

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 20 December 2024.[1] 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, 84 human cases of avian influenza H5N1 clade 2.3.4.4b have been reported in Europe (8 cases), Asia (2 cases) and the Americas (74 cases¹). Eighty one cases had direct or indirect exposure to sick poultry/birds (40 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]

On 5 February 2025, the US Department of Agriculture (USDA) announced the detection of the second known spillover event from birds into dairy cattle.[4] Genotype D1.1 was detected in milk samples from Nevada dairy farms in early January. Prior to this, all detections in dairy cattle were genotype B3.13. **Genetic analysis suggests this spillover may have occurred in early December.**[5] Genotype D1.1 is the predominant strain circulating in migratory wild birds on all four North American flyways. On 13 February, the USDA confirmed the second spillover of genotype D.1.1, into dairy cattle in Arizona.[6] Genetic analysis identified this second spillover event, which may indicate an increased risk of A(H5N1) genotype D1.1 introduction from wild birds into dairy farms. Genotype D1.1 previously caused the fatal case in Louisiana who was infected by backyard poultry and the severe case in Canada with unknown source, as well as mild infections in several poultry farm workers in Washington. On 10 February, Nevada reported a human case due to genotype D1.1 in a dairy worker.[7] They reported mild illness (conjunctivitis) and recovered. **Virus isolated from this patient had a mutation in the PB2 protein which is associated with more efficient replication in mammalian cells and was previously detected in the human case in Chile in 2023.**[8] There were no mutations associated with reduced effectiveness of antivirals or existing candidate vaccine viruses.

On 27 January 2025, the United Kingdom Health Security Agency (UKHSA) reported a human case of infection with influenza A(H5N1).[9] The case was a poultry farm worker exposed to birds infected with genotype D1.2, which is distinct from the genotypes causing human cases in the US. The UKHSA has assessed the risk to the public as very low.

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

On 6 January 2025, the first fatal human case of infection with A(H5N1) in the United States (US) was reported, in a Louisiana case infected with genotype D1.1 following exposure to sick and dead birds in a backyard flock.[10] The virus was 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. Genetic analysis of virus isolated from this case showed some mutations in the HA segment, which are rare in human cases but have been detected in some severe cases in other countries.[11] One mutation was also detected in the recent severe case in Canada, suggesting the changes occurred over the course of the patient's infection. There was no evidence of reduced susceptibility to antiviral drugs, and the virus remains closely related to existing A(H5N1) candidate vaccine viruses (CVVs).

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.[12] The virus is clade 2.3.4.4b, genotype A3.[13] 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.[14] A positive wastewater detection from a second island, Hawaii island has been confirmed, while low level detections have been reported on a third island, Kaua'i.[15] [16] No human cases of A(H5N1) have been detected in Hawaii.

On 13 November 2024, the Public Health Agency of Canada confirmed a human case of infection with influenza A(H5N1) in British Columbia.[17] This is the first domestically acquired case in Canada. The teenager had no underlying conditions and was hospitalised with severe illness.[18] Public health investigations did not identify a source of infection.[19] 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.[20] These mutations may have evolved during the patient's infection.[21] The Public Health Agency of Canada continues to assess the risk to the general public in Canada as low.[17]

The US have confirmed three human cases of infection with influenza A(H5N1) where the source of infection is unknown. There is no evidence of human-to-human transmission in any of these cases. The first case was identified through seasonal influenza surveillance in Missouri in September 2024.[22] Investigations identified a household member who was symptomatic at the same time and had serology results indicating possible previous infection, suggesting a common source exposure.[23]. The virus from the confirmed case was genomically related to the ongoing US cattle outbreak, despite no outbreaks in dairy cattle being reported in the state to date, [24]. Two cases of unknown source have also been reported in different counties in San Francisco; one in November 2024 and one in January 2025. Both children experienced mild symptoms and recovered. Genomic analysis of virus isolated from the November case showed the virus is similar to those isolated from dairy cattle, poultry and some dairy workers in California. In November 2024, the California Department of Health investigated a third suspect case of A(H5) in a child in San Francisco who had consumed contaminated raw milk prior to illness onset. The CDC was unable to confirm the case, therefore it remains a suspect case.[25]

As of 18 January 2024, the CDC has reported 41 human cases of infection with influenza A(H5) among dairy farms workers in California (36 cases), Michigan (2 cases), Colorado (1 case), Nevada (1 case), and Texas (1 case).[3]. 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.[26] A study among dairy farm workers in Michigan and Colorado found that 7% of participants had evidence of recent infection with influenza A(H5).[27] A serosurvey of 150 bovine veterinary practitioners identified three people who had evidence of recent A(H5N1) infection with no known exposure, one of whom worked in a state with no known infected cattle, and two who were not exposed to cattle known to be infected.[28]

Influenza A(H5N1) has been detected in 973 dairy herds in 17 states. In the past 30 days (to 25 February 2025), there have been detections in 23 herds in 3 states, with the majority in California (15 herds).[29] Detections in other farm animals, including mice, domestic cats, and alpacas have also been reported in multiple states.[30] 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.[31]

As of 24 February 2025, the CDC has reported 24 confirmed cases of A(H5) in poultry farm workers since 2024, in Washington (11 cases), Colorado (9 cases), Ohio (1 case), Oregon (1 case), Iowa (1 case) and Wisconsin (1 case).[3] Both genotype B3.13 and D1.1 have been detected among these cases.[32] Two cases have also been detected in owners of infected backyard poultry flocks, in Louisiana and Wyoming [8]. Genomic sequencing of virus isolated from Washington cases shows a mutation that may be associated with reduced susceptibility to the neuraminidase inhibitor oseltamivir (Tamiflu).[33] Twenty-eight states have reported outbreaks in commercial or backyard poultry flocks in the past 30 days (as of 26 February).[34]

The US are continuing to report detections of A(H5N1) in outdoor and indoor domestic cats. Infections have been associated with consumption of raw pet food containing contaminated poultry products, contaminated raw milk sold for human consumption, and possible fomite transmission from their owners who worked at dairy farms not known to be infected with A(H5N1).[35, 36]

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.[37] 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.[38]

Clade 2.3.2.1.c

On 10 January 2025, Cambodia reported a fatal human case of infection with influenza A(H5N1). The case was exposed to sick poultry prior to illness onset.[39] The virus was confirmed as clade 2.3.2.1c and is closely related to virus circulating among birds in Cambodia.

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.[40] 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.[41]

Clade unknown

On 14 November 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. [42]

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

On 18 February 2025, Hong Kong's Centre for Health Protection reported two human cases of infection with avian influenza A(H9N2) in China. Both cases were adults from the same province,[43] No further information is available at this time. Since 2015, 114 human cases of A(H9N2) infection have been reported from China to WHO.

On 11 February 2025, Hong Kong's Centre for Health Protection reported two human cases of infection with avian influenza A(H9N2) in China.[44] Both cases were children from the same province. No further information is available at this time

On 7 February 2025, the US CDC reported a human case of infection with influenza A(H1N2) variant virus in Iowa. The case was hospitalised and has since recovered.[45] Investigations did not identify any direct or indirect exposures to swine prior to illness onset. No additional cases have been identified. Since 2011, the US have reported 42 human cases of A(H1N2)v infection.[46]

From 2 November to 20 January 2025 there were 11 human cases of infection with influenza A(H9N2) and one human case of infection with influenza A(H10N3) in China.[39, 47] All A(H9N2) cases were likely exposed to poultry prior to illness onset, and influenza A(H9) was detected in the poultry-related environments in 10 cases. Three of the 11 cases were hospitalised with severe infection, and all cases recovered. None of the cases were epidemiologically linked, and there were no additional cases identified among their close contacts. The case of A(H10N3) was exposed to poultry prior to illness onset. They hospitalised with severe illness but since recovered, All close contacts and environmental samples tested negative.

Australia is responding to outbreaks of HPAI H7N8 in four commercial poultry flocks in Victoria.[48] 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 20 January 2025, 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.[39]

Middle East respiratory syndrome coronavirus (MERS-CoV)

In 2024, five MERS-CoV cases were reported in Saudi Arabia, with the most recent case reported in September. All five cases were fatal. The WHO's risk assessment remains moderate at the global and regional levels.[49] 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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