

Stage one: Epidemiological dynamics assessment

An automated statistical risk assessment algorithm based on the daily incidence of cases and deaths reported over the previous week was used to predict the number of COVID-19 associated deaths (a proxy for disease severity) within the next five weeks per one million population. This stage produced an initial alert level.

Stage two: Context assessment

Additional contextual factors were manually assessed using signals for each country based on three indicators: (i) health system pressures; (ii) other concerning epidemiological signals (e.g.: concurrent outbreaks, testing-related concerns, changes in circulating variants of concern, etc.); and (iii) factors affecting response - such as mass gatherings, population movement or instability related to acute events resulting in logistical challenges. Data were obtained from event-based surveillance including Epidemic Intelligence from Open Sources (EIOS), internet search engines, WHO Regional Office situation reports, Ministry of Health websites and the WHO variant tracking database. This was combined with information on vaccination coverage and public health and social measures. An assessment of the trust in available data was attributed for each indicator, ranging from high (reliable data from a trusted source) to unknown (no information consistently output from a country, with limited or no media access). All indicators, and associated trust levels, were combined to produce a recommendation on whether a country should be maintained at the initial alert level, or whether this alert level should be updated. Based on this, teams at WHO global and regional levels jointly agreed on a final classification for each country.

Stage three: Response

Based on the final classifications, a weekly operational watchlist of countries considered at moderate to critical risk was produced and shared at WHO global and regional level. The WHO response teams at both levels utilized this to prioritize and prompt response actions. The global situation alert system has facilitated the release of more than USD 27 million from internal emergency funding to help expedite

response activities in at-risk contexts and has enabled the rapid release of operational and technical support, including: over 450,000 antigen rapid diagnostic tests over 6,000 oxygen concentrators; support to deploy and establish COVID-19 treatment centers; and the deployment of rapid response teams.

Next steps

A retrospective qualitative and quantitative review of the process was undertaken between April and June 2022, to inform the use of the system for COVID-19 and of similar systems in future epidemics. Preliminary results suggest that the mixed methods approach, incorporating multiple data sources and allowing for differences in data quality, may have improved the capacity to rapidly identify deteriorating contexts, particularly when there were gaps or delays in official reporting of cases and deaths. This therefore helped to improve the situational assessments. However, developing a standardised global system remained challenging as data availability varied by country over the course of the pandemic. Moreover, despite the benefits of the qualitative assessment, this added a degree of subjectivity based on differing perceptions of risk.

Based on the current trajectory of the pandemic, and the decreased level of global operational support required for country response to COVID-19 (due to preparedness and lessons learned over the past two years), a decision was made to pause the WHO global situational alert system for COVID-19 in May 2022. However, some regions continue to utilize the system at a regional level. Triggers which may prompt the reimplementation of the global system for COVID-19 are currently being drafted. Lessons learned are being documented, and the statistical risk assessment algorithm continues to be active, for potential adaptation to a novel epidemic or pandemic. Should it be decided to utilize the WHO situational alert system for a different health emergency, the parameters and indicators will need to be adjusted.

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The Urgepi project: Preventing and responding to measles epidemics in the Democratic Republic of the Congo (DRC)

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Measles outbreaks in the DRC remain recurrent and a leading cause of mortality and morbidity among children. One of the greatest challenges is to identify mechanisms to prevent rather than simply to chase after outbreaks across the country. The Epicentre-MSF project started in 2018, in collaboration with the Ministry of Health (MoH), covering 4

provinces of the Democratic Republic of Congo (DRC) Grand-Katanga Region (Haut Katanga, Haut Lomami, Lualaba, Tanganyika). The project combines activities to control measles epidemics (prevention - vaccination, surveillance, biological confirmation, outbreak response – vaccination and case management) with an operational research component to improve measles prevention / response strategies.

Applying an IOA lens to measles risk assessment and outbreak response:

The project uses multiple data sources and considerations to identify areas at high risk of large measles outbreaks. The prevention and response strategy is targeted towards these high risk areas, that were identified based on the estimated susceptible pool of children. In addition, the project seeks to look beyond surveillance and vaccination data, and to consider community information explaining barriers to vaccination (including behavioural data). Overall, the Epicentre- MSF field and research teams, in support and collaboration with ministry of health actors, consider multiple data sources and methods to identify and respond to measles risk in the DRC.

Step 1: Risk prioritization: The project acknowledges health zones may differ in their characteristics, resulting in differences in epidemic risk. As a first step, in collaboration with Penn State University, models were developed to rank all health zones within each province, identifying those most at risk of outbreak by quantifying the pool of susceptible individuals. Every year about 20 high-risk health zones are selected for supplementary actions (e.g. preventive activities, enhanced surveillance).

Step 2: Two-pronged surveillance: Surveillance in all 68 health zones of the 4 provinces is based on the national surveillance data collected by the MoH. Alerts of measles outbreaks are identified based on the number of suspected measles cases notified per health zone on a weekly basis through the national surveillance system.

To intervene faster in health zones where large measles epidemics are likely, a more sensitive and less specific alert threshold is implemented in the high-risk health zones.

Additionally, in the selected high-risk health zones, regular contact is maintained with the MoH at the health zone level to collect supplementary real-time information (e.g. geographic distribution of cases, case characteristics, investigation reports).

Alerts in all 68 health zones are either investigated by the MoH, by MSF in collaboration with the MoH, or other partners. In the high-risk health zones, additional financial and technical support may be provided for investigations by the Epicentre-MSF teams.

Step 3: Biological confirmation: MSF supports activities of a laboratory in Lubumbashi, where biological samples from all 68 health zones of the 4 provinces can be analysed. Having provincially available laboratories means that delays in laboratory confirmation of outbreaks are reduced due to shorter transit times (compared to sending samples all the way to Kinshasa). This also can help reducing intervention delays, as laboratory confirmation is needed before the start of an intervention. In addition, in the high-risk health zones, there is additional support for rapid sample collection and transport provided by MSF.

Step 4: Managing multiple simultaneous alerts, using a multiple indicator algorithm to make decisions: At present, we are dealing with high numbers of simultaneous alerts and therefore we are obliged to prioritize some response over others. The algorithm to make these decisions is based on:

- Epidemiological trends: Number of cases, trends of case numbers, case fatality, biological confirmation, evolution of the epidemic (delay of intervention)
- Epidemiological context: High-risk health zone, timing and date of last epidemic, vaccination coverage, neighbouring health zones in epidemic
- Other criteria (logistic, security, presence of other partners) are considered for the final decision

This algorithm is used for the prioritisation of health zones for investigations, the final decision to intervene or not is based also on the results of the investigation.

As part of the operational research component of the project, we are trying to better understand the spatial heterogeneity in susceptible individuals, i.e. where to find the children at most need of vaccination. Therefore, we are carrying out vaccination coverage surveys or seroprevalence studies.

Vaccination coverage surveys: To improve vaccination strategies, it is important to understand where and why we have low or high rates of vaccination in different areas. For example, during a vaccination campaign in one health zone vaccination teams reported a large number of vaccine refusals and a vaccine coverage survey confirmed that only 68% of children were being vaccinated.

The survey allowed to understand that many reasons for non-vaccination were related to absence/unavailability of caregivers; refusal of vaccination (including parents' fears around vaccines following the start of COVID-19 vaccination); difficult access; and lack of information about the campaign. This is critical information to improve the planning of vaccination activities and subsequently their impact. It also highlights that often; barriers are not only due to refusal but also related to inability rather than unwillingness and require adaptations on the programme side rather than behavioural changes.

Seroprevalence surveys: Another way to quantify the number of immunised children (through vaccination or naturally) are seroprevalence surveys, where blood samples are tested for measles antibodies and questions about vaccination and infection history are asked to participants. With these, we try to answer three main questions:

1. In a given health zone, where are the geographic areas with the least immunized children (planning)?
2. Did we succeed in vaccinating all children (evaluation)?
3. Are we vaccinating the same children (conduct during the response/ vaccination campaigns)?

These surveys can help to better locate areas with high numbers of non-immunized children and identify where and how to strengthen vaccination programmes (routine, prevention, or response). The seroprevalence data can also tell us if we've succeeded in vaccinating a sufficient number of susceptible children during a vaccination campaign. In combination with information on vaccination history, we can identify areas with potential cold-chain issues (for example where children reported to have been vaccinated, however have not developed antibodies against measles). It can also tell us if we are re-vaccinating children that are already immunized by quantifying seroprevalence among children attending one of our vaccination sites, can allow us to compare different vaccination strategies. For example, if we wanted to

implement a new vaccination strategy, we could see whether one is more efficient than the other to reach the non-immunized children in a community.

Planning based on risks maps, epidemiological trends and community data: The risk mapping and analysis of epidemiological trends help us identify where to respond. However, to increase the impact of our activities, understanding the factors causing those risks is key. By including community data from surveys into our considerations we can develop prevention and response strategies in these pre-identified areas which also take the

underlying reasons into account. If it's about information, how can we ensure that people have the information they need? Are we communicating early enough and through the right channels? If people are absent, then we need to find out what would be the optimal timing for intervention? Is this a time of day, a day in the week, or a specific month in the year? Are there approaches better than mass vaccination? For example, more decentralized, locally available options and locations? We are currently determining what would be the best qualitative data to respond to these critical questions in the coming year.

Harnessing Community Knowledge to Track Emerging Infectious Pathogens

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There is increasing recognition of the need to develop new, innovative and sustainable surveillance systems for tracking emerging infectious diseases globally.¹ The majority of these emerging diseases are zoonoses with sources often attributed to non-domesticated animal species.² The impact and increase of wildlife-sourced zoonoses on human populations as globalisation, climate change and ecosystem alterations bring people and wildlife into closer contact raises concerns, particularly in the light of the Covid-19 pandemic and recent outbreaks of Ebola virus, Swine Flu, Marburg, Nipah, Anthrax and Rift Valley Fever.³ As such, there is a requirement to develop One Health-aligned dynamic approaches to understanding and preventing pathogen spillover, those that address both the biological and social factors.

Our case study discusses the co-development of a novel, sustainable, community-led self-reporting system that assists with the prediction of pathogen spillover in Southern Uganda (Figure 1). It does so by harnessing community knowledge of animal behaviour and population changes, identifying carcasses of known hosts (for example of Ebola virus (EBOV)) such as bush pigs, bats, porcupines and certain primate species, and conducting large scale qualitative data collection and community engagement activities to better understand human behaviours surrounding the collection, consumption and movement of wild animal products in and around Bwindi Impenetrable Forest.



Fig 1: Bwindi Impenetrable National Park, Uganda

How it works

Concurrent with previous human Ebola Virus Disease (EVD) epidemics, biologists have reported high mortality rates in western lowland gorillas and chimpanzees in Republic of Congo, Cameroon and Gabon. EBOV was detected in a number of these carcasses and 5000 apes were believed to have died before human cases were identified.⁴ Examples like this have also been reported in a number of other species, diseases and contexts.⁵ As some epizootic disease outbreaks (diseases of epidemic proportion within animal populations) are correlated with zoonotic disease outbreaks (diseases that can be transmitted from animals to humans) such as certain Ebola virus strains, identifying, tracking and responding to the emergence of both zoonotic and epizootic pathogens in animals, in an attempt to be one step ahead in predicting spillover into human populations, provides a possible solution to the prevention of a public health emergency.

1 Holmes EC, Rambaut A, Andersen KG. 2018 Pandemics: spend on surveillance, not prediction. *Nature* 558, 180–182. (doi:10.1038/d41586-018-05373-w); Morse SS, Mazet JAK, Woolhouse M, Parrish CR, Carroll D, Karesh WB, Zambrana-Torrel C, Lipkin WI, Daszak P. 2012 Prediction and prevention of the next pandemic zoonosis. *Lancet* 380, 1956–1965. (doi:10.1016/S0140-6736(12)61684-5); Olival KJ, Hosseini PR, Zambrana-Torrel C, Ross N, Bogich TL, Daszak P. 2017 Host and viral traits predict zoonotic spillover from mammals. *Nature* 546, 646–650. (doi:10.1038/nature22975)

2 Kruse, H., Kirkemo, A. M., & Handelnd, K. (2004). Wildlife as source of zoonotic infections. *Emerging infectious diseases*, 10(12), 2067–2072. <https://doi.org/10.3201/eid1012.040707>

3 National Research Council (US) Committee on Achieving Sustainable Global Capacity for Surveillance and Response to Emerging Diseases of Zoonotic Origin; Keusch GT, Papaioanou M, Gonzalez MC, et al., editors. *Sustaining Global Surveillance and Response to Emerging Zoonotic Diseases*. Washington (DC): National Academies Press (US); 2009. 3. Drivers of Zoonotic Diseases. Available from: <https://www.ncbi.nlm.nih.gov/books/NBK215318/>

4 Bermejo M, Rodriguez-Teijeiro JD, Illera G, Barroso A, Vila C, Walsh PD. 2006 Ebola outbreak killed 5000 gorillas. *Science* 314, 1564. (doi:10.1126/science.1133105)

5 Rouquet P et al. 2005 Wild animal mortality monitoring and human Ebola outbreaks, Gabon and Republic of Congo, 2001–2003. *Emerg. Infect. Dis.* 11, 283–290. (doi:10.3201/eid1102.040533)