

OVERSEAS EMERGING RESPIRATORY VIRUS INTELLIGENCE

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

Highly Pathogenic Avian Influenza A(H5NX)

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, 74 human cases of avian influenza H5N1 clade 2.3.4.4b have been reported in Europe (7 cases), Asia (2 cases) and the Americas (65 cases¹). All but three cases had direct or indirect exposure to sick poultry/birds (34 cases) or dairy cattle (37 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]

On 18 December 2024, the US Centers for Disease Control and Prevention reported the first severe human case of infection with A(H5N1) in the United States (US), in Louisiana.[4] The case had exposure to sick and dead birds in a backyard flock. The genotype was identified as D1.1 and is related to virus recently detected in poultry and wild birds in the US, and the recent severe human case in Canada. The CDC continues to assess the immediate risk to the public from A(H5N1) as low.

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.[5] The virus is clade 2.3.4.4b, genotype A3.[6] This genotype was first identified in Alaska in 2022 which supports the theory that it was introduced to Hawaii from the mainland United States via wild birds migrating along the Pacific flyway. On 25 November, the State of Hawaii Department of Agriculture confirmed the detection of A(H5) in a wild duck on the same island as the infected backyard flock.[7] No human cases of A(H5N1) have been detected in Hawaii. Contact tracing was undertaken following potential public exposures to birds at a Pet Fair but no human cases arose.[6]. On 10 December 2024, the State of Hawaii Department of Health announced the first wastewater detection of A(H5) on Hawaii Island, in a sample collected on 2 December.[8]

On 13 November 2024, the Public Health Agency of Canada confirmed a human case of infection with influenza A(H5N1) in British Columbia.[9] This is the first domestically acquired case in Canada. The teenager had no underlying conditions and was hospitalised with severe illness.[10] Public health investigations did not identify a source of infection.[11] The virus is clade 2.3.4.4b genotype D1.1, the same strain currently circulating in wild birds and poultry in British Columbia, and distinct from the genotype associated with the dairy cattle outbreak in the United States (B3.13). The virus is most closely associated with wild birds in the area where the case resides and is not directly related to the poultry outbreaks. Genomic sequencing has identified three mutations associated with enhanced cell-receptor binding and ability to bind to human lung receptors.[12] These mutations may have evolved during the patient's infection. The Public Health Agency of Canada continues to assess the risk to the general public in Canada as low.[9]

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

On 22 November 2024, the US Centers for Disease Control and Prevention (CDC) confirmed a human infection with influenza A(H5N1) in a child in California.[13] The child was identified through routine influenza surveillance. They had mild symptoms and low-level virus detection in the initial sample, with negative samples several days later. They were positive for other common respiratory viruses which may explain their symptoms. All household members were symptomatic but were negative for influenza H5. There is no evidence of human-to-human transmission.[13] Genomic analysis showed the virus is similar to virus detected in dairy cattle, poultry and some dairy workers in California. Epidemiologic and environmental investigations did not identify a source of infection.[14]

In November, the California Department of Health investigated a suspect case of A(H5) in a second child in a nearby county. The child consumed contaminated raw milk prior to illness onset. Due to low levels of virus, confirmatory testing was unable to determine whether the case was infected with seasonal influenza A or A(H5), therefore they remain a suspect case.[15]

In September 2024, the CDC investigated a confirmed case of influenza A(H5N1) in Missouri identified through seasonal influenza surveillance. They subsequently identified a household member who was symptomatic at the same time and had serology results indicating previous infection, suggesting a common source exposure.[16] The source of these cases remains unknown. The virus from the confirmed case was genomically related to the ongoing US cattle outbreak, [17] There were no mutations associated with enhanced infectivity or capacity for human-to-human transmission. H5 avian influenza outbreaks have been detected in poultry in Missouri in 2024 and in wild birds there in the past. No A(H5N1) dairy cattle outbreaks have been reported in the state to date.

As of 17 December 2024, the CDC has reported 37 human cases of infection with influenza A(H5) among dairy farms workers in California (33 cases), Michigan (2 cases), Colorado (1 case) and Texas (1 case).[3] All cases had occupational exposure to infected cattle and experienced mild symptoms, with many reporting only eye redness or conjunctivitis. 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 generally poor ability of this virus to transmit to humans.[18] A recent study among dairy farm workers in Michigan and Colorado found that 7% of participants had evidence of recent infection with influenza A(H5).[19]

Influenza A(H5N1) has been detected in 865 dairy herds in 16 states. In the past 30 days, there have been detections in 315 herds in 2 states, with the majority in California (313 herds)[20] Detections in other farm animals, including mice, domestic cats, and alpacas have also been reported in multiple states.[21] There has also been evidence of transmission of A(H5N1) from dairy to poultry farms. Epidemiological findings from Michigan suggest that the majority of transmission between farms is through shared movement of people, vehicles and equipment between premises.[22]

As of 17 December 2024, the CDC has also reported 21 confirmed cases of A(H5) in poultry farm workers in 2024, in Washington (11 cases), Colorado (9 cases) and Oregon (1 case).[3] Genomic analysis of virus isolated from three of the Colorado workers showed they are closely related to the dairy cattle clade 2.3.4.4b, genotype B3.13 outbreak, while virus from the Washington cases is genotype D1.1.[23] Genomic sequencing of virus isolated from Washington cases shows a mutation that may be associated with reduced susceptibility

to the neuraminidase inhibitor oseltamivir (Tamiflu).[24] Twenty-two states have reported outbreaks in commercial or backyard poultry flocks in the past 30 days (as of 18 December).[25]

The US Department of Agriculture has confirmed the first detections of A(H5N1) in swine in the US, in a non-commercial farm which included other livestock and A(H5N1)-infected poultry.[26] Two pigs were positive for A(H5N1), with the sharing of water sources, housing and equipment between livestock and infected poultry likely facilitating transmission from poultry. Low levels of virus were isolated from the pigs, and partial genomic sequences indicates the virus was genotype D1.2, and genomically similar to samples from migratory birds in the area. Genomic sequencing of virus isolated from the poultry does not show any changes to suggest increased transmissibility between humans.

On 9 August 2024, the CDC published their assessment of potential pandemic risk posed by currently circulating influenza A(H5N1) viruses, based on virus isolated from the first human case of infection following exposure to infected dairy herds. The current overall individual and population health risk to the general public from this virus remains low, and the future pandemic risk is assessed as moderate, which is similar to previous assessments of earlier influenza A(H5N1) viruses.[27]

On 14 August 2024, the joint FAO/WHO/WOAH assessment on the recent influenza A(H5N1) virus situation in animals and people was updated.[1] The global public health risk of influenza A(H5N1) is assessed as low, and the risk for occupationally exposed persons as low to moderate, depending on risk mitigation measures in place. Additional human infections in those exposed to infected animals or contaminated environments are likely to occur, however the public health impact of these infections is minor at the global level.

Clade 2.3.2.1.c

On 2 September 2024, the WHO published a risk assessment for avian influenza A(H5N1) in Cambodia following the notification of a confirmed case due to clade 2.3.2.1c in a 15 year old child.[28] Cambodia has reported 10 human cases of infection due to influenza A(H5N1) in 2024, most of whom had known exposure to dead or sick poultry prior to illness onset. Available evidence suggests that the virus has not acquired the capacity for sustained human-to-human transmission. Further cases are expected as the virus continues to circulate among poultry in Cambodia. The overall public health risk posed by this virus was assessed as low.

Clade 2.3.2.1a

On 22 May 2024, the Victorian Department of Health (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.[29]

Clade unknown

On November 14 2024, Vietnamese health authorities were notified of a human case of infection with influenza A(H5). Characterisation of the N gene is pending. The case had exposure to dead poultry at their home prior to illness onset and was hospitalised. The last human case of A(H5N1) in Vietnam was reported in March 2024. A reassortment of H5N1 in south-east Asia, 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 Vietnam, since 2023 and has previously caused human infections. [30]

ESR public health risk assessment

Given the 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

In November 2024, there was one human case of infection with influenza (H9N2) in a child in China. There is no further information available at this time.[31]

From 28 September to 1 November 2024, there was one human case of infection with influenza A(H9N2) in China. The child had mild illness and has recovered. Environmental samples taken from the live poultry market the case visited prior to illness onset were positive for influenza A(H9) viruses.[32]

In 2024, Australia has 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.[33] No new outbreaks have been reported since late July. There has been no associated human illness.

WHO risk assessment for influenza at the human-animal interface

As at 1 November, the WHO advises that the overall public health risk from currently known influenza viruses at the human-animal interface has not changed, and that sustained human-to-human transmission of these viruses is currently considered unlikely. Human infections with viruses of animal origin are not unexpected at the human-animal interface wherever these viruses circulate in animals.[32]

Middle East respiratory syndrome coronavirus (MERS-CoV)

On 5 September 2024, the WHO was notified of a human case of MERS-CoV in Saudi Arabia.[34] The case had underlying conditions, did not have a history of contact with camels and was not a healthcare worker. Prior to this case, four MERS-CoV cases, all fatal, had been reported in 2024.[35] All cases were from Saudi Arabia, with the most recent reported in April . The WHO's risk assessment remains moderate at the global and regional levels.[34] 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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