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# Global updates on COVID-19 and other diseases

Prepared by the Science Team, SIDC
Edited by Prof Andrew Kiyu (Faculty of Medicine and Health Sciences, UNIMAS)

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## Summary

- COVID-19 has not reached seasonality.
- The WHO has granted prequalification to Xpert® MTB/RIF Ultra (Cepheid Inc.), a molecular diagnostic test for tuberculosis (TB).
- The WHO reported progress in the fight against soil-transmitted helminths.
- The WHO reported positive trends in global malaria control.
- Malaria remains a threat in the African continent.
- Administrators in Indonesia's new capital Nusantara have begun to make plans to mitigate vector-borne diseases there.
- Dengue cases continue to increase in Malaysia.
- PAHO continues to report increasing incidences of dengue cases.
- Sporadic outbreaks have been reported in multiple countries across Asia.
- Outbreaks of various types of avian influenza continue across the globe.
- New Zealand reported its first case of H7N6 in poultry.
- Human infections of HPAI H5N1 continue to be detected.
- Backyard flocks remain a threat as sources of human avian influenza infection.
- The UKHSA has begun stockpiling vaccines against the H5 avian influenza.
- Mpox remains uncontrollable in the African continent mainly due to the lack of resources.
- Continued diligence is required to control the spread of African swine flu (ASF) in Asia and the rest of the world.
- The US and 8 other countries across Asia and Europe have reported clade Ib MPXV.
- Australia reported an unprecedented outbreak of mpox.
- The WHO continues to make concerted efforts to control mpox in Africa.
- The Marburg outbreak in Rwanda has officially ended.
- The mysterious outbreak in the DRC is linked to severe malaria co-infection and malnutrition.

- The pandemic agreement has not been finalised in 2024.

# 1.0 COVID-19 and related issues

## 1.1 World Health Organization updates

Periodic waves of COVID-19 occur in some countries as the SARS-CoV-2 virus continues circulating. Currently, there is no indication of links to seasonality. The virus can cause severe acute disease, and the outcome of the infection is post-COVID condition (PCC)[Footnote1]. Changes to national policies, resources and access to countermeasures, and the circulating variant cause variations in the impact of the virus.

During the 14 October to 10 November 2024 (28-day) reporting period, the SARS-CoV-2 virus positivity reduced (from 13.6% to 10.8%). Globally, 77 countries reported COVID-19 cases and 27 countries reported deaths; the number of reported cases decreased by 39% while the number of new deaths by 36%. However, note that the actual number of countries experiencing cases or deaths may not be accurately represented, as many have either halted or altered their reporting schedules. Additionally, the trends in newly reported cases and deaths should be approached with caution due to reduced testing and sequencing, as well as reporting delays in numerous countries. Wastewater surveillance (WWS), reported by about 30 countries in 5 WHO regions, has estimated the circulation of the SARS-CoV-2 virus as approximately 2 – 19 times higher than identified and reported cases.[2]

As of December 2024, KP.3.1.1, is the most prevalent Omicron JN.1 descendent, followed by XEC, the latest designated variants under monitoring (VUMs), which is increasing in prevalence. It is currently the only VUM (of 6 circulating) with increasing prevalence globally. This variant is a recombinant of two Omicon JN.1 lineages, KS.1.1 and KP.3.3. It was first detected in late June 2024 and was designated as a VUM on 24 September 2024. The World Health Organization (WHO) risk assessment for the XEC is low based on the public health risk posed by the variant relative to others circulating. According to the WHO's Technical Advisory Group on Virus Evolution (TAG-VE), because of its limited escape from JN.1- or KP.2-based booster vaccines, the continued spread from the XEC variant alone is unlikely to increase the burden on national public health systems compared to other Omicron sublineages. The WHO and TAG-VE continue to recommend Member States to address the uncertainties related to antibody escape and disease severity. [3]

## 1.2 Centers for Disease Control and Prevention updates

COVID-19 indicators – shown by wastewater detections, emergency department (ED) visits, and test positivity – have started to rise from low levels. It is predicted that COVID-19 illness

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[1] Also known as long-COVID (LC) or post-COVID syndrome (PCS). It represents a myriad of symptoms that can persist long after a SARS-CoV-2 infection. [1]

levels will increase in the coming colder (winter) months. However, it is not expected to rise above that in previous winters.[4,5]

According to the latest estimates by the CDC, in 2023, approximately 8.4% of adults in the US reported having experienced long-COVID (LC, or post-COVID condition, PCC), while those who currently suffered from the condition or currently had activity-limiting LC were both < 4%. The outcome was based on 29,522 adult respondents to the National Health Interview Survey.[6] Serological data from the CDC revealed that by the end of 2023, approximately 87.2% of Americans had infection-induced antibodies to the SARS-CoV-2 virus (indicating past infection).[7]

Previous studies published this year reported differing prevalences of LC – generally higher than the current study. This was mainly because of differing study designs used, for example, the definition of LC used, target population, predominant SARS-CoV-2 variant, and vaccination rates, among the few.[6,8–12]

Regardless of this, when extrapolated to the entire US population, the current study suggests that LC is a serious problem that demands attention.

### 1.3 European Centre for Disease Prevention and Contol updates

According to the latest European Centre for Disease Prevention and Contol (ECDC) Communicable Disease Threats Reports (CDTR) and the European Respiratory Virus Surveillance Summary (ERVISS), in general, consultation rates for acute respiratory illness (ARI) and influenza-like illness (ILI) have been increasing in several countries in recent weeks. However, the rates of severe acute respiratory illness (SARI) are similar to, or lower than, levels observed at weeks 50 – 52 during previous years. Influenza and respiratory syncytial virus (RSV) activities are increasing.

The SARS-CoV-2 virus activity continues to decrease; however, it remains elevated in some reporting countries, with individuals aged ≥ 65 years at greatest risk of severe disease. Disease severity continues to decrease or remain stable in the EU/EEA, with levels lower than observed in 2023. However, the agency emphasises that countries continue monitoring the impact of the virus at national and regional levels; this includes submitting genetic sequences from COVID-19-positive cases to the Global Initiative on Sharing All Influenza Data (GISAID) and/or The European Surveillance System (TESSy).[13–15]

### 1.4 Singapore

The Ministry of Health (MOH) continues to remind the public that the SARS-CoV-2 virus still circulates in communities and remains a global health risk. The MOH has also updated the availability of COVID-19 vaccines as the supply of the (older) Omicron XBB.1.5 variant-based version has ended, and current stocks will expire on 31 December 2024. The public will continue to have access to the updated JN.1-based mRNA vaccines (Pfizer-

BioNTech/Comirnaty and Moderna/Spikevax) under the National Vaccination Programme (NPV).[16,17]

## 2.0 Tuberculosis

The WHO has granted prequalification to Xpert® MTB/RIF Ultra (Cepheid Inc.), a molecular diagnostic test for tuberculosis (TB). It is the first test for TB diagnosis and antibiotic susceptibility testing that meets the WHO's prequalification standards. It detects the genetic material of *Mycobacterium tuberculosis* in sputum samples and provides results within hours. It also identifies mutations associated with rifampicin resistance, which is a key indicator of multidrug-resistant TB.[18]

The prequalification supports countries in scaling up and accelerating access to high-quality TB assays that meet both WHO recommendations and its stringent quality, safety and performance standards.

The WHO's assessment for prequalification of Xpert MTB/RIF Ultra was based on information submitted by the manufacturer, and reviewed by Singapore's Health Sciences Authority. To improve access to quality-assured TB tests and expand diagnostic options for countries, the WHO is currently assessing 7 additional TB tests.

## 3.0 Soil-transmitted helminth, update from the World Health Organization

The WHO's 2023 report on soil-transmitted helminthiasis (STH) highlights progress in fighting helminth infections. A key approach is Preventive Chemotherapy (PC), which involves regularly giving medicine to at-risk groups to stop these infections and reduce their impact, aiming to eventually eliminate the disease.[19]

In 2023, 86 countries needed PC for STH, affecting 253.1 million pre-school-age children (pre-SAC) and 623.1 million school-age children (SAC). Additionally, 247 million women of reproductive age (WRA) also needed treatment. In total, 451.4 million children (97.7 million pre-SAC and 353.7 million SAC) received PC in 2023, giving a global coverage rate of 51.5% (38.6% for pre-SAC and 56.8% for SAC). An estimated 111.8 million women received STH treatment through lymphatic filariasis programmes. In Southeast Asia, 63.8% of children (308.2 million) were covered by PC. India treated the most children (200.7 million), followed by Indonesia (50.2 million) and Bangladesh (38.3 million). India also treated 57.1 million adolescents (ages 15-18 years) with albendazole, however, these treatments are not included in global reports, as the global target for STH treatment is for those < 15 years old.

The agency advises countries with high levels of STH to gather data after 5 years of giving PC (with ≥75% coverage) to assess the impact and improve strategies. The WHO's 2024 framework for monitoring and evaluating STH programmes helps countries strengthen their control efforts and track their progress. Over the past 20 years, 31 out of the 86 affected countries have given over 10 years of treatment. In June 2024, the WHO introduced new guidelines for controlling strongyloidiasis, another type of helminth infection.[20] These guidelines recommend giving ivermectin (200 µg/kg) annually to all people aged ≥ 5 years old in areas where strongyloidiasis is common (prevalence ≥ 5%). The WHO also encourages countries to understand the disease better, improve testing, and expand treatment programmes.

PC remains a key tool in fighting helminth infections. As countries continue to improve their treatment programmes and follow the new guidelines, ongoing efforts to strengthen monitoring and increase coverage will be essential to reduce the spread of these diseases. By taking these actions, significant progress can be made toward achieving global health goals and ensuring a healthier future for all at-risk groups.

# 4.0 Vector-borne diseases

## 4.1 Malaria

### 4.1.1 World Malaria Report 2024

The World Malaria Report (WMR) highlights positive trends in global malaria control with emphasis on the ongoing challenges. Since 2000, approximately 2.2 billion cases and 12.7 million deaths have been averted. However, malaria remains a significant global health threat, particularly in the WHO African Region. In 2023, there were an estimated 263 million malaria cases and 597,000 deaths globally, with 95% of the deaths occurring in Africa.[21]

Despite progress, the disease's incidence rate in 2023 was 60.4 cases per 1,000 population- three times higher than the target rate of 21.3 needed to reach the 2025 goal of reducing case incidence and death rates by 75%. Similarly, the death rate was 13.7 per 100,000 population, exceeding the target of 5.5.

Countries face several challenges, including fragile health systems, weak surveillance, funding gaps, and rising threats such as drug and insecticide resistance. Additional challenges come from conflict, climate change, and displacement.

Notable advancements include the rollout of the WHO-recommended malaria vaccines in 17 African countries, including Nigeria, and the widespread use of improved insecticide-treated nets (ITNs). In 2023, seasonal malaria chemoprevention reached 53 million African children, a significant increase from just 170,000 in 2012.

### 4.1.2 Vaccines

Two new malaria vaccines[Footnote2], projected to save 180,000 children's lives by 2030, were introduced in 2024 after decades of research. However, an estimated 2.5 million children will remain unvaccinated and die from malaria due to limited funding. Nigeria, which accounts for a third of global malaria deaths, has a health budget of USD10 per capita and cannot afford

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[2] Current vaccines against malaria are targetted towards *P. falciparum*, the main malaria parasite that circulates in the African Region and the main cause of global deaths from malaria. [22,23]

the USD15 per child cost for the R21\Matrix-M vaccine (co-developed by the University of Oxford and the Serum Institute of India, SSI). Poorer countries, such as the Democratic Republic of Congo (DRC), face challenges in ensuring vaccine uptake without extra spending on outreach and cold-chain management. Despite these financial hurdles, malaria vaccines are cost-effective at USD2-4 per life saved, making them a highly efficient health investment. To fully roll out vaccines would require USD2 to USD3 billion more than Gavi's current malaria budget over the next 5 years.[24]

Seventeen African countries, representing 70% of the global malaria burden, have begun offering malaria vaccines through routine childhood immunisation programmes. Over 12 million vaccine doses have been delivered since 2023, co-funded by the United Nations Children's Fund (UNICEF), Gavi, the Vaccine Alliance, and the countries themselves. In 2024, 14 countries introduced the vaccines, with an additional 8 to join in 2025. The RTS,S malaria vaccine (or RTS,S/AS01, trade name Mosquirix; GSK) recommended by WHO in 2021, has reduced child deaths by 13% in Ghana, Kenya, and Malawi and reached over 3 million children. The WHO also recommends the R21/Matrix-M vaccine for high-risk areas.[25–27]

While UNICEF plays a crucial role in ensuring the timely delivery of vaccines by forecasting needs, securing financing, and establishing supplier contracts, health workers are key to the success of these programmes: raising awareness, administering vaccines, and ensuring follow-up, driven by their own experiences with malaria's impact on their communities. The WHO's peer-learning workshops emphasise community engagement as key to increasing vaccine uptake.

To maximise impact, the malaria vaccine is combined with other WHO-recommended interventions, including ITNs, chemoprevention, and indoor spraying, tailored to local needs. The vaccine, which requires four doses for full protection, is being introduced alongside vaccines for pneumococcal disease and rotavirus as part of a broader effort to reduce child mortality in Africa.

### 4.1.3 Other updates

To date, a total of 44 countries and 1 territory have been awarded a malaria-free status by the WHO with Cabo Verde and Egypt joining the list in 2024.[28]

In 2024, the Global Malaria Programme published guidance that spanned a range of technical areas including a field guide on community-based deployment of intermittent preventive treatment of malaria during pregnancy (IPTp-SP)[29], controlling malaria vectors through indoor residual spraying[30], response plan for *Plasmodium falciparum* mutation[31], and implementation guide on multiple first-line therapies.[32]

### 4.1.4 Indonesia, mitigating risks of malaria and other vector-borne diseases in the new capital city

Large-scale infrastructure projects, such as Indonesia's new capital, Ibu Kota Nusantara (IKN), present emerging risks for malaria and other vector-borne diseases. Deforestation and urbanisation in malaria-endemic areas heighten the risk of zoonotic diseases such as *P. knowlesi* and malaria transmission. Environmental changes may also contribute to the spread of diseases like dengue and chikungunya, necessitating enhanced surveillance and control measures.[33]

Proactive disease surveillance and control, such as the IKN Malaria Free Task Force established in 2024, are crucial to mitigate these risks. This task force implements malaria screening, vector control, and surveillance, especially for high-risk groups (for example, migrant workers). Despite challenges with undocumented workers and environmental changes, a pilot programme targeting these issues will be expanded in 2025.

Further research is needed to understand the risks of malaria and emerging vector-borne diseases, particularly in the context of environmental changes and human mobility. Remote sensing and artificial intelligence (AI) tools present new opportunities to monitor these risks and improve surveillance and control measures. It was noted that large-scale infrastructure projects such as IKN must balance economic development, conservation, and public health goals, with cross-border collaboration and multidisciplinary approaches necessary to address the spread of diseases beyond IKN into surrounding regions.

### 4.1.5 Enhancing decision-making for malaria elimination, study findings

A high sensitivity and specificity surveillance system is required to assess local malaria elimination accurately. The current WHO standard for declaring malaria elimination – observing no locally acquired cases for 3 consecutive years – can lead to premature relaxation of control measures, risking resurgence.

A team of researchers from Scotland, Indonesia and the US developed a statistical inference framework that efficiently models four key components: spatial patterns, dynamic temporal patterns, an observation process, and an epidemiological process to improve decision-making for malaria elimination by providing health systems with a tool that more accurately captures the complexities of disease transmission and detection. The goal is to enhance resource allocation and contribute to the ultimate eradication of malaria. The study also highlighted the limitations of the traditional elimination criteria, which can misinterpret ongoing transmission and put communities at risk. It calls for a reassessment of current methods for confirming malaria elimination, emphasising the need for comprehensive modelling to guide decisions and maintain surveillance effectiveness.[34]

## 4.2 Dengue

### 4.2.1 World Health Organization/Pan American Health Organization updates

#### *4.2.1.1 Malaysia*

The number of dengue cases in Malaysia increased from 1,384 in epidemiology week 50 (EW50/2024; 8 – 14 December 2024) to 1,407 in EW51/2024 (15 – 21 December 2024). The total cumulative cases increased to 121,082, compared to 120,418 in the same period of 2023. Two fatalities due to dengue complications were reported, bringing the death toll to 116 for 2024, up from 96 in 2023. Although the number of cases has risen, the number of hotspot localities has decreased from 27 to 18. The hotspots were predominantly in Selangor, Negeri Sembilan, Kuala Lumpur, Putrajaya, Pahang, and Penang. Health authorities are urging the public to eliminate mosquito breeding sites, particularly during the holiday season, when increased movement could aid in the spread of dengue.[35]

#### *4.2.1.2 Report on the epidemiological situation of dengue in the Americas*

According to the latest updates from the Pan American Health Organization (PAHO), up to EW48/2024, a total of 12,780,728 suspected dengue cases were reported across the region, marking a significant increase of 195% compared to 2023 and 371% compared to the average of the last 5 years. Out of these, 53% were laboratory-confirmed, and 0.17% were classified as severe dengue, resulting in 7,822 fatalities and a case fatality rate (CFR) of 0.061%.[36]

In EW48/2024, 20 countries and territories reported 57,267 new suspected cases, with 223 classified as severe dengue and 49 deaths, yielding a CFR of 0.085%. Region-specific data includes:

- Central America and Mexico:
  17,131 new suspected cases, showing an 83% increase compared to the same week in 2023 and a 198% increase compared to the last five years.
- Caribbean:
  993 new suspected cases, with a 27% decrease compared to 2023 but a 30% increase compared to the five-year average.
- Andean:[Footnote3]
  6,684 new suspected cases, reflecting a 22% increase from 2023 and a 170% increase from the five-year average.
- Southern Cone: [Footnote4]
  32,459 new suspected cases, with a 252% increase from 2023 and a 435% increase from the five-year average, particularly driven by Brazil.

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[3] Area which runs along the western coast of South America including Columbia, Ecuador, Peru, Bolivia, Chile and Argentina.

[4] Geographic regions located in the southern part of South America, encompass Argentina, Chile, Uruguay, and parts of Paraguay and Brazil.

# 5.0 Rabies

## 5.1 Regional Developments: Southeast Asia

In Southeast Asia, rabies remains endemic in several countries, with new outbreaks reported in rural and remote areas.

### 5.1.1 Sarawak, Malaysia

Sarawak reported two cases in December 2024 involving a pet dog and a rabid cat. Local authorities have urged the public to remain vigilant, avoid contact with stray animals, and ensure their pets are vaccinated. Public education campaigns have been intensified to inform communities about the risks of rabies and the importance of seeking immediate medication attention if exposed. Vaccination drives for domestic pets and efforts to manage stray animal populations are part of the state's ongoing response to the situation. [37]

### 5.1.2 VietNam

Over 80 rabies-induced (human) deaths were recorded in 2024, with two particularly tragic incidents highlighting the severity of the issue. An 11-year-old boy succumbed to rabies two months after being bitten by a rabid dog due to delayed medical intervention.[38] Similarly, the owner of a dog meat restaurant died after being bitten by a rabid dog [39], reflecting the gaps in public awareness and vaccine accessibility. These cases emphasise the need for enhanced public education on the urgency of post-exposure prophylaxis (PEP).

### 5.1.3 India

In Thane, India, a 27-year-old man succumbed to rabies after delaying the administration of a rabies vaccine following bites from a stray dog and cat. This tragic incident, attributed to a lack of awareness and prompt action, underscores the critical importance of immediate medical attention post-exposure.[40]

### 5.1.4 China

A recent rabies death in Changsha County, Hubei, linked to a bite from a pet dog has raised concerns. The Changsha County Center for Disease Control and Prevention (CDC) has confirmed this fatal rabies case. Local authorities are urging vaccinations for domestic dogs and controlling stray populations. China faces a high rabies death toll, largely due to low vaccination rates. Experts recommend immediate rabies vaccination for anyone bitten and highlight the need for regular pet vaccinations.[41]

## 5.2 Global Perspective

The WHO and the Global Alliance for Rabies Control (GARC) have reaffirmed their commitment to the "Zero by 30" strategy, which aims to eliminate human deaths from dog-mediated rabies by 2030. For 2024, their efforts focused on increasing community engagement, scaling up mass dog vaccination campaigns, and improving access to post-exposure prophylaxis (PEP), particularly in underserved regions. Rabies prevention programmes continue to emphasise the interconnectedness of human and animal health, reinforcing the need for a One Health approach. [42]

# 6.0 African swine flu

## 6.1 Situation update: Asia-Pacific region

The African swine flu (ASF) situation in Southeast Asia is summarised as follows (**Table 1**) from reports from the Food and Agriculture Organization (FAO) and the World Organisation for Animal Health (WOAH). [43,44]

**Table 1**. Country-wise ASF outbreaks in 2024 in the Asia-Pacific region. The information was extracted from the ASF situation in Asia & Pacific update.

| REGION | COUNTRY/ AREA | SITUATION UPDATE |
|---|---|---|
| EAST ASIA | Republic of Korea (South Korea) | A total of 4,200 wild boar were confirmed affected as of 6 December 2024.[45] The number has increased by 21 since 13 November 2024. |
| | China | The Agriculture and Rural Affairs Department of Guangxi Zhuang Autonomous Region reported that monitoring results revealed the continued presence of ASF virus contamination in various locations, including harmless treatment plants, slaughterhouses, farmers' markets, and farms, albeit at a lower level. Additionally, nucleic acid detection was observed in some parts of the breeding environment. [46] |
| SOUTHEAST ASIA | The Philippines | A total of 365 barangays in 19 provinces are active as of 6 December 2024. [47] |
| | Malaysia | An outbreak in December 2024 in Serian, Sarawak, has led to the culling of all pigs in affected backyard farms at Kampung Mapu and Bunan to contain the spread. [48–50]<br>The Department of Veterinary Services Sarawak (DVSS) compensates farmers and emphasises stricter biosecurity measures, including movement controls, proper fencing, and avoiding uncooked feed. Farmers are urged to promptly report any ASF symptoms, such as fever, skin issues, and respiratory distress. |
| | Indonesia | Indonesia is on the alert after the situation reports from Sarawak were shared with their authorities. The West Kalimantan Animal, Fish and Plant Quarantine Center (BKHIT) PLBN Nanga Badau Satpel (*Balai Karantina Hewan, Ikan dan* |

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|---|---|---|
| | | *Tumbuhan (BKHIT) Kalimantan Barat Satpel PLBN Nanga Badau*) together with CIQS PLBN Badau, RI-MLY Pamtas Task Force and Forkopimcam (*Satgas Pamtas RI-MLY* and *Forkopimcam*) have been monitoring the situation at areas bordering Indonesia and Sarawak for signs of the disease.[51]<br>In mid-December 2024, Indonesian authorities reported that multiple cases of ASF had been detected in 32 of 38 Indonesian provinces, including key pig farming regions such as Bali, North Sumatra, East Nusa Tenggara, and Papua. They also noted that the highest density of cases was in the provinces of East Nusa Tenggara, North Kalimantan, South Sulawesi and Riau, and urged local leaders to boost awareness and report more cases to authorities. The outbreak has led to the deaths of thousands of pigs, impacting pork supply during the year-end holiday season. The government plans to establish a task force by the end of 2024 to address the outbreak. [52,53] |
| | VietNam | ASF re-emerged in Cho Moi District, Bac Kan Province, and affected 6 villages. [54]<br>In Central VietNam's Nghe An Province, the outbreaks surged following two typhoons in September. By 2 December 2024, 250 outbreaks had been confirmed in the province. [55]<br>Pu Mat National Park, located in the north-central VietNam, which spans Anh Son, Con Cuong, and Tuong Duong districts in Nghe An, reported 21 wild boar deaths during November 2024 patrols, raising concerns about potential disease circulation within the wild boar population. [56] |
| SOUTH ASIA | Nepal | ASF was confirmed in Lalitpur, Nepal, with over 200 pig deaths reported in Chunikhel and the Nakkhu River corridor. The disease has been spreading since October 2024, prompting authorities to urge strict biosecurity measures. [57,58] |
| | India | Between January and 2 December 2024, a total of 14,807 pigs have died, and at least 24,090 pigs have been culled. In Mizoram State, 6 additional pig deaths were attributed to ASF. [59] |
| | Sri Lanka | ASF has been confirmed in the Western Province (Ganemulla and Ja-Ela towns) and the North Western Province (Madampe Town), with vehicles and swill feeding identified as sources of infection. [60] |

# 7.0 Avian influenza

## 7.1 Human cases

### 7.1.1 H5N1

### *7.1.1.1 The US, multistate*

Louisiana reported the first severe human case of H5N1 on 13 December 2024. The 65-year-old patient had contact with sick and dead birds in a backyard flock and was infected with the D1.1 genotype of the virus. This genotype differs from the B3.13 genotype detected among dairy cows, sporadic human cases in multiple states and some poultry outbreaks in the US. This is the first case of H5N1 bird flu in the US that has been linked to exposure to a backyard flock. A sporadic case of severe H5N1 bird flu illness in a person is not unexpected. The virus has previously been associated with severe human illness in other countries in 2024 and the years before, including illness resulting in death. No human-to-human transmission has been detected. The CDC's overall assessment of immediate risk to the public's health from avian influenza remains low. [61]

The Wisconsin Department of Health Services reported the state's first human case of H5N1. This occurred in an adult who worked at a poultry facility where the virus had been detected in birds. The individual experienced respiratory symptoms and tested positive for influenza A(H5) virus through state and CDC laboratory testing.[62–64]

The Iowa Department of Health and Human Services reported the state's first human case of H5N1. This occurred in an adult who worked at a poultry facility where the virus had been detected in birds. The individual experienced conjunctivitis and respiratory symptoms and tested positive for influenza A(H5) virus through state and CDC laboratory testing. [62]

On 18 December 2024, the California Department of Public Health reported three cases of H5N1 in adult workers employed at commercial dairy cattle farms located in regions where the virus had been detected in cows. These individuals experienced mild symptoms and voluntarily reported their health concerns to local health officials.[62]

As of 31 December 2024, there have been 66 confirmed cases of human infection in the US.[65]

Update on sequencing H5N1 bird flu infection in a child in California on 22 November 2024

Initial sequencing efforts were challenging due to low viral RNA levels in the patient's sample. However, researchers used advanced techniques to obtain partial viral gene sequences, including full-length neuraminidase and nucleoprotein genes. Subsequent analysis of limited viral gene sequences revealed the virus to be a clade 2.3.4.4b H5N1 that is closely related to those found in dairy cattle and poultry in the US. Phylogenetic analysis showed similarity to influenza A (H5N1) or the highly pathogenic avian influenza (HPAI) viruses from previous human infections in dairy workers in California. The virus showed no signs of concerning mutations that might increase its infectivity or transmissibility in humans or reduce its susceptibility to antivirals. While the source of the child's exposure remains unidentified, these findings indicate that the virus detected in this case is similar to most other H5N1 viruses circulating in the US and does not pose a significant public health concern. [66]

### *7.1.1.2 VietNam*

In early December 2024, a case of H5N1 was reported in an 18-year-old man in Long An province. The patient is was hospitalised in Ho Chi Minh City with severe pneumonia and respiratory failure after experiencing symptoms such as fever, headache, and muscle pain. Chest X-ray revealed alveolar damage in both lungs. The patient was subsequently transferred to the Ho Chi Minh City Hospital for Tropical Diseases for further treatment and was reported to be in stable condition. Following initial reports of severe pneumonia, the Long An Center for Disease Control (CDC) collected samples from the patient and sent them to the Pasteur Institute in Ho Chi Minh City for testing. The results confirmed the presence of influenza A(H5N1) virus. Investigations conducted at the patient's residence revealed a significant number of dead poultry, suggesting potential exposure. This information was initially reported by foreign language media outlets and subsequently shared on the *FluTrackers* infectious disease news message board. [67–69]

### *7.1.1.3 Canada, update on the critically ill teenager with the H5N1 on November 2024*

Canadian public health officials have concluded their investigation into the critically ill teenager infected with H5N1 avian influenza. Despite thorough investigations, the source of infection remains unidentified. While the patient's pet dog was ill concurrently, investigations ruled out H5N1 infection in the animal. Genetic analysis revealed that the patient was infected with a clade 2.3.4.4b H5N1 strain that closely matches those found in wild birds in the Fraser Valley, unrelated to poultry farm outbreaks. Notably, the investigation identified genetic mutations in the virus, including one potentially enhancing its ability to bind to lung receptors and cause severe illness. [70]

### **7.1.2 H9N2**

#### *China*

From 6 to 12 December 2024, two cases of human infection with H9N2 were reported from China. The first case was a one-year-old girl from Guizhou Province who experienced mild symptoms after contact with backyard poultry. The second case, also a one-year-old girl from Guangxi Province, developed mild symptoms following exposure at a live poultry market. Both cases have since recovered. Investigations revealed no epidemiological link between the cases or any family clusters. Samples from backyard poultry in the first case and the live poultry market in the second case tested positive for the virus, while all human contacts in both instances tested negative. [71]

## 7.2 Outbreaks in animals

Multiple outbreaks were reported across the globe in December 2024, simplified as follows.

## 7.2.1 H5N1

### *7.2.1.1 Asia/Western-Pacific*

#### 7.2.1.1.1 Japan

An H5N1 outbreak was reported in Kawaminami-Town, Miyazaki Prefecture to the World Organisation for Animal Health (WOAH). The outbreak, which occurred on 9 December 2024, resulted in the infection and subsequent death of 955 domestic birds. As a response, all affected birds were culled and disposed of, and all necessary control measures at the outbreak site were implemented. [71,72]

A broiler farm in Kagoshima Prefecture reported increased mortality in their flock on 19 December. Subsequent testing by the Livestock Hygiene Service Center confirmed the presence of influenza A virus. Further analysis by RT-PCR and rRT-PCR on 20 December identified the virus as H5 subtype. Immediate response measures were implemented, including movement and shipment restrictions within 3 km and 10 km radii of the affected farm. The stamping-out of the infected flock and disinfection measures were completed by 23 December 2024. On 26 December 2024, the National Institute of Animal Health confirmed the virus subtype as H5N1.[73]

#### 7.2.1.1.2 (South) Korea

Positive cases of H5N1 from wildlife species in Sangsin-gil, Daesowon-myeon, Haemajihaean-ro, Wondang-gil and Ojo-ro. [74]

#### 7.2.1.1.3 Chinese Taipei

A positive case of H5N1, specifically clade 2.3.4.4b of the Fully Eurasian lineage, was detected in a wild Black-faced Spoonbill. The bird was found at locations including kilometre 276 southbound on Route 61 in Budai Township and the coastal road west of Budai Township as well as from Tainan Black-Faced Spoonbill Conservation Association, Taiwan Biodiversity Research Institute, and Tainan City Bird organisation. The deceased bird was subsequently transferred to the animal protection department for inspection. [75]

The H5N1 virus, specifically Clade 2.3.4.4b of the Fully Eurasian lineage, was detected from meat geese poultry in Tainan. [76]

#### 7.2.1.1.4 India

A positive case of H5N1 in multiple regions in Kerala from poultry farms, as confirmed by the National Institute of High-Security Animal Diseases (NIHSAD), Bhopal, India. [77]

### *7.2.1.2 The Americas*

#### 7.2.1.2.1 The US

A State of Emergency was declared in California to expedite the state's response to the Avian influenza A (H5N1) outbreak. This decision follows the detection of cases of dairy cows on farms in Southern California. As of 19 December, The US Department of Agriculture (USDA) has confirmed H5N1 avian influenza in 266 dairy farms in California over the past 30 days, following investigations by the California Department of Food and Agriculture (CDFA) and rapid disease detection by the California Animal Health and Food Safety Laboratory System (CAHFS). [78,79]

H5N1 outbreaks have been reported across several US states, impacting both commercial and backyard flocks. In Michigan, the virus was detected in two commercial turkey operations in Ottawa County, affecting a total of 188,700 birds. Additionally, three backyard flocks and two commercial poultry facilities, including a layer farm with approximately 1 million birds, tested positive in Michigan, Ohio, as well as California. Ohio also experienced a second HPAI detection in December 2024, while Missouri reported an outbreak in a backyard flock of 70 birds in Pemiscot County. [80]

The USDA's Animal and Plant Health Inspection Service (APHIS) has confirmed 32 new outbreaks of H5N1 in dairy cattle on 12 December 2024, and 13 new outbreaks on 14 December 2024[81], all located in California, bringing the state's total to 630 affected farms and the national total to 845 across 16 states. APHIS has also confirmed additional outbreaks in poultry across 5 states. In California, the virus impacted a large-scale broiler farm in Tulare County with > 330,000 birds, along with a duck breeder in Stanislaus County and another farm in Kern County. Missouri reported two new outbreaks, one on a commercial farm in Daviess County and another in a backyard flock in Cedar County. South Dakota, which has experienced significant recent outbreaks in turkey farms, reported three new cases in Beadle, Charles Mix, and Moody counties. Finally, Colorado and Idaho each reported outbreaks in backyard flocks, specifically in La Plata County, Colorado, and Jefferson County, Idaho. [82] H5N1 outbreaks were reported in two backyard flocks in Arkansas (Craighead and Pope counties) and on commercial turkey farms in Sac County, Iowa, and Kingsbury County, South Dakota. [81]

Notably, 5 new mammalian cases were reported, including a polar bear in Alaska, a mountain lion in Montana, and a domestic cat, a mouse, and a coyote in California and Washington, respectively. [81]

A breakdown of the infection involving cats is summarised in **Table 2.** These cases represent the first confirmed H5 bird flu infection in cats in the US. Furthermore, these are the first reported cases of animal illness resulting from the ingestion of raw milk purchased from a store before it was recalled due to H5 avian influenza contamination. To date, no evidence of cat-to-cat, cat-to-human, or human-to-human spread of the H5 avian influenza has been observed. The risk to the general public remains low.

**Table 2.** First confirmed instances of H5 bird flu infection in cats in the US summarised from multiple reports.

| Location | Details of the cases |
|---|---|
| California | 8 cats in a single household in Los Angeles County consumed raw milk from Raw Farm, LLC, which was later recalled due to H5N1 avian influenza contamination. |

| Location | Details of the cases |
|---|---|
| | 7 of these cats subsequently became ill, exhibiting symptoms such as fever, lethargy, anorexia, and neurologic issues; 5 cats died or were euthanised, while the remaining two were under quarantine and improving. PCR testing confirmed H5N1 avian influenza infection in four deceased cats, with viral sequencing matching the contaminated milk. These cases represent the first confirmed H5N1 infection in cats within Los Angeles County and highlight the potential risk of consuming contaminated raw milk. [83]<br>Veterinary Public Health in Los Angeles County is investigating an illness outbreak in 5 indoor-only cats suspected to have consumed two different raw pet food diets containing raw poultry and beef. Two cats developed acute respiratory distress and were euthanised, while others exhibited lethargy, reduced appetite, and various ocular and neurologic issues. One cat tested presumptive positive for Influenza A and Feline Calicivirus, and subsequent testing at the California Animal Health and Food Safety (CAHFS) Laboratory confirmed the presence of H5 avian influenza. [83,84]<br>As of 23 December 2024, the Santa Barbara County Public Health Department announced the confirmation of two cases of H5 avian influenza in domesticated cats from separate households. Following a positive influenza A test, both cats experienced severe neurological illness and unfortunately died. The source of infection for these cases is currently under investigation. [85,86] |
| Oregon | The Oregon Department of Agriculture reported that a house cat died from H5N1 avian influenza after consuming raw frozen pet food produced by Northwest Naturals. This led to a voluntary recall of the company's 2lb *Feline Turkey Recipe raw & frozen pet food*, which was distributed nationwide across 12 states and in British Columbia. Genetic testing confirmed a match between the virus in the cat and the virus found in the recalled pet food. Oregon's state veterinarian emphasised that the cat was strictly indoor and therefore likely contracted the virus solely from the contaminated food. [85] |
| Washington | On 25 December 2024, animal health officials confirmed a devastating outbreak of HPAI H5N1 at the Wild Felid Advocacy Center of Washington. Between late November and mid-December, 20 big cats, including a half-Bengal tiger and four cougars, succumbed to the virus. Three cats have recovered, while one remains critically ill. The outbreak began with the death of a cougar on 23 November 2024, prompting immediate concern as other cats began to exhibit signs of illness. An African serval was the last cat to succumb to the virus on 13 December. The remaining 17 cats at the sanctuary are currently being closely monitored. |

| Location | Details of the cases |
|---|---|
| | The following wild cats have died: 1 Bengal Tiger, 4 Cougars, 1 African Caracal, 2 Canada Lynx, 1 Geoffroy Cat, 1 Bengal Cat, 1 Eurasian Lynx, 4 Bobcats, 5 African Servals[87]. The centre is working with officials to determine the origin of the outbreak. Possible entry points for the virus include contaminated wild bird droppings entering cat habitats or the presence of the virus in the meat used to feed the animals. As a precautionary measure, the sanctuary removed 8,000 pounds (~3,628.7 kg) of stored food and initiated a thorough sanitation process, which is expected to take several months to complete. [88] |

The H5 subtype of avian influenza was detected via wastewater monitoring in Maricopa County, Arizona. However, no human cases have been identified. This detection occurred across all three cities within the county conducting wastewater monitoring: Phoenix, Surprise, and Tempe. Genetic analysis indicates that the virus is related to that circulating in wild birds, distinct from the strain affecting dairy cattle, which has not been found in Arizona. Though the precise source location of the wastewater detections remains unknown, officials emphasised that the overall risk of avian influenza to humans in Maricopa County currently remains low due to the absence of human cases and limited evidence of human-to-human transmission. [80]

#### 7.2.1.2.2 Mexico

H5N1 was detected in two falcons used for wild duck hunting in Aguascalientes, Mexico. These birds presented with clinical signs including hyporexia, lethargy, emesis, dyspnea, and paralysis. A veterinarian was consulted, and the falcons were immediately isolated as a precautionary measure. [89]

#### 7.2.1.2.3 Falkland Islands

An H5N1 was detected in wild animals, namely, a Southern elephant seal [90] and Gentoo penguins at three different locations. [91]

#### 7.2.1.2.4 Columbia

An H5N1 outbreak was reported in backyard ducks and hens on a farm in Familia Borja De La Rosa in Corral Viejo, Remolino, Magdalena. In response, birds in contact with the infected flock were culled. Active epidemiological surveillance was conducted within a 2km radius of this location. This surveillance involved visiting 417 premises, monitoring > 4,000 birds, and collecting samples from 190 birds across different zones. [92]

### *7.2.1.3 The UK and Europe*

#### 7.2.1.3.1 The UK

HPAI H5N1 was confirmed in two commercial poultries near Yorkshire on 28 and 31 December. A 3km protection and 10 km surveillance zone have been declared around the affected premises. All poultry on the premises would be humanely culled. Fifteen HPAI H5N1 outbreaks and one H5N5 outbreak were reported in England since the first confirmed case on 5 November [93].

#### 7.1.2.3.2 France

Two outbreaks of HPAI were reported in the northwestern region of Normandy. These outbreaks occurred on 27 and 28 December, affecting farms with 25,000 and 540 poultry birds, respectively. As a precautionary measure, the entire flocks on both farms have been culled. [94]

A positive case of H5N1, Clade 2.3.4.4b was detected in wild birds at Auvergne-Rhône-Alpes, Île-de-France[95] and Bretagne. [96]

#### 7.2.1.3.3 Germany

Multiple outbreaks of H5N1 were confirmed in December, as follows:

- On 5 December 2024, positive cases were detected in wild birds, including Laridae, Anatidae, and Cygnus, in Hamburg and Bayern. [97]
- On 6 December 2024, outbreaks were confirmed in poultry flocks, including laying hens, in Niedersachsen [98,99], Baden-Württemberg [100], and Schleswig-Holstein.[101]
- On 7 December 2024, outbreaks were detected in poultry flocks, including turkeys for fattening, in Nordrhein-Westfalen [102] and Mecklenburg-Vorpommern. [103]
- On 23 and 27 December 2024, outbreaks were detected in poultry flocks, in Rostock and Prohn, Mecklenburg-Vorpommern. This detection prompted immediate action, which resulted in the culling of 23 birds and the disposal of 40 deceased birds to prevent further spread of the disease. [104]

A positive case of H5 (N Subtypes) was detected in a backyard poultry farm at Lehrberg, Bayern on 23 December 2024. This detection prompted immediate action, resulting in the culling of 15,700 birds and the disposal of 300 deceased birds to prevent further spread of the disease. [105]

#### 7.2.1.3.4 Austria

Multiple outbreaks of H5N1 were confirmed in:

- In Niederösterreich, positive cases were detected in both poultry and wild birds, including Great Egrets and Mute Swans. [106,107]
- In Oberösterreich, Steiermark, and Burgenland, positive cases were detected in wild birds, specifically Mute Swans and Mallards. [106]

#### 7.1.2.3.5 Hungary

Multiple outbreaks of H5N1 were confirmed on 4 December in the following locations:

- Bács-Kiskun county, positive cases were detected in poultry, including *foie gras* geese, breeding ducks, and fattening ducks. [108]

- Békés county, positive cases were detected in a breeding turkey flock. [109]
- Jász-Nagykun-Szolnok county, positive cases were detected in *foie gras* geese, breeding geese, and fattening geese. [110]

#### 7.1.2.3.6 Italy

Multiple outbreaks of H5N1 were confirmed at the following locations: [111]

- Veneto, the virus was detected in several wild bird species, including Eurasian Wigeon, Eurasian Collared-Dove, European Robin, Yellow-legged Gull, and a hunted Common Teal.
- Lombardia, the virus was detected in wild birds such as Western Marsh Harriers, Little Owls, Grey Herons, and hunted Eurasian Wigeon.
- Friuli-Venezia Giulia, the virus was detected in a Mute Swan.
- Italian Exclusive Economic Zone, the virus was detected in a hunted Common Teal.
- Emilia-Romagna, the virus was detected in a hunted Common Teal.
- Outbreaks were confirmed in multiple commercial poultry including a fattening turkey farm in Guidizzolo, Mantua Province, and a multispecies farm in Roncade, Treviso Province. [112]

#### 7.1.2.3.7 The Netherlands

A H5N1 outbreak in both poultry and wild birds in Friesland was reported on 9 December 2024. [113]

#### 7.1.2.3.8 Switzerland

A H5N1 outbreak in wild mute swan on 4 December 2024. [114]

#### 7.1.2.3.9 Czech Republic

Five outbreaks of H5N1 were detected in non-commercial backyard flocks across various regions of the country. [115]

- On 9 December 2024, a case was confirmed in a flock of hens in the Kraj Vysočina region.
- On 10 December 2024, an outbreak occurred in a flock of hens in the Moravskoslezský region.
- A subsequent outbreak was detected in a flock of hens in the Královéhradecký region.
- On 19 December 2024, a case was confirmed in a flock of hens, geese, ducks, quails, guinea fowls, and pigeons in the Karlovarský region.
- Finally, another outbreak was identified on 19 December 2024 in a flock of hens in the Jihomoravský region.

#### 7.1.2.3.10 Poland

A positive case of H5N1 has been detected in a poultry farm at Śląskie on 23 December 2024. [116]

#### 7.1.2.3.11 Slovenia

Six outbreaks of H5N1 were detected in wild Mute Swan across Obalno-kraška, Podravska, Jugovzhodna Slovenija, Pomurska and Osrednjeslovenska regions.[117]

7.1.2.3.12 Portugal

A positive case of H5N1 has been detected from wild Yellow-legged Gull at Olhão. [118]

7.1.2.3.13 Ukraine

A positive case of H5 (N untyped) has been detected from wild Egyptian Goose, Fulvous Whistling Duck, Common Shelduck in Mykolayiv [119] and Non-poultry birds in Kirovohrad. [120]

7.1.2.3.14 Moldova

A positive case of H5N1 was detected in a poultry bird in a village at Balauresti, Nisporeni on 25 December 2024. This detection prompted immediate action, resulting in the culling of 60 birds and the disposal of 20 deceased birds to prevent further spread of the disease. [121]

7.1.2.3.15 Albania

A positive case of H5N1 was detected in a backyard poultry bird at Cekrez, Morine, on 27 December 2024. This detection resulted in the culling of 135 birds and the disposal of 265 deceased birds to prevent the further spread of the disease. [122]

### 7.2.2 H5N5

#### *7.2.2.1 Iceland*

Multiple outbreaks of H5N5 were confirmed in the following locations:

- Ölfus, Suðurland, positive cases were detected in a flock of fattening turkeys, following the onset of clinical signs and deaths on 2 December 2024. As a precautionary measure, samples were collected from all flocks within a 10-kilometer restriction zone before slaughter. [123]
- Höfuðborgarsvæði, positive cases were detected in wild black-headed gull birds. [124]
- Hálshreppur, positive cases were detected in wild herring gull birds. [124]

#### *7.2.2.2 Norway*

A positive case of H5N5 was detected in dead wild Eurasian lynx at Burfjord, Kvænangen kommune, Troms Og Finnmark on 19 December 2024[125]

### 7.2.3 H7N6

#### *New Zealand*

An H7N6 outbreak was reported at a single farm in Otago. Following extensive testing of connected farms, officials expressed confidence in the eradication of the virus. While the farm remains under strict biosecurity measures for cleaning and decontamination, the government has stated that they are on track to eliminate the disease. This outbreak, unlike the globally prevalent H5N1 strain, has not shown evidence of human transmission. Following the virus's discovery, a temporary suspension of all poultry exports was implemented. [104,126]

## 7.3 Research findings

### 7.3.1 Persistence of Influenza A Virus in Raw Milk

This study examined the persistence of influenza A virus (IAV) H1N1 PR8 in raw cow milk stored at 4°C. Results showed that infectious virus was detectable for up to 2.3 days, while viral RNA remained detectable for at least 57 days. Pasteurisation significantly reduced infectious viruses to undetectable levels, however, only a minor reduction in viral RNA was observed. These findings emphasise the potential risk of zoonotic influenza transmission through raw milk consumption, highlighting the critical importance of pasteurisation for food safety.[127]

### 7.3.2 Rare H5N1 infection in a child after travel to India

A recent study published in *Emerging Infectious Diseases* reports a case of HPAI H5N1 infection in a young child who travelled to Kolkata, India. This infection, caused by clade 2.3.2.1a HPAI H5N1, is rare in humans, with only two previously reported cases. While poultry outbreaks caused by this clade are common in South Asia, particularly India and Bangladesh, human infections remain infrequent. With human infections with this clade uncommon, this case highlights the zoonotic potential of this virus. Genetic analysis revealed the virus retained avian-like characteristics and exhibited preferential binding to avian receptors, suggesting a low risk of human-to-human transmission. The child recovered after treatment with the antiviral oseltamivir. This case highlights the ongoing zoonotic threat posed by HPAI H5N1, particularly clade 2.3.2.1a, which is prevalent in South Asia and associated with poultry outbreaks.[128]

### 7.3.3 H5N1 risk in live poultry markets, China: Increased risk of human infection

A recent correspondence published in *The Lancet Microbe* underscores the critical findings concerning the emergence of HPAI H5N1 viruses, particularly their significant presence within live poultry markets in China. These viruses, belonging to the 2.3.4.4b sublineage, exhibited an enhanced binding affinity for human-type receptors, a key factor in human infection. Specifically, the presence of the N193K substitution in the haemagglutinin (HA) protein enables these viruses to bind to human-type sialic acids, a critical step for human infection. This finding is significant as the N193K mutation was more prevalent in human H5N1 isolates compared to avian strains, suggesting its potential role in human adaptation. These findings highlight the ongoing threat posed by H5N1 viruses, particularly those circulating in live poultry markets, and emphasise the need for continued surveillance and public health interventions to mitigate the risk of future pandemics. [129]

### 7.3.4 Spillover infections of H5N1 influenza virus in horses from Mongolia

This study investigated the potential for spillover infections of the H5N1 influenza virus in horses from Mongolia. Researchers collected serum samples from horses across different regions and tested them for antibodies against H5N1. The results identified two horses with positive H5N1 antibodies, suggesting they had been infected with the virus. These findings highlight the susceptibility of horses to H5N1 and the possibility of frequent spillover events from infected birds. This raises concerns about the potential emergence of new influenza viruses through reassortment between equine influenza virus and H5N1, particularly in North America, where these viruses co-circulate in horses, cattle, and wild birds. The study authors recommend serological surveys in horse populations to enable early detection of H5N1 infections and inform control measures to prevent future influenza outbreaks. [130]

### 7.3.5 Airborne transmission of recent H5N1 strains in ferrets

The study involved infecting ferrets with various H5N1 strains, including those isolated from a Texas dairy worker, a European polecat, and an Ohio dairy cow, and measuring airborne viral shedding. While the highly transmissible 2009 H1N1 virus[Footnote5] was readily detected in the air, no airborne transmission was observed for older wild-type or recent bovine H5N1 strains. However, limited airborne shedding was identified in one out of four ferrets infected with the 2022 polecat strain and the 2024 worker strain. The researchers suggest that the lack of airborne transmission for older strains might be due to the absence of mutations promoting mammalian adaptation, rather than a complete inability to spread through the air. They emphasise the importance of understanding how H5N1 spreads among cattle, its potential to adapt to mammals, and its airborne transmission capacity, given the ongoing outbreaks in cattle and the high exposure risk for farm workers and animals. [132]

### 7.3.6 Rapid diagnostic kit for detecting highly pathogenic avian influenza (HPAI) H5N1 virus

The Diagnostics Development Hub (DxD Hub) in Singapore, in collaboration with the National Institute for Environmental Studies (NIES) in Japan and the A*STAR Bioinformatics Institute, has developed *Steadfast*, a rapid diagnostic kit for detecting HPAI H5N1 virus. This innovative kit can differentiate between HPAI and low pathogenic avian influenza (LPAI) strains within three hours, significantly faster than conventional sequencing methods. Validated by NIES, *Steadfast* accurately classified avian influenza viruses detected in wild birds in Japan, enabling timely detection and control measures for this critical public health concern.[133]

## 7.4 Outbreak preparedness, the UK

The UK Health Security Agency (UKHSA) has announced a contract with CSL Seqirus to procure > 5 million doses of human H5 avian influenza vaccine as a precautionary measure against a potential pandemic. This move aligns with broader plans to ensure access to vaccines for various pandemic-threatening pathogens. The vaccine, based on a current H5 strain, is intended for use only if human-to-human transmission of the virus begins. If necessary, it will be utilised while a more specific pandemic vaccine is developed and produced. This proactive measure mirrors similar efforts by other nations, including the US, the European Union (EU),

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[5] Also known as A(H1N1)pdm2009 or H1N1pdm09, the cause of the influenza pandemic in 2009. It continues to circulate today. [131]

and Japan, who are also stockpiling H5 vaccines as part of pandemic preparedness strategies.[134,135]

# 8.0 Outbreaks

## 8.1 Mpox, updates from the World Health Organization

### 8.1.1 Risk assessment

The WHO updated the latest risk assessment of different mpox clades in the *Multi-country External Situation Report no. 44 (23 December 2024)* based on data and information available in November 2024.[136] The public health and geographical spread risks of the mpox virus (MPXV) are stated in **Table 3**.

**Table 3**. Overall public health risk and risk of national and international spread, by MPXV clade, as assessed by the WHO. The information was obtained from Multi-country outbreak of mpox, External situation report#44 - 23 December 2024.

| MPXV Risk Groups | Epidemiology/mode of transmission | Overall public health risk | Risk of national & international spread | Confidence in the available information |
|---|---|---|---|---|
| **Clade Ib** | • Affecting **non-endemic areas** in The Democratic Republic of Congo (DRC) and neighbouring countries.<br>• Transmitted through close human-to-human contact. Persistent transmission is likely through sexual, household, and community contact.<br>• International spread largely ties to sexual contact, particularly among young adults. | **High** | **High** | Moderate |
| **Clade Ia** | • Affecting mpox **endemic areas** in DRC.<br>• Sporadic reports in Central and East African regions.<br>• Associated with zoonotic spillover events from animal reservoirs. | **High** | **Moderate***<br>*A concerning trend was observed in the Kinshasa sexual network, where emerging evidence shows sustained human-to-human transmission. | Moderate |

| MPXV Risk Groups | Epidemiology/mode of transmission | Overall public health risk | Risk of national & international spread | Confidence in the available information |
|---|---|---|---|---|
| | • Transmitted through human physical contact is observed. | | | |
| **Clade IIa** | • **Endemic** in Nigeria, West and Central African Countries.<br>• Sustained community transmission found in Côte d'Ivoire and Liberia.<br>• Transmitted through human physical contact and zoonotic spillover events. | Moderate | Moderate | Moderate |
| **Clade IIb** | • **Global risk**.<br>• Males having homosexual activities are a high-risk group. | Moderate | Moderate | Moderate |

### 8.1.2 Situation update

#### *8.1.2.1 African Countries*

African countries reported 1,904 confirmed cases from 4 November to 15 December 2024, bringing the total count in 2024 to 13,769. High case counts continue to be driven by outbreaks in the DRC, Burundi, and Uganda. Fourteen African countries have active outbreaks, with cases reported in the last 6 weeks, which equates to two maximum incubation periods of 21 days. [137] Six countries, Gabon, Mauritius, Morocco, South Africa, Zambia and Zimbabwe, entered the control phase with no confirmed cases within that same period. [137] Two countries with controlled status, the Republic of Congo (RC) and Ghana, returned to active transmission status. [138]

#### *8.1.2.2 The Democratic Republic of the Congo, co-circulating Clade Ia and Ib*

The DRC reported 3,046 suspected cases within the same period, with only 137 confirmed, due to limited access to PCR testing. In contrast, most mpox cases (> 95%) in other African countries were confirmed with laboratory tests, and no backlogs of suspected cases were reported. [137]

The outbreaks in the DRC are driven by clade Ia and Ib strains. Two new provinces in the DRC, namely Haut-Katanga and Mai'Ndombe, reported clade Ib MPXV, bringing the total number of affected provinces to 8. The other 6 provinces are South Kivu (most severe with up to 800 weekly reports), North Kivu, Kinshasa, Kasai, Tshopo, and Tanganyika.[137] Other provinces outside the 8 reported mostly the historically endemic clade Ia MPXV. [139]

The epidemiological pattern of clade Ib in the eastern part of the DRC evolved from predominantly affecting adults at earlier outbreaks (January to October 2024) to an increased proportion of children patients more recently (October to December 2024). This reflects that the mode of transmission has transitioned from initially sexual contact to a broader community spread through close physical contact, especially among household members. A similar shift in the epidemic dynamics from primarily young adults to increased children cases was observed in other severely affected countries, such as Burundi and Uganda. [137]

### 8.1.3 Geographical expansion of clade Ib MPXV

Nine countries outside Africa have detected clade Ib MPXV as of 23 December 2024, summarised in **Table 4**. [137,140–142]

**Table 4.** Countries which have reported clade Ib MPXV.

| Countries | Number of cases | Note |
|---|---|---|
| Sweden | 1 | Travellers from affected African countries. |
| Belgium | 1 | |
| Thailand | 1 | |
| USA | 1 | |
| Canada | 1 | |
| India | 1 | Travellers from the United Arab Emirates (UAE). |
| Pakistan | 1 | |
| Germany | 5 | Secondary transmission was reported in December 2024. |
| UK | 5 | Two travellers plus three household contacts of one of the travellers. |

### 8.1.4 Multicountry reports

#### *8.1.4.1 Australia*

Australia is experiencing an unprecedented outbreak of clade IIb MPXV, with 1,352 confirmed cases reported as of 30 November 2024. The virus is found mainly in men who have sex with men (MSM). The number of monthly cases shows an early indication of plateauing in recent months. [137]

#### *8.1.4.2 Kosovo*

The country's health authorities reported the first case of mpox in a 30-year-old citizen who returned from a West African country. [143]

#### *8.1.4.3 The Sultanate of Oman*

The country reported its first recorded case of mpox due to clade I MPXV. The case is an adult male who travelled to the UAE from 20-25 November 2024. The subclade is undetermined at the time of preparing this report.[137]

#### *8.1.4.4 India*

Two men in Kerala tested positive for mpox after returning from the UAE. The clade type was not shared.[144]

### 8.1.5 Public health efforts

#### *8.1.5.1 Diagnostics*

Access to essential testing supplies has been the major hindrance in controlling the mpox outbreak in the African region. In light of that, the African CDC and the WHO initiated a joint continental plan to address the diagnostic challenge. [145] The strategies to scale up mpox testing capacity include centralised PCR sites, increased testing sites, point-of-care testing (POCT) applications, laboratory personnel training, and ensuring adequate testing supplies. [145] The Singapore government supports the continental plan by promising 50,000 mpox diagnostic kits to bolster the African CDC's disease management capacity. [145]

The WHO has changed its stance on using rapid antigen tests to detect MPXV. In the latest report, the organisation encourages research on point-of-care rapid antigen tests, which could significantly expand diagnostic access to remote areas**.** This will especially benefit the DRC, which missed the window of verifying most suspected cases. The WHO collaborates with the Foundation for Innovative New Diagnostics (FIND) and the DRC to evaluate 6 rapid antigen tests (RATs). [137]

To date, the WHO has approved three mpox virus *in vitro* diagnostics (IVD), namely *Alinity m MPXV assay kit*, *cobas MPXV Qualitative assay kit*, and *Xpert Mpox*, for Emergency Use Listing (EUL). The WHO is currently assessing four other submissions and expecting another two dossiers. [137]

#### *8.1.5.2 Vaccines*

The distribution of mpox vaccines through the Access and Allocation Mechanism (AAM) is ongoing. A supply of 4,778,000 vaccines will be available for future allocation to affected countries. [137] A previous report claimed that the African CDC had allocated 899,000 doses to 9 African Countries[146].

Japan pledged 3 million doses and bifurcated needles from its LC16 vaccine stockpiles for vaccine administration in African countries. The first batch will be delivered to the DRC to fill the child vaccination gap. [138] The ongoing Bavarian Nordic vaccination is only indicated for people ≥ 12 years old. [138]

Nigeria launched a vaccination campaign (Bavarian Nordic's JYNNEOS) targeting three priority groups: frontline healthcare workers, close contacts, and people living with HIV. Three sites in 7 states (FCT, Bayelsa, Enugu, Akwa Ibom, Rivers, and Cross River) have been selected for the campaign. [146]

### 8.1.6 Other WHO efforts

Multiple efforts have been made by the WHO in collaboration with its partners and affected countries to control the mpox situation globally, specifically, in the African continent which is hardest hit by the outbreak. These include the following. [137]

a. Emergency coordination:
   The joint WHO-Africa CDC Continental Mpox Response Taskforce conducted an Intra-Action Review (IAR) on affected African Countries. IAR is a qualitative review process that evaluates actions in response to an emergency. Such evaluation aims to identify best practices and areas of improvement to be better prepared for the future. It also indicates the national capacities for preparedness and response to public health emergencies.
b. Collaborative surveillance:
   The WHO guided the implementation of the WHO mpox transmission protocol in the DRC, the epicentre of the mpox epidemic. The protocol is a template for the member states and partners to standardise the investigation of mpox outbreaks, thus enabling similar investigations across different settings for more comparable analysis.
c. Community protection:
   The technical areas covered include risk communication and community engagement, infodemic management, infection prevention and control, community-based surveillance, human-animal interface, and border health. The WHO also published technical briefs and advice, disseminating practical information to local communities to strengthen response, protection, awareness, and care while addressing stigma and discrimination related to mpox.
d. Scalable care**:**
   WHO updated the interim guidance on case management for mpox according to the latest available evidence following a Guideline Development Group meeting of experts. The Monitored Emergency Use of Unregistered Investigational Interventions (MEURI) process is ongoing to access tecovirimat for treating severe diseases outside research settings. Notably, the antiviral drug (branded as Tpoxx for smallpox treatment) did not speed up lesion healing or pain relief as compared to placebo in two independent randomised clinical trials—the Study of Tecovirimat for Mpox (STOMP) targeting mild to moderate clade 2 mpox and the PALM007 trial in DRC targeting clade I mpox. [147,148]

## 8.2 Marburg, update

The Ministry of Health of Rwanda declared the end of the Marburg virus disease (MVD) outbreak on 20 December 2024 per the WHO recommendation. [149] The declaration came after two consecutive incubation periods (42 days from 8 November 2024) without a new confirmed case since the second negative PCR test of the last confirmed patient (reported on 30 October 2024). The outbreak statistics finalised at 66 confirmed cases, 15 deaths (case fatality ratio, CFR, 23%), and 51 recovered cases. [149]

The risk of MVD re-emergence remains after the official end-of-outbreak declaration concerning viral persistence in body fluids such as the semen of recovered patients and human-animal interaction in the country.[149] The source of the recent outbreak in Rwanda was linked to exposure in a cave inhabited by fruit bats. Continuous surveillance of the miners working in the caves was in place to detect new cases. The WHO also encourages maintaining early detection and care capacities to minimise the spread of the disease and save more lives should it re-emerge.[149]

Following the end of the outbreak in Rwanda, the WHO updated the risk of MVD to low at the national, regional, and global levels. The WHO advises against any travel or trade restrictions with Rwanda.[149]

### 8.3 Mysterious outbreak, the DRC

An unknown disease with symptoms of fever, headache, cough, runny nose, and body aches emerged in the Panzi health zone in Kwango Province of the DRC between 24 October and 5 December 2024.[150] Severe cases are associated with anaemia, respiratory distress, and malnutrition. Reported cases reached 406, with 31 deaths registered as of the WHO update on 8 December 2024.[150] *Euronews* later reported that the confirmed cases reached 592 infected, and the death toll was 37 on 20 December 2024.[151] Children aged 0-14 years represent 64.3% of all reported cases, with those < 5 years old accounting for 53% of cases.[150] Similarly, 54.8% of the total deaths are children < 5 years old.[150]

Among the suspected aetiologies of this outbreak are acute pneumonia, influenza, COVID-19, measles, and malaria, with malnutrition potentially contributing to the severe cases.[150] Ten of the 12 initial samples collected were confirmed positive for malaria, a common disease there.[152] Nevertheless, the WHO and the African CDC have not officially confirmed the diagnosis, with more laboratory testing underway.[150,153]

Congo's health ministry announced severe malaria was the culprit on 20 December 2024. Concurrent health complications in the province, such as malnutrition and other viral infections, might have exacerbated the disease severity.[154]

Multiple factors complicate the mysterious outbreak:

1. Logistic challenge:
   The Panzi health zone is approximately 700 km from the capital (Kinshasa). Travelling to the region by road can take up to 48 hours in the current rainy season.[150] Limited diagnostic accessibility in the area means the samples must be transported to Kikwit, > 500 km away, for testing.[151] This makes mobilising resources and a response team to the region difficult and delays the identification of the cause.
2. Food insecurity:
   The region has suffered from food insecurity in recent months, which has increased from Integrated Food Security Phase Classification (IPC) level 1 (IPC1, acceptable) to

IPC3 (crisis level).[150] The high risk of severe acute malnutrition in the region might impact immunity and increase people's vulnerability to the disease.

3. Concurrent infection:
   A recent death with symptoms of haemorrhagic fever raised concern over co-infection by a still-unidentified virus.[151] Haemorrhagic fever is not generally associated with malaria. The African CDC did not dismiss the possibility of the secondary hypothesis of a viral infection happening alongside malaria and malnutrition. [153]
4. Low vaccination:
   Information on vaccination coverage (including childhood coverage) is lacking.[150] Vaccine deprivation probably hampered population immunity in Panzi, making the children more vulnerable to the mysterious infection.

The overall risk level of the unknown disease is high for the affected communities, moderate at the national level considering the localised nature, and low at the regional and global levels. However, neighbouring regions and nations should heighten the alert on potential cross-region/border transmission. [150]

# 9.0 Other news

## 9.1 Intergovernmental Negotiating Body, update

The Intergovernmental Negotiating Body (INB) resumed the 12th meeting on 2-6 December 2024 to draft and negotiate a convention, agreement or other international instrument under the Constitution of the World Health Organization, to strengthen pandemic prevention, preparedness and response. [155,156]

The meeting did not yield a pandemic agreement by the end of 2024. However, the week-long meeting made some progress, particularly on research and development (Article 9) and financing (Article 20). While some disagreement remains on a few of “key obstacles”, informal talks will continue alongside the formal talks. With only 10 days allotted aside in 2025 for these talks, scheduled sometime in February and April, there are some doubts that an agreement may still not be reached come the May 2025 deadline. [157]

However, the Director General of the WHO remains optimistic that an agreement will be finalised by the dateline. Member states (194 countries) have been negotiating for two years on an agreement that could increase collaboration before and during pandemics after noted failures during COVID-19.[158]

## 9.2 The WHO academy

On 18 December 2024, the World Health Organization (WHO) Academy in Lyon, France, officially opened its doors. The WHO Academy is a revolutionary project which will contribute to a better trained health workforce globally, through the most ambitious lifelong training programme ever designed in the field of public health. Trainings are delivered in Lyon and everywhere in the world on its online platform. It will give access to the critical skills and competencies as well as to the latest knowledge and know-how in terms of public health to health professionals, policy-makers, and the WHO's workforce.[159]

The WHO Academy intends to address identified weaknesses in health systems – the first of many is the growing global shortage of health and care workers, projected to reach 10 million by 2030, and also the widening gap in terms of access to the latest research and innovation. The majority of this shortfall will be felt in low- and middle-income countries, particularly in Africa. With the view to build and share access to the most advanced technology for health and care and research and development in the field of health, including AI, the Academy will bring additional capacity and efficiency directly to health systems.

The WHO Academy was launched 7 years ago, with support from the Government of France, the Auvergne-Rhône-Alpes region, Lyon City and Métropole, and other global partners. The state-of-the-art campus spans 11,000 $m^2$ and includes: 22 training rooms, two distance-learning rooms, a simulation centre, an emergency operations centre, a TV recording studio, a modern auditorium and a library.

The Academy aims to train 3 million healthcare workers, including nurses, clinicians, and midwives, along with 900 senior decision-makers and 13,000 public health managers by 2080. The WHO Academy will produce 50 to 80 courses annually from 2025 to 2028, totalling approximately 260 new courses by 2028.

## Implications for Sarawak based on the views of SIDC

COVID-19 continues to persist. In their year-end message for 2024, the WHO emphasised the 5-year mark since China reported the first cases of viral pneumonia. The agency urged for a commitment to learning from the lessons of the COVID-19 health crisis to build a healthier future. [160]

This health emergency hit Sarawak and Sarawakians hard. Public health resources had to be shared nationally and were spread thin. The daily lives of many were disrupted, and the impact is still being felt until now.

The question *"Is the world better prepared for the next pandemic than we were for COVID-19?"* is taken to heart by Sarawak and SIDC.

We need to be prepared for the next public health outbreak. This means actively engaging the community in awareness of the current health issues locally and globally, and encouraging/growing a mindset towards a healthy Sarawak using the One Health approach. Having sufficient resources and tools to monitor diseases and conduct surveillance is as important as the sharing of these resources and tools. Data consolidation and sharing are keys to understanding the 'whole picture', to better make patterns and links to diseases and healthcare (human and animal).

The threat of zoonotic influenza, particularly avian influenza is not far away. The virus has been detected in birds and mammals (wild and farmed and domesticated animals). The East Asian-Australasian Flyway brings wild birds that have travelled from faraway places, possibly including areas with known cases of human avian influenza, into Borneo annually. These birds can harbour pathogens. While there are no reports of avian influenza in Sarawak's agriculture industry, nor reports of human infections, it is not unlikely that the virus is already on our shores.

SIDC has been highlighting animal-linked human avian influenza infections throughout 2024. Studies summarised in this report as well as others have indicated the potential for spillover events, where the virus 'jump species' to humans as it continues to mutate while circulating among animals. [161,162] Both active and passive surveillance to look for these genetic mutations in animals within our borders can help determine the direction/threat of the disease.

Likewise mpox. To date, only 10 cases have been reported, all males, with a history of 'high-risk behaviour', all clade II MPXV infection. The last case was reported in September 2024 without a history of travel. The threat of a disease associated with sexual transmission poses a problem in health-seeking behaviour with many may go undetected. Furthermore, the urgency of a mpox infection may not seem as high as the other sexually transmitted diseases (STDs) as it is seen as related to taboo behaviour (MSM). However, the picture in Africa serves as a caution as household transmission of MPXV is more prevalent for the clade Ib virus. The clade Ib is spreading, and it is a matter of time before a case involving a member of a household is reported.

Lessons from the African continent on the management of the multiple outbreaks in a resource-poor and disease-challenged environment, and geographically difficult terrains such as those found in Central Africa should be heeded. Outbreak management training with this scenario in mind will enable associated personnel here in Sarawak to adapt and adopt the best methods to mitigate infection control as Rwanda did successfully for the Marburg outbreak.

Irrespective of whether malaria is caused by the four main human malaria (*P. falciparum*, *P vivax*, *P. malariae* and *P. ovale*) or zoonotic malaria (for example, *P. knowlesi*), mitigating the number of cases requires a concerted effort of many agencies. A similar framework from the study mentioned in this report can be adapted to support Sarawak's goal of minimising human zoonotic malaria cases caused by *P. knowlesi*, as indigenous human malaria cases are already under control. The four key components, along with weather patterns, could be integrated to study the breeding seasons of malaria vectors, serving as a tool to predict potential spikes in *P. knowlesi* malaria cases. Additionally, the current elimination criteria in Sarawak should be reassessed to address local limitations, particularly in terms of health inequity and access to healthcare.

The outbreak of African Swine Fever (ASF) recently is a reminder that the virus continues to circulate within the region. Due diligence is required to ensure all farms including backyard breeders get their animals tested. The research and development of effective vaccines for the swine industry in Sarawak could ensure the industry's safety.

As the WHO and the Global Alliance for Rabies Control (GARC) reaffirmation of their commitment to the "Zero by 30" strategy to eliminate human deaths from dog-mediated rabies by 2030, so does Sarawak. The One Health approach of community education and engagement, scaling up mass dog vaccination campaigns (vaccines are already provided for free by the Department of Veterinary Services Sarawak, DVSS) and improving access to PEP are key to the rabies prevention programme. It goes hand-in-hand with responsible pet ownership, elimination of illegal breeding practises as well as humane animal population control (trap-neuter-vaccinate) and adherence to the local by-laws. Suggestions from modelling dynamics studies to control the rabies problem in Sarawak should continue to be considered [163–165] whilst the local development of vaccines ensures the supply chain is not disrupted.

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