Global updates on COVID-19 and other diseases

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Contents

Summary

- COVID-19 is under control in Malaysia.
- There are now 7 SARS-CoV-2 variants under monitoring (VUM) circulating globally, without any evidence of severe disease.
- The origin of SARS-CoV-2 virus remains inconclusive.
- Long-COVID symptoms in children are age-specific, with the syndrome linked to poorer health outcomes.
- Mpox remains a public health emergency of international concern (PHEIC).
- The DRC's TB crisis is mainly centred on one region.
- Singapore reported 2 cases of Zika in June.
- An integrated approach is needed for mitigating zoonotic malaria.
- The elimination of neglected tropical diseases in Malaysia, such as lymphatic filariasis, is possible.
- Evidence of African Swine Fever was found in wild boar carcasses in Selangor.
- 9 human cases of avian influenza H5N1, including 2 deaths, were reported in June 2025 by Bangladesh and Cambodia, collectively.
- Unpasteurised raw milk can serve as a transmission source for the H5N1 virus.
- Genetic analysis revealed that MPXV was present well before the onset of the global mpox outbreak.
- Measles in the US and Europe underscores the roles of under-vaccination and travel in outbreaks of vaccine-preventable diseases.

1.0 COVID-19 and related issues

1.1 World Health Organization updates

1.1.1 Global situation

Globally, the SARS-CoV-2 virus positivity remained stable and low across the majority of reporting countries. Positivity was elevated (>10%) in a few countries in Central America and the Caribbean, Tropical South America, Northern and South-West Europe and in Western, Southern and South-East Asia, with small increases in activity reported in some countries. As with other respiratory viruses, such as the influenza virus, the agency continues to monitor the situation, as the SARS-CoV virus co-circulates with them.[1]

On 25 June 2025, the World Health Organization (WHO) Technical Advisory Group on Virus Evolution (TAG-VE) added the Omicron XFG to its SARS-CoV-2 variants under monitoring (VUM) list—now 7—including LP.8.1, thought to be responsible for the surge of cases observed in most regions recently, as global proportions increase rapidly. In its initial risk assessment, the public health risk is currently low.

XFG is a recombinant of Omicron lineages LF.7 and LP.8.1.2, with the earliest sample collected on 27 January 2025. In May 2025, the proportion of XFG viruses rose in all three WHO regions (Western Pacific, Americas and European) that consistently share SARS-CoV-2 sequences, as well as the Southeast Asia Region. Cases and hospitalisations are rising in countries where XFG proportions are high. However, currently there is no sign that infections are more severe.[2]

1.1.2 Origins of the COVID-19 pandemic

The World Health Organization (WHO) published the independent assessment report of the origins of the SARS-CoV-2 virus, the cause of the COVID-19 pandemic, on 27 June 2025. This update, built on the preliminary findings in 2022 and based on accessible scientific evidence, maintains the hypotheses initially presented in 2022: the possibility of a species jump from animals to people and an accidental lab-related event.[3]

The WHO acknowledged that not all information and intelligence reports were shared by the nations that had them for the completion of the report. The agency reiterated that understanding the origin and dynamics of an outbreak is important in preventing another one.

The link to the full 2025 report is as follows: Independent assessment of the origins of SARS-CoV-2 by SAGO. The findings from the preliminary report published in 2022 can be found at SAGO Preliminary Report.

1.2 Country updates

1.2.1 Malaysia

The nationwide situation remains under control, and cases are below the national threshold, despite an increase in cases observed in the second week of June 2025 (epidemiology week 24, EW24/2025).[4] The first fatality for 2025 was also reported in EW24/2025; the deceased had comorbidities and had not taken the second (vaccine) booster. All 6 (severe cases) intensive care admissions reported in EW24/2025 had comorbidities. The last fatality linked to the disease was reported on 26 May 2024, with a cumulative of 57 deaths reported that year.

KKM encourages the public, especially those in high-risk groups (elderly, people with comorbidities, the homeless, immunocompromised individuals, pregnant mothers, healthcare workers and those who have not been vaccinated against COVID-19), to keep up-to-date with their vaccination/boosters. However, getting boosted is voluntary. The public was also reminded to maintain the use of public health and social measures (PHSM) as they live with the virus.[4]

KKM will be updating the standard operating procedure for COVID-19 soon. This is part of the transition from endemicity to living with the virus.[5]

1.2.2 Hong Kong

The COVID-19 situation in Hong Kong continues to decrease after the latest surge in April 2025, according to the latest update from the Centre for Health Protection (CHP).[6] The latest sewage surveillance data and analysis of samples from positive cases showed that Omicron NB.1.8.1 subvariant has become the dominant strain in Hong Kong. This variant was listed as a variant under monitoring (VUM) by the WHO on 23 May 2025. Based on available evidence, NB.1.8.1 poses low risk to global public health and currently approved COVID-19 vaccines are expected to be effective against this VUM. There is no evidence to suggest this VUM will cause more serious disease.

1.3 Long-COVID, children

The study "*Characterizing Long COVID Symptoms During Early Childhood*," published in *JAMA Pediatrics* recently, analysed prolonged COVID-19 symptoms in children (0-5 years old) using data from the RECOVER-Pediatrics cohort. Researchers studied 472 infants/toddlers (0-2 years) and 539 preschoolers (3-5 years), comparing those with and without prior COVID-19 infection.[7]

The findings showed age-specific symptom patterns: infants and toddlers with long-COVID (LC) often had trouble sleeping, fussiness, poor appetite, stuffy nose, and cough, while preschoolers commonly experienced dry cough and daytime tiredness. These symptoms differ from those in older children and adults, highlighting unique impacts in early childhood. The study developed age-specific symptom indexes to aid diagnosis and research. It also found that LC in young children is linked to poorer health, reduced quality of life, and developmental delays. It also highlighted the importance of caregiver reports, as young children cannot always express symptoms clearly.

The findings further underscore the need for tailored clinical care for young children with LC.

2.0 Tuberculosis

The Democratic Republic of Congo

According to authorities, > 13,000 cases of tuberculosis (TB), including 343 deaths, were reported from the Ituri province,[footnote1] located in the northeast region of the Democratic Republic of The Congo (DRC) in 2024. Approximately 71% of the cases were from one location. Despite the efforts to control the disease in the Ituri province, TB remains a threat to the people there and the general population in the DRC.[9]

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[1] There are a total of 26 provinces in the DRC. These are further subdivided into smaller administrative sections. [8]

3.0 Vector-borne diseases

3.1 Zika, Singapore

Singapore confirmed two local Zika cases, both female, in Woodlands on 19 June 2025.[10] Neither were pregnant at the time their infection was detected. They resided in areas that had active dengue clusters. The National Environment Agency (NEA) found evidence of persistent signals for the Zika virus in residential areas around those linked to these cases based on wastewater and mosquito surveillance. The NEA's update showed that as of 27 June 2025, Singapore has had a total of 9 Zika cases nationwide.[11] Zika virus is transmitted by the same mosquito that transmits dengue (*Aedes*) and the clinical presentation is similar to dengue. The public, especially those living in Zika-affected areas, were reminded to remain vigilant for the disease and take necessary precautions to prevent bites and the spread of the disease.[12]

3.2 Malaria

3.2.1 Technical consultation on control of zoonotic malaria: 2024 meeting report

The Technical Consultation on Control of Zoonotic Malaria was convened by the WHO Global Malaria Programme in Geneva from 5 to 7 November 2024. The meeting gathered national malaria programme managers from Indonesia, Malaysia, the Philippines, and Thailand, alongside members of the Malaria Policy Advisory Group, the Technical Advisory Group on Malaria Elimination and Certification, and research experts.[13]

The key points from the consultation include:[13]

- Focus on *Plasmodium knowlesi* malaria, a zoonotic malaria species increasingly affecting humans.
- Review of the epidemiological and programmatic challenges posed by *P. knowlesi*.
- Discussion on current practices in diagnosis, treatment, and vector control.
- Consideration of the implications for malaria elimination certification due to zoonotic transmission.
- Identification of priority research questions to develop effective strategies to reduce transmission risk and achieve zero malaria deaths.
- Emphasis on the need for intersectoral collaboration and strong community engagement for effective control.

- Agreement that coordinated efforts are urgently required as the burden of *P. knowlesi* malaria increases.
- Next steps include conducting priority research to inform WHO guidelines on *P. knowlesi* control and addressing certification challenges related to zoonotic malaria transmission.

The consultation concluded that controlling zoonotic malaria will require integrated approaches involving multiple sectors and the active participation of affected communities to reduce transmission and mortality effectively.

The meeting report provides a strategic framework for advancing zoonotic malaria control and highlights the urgency of addressing this emerging public health challenge.

3.2.2 Australia, locally-acquired malaria cases

Queensland health authorities are investigating the second locally-acquired malaria case reported in the Torres Strait in June 2025—a week after the first.[14,15] This follows a previous locally acquired case and coincides with a rise in imported malaria cases, primarily from Papua New Guinea (PNG) and the Solomon Islands in 2025. The local transmission is believed to be caused by the cross-border movement of infected mosquitoes from PNG, facilitated by the region's tropical climate and presence of *Anopheles* mosquitoes, which are malaria vectors. Queensland Health has implemented focused containment and mosquito control measures to prevent further spread of the disease. Malaria in Australia is mostly seen in returned travellers; however, local transmission in the Torres Strait is not uncommon due to proximity to high-risk areas. The last outbreak of locally acquired malaria in the Torres Strait occurred in 2023, with 5 cases detected. The mainland last saw an outbreak in 2002. As of early June 2025, there have been 71 malaria notifications in Queensland, with 97% related to international travel. Investigations into the locally acquired cases are ongoing to control and prevent further transmission.[16,17]

3.3 Filariasis, lymphatic filariasis elimination efforts in Malaysia: progress and current status

Malaysia remains firmly committed to eliminating lymphatic filariasis (LF) by 2025 through comprehensive surveillance efforts, treatment and public health outreach.[18,19]

Mass drug administration (MDA) is a key strategy to interrupt LF transmission by reducing infection levels below thresholds that prevent mosquito-borne spread, and the WHO recommends Transmission Assessment Surveys (TAS) to determine when MDA can be stopped and to monitor post-MDA infection levels at intervals of 2 - 3 and 4 - 6 years to detect any resurgence. [20,21]

The National Lymphatic Filariasis Elimination Programme (PEFLK) has been held since 2002 in 127 endemic sub-districts in 8 states (Kedah, Perak, Johor, Pahang, Terengganu, Kelantan, Sabah and Sarawak) with the target to reduce the infection prevalence to ≤ 2% or fewer than two people per 100 population screened in endemic areas. This target was achieved in 2021. [22] However, it was noted that three sub-districts in Sarawak [footnote2] and two in Sabah had yet to achieve it in 2021. [22]

According to the statistics from the Kementerian Kesihatan Malaysia (KKM; Filariasis Unit, Vector-borne Disease Sector), from 2022 until mid-June of 2025, the number of cases in Sarawak has shown an upward trend, with most cases occurring among nationals. [23–26] In June 2025, most cases were reported from Debak District. [27]

4.0 African swine flu

Malaysia, wild boar carcasses

Six wild boar carcasses found between 28 April and 15 May in Selangor tested positive for the African Swine Fever virus (ASFV).[28] The discovery of the carcasses was reported to the Selangor Department of Wildlife and National Parks (Perhilitan). The confirmatory tests were reported by the Veterinary Services Department laboratories. Both departments, together with the local authorities and other agencies, have continued to monitor the situation, disposed of carcasses and disinfected affected areas as required by the existing biosecurity protocols. Surveillance for the ASFV on newly discovered carcasses in nearby areas is ongoing. Wildlife populations' health in high-risk zones is being monitored. All related agencies have enhanced surveillance and preparedness in anticipation of similar outbreaks elsewhere. The public has been advised not to touch, move or approach any wild animal carcasses found, particularly wild boars, and to report sightings of animal carcasses to the authorities. They were also reminded to refrain from spreading any unverified information to avoid causing unnecessary public concern.

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[2] The names of the sub-districts were not mentioned in the article.

5.0 Avian/zoonotic influenza: H5N1

5.1 Human cases

5.1.1 Bangladesh

Bangladesh has reported two recent human infections with H5N1 avian influenza to the WHO, detected in May and June 2025. Genetic analysis confirms the virus belongs to an older clade circulating in local poultry, with no signs of human-to-human transmission. Though details are limited, both cases are linked to exposure to infected birds. The situation highlights ongoing zoonotic risks and the importance of surveillance, early detection, and biosecurity measures. Antiviral treatments remain effective, and the authorities stress continued vigilance through a One Health approach.[29]

5.1.2 Cambodia, highest case load in June 2025

Cambodia emerged as the primary hotspot for human H5N1 infections in June 2025, with three new cases reported to the WHO during the period of 20 – 26 June 2025.[30,31] The cases included:

- Takeo Province: A 65-year-old female (onset 4 June 2025) and a 19-month-old male (onset 7 June 2025)
- Svay Rieng Province: A 52-year-old male (onset 14 June 2025)

Tragically, two of those three cases resulted in death. All patients had documented exposure to sick or dead poultry before becoming ill. By the end of June, Cambodia's total for 2025 reached 10 human cases with 5 deaths [32,33], representing a significant increase from previous years.

Additional cases were identified in Siem Reap Province, including a 41-year-old woman confirmed positive on 23 June 2025, bringing the total to 7 cases by late June 2025. [34,35] Most concerning was the discovery of two additional cases: a 46-year-old mother and her 16-year-old son, living approximately 20 metres from another confirmed case, suggesting potential clustered transmission.

5.2 Animal Outbreaks

5.2.1 The US

Dairy cattle remained significantly affected, with 1,074 dairy herds confirmed positive across 17 states as of June 2025. California led with the highest number of affected herds. The United States Department of Agriculture (USDA) extended its H5N1 testing program for dairy cattle through September 2025, examining approximately 800 muscle tissue samples from asymptomatic cows.[36] Wild bird detections continued at high levels, with 13,324 wild birds testing positive as of June 2025, across 51 jurisdictions. Commercial poultry remained heavily impacted, with 174.8 million birds affected as of June 2025. [37]

5.2.2 Europe

European surveillance detected 365 highly pathogenic avian influenza (HPAI) A(H5) virus cases in domestic and wild birds across 24 countries between March and June 2025. The detections were predominant, particularly in western, central, and southeastern Europe. [38] Notably, the first-ever detection of H5N1 in a sheep was reported in the UK in March 2025. Several European countries reported new poultry outbreaks in June 2025, including commercial facilities in Wales and North Yorkshire in the UK.[39]

5.2.3 Asia-Pacific Region

The region continues experiencing widespread circulation, with H5N1, H5N2, H5N9, H9N2, and H10N3 subtypes reported during March-June 2025.[40] Meanwhile, Australia successfully eradicated an HPAI H7N8 outbreak in northern Victoria: all infected properties were cleared by 13 June 2025, control zones lifted, and Australia formally declared disease freedom in poultry to the World Organisation for Animal Health (WOAH).[41]

5.3 H5N1 virus found to persist in raw milk

A new study has found that live H5N1 avian influenza virus can persist in raw milk for >1 day at room temperature and >7 days when refrigerated, raising concerns about potential zoonotic transmission through unpasteurised dairy. While the infectious dose for humans remains unclear, the findings underscore risks for raw milk consumers and dairy workers if animals are infected. Pasteurisation effectively inactivates the virus, reinforcing the importance of avoiding raw milk and maintaining strict biosecurity in dairy operations.[42,43]

6.0 Other diseases/current outbreaks

6.1 Mpox

6.1.1 World Health Organization updates

The fourth Emergency Committee meeting, convened on 5 June 2025, regarding the upsurge of mpox in 2024, unanimously agreed and advised the WHO Director-General that the disease remains a public health emergency of international concern (PHEIC).[44]

The WHO's Rapid Risk Assessment assessed clade Ib as high risk, while clades Ia, IIa, and IIb were classified as moderate risk. The Director-General concurred with the advice and issued a set of revised Temporary Recommendations to State Parties experiencing mpox virus (MPXV) transmission.

These recommendations are updated or extended from the set of recommendations issued on 27 November 2024 and are available on the official WHO site: Fourth meeting of the International Health Regulations (2005) Emergency Committee regarding the upsurge of mpox 2024 – Temporary recommendations.

6.1.2 Situation in Africa

Mpox continues to ravage the WHO African Region, where the majority of global cases have been reported. Active transmission has been observed in 18 countries across Western, Central, and Eastern Africa over the past 6 weeks. The DRC remains the most affected, recording 12,208 confirmed cases in 2025—more than twice the number reported in Uganda (5,636). A rapid surge in Sierra Leone has driven the recent wave, with 53% of cases reported there (as of 7 June 2025). While a sustained decline in cases is being reported on 27 June 2025, it may reflect delays in case reporting instead of a true drop, therefore, warrants cautious interpretation. The virus has also reached new regions, with Ethiopia and Togo reporting confirmed cases for the first time, underscoring the risk of further geographical spread.[45]

6.1.3 Phylogenetic study of clade IIb epidemic in Nigeria and Cameroon

A genomic study of 118 mpox virus (MPXV) samples from Nigeria and Cameroon revealed contrasting transmission patterns between the two countries.[46]

In Nigeria, 105 of 109 cases were linked to human-to-human spread, while all 9 cases from Cameroon were the result of animal-to-human (zoonotic) transmission. Although zoonotic spillover is less common in Nigeria (around 3.7%), it remains a contributing factor in the country's mpox epidemiology. The forested border regions between Nigeria and Cameroon host diverse wildlife populations that may serve as a reservoir for the mpox virus (MPXV), facilitating continued transmission across the region. The presence of zoonotic cases in these areas signals a persistent risk of mpox emergence and re-emergence, particularly among communities living near forested areas and wildlife habitats. This risk is likely underreported due to gaps in case detection, limited active surveillance, and insufficient genomic data.

The study also suggests that the human MPXV may have been circulating in Nigeria for several years before its detection, based on an unexpectedly high number of genetic mutations. Phylogenetic analysis supports this, showing that the ancestor of the current outbreak strain likely originated in animals around November 2013. It then spilled over to humans in southern Nigeria in August 2014 and silently spread across 11 states in the country for three years before the first reported human cases in 2017. International outbreaks involving the same strain began 5 years later, indicating that the virus had been evolving unnoticed in Nigeria for at least 8 years.

These findings underscore the urgent need to strengthen surveillance in both animal and human populations to better understand how MPXV is maintained and transmitted. Such data are essential for timely and targeted public health interventions to prevent wider outbreaks. However, efforts to control mpox in Africa continue to face significant challenges, particularly due to unequal access to diagnostic tools, vaccines, and treatments. Without improved control measures, ongoing transmission risks trigger future multi-country outbreaks while sustaining avoidable illness and death in affected regions.

6.2 Measles

6.2.1 The US, ongoing

As of 25 June 2025, the Centers for Disease Control (CDC) has reported 1,227 confirmed measles cases across 37 jurisdictions, rapidly approaching the 2019 peak of 1,274 cases

– the highest since measles was declared eliminated in 2000. So far this year, 23 outbreaks have been reported, with 89% of reported cases linked to these events. The largest outbreak is centred in West Texas, accounting for 750 cases (62% of the US total). Alarmingly, 95% of infections occurred in unvaccinated individuals or those with unknown vaccination status. This surge coincides with a decline in measles-mumps-rubeola (MMR) vaccination coverage, now at 92.7% among kindergartners (2023/2024 school year), with overall rates falling in 78% of US counties since the pandemic. This is well below the 95% threshold needed to achieve herd immunity and sustain measles elimination status. The disease was eliminated in the US in 2000; the current surge began in January 2025.[47]

The situation in the US underscores the urgent need to boost MMR vaccination to protect communities from the disease resurgence.

6.2.2 Europe, warning for holidaymakers

In Europe, the measles situation remains concerning, with an expected increase in the EU/EEA region in the coming months, with an observed seasonality. This is due to sub-optimal vaccination coverage as well as a high probability of importation from locations with high virus circulation. Most countries in the region have been reporting locally transmitted cases, with some cases related to international travel. The European Centre for Disease Prevention and Control (ECDC) strongly recommends increasing vaccination uptake, enhancing surveillance, and raising public and healthcare awareness to curb the ongoing resurgence of this preventable disease.[48]

6.3 Vaccination and anti-microbial resistance: data gap

Vaccination can play a pivotal role in addressing antimicrobial resistance (AMR), both by directly preventing infections caused by drug-resistant pathogens and indirectly reducing the need for antimicrobial use, thereby slowing the development of resistance. A Wellcome-funded initiative supported 13 diverse projects to examine these links. Of these, 11 studies indicated that vaccination has the potential to reduce antibiotic use and the prevalence of AMR genes. However, the magnitude of this impact varies significantly depending on the pathogen, healthcare setting, and system-level behaviours.[49]

The causal pathway from vaccination to reduced AMR is non-linear and shaped by a complex interplay of microbial ecology, prescribing practices, and vaccine coverage. While encouraging results have emerged—particularly concerning typhoid, pneumococcal infections, malaria, and diarrhoeal diseases—the overall evidence base remains limited, especially in low- and middle-income countries (LMICs). The findings highlight an urgent need for more robust, standardised, and interdisciplinary research to gather empirical evidence. Strengthening this evidence base is essential to guide policy, incorporate AMR considerations into immunisation strategies, and inform future vaccine development and deployment.

7.0 Implications for Sarawak based on the views of SIDC

The implications of outbreaks of vaccine-preventable diseases are many, some of which are listed as follows: [50–52]

- Increase mortality and morbidity, as diseases such as measles and diphtheria can cause severe disease complications and death, placing vulnerable populations (very young, elderly, people with comorbidities, the immunocompromised, and many more) at risk.
- Impact education progress, affecting the potential of youths as the next generation to build society and the nation.
- Outbreaks reverse years of progress made in controlling vaccine-preventable diseases or their elimination, or near-elimination. It also reverses progress made in preventing child mortality and improving population health.
- The healthcare system will be strained. Outbreaks result in increased healthcare costs due to treatment and outbreak response efforts. They also cause disruptions in healthcare services, including absenteeism among healthcare workers, which further compromises patient care and infection control.
- The economic impact/burden of these outbreaks extends well beyond immediate medical expenses. Broader repercussions include reduced productivity, due to workforce shortages, and heightened public health expenditures aimed at containing a disease that vaccines could have prevented in the first place.
- Potential for disease resurgence post-pandemic. Disruptions to vaccination programmes during the COVID-19 pandemic have led to declines in vaccine coverage, increasing the risk of outbreaks and excess deaths from diseases (for example, measles and polio) in the coming years.

These, as well as science-based evidence of the benefits of vaccines, should be reiterated to the public. Addressing misinformation and ‘popular’ science is important. Misinformation about vaccines contributes to lower immunisation rates, leading to

—causing resources to be redirected to address these outbreaks. Vaccine hesitancy undermines herd immunity and allows diseases to resurge even in communities where vaccines are available.

Mosquitoes are bearers of a multitude of diseases. The *Aedes* mosquito can transmit multiple types of pathogens that cause diseases such as Zika, dengue and chikungunya. Challenges in diagnosing these diseases can arise because all three can present with similar symptoms, and in settings where the mosquito vector can be found, differential diagnosis for all three should be made. This will allow for the correct management of the disease. Mosquito surveillance, as well as environmental surveillance, together with incident reports, serve as surveillance tools in monitoring the progression of these diseases in affected localities and their neighbouring areas. The public should also be made aware of any reported case(s) so that they are aware of why mitigation is being made.

Lymphatic filariasis (LF) is a neglected tropical disease that many thought had been eliminated. However, reports of sporadic cases in Malaysia, specifically in Sarawak, meant that the parasite remains in circulation. The parasite is transmitted by different types of mosquitoes, namely, *Mansonia*, *Culex* and *Anopheles*.[54] Controlling the vector is one way of controlling the disease. However, as cases continue to be reported despite the efforts of the public health services, including controlling the vector, the possibility of zoonotic strains cannot be ruled out.[55] Active surveillance of mosquitoes and the animals that can serve as reservoirs (patent filaria infection) for the parasite, such as primates and dogs, should be conducted to confirm or negate this hypothesis. Awareness of the disease, including how it is transmitted, should also remain an ongoing public health initiative to bring the number of cases down.

The burden of zoonotic malaria, *P. knowlesi*, is mostly felt in Sarawak. Of approximately 3,200 cases reported in 2023, 87% were from Sarawak and Sabah, with the majority reported from the former. Diagnostic tools such as nucleic acid amplification methods are limited, and rapid diagnostic tests (RDTs) are not specific. Microscopy, while being the ‘Gold Standard’ for the diagnosis of malaria, is only useful in the hands of an experienced microscopist who can differentiate *P. knowlesi* and *P. malaria* and *P. falciparum*—all three have features that look like one another at different stages of their blood lifecycle. The development of a specific RDTs for *P. knowlesi* is most urgent to address healthcare providers' diagnostic capabilities, and the swiftness of treatment initiation.

The scenario of TB in the DRC is one that Sarawak intends to avoid. Active surveillance for latent TB infection means being able to treat individuals before they become active cases. A TB-free Sarawak is achievable with the right (planned) strategies involving the efforts from both public and private entities, and the people.

The research on antimicrobial resistance in TB needs to be investigated. This includes the emergence of mutation markers for the current treatment regimen used in Sarawak. Tracking mutation patterns can predict emerging resistance, help policymakers determine when to change the management of cases, and help (pharmaceutical) researchers formulate new antimicrobials to combat the infection.

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