OVERSEAS EMERGING RESPIRATORY VIRUS INTELLIGENCE

Major content updates from the previous report are highlighted in green.

Highly Pathogenic Avian Influenza A(H5NX)

The joint FAO/WHO/WOAH assessment on the recent influenza A(H5N1) virus situation in animals and people was updated on 17 April 2025.[1] The assessment concludes that the global public health risk of influenza A(H5N1) remains low, and the risk for occupationally exposed persons remains low to moderate, depending on risk mitigation measures in place and the local avian influenza epidemiological situation. Additional human infections in those exposed to infected animals or contaminated environments are likely to occur, however the public health impact of these infections remains minor at the global level.

Clade 2.3.4.4b

Avian influenza A(H5N1) clade 2.3.4.4b has spread throughout poultry and wild birds across Africa, Asia, Europe and the Americas, and was detected on Antarctica's mainland in February 2024.[1, 2] It has never been detected in New Zealand, Australia or Pacific Island Countries or Territories.

Since January 2022, 85 human cases of avian influenza H5N1 clade 2.3.4.4b have been reported in Europe (8 cases), Asia (2 cases) and the Americas (75 cases[1]). Eighty-two cases had direct or indirect exposure to sick poultry/birds (41 cases) or dairy cattle (41 cases) before illness onset, while three cases have no immediately known animal exposure. There is no evidence of sustained human-to-human transmission.[1, 3]

United States

There have been three known spillover events of A(H5N1) clade 2.3.4.4b from birds into dairy cattle in the US. Genotype B3.13 was first detected in cattle on 25 March 2024, and two spillovers of genotype D1.1, the predominant strain circulating in migratory wild birds in the US, were detected in February 2025.[4, 5] Influenza A(H5N1) has been detected in 1,047 dairy herds in 17 states. In the past 30 days (to 29 April 2025), there have been detections in 48 herds in 3 states, with the majority in Idaho (40/48).[6]

As of 30 April 2025, the US Centers for Disease Control and Prevention (CDC) has reported 41 human cases of infection with influenza A(H5) among dairy farms workers, mostly in California.[3] The majority of cases have been due to genotype B3.13, have had mild illnesses and recovered. There is no evidence of human-to-human transmission. Studies have demonstrated that seroprevalence to HPAI A(H5N1), even among workers with known exposures, is low reflecting the generally poor ability of this virus to transmit to humans.[7]

Between 2024 and 30 April 2025, the CDC has reported 24 confirmed cases of A(H5) in poultry farm workers .[3] Genotypes B3.13, D1.1 and D1.3 have been detected among these cases [8] Two cases have also been detected in owners of infected backyard poultry flocks [9]. Nine states have reported outbreaks in commercial or backyard poultry flocks in the past 30 days (as of 30 April).[10]

There have been three severe cases of A(H5N1) infection in the US (one death, two hospitalisations), all associated with poultry and all due to genotype D1.1.[11, 12]

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[1] This includes H5 cases linked to outbreaks of A(H5N1) clade 2.3.4.4b but not further typed.

The US have confirmed three human cases of infection with influenza A(H5N1) where the source of infection is unknown; one in Missouri and two in California.[13-16] There is no evidence of human-to-human transmission in any of these cases.

Influenza A(H5N1) was confirmed in two pigs on a non-commercial farm with infected poultry in late 2024.[17] The genotype was D1.2 and similar to virus isolated from migratory birds in the area. No detections in pigs have been reported since.

On 15 November 2024, the State of Hawaii Department of Health confirmed the first detection of influenza A(H5N1) in Hawaii in a backyard flock of various birds.[18] It is likely that the virus (genotype A3) arrived via wild birds on the Pacific flyway. It has been detected in wastewater on two other islands since.[19, 20] No human cases have been detected in Hawaii.

Canada

On 13 November 2024, the Public Health Agency of Canada confirmed their first domestically acquired human case of infection with A(H5N1) in British Columbia.[21] The case, a teenager, had no underlying conditions, was hospitalised in critical condition but has since recovered. The virus was clade 2.3.4.4b genotype D1.1, the same strain currently circulating in wild birds and poultry in British Columbia.[22] The source of infection was never identified.

United Kingdom

On 27 January 2025, the United Kingdom Health Security Agency (UKHSA) reported a human case of infection with influenza A(H5N1).[23] The case was a poultry farm worker exposed to birds infected with genotype D1.2. Prior to this, the UK has detected two cases in poultry workers involved in depopulation activities.

On 24 March 2025, the United Kingdom Department for Environment, Food & Rural Affairs reported the world’s first detection of influenza A(H5N1) in sheep.[24] A single positive sheep was identified via routine surveillance on a farm with A(H5N1)-infected captive birds. The only clinical sign was mastitis. Influenza A(H5N1) was detected in a milk sample and a blood sample was positive for A(H5) antibodies.[25] There have been no additional detections among sheep or other mammals on the premises.

Mexico

On 2 April 2025, Mexico notified the WHO of a human case of infection with influenza A(H5N1), the first confirmed case reported in the country.[26] The case, a child, had no underlying conditions and died in hospital. The virus was confirmed as clade 2.3.4.4b genotype D1.1. The source of infection remains under investigation. Influenza A(H5N1) has been detected in wild and captive birds in same state where the case resided in 2025. All contacts tested were negative for influenza A(H5N1).

Clade 2.3.2.1.e (previously classified as clade 2.3.2.1c)

A reassortment of A(H5N1), with surface genes from clade 2.3.2.1.c and internal genes from clade 2.3.4.4b has been circulating in the Greater Mekong subregion, including Cambodia and Vietnam, since 2023 and has caused human infections. [27]

In 2025, Cambodia has reported three fatal cases of influenza A(H5N1).[28] All three cases were exposed to sick poultry prior to illness onset. The clade has been confirmed as 2.3.2.1e in two cases. Since February

2023, 19 cases of A(H5N1) have been reported in Cambodia, of which all cases with known clade were clade 2.3.2.1e [29]

Clade 2.3.2.1a

On 22 May 2024, the Victorian Department of Health in Australia reported the retrospective identification of a human case of infection with influenza A(H5N1) clade 2.3.2.1a. The case was a child who acquired infection in India in March before returning to Australia and recovered following severe infection. There was no evidence of onwards human transmission. This clade has previously been detected among birds in India.[30]

Clade unknown

On 14 November 2024, a human case of infection with A(H5) was reported in Vietnam.[31] The N gene has not been reported for this case, although A(H5N1) detections in wild birds from the area were clade 2.3.2.1c. This case was exposed to sick poultry prior to illness onset and died from their infection.

On 18 April 2025, Vietnam reported a human case of infection with A(H5N1).[32] The child had an underlying health condition and developed encephalitis. They had contact with sick birds two weeks before illness onset.

ESR public health risk assessment for H5N1 in New Zealand

Given the current absence of infected animals in New Zealand, potentially high impact of the disease, very low likelihood of sustained human-to human transmission and very low likelihood of importation of a human case of influenza A(H5N1), the overall public health risk of avian influenza A(H5N1) to Aotearoa New Zealand is low. However, due to the pandemic potential of avian influenza viruses should there be a change in viral transmissibility, national preparedness activities led by the Ministry for Primary Industries, Health New Zealand and the Public Health Agency are ongoing.

Other human cases of avian and swine influenza

From 21 January to 24 March 2025, there were four human cases of infection with influenza A(H9N2), one human infection with influenza A(H1N1) variant virus, and one human infection with influenza A(H1N2) variant virus.[33]

All four cases of A(H9N2) were reported in three provinces of China and had no epidemiological links. One case had underlying conditions and was hospitalised while the other cases had mild illness. All cases had contact with poultry prior to illness onset.

The A(H1N1)v infection was reported in a child in China who had exposure to backyard swine prior to illness onset, although the swine tested negative for A(H1N1) viruses. Close contacts tested negative and were asymptomatic.

The influenza A(H1N2)v infection was reported in an adult in Iowa, US. The case was hospitalised and recovered. Investigations did not identify any direct or indirect exposure to swine. The clade (1B.2.1) circulates among swine in the US.

Australia is responding to outbreaks of HPAI H7N8 in four commercial poultry flocks in Victoria.[34] In 2024, Australia responded to outbreaks of HPAI H7 viruses in 16 commercial and domestic poultry flocks; eight in Victoria, six in New South Wales and two in the ACT. There has been no associated human illness.

WHO risk assessment for influenza at the human-animal interface

As at 19 March 2025, the WHO advises that the overall public health risk from currently known influenza viruses at the human-animal interface remains low. Sustained human-to-human transmission of these viruses is currently considered unlikely, however, infections with viruses of animal origin are not unexpected at the human-animal interface wherever these viruses circulate in animals.[33]

Middle East respiratory syndrome coronavirus (MERS-CoV)

In 2025, one MERS-CoV case has been reported in Saudi Arabia.[35] Eight cases were reported in Saudi Arabia in 2024. As of 13 March 2025, the WHO's risk assessment remains moderate at the global and regional levels. The WHO expects additional cases of MERS-CoV to be reported from the Middle East and/or other countries where MERS-CoV is circulating in dromedaries.

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