

WEEKLY BULLETIN

Communicable Disease Threats Report

Week 14, 31 March to 6 April 2024

This week's topics

- 1. Overview of respiratory virus epidemiology in the EU/EEA weekly monitoring
- 2. SARS-CoV-2 variant classification
- 3. Cholera Comoros and Mayotte 2024 Weekly monitoring
- 4. Highly pathogenic avian influenza A(H5N1) in cattle and a related human case United States 2024
- 5. Human cases infected with swine influenza A(H1N2) variant virus Multi-country 2023
- 6. Middle East respiratory syndrome coronavirus (MERS-CoV) Multi-country Monthly update

Executive Summary

Overview of respiratory virus epidemiology in the EU/EEA - weekly monitoring

- Syndromic surveillance in primary and secondary care indicates that acute respiratory infections continue to decrease and have returned to baseline levels in most EU/EEA countries.
- Seasonal influenza activity at EU/EEA level continues to decrease and is no longer above the 10% positivity threshold.
- The primary care pooled test positivity at EU/EEA level has been below 10% for two consecutive weeks, with half of countries reporting test positivity below 10%. Similarly, the pooled test positivity in secondary care was below 10% and is continuing to decrease.
- Seasonal influenza activity decreased earlier this winter period compared to the trends observed in the past five years (excluding the 2020/2021 season with almost no activity).
- Most countries now report baseline or low levels of influenza intensity and baseline rates of
 influenza-like illness (ILI). Countries continue to report a mix of geographical spread, indicating
 continued heterogeneity of influenza activity at country level.
- In week 13, B/Victoria lineage was the most detected virus in the EU/EEA. For the first time this
 season, there was more Influenza B than Influenza A detected, although the detections remain
 low and continue to decrease.
- RSV activity continued to decrease to low levels at the EU/EEA level and in most reporting countries.
- SARS-CoV-2 activity remained low in all EU/EEA countries.

SARS-CoV-2 variant classification

Since the last update on 15 March 2024, and as of 5 April, **no 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.

As of 15 March 2024, given the low levels of circulation for **XBB.1.5-like**, **XBB.1.5-like+F456L** and **XBB.1.5-like+L455F+F456L**, these will be merged into a single VOI designation: **XBB.1.5-like**. This update will simplify the presentation of SARS-CoV-2 variant data in <u>ERVISS</u> from week 11, 2024 and does not require any change in current reporting of SARS-CoV-2 variants by countries.

The variant landscape in the EU/EEA is clearly dominated by **BA.2.86**. As of 1 April 2024, the median proportion for BA.2.86 in the EU/EEA for week 11 (11–17 March 2024) is 85.1% (range: 73.5–96.7%).

BA.2.87.1 lineage was classified as a VUM on 2 February 2024. Nine sequences of this lineage were detected in South Africa, with collection dates ranging from 20 September to 12 December 2023. As of 1 April 2024, BA.2.87.1 has not been detected outside South Africa. This lineage has been circulating in South Africa at low levels since September 2023, without any clear signs of an increase in proportion 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 potentially be associated with a significant shift in antigenic properties. However, to date no virus neutralisation data are 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.

XBB.1.5-like lineages are circulating in very low proportions in the EU/EEA, with a median proportion of 0% (range: 0.0-0.0%).

Cholera - Comoros and Mayotte - 2024 - Weekly monitoring

- On 19 March 2024, the prefect of Mayotte reported the first imported confirmed case of cholera in the French territory of Mayotte since 2000. According to media, the case recovered and no additional cases have been detected in Mayotte.
- In light of the information available, the risk of community transmission in Mayotte remains high.
- Since the last available update on 22 March 2024, and as of 31 March, 199 new cholera cases and four new deaths have been reported in Comoros. As of 31 March, 655 confirmed cholera cases and 16 deaths have been reported.

Highly pathogenic avian influenza A(H5N1) in cattle and a related human case – United States – 2024

- One human case of influenza A(H5N1) has been detected in the state of Texas, United States (US), in a person with previous exposure to presumably infected cattle.
- The virus isolated from this case belongs to the HA clade 2.3.4.4b HPAI A(H5N1) and is closely related to the virus detected in dairy cattle in Texas.
- Highly pathogenic avian influenza has been detected in cattle in several farms in multiple states in the US.
- The US Department of Agriculture highlights that commercially produced pasteurised milk is safe to consumers. However, the US Food and Drug Administration has recommended not to manufacture or sell raw milk or raw/unpasteurised milk and cheese products made with milk from cows showing symptoms of illness.
- A multi-sectoral investigation is ongoing and farmers and veterinarians are encouraged to report any illness in cattle promptly.
- The US Centers for Disease Control and Prevention has issued interim recommendations for prevention, monitoring and public health investigations of HPAI A(H5N1) in animals.

Human cases infected with swine influenza A(H1N2) variant virus - Multi-country - 2023

• One new case of human infection with influenza A(H1N2) variant virus of swine origin has been reported in the state of Pennsylvania, United States (US). This is the first human case with swine influenza A(H1N2)v infection detected in the US this year.

- Previously, swine influenza A(H1N2)v cases were reported in the US in 2023 (two cases), 2022 (six cases) and 2021 (four cases). All the cases were from different regions of the US and were considered sporadic cases.
- Overall, 27 cases have been reported globally since 2019, including four cases reported in EU/EEA countries (Austria, Denmark, France and the Netherlands). The last case in the EU/EEA was reported in the Netherlands in 2022. The last four cases reported in 2023 were from Taiwan (one case), the United Kingdom (one case) and the US (two cases).
- These events are rare and no human-to-human transmission has been detected.

Middle East respiratory syndrome coronavirus (MERS-CoV) - Multi-country - Monthly update

• Since the beginning of 2024, and as of 3 April, no MERS-CoV cases have been reported by the World Health Organization (WHO) or national health authorities. The last reported case was in Saudi Arabia, with date of onset on 26 October 2023.

1. Overview of respiratory virus epidemiology in the EU/EEA – weekly monitoring

Overview:

Respiratory virus activity

- ILI and acute respiratory infection (ARI) consultation rates continue to decrease or remain stable at low levels (20 reporting countries). Moving Epidemic Method (MEM) thresholds were available for 18 countries, five of which observed consultation rates above baseline levels. Short-term forecasts of ILI and ARI rates in EU/EEA countries are published on ECDC's RespiCast.
- In primary care sentinel settings, the median test positivity at the EU/EEA level was highest for influenza, at 10% (pooled country data: 7.1%; interquartile range (IQR) of country values: 6–18%), with stable or decreasing trends observed in most countries. In week 13, half of the countries reported a test positivity below 10%. Qualitative assessments of seasonal influenza activity from 22 countries indicate decreasing intensity in recent weeks (eight baseline, eight low, six medium). Eight of 21 countries reported widespread geographical spread of seasonal influenza.
- Among the 108 sentinel primary care detections of seasonal influenza, 62 (57%) were typed as influenza virus type B and 46 (43%) were typed as influenza virus type A. Of the influenza type B detections, 43 were further defined as B/Victoria lineage, while the remaining 19 were of unknown lineage. Of the influenza type A detections that were further subtyped, 21 (46%) were A(H1)pdm09 and seven (15%) were A(H3). The remaining 18 influenza type A detections were of unknown subtype.
- The median sentinel primary care RSV positivity was 0% (pooled: 2.3%; IQR: 0-4%). Decreasing or stable trends were observed at the country level in both sentinel positivity and non-sentinel detections.
- The median sentinel primary care positivity for SARS-CoV-2 remained low at 0% (pooled: 1.5%; IQR: 0–1%). Decreasing or stable trends were observed at the country level in both sentinel positivity and non-sentinel detections.

Severe disease

- Rates of severe acute respiratory infection (SARI) from sentinel secondary sites were stable or decreasing and at levels comparable to the same time last year in most of the seven countries reporting data up to week 13.
- The median SARI test positivity for seasonal influenza was 4% (pooled: 3.6%; IQR: 2–5%), with decreasing or stable trends observed in all six countries reporting this indicator. All countries reporting non-sentinel hospital or ICU data observed decreasing trends.
- The median SARI test positivity for RSV was 2.8% (pooled: 2.8%; IQR: 1–3%), with decreasing or stable trends observed in all six countries reporting this indicator. The highest pooled test positivity continued to be in children aged 0–4 years, but a decreasing trend has been observed since week 52, 2023.
- The median SARI test positivity for SARS-CoV-2 was 2% (pooled: 2%; IQR: 1–5%). Both SARI positivity and non-sentinel indicators of severity have shown a gradually decreasing trend since week 50 and low levels in all countries.

<u>EuroMOMO</u> pooled estimates of weekly excess all-cause mortality showed mortality is within
expected levels for this time of the year for the participating European countries, following a
longer period of elevated mortality.

Virus characterisation

Influenza

- The World Health Organization (WHO) <u>recommends</u> that trivalent vaccines for use during 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).
- From week 40, 2023 to week 13, 2024, 2 933 A(H1)pdm09, 1122 A(H3) and 157 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, 1 957 were reported as clade 5a.2a and 965 were subclade 5a.2a.1. Of the A(H3) viruses that have been assigned to a clade, 10 were reported as clade 2a.3a, 1 078 were subclade 2a.3a.1, one was subclade 2a.3b, and 30 were subclade 2a. All B/Victoria viruses were reported as subclade V1A.3a.2.
- Antigenic characterisation data presented in the WHO <u>2024-2025 northern hemisphere vaccine</u> <u>composition report</u> indicate current northern hemisphere vaccine components are well matched to circulating 5a.2a and 5a.2a.1 A(H1N1)pdm09 subclades and V1A.3a.2 B/Victoria subclades. While components also appear well matched for 2a.3a A(H3) clade viruses, 2a.3a.1 clade viruses are less well matched. Based on human post-vaccination serology studies, haemagglutination inhibition and virus neutralisation against some recent 2a.3a.1 viruses were significantly reduced for some serum panels.
- ECDC has <u>published</u> interim influenza vaccine effectiveness estimates for the 2023–2024 season. Analysis of data submitted from multi-country primary care and hospital study sites between September 2023 and January 2024 indicated that up to 53% and 44% of vaccinated individuals in primary care or hospital settings, respectively, were protected against mild and severe influenza.
- Updated WHO <u>recommendations</u> for the composition of trivalent vaccines for use during the 2024–2025 influenza season in the northern hemisphere are as follows (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/Thailand/8/2022 or A/Massachusetts/18/2022 (H3N2)-like virus (subclade 2a.3a.1); and a B/Austria/1359417/2021 (B/Victoria lineage)-like virus (subclade V1A.3a.2).

SARS-CoV-2 variants for weeks 11-12 (11 March to 24 March 2024)

• The estimated distribution (median and IQR of proportions from eight countries) of variants of concern (VOCs) or variants of interest (VOIs) was 95% (75–97%) for BA.2.86 (which includes JN.1 isolates) and 0% (two detections overall) for XBB.1.5-like (which now includes XBB.1.5+F456L). These proportions have been stable since week 5.

Period overview (week 25, 2023 to week 13, 2024)

Following relatively low respiratory illness transmission over the summer period, consultation rates increased in primary care settings from September. Consultation rates reached their peaks at different timepoints in each country during the winter period, with peak rates between week 50, 2023 and week 7, 2024. As of week 13, consultation rates continued to decrease and have returned to baseline levels in most EU/EEA countries. 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. Activity is currently low in most EU/EEA countries. Similarly, a steady decrease in severe disease has been observed since week 50. COVID-19 has predominantly affected individuals aged 65 years and above. Week 50 marked the start of the seasonal influenza epidemic. A decreasing trend in influenza activity has been observed since week 4, with half of the countries reporting below 10% positivity as of week 13. Compared to trends observed in previous influenza epidemics, the seasonal influenza activity decreased earlier this season. Severe disease due to influenza has affected all age groups. Since week 6, a decrease in the severe disease indicators for seasonal influenza has been observed in most EU/EEA countries. Both influenza type A and type B viruses have been detected, with a dominance of A(H1)pdm09 viruses in the first part of the season. As of week 13, B/Victoria lineage was the most detected virus, but with relatively low numbers of detections. RSV activity began increasing around week 41, reaching a peak in week 50, followed by a decreasing trend. RSV has had 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 primary care sentinel systems during week 13, 2024. Influenza activity at EU/EEA level continues to decrease and pooled positivity in primary care has been below the 10% positivity threshold for two consecutive weeks. Even if the respiratory virus circulation is decreasing, it remains essential to closely monitor the impact of influenza and other respiratory viruses on hospital and ICU admissions.

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 (<u>ERVISS.org</u>). 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 <u>Operational considerations for respiratory virus surveillance in Europe</u>'.

ECDC published an <u>epidemiological update</u> that describes the epidemiological situation for acute respiratory infections in EU/EEA countries and provides updated ECDC recommendations to mitigate their impact.

ECDC published guidance on <u>vaccination rollout for autumn/winter 2023</u> which stresses the importance of influenza and COVID-19 vaccination to protect individuals at increased risk of severe disease – e.g. people aged 60 years and above, 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: 22 March 2024

2. SARS-CoV-2 variant classification

Overview:

Weekly update on SARS-CoV-2 variants:

Since the last update on 15 March 2024, and as of 5 April 2024, no 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.

As of 15 March 2024, given the low levels of circulation for **XBB.1.5-like**, **XBB.1.5-like+F456L** and **XBB.1.5-like+L455F+F456L**, these will be merged into a single VOI designation: **XBB.1.5-like**. This update will simplify the presentation of SARS-CoV-2 variant data in <u>ERVISS</u> from week 11, 2024 and does not require any change in current reporting of SARS-CoV-2 variants by countries.

The variant landscape in the EU/EEA is clearly dominated by **BA.2.86**. As of 1 April 2024, the median proportion for BA.2.86 in the EU/EEA for week 11 (11–17 March 2024) is 85.1% (range: 73.5–96.7%). Among the two EU/EEA countries reporting at least 20 sequences to GISAID EpiCoV for week 11, the proportions of BA.2.86 lineages were as follows: France (73.5%) and Germany (96.7%).

A large proportion of the BA.2.86 sequences belong to the sublineage **JN.1**. As of 19 December 2023, due to its rapid increase in proportion, <u>WHO classified</u> 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.

BA.2.87.1 lineage was classified as a VUM on 2 February 2024. Nine sequences of this lineage were identified in South Africa, with collection dates ranging from 20 September to 12 December 2023. As of 1 April 2024, BA.2.87.1 has not been detected outside South Africa. This lineage has been circulating in South Africa at low levels since September 2023, without any clear signs of an increase in proportion 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, to date no virus neutralisation data are 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.

XBB.1.5-like lineages are circulating in very low proportions in the EU/EEA, with a median proportion of 0% (range: 0.0-0.0%).

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 <u>ECDC's webpage on variants</u>. 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 <u>European Respiratory Virus Surveillance Summary (ERVISS)</u>.

Last time this event was included in the Weekly CDTR: 22 March 2024

3. Cholera – Comoros and Mayotte – 2024 – Weekly monitoring

Overview:

Update

On 19 March 2024, the <u>prefect</u> of Mayotte reported the first imported confirmed case of cholera on the island since 2000. The <u>patient</u> is a woman who arrived from Anjouan by kwassa in the north of the island of Mayotte on 17 March. She called the Samu (Emergency Medical Aid Service) after vomiting on 18 March. She was hospitalised at the Mayotte Central Hospital and isolated. <u>According to media</u> reports, she was living in Passamainty (a village in the commune of Mamoudzou, the capital city of Mayotte) when the symptoms arose.

Following the detection of the imported cholera case in Mayotte, the prefect of the French Territory released a public <u>statement</u> listing the public health measures taken. An initial medical and paramedical investigation team went to the patient's home to identify contacts and co-exposed cases and provide them with initial treatment. On 19 March, a second team was deployed to disinfect the site, carry out environmental analyses and provide health recommendations to people in the neighbourhood.

According to media, the imported cholera case recovered and no additional cases have been detected in Mayotte.

In Comoros, since 22 March and as of 31 March, <u>Comoros health authorities</u> reported 199 new cholera cases and four new deaths.

Since the outbreak was declared on 2 February in the Union of the Comoros*, a total of 655 cases, including 16 deaths, have been reported on the three islands. Of these cases, 581 have recovered and 58 are hospitalised.

* Note that the report from other sources is irregular and data on the date of symptom onset are not available.

Summary

On 31 January 2024, a boat from Tanzania carrying 25 people <u>arrived in Moroni</u>, the capital of the Comoros archipelago. One person on board died of suspected cholera and several others were symptomatic. The Comoros Ministry of Health <u>declared</u> a cholera outbreak on 2 February. The first locally transmitted cases in Comoros were reported on 5 February in Moroni. Cholera cases were also detected in Moheli and Anjouan by the end of February and the first week of March. On 18 March 2024, Mayotte reported the detection of the first confirmed case on the island.

Following the increase in cholera cases in Comoros during February, the Mayotte Regional Health Agency (ARS Mayotte) <u>announced</u> that health surveillance capacities would be strengthened on the island, including risk communication for health professionals and passengers. The first imported cholera case was detected in Mayotte on 19 March.

Background

There is frequent undocumented population movement between the Comoros archipelago and the French territory of Mayotte. No cholera cases had been recorded in Mayotte since 2000.

Cholera is a bacterial disease caused by the bacterium *Vibrio cholerae*. The main risk factors are associated with poor water, sanitation and hygiene practices. Several countries in eastern and southern Africa are currently responding to cholera outbreaks. Response efforts are constrained by global shortages of cholera vaccines.

ECDC assessment:

Following importation of the first confirmed case of cholera to Mayotte, ECDC assesses the likelihood of cholera community transmission in Mayotte as high. The impact of a cholera outbreak in Mayotte is considered to be moderate. The overall risk of cholera for the population in Mayotte is therefore assessed to be high.

The imported case was isolated early, although the number of contacts and possible exposed people remains uncertain. Early detection and response activities are essential and have been reinforced in Mayotte, as well as increasing awareness among healthcare workers and at points of entry.

Actions:

ECDC is in contact with French authorities and relevant partners and is monitoring the situation through epidemic intelligence activities.

Last time this event was included in the Weekly CDTR: 27 March 2024

4. Highly pathogenic avian influenza A(H5N1) in cattle and a related human case – United States – 2024

Overview:

Following the detection of highly pathogenic avian influenza (HPAI) A(H5N1) in diary cattle in the United States (US) on 25 March 2024 by the US Department of Agriculture (<u>USDA</u>), a related human case in Texas was reported on 1 April by the US Centers for Disease Control (<u>CDC</u>) and the <u>Texas Department of State Health Services</u> (DSHS). The person had exposure to dairy cattle in the state that were presumed to be infected with A(H5N1) virus. The case presented with conjunctivitis as the only symptom on week 13 (ending 31 March 2024) and is recovering. The person has been isolated and treated with antivirals (Oseltamivir). This is the second human case with avian influenza A(H5N1) infection reported in the US and the first linked to an exposure to cattle. The US authorities maintain that the risk to the general public remains low.

On 2 April 2023, the <u>US CDC</u> published a technical update regarding the influenza virus genome sequence from the reported human infection with avian influenza A(H5N1) in Texas. The virus sequences are HA clade 2.3.4.4b HPAI A(H5N1) and are closely related to other viruses detected in dairy cattle in Texas. Compared with the sequences from dairy cattle, the human isolate had one change (PB2 E627K) known to be associated with viral adaptation to mammalian hosts that has been detected before in other persons and mammals infected with avian influenza A(H5N1). Both the cattle and human sequences have avian genetic characteristics and they lack major changes for better adaptation to mammals.

Update on the situation in cattle:

As of 3 April 2024 and since 25 March 2024, the <u>USDA</u> reports detection of HPAI A(H5N1) in six states, affecting 15 herds: Texas (seven herds), Kansas (three herds), New Mexico (two herds), Michigan (one herd), Idaho (one herd) and Ohio (one herd).

Earlier, on 29 March, the <u>Michigan Department of Agriculture and Rural Development</u> reported that a farm in Michigan state had recently received cattle from an affected premises in Texas before that herd had shown any sign of disease. Authorities called upon farmers to contact their veterinarian if they have any concern about their animals, regardless of species. The <u>Idaho State Department of Agriculture</u> also reported the detection of HPAI (A(H5N1) in cattle herds in a facility that had recently imported cattle from another state that has identified cases of HPAI in cattle.

According to the World Organisation for Animal Health (WAHIS) on 27 March 2024, HPAI A(H5N1) Eurasian lineage goose/Guangdong clade 2.3.4.4b was confirmed in samples from sick cattle collected from at least one dairy farm in Kansas and at least one dairy farm in Texas. The initial sequences represent a sporadically detected four gene reassortant (B3.13 per GenoFlu) descended from the previously predominant genotype B3.2 first observed in wild birds in November 2023. No markers for mammalian adaptation nor antiviral resistance were observed. In addition, according to US veterinary experts, the unexplained illness syndrome was reported since late January 2024, and there is not enough evidence that HPAI is the only causative agent. They also discussed the difficulties of implementing biosecurity measures in cattle farms.

Authorities continue to emphasise that pasteurised milk is safe for consumers, but are worried about the effects of HPAI on the production of milk. While cases among humans in direct contact with infected animals are possible, this indicates that the current risk to the public remains low. The US FDA has recommended that farmers and the milk industry do not manufacture or sell raw milk or raw/unpasteurised milk cheese products made with milk from cows showing symptoms of illness. At this time, the US FDA is not aware that any milk or food product from symptomatic cows is entering interstate commerce.

On 25 March 2024, the USDA reported that highly pathogenic avian influenza (HPAI) has been detected in unpasteurised milk samples from cattle at two dairy farms in Kansas, one in Texas, and an oropharyngeal swab from cattle in another dairy farm in Texas. Clinical signs of reduced milk yield and decreased appetite among mainly older dairy cattle has been observed at affected farms. There appears to have been no or limited mortality reported in affected animals. Dead wild birds have been reported on the properties.

The <u>USDA</u> emphasises that the detection of HPAI in cattle does not affect the safety of consuming commercially produced milk. Milk from affected cattle is removed from the human food chain and pasteurisation of milk inactivates viruses such as influenza. Sale of unpasteurised milk is allowed in some states in the US, according to the <u>USDA</u>.

There is no indication that the detected virus would be more transmissible to humans. Information on the subtype and clade of HPAI has not been shared yet. Additional investigation, such as genome sequencing and characterisation of the virus, is being carried out. Furthermore, farmers and veterinarians are being encouraged to report illness in cattle to identify any additional cases.

On 29 March 2024, the <u>US CDC issued interim recommendations</u> for prevention, monitoring and public health investigations of HPAI A(H5N1) in animals. For the public, these focus on the prevention of unprotected exposure to sick or dead animals and the need to monitor for symptoms. For occupational exposures, wearing the recommended personal protective equipment is stressed, after appropriate training. Clinicians should consider the possibility of A(H5N1) infection in persons showing compatible symptoms of respiratory illness and exposure history. Standard, contact and airborne precautions are recommended, as well as prompt initiation of antiviral treatment. Prompt testing of exposed persons is recommended and a case definition for surveillance purposes.

Sources: <u>US CDC</u>, <u>the Texas Department of State Health Services</u>, <u>WAHIS</u>, <u>Michigan Department of Agriculture and Rural Development</u>, <u>USDA APHIS | Federal and State Veterinary</u>, <u>Public Health Agencies Share Update on HPAI Detection in Kansas</u>, <u>Texas Dairy Herds</u>

ECDC assessment:

A human case of HPAI A(H5N1) has been reported in the US with previous exposure to presumably infected cattle. The US CDC assesses the risk to the general public as low. For occupationally exposed individuals, wearing personal protective equipment (PPE) is recommended to decrease the individual risk of infection (<u>ECDC</u>). In general, sick and dead wild birds or mammals should not be touched without proper precautionary measures such as wearing gloves, at a minimum (<u>ECDC</u>). Pasteurisation has shown to inactivate HPAI viruses (Chmielewski et al., 2013). The USDA highlights that commercially produced milk is safe for consumers and that milk from affected cattle has been removed from the human food chain (USDA, 2024).

To date, HPAI has not been reported in cattle in the EU/EEA. Close cross-sectoral cooperation and communication between animal and public health authorities are recommended to better understand the circulating HPAI viruses in order to implement safety measures and prevent zoonotic transmission events. However, occupational safety and health measures should be taken in all premises where zoonotic influenza is suspected and/or identified, including avoidance of aerosol and dust, ventilation, separation of work and personal clothing, and measures to prevent contamination of worker accommodations. In addition, public health professionals and clinicians should be aware of the need to test for zoonotic influenza virus infection in patients with respiratory illnesses and recent exposure to animals potentially infected with influenza virus.

ECDC relevant publications:

- 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
- Enhanced surveillance of severe avia influenza virus infections in hospital settings in the EU/EEA.
- Investigation protocol of human cases of avian influenza virus infections in the EU/EEA
- <u>Joint ECDC-EFSA Drivers for a pandemic due to avian influenza and options for One Health mitigation measures</u>

Actions:

ECDC is in contact with US Centers for Disease Control and Prevention for further information and closely follows any updates on the event. 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.

Last time this event was included in the Weekly CDTR: -

5. Human cases infected with swine influenza A(H1N2) variant virus - Multi-country - 2023

Overview:

On 29 March 2024 (week 12), the <u>United States Centers for Disease Control and Prevention</u> (US CDC) reported a human infection with influenza A(H1N2) variant virus of swine origin (A(H1N2)v) in the state of Pennsylvania in a person below 18 years of age who had contact with pigs prior to onset of symptoms. The person required hospitalisation and was later discharged.

Further investigations identified mild symptoms that began prior to the case's onset of symptoms in two contacts who were also exposed to swine. No person-to-person transmission of A(H1N2)v has been associated with this case. Investigations are still ongoing.

This is the first reported human infection with influenza A(H1N2)v of swine origin detected in the US this year. Previously, cases were reported in 2023 (two cases), 2022 (six cases) and 2021 (four cases). All the cases were from different regions in the US and were considered sporadic cases.

Summary: Overall, 27 cases have been reported globally since 2019, of which four were reported in the EU/EEA: Austria (in 2021), Denmark (in 2019), France (in 2021) and the Netherlands (in 2022). Outside the EU/EEA, cases have been reported in Brazil (three cases), Canada (three cases), Taiwan (three cases), the United Kingdm (one case) and the US (thirteen cases).

Source: <u>US Centers for Disease Control and Prevention</u>

ECDC assessment:

Sporadic human cases infected with an influenza virus of swine origin have been reported from several countries globally. To date, no human-to-human transmission has been detected. Exposure to pigs or pig products have been reported in the past and represent the most common risk factor. Transmission events have also been observed in healthy people without underlying conditions. All cases need to be thoroughly followed up to exclude human-to-human transmission and implement control measures. Influenza viruses from patients with severe infection should be further characterised, as well as shared with the national influenza reference laboratories and World Health Organization (WHO) Collaborating Centres.

Actions:

ECDC is monitoring zoonotic influenza events through its epidemic intelligence activities and disease experts in order to identify significant changes in the epidemiology of the virus. Cases should be immediately reported to the Early Warning and Response System (EWRS) and International Health Regulations (IHR).

ECDC has published guidance in October 2022: <u>Testing and detection of zoonotic influenza virus infections in humans in the EU/EEA</u>, and occupational safety and health measures for those exposed at work and in June 2023 <u>Enhanced surveillance of severe avian influenza virus infections in hospital setting in the EU/EEA</u>.

Sources: 2022-E000482

Last time this event was included in the Weekly CDTR: 29 September 2023

6. Middle East respiratory syndrome coronavirus (MERS-CoV) – Multi-country – Monthly update

Overview:

Update: Since the previous update on 4 March 2024, and as of 3 April, no new MERS-CoV cases have been reported by the World Health Organization (WHO) or national health authorities.

Summary: Since the beginning of 2024, and as of 3 April, no MERS-CoV cases have been reported by WHO or national health authorities. The last reported case was in Saudi Arabia, with date of onset on 26 October 2023.

Since April 2012, and as of 3 April 2024, a total of 2 621 cases of MERS-CoV, including 949 deaths, have been reported by health authorities worldwide.

Sources: ECDC MERS-CoV page | WHO MERS-CoV | ECDC factsheet for professionals | WHO updated global summary and assessment of risk (November 2022) | Qatar MoPH Case #1 | Qatar MoPH Case #2 | FAO MERS-CoV situation update | WHO DON Oman | WHO DON Saudi Arabia | WHO DON UAE | WHO DON Saudi Arabia | WHO IHR | WHO EMRO MERS Situation report

ECDC assessment:

Human cases of MERS-CoV continue to be reported in the Arabian Peninsula. However, the number of new cases detected and reported through surveillance has dropped to the lowest levels since 2014. The risk of sustained human-to-human transmission in Europe remains very low. The current MERS-CoV situation poses a low risk to the EU, as stated in the Rapid Risk Assessment published by ECDC on 29 August 2018, which also provides details on the last case reported in Europe.

ECDC published a technical report, <u>Health emergency preparedness for imported cases of high-consequence infectious diseases</u>, in October 2019, which is still useful for EU Member States wanting to assess their level of preparedness for a disease such as MERS-CoV. ECDC also published <u>Risk assessment guidelines for infectious diseases transmitted on aircraft (RAGIDA) – Middle East respiratory syndrome coronavirus (MERS-CoV) in 22 January 2020.</u>

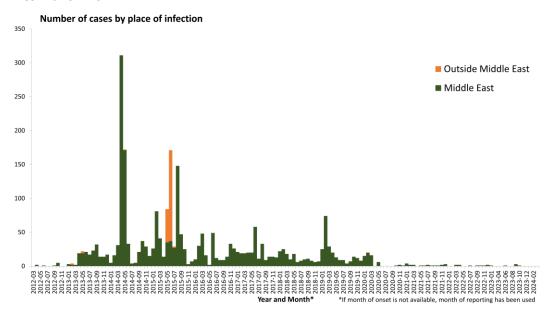
Actions:

ECDC is monitoring this situation through its epidemic intelligence activities and reports on a monthly basis or when new epidemiological information is available.

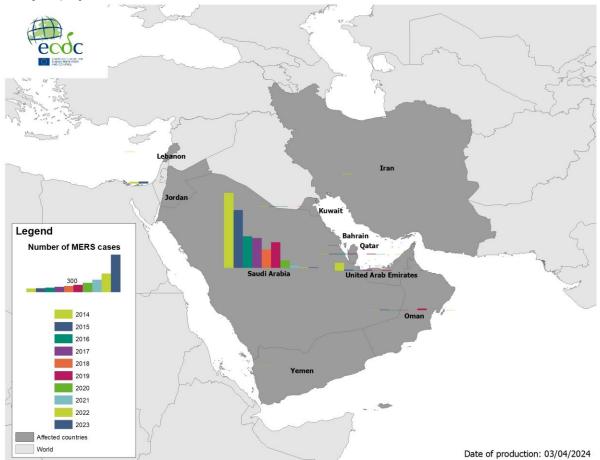
Last time this event was included in the Weekly CDTR: 8 March 2024

Maps and graphs

Figure 1. Confirmed cases of MERS-CoV by place of infection and month of onset, March 2012 to March 2024



Source: ECDC



Source: ECDC