SURVEILLANCE & MONITORING

Zoonotic influenza

Annual Epidemiological Report for 2024

Key facts

- Nine countries reported sporadic human infections with avian influenza virus subtypes A(H5N1), A(H5N2), A(H5N6), A(H5Nx), A(H9N2), A(H10N3) for 2024.
- Four countries reported human infections with influenza A(H1N1) variant (v), A(H1N2)v and A(H3N2)v viruses of swine origin for 2024.
- No human cases of infection with avian influenza viruses or influenza variant virus of swine origin were reported in the EU/EEA in 2024.
- Considering the widespread transmission of zoonotic influenza viruses in animal populations, reported transmission to humans with zoonotic influenza viruses remains infrequent.

Introduction

Animal influenza viruses that usually circulate in animal species can, in rare instances, transmit to humans and cause zoonotic influenza virus infections. In Europe, there has been widespread transmission of highly pathogenic avian influenza (HPAI) A(H5N1) in wild birds since 2020, causing outbreaks in poultry establishments. Since late 2022, HPAI A(H5N1) has also been detected more frequently in mammals such as wild carnivores, marine mammals, fur farm animals, and pets both in Europe and globally [1,2]. In March 2024, HPAI A(H5N1) was detected for the first time in dairy cattle in Texas, United States [3], and was subsequently confirmed in other states in the country [4,5].

Most human infections with zoonotic influenza viruses are caused by avian influenza viruses that circulate in wild birds and spill over to farmed poultry or swine influenza viruses that are present in pig populations. Since 2024, human infections have also resulted from exposure to infected dairy cattle [6-8]. Infections are typically related to direct contact with infected animals or contaminated environments. Infections can result in asymptomatic, mild or severe disease, causing symptoms which range from fever, conjunctivitis and cough to severe pneumonia, but can also cause less frequently reported symptoms such as gastroenteritis or neurological symptoms. The mortality among reported cases of zoonotic influenza in human varies depending on the subtype, ranging from 1% for subtype A(H9N2), to 39% for A(H5N6) and 50% for A(H5N1). Nevertheless, less severe cases may not be detected and reported in the absence of targeted surveillance of individuals exposed to infected animals, affecting the estimated mortality for the different subtypes [9].

This annual epidemiological report provides a description and summary of human infections with zoonotic influenza virus reported globally for 2024.

Suggested citation: European Centre for Disease Prevention and Control. Zoonotic influenza. In: ECDC. Annual epidemiological report for 2024. Stockholm: ECDC; 2026.

Stockholm, January 2026

Methods

Data on human infections with zoonotic influenza virus reported globally were systematically collected from official, public sources identified through ECDC's epidemic intelligence activities and compiled in a line list, as described in [9]. This report includes events and data from 2024, retrieved from the ECDC line list in August 2025. The date of identification or onset of symptoms was used, and if not available, the date of sampling or reporting.

Since September 2017, ECDC, together with the European Food Safety Authority (EFSA) and the European Union Reference Laboratory for Avian Influenza (EURL), have been publishing quarterly updates on the avian influenza situation in the EU/EEA and globally (see link). The avian influenza detections in humans for 2024 listed in the subsequent sections have been described in the avian influenza situation reports [10-14].

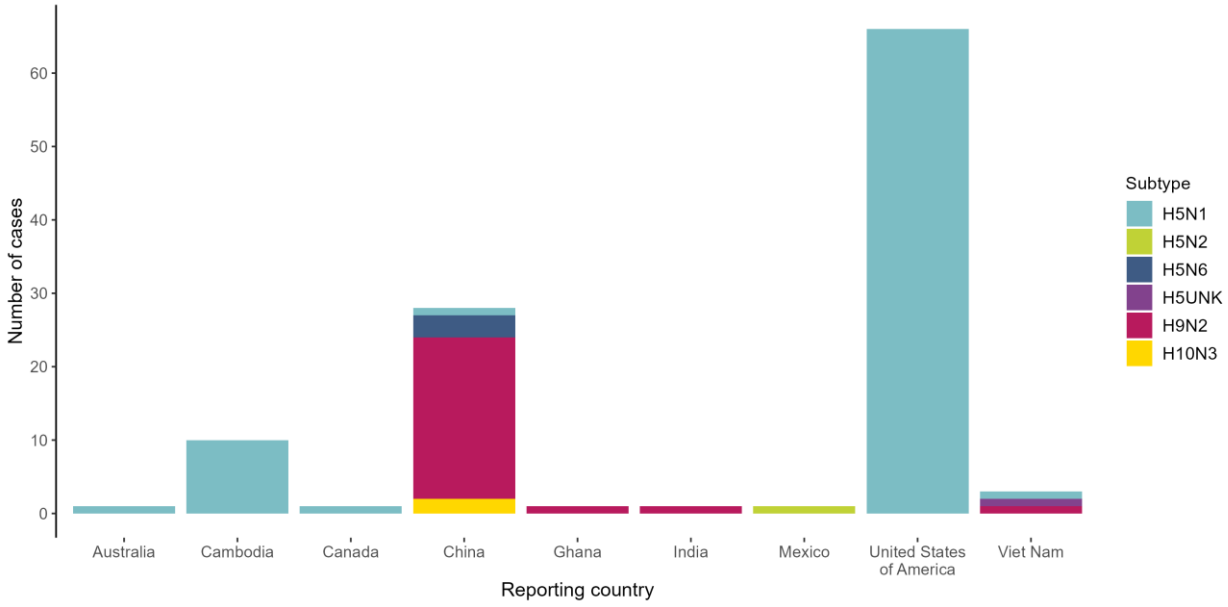
Epidemiology

Avian influenza in humans

Nine countries reported a total of 112 human cases or detections of avian influenza virus with onset of symptoms or identification in 2024, including subtypes A(H5N1), A(H5N2), A(H5N6), A(H5Nx), A(H9N2), and A(H10N3). The majority of cases were reported by the United States (66 cases), followed by China (28 cases) Cambodia (10 cases), and Viet Nam (three cases). Australia, Canada, Ghana, India, and Mexico all reported one case each for 2024.

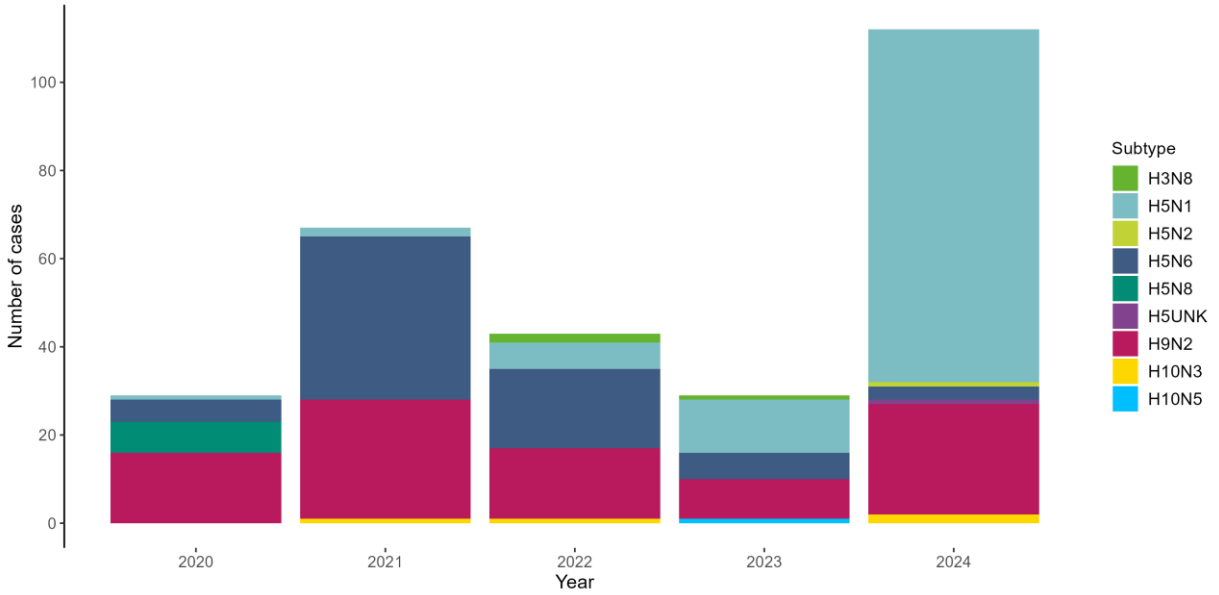
Out of those cases for which information on hospitalisation (n=103) was provided, 30 (29%) were hospitalised, and eight (7%) out of the total 112 cases died. The majority of reported human cases (94%, n=101/108) had a history of known exposure to animals or a contaminated environment, specifically poultry (54%, n=60), cattle (36%, n=40), and two (2%) had reported exposure to wild birds. It is possible to report exposure to more than one animal species. For seven of the cases (6%), no epidemiological exposure was identified following investigation, and four of the cases (4%) had no reported or publicly available information on animal exposure. Reported human cases and detections of avian influenza virus in 2024 are illustrated in Figure 1 by subtype. An increase in reported cases of avian influenza in humans was observed in 2024 compared to recent years (Figure 2) as a result of a rise in documented cases of subtype A(H5N1). In contrast, reported human cases of subtype A(H5N6) has been decreasing since 2021, with the lowest number of human cases of subtype A(H5N6) being reported in five years.

Figure 1. Reported cases of avian influenza virus in humans with onset or identification in 2024 by country and subtype



Human cases of A(H5) epidemiologically linked to A(H5N1) outbreaks in poultry and dairy cattle farms in the United States are included in the reported number of A(H5N1) cases.

Figure 2. Reported human cases and detections of avian influenza virus by subtype between 2020 and 2024



Avian influenza A(H5N1) virus

For 2024, 80 cases of avian influenza A(H5N1) virus in humans were reported globally. No human cases of influenza A(H5N1) were reported in Europe in 2024.

The first human infection with avian influenza A(H5N1) detected in Australia was reported in 2024, which was identified through enhanced surveillance for novel strains of influenza virus. The individual had a travel history to India, where exposure to infection likely occurred. The individual was a two-and-a-half-year-old child, who experienced initial symptoms while abroad, including fever, coughing, reduced appetite, vomiting, and irritability. The child was hospitalised upon return to Australia with severe symptoms and has since recovered. The child had no known exposure to live birds, animals or sick persons while in India. No additional cases were identified from contact tracing. The virus belonged to A(H5) clade 2.3.2.1a, which has been detected in poultry and human cases in South Asia [13,15,16].

In Asia, Cambodia reported 10 cases of avian influenza A(H5N1) virus infection in three children below five years of age, six children aged 5-17 years, and one adult above 65 years of age. Two out of 10 cases (20%) were fatal. For those where information was available (n=9), seven were hospitalised. Symptoms included fever, respiratory signs, weakness, and irritability or confusion. The two cases that did not require hospitalisation were identified through contact tracing, out of which one was asymptomatic [17] and the other had mild symptoms, including fever [18]. All cases, including the two identified through contact tracing, had exposure to domestic poultry in a backyard setting before onset of symptoms or detection of infection. Where virus sequences were available (n=5), phylogenetic analysis showed the strains belonged to a reassortant of A(H5) clade 2.3.2.1e (previously classified as 2.3.2.1c), which contains internal segments from clade 2.3.4.4b, and has dominated among sequenced viruses of A(H5N1) in Cambodia since late 2023 [10,12,19]

One human infection with influenza A(H5N1) was reported by China in a 33-year-old woman from Viet Nam. The case was detected through routine surveillance at the port of entry from Viet Nam to China. The individual had exposure to poultry before onset of symptoms of respiratory illness. No additional cases were detected among close contacts [20].

There was one fatal case of influenza A(H5N1) reported in Viet Nam in a 21-year old man, who developed a fever, respiratory and gastrointestinal symptoms, followed by severe pneumonia. The individual had exposure to wild birds during hunting a few weeks before onset of symptoms. No additional cases were identified among close contacts. The virus sequence belonged to clade 2.3.2.1e [13].

In the Americas, Canada reported one case of avian influenza A(H5N1) in a 13-year-old child with underlying conditions (asthma, elevated body-mass index). The case was identified through enhanced hospital surveillance for influenza. The individual presented with fever and conjunctivitis, and subsequently developed respiratory and gastrointestinal symptoms, and was hospitalised with critical illness (pneumonia, respiratory failure, acute kidney injury, haemodynamic instability, thrombocytopenia, leukopenia). Following treatment in intensive care unit, including extracorporeal membrane oxygenation, the patient improved clinically.

The source of infection was not identified. The sequenced virus belonged to A(H5) clade 2.3.4.4b, genotype D1.1, and was most closely related to viruses found in wild birds in the geographical area around the same time period. No additional human cases were identified from contact tracing [11,21,22].

The United States reported 66 cases of A(H5) in 2024, out of which the majority (61%, n=40/66) had occupational exposure to dairy cattle presumed or confirmed to be infected with avian influenza A(H5N1). The first human case of influenza A(H5N1) following exposure to dairy cattle was reported on 1 April 2024 in Texas, and appears to have been the first human infection with influenza A(H5N1) associated with exposure to infected mammals. Affected individuals were either above 18 years of age or the age was not reported. Symptoms experienced by cases with occupational exposure to A(H5N1) infected dairy cattle were mild and included conjunctivitis (100%, n=35/35), and occasionally mild respiratory illness, fever, headache, and muscle pain. None of the cases required hospitalisation. Where virus sequences were available, they belonged to A(H5N1) clade 2.3.4.4b, genotype B3.13, and were closely related to the virus detected in dairy cattle [6-8,11-13].

Out of the 66 cases of A(H5) in 2024 reported by the United States, 23 cases (35%) had occupational exposure to domestic poultry, mostly during depopulation of poultry at farms with HPAI A(H5N1) outbreaks. Where age was reported, affected individuals were above 18 years of age. Symptoms reported were mild and included conjunctivitis, fever, and respiratory illness. None of the cases required hospitalisation. Sequences that were available of A(H5N1) viruses from cases with occupational exposure to poultry were identified as clade 2.3.4.4b, where strains of cases in Colorado belonged to genotype B3.13, and were closely related to viruses belonging to genotype B3.13 found in dairy cattle in the country, while strains available from viruses of cases in Washington State were genotype D1.1 [7,8,11,12,23,24].

One case was reported in an individual over 65 years of age with underlying conditions. The patient was hospitalised in a critical condition with pneumonia and passed away. The case had exposure to backyard poultry and had observed deaths among domestic and wild birds on the property before onset of symptoms. Poultry on the property tested positive for avian influenza A(H5). The sequenced virus from the case belonged to A(H5) clade 2.3.4.4b, genotype D1.1 [14].

In addition, there were two human cases of avian influenza A(H5N1) reported in individuals with no known animal exposure identified. The first case, which was detected through routine surveillance for seasonal influenza, was in an adult hospitalised because of underlying medical conditions. The patient presented with chest pain, gastrointestinal signs, and weakness, but was not severely affected. The case subsequently recovered. Virus sequences were assigned to clade 2.3.4.4b and were closely related to viruses belonging to genotype B3.13 found in dairy cattle in the United States [7,12]. The second case, which was identified through routine surveillance for influenza, was in a child who experienced mild symptoms, including conjunctivitis and cough, and did not require hospitalisation. Close contacts tested negative for influenza A(H5N1). Analysis of the partial HA sequence suggested the virus belonged to clade 2.3.4.4b genotype B3.13 [8,11]

Avian influenza A(H5N2) virus

The first laboratory-confirmed human case of influenza A(H5N2) globally was reported in Mexico in a 59-year-old man with multiple comorbidities who developed respiratory symptoms. The patient was hospitalised but died from complications related to his underlying conditions. The individual had no known history of exposure to poultry or other animals and had been bed-ridden for three weeks before onset of symptoms. The virus had 99% similarity to low pathogenic avian influenza strains detected in birds in Mexico. No additional cases were identified from contact tracing [13].

Avian influenza A(H5N6) virus

China reported three human cases of avian influenza virus A(H5N6) with onset or detection in 2024 in adults aged between 41 and 70 years. All three individuals were hospitalised and had a fatal outcome. All had a known history of exposure to domestic poultry in a backyard or wet market setting (ECDC line list).

Avian influenza A(H5Nx) virus

One case of influenza A(H5Nx) was reported in Viet Nam in an 18-year-old man with an underlying medical condition who developed influenza-like symptoms. The patient was hospitalised with severe pneumonia following a worsening condition but has since recovered. The individual had exposure to sick and dead poultry at home. No additional cases were identified from contact tracing [11,22].

Avian influenza A(H9N2) virus

In 2024, there were 25 cases of avian influenza A(H9N2) virus in humans reported globally. In total, 22 human cases of avian influenza A(H9N2) were reported by China with onset or identification in 2024. The majority (86%, n=19/22) of the cases were in children, of which 13 were aged below five years, and six were aged 5-17 years. The remaining three cases were in adults. For those which information was available (n=15), 10 (67%) were hospitalised. Most of the cases (90%, n=18/20) had a history of exposure to poultry in a backyard (47%, n=9/19) or wet market (53%, n=10/19) setting. For two cases, no epidemiological exposure was identified following investigation. No information on animal exposure was reported or publicly available for the other two cases. (ECDC line list).

India reported the second case of influenza A(H9N2) in the country in a three-year-old child with recurrence of severe respiratory distress. A month earlier, the patient had tested positive for influenza B and adenovirus, and at the time of testing positive for influenza A(H9N2), was also positive for rhinovirus. The patient was hospitalised and subsequently recovered. The patient had exposure to poultry at home. No additional cases were identified from contact tracing [13].

The first case of influenza A(H9N2) in Viet Nam was reported in a 37-year-old man with underlying conditions, who experienced severe symptoms and was hospitalised, but recovered. Although no direct exposure to poultry was reported, the patient lived in front of a live poultry market [13].

Ghana also reported its first human case of influenza A(H9N2) in a child who developed influenza-like illness. The case had no known exposure to poultry before onset of symptoms. No additional cases were identified through contact tracing [12].

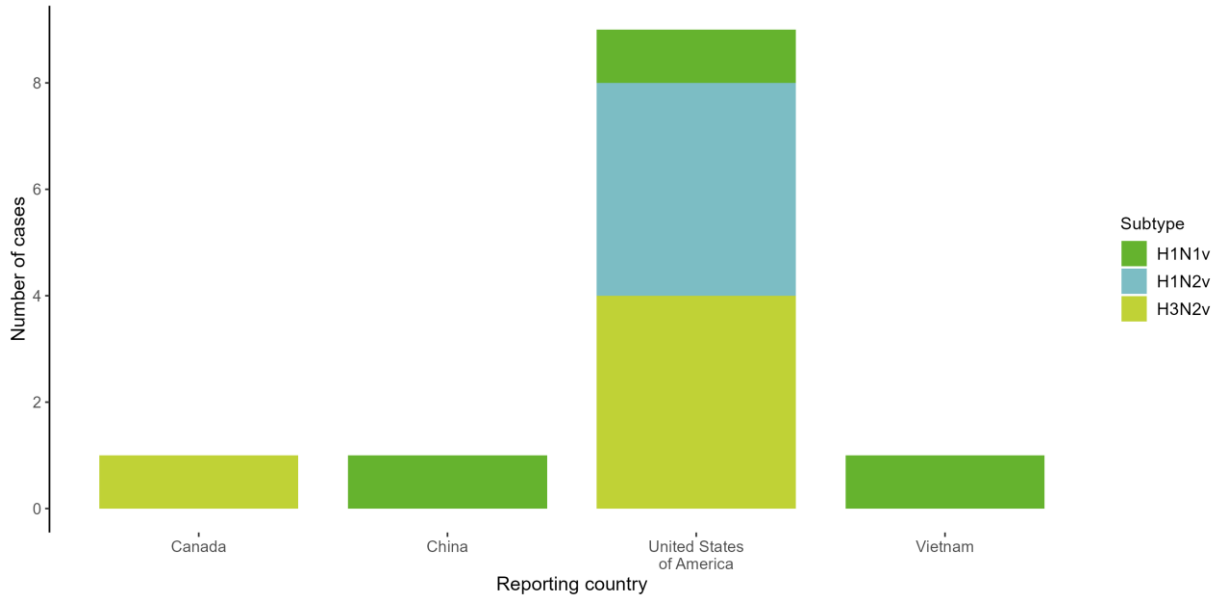
Avian influenza A(H10N3) virus

In 2024, two human cases of avian influenza A(H10N3) were reported in China in a 23-year-old woman with underlying conditions, and in a 51-year-old man. Both individuals were hospitalised with severe pneumonia but have since recovered. Both individuals had exposure to domestic poultry before onset of symptoms. No additional cases were identified form contact tracing [13,14]

Swine influenza in humans

Four countries reported a total of 12 human cases of influenza variant (v) viruses of swine origin with onset of symptoms or identification in 2024, including subtypes A(H1N1)v, A(H1N2)v and A(H3N2)v. The United States reported nine cases, while Canada, China, and Viet Nam all reported one case each (Figure 3).

Figure 3. Reported human cases of infection with influenza A variant viruses of swine origin with onset or detection in 2024 by country and subtype



Swine influenza A(H1N1)v virus

Three human cases of infection with swine influenza A(H1N1)v virus were reported globally with onset or detection in 2024. China reported one case in a child below five years of age who experienced mild respiratory illness. The child had exposure to pigs in a backyard setting. The United States reported a case in an adult with underlying conditions who developed mild symptoms. The individual was hospitalised for observation. The case had attended an agricultural fair before onset of symptoms. Both cases recovered. Viet Nam reported a fatal case of infection with influenza A(H1N1)v virus in a 70-year-old woman who had underlying conditions, for which no known source of exposure was identified [25,26].

Swine influenza A(H1N2)v virus

The United States reported four cases of human infection with swine influenza A(H1N2)v virus for 2024. One case was in a child below five years of age and the remaining three cases were in adults. Three of the individuals were hospitalised, one due to underlying medical conditions. All individuals recovered from the infection. All individuals also had known exposure to pigs: one in their home, two had attended an animal auction, and one in an occupational setting [25,27,28].

Swine influenza A(H3N2)v virus

In 2024, there were five reported cases of human infection with swine influenza A(H3N2)v virus by the United States (4 cases) and Canada (1 case). All cases were in children below 18 years of age. One of the individuals, who had an underlying condition, was hospitalised. All individuals recovered. Three of them had attended agricultural fairs where they had direct or indirect contact with pigs, one person had no reported direct contact with pigs but lived on a farm with pigs, while the likely source of infection was not identified for the remaining case [25].

Discussion

In 2024, sporadic cases of infection with avian influenza viruses were reported in humans globally, most of which had had a history of direct contact with infected poultry, cattle or exposure to a contaminated environment. However, no sustained human-to-human transmission has been observed. In the EU/EEA, despite many detections and outbreaks of highly pathogenic influenza A(H5N1) reported in wild and domestic birds in 2024 [2,10-14], there have been no confirmed infections with avian influenza A(H5N1) in humans.

Human infections with influenza viruses of swine origin were detected globally, with cases of A(H1N1)v, A(H2N3)v, and A(H3N2)v being reported sporadically outside of the EU/EEA. Several of the individuals reported to have experienced mild respiratory illness. However, infections can be severe and six people were hospitalised, including one person who died. The majority of the cases had known exposure to pigs or their environment.

Considering the extensive circulation of zoonotic influenza viruses in animal populations, with frequent human exposures in recent years, reported human infection with zoonotic influenza viruses remains infrequent. However, sporadic infections with zoonotic influenza viruses in humans are likely to continue occurring in areas where zoonotic influenza viruses are prevalent and individuals have unprotected exposure to infected animals or their environment. Influenza viruses in animals also continue to reassort and evolve genetically. This underlines the need to continuously monitor the current situation and identify changes that could contribute to adaptation to mammals, including humans.

Human infections with influenza viruses of animal origin need to be tackled through an integrated One Health approach. Timely sharing of information on outbreaks in animals as well as virus characteristics are key for situation assessments and implementation of prevention and control measures. Transmission events of zoonotic influenza viruses to humans should be identified and reported as early as possible to investigate any human-to-human spread and facilitate implementation of necessary mitigation measures [9,29].

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