Sarawak Infectious Disease Centre

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Global updates on COVID-19 and other diseases

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Summary

- The outcome of the 10th International Negotiating Body (INB) is eagerly awaited.
- The WHO has updated the Laboratory Biosecurity Guidance.
- Though the data on COVID-19 may not be complete, whatever is available says it can still kill.
- Studies have offered more glimpses into the mechanism of long-COVID.
- Resurgence of lymphatic filariasis may be linked to increasing urbanisation trends and migration from previously endemic regions.
- H5N1 continues to affect more dairy herds in the US.
- Experiments using ferrets found that H5N1 did not easily spread in the air.
- Mpox remains a global health threat, with the outbreak in DRC not showing signs of slowing.
- Dengue and other arboviruses remain a global disease that is difficult to control.
- African Swine Fever (ASF) has been reported by multiple countries in Asia.
- Preparing for a massive sporting event such as the 2024 Olympics includes a risk assessment of currently important pathogens.

1.0 Situational summary: cases and related issues

According to the WHO, COVID-19 still kills an average of 1,700 people globally every week. Data shows that vaccine coverage has declined among health workers and people > 60 years old, which are two of the most at-risk groups. The agency recommends that people in the highest risk groups receive a COVID-19 vaccine within 12 months of their last dose.[1]

The Americas

The US

COVID-19 activity has been rising steadily in the US. Wastewater surveillance showed high levels of SARS-CoV2 (**Figure 1**), [2] [3] as with other indicators (emergency department visits [ED], test positivity, hospitalisations); older people ≥ 65 years old and people in the country's western states are especially affected. [4]

The percentage of ED visits rose 23.5% last week compared to the week before. Levels were higher in the West and the South than in the rest of the country. [5]

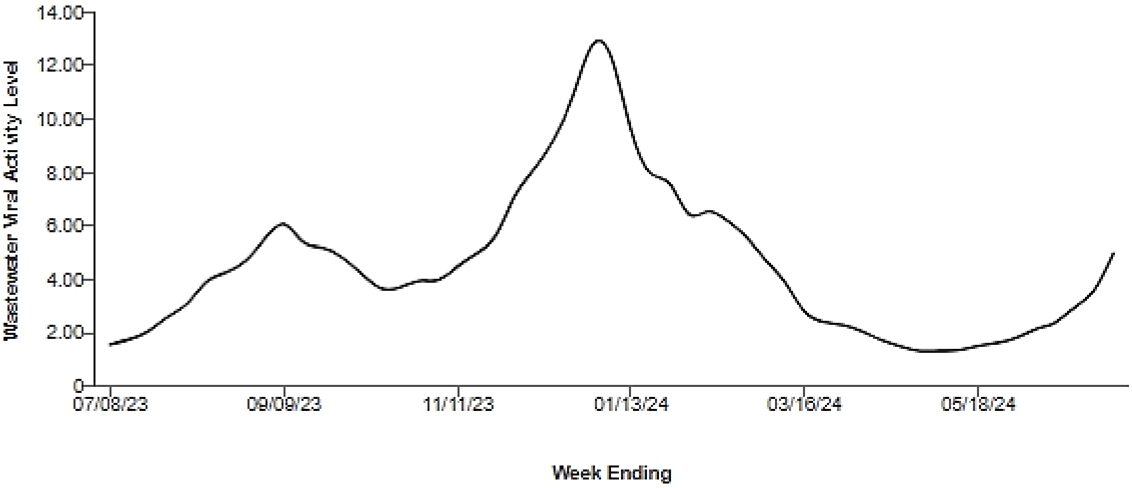

Figure 1. The SARS-CoV-2 viral activity in wastewater for one year in the US. The current positive trend began in mid-May and continues into early July (latest data 6 July). The graph was obtained from [NWSS Wastewater Monitoring in the U.S. | National Wastewater Surveillance System | CDC](#)

Officials at the New York City Department of Health and Mental Hygiene have advised people, especially seniors and people with underlying medical conditions, to consider wearing masks in crowded indoor settings.[6]

The latest variant update from the CDC showed the proportion of KP.3 detections continues to rise (**Figure 2**). As with KP.2, KP.3 is a sublineage of Omicron JN.1. They have mutations that allow for better immune evasion from earlier infection or vaccination. Another variant that expanded its proportion is LB.1, which rose slightly from 13.0% to 14.9%.[7]

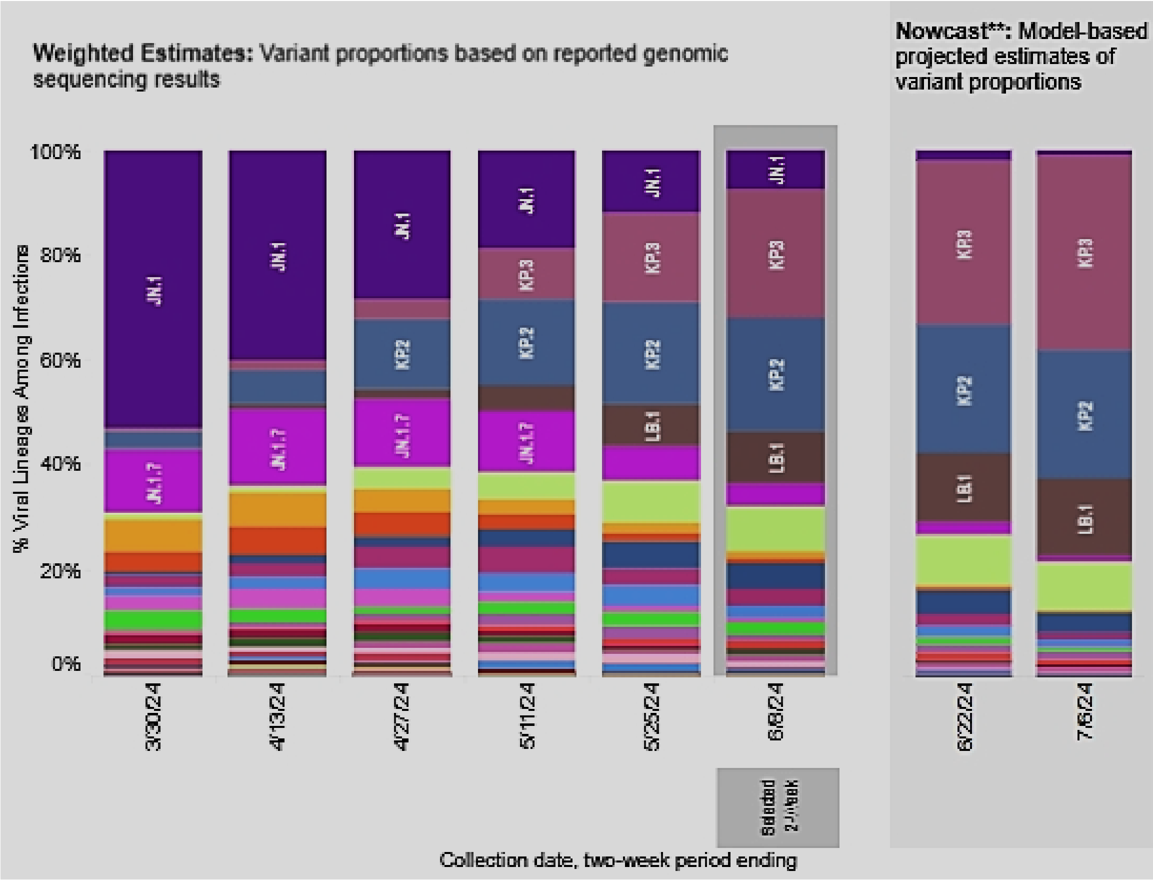

Figure 2. The projected proportion of the SARS-CoV-2 virus variants circulating in the US from March to early July 2024. The estimated proportion of KP.3 (annotated and dusky pink colour in the chart) rose from 31.3% in the week ending 22 June to 36.9% in the week ending 6 July. The chart and notation were adapted from CDC COVID Data Tracker: Variant Proportions.

2.0 Variants

KP.3 variant (B.1.1.529.2.86.1.1.11.1.3)

KP.3 is a variant form of the Omicron Variant of Interest (VOI), an offspring of JN.1, which is the descendent of BA.2.86. KP.3 is the direct descendent of KP.2—also an offspring of JN.1, a member of the "FLiRT" group of subvariants due to the mutations to its spike proteins.[8]

KP.3 is "FLuQE" subvariant, referring to the additional substitutions in the spike proteins, S:Q493E, where glutamine is replaced by glutamic acid at position 493 of the 1,273-amino-acid-long molecule. This alteration may enhance the virus' ability to infect human cells, making it more contagious and able to drive up cases and hospitalisations.[9]

KP.3 has been detected in > 40 countries worldwide including the US, the UK, Spain, Japan, Ireland, New Zealand, Canada, Denmark, France, Singapore, Costa Rica, China and Malaysia. It has become dominant in the US and Australia. [10] [11] [12]

According to experts, widespread transmission of and infection with FLiRT and FLuQE variants is expected, and with it, population immunity to these variants will mature. However, in time, their dominance will be supplanted by the next immune-evasive variant.[13]

"The tug of war between our immune system and SARS-CoV-2 evolution continues."

Professor Nathan Bartlett, School of Biomedical Sciences and Pharmacy, University of Newcastle, in *The Conversation* (10 July 2024).

The current issue the world population faces is that vaccines do not sufficiently protect from the SARS-CoV-2 infection nor prevent the virus' transmission. They are still good at protecting against severe diseases; however, the virus still infects many people.

Meanwhile, other JN.1 descendants are rising, trailing close behind KP.1, KP.2, LB.1 and KP.3.

3.0 Vaccines and vaccinations

Expired vaccines, Malaysia

Over 9 million doses of COVID-19 vaccines (or 10.8%) out of almost 84.5 million doses received have expired as of 11 July 2024. They were worth RM185 million. The vaccines, from various brands, were either procured or donated since 2020. The expired vaccines must be disposed of according to asset and stock management procedures.[14]

4.0 Outcome

4.1 Prevalence of asthma lower in children with COVID-19 vaccination

According to a cross-sectional study, higher COVID-19 vaccination rates are linked to reduced asthma symptoms in children, highlighting broader health benefits of vaccination during the pandemic. The reduction occurred amid significant public health efforts to control COVID-19, such as widespread vaccination and mandatory face masks.[15] [16]

For every increase of 10% in vaccination coverage, parent-reported child asthma symptom prevalence decreased by 0.36 percentage points ($P=0.04$). The mean state-level prevalence of parent-reported childhood asthma symptoms decreased from 7.77% in 2018-2019 to 6.93% in 2020-2021 ($P<0.001$).

There was no significant association observed between asthma symptoms and COVID-19 death rates or face mask mandates at the state level.

The analysis used multiple sources of data:

- state-level data on parent-reported current asthma symptom prevalence in their children from the National Survey of Children's Health for 2018-2019 and 2020-2021;
- CDC data on age-adjusted COVID mortality rates in 2020 and 2021 and on the proportion of children ≥ 5 years old who completed their primary vaccination series in 2020-2021; and
- data on face mask requirements for enclosed spaces through August 2021 from 20 states and the District of Columbia.

The findings suggested that COVID-19 vaccination provided prophylactic benefits against SARS-CoV-2 infection for individual children. It may also protect against other human coronaviruses through cross-reactive antibody responses. Furthermore, community-level immunity in states with higher vaccination rates may have contributed to reducing the risk of asthma in children.

However, the study had one limitation as it could not assess for differences in symptomatic asthma among vaccinated versus unvaccinated children.

4.2 Long-COVID

4.2.1 Prolonged immune activation, update

People who have long COVID symptoms can display signs of abnormal immune-cell activation in many of their organs and tissues. They can also have "leftover" SARS-CoV-2 RNA in the gut for > 2 years post-infection.[17] [18] [19]

The findings were from a small study, with 24 participants, which involved whole-body positron emission tomography (PET) imaging at time points ranging from 27 to 910 days (~2.5 years) after acute illness of COVID-19; 18 patients had long-COVID.

The study found that certain tissues were enriched for activated T cells in people with long-COVID compared with those who have never had a SARS-CoV-2 infection (prepandemic controls). The T-cell activation correlated with symptoms of long-COVID (for example, those who reported persistent lung problems had stronger signs of T-cell immune activation in the lungs). Furthermore, the gut from 5 patients with long-COVID all had sites of activated T-cell enrichment, and all 5 contained SARS-CoV-2 RNA.

While the findings are only correlative, they provide "compelling evidence that long-COVID is tied to the persistence of the SARS-CoV-2 virus in the body and abnormal immune activity".

Previous studies have shown that 'long haulers' can suffer from lingering issues in various organs including the tissues in the heart, brain, lungs, skin, kidneys, liver, spleen, gut, thyroid, and ovaries.[20] [21] [22]

One explanation for this widespread effect involves the activity of the immune system. Scientists have found biomarkers of inflammation and immune activation are often present in a patient's blood after the acute phase of a viral infection.

4.2.2 Altered sense of smell in healthcare workers common, Sweden

A new study based on 2,149 healthcare workers (HCWs) employed at Danderyd Hospital in Stockholm showed a significant proportion of those who had COVID-19 experienced lasting changes to taste and smell. Approximately 45% reported olfactory disorders 15 months after infection. A further 24% continued to experience symptoms 2.5 years after infection.[23]

The HCWs were recruited between January and May 2020 during the first wave of the pandemic in Sweden. The study began in April 2020 and involved testing the HCWs for SARS-CoV-2 antibodies every 4 months. They were compared to healthy controls.

A summary of all the findings is as follows (paraphrased):[24]

- 37% of people in the COVID-positive group suffered quantitative olfactory dysfunction, with 4 people exhibiting anosmia (loss of sense of smell), and 32 people exhibiting hyposmia, or decreased sense of smell.
- In the COVID-negative group, 20% showed quantitative olfactory dysfunction, all of whom had hyposmia.
- Overall, first-wave infections almost doubled the prevalence of olfactory dysfunction in the study population, from 20% to 36%, and increased the prevalence of any form of olfactory dysfunction by a full 41 percentage points compared to those without COVID.
- For all tested COVID-19 survivors, 24% still experience parosmia 2.6 years after COVID-19 diagnosis, nearly half of which experience medium to severe symptoms.

5.0 Planning

5.1 International Negotiating Body

The world is at a critical juncture with the International Negotiating Body, INB10, meeting to define the modalities approaching on 16-17 July 2024. [25]

The process is to achieve a pandemic agreement rather than the content of an agreement. Anticipated agenda items include decisions on timeline, co-chairs, and stakeholder engagement and inclusion process.[26]

A draft work plan has laid out a process that could result in a special World Health Assembly (WHA) session as early as the week of 16 December 2024. [27]

5.2 Laboratory biosecurity guidance updated, the WHO

The WHO issued an updated guidance for national authorities and biomedical laboratories to manage biological risks recently on 21 June 2024.[28]

The updated guidance provides best practices and recommendations while encouraging Member States to adopt a risk-based approach, as stipulated in the resolution on *'Strengthening laboratory biological risk management'* that was adopted at the World Health Assembly (WHA 77) this year.[29] [30]

The updated guidance includes (paraphrased):

- The strengthening of cybersecurity measures and handling of confidential information such as patient records;
- Reducing risks from new technologies, including those related to genetic modification and manipulation of pathogens, and artificial intelligence (AI); and
- Advice on keeping laboratories safe and secure during emergencies like wars, civil unrest, and disasters from natural hazards.

5.3 Preparing for the 2024 Olympics, France

Authorities from the French national public health agency have developed a model framework to identify priority pathogens for wastewater surveillance (WWS) at the upcoming summer Olympic and Paralympic Games in Paris. They have prioritised viruses that cause flu and polio.[31]

The selection of 6 target pathogens, including those that cause polio and flu, is based on peer-reviewed publications and expert opinion suitable for WWS at mass gatherings, where it can monitor disease levels and guide public health decisions. The process is as follows (paraphrased):[32]

- An initial 60 pathogens were listed based on the criteria informed by the European Centre for Disease Prevention and Control (ECDC), the Olympic and Paralympic Games, and the WHO.
- The list of pathogens was then associated to disease categories identified as priorities for the Games by France's national public health agency and included on a risk map for the event, including notifiable diseases, those associated with foodborne illnesses, acute respiratory infections, emerging infectious diseases, and zoonotic diseases, in addition to 6 other infectious diseases considered for WWS.
- The list (of 60) is further narrowed to 25 pathogens based on pathogen analytical feasibility, relevance to the event and pathogen characteristics, and value in guiding public health decision-making (for example, allocation of hospital beds and physical distancing).
- The final list consists of 6 target pathogens: the viruses that cause polio, influenza A, influenza B, mpox, COVID-19, and measles.

WWS was chosen because of its wide deployment in monitoring the COVID-19 pandemic: a collection of data “regardless of symptomatic or asymptomatic status, freedom from the availability of testing or test-seeking behaviour, low cost, early-warning function, passive provision of community-level data, ability to quantify virus and evaluate genetic diversity, and its use to guide public health decision making”.

The WWS will be using France’s existing wastewater treatment network of 54 plants.

The 2024 Olympics will begin on 26 July 2024, and the Paralympics start on 28 August 2024.

5.4 Precision medicine: DNA for science, multi-country example

Biobank data release is a growing trend among population health studies with several ongoing globally.[33]

In Estonia >200,000 Estonians or 20% of the adult population have contributed samples to the country’s biobank. It will allow them to access to learn about some of their genetic traits, including disease risk and ancestry markers. This element was mandated by law when the Estonian Biobank was created in 2000.[34] Sharing the results with the people who provided their samples is one way of recognising the value of participants’ contributions. Furthermore, participants will be counselled by specialists individually (though not without hiccups because of the number of participants) if their results are flagged for genetic risk of certain conditions.

The US is also conducting similar studies. The ‘All of Us’ study, also launched in 2000, aims to collect genome and health data from > 1 million people from diverse backgrounds and allow all participants to receive their genetic results; so far, > 100,000 participants have received theirs. The study examines a set of 59 genes for genetic variations linked to diseases that can be treated or prevented. [35]

Note:

Biobanking is the act of collecting, processing and storing biological samples and data for research. Biobanks are large collections of biospecimens linked to relevant personal and health information (health records, family history, lifestyle, genetic information) that are held predominantly for use in health and medical research. Hence, biobanks are subject to legal and ethical constraints. [36] [37] [38]

Ideally, the availability of high-quality biological samples through biobanks has the potential to advance global health research and speed up progress towards Sustainable Development Goals (SDG), including achieving universal health (SDG3).

The set-up is not without problems, among which include, though not restricted to, funding, ethically obtained samples (bioethics), and timely sharing of results with participants for a timely intervention/management of health risk(s). [33]

6.0 Others

6.1 Avian influenza

6.1.1 Warning from the WHO

The WHO warned that its ability to manage the risk of the virus to humans is being compromised by "patchy" or limited surveillance of the virus in animals globally. The warning came as more human infections of H5N1 were reported last week. The World Organisation for Animal Health (WOAH) has continuously reported the number of farmed, domesticated or wild animals affected.[39] [1]

Currently, no human-to-human transmission has been reported—that is the reason the WHO continues to assess the risk to the general public as low.

The agency continues to call upon all countries to step up influenza surveillance and reporting in animals and humans, as well as research about the virus. Countries are also encouraged to share samples and genetic sequences. Better protection should also be given to people or workers who may be exposed to the virus via infected animals. Closer cooperation between the animal and human health sectors is also encouraged.

The management and eradication of an outbreak that affects domesticated animals in general would be easier because the location of the animals is known, and containment measures can be applied.

6.1.2 H5

6.1.2.1 Human infection, Cambodia

Two human cases of highly pathogenic avian influenza (HPAI) H5N1 were reported in Preah Bat Choan Chum commune, Kirivong district, Takeo province. The first, which was reported on 6 July 2024, was a 3-year-old boy. According to the local authorities, the boy had previously had contact with a dead chicken.[22] On 10 July 2024, another case of infection occurred to a 5-year-old girl who was the cousin of the boy who contracted H5N1. Both relatives were living in the same household. The girl had a mild symptom and is currently under intensive care.[18]

An outbreak of HPAI H5N1 was reported by Cambodia's agriculture ministry in village birds from the same location where two human cases were recently reported.[40] The virus killed 474 of 1,168 susceptible birds, and the remaining ones were culled to curb the spread of the virus. The outbreak began on 5 July 2024. The H5N1 findings were confirmed on 7 July 2024. The clade was not noted in the WOAH report. However, an older 2.3.2.1c clade is known to circulate in Cambodia and has been implicated in other recent human infections in the country.[41]

6.1.2.2 Updates, the US

More dairy herds are being infected by the H5N1—5 in 3 states. The outbreak has now been confirmed in 145 dairy herds across 12 states by the US Department of Agriculture (USDA) Animal and Plant Health Inspection Service (APHIS). [42] [43]

APHIS confirmed H5N1 detections in three more domestic cats, two from Minnesota (feral barn cats) and one from Michigan, raising the total since 2022 to 33. The cats were either from the same facility that is affected by the virus or in the same location (county) where dairy farms are affected. A wild raccoon from the same area in Michigan was also found positive for the HPAI H5N1.

APHIS reported four H5N1 detections in wild birds from two Iowa counties: red-winged blackbird, robin, turkey vulture, and barn swallow. Sampling was conducted by an all-agency effort in June 2024.[44]

6.1.2.3 Animal experiments: H5N1 does not spread easily through respiratory routes

Scientific experiments designed to assess the threat from H5N1 avian flu in the milk of infected cows reported that the virus can bind to both avian and human-type cell receptors. However, the investigations found that the virus does not easily spread through respiratory routes.[45] [46]

The experiment consisted of two parts. One involved intranasally infecting mice and ferrets with milk from infected cows (the contaminated milk was dripped into the noses of these animals), which caused severe disease in the animals. Ferrets were used to examine potential influenza A transmission patterns in humans because the animals show similar clinical symptoms and immune responses. The infectivity of three different viruses was compared in these experiments: H5N1 from cows, a Vietnamese H5N1 strain, and seasonal H1N1. To gauge transmission, H5N1-infected ferrets were placed in cages that were near, though not touching, the cages of uninfected ferrets. Finally, the H5N1 virus from cows was mixed with different types of receptors, which the virus uses to enter cells.

A summary of the results is as follows (paraphrased):[47]

- Intranasal inoculation:
    - Mice which received H5N1 had high virus levels in respiratory and non-respiratory organs, including mammary tissues and muscles; H1N1 was found only in respiratory tissues. The virus was also able to spread from mice mothers to their pups, likely via infected milk.
    - The mice became ill after drinking a small amount of raw milk from an infected cow. [footnote1]
    - In ferrets, the H5N1 virus was found only in the respiratory system.
- Transmission experiments:
    - One of the four exposed ferrets (25%) got sick or tested positive for the virus. Follow-up tests, however, found that one ferret had antibodies to the H5N1 virus.
    - When the same experiment was repeated with seasonal flu, efficient noncontact spread was found.
- Receptor mix experiment:

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[1] Similar findings were published in the New England Journal of Medicine (NEJM) in May 2024. [103]

- The H5N1 virus from cows was able to bind to receptors that can recognise both avian and human influenza viruses.

The findings add more evidence that the virus may be adapting to human hosts and that it may have the ability to bind to cells in the human upper respiratory tract. These experiments suggested that bovine H5N1 viruses may differ from previously circulating HPAI H5N1 viruses by possessing dual human/avian-type receptor-binding specificity with limited respiratory droplet transmission in ferrets.[48]

6.2 *Haemophilus influenza*, ECDC annual update

The European Centre for Disease Prevention and Control (ECDC) reported that the invasive form of the disease caused by *Haemophilus influenza* type b (Hib) rose sharply in EU/EEC in 2022 compared to the previous 2 years. In 2022, 3,967 confirmed cases were reported, in 2021, 1,694 cases and in 2020, 1,849. The increase coincided with the lifting of COVID-19 restrictions and measures in Europe.[41] [49]

The notification rate was 0.9 cases per 100,000 population; it was 0.4 cases per 100,000 population on 2020 and 2021. The rates were highest in infants < 1 year old, followed by seniors (≥ 65 years old) at 7.0 cases per 100, 000 population for males and 4.5 for females, and 2.5 cases per 100,000 population for males and 2.0 for females, respectively.

Serotyping data were available for 58% of the confirmed cases. Of the known cases, non-capsulated strains were the most common among all age groups and caused 73% of the cases overall. Serotype f was the most common capsulated serotype observed (10%). According to the ECDC, there was a slight increase in 2022, which represented 9.1% (n=211) of cases compared to 7% (n=153) in 2018.

Note:

Haemophilus influenza disease is caused by the bacteria *Haemophilus influenzae* which is commonly found in the upper respiratory tract. Similar to the flu and colds, the bacteria is transmitted by droplets (from coughing or sneezing) from infected people (may be asymptomatic) to those who are susceptible.[50] [51] [52]

The bacteria is generally classified into encapsulated and non-encapsulated types. Based on the capsule types, the encapsulated bacterium is further subdivided into subtypes (a through f). The most common form is subtype b, Hib, which infects mostly children <5 years old and immunocompromised individuals. Hib can cause lower respiratory tract infections such as pneumoniae.[53]

The time between infection with Hib and the appearance of symptoms is 2 to 10 days. The bacteria become 'invasive' when they enter the bloodstream. They can cause pneumonia, meningitis, sepsis, or other serious diseases. If the bacteria spread to the sinuses or the middle ear, it can cause sinusitis or otitis media, which leads to a painful ear infection. Hib meningitis can lead to complications such as blindness, deafness, and learning disabilities. Infections sometimes lead to death.[50] [52]

According to the WHO, antibiotic resistance is a growing challenge, with strains now found across all regions.[50] Vaccination remains the only effective means of preventing the disease and is becoming increasingly important as Hib antibiotic resistance grows.

As people can get the disease, including Hib, more than once, maintaining healthy habits, such as washing hands often and not having close contact with people who are sick, helps prevent the disease. [52] [54]

6.3 Pertussis/whooping cough, the UK

According to the UK Health Security Agency (UKHSA), the UK has reported its highest pertussis level in decades so far. [footnote2]

Monthly cases have been rising since January (**Figure 3**). There were approximately 2,600 cases reported in England in May 2024, with the year's total approaching 7,600 cases. [55] [56] [57] Approximately 53% were in people aged ≥ 15 years old who usually experience mild disease.

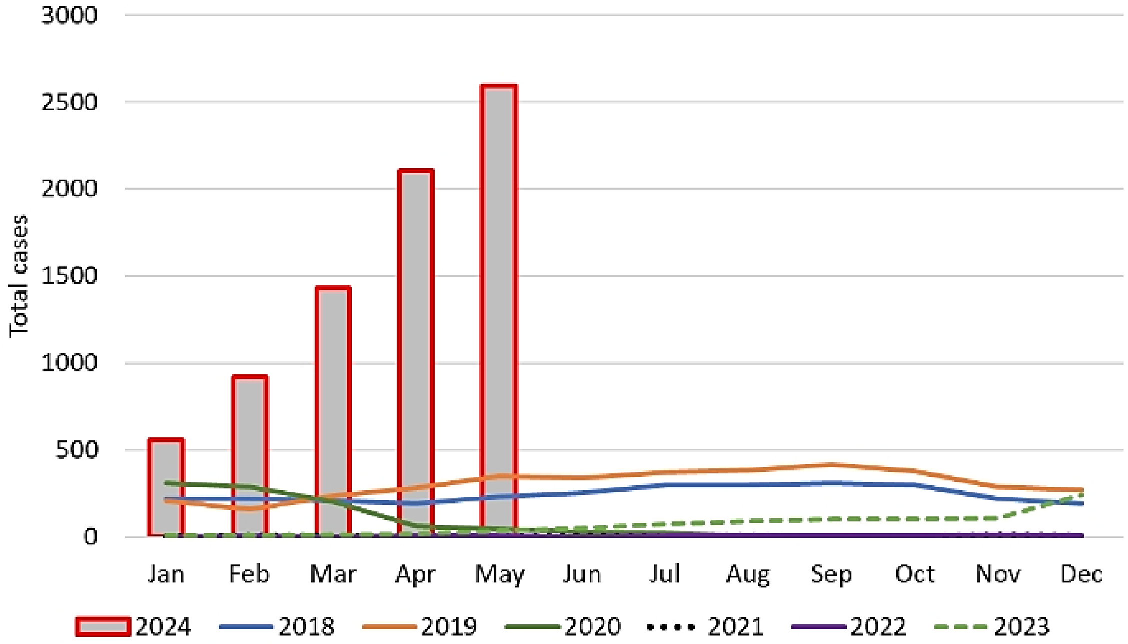

Figure 3. Laboratory confirmed cases of pertussis by month in England from 2018 to May 2024. There were 555 cases in January, 920 in February, 1,427 in March and 2,106 in April. The last cyclical rise in cases occurred in 2016. The graph was modified from [Confirmed cases of pertussis in England by month - GOV.UK (www.gov.uk)](https://www.gov.uk).

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[2] Last reported in Report 2024-R19, Section 5.4

High numbers (262 cases) continue to be reported in babies < 3 months old who are at greatest risk from the infection. To date, 9 infant deaths have been reported since pertussis activity began rising in November 2023.

Timely vaccination in childhood and pregnancy is crucial to protect babies. The latest uptake data revealed that vaccination offered to pregnant women to protect newborn infants against whooping cough continues to decline. Coverage in March 2024 was at 58.9% compared to the peak coverage (72.6%) in March 2017.

6.4 Diphtheria, VietNam

A case of fatal diphtheria was recorded in Nghe An, VietNam. The victim was an 18-year-old female who died 10 days after contracting the disease. This case is the first death recorded in 2024. The deceased had presented with coughing and fever. Two other girls who shared a room with the deceased also contracted the disease. Both are being kept under observation. All close contacts with the patients are undergoing quarantine.[58]

Another case of diphtheria was detected in Bac Giang, in a 29-year-old female. The woman showed no symptoms and remains in normal health.[80]

6.5 Measles

6.5.1 Morocco

There has been an increase in measles infection detected in Souss-Massa, Morroco. As of 6 July 2024, 400 cases and 2 deaths have been reported.[59]

6.5.2 The US

As of 11 July 2024, 167 cases of measles have been reported from 24 US jurisdictions. These included 110 cases from 13 outbreaks.[footnote3] Among the confirmed-case-patients, 84% were unvaccinated or had an unknown vaccination status, and 53% were hospitalised for measles complications.[60]

Among the jurisdictions which reported cases, New Hampshire's Department of Health and Human Services confirmed a measles infection in an unvaccinated resident. The case was likely exposed to an infected international traveller who visited New Hampshire in late June 2024. This case follows another which was also linked to the same international traveller bringing the cluster of cases to three. Investigations found the latest case visited several public places while infectious, including a restaurant, stores, and medical facilities; the person could have transmitted measles to people who are not immune to the disease.[61]

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[3] Report 2024-R15. Most were linked to migrant shelters.

6.6 Plague,

6.6.1 Human case, the US

A human case of plague was reported in Pueblo, Colorado on 6 July 2024. The case is currently under investigation by the Pueblo Department of Public Health and Environment, in collaboration with the Colorado Department of Public Health and Environment.[62]

6.6.2 Plague in ruminants, Greece

Greece reported the first case of "pestes des petits" viral infection in the country. The source of infection is not determined. [63]

Peste des petits ruminants (PPR) is caused by a morbillivirus closely related to rinderpest virus. It affects goats, sheep, and some wild relatives of domesticated small ruminants, as well as camels. It is characterised by severe morbidity and mortality rates and has a high economic impact in areas of Africa, the Middle East, and Asia, where small ruminants contribute to guaranteeing livelihoods.

6.7 Rabies, Uruguay

Uruguay's Veterinary Laboratories Directorate (DILAVE) confirmed a positive case of rabies in a domesticated cat living in the city of Salto. The animal showed an acute change in behaviour characterised by aggressiveness before suddenly dying.[64] [65] The last human rabies reported in Uruguay was in 1966 and the last case of canine rabies was in 1983.

According to authorities, the virus remains active in haematophagous (animals that feed on blood) and insectivorous bats, implying a constant risk of transmission to other species and humans. The recent discovery marks the first confirmation of a species jump (cross-species infection) in the country, underlining the importance of "properly managing the situation".

6.8 Hantavirus, the US

Arizona has reported a total of 7 Hantavirus Pulmonary Syndrome (HPS) in the past 6 months; 3 were fatal cases. Coconino County, which has not reported a case since 2016, reported 3 cases, 2 of which were fatal (67% mortality rate).[66]

The virus is spread from rodents (primarily the deer mouse in Arizona) to people through airborne transmission of viral droplets. It can also spread through handling or stirring up materials contaminated with rodent urine, saliva, or faeces. Hantavirus does not spread from person to person.

Note:

Hantaviruses belong to the group of viruses from the *Bunyaviridae* family. The members are normally carried by rodents, such as rats, mice and voles. They are present globally and cause a range of diseases in humans—from mild, flu-like illness to severe respiratory illness or haemorrhagic disease with kidney involvement. Old World hantaviruses are present in Europe, Asia and Africa. They tend to cause haemorrhagic and kidney disease (haemorrhagic fever with renal syndrome, HFRS). New world hantaviruses tend to cause severe respiratory disease (hantavirus pulmonary syndrome, HPS). Both can be deadly.[67] [68] [69]

Symptoms of HPS usually start to show 1 to 8 weeks after contact with an infected rodent, while it takes 1 to 2 weeks for symptoms to develop for HFRS.

Simple hygiene precautions such as washing hands after handling rats or their bedding and cage should be applied to reduce the risk of infection. Ensuring homes and surrounding areas are clean will also minimise the chances of attracting rats.

6.9 Haemorrhagic fever

6.9.1 Argentine Hemorragic Fever

As of 15 June 2024, there have been 238 suspected cases of Argentine Hemorrhagic Fever (AHF) reported. Thirteen have been confirmed 174 ruled out, and 51 still under investigation. The districts of San Nicolás and Pergamino, endemic areas for AHF, have the highest number of confirmed cases, with San Nicolás registering 12 infections. According to the Buenos Aires Ministry of Health, only one confirmed case did not receive convalescent immune plasma, and none had a history of vaccination. All confirmed cases required hospitalisation, with two fatalities reported.[70] [71]

The number of suspected cases reported in 2024 was a significant increase from that to 2023. For the same 6 month period in 2023, 98 suspected cases were reported, with 4 confirmed cases in Colón, Olavarría, Pergamino, and San Nicolás. This marked rise highlights the ongoing health concern and the need for increased monitoring and preventative measures in the affected districts, particularly in disease-endemic areas.[70]

Note:

AHF is a severe haemorrhagic fever that is rodent-borne and caused by the arenavirus, Junin virus (JUNV). It is endemic to the humid pampas of Argentina.[72] The rodent *Calomys musculinus* has been identified as its principal reservoir. AHF has had significant morbidity since its emergence in the 1950s, with a case-fatality rate, CFR, of the illness without treatment between 15% and 30%. Human exposure to JUNV is believed to occur through inhalation of aerosolised body fluids or excretions of infected rodents, which occur typically during agricultural work.[73]

6.9.2 Crimean-Congo Haemorrhagic Fever

6.9.2.1 Iraq

The number of Crimean-Congo Haemorrhagic Fever (CCHF) cases continues to increase in Iraq. It reached 133 in Baghdad, with 14 fatalities. In Dhi Qar, 31 cases were recorded, with 4 deaths.[74]

6.9.2.2 Pakistan

As of 14 July 2024, Quetta reported an additional case of CCHF infection, bringing the total number to 15 cases since January 2024. There have been three fatalities so far.[79]

The disease is widespread in Eastern and Southern Europe, the Mediterranean, northwestern China, central Asia, Africa, the Middle East, and the Indian subcontinent. Healthcare workers and those in close contact with livestock are at higher risk. [footnote4]

6.10 Dengue

6.10.1 Iran

There has been an increasing incidence of dengue fever in many provinces of Iran. Since March 2024, there have been 155 recorded cases, with one fatality. It is considered an emerging disease, particularly in the southeast region of Iran. This could be due to the prevalence of cases in neighbouring countries Pakistan and Afghanistan.[75]

6.10.2 Bangladesh

Dhaka reported 103 cases of dengue within 24 of 10 July. It brings the total since January 2024 to 4,311 cases with 47 deaths.[76] In 2023, a total of 1,705 died from the disease, making it the deadliest year on record. [77]

6.11 Japanese encephalitis, India

A case of human Japanese encephalitis (JE) was reported in the Tirap district of Arunachal Pradesh in early July 2024. The patient was admitted to the intensive care unit (ICU). No further information was provided regarding this case. Another outbreak was recorded in Sivasagar, Assam, with 3 fatalities and 12 infected. The increase in cases could be due to prolonged flood conditions, leading to an increase in mosquito breeding grounds.[78]

6.12 Zika, India

Maharashtra (western peninsular region of India) reported a rise in Zika infections. The state recorded 12 patients, 6 of which were pregnant women. The first case was detected on 20 June 2024 and was confirmed by the laboratories at the National Institute of Virology (NIV) on 6 July 2024. [79]

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[4] Pakistan and Türkiye both reported cases recently; Report 2024-R25, Section 6.7.

The source of the infection remains unclear. The NIV did not find the virus in any mosquito samples collected from affected areas. Of the 10,000 homes that have been inspected, 311 were found to have mosquito-breeding sites.footnote[5] The Zika-causing mosquitoes might have been eliminated during the fogging exercises initiated by the civic authorities to control the disease transmission.

A suspected Zika death was reported in the Shivamogga district in Karnataka (state neighbouring Karnataka). The deceased was 74-year-old man.

6.13 Rift Valley Fever, Uganda

Endemic cases of Rift Valley fever were reported in western Uganda. So far, 9 confirmed cases of human infections have been recorded, 3 of which were fatal. To stop the spread of the disease, the authorities have initiated vector control, contact tracing, and public awareness campaigns, especially on handling dead animals. [80]

Note:

Rift Valley Fever (RVF) is a vector-borne viral zoonosis that primarily affects animals. The virus belongs to the genus *Phlebovirus*. It was first identified in 1931 in a sheep epidemic on a farm in the Rift Valley of Kenya. [81] [82] [83] [84]

The virus can also infect humans. It is transmitted by mosquitoes (*Culex* and *Aedes*) and blood-feeding flies. People can also become infected from contact with the blood or organs of infected animals as well as ingestion of raw or unpasteurised milk from infected animals. The disease is an occupational risk for people who work with animals (for example, veterinarians, herders, farm workers and people who work in slaughterhouses).

In humans, the disease ranges from a mild flu-like illness to severe haemorrhagic fever that can be lethal. It has been identified by WHO as one of the nine priority diseases due to its potential outbreak.

There are no approved vaccines or effective treatments for use in humans. Vaccines are available for animals; hence, the best way to prevent the spread to humans. The lack of diagnostic and surveillance tools means that the true prevalence of RVF is unknown.

6.14 Lymphatic filariasis, Columbia

The report of lymphatic filariasis (LF) in a 14-year-old boy in Columbia raises the concern about the resurgence of the disease. [85]

The patient had a history of progressive lymphoedema (swelling of the lymph nodes) which lasted 3 years. His symptoms began after a hunting trip in a forested area. Symptom onset

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[5] No documented reports of mosquito larvae found, therefore, it is assumed that none were found during the inspection.

started when he was 11 years old; he had presented with enlarged testicles, which became painful, recurrent episodes of fever, erythema (redness on the skin or mucous membranes) including red patches on the skin, itching, and pain in the left lower limb. He was initially diagnosed with malformed arteries with filariasis, as suspected. The diagnosis was only confirmed by a filarial-based polymerase chain reaction test.

The case shows the potential for the reemergence of LF in Colombia and highlights the disease manifestation in children, which had presented similarly to that in adults.

The last case of filariasis in Columbia was recorded in 2016, which involved a 33-year-old male patient. However, the parasite's presence or verification of a travel history or residency in endemic areas was not determined. LF was common in Columbia from the 16th century until the mid-20th century. Areas along the Magdalena River that are associated with oil prospecting were endemic for the disease. A decline in cases was observed in the 1960s and 70s, with only sporadic and subclinical cases reported. The disease disappeared subsequently, but the cause of the disappearance was unknown.

Note:

LF, commonly known as elephantiasis, is a neglected tropical disease (NTD). It is caused by an infection with filarial nematodes or parasitic roundworms such as *Wuchereria bancrofti*, *Brugia malayi*, and *Brugia timori*. The disease is mosquito-borne, and transmission occurs in various tropical and sub-tropical regions around the world, including Africa, Southeast Asia, and the Western Pacific. The nematodes circulate in the blood as microfilaria (**Figure 4**). The species of mosquito vector varies; *Culex* is widespread across urban and semi-urban areas, *Anopheles*, in rural areas, and *Aedes*, mainly in endemic islands in the Pacific. [85] [86] [87]

While infection is usually acquired in childhood, disease manifestation occurs much later in life. The hidden damage to the lymphatic system causes temporary or permanent disability; the infection impairs the lymphatic system and can lead to the abnormal enlargement of body parts, causing pain, severe disability and social stigma. In endemic countries, lymphatic filariasis has a major socioeconomic impact.

Lymphatic filariasis may be linked to increasing urbanisation trends and migration from previously endemic regions.

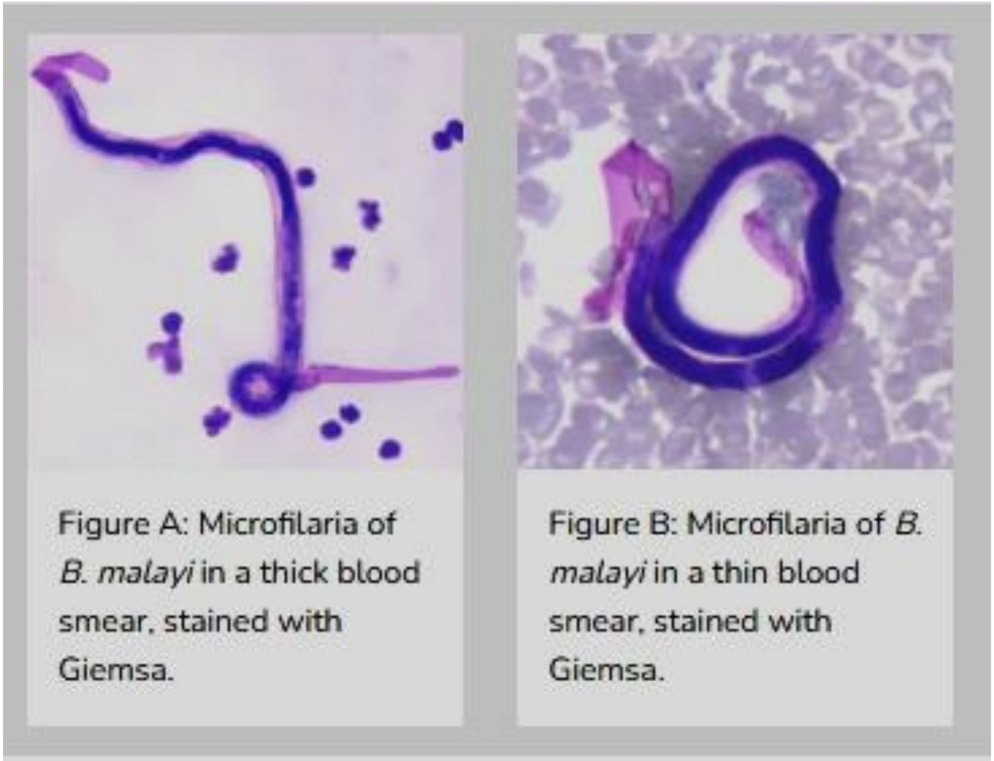

Figure A: Microfilaria of *B. malayi* in a thick blood smear, stained with Giemsa.

Figure B: Microfilaria of *B. malayi* in a thin blood smear, stained with Giemsa.

Figure 4. Photomicrograph of microfilariae (*Brugia malayi*) observed under 500x magnification. The image was modified from CDC - DPDx - Lymphatic Filariasis. Humans get infected from the bite of a microfilaria-infected mosquito. These mature in the lymphatics and subsequently migrate to the peripheral blood circulation where it can be taken up by mosquitoes during a blood meal.

6.15 Amoebic meningoencephalitis, India

Kerala reported a case of amoebic meningoencephalitis. This case is the fourth since May 2024, all of which involved children < 15 years old, three of which have died. The current case, a 14-year-old boy, is reportedly improving after he was hospitalised on 1 July 2024. [88]

Note:

Amoebic meningoencephalitis is also known as primary amebic meningoencephalitis (PAM). It is caused by the free-living amoeba *Naegleria fowleri,* which can be found in freshwater, lakes, rivers and soil around the world. The infection is rare, though usually fatal, even with treatment. It has a high mortality rate of > 90%.

Swimming in contaminated water exposes nasal mucous membranes to the organism, which gains entrance to the central nervous system via the nerves located there. Most patients are healthy children or young adults. [89] [90] [91]

6.16 Polio, multicountry

6.16.1 Wild poliovirus type 1

The wild poliovirus type 1 continues to circulate in countries where it is still endemic: [92]

- Afghanistan reported three wild poliovirus type 1 (WPV1) cases, all in Kandahar, raising the country's total for the year to 9. Last year Afghanistan reported a total of 6 WPV1 cases.
- Pakistan reported 8 new environmental cases of WPV1.

6.16.2 Vaccine-derived polio

Six countries, mostly in Africa, reported more polio cases involving two different vaccine-derived types: [92]

- Angola reported two circulating vaccine-derived poliovirus type 2 (cVDPV2) cases in two provinces, bringing its total for the year to 5.
- Chad reported one more case; the total for 2024 is 5.
- The Democratic Republic of the Congo (DRC) reported two additional cVDPV2 cases, as well as its fifth infection involving circulating vaccine-derived poliovirus type 1 (cVDPV1).
- Guinea reported its fourth cVDPV2 case of the year.
- Mozambique reported its first cVDPV1 case of 2024.

In the Middle East, Yemen reported 6 more cVDPV2 cases, bringing the total so far to 21.

6.17 Mpox

6.17.1 South Africa

An outbreak notice was released by the WHO about a spike in mpox cases in South Africa. The outbreak has resulted in 20 confirmed illnesses with 3 fatalities since May 2024. Cases were reported in three of the country's nine provinces: Gauteng, Western Cape, and KwaZulu-Natal. All of the cases are in men ages 17 to 43, 11 of whom had sex with men (MSM). At least 15 of the patients have HIV. [93] [94]

Exposures were related to sexual contact. The sudden appearance of the cases in people without international travel, the high HIV prevalence, and the high case-fatality rate suggested only a small portion of cases have been confirmed and that community transmission of the global clade 2 strain in South Africa is ongoing.

These cases are the first since 2022 when 5 cases were reported without fatalities.

6.17.2 Democratic Republic of Congo

Democratic Republic of Congo (DRC) has detected at least 25 new cases of clade 1 mpox in Goma, mainly in displacement camps. The new strain has been spreading in South Kivu province. [95] Goma is the capital and largest city of the neighbouring North Kivu province.[footnote6]

Twenty-thousand cases and > 1,000 deaths have been reported since 2023. Deaths mainly occurred among children. Over 11,000 cases including 443 deaths have been reported so far in 2024.

While vaccines have been approved to tackle the upsurge,[96] none are currently available outside of clinical trials.

6.18 Multiple diseases, multicountry

6.18.1 Chickenpox and hand, foot and mouth disease, Maldives

On the last week of June 2024 (epidemiology week 25), the Maldives reported a total of a total of 107 cases of chickenpox, 35 cases of hand, foot and mouth disease, and 737 cases of conjunctivitis. [97]

6.18.2 Foot and mouth-like disease, India

Foot and mouth disease-like illness has affected livestock in Kargil, India for the past 3 weeks. However, the absence of owners has been a major concern for the authorities as the lack of care from owners will cause unnecessary loss of livestock. [98]

6.19 African Swine Fever

6.19.1 Thailand

Reports of the reoccurrence of African Swine Fever (ASF) have been reported from various areas in Chiang Mai, Thailand. The possible reason could be due to the feed—known as swill feeding. The practice, which involves feeding pigs with food waste, is closely linked to the spread of the virus through contaminated feed, water, and the environment. [99]

6.19.2 Bhutan

Bhutan reported its first ASF outbreak in 2020, linked to stray pigs. It has since spread to 10 districts in the country. Between 2020 and 2024, 2,740 pigs have been culled to curb ASF, including 273 culled during the latest outbreak last month. The latest outbreak of ASF was confirmed in a commercial piggery farm in Wangdue, on 28 June 2024 and at Tshether farm in Punakha on 29 June 2024. On 27 June 2024, a sow died at a commercial piggery farm in Zawakha, 9 piglets died three days after the index case.[100]

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[6] A case in North Kivu was confirmed on 1 July 2024 and was reported to the WHO. It was linked to a suspected case from South Kivu. Refer to Report 2024-R24, Section 5.2.1.

6.19.3 South Korea

The ASF outbreak continues in South Korea with the the sixth case reported in North Gyeongsang Province. footnote[7] Authorities have planned on disinfecting the farm and culling the pigs as a precautionary step to prevent the disease from spreading.[101]

6.20 Norovirus outbreak, South Korea

Contaminated kimchi (fermented vegetables) has sicked at least 1,000 people in South Korea. They are staff and students from 24 schools. The food was likely contaminated with norovirus which was distributed through school meals. The virus was detected from environmental samples and the patients. Authorities (disaster and safety department) temporarily halted the production and sale of the product. [102]

7.0 Implications for Sarawak based on the views of SIDC

We may no longer actively track the SARS-CoV-2 virus as before, during the acute phase of the pandemic, however, we need to be constantly aware that it is still with us. As with other respiratory viruses, using the tools learnt is essential in preventing its spread. The virus continues to mutate, supplanting the current version that is circulating regionally and globally. As COVID-19 still kills, especially the vulnerable and those who at at higher risk of the disease, getting them vaccinated against the virus would help protect them against severe disease.

COVID-19 and other respiratory pathogens are to be considered for surveillance in the coming 2024 Olympics. Similar preparations should be considered by organisers in Sarawak when organising large-scale events. Participants and eventgoers should be made aware of the current situation of COVID-19 and other diseases of interest before travelling into the territory. Knowing the risks allows for better preparation. Foodborne diseases or illnesses should also be considered during the planning of any event to ensure the safety of all involved. Having the ‘people’s backs’ reassures eventgoers that they are always being considered and not left out in the planning of events.

Long-COVID is without a known mechanism (no single cause) or cure. Far from being psychosomatic, new studies have added weight that the condition is biological. Furthermore, the aftereffects of COVID-19 (the infection) linger.

Healthcare workers or agencies using OneHealth to manage diseases should be aware that lymphatic filariasis can enter Sarawak via the migration of people from endemic regions, and is likely linked to increasing urbanisation trends. To reiterate, active surveillance for the

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[7] The circulation of ASF has not stopped since 2021. Refer to Report 2024-R25, Section 6.3.

disease can be a beneficial tool for screening and containing transmission; we do not have to wait until a case manifests before acting on it.

Vector-borne diseases highlight the importance of knowing the endemicity of viral families and the possible vectors and/or hosts involved. These diseases involve not only humans (travellers/tourists) but also the agriculture industry that Sarawak relies on for its income.

The reports of the plague are a reminder that the disease never went away. While the disease may not have been reported in the ASEAN region, we need to be aware that is still around, and travel to endemic countries may expose a person to it.

Precision medicine is a tool that will enable treatment to be catered to an individual's needs. Biobanking would be the first phase of pioneering this effort in Sarawak.

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