

## WEEKLY BULLETIN

# Communicable Disease Threats Report

Week 5, 28 January to 3 February 2024

## This week's topics

1. Overview of respiratory virus epidemiology in the EU/EEA
2. SARS-CoV-2 variant classification
3. Human infection with swine influenza A(H1N1) variant virus – Spain – 2024
4. Human case of co-infection with seasonal influenza A(H3N2) and avian influenza A(H10N5) – China – 2024
5. Influenza A(H5N1) – Multi-country (World) – Monitoring human cases
6. Western equine encephalitis – Argentina – 2023

## Executive Summary

### Overview of respiratory virus epidemiology in the EU/EEA

- At the end of week 4 (ending 28 January 2024), rates of respiratory illness (influenza-like illness (ILI) and/or acute respiratory infection (ARI)) in the community remained elevated and at levels above the baseline (based on moving epidemic method (MEM) thresholds) in most EU/EEA countries. Rates of severe acute respiratory infection (SARI) cases presenting to sentinel secondary care were higher than at the same time last year in three of the five countries reporting data to week 4.
- All indicators pointed to continued high influenza activity in the EU/EEA. All reporting countries were above the 10% sentinel primary care positivity threshold for influenza, with increasing trends observed in most. The majority of reporting countries observed medium or high levels of influenza intensity, widespread geographic spread and above-baseline ILI MEM threshold), driven predominantly by A(H1)pdm09. RSV activity was decreasing overall at the EU/EEA level, although the country-level picture was mixed. SARS-CoV-2 activity was decreasing or low in all countries.

### SARS-CoV-2 variant classification

Since the last update on 19 January 2024 and as of 2 February 2024, **the following changes** have been made to ECDC variant classifications for variants of concern (VOCs), variants of interest (VOIs), variants under monitoring (VUMs) and de-escalated variants:

- The newly designated SARS-CoV-2 lineage **BA.2.87.1** was classified as a VUM. Currently, a small number of sequences of this lineage (9) were identified in South Africa, with collection dates ranging from 20 September to 12 December 2023. This lineage has been circulating at low levels since September 2023, without any clear

signs of an increase in proportions or an impact on epidemiological indicators. BA.2.87.1 is genetically distinct from currently circulating variants, carrying around 100 mutations compared with the parental lineage BA.2. It also has a distinct N-terminal domain in the spike protein, including several large deletions, and could therefore potentially be associated with a significant shift in antigenic properties. However, so far there are no virus neutralisation data available for BA.2.87.1 and further studies are needed to elucidate the properties of this variant. BA.2.87.1 is unlikely to have an impact on the epidemiological situation in the EU/EEA in the near future.

The variant landscape in the EU/EEA is clearly dominated by **BA.2.86**, which was classified as a VOI on 24 November 2023. The increasing trends consistently observed in recent months appear to have levelled off in December 2023. As of 29 January 2024, the median proportion for BA.2.86 in the EU/EEA for week 2 (8 January 2024 to 14 January 2024) is 93.7% (range: 81–100%).

**XBB.1.5-like+F456L** lineages are circulating with a median proportion of 4.3% in EU/EEA countries (range: 0–16.4%). The overall proportion of XBB.1.5-like+F456L variants is declining in the EU/EEA.

**XBB.1.5-like+L455F+F456L** variants show a declining trend in the EU/EEA, with a median proportion of 3.7% (range: 0–11%).

Other **XBB.1.5-like** lineages are circulating in very low proportions and are declining in the EU/EEA, with a median proportion of 1.3% (range: 0.0–5.5%).

#### **Human infection with swine influenza A(H1N1) variant virus – Spain – 2024**

- A new possible case of human infection with swine influenza A(H1N1)v has been reported by Spanish authorities in an adult man who worked in a pig farm in the Catalonia region.
- No human-to-human transmission has been detected.

#### **Human case of co-infection with seasonal influenza A(H3N2) and avian influenza A(H10N5) – China – 2024**

- On 30 January 2024, Chinese authorities reported a human case of co-infection with seasonal influenza A(H3N2) and zoonotic A(H10N5) in Zhejiang province.
- The case was a 63-year-old woman with multiple underlying conditions from Anhui province who developed symptoms on 30 November 2023 and died on 16 December 2023.
- The investigation by Chinese authorities did not find secondary cases among contacts.
- The risk to human health in the EU/EEA is currently assessed as very low.

#### **Influenza A(H5N1) – Multi-country (World) – Monitoring human cases**

##### **Summary:**

- Worldwide, 884 human cases of avian influenza A(H5N1), including 461 deaths (case-fatality rate (CFR): 52%), have been reported in 23 countries since 2004.
- On 28 January 2024, the Cambodian Ministry of Health reported a second new human case of avian influenza A(H5N1) infection detected this year. The case is a 69-year-old man from Siem Reap province.
- The man raised about 50 to 60 chickens that have been dying for about two weeks prior to his diagnosis.
- To date, no human-to-human transmission associated with this event has been reported.
- The clade of the virus was not reported for this case. In Cambodia, clade 2.3.2.1c viruses have been circulating and caused human cases earlier in 2023.
- The risk of zoonotic influenza transmission to the general public in EU/EEA countries is considered low. The risk to occupationally exposed groups, such as cullers, is considered low-to-medium.

#### **Western equine encephalitis – Argentina – 2023**

- Western equine encephalitis (WEE) cases were reported for the first time since 1996 in Argentina.
- The first case presented with symptoms in November 2023 and, overall, 39 cases (including five deaths) were confirmed as of 26 January 2024. Most cases were reported in adult males.
- WEE is a mosquito-borne disease caused by the WEE virus. Birds are the main reservoir, while equines and humans are dead-end hosts. Outbreaks in equines have been reported in Argentina and Uruguay.
- The risk for the EU/EEA is very low because humans and horses are dead-end hosts, there is no direct migration of birds from South America to Europe, and conditions in Europe are currently unfavourable for vector-borne transmission.

# 1. Overview of respiratory virus epidemiology in the EU/EEA

## Overview:

### Respiratory virus activity

- Consultation rates of patients presenting to general practitioners with respiratory illness (ILI and/or ARI) were reported by 20 EU/EEA countries up to week 4. MEM thresholds were available for 18 of these countries (eight for ARI, 17 for ILI), with 12 countries reporting consultation rates above baseline levels in at least one indicator: ARI rates were medium in three countries and high in one; ILI rates were low in four countries, medium in six and high in one.
- Short-term forecasts of ILI and ARI rates in EU/EEA countries are published on [ECDC's RespiCast](#).
- Among countries that reported data on testing in primary care sentinel settings for seasonal influenza, RSV and/or SARS-CoV-2, the median test positivity at the EU/EEA level was highest for influenza at 39% (pooled country data: 34%; IQR of country values: 31–50%), with an increasing trend observed. All 20 countries reporting at least 10 tests observed seasonal influenza activity above the 10% positivity threshold in sentinel primary care. Of 21 countries reporting qualitative assessments of seasonal influenza activity, 20 reported levels above baseline, including five with high activity. Seventeen of 21 countries reported widespread geographical spread of seasonal influenza. The vast majority of countries reported increasing trends in both sentinel and non-sentinel sources.
- Among the 1 270 sentinel primary care detections of seasonal influenza, 1 231 (97%) were typed as influenza virus type A and 36 (3%) were typed as influenza virus type B. Of the influenza type A detections that were further subtyped, 812 (82%) were A(H1)pdm09 and 181 (18%) were A(H3). Seventeen of the influenza type B detections were further defined as B/Victoria lineage, while the remaining 19 were of unknown lineage.
- The median sentinel primary care positivity for SARS-CoV-2 was 4% (pooled country data: 5%; IQR of country values: 2–6%). This indicator has been decreasing since week 49, 2023. Both primary care sentinel and non-sentinel data at the national level show decreasing or stable trends in all countries reporting data to week 4.
- The median sentinel primary care RSV positivity was 4% (pooled: 6%; IQR: 2–7%), decreasing compared to the last week. Country-level variation was present, with some continuing to report elevated sentinel positivity and/or increasing or elevated counts of non-sentinel detections.

### Severe disease

- Rates of severe acute respiratory infection (SARI) from sentinel secondary sites were higher than at the same time last year in three of the five countries reporting data to week 4. These countries all reported testing data for all three pathogens.
- The median SARI test positivity for seasonal influenza was 32% (pooled test positivity: 30%; IQR of country values: 22–38%), with a slight decreasing trend driven by a mixed picture in country-level data. The highest positivity (pooled test positivity 49%) this week was observed in people aged 5–14 years, but was over 20% in all age groups.
- The median SARI test positivity for RSV was of 12% (pooled: 14%; IQR: 9–14%). The highest pooled test positivity (48%) continued to be observed in children aged 0–4 years; it was below 8% in all other age groups.
- The median SARI test positivity for SARS-CoV-2 test positivity decreased to 5% (pooled: 6%; IQR: 5–9%). Pooled positivity remained highest at 8% among people aged 65 years and above. Overall, rates for non-sentinel hospital admissions, ICU admissions and deaths have gradually decreased since week 50, with decreasing or stable trends in all reporting countries.
- [EuroMOMO](#) pooled estimates of weekly excess all-cause mortality showed a 'substantial elevated level of mortality, overall and in the age groups above 45 years of age'.

### Virus characterisation

#### Influenza

WHO recommends that trivalent vaccines for use in the 2023–2024 influenza season in the northern hemisphere contain the following (egg-based and cell culture or recombinant-based vaccines respectively): an A/Victoria/4897/2022 or A/Wisconsin/67/2022 (H1N1)pdm09-like virus (subclade 5a.2a.1); an A/Darwin/9/2021 or A/Darwin/6/2021 (H3N2)-like virus (clade 2a); and a B/Austria/1359417/2021 (B/Victoria lineage)-like virus (subclade V1A.3a.2).

During weeks 40, 2023 to 4, 2024, 1 142 A(H1)pdm09, 447 A(H3) and 43 B/Victoria viruses from sentinel and non-sentinel sources were genetically characterised. Of the A(H1)pdm09 viruses that have been assigned to a clade, 600 were reported as clade 5a.2a and 535 were subclade 5a.2a.1. Of the A(H3) viruses that have been assigned to a clade, eight were reported as clade 2a.3a, 434 were subclade 2a.3a.1 and one was subclade 2a.3b. All of the B/Victoria viruses were reported as subclade V1A.3a.2.

### **SARS-CoV-2 variants for weeks 2–3 (8–21 January 2024)**

The estimated distribution (median and IQR of proportions from 14 countries) of variants of concern (VOCs) or variants of interest (VOIs) was 93% (84–95%) for BA.2.86 (which includes JN.1 isolates), 5% (3–10%) for XBB.1.5+F456L and 1% (0.6–2%) for XBB.1.5-like. The proportion of BA.2.86 continues to grow, with XBB.1.5-like+F456L and XBB.1.5 showing decreasing trends.

### **Period overview (week 25, 2023 to week 4, 2024)**

Following relatively low respiratory illness activity over the summer period, consultation rates increased in primary care settings from September. Transmission of SARS-CoV-2 began increasing in late summer, with clear increases observed at the EU/EEA level up to week 49 and decreases in activity thereafter, with activity currently decreasing or low in all countries. COVID-19 predominantly had an impact on individuals aged 65 years and above. Week 50 marked the start of the seasonal influenza epidemic. Activity remains high, with a mixed picture in trends for sentinel weekly test positivity at country level. Severe disease due to influenza has mainly affected people aged 15 years and above. Both influenza type A and type B viruses have been detected, with a dominance of A(H1)pdm09 viruses in most countries, and A(H3) also dominant or co-dominant in a small number of countries. RSV activity began increasing around week 41, reaching a peak in week 50 followed by a decreasing trend, although in recent weeks a mixed epidemiological picture has been observed, with increasing and decreasing trends at the national level. RSV continues to have the greatest impact among children aged 0–4 years.

### **ECDC assessment:**

After marking the start of the seasonal influenza epidemic in the EU/EEA in week 50, 2023, seasonal influenza continued to circulate at higher levels than SARS-CoV-2 and RSV in week 4, 2024. With continued co-circulation of all three respiratory viruses, it remains essential to continue to monitor the impact on hospital and ICU admissions closely. The combined effect of co-circulating acute respiratory pathogens is likely to convey an increased burden of severe respiratory disease in the EU/EEA, which may result in further significant pressure on healthcare systems in the coming weeks.

### **Actions:**

ECDC monitors rates of respiratory illness presentation and respiratory virus activity in the EU/EEA, presenting findings in the European Respiratory Virus Surveillance Summary ([ERVISS.org](https://www.ecdc.europa.eu/en/er viss)). Updated weekly, ERVISS describes the epidemiological and virological situation for respiratory virus infections across the EU/EEA and follows the principles of integrated respiratory virus surveillance outlined in [Operational considerations for respiratory virus surveillance in Europe](#).

ECDC has published an [epidemiological update](#) that describes the epidemiological situation of acute respiratory infections in EU/EEA countries and provides updated ECDC recommendations for mitigating their impact.

ECDC has published guidance on [vaccination roll-out for autumn/winter 2023](#), which stresses the importance of influenza and COVID-19 vaccination to protect individuals at increased risk of severe disease, e.g. people aged over 60 years and other vulnerable individuals (such as those with underlying comorbidities), irrespective of age.

**Sources:** [ERVISS](#)

**Last time this event was included in the Weekly CDTR:** 26 January 2024

## 2. SARS-CoV-2 variant classification

### Overview:

#### Weekly update on SARS-CoV-2 variants:

Since the last update on 19 January 2024 and as of 2 February 2024, **the following changes** have been made to ECDC variant classifications for variants of concern (VOCs), variants of interest (VOIs), variants under monitoring (VUMs) and de-escalated variants:

- The newly designated SARS-CoV-2 lineage **BA.2.87.1** was classified as a VUM. Currently, a small number of sequences of this lineage (9) were identified in South Africa, with collection dates ranging from 20 September to 12 December 2023. This lineage has been circulating at low levels since September 2023 without any clear signs of an increase in proportions or an impact on epidemiological indicators. BA.2.87.1 is genetically distinct from currently circulating variants, carrying around 100 mutations compared to the parental lineage BA.2. It also has a distinct N-terminal domain in the spike protein, including several large deletions, and could therefore potentially be associated with a significant shift in antigenic properties. However, so far there are no virus neutralisation data available for BA.2.87.1 and further studies are needed to elucidate the properties of this variant. BA.2.87.1 is unlikely to have an impact on the epidemiological situation in the EU/EEA in the near future.

The variant landscape in the EU/EEA is clearly dominated by **BA.2.86**, which was classified as a VOI on 24 November 2023. The increasing trends consistently observed in recent months appear to have levelled off in December 2023. As of 29 January 2024, the median proportion for BA.2.86 in the EU/EEA for week 2 (8 January 2024 to 14 January 2024) is 93.7% (range: 81–100%). Among the 13 EU/EEA countries reporting at least 20 sequences to GISAID EpiCoV for week 1, the proportions of BA.2.86 lineages were as follows: Austria (80.8%), Croatia (70.6%), Denmark (95.0%), France (94.9%), Germany (92.5%), Ireland (84.4%), Italy (85.5%), Luxembourg (100.0%), the Netherlands (95.1%), Norway (100.0%), Poland (100.0%), Spain (95.0%) and Sweden (83.7%).

A large proportion of the BA.2.86 sequences belong to the sub-lineage **JN.1**. As of 19 December 2023, due to its rapid increase in proportion, [WHO classified JN.1](#) as a separate VOI from the parent lineage BA.2.86. The most probable driver of the success of BA.2.86-descendant lineages is immune escape in a population where immunity is increasingly derived from XBB-variants.

As of 29 January 2024, and for week 1 2024, **XBB.1.5-like+F456L** lineages are circulating with a median proportion of 4.3% in EU/EEA countries (range: 0–16.4%). The overall proportion of XBB.1.5-like+F456L variants is declining in the EU/EEA.

**XBB.1.5-like+L455F+F456L** variants show a declining trend in the EU/EEA, with a median proportion of 3.7% (range: 0–11%). Virtually all the lineages are already included in the existing VOIs XBB.1.5-like+F456L, but those carrying L455F are being monitored specifically as this VUM.

Other **XBB.1.5-like** lineages are circulating in very low proportions and are declining in the EU/EEA, with a median proportion of 1.3% (range: 0.0–5.5%).

For the latest information on variants, please see ECDC's [webpage on variants](#).

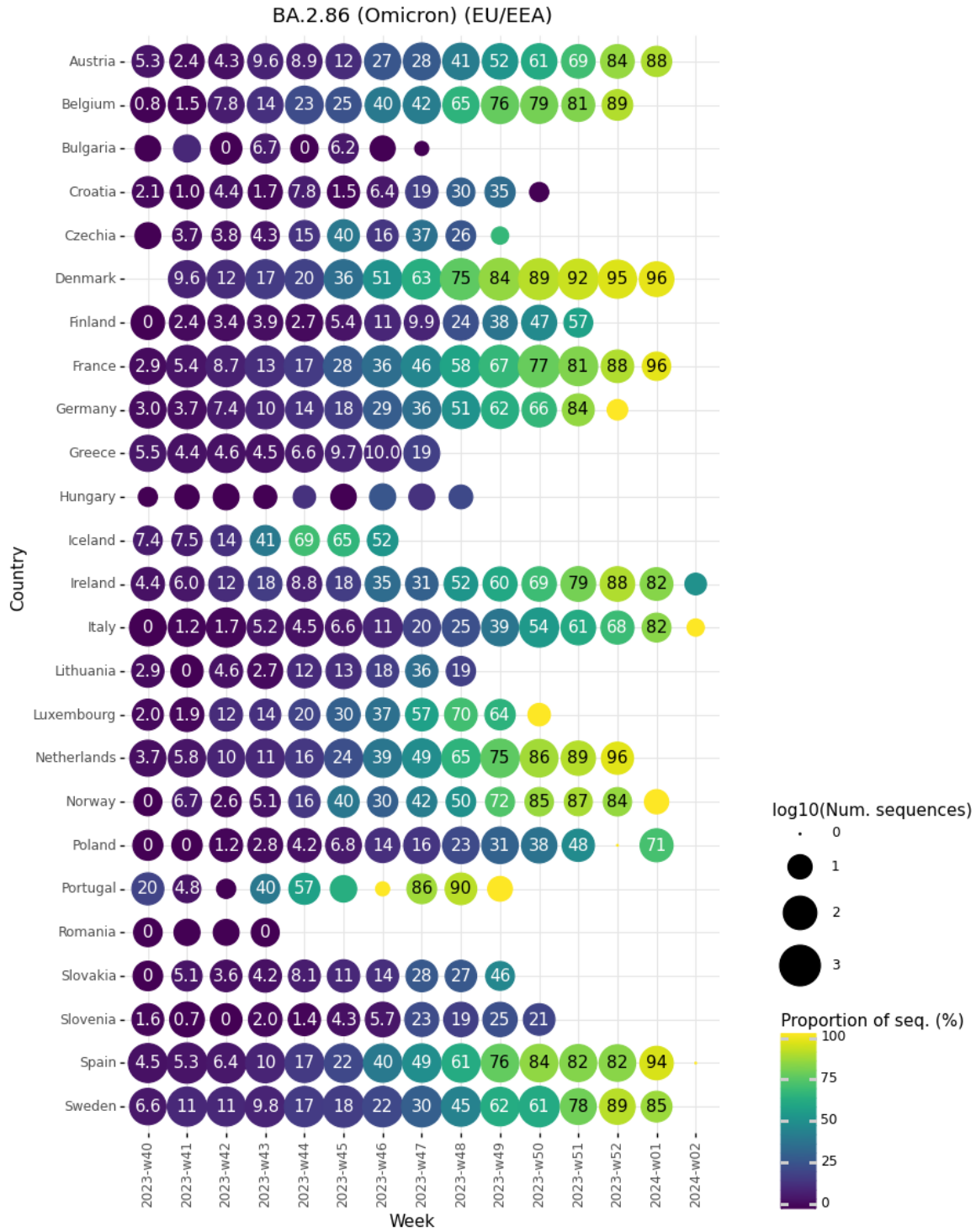
### Actions:

For the latest update on SARS-CoV-2 variant classifications, please see [ECDC's webpage on variants](#). Variant surveillance data, including the distribution of VOC and VOI variant proportions in the EU/EEA and detailed country-specific COVID-19 updates, are available as part of the [European Respiratory Virus Surveillance Summary \(ERVISS\)](#).

**Last time this event was included in the Weekly CDTR:** 26 January 2024

## Maps and graphs

**Figure 1. Proportion of sequences belonging to BA.2.86 lineages per sample collection week, reported by EU/EEA countries to GISAID EpiCoV as of 15 January 2024**



Source: ECDC

## 3. Human infection with swine influenza A(H1N1) variant virus – Spain – 2024

### Overview:

On 29 January 2024, the Spanish authorities reported a possible case of human infection with swine influenza A(H1N1) variant virus (A(H1N1)v) in an adult male worker in a pig farm. The patient has no history of underlying conditions, lives in the Region of Catalonia and developed symptoms (cough with muco-purulent expectoration, fever, malaise and myalgia) on 25 November 2023. He contacted an outpatient clinic three times within three weeks from the start of the symptoms. There were no signs of pneumonia following chest x-ray and the patient was diagnosed with bronchitis. On 12 December 2023, a nasal and oropharyngeal exudate sample tested positive for influenza A, which could not be subtyped. It was further analysed in the regional reference laboratory in Catalonia and was identified as swine influenza A(H1N1)v. The sample was sent for confirmation to the National Institute of Microbiology and the virus isolate will be shared with the WHO Collaboration Centre.

The patient has fully recovered. To date, no new cases have been detected among close contacts (family members) of this case, nor among co-workers in the farm through the epidemiological investigation, which according to Spanish authorities, is considered closed.

The sequences are available on GISAID (isolate ID: EPI\_ISL\_18782577). According to the assessment by ECDC experts all genes match currently circulating swine viruses.

**Background:** overall, and since 2011, 73 cases of A(H1N1)v infection have been reported globally, from Brazil (2), Canada (1), China (42), Denmark (2), Germany (5), Italy (1), the Netherlands (6), Spain (2), Switzerland (3) and the United States (9). In 2023 (by year of diagnosis or onset), six cases of A(H1N1)v were reported, including two cases detected in EU/EEA countries: Spain (1) and the Netherlands (1). The previous case in Spain was reported with date of onset in 2022.

Source: [EWRS notification](#)

### ECDC assessment:

Sporadic transmission of influenza viruses of swine origin to humans causing mild to severe infections have been reported from several countries, including in the EU/EEA. Swine influenza viruses circulate widely in the pig population and direct human exposure to pigs represents the most common risk factor for infection. Therefore, this A(H1N1)v case from Spain is not unexpected. Cases have also occurred among otherwise healthy people and sporadic infections cannot be excluded when people have unprotected direct contact with infected animals.

When a human infection is detected, it is necessary to perform contact tracing to exclude onward transmission to contacts and to implement control measures to prevent human-to-human spread. Zoonotic influenza viruses isolated from patients should be further sequenced and characterised, as well as shared with the national influenza reference laboratories and WHO Collaborating Centres.

The overall risk of spread of this type of influenza is very low for the general population and low for occupationally exposed individuals due to the high prevalence of swine influenza viruses in the pig population. Sporadic cases can be expected.

ECDC published a [Testing and detection of zoonotic influenza virus infections in humans in the EU/EEA, and occupational safety and health measures for those exposed at work](#) in October 2022 and [Threat Assessment Brief on Eurasian avian-like A\(H1N1\) swine influenza viruses](#) in July 2020.

### Actions:

ECDC is monitoring zoonotic influenza events through its epidemic intelligence activities in collaboration with disease experts to identify potential significant changes in the epidemiology of the virus. Human cases of zoonotic influenza should be reported immediately to EWRS and IHR.

**Last time this event was included in the Weekly CDTR: –**

## 4. Human case of co-infection with seasonal influenza A(H3N2) and avian influenza A(H10N5) – China – 2024

### Overview:

On 30 January 2024, the [National Disease Control and Prevention Administration in China](#) has reported a human case with co-infection of influenza A(H3N2) and zoonotic A(H10N5) in Zhejiang province. The case is a 63-year-old woman from Xuancheng, Anhui province, with multiple underlying conditions. She developed symptoms (cough, sore throat and fever) on 30 November 2023, and was admitted to a local healthcare facility on 2 December due to worsening clinical conditions. On 7 December, she was admitted to a hospital in Zhejiang Province where she died on 16 December.

Microbiological investigations carried out at the laboratory in Zhejiang Province on 22 January 2024 revealed the presence of both seasonal influenza A(H3N2) and avian influenza A(H10N5). These findings were confirmed by the Chinese CDC on 26 January 2024.

No additional cases have been identified among close contacts of the case.

Chinese authorities have instructed Zhejiang and Anhui provinces to carry out prevention and control measures and organised experts to conduct risk assessments. According to the expert assessment in China, the whole genome analysis of the virus showed that the A(H10N5) virus was of avian origin and did not have the ability to effectively infect humans, and the case represented an occasional poultry-to-human cross-species transmission. Chinese authorities assessed the risk of the virus infecting people to be low and excluded human-to-human transmission.

The sequences are available on GISAID (Isolate ID: EPI\_ISL\_18846022).

**Background:** This is the first documented human infection with avian influenza A(H10N5). To date, information on exposure history of this case has not been provided.

**Source:** [National Disease Control and Prevention Administration, China](#)

### ECDC assessment:

This is the first human case of avian influenza A(H10N5) reported. No human-to-human transmission has been observed for this influenza subtype so far. However, the source of exposure of the current case has not been identified yet. Despite co-infection with H3N2 seasonal influenza virus in the patient, genomic analysis showed that the A(H10N5) influenza virus genes were all of avian influenza origin, thus ruling out possible genetic recombination between the two viruses.

The risk to human health in the EU/EEA is currently assessed as very low. ECDC closely follows any updates on the current case and will update the assessment as more information becomes available.

Direct contact with infected birds or contaminated environments is the most likely source of human infection with avian influenza. The use of personal protective measures for people exposed to sick or dead birds and their droppings will reduce the associated risk.

### Actions:

ECDC monitors avian influenza strains through its epidemic intelligence and influenza surveillance activities in collaboration with the European Food Safety Authority (EFSA) and the EU reference Laboratory for Avian Influenza to identify significant changes in the epidemiology and characteristics of the virus. ECDC works with EFSA and the EU reference laboratory to produce a quarterly [report on the avian influenza situation](#). The [most recent report](#) was published in December 2023.

**Last time this event was included in the Weekly CDTR:** –



## 5. Influenza A(H5N1) – Multi-country (World) – Monitoring human cases

### Overview:

**Update:** on 28 January 2024, a second new human case of avian influenza A(H5N1) infection was reported in Cambodia by the [Ministry of Health](#). The case is a 69-year-old man from Pbat village, Prey Chrouk commune, Puok district, Siem Reap province (450–500 km away from Kampong Trabek district, Prey Veng province, where a 3-year-old boy was diagnosed with A(H5N1) infection on 25 January 2024). The man's infection was confirmed on 27 January 2024. He is receiving intensive care.

Contact tracing and laboratory investigation are ongoing and close contacts have received antiviral treatment (Tamiflu). The man raised 50 to 60 chickens that have been dying for about two weeks. To date, there is no information on the clade of the virus related to this case.

Previously, virus clade 2.3.2.1c was identified in human cases reported in 2023 in Cambodia (GISAID EPI\_ISL\_18540514).

This is the second case reported in Cambodia in 2024. Overall, six cases, including three deaths, due to A(H5N1) were reported in Cambodia in 2023: two cases reported in February, two in October and two in November. Since 2005, Cambodia has reported 64 cases of avian influenza A(H5N1) infection, including 40 deaths (CFR: 64%).

### Summary:

As of 29 January 2024, there have been 884 human cases\* worldwide, including 461 deaths (CFR: 52%), from infection with avian influenza A(H5N1) reported in 23 countries since 2004. To date, no human-to-human transmission has been detected.

**\*Note:** this includes six detections due to suspected environmental contamination and no evidence of infection that were reported in 2022 by Spain (2 detections) and the United States (1), as well as in 2023 by the United Kingdom (3).

**Sources:** [report on Facebook account of the MoH of Cambodia](#) (second case), [media report](#) (second case), [media report](#) (first case), [report on Facebook account of the MoH of Cambodia](#) (first case), [ECDC Avian influenza](#), [ECDC Avian influenza overview: Latest situation update of the avian influenza in the EU/EEA](#)

### ECDC assessment:

Sporadic human cases of different avian influenza A(H5Nx) subtypes have previously been reported globally. Current epidemiological and virological evidence suggests that A(H5N1) viruses remain avian-like. Transmission to humans remains a rare event and no sustained transmission between humans has been observed.

Overall, the risk of zoonotic influenza transmission to the general public in EU/EEA countries is considered low. The risk to occupationally exposed groups, such as cullers, is considered low-to-medium.

Direct contact with infected birds or a contaminated environment is the most likely source of infection, and the use of personal protective measures for people exposed to dead birds or their droppings will minimise the remaining risk. The recent severe cases in Asia and South America in children and people exposed to infected, sick or dead backyard poultry underline the risk of unprotected contact with infected birds in backyard farm settings. This would also suggest the importance of using appropriate personal protective equipment.

### Actions:

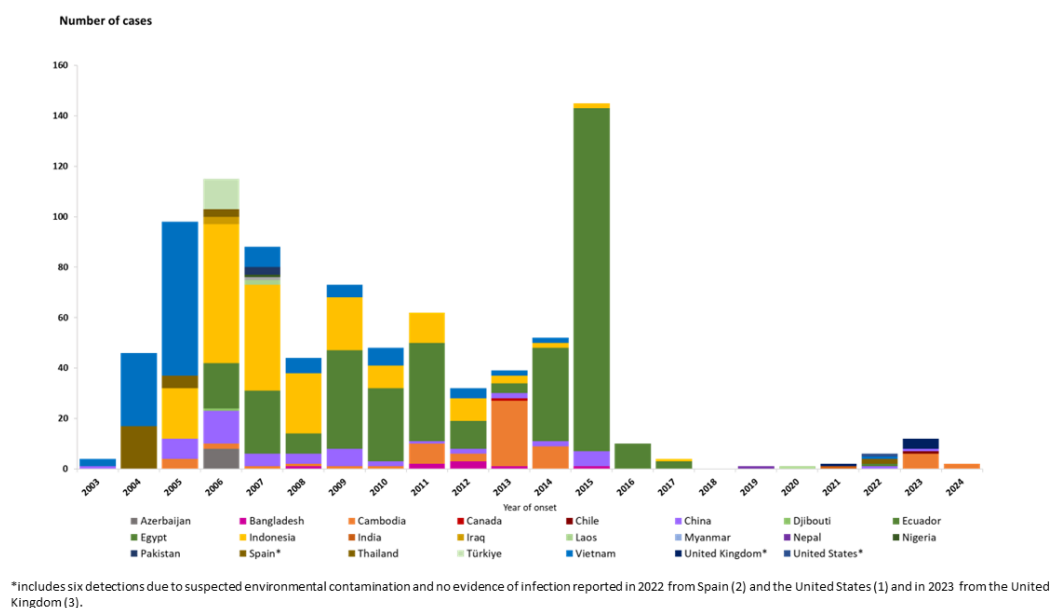
ECDC monitors avian influenza strains through its influenza surveillance programme and epidemic intelligence activities in collaboration with the European Food Safety Authority (EFSA) and the EU Reference Laboratory for Avian Influenza in order to identify significant changes in the virological characteristics and epidemiology of the virus. Together with EFSA and the EU Reference Laboratory for Avian Influenza, ECDC produces a quarterly updated report of the [avian influenza situation](#).

**Sources:** [42877](#) | [2023-E000065](#)

**Last time this event was included in the Weekly CDTR:** 26 January 2024

## Maps and graphs

**Figure 1. Confirmed human cases of avian influenza A(H5N1) virus infection by year of onset and country, 2003 to 29 January 2024 (n = 884)**



Source: ECDC

## 6. Western equine encephalitis – Argentina – 2023

### Overview:

On 20 December 2023, the Ministry of Health of Argentina [reported](#) that a case of Western equine encephalitis (WEE) was detected in Santa Fe. The report was followed by a [Disease News Item \(DON\) published by WHO on 28 December 2023](#). According to the DON, the patient developed symptoms in November and was working in an area where WEE cases were reported in equines. Human WEE cases were reported previously in Argentina in 1983 and 1996.

Epidemiological surveillance of WEE in humans was initiated on 28 November 2023, after the initial alert at the national level. [According to the epidemiological bulletin of the Ministry of Health of Argentina](#), until 26 January 2024, 213 suspected WEE cases were reported, of which 39 were confirmed, including five deaths (in people between 36 and 74 years old, three males and two females). Of the 39 confirmed cases, 10 were reported in Santa Fe, 23 in Buenos Aires, three in Entre Rios, two in Córdoba and one in Santiago del Estero. The median age of the cases is 55 years (range: 9 months to 81 years) and most cases were reported in males (89%). All were hospitalised and all have confirmed epidemiological links with a rural environment (living, working or carrying out recreational activities).

WEE is a mosquito-borne disease caused by the Western equine encephalitis virus (WEEV; genus Alphavirus, family Togaviridae). The main reservoir for WEEV is birds, while humans and equines are dead-end hosts. Up to 18 January 2024, 47 and 1 171 outbreaks in equines have been reported to [WAHIS](#) in Uruguay and Argentina, respectively. Prior to this event, the last outbreaks in equines were reported in Mexico in 2019, after which the situation was resolved. The most recent human case was in [Uruguay](#) in 2009.

Detailed laboratory guidelines for the detection of WEEV infection in humans were [published](#) by WHO PAHO on 20 December 2023. The European Union reference laboratories for equine diseases provide a Standard Operating Procedure for the detection of WEE in equine animals ([WOAH, accessed on 23/01/2024](#)), and the requirements for diagnostics techniques and vaccines for WEE are described in Chapter 3.6.5 of the [diagnostic manual](#) of the WOAH.

**ECDC assessment:**

WEE used to be widespread in the Americas, from Canada to Argentina, with epidemics with thousands of cases in the 1940s. Since then, case numbers have decreased, with no human cases since 2009. There is no clear explanation for the decline that was observed in the last decade. More specifically, lack of evidence for a decline in virulence of WEEV has been reported, but ecological factors have been hypothesised to play a role ([Forrester et al., 2008](#)). Serological studies provide only patchy evidence of potential virus circulation in South America. For instance, there is some serological evidence of WEEV circulation in horses in 2007, both in Central-West Brazil ([Pauvolid-Correa et al, 2010](#)) and Uruguay ([Burgueno et al., 2018](#)). A study in Argentina, carried out from 2013 to 2016, did not collect any serological evidence of WEEV circulation in horses ([Albrieu-Llinas et al., 2021](#)). Other studies investigating seroprevalence in 182 humans in the S. Paulo State in 2000 delivered only negative test results ([Romano Lieber et al, 2000](#)) and this was the same for 298 young men tested in 2021 in the Amazonas State in Brazil ([Salgado et al, 2021](#)). Also, studies carried out in Trinidad did not find any serological evidence of virus circulation in humans ([Thompson et al., 2012](#)).

There is not much information yet about the current prevalence of WEEV in mosquitoes and wild birds, but knowing that equines and humans (which are dead-end hosts) are being affected, it can be assumed that it is circulating among mosquitoes and wild birds. Therefore, to reduce the potential exposure to humans, personal protective measures against mosquito bites should be applied in affected areas. These include the use of repellents, protective clothing, door and window screens, and mosquito nets.

The risk for the EU/EEA is very low because humans and horses are dead-end hosts, there is no direct migration of birds from South America to Europe, and conditions in Europe are currently unfavourable for vector-borne transmission.

**Actions:**

ECDC is monitoring the event through epidemic intelligence.

**Further information:**

- [Equine encephalomyelitis \(Western\) - WOA - World Organisation for Animal Health](#)
- [Epidemiological alert - Risk to human health associated with Western Equine Encephalitis Virus infection in Equines - 19 December 2023 - PAHO/WHO | Pan American Health Organization](#)
- [Ministerio de Salud Argentina - Encefalitis Equina del Oeste: Circular para la vigilancia epidemiológica y laboratorial, la prevención y el control \(08/12/2023\)](#)

**Last time this event was included in the Weekly CDTR:** 5 January 2024