype were reported previously in swine by the Harbin Veterinary Research Institute, China in a 2016 publication, and G4 genotype viruses have been the dominant genotype in swine population in China since 2016. The reported seroprevalence rate was based on a moderately small sample size and might not be solely attributed to the “new” G4 viruses. Other factors e.g. study design and context need to be taken into consideration. On the other hand, it highlights the importance of surveillance of swine influenza. Sporadic zoonotic infections in humans with G4 genotype swine influenza viruses have been reported from China with the most recent human case reported in November 2019. In line with the findings of this paper, the influenza division of the Centers of Disease Control and Prevention (CDC) in the United States (US) has performed risk assessments of related viruses (though not G4 genotype) in 2019 and confirmed that they are transmissible in a ferret model by both direct contact and respiratory droplet. In collaboration with the OIE-FAO Network of expertise on animal influenza (OFFLU), the WHO Global Influenza Surveillance and Response System (GISRS) has been monitoring swine influenza viruses from the public health perspective. A candidate vaccine virus (CVV) from a closely related Eurasian avian-like A(H1N1) virus has been developed by the WHO Collaborating Centre at the Chinese Center for Disease Control and Prevention (China CDC) and is available for vaccine development for pandemic preparedness purposes. Preliminary evaluation shows that the CVV covers well the G4 viruses from human infections, and evaluation with viruses from swine is ongoing.

The G4 genotype and other swine and avian influenza viruses are continuously evolving. WHO, in collaboration with partners from the animal health sector, will continue monitoring their evolution and assess the associated risk. Animal influenza viruses continue to challenge human public health; surveillance of swine influenza viruses is as equally important as avian influenza viruses. Effective surveillance of these viruses significantly improves pandemic preparedness.

### Overall Risk Management Recommendations:

- **WHO does not advise special traveler screening at points of entry or restrictions with regards to the current situation of influenza viruses at the human-animal interface.** For recommendations on safe trade in animals from countries affected by these influenza viruses, refer to OIE guidance.
- **WHO advises that travelers to countries with known outbreaks of animal influenza should avoid farms, contact with animals in live animal markets, entering areas where animals may be slaughtered, or contact with any surfaces that appear to be contaminated with animal excreta. Travelers should also wash their hands often with soap and water.** Travelers should follow good food safety and good food hygiene practices.
- **Due to the constantly evolving nature of influenza viruses, WHO continues to stress the importance of global surveillance to detect virologic, epidemiologic and clinical changes associated with circulating influenza viruses that may affect human (or animal) health. Continued vigilance is needed within affected and neighbouring areas to detect infections in animals and humans. Collaboration between the animal and human health sectors is essential. As the extent of virus circulation in animals is not clear, epidemiological and virological surveillance and the follow-up of suspected human cases should remain high.** Guidance on investigation of non-seasonal influenza and other emerging acute respiratory diseases has been published on the WHO website here [www.who.int/influenza/resources/publications/outbreak_investigation_protocol/en/](https://www.who.int/influenza/resources/publications/outbreak_investigation_protocol/en/).
- **In the current COVID-19 pandemic, vigilance for the emergence of novel influenza viruses of pandemic potential should be maintained.** WHO is developing practical guidance to prepare for

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6 [https://www.who.int/influenza/vaccines/virus/candidates_reagents/summary_a_h1v_cvv_nh2020_21_20200228.pdf?ua=1](https://www.who.int/influenza/vaccines/virus/candidates_reagents/summary_a_h1v_cvv_nh2020_21_20200228.pdf?ua=1)
the upcoming influenza season and influenza emergencies in the context of the cocirculation of SARS-CoV-2 and influenza viruses.

- All human infections caused by a new subtype of influenza virus are notifiable under the International Health Regulations (IHR, 2005).\(^7\) State Parties to the IHR (2005) are required to immediately notify WHO of any laboratory-confirmed\(^8\) case of a recent human infection caused by an influenza A virus with the potential to cause a pandemic\(^9\). Evidence of illness is not required for this report.

- It is critical that influenza viruses from animals and people are fully characterized in appropriate animal or human health influenza reference laboratories. Under WHO’s Pandemic Influenza Preparedness (PIP) Framework, Member States are expected to share their influenza viruses with pandemic potential on a regular and timely basis\(^10\) with the Global Influenza Surveillance and Response System (GISRS), a WHO-coordinated network of public health laboratories. The viruses are used by the public health laboratories to assess the risk of pandemic influenza and to develop candidate vaccine viruses.

Links:
WHO Human-Animal Interface web page
WHO Protocol to investigate non-seasonal influenza and other emerging acute respiratory diseases
Cumulative Number of Confirmed Human Cases of Avian Influenza A(H5N1) Reported to WHO
Avian Influenza A(H7N9) Information
WHO Avian Influenza Food Safety Issues
http://www.who.int/foodsafety/areas_work/zoonose/avian/en/
World Organisation of Animal Health (OIE) web page: Web portal on Avian Influenza
Food and Agriculture Organization of the UN (FAO) webpage: Avian Influenza
OFFLU
http://www.offlu.net/index.html

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\(^7\) World Health Organization. Case definitions for the four diseases requiring notification in all circumstances under the International Health Regulations (2005). Available at: www.who.int/ihr/Case_Definitions.pdf
\(^9\) https://www.who.int/influenza/resources/pip_framework/en/