Sarawak Infectious Disease Centre

23 September 2024

Global updates on COVID-19 and other diseases
Sarawak Infectious Disease Centre (SIDC)

Prepared by Geraldine Lee Phey Siing, Angelesa Runin Unggit and Sunita Shamsul
(Science Team, SIDC)
Edited by Prof Andrew Kiyu (FMHS, UNIMAS)

Contents

Summary

- New COVID Variant XEC may outpace others this autumn (northern hemisphere).
- Molnupiravir provides only modest benefits for vaccinated, higher-risk adults with COVID-19.
- Researchers have discovered an antibody that could counter all known coronavirus variants.
- Research suggests that immune-ecological interaction will determine population immunity against the SARS-CoV-2 virus, irrespective of variant.
- Wastewater surveillance again has been proven a better way to detect pathogens.
- Malaysia confirmed a local case of clade II mpox.
- Nipah virus kills another person in India.
- HPV viral genotypes have variable effects on the quality of sperm.
- The toll of drug-resistant infections is predicted to rise by 70% by 2050.

1.0 Variants

Omicron XEC subvariant

XEC is likely a recombinant of the KP.3.3 and KS.1.1 subvariants, both of which are among the many sub-lineages derived from the BA.2.86 variant that emerged in 2023 and has dominated since.

XEC was first identified in Germany in June 2024 and has been gradually increasing in frequency. It has now been detected in Europe, North America, and Asia, with over 500 cases sequenced to date. It is most prevalent in Central Europe, where it accounts for more than 10% of all COVID-19 infections.

While it is less common in other regions, its global frequency is on the rise, potentially becoming the dominant subvariant this winter. In August 2024, experts suggested that the variant might take weeks to several months to spread more widely. According to the CDC's data from 14 September 2024, XEC may eventually surpass the current dominant subvariant circulating in the US—KP.3.1.1 constitutes approximately 52.7% of cases. [1–5]

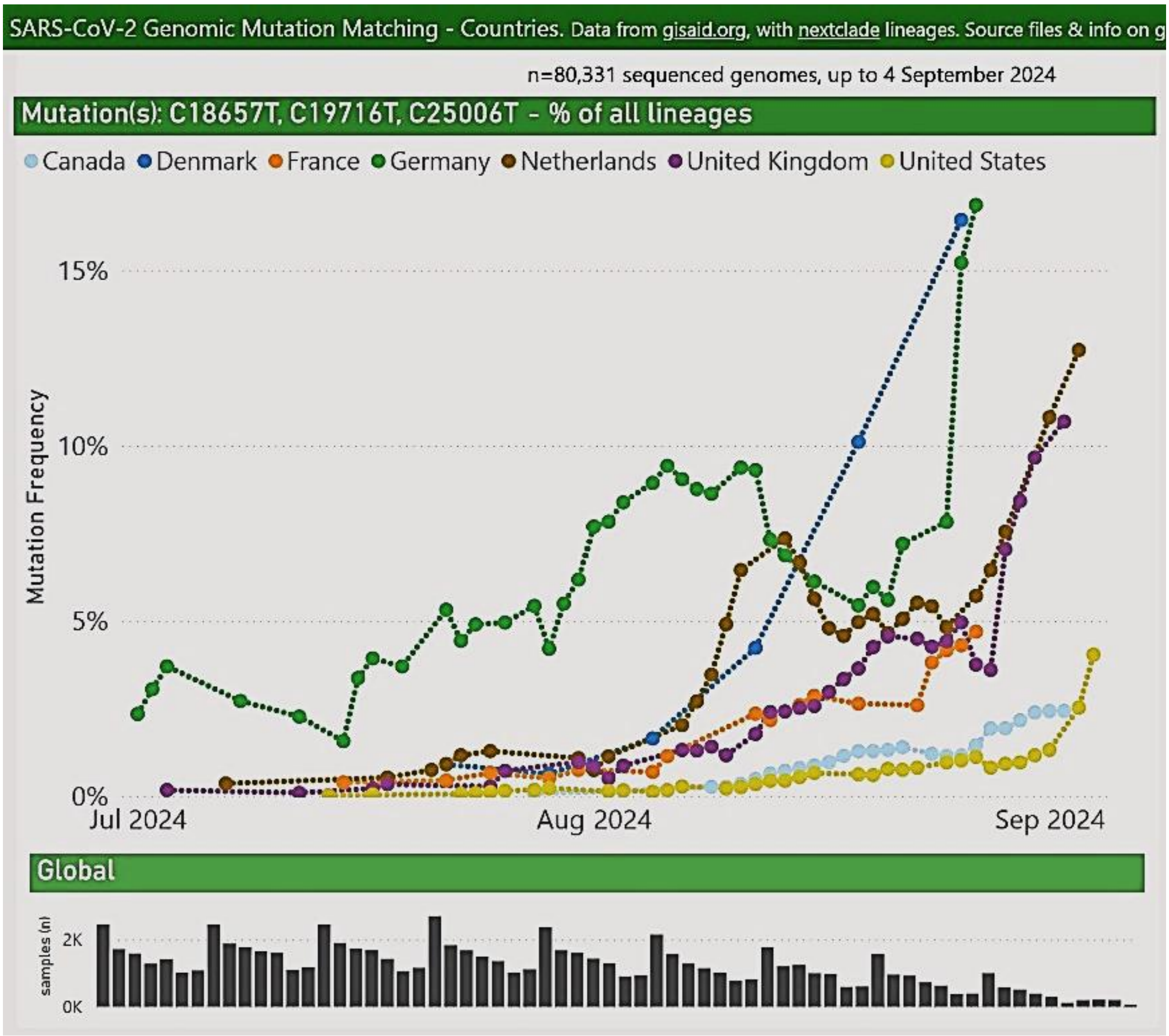

Figure 1. A graph showing the leading countries reporting the XEC subvariant as of 4 September. Strong growth is observed in Denmark and Germany (dark blue dots and green dots, respectively, at 16-17%), and in the UK and Netherlands (purple dots and brown dots, respectively, at 11-13%). The subvariant's activity is picking up in the US and Canada.
The figure was obtained from the blog post https://x.com/Mike_Honey_/status/1835107922797588806/photo/1.

XEC infection causes similar symptoms to previous COVID-19 variants, including fever, sore throat, cough, loss of smell, loss of appetite, and body aches. As part of the Omicron lineage, vaccines and booster shots are expected to provide adequate protection against severe illness and hospitalisation. Experts continue to monitor the XEC variant to gain a better understanding of its symptoms and impact.

Note:
KS.1.1, known as a FLiRT variant, is characterised by mutations in the virus's spike protein, where phenylalanine (F) changes to leucine (L) and arginine (R) to threonine (T). KP.3.3, classified as a FLuQE variant, involves a mutation where glutamine (Q) is replaced by glutamic acid (E) in the spike protein, enhancing the virus's binding to human cells.

2.0 Origins, update

New genetic analysis for the origins of COVID-19 has narrowed down to a short list of animals that possibly helped spread it to people. [6,7] The list included the raccoon dog, hoary bamboo rat, dog, European rabbit, Amur hedgehog, Malayan porcupine, Reeves's muntjac, Himalayan marmot, and masked palm civet. It was suspected that the infected animals were first brought to the Wuhan market in late November 2019, which subsequently triggered the pandemic. Subpopulations of these animals—originally found near or together with the animals listed—are known to be natural reservoirs of related SARS-like coronaviruses. [8]

Scientists from Europe, the US and Australia analysed data previously released by experts at the Chinese Center for Disease Control and Prevention. It included 800 samples of genetic material Chinese workers collected on 1 January 2020 from the Huanan seafood market, the day after Wuhan municipal authorities first raised the alarm about an unknown respiratory virus.

When scientists from China published genetic sequences they found last year, the materials did not identify any animals possibly infected with the coronavirus. These new findings used evolutionary analysis of the genetic material. It estimates when a virus first emerged and what its closest genetic relation might be (similar to carbon dating). It is then possible to determine the virus's age by understanding how quickly the SARS-CoV-2 virus mutates. The analysis can identify specific organisms from any mixture of genetic material collected in the environment providing a snapshot of the situation at the market before the pandemic began.

This significant finding shifts to favour animal origins of the pandemic, moving away from the laboratory leak theory. It also closely aligns with the initial findings shared by Chinese researchers in the journal *Nature* in 2023. [9]

Questions, however, remain about how the animals got to the market.

In April 2024, it was reported that the Chinese government froze meaningful domestic and international efforts to trace the virus from the first weeks of the outbreak—as early as December 2020—despite statements supporting open scientific inquiry. The efforts became a victim of political infighting which caused missed opportunities by local and global health officials to narrow the possibilities in search for the origins. [10,11]

3.0 Immunity and seroprevalence

Antibody vs COVID-19 infection

Researchers have discovered an antibody that could counter all known coronavirus variants that cause COVID-19, and others related that can infect animals. The SARS-CoV-2 virus uses the spike (S) protein to enter the host cell, and antibodies against the S-protein could effectively block its entry.

The neutralising plasma antibody SC27 (**Figure 2**) was isolated using Ig-Seq.[Footnote1] This method has paved the way for its large-scale production for future treatments and research on hybrid immunity against the SARS-CoV-2 virus. The virus has evolved rapidly, with each variant exhibiting unique characteristics, often leading to increased resistance to vaccines and other treatments. The SC27 antibody, however, recognises these varying features of the spike proteins across different COVID-19 variants. [12,13]

Protective antibodies function by binding to the spike protein, a key component the virus uses to attach to and infect body cells. By blocking this protein, antibodies can prevent infection. SC27 has demonstrated the ability to recognise the diverse characteristics of spike proteins in various COVID-19 variants. The decoding of the original spike protein's structure was a significant milestone, enabling the development of vaccines and other treatments and validating SC27's effectiveness.

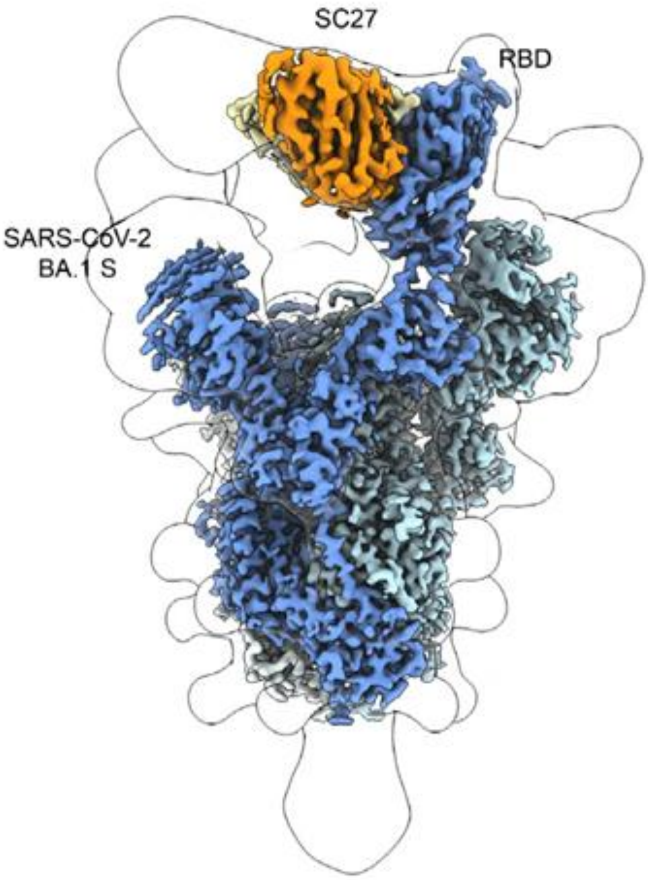

Figure 2. A Coulomb potential map[Footnote2] shows SC27 (in orange and yellow) bound to the SARS-CoV-2 BA.1 S-protein (in blue). The SC27 antibody blocks the receptor binding domain (RBD) from attaching to the host cell, preventing the virus from fusing with and entering the cell. The figure was adapted from the original in Hybrid immunity to SARS-CoV-2 arises from serological recall of IgG antibodies distinctly imprinted by infection or vaccination (cell.com).

---

[1] A high throughput method to sequence antibodies/immunoglobulins. [48]

[2] These maps show the electrical charge distribution of molecules three-dimensionally, enabling the visualisation of variably charged regions of a molecule. Knowledge of the charge distributions can then be used to determine how molecules interact. [49,50]

4.0 Tools

Wastewater surveillance better at detecting pathogens

Following the launch of the National Wastewater Surveillance System (NWSS), the National Academies of Sciences, Engineering and Medicine recommended 5 actions for a more robust NWSS to support public health including better readiness for future pandemics. This report is the second and final part of the Academies' Committee on Community Wastewater-Based Infectious Disease Surveillance evaluation of wastewater surveillance (WWS).[14,15]

It details the technical constraints and opportunities to improve wastewater surveillance for the prevention and control of infectious diseases in the US. The 5 recommendations involve improvements in the consistency and quality of national wastewater sampling, testing, and data analysis. It also identified research and technology development needs for an NWSS that can serve ongoing and changing public health needs in the country: [16]

1. Optimise state and local sampling sites while improving the representativeness of wastewater data through the use of statistical tools and methods. This can boost equity in unrepresented areas and increase the value of investments in the system.
2. Substantially improve the quality and comparability of wastewater data across localities by determining optimal sampling, lab analytic methods, or performance criteria and requiring them as a condition of participation in the NWSS.
3. Increase data analysis, visualisation, and interpretation by working with external partners to build models that integrate wastewater and other forms of surveillance data and strengthen its role in forecasting and estimating disease prevalence.
4. Strategically add more endemic pathogens, for example, respiratory syncytial virus (RSV) and influenza, to SARS-CoV-2 routine surveillance.
5. Increase capacity for early detection of emerging pathogens, including those with pandemic potential, to facilitate early intervention.

Though a cost-benefit analysis was not conducted, investing in wastewater surveillance (WWS) capacity should consider the vast economic and social cost of responding to infectious disease spread when it is not detected and arrested early.

The phase I report, released in 2023, examined the usefulness of the NWSS during the COVID-19 pandemic. It described the potential value of a robust national wastewater surveillance system beyond COVID-19 and provided recommendations to increase the public health impact of such a system.[17]

Both reports were produced at the request of the CDC.

5.0 Outcome

5.1 COVID-19 antiviral: molnupiravir, update from the UK

New research from the **P**latform **A**daptive trial of **NO**vel antivi**R**als for e**A**rly treat**M**ent of covid-19 **I**n the **C**ommunity. (PANORAMIC) showed that the antiviral, molnupiravir, provides only modest benefits for vaccinated, higher-risk adults with COVID-19. The study included 577 participants in the UK, who were randomly assigned to receive either a 5-day course of molnupiravir or standard care without antiviral treatment. [18,19]

Initially, molnupiravir reduced the patients' viral load faster than standard care. By day 5, 14% of the molnupiravir group had cleared the virus, compared to just 2% in the standard care group. However, after this point, the rate of viral clearance in the molnupiravir group slowed down. By day 9, only 48% of patients treated with molnupiravir had cleared the virus, while 56% of those in the standard care group had done so.

The study also found that the SARS-CoV-2 virus from the molnupiravir group had more mutations than those in the standard care group. Some of these mutated viruses were grown in the lab from samples taken up to 9 days after treatment, indicating the possibility of transmission from treated patients.

The researchers suggested that a longer course of molnupiravir might be needed to clear the virus and prevent its spread fully. The body's immune response is examined by measuring S protein antibody levels. The molnupiravir group had 6,200 U/mL of antibodies after treatment, compared to 8,400 U/mL in the standard care group. This lower antibody response could be because the initial viral load was reduced, leading to a weaker immune reaction. As a result, patients treated with molnupiravir might be more susceptible to reinfection than those who received standard care. These findings raise important questions about the effect of molnupiravir on long-term immunity.

5.2 SARS-CoV-2 virus and population-wide immunity

A study examined the combined effect of individual immune responses to the SARS-CoV-2 virus on population-level immunity. The research was conducted on 1,045 participants (aged ≥5 years) from the Northwest and Southeast regions of the Dominican Republic. It aimed to understand how population-wide immunity against high-transmission pathogens, which provide only partial and temporary immunity, is influenced by infection or vaccination. [20,21]

The findings suggest that immune-ecological pressures resulted in a single, population-wide peak in antibody levels (immune markers) against SARS-CoV-2 S-proteins, regardless of the number of infections or vaccinations. It also indicates the existence of an "optimal" population-wide antibody titre threshold. In individuals with antibody levels below this threshold, concentrations rise until the threshold is reached. Conversely, the titres gradually decrease in those with higher antibody levels (due to recent infection or vaccination), converging towards the population-wide optimal level.

The study revealed that population-level immune responses to COVID-19 follow a distinct pattern, differing from individual immune responses, where antibody titres fluctuate based on exposure. At the population level, immune responses tend to stabilise around a set point, unaffected by antigen exposure, age, gender, or geography. These findings are crucial for epidemiologists and policymakers, as the population-wide immune responses are not random but follow predictable patterns.

5.3 Transmission risk in various settings

The association between SARS-CoV-2 transmission and different environments was studied in France between 27 October 2020 and 2 October 2022, involving 175,688 cases and 43,922 controls. Participants completed an online survey providing information about their demographics, health, household, and recent exposures within 10 days before symptoms or diagnosis. The study found a consistent increase in infection risk across various settings (**Table 1**). [22,23]

Table 1. Summary of the increased risk of infection for settings and activities extracted from Risk of SARS-CoV-2 infection in professional settings, shops, shared transport, and leisure activities in France, 2020–2022.

Location/ Activity	Odds Ratio (OR) Range
Open-space offices	1.12 to 1.57
Long-distance trains	1.25 to 1.88
Convenience stores	1.15 to 1.44
Takeaway delivery	1.07 to 1.28
Carpooling with relatives	1.09 to 1.68
Taxis	1.08 to 1.89
Airplanes	1.20 to 1.78
Concerts	1.31 to 2.09
Night-clubs	1.45 to 2.95

No increased risk was found in short-distance shared transport, carpooling through platforms, markets, supermarkets, malls, hairdressers, museums, cinemas, outdoor sports events, or swimming pools. The lack of increased risk in retail spaces, hairdressers, and beauty salons suggested that these venues maintained low occupancy and effective health measures. After an initial period of increased risk (odds ratio, OR, 1.97), bars and restaurants were no longer tied to an increased risk of transmission after reopening in 2021, except for bar patrons <40 years old.

The settings linked to higher infection risk shared common traits: mostly indoor, have limited air circulation, involve close, maskless interactions, sometimes include loud speaking or singing, and typically involve prolonged exposure. Improving ventilation and air filtration in these spaces could reduce the risk of transmission. Although costly, such measures could offer long-term public health benefits and should be evaluated for feasibility and effectiveness. [22]

6.0 Mpox

6.1 Malaysia

Kementerian Kesihatan Malaysia (KKM) confirmed a new case of mpox on 16 September 2024. This is the 10th case since the first was confirmed in July 2023. This latest case involved the clade II mpox virus (MPXV) detected in a Malaysian male who did have a history of travel within 21 days before the onset of symptoms. He presented with fever, headache, and cough on 11 September, with a rash appearing on 12 September 2024. The patient is currently in isolation and is reportedly in stable condition. All contacts of the patient are being identified, and their health status will be monitored as per KKM protocols.[24,25]

KKM is using various media and social media channels to inform the public, encouraging increased preparedness and better self-health practices. Suspected cases should be offered mpox testing and reported to the nearest District Health Office (PKD) via the e-notification system for further investigation, prevention, and control measures.[26,27]

This latest case was allegedly shared on ‘X’ (previously known as Tweeter) before KKM’s confirmation. According to reports, the post related to an individual’s inquiry about the mpox test. It also shared images of lesions/rash. It was criticised for fearmongering as it implied specific activity (in this case, shared sauna space) and groups of people (lesbian-gays-bisexual-transgender, LGBT) with the disease’s transmission. It was subsequently deleted. [26]

KKM reiterated for the public to refer to (trusted) KKM social media accounts for information regarding mpox. [28]

6.2 Vaccines

6.2.1 Canada

Canada is donating 'up to 200,000' doses of Imvamune (another name for the Bavarian Nordic Jynneos vaccine) mpox vaccine. The number to be donated would depend on the receiving countries' capacity for storage and administration. The donation is meant to address the inequity of vaccine access for the outbreak in the African continent. Canada has a sufficient supply of mpox vaccines for its own needs. [29]

6.2.2 Rwanda

Rwanda began vaccinating its people against mpox on 18 September 2024. To date, approximately 500 people have been vaccinated, while the country has received a total of 1,000 doses of the mpox vaccine. The campaign is focused on the 7 districts bordering the Democratic Republic of Congo (DRC) which has been the main focus of the outbreak that accounted for 90% of the continent’s cases. The vaccines are targeted at high-risk people, including truck drivers and sex workers. [30]

7.0 Others

7.1 Influenza H5N1: observed, the US

The risk of H5N1 spreading to humans is still low, but as it continues to circulate in cattle, there's a greater chance it could mutate and trigger a flu pandemic. Six months into the outbreak, H5N1 is still spreading among US dairy cattle and farmworkers. So far, the virus has been detected in 192 cattle herds across 13 states, 13 people, and 6 cats. Despite this, there are still many unanswered questions about the outbreak. [31,32]

Federal officials mentioned the virus causes only mild symptoms in cows. However, a study found that cows on infected farms were dying at twice the normal rate, and some were infected without showing symptoms. H5N1 doesn't seem to spread easily through cattle's respiratory systems. Instead, most cases seem to come from contaminated milk, milking equipment, vehicles, or farmworkers' clothing.

Experts suggest that the virus spreads mechanically (through objects or people) and emphasise that this method of transmission makes the outbreak controllable since there is no wildlife reservoir for the virus. However, the current measures aren't strong enough to stop the spread. Ideally, farms would test pooled milk samples and limit cattle and worker movement until the virus is eradicated. However, federal guidelines only require testing when cattle are moved between states, and many states only test cows that show obvious signs of illness. So far, only Colorado has required bulk milk testing, which led to the discovery of 10 more infected herds within two weeks of the rule going into effect on 22 July 2024. The Agriculture Department has introduced a voluntary testing program, but out of about 24,000 US dairy farms, only 30 are participating. [33]

Genetic data suggests the outbreak in the US started with a single spillover from birds to cattle and then spread across the country. There's a small possibility that the virus could die out on its own, but this might take months or even years if it happens at all.

7.2 Nipah virus, India

Kerala, a southern state in India, reported a death from the Nipah virus on 16 September 2024. The deceased, a 24 year old student from Malappuram district, began showing fever symptoms on 4 September 2024; he had visited several hospitals before his symptoms were flagged as suspected Nipah infection. He died 5 days later. The confirmation was made on 9 September 2024 by the National Institute of Virology in Pune. [34]

According to the WHO, initial symptoms include fever, headaches, myalgia (muscle pain), vomiting and sore throat. Neurological signs including encephalitis can develop after.

Approximately 151 people who came into contact with the deceased (primary contact) have been under observation to prevent the spread of the virus. Five other people who have developed primary symptoms of a Nipah infection have had blood samples sent for tests. This is the second death caused by NiV since July 2024; the first victim was a 14 year old boy also from the same district.

Kerala is a hotspot for NiV. This incident is the sixth since 2018 where Kerala faces an outbreak, coinciding with the Onam (religious) festival. The festivities have been overshadowed by fears of the virus.

7.3 Polio

7.3.1 Gaza

The first round of the vaccination campaign which began on 1 September 2024 has reached 90% coverage. According to the United Nations Relief and Works Agency for Palestine Refugees (UNRWA), over 446,000 children ≤10 years old in central and south GAZA had received the first dose. Despite access restrictions, evacuation orders and shortages of fuel, the second and final round began on 10 September intending to vaccinate 200,000 children in the north of the Palestinian territory.[35,36]

7.3.2 Multicountry updates

Three more countries have reported new polio cases as of 18 September 2024: [37,38]

<u>Wild poliovirus type 1</u>:

- Afghanistan reported one case of wild poliovirus type 1 (WPV1) in the Kandahar province, bringing the total number of cases for 2024 to 19.

<u>Circulating vaccine-derived poliovirus type 2 (cVDPV2)</u>:

- Cameroon reported two cases from Est province. These are the first cases for the country in 2024.
- Nigeria reported four cases from the Yobe province, bringing the total in 2024 to 53.

Positive environmental isolates were obtained from the following countries:

- Afghanistan; 5 WPV1.
- Niger; one CVDPV2
- Chad, South Sudan and Zimbabwe each reported two cVDPV2, and
- Pakistan; 30 WPV1.

7.4 Ebola research, the US

Emergent Biosolutions has been awarded with a contract modification executing an option period by the Biomedical Advanced Research and Development Authority (BARDA), part of the US Department of Health and Human Services. The award, valued at USD 41.9 million, is a research and development option to further develop and scale up the drug 'Ebanga'.

Research and development will cover engineering and scale-up process validation, long term stability, and commercial readiness. The drug was previously approved by the US Food and Drug Administration (FDA) in December 2020 as a single infusion for the treatment of Ebola Zaire virus disease.[39,40]

7.5 HPV linked to changes in sperm

Researchers from Argentina have found that the human papillomavirus (HPV) is linked to alterations towards human sperm. HPV has long been tied to most cervical cancer cases. However, a new study has suggested that high-risk HPV strains are associated with a higher percentage of sperm deaths. Studies on semen samples from those infected with high-risk strains found that there was a lower count of white blood cells and an elevation of reactive oxygen species (ROS), which can damage and alter the DNA of sperms. However, this correlation was not found in semen samples from individuals infected with low-risk HPV. [41]

The results of this study were supported by a previous study done on the effects of HPV on lower sperm count, reduced motility and viability, indicating the negative health impact it has on male fertility. [42]

7.6 Drug-resistance and deaths

A systematic analysis found that antimicrobial-resistant (AMR) bacterial infections directly caused more than 1 million deaths worldwide annually from 1990 to 2021. The number is projected to increase by almost 70% over the next 25 years.[43]

The global study relied on a statistical modelling approach which used 520 million individual records from a variety of sources (such as hospital data, death records, antibiotic use surveys, pharmaceutical sales data, insurance claims data, and published scientific studies). It included 22 pathogens, 84 pathogen-drug combinations, and 11 infectious syndromes from 204 countries and territories. [44]

The analysis is summarised as follows (paraphrased): [44,45]

- Data from 2021 showed that globally, 1.14 million deaths were attributable to bacterial AMR, a little higher than the 1.06 million deaths that were reported in 1990. Bacterial AMR was also associated with an estimated 4.71 million deaths in 2021; similar to that in 1990.
- Forecasting analysis showed that by 2050, an estimated 1.91 million AMR-attributable deaths and 8.22 million AMR-associated deaths could occur every year worldwide.

From 2025 to 2050, a cumulative of 39.1 million deaths attributable to AMR could occur.

  - With improved access to healthcare and antibiotics, however, an estimated 92 million lives could be saved.
- Age-wise:
  - AMR-attributable deaths among children <5 years old decreased by 60.4% from 1990 to 2021, and deaths associated with AMR decreased by 63.3%.
    - Sepsis deaths among children <5 years old decreased by over 60% over this period; however, they are harder to treat.
    - The decline in deaths in young children coincided with widespread paediatric vaccination efforts and improved access to WASH (water, sanitation, and hygiene), and infection prevention and control strategies which proved highly effective in reducing AMR burden.
    - The former could prevent an estimated 430,000 AMR-associated deaths, from both direct prevention of resistant infections and reduction of antibiotic use.
  - Among those ≥70 years old, deaths directly attributable to AMR increased by 89.5%, and AMR-associated deaths increased by 81.3%, from 1990 to 2021.
    - Improved access to antibiotics and better care could have the greatest benefits in South Asia, sub-Saharan Africa, and parts of Southeast Asia, East Asia, and Oceania.
  - South Asia, Latin America, and the Caribbean will be the regions with the highest all-age AMR mortality rate; the largest increases in deaths attributable to AMR would be among those ≥70 years old (65.9%).
- From 1990 to 2021, there was an increase in AMR-attributable deaths for 12 pathogens.
  - In 2021, 6 pathogens were associated with at least 100,000 AMR-attributable deaths annually: *Staphylococcus aureus*, *Acinetobacter baumannii*, *Escherichia coli*, *Klebsiella pneumoniae*, *Streptococcus pneumoniae*, and *Pseudomonas aeruginosa*.
  - Deaths due to methicillin-resistant *S. aureus* (MRSA) increased the most globally, leading to 130,000 AMR-attributable deaths in 2021—doubling from 57,200 in 1990.
  - Among Gram-negative bacteria, resistance to carbapenems increased more than any other type of antibiotic, from 127,000 in 1990 to 216,000 in 2021.
  - *S. pneumoniae* had the most substantial decline in both AMR-associated and AMR-attributable deaths—from 258,000 in 1990 to 155,000 in 2021.
- Deaths attributable to AMR varied across regions.
  - 5 regions—Western sub-Saharan Africa, tropical Latin America, high-income North America, Southeast Asia, and South Asia—had increases of >10,000 AMR-attributable deaths over the 31 years (1990 -2021).

  - Among children <5 years old, AMR-attributable and -associated deaths decreased in all regions except Oceania.
  - Among those >5 years old, AMR mortality increased in all regions except western and central Europe.

The findings highlighted that AMR has been a significant global health threat for decades; the threat is growing. However, with the right mitigation/tools, for example, through vaccination programmes, WASH, and the correct use of antibiotics, the threat can be controlled. There is much to be done to address AMR and develop new antimicrobials to circumvent this issue.

7.7 Salmonellosis, the US

Salmonellosis was detected in 65 individuals from across 9 states in the US. No fatalities have been reported and 24 of the individuals were hospitalised. These additional cases are part of the ongoing multistate *Salmonella* outbreak which began in May 2024. The eggs were recalled after environmental samples were tested positive for the bacteria (*Salmonella sp*.). Most of the cases were reported from Wisconsin and Illinois, while others came from California, Utah, Colorado, Minnesota, Iowa, Michigan and Virginia.

This is the second reported outbreak of salmonella after a similar outbreak tied to cucumbers, in which the cause of the outbreak was blamed on unethical usage of untreated canal water by farmers to grow cucumbers. [Footnote 3]

7.8 Oropouche virus, the US

The CDC has reported 22 new cases of Oropouche virus (OROV) as of 18 September 2024. The cases were all imported. This brings the total cases to 74 in 5 states (Florida, New York, Kentucky, Colorado and California; **Figure 3**). To date, one neuroinvasive form of the disease has been reported. Most of the illnesses were reported from Florida (70 cases), all of which had just returned from Cuba with the majority from Miami-Dade County. Although not a serious condition, an alert was issued by the CDC in August 2024 on a sudden rise in imported cases and encouraged jurisdictions to report cases to their ArboNET surveillance system. [46,47]

---

[3] Report 2024-R37, Subsection 6.11

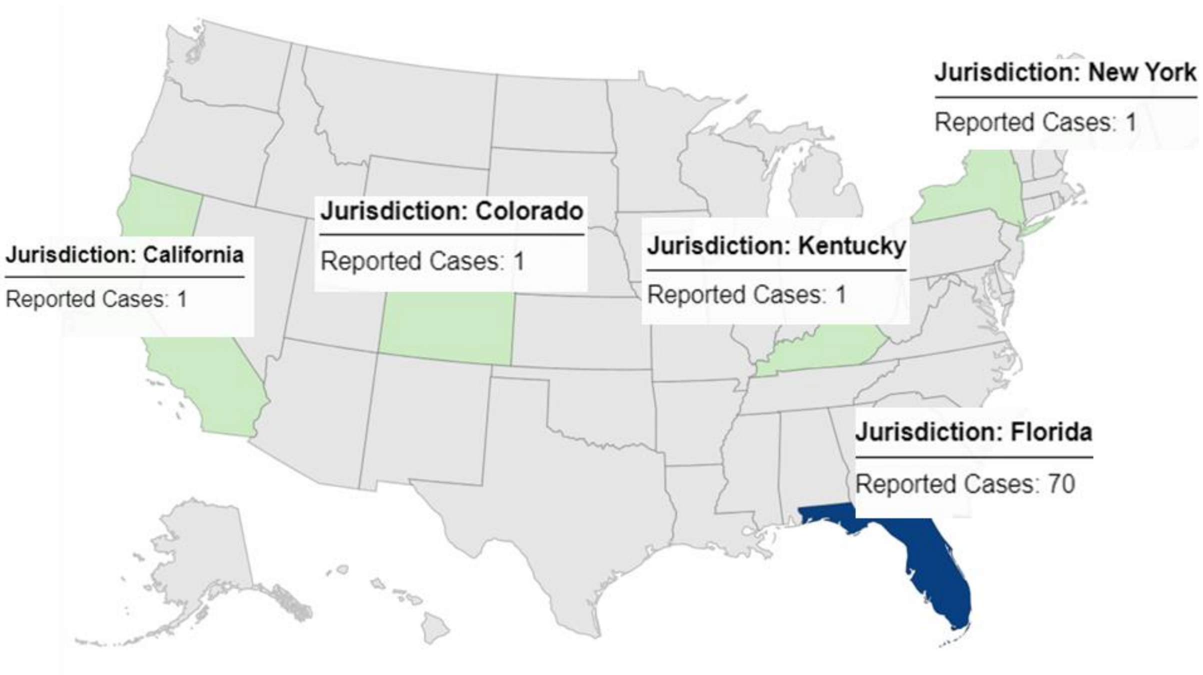

Figure 3. Geographical distribution of OROV infections in the US as of 19 September 2024. Image obtained from Current Year Data (2024) | Oropouche | CDC

The Americas region has seen a rapid rise in OROV cases since August 2024 and has been linked to adverse foetal defects, some resulting in foetal deaths, birth defects and miscarriages. Transmitted by infected midges, its initial symptoms are like those of dengue, Zika, and Chikungunya; including fever, chills headaches and myalgia. Footnote [4]

8.0 Implications for Sarawak based on the views of SIDC

The latest update about COVID-19 transmission suggests that the risk for transmission still exists especially when indoors, in small places with poor ventilation where people are in close proximity to one another (karaoke rooms are an example).

The COVID-19 pandemic sparked widespread implementation of wastewater surveillance (WWS) in communities across the US to help track the spread of the disease. In contrast to clinical laboratory testing that tracks individual cases of infection, WWS provides a way to measure the amount of genetic material from pathogens coming from homes, businesses, and other institutions that share a sewer system.

WWS should be harnessed by Sarawak to know “what is out there” to subsequently narrow down the area(s) that need the necessary mitigation exercise(s). It acts similarly to a triage, especially when manpower and logistics are a problem. WWS will work well in urban or semi-urban settings. However, disease surveillance in rural areas needs other methods.

---

[4] Report 2024-R36, Section 4.3.2

Likewise, surveillance in farms and agriculture settings. The methods for the latter two (rural settings and farms and agriculture) need to be planned to capture as much of the disease status of our population and the health of our waterways. AMR surveillance can be incorporated into population WWS. We in Sarawak should know if we have an AMR problem and if there is, the extent of it.

Understanding the origin of the SARS-CoV-2 virus is very important: to understanding what happened with COVID-19, and understanding how future pandemics emerge. It also raises the issue of improving laboratory safety and the potential for the accidental release of dangerous pathogens. The latest update also points to the role of wildlife and farmed animals in disease outbreaks. Unregulated trade of the former can pose a serious risk to future outbreaks. Disease surveillance also not only includes the survey of farmed animals but also wildlife.

Human Papilloma Virus (HPV) may permanently ruin both male and female fertility if it is still predominantly seen as a "woman's problem." Educating males of their role in keeping the virus in check is as important as getting young people (females and males) vaccinated against the infection.

Reference

1. Lombardi, J. COVID-19: New XEC Strain ‘Just Getting Started’ Sparks Concern Amid Summer Wave Of US Cases. *Daily Voice* https://dailyvoice.com/new-york/whiteplains/covid-19-new-strain-just-getting-started-sparks-concern-amid-summer-wave-of-us-cases/ (2024).

2. CDC. *COVID Data Tracker*. https://covid.cdc.gov/covid-data-tracker/#variant-proportions (2024).

3. Mike Honey@Mike_Honey_.(Sep 15,2024). Recombinant variant XEC is continuing to spread, and looks a likely next challenger against the now-dominant DeFLuQE variants (KP.3.1.1.*). https://x.com/Mike_Honey_/status/1835107922797588806.

4. Putka, S. New COVID Variant XEC May Outpace Others This Fall. *MedPage Today* https://www.medpagetoday.com/special-reports/features/112016?xid=nl_mpt_DHE_2024-09-18&mh=2e0e77d706cf2574d6370ea746f61244&utm_source=Sailthru&utm_medium=email&utm_campaign=Daily Headlines Evening 2024-09-18&utm_term=NL_Daily_DHE_dual-gmail-definition (2024).

5. expert comment on XEC COVID-19 variant. *Science Media Centre* https://www.sciencemediacentre.org/expert-comment-on-xec-covid-19-variant/ (2024).

6. New Genetic Analysis of Animals in Wuhan Market in 2019 May Help Find COVID's Origin. *MedPage Today/AP* https://www.medpagetoday.com/infectiousdisease/covid19/112034?xid=nl_mpt_DHE_2024-09-19&mh=2e0e77d706cf2574d6370ea746f61244&utm_source=Sailthru&utm_medium=email&utm_campaign=Daily Headlines Evening 2024-09-19&utm_term=NL_Daily_DHE_dual-gmail-definition (2024).

7. Goodman, B. New analysis of samples from Wuhan animal market supports its role as a central site of early spread of Covid-19. *CNN* https://edition.cnn.com/2024/09/19/health/huanan-animal-market-analysis-covid-19/index.html (2024).

8. Crits-Christoph, A. *et al.* Genetic tracing of market wildlife and viruses at the epicenter of the COVID-19 pandemic. *Cell* **187**, 5468-5482.e11 (2024).

9. Liu, W. J. *et al.* Surveillance of SARS-CoV-2 at the Huanan Seafood Market. *Nature* **631**, 402–408 (2024).

10. Kang, D. & Cheng, M. Toxic: How the search for the origins of COVID-19 turned politically poisonous. *AP News* https://apnews.com/article/china-covid-virus-origins-pandemic-lab-leak-bed5ab50dca8e318ab00f60b5911da0c (2024).

11. Kang, D., Cheng, M. & McNeil, S. China clamps down in hidden hunt for coronavirus origins. *AP News* https://apnews.com/article/united-nations-coronavirus-pandemic-china-only-on-ap-bats-24fbadc58cee3a40bca2ddf7a14d2955 (2020).

12. Antibody that can counter all variants of COVID-19 discovered-Here's what we know so far. *Financial Express, PTI* https://www.financialexpress.com/life/science-antibody-that-can-counter-all-variants-of-covid-19-discovered-heres-what-we-know-so-far-3606529/ (2024).

13. Voss, W. N. *et al.* Hybrid immunity to SARS-CoV-2 arises from serological recall of IgG antibodies distinctly imprinted by infection or vaccination. *Cell Rep Med* **5**, 101668 (2024).

14. National Wastewater Surveillance Strengthens U.S. Public Health Efforts and Future Pandemic Prevention, Says New Report. Preprint at https://www.nationalacademies.org/news/2024/09/national-wastewater-surveillance-strengthens-u-s-public-health-efforts-and-future-pandemic-prevention-says-new-report#:~:text=WASHINGTON — Wastewater surveillance for both,Sciences%2C Engineering%2C and Medic (2024).

15. Beusekom, M. Van. National Academies: Wastewater surveillance could be even better for detecting pathogens. *CIDRAP (University of Minnesota)* https://www.cidrap.umn.edu/covid-19/national-academies-wastewater-surveillance-could-be-even-better-detecting-pathogens (2024).

16. *Increasing the Utility of Wastewater-Based Disease Surveillance for Public Health Action. A Phase 2 Report*. https://nap.nationalacademies.org/read/27516 (2024).

17. *Wastewater-Based Disease Surveillance for Public Health Action*. https://nap.nationalacademies.org/catalog/26767/wastewater-based-disease-surveillance-for-public-health-action (2023).

18. Harris, V. *et al.* Health outcomes 3 months and 6 months after molnupiravir treatment for COVID-19 for people at higher risk in the community (PANORAMIC): a randomised controlled trial. *Lancet Infect Dis* (2024) doi:10.1016/S1473-3099(24)00431-6.

19. Antiviral molnupiravir offers only modest longer-term benefits for COVID-19, finds new paper from the PANORAMIC trial. *Nuffield Department of Primary Care Health Care Health Science, University of Oxford* https://www.phc.ox.ac.uk/news/antiviral-molnupiravir-offers-only-modest-longer-term-benefits-for-covid-19-finds-new-paper-from-the-panoramic-trial (2024).

20. Nilles, E. J. *et al.* Convergence of SARS-CoV-2 spike antibody levels to a population immune setpoint. *EBioMedicine* **108**, 105319 (2024).

21. de Souza, H. F. Study reveals population-wide immune setpoint for SARS-CoV-2 antibodies. *News Medical* https://www.news-medical.net/news/20240910/Study-reveals-population-wide-immune-setpoint-for-SARS-CoV-2-antibodies.aspx?utm_source=news_medical_newsletter&utm_medium=email&utm_campaign=covid_19_newsletter_11_september_2024 (2024).

22. Mary Van Beusekom, M. Offices, long-distance shared transport, some activities tied to COVID spread. *CIDRAP (University of Minnesota)* https://www.cidrap.umn.edu/covid-19/offices-long-distance-shared-transport-some-activities-tied-covid-spread (2024).

23. Galmiche, S. *et al.* Risk of SARS-CoV-2 infection in professional settings, shops, shared transport, and leisure activities in France, 2020–2022. *BMC Public Health* **24**, 2411 (2024).

24. Malaysia reports new mpox case of less severe variant. *Reuters* https://www.reuters.com/business/healthcare-pharmaceuticals/malaysia-reports-new-mpox-case-clade-2-variant-2024-09-17/?utm_source=Sailthru&utm_medium=Newsletter&utm_campaign=Health-Rounds&utm_term=091724&user_email=3b5e227eb43ca086a7f49e8924d7dc4a0ff3f5d6 (2024).

25. Health Ministry says one positive mpox case detected yesterday, but with milder clade II strain and no history of international travel. *MSN/Malay Mail* https://www.msn.com/en-my/health/other/health-ministry-says-one-positive-mpox-case-detected-yesterday-but-with-milder-clade-ii-strain-and-no-history-of-international-travel/ar-AA1qGxDR?ocid=msedgntp&pc=HCTS&cvid=9d451837a564495cb2487fb2d377f3dc&ei=10 (2024).

26. Malaysia Records First Monkeypox Case For 2024, Health Ministry Urges Vigilance. *MSN/The Rakyat Post* https://www.msn.com/en-my/lifestyle/other/malaysia-records-first-monkeypox-case-for-2024-health-ministry-urges-vigilance/ar-AA1qGFdE?ocid=msedgntp&pc=HCTS&cvid=4d7b170cc846471faf3285e0be9c0389&ei=5 (2024).

27. KKMalaysia@KKMPutrajaya. (Sep17, 2024). Kenyataan Media Kementerian Kesihatan Malaysia. Situasi Terkini Mpox di Malaysia. https://x.com/KKMPutrajaya/status/1835865840727818252/photo/3. Preprint at (2024).

28. KKM - FAQ mpox (MB-MY) (kemaskini 17 Sep 2024). Preprint at bit.ly/KKM-FAQ-mpox (2024).

29. Paperny, A. M. Canada to donate ‘up to 200,000’ doses of mpox vaccine. *Reuters* https://www.reuters.com/business/healthcare-pharmaceuticals/canada-donate-up-200000-doses-mpox-vaccine-2024-09-11/?utm_source=Sailthru&utm_medium=Newsletter&utm_campaign=Health-Rounds&utm_term=091224&user_email=3b5e227eb43ca086a7f49e8924d7dc4a0ff3f5d64ef5 (2024).

30. Rwanda launches mpox vaccine campaign. *CIDRAP (University of Minnesota)* https://www.cidrap.umn.edu/mpox/rwanda-launches-mpox-vaccine-campaign (2024).

31. Zimmer, C. How Does Bird Flu Spread in Cows? Experiment Yields Some ‘Good News.’ *The New York Times* https://www.nytimes.com/2024/06/29/health/bird-flu-dairy-cows-infection.html (2024).

32. Mandavilli, A. How U.S. Farms Could Start a Bird Flu Pandemic. *The New York Times* https://www.nytimes.com/2024/08/21/health/bird-flu-cattle-pandemic.html (2024).

33. Caserta, L. C. *et al.* Spillover of highly pathogenic avian influenza H5N1 virus to dairy cattle. *Nature* (2024) doi:10.1038/s41586-024-07849-4.

34. Devasia, J. One dead from Nipah virus in India’s Kerala; second death this year. *Reuters* https://www.reuters.com/world/india/one-dead-nipah-virus-indias-kerala-second-death-this-year-2024-09-16/ (2204).

35. UNRWA chief: Gaza polio vaccination coverage has reached 90%. *Reuters* https://www.reuters.com/world/middle-east/unrwa-chief-gaza-polio-vaccination-coverage-has-reached-90-2024-09-16/?utm_source=Sailthru&utm_medium=Newsletter&utm_campaign=Health-Rounds&utm_term=091724&user_email=3b5e227eb43ca086a7f49e8924d7dc4a0ff3f5d64ef521 (2024).

36. The first round of the polio vaccination campaign ended successfully. 16 September 2024. Preprint at https://www.unrwa.org/newsroom/official-statements/1st-round-polio-vaccination-campaign-ended-successfully (2024).

37. Quick takes: Measles uptick in US, more polio cases in 3 countries. *CIDRAP (University of Minnesota)* https://www.cidrap.umn.edu/measles/quick-takes-measles-uptick-us-more-polio-cases-3-countries (2024).

38. Polio. Country updates as of 18 September 2024. *Global Polio Eradication Initiative (GPEI)* https://polioeradication.org/about-polio/polio-this-week/ (2024).

39. Emergent BioSolutions awarded BARDA contract for Ebola treatment. *CIDRAP (University of Minnesota)* https://www.cidrap.umn.edu/avian-influenza-bird-flu/emergent-biosolutions-awarded-barda-contract-ebola-treatment (2024).

40. Emergent BioSolutions Awarded Research and Development Option valued at $41.9 Million for continued Advanced Development and Procurement of Ebanga^{TM} Treatment for Ebola. *Globe News Wire* https://www.globenewswire.com/news-release/2024/09/12/2945192/33240/en/Emergent-BioSolutions-Awarded-Research-and-Development-Option-valued-at-41-9-Million-for-continued-Advanced-Development-and-Procurement-of-Ebanga-Treatment-for-Ebola.html (2024).

41. Olivera, C. *et al.* Impact of high-risk and low-risk human papillomavirus infections on the male genital tract: effects on semen inflammation and sperm quality. *Front Cell Infect Microbiol* **14**, (2024).

42. Sucato, A. *et al.* Human Papillomavirus and Male Infertility: What Do We Know? *Int J Mol Sci* **24**, 17562 (2023).

43. Katherine Kahn. Drug-Resistant Bacteria Deaths Projected to Rise 70% by 2050 — New antibiotics, access to care access to care could prevent millions of deaths, researchers say. *MedPage Today* https://www.medpagetoday.com/infectiousdisease/generalinfectiousdisease/111981?xid=nl_mpt_DHE_2024-09-17&mh=2e0e77d706cf2574d6370ea746f61244&utm_source=Sailthru&utm_medium=email&utm_campaign=Daily Headlines Evening 2024-09-17&utm_term=NL_Daily_DHE_dual-gm (2024).

44. Naghavi, M. *et al.* Global burden of bacterial antimicrobial resistance 1990–2021: a systematic analysis with forecasts to 2050. *The Lancet* (2024) doi:10.1016/S0140-6736(24)01867-1.

45. Kariuki, S. Global burden of antimicrobial resistance and forecasts to 2050. *The Lancet* (2024) doi:10.1016/S0140-6736(24)01885-3.

46. Imported Oropouche virus cases continue steady US rise. *CIDRAP (University of Minnesota)* https://www.cidrap.umn.edu/oropouche-virus/imported-oropouche-virus-cases-continue-steady-us-rise (2024).

47. Oropouche. Current Year Data (2024). Data are current as of September 17, 2024. *Centres for Disease Control and Prevention, CDC* https://www.cdc.gov/oropouche/data-maps/current-year-data.html (2024).

48. Ig-Seq/Rep-Seq/MAF. *Illumina* https://www.illumina.com/science/sequencing-method-explorer/kits-and-arrays/ig-seq-rep-seq-maf.html (2024).

49. Marques, M. A., Purdy, M. D. & Yeager, M. CryoEM maps are full of potential. *Curr Opin Struct Biol* **58**, 214–223 (2019).

50. Electrostatic Potential maps. *LibreTexts. Chemistry* https://chem.libretexts.org/Bookshelves/Physical_and_Theoretical_Chemistry_Textbook_Maps/Supplemental_Modules_(Physical_and_Theoretical_Chemistry)/Chemical_Bonding/Fundamentals_of_Chemical_Bonding/Electrostatic_Potential_maps (2024).