

# Detect and suppress future zoonotic‐derived outbreaks: A lesson from the last two decades

To the Editor,

COVID‐19 has revealed how naive we are when dealing with a global threat. Looking back on the last few decades, there is a shared pattern. These outbreaks emerged as harmless zoonotic diseases within a favorable environment (notably in low‐ and middle‐income countries, LMIC), then spilled over to humans and eventually spread to become outbreaks. Most of these are respiratory viruses (particularly Orthomyxoviridae or Coronaviridae families), which are highly transmissible and can be easily spread (see Table [1\)](#page-1-0). These raise an urgent need for innovative and multidisciplinary approaches that prepare for future outbreaks, taking into account the interconnection between human, environmental, and animal fields.

Although we already have numerous centers to keep track of infectious diseases globally, most focus on human pathogens (e.g., influenza, RSV, tuberculosis). Nevertheless, many recent worldwide outbreaks are zoonotic‐derived and genetically related (Table [1](#page-1-0)). These pathogens require specific environmental conditions to flourish, particularly optimal temperature, moisture, hygiene conditions, population density, and so forth, in tropical climate areas and LMIC. A poor response at the beginning is likely to enable pathogenic spread to the border regions and then globally. Since the interplay between animals and environmental sectors poses a threat to another spillover pandemic, those countries need more resources to early detect and suppress future threats.

Nevertheless, we are now facing an imbalance in health resource allocation: most outbreaks originate in LMIC while a large number of centers are located in high‐income countries. We need more proactive and on-site surveillance centers to deal with high-risk situations. Some factors should be considered to decide whether an area is ideal to establish a new center, including environmental pollution, ideal moisture, and temperature for pathogenic spread, dense population, and wildlife adhesion. It should take into account the endemic and current emerging strains in both humans and animals to keep track of any zoonotic viruses that will be likely to spill over to humans (e.g., Coronaviridae, Orthomyxoviridae—see Table [1](#page-1-0)). Data should be collected through fieldwork and event-based surveillance systems to generate publicly available weekly reports. Wastewater surveillance can be of foremost interest because it can help identify contaminated samples in infected wastewater with reasonable costs regardless of transmission routes. Understanding the microbiome of the water source would also lead to a better understanding of samples and alert authorities to potential epidemics. Wastewater samples and the resources invested can also be used to

track antibiotic‐resistant strains or other pathogens as needed and optimize cost-effectiveness. Additionally, these centers should expand multidisciplinary collaborations to comprehend the humanwildlife interaction and understand the epidemiology within regions, which plays an essential role in managing and controlling a pandemic outbreak.

With the raw data collected, the surveillance centers can utilize these data, model the diseases, and determine how and when the region will have to respond to a cluster of illnesses or health events. The quality of output data plays a vital role in determining future responses; hence, it requires well‐designed analysis plans with careful checkpoints and sufficient mathematical intellect. The data will enable us to build monitoring systems capable of tracking the expected levels and types of disease and watching closely for changes that could trigger any unusual spike in cases. These centers should work cooperatively with the government to propose actionable plans for preventing and controlling the identified risk factors. Experts from the surveillance centers can work with policymakers to develop fast and practical guidelines to respond to upcoming disease threats. Besides, the surveillance centers also assist the government in sharpening communication with citizens so they can respond rapidly and effectively. In cooperation with the government's adequate response, the surveillance center will strengthen the understanding of risk factors and create impactful positive effects on the region epidemiologically.

Besides assisting in analyzing data, promoting a monitoring system, and initiating appropriate policy‐making, separated surveillance centers in different regions can exchange information. This effort would provide deep epidemiology understanding, initiate an impactful response to the pandemic burden between countries, support healthcare resource distribution, and direct agencies to health research investment. By having high‐quality surveillance centers located in LMICs or regions with high risks of pandemic burden, we are preventing a possible outbreak from the very beginning.

Despite the undeniable advantages, this tactic possesses some limitations. LMICs that pose a high risk of endemic usually lack the capability to build these surveillance centers, which require sufficient infrastructure supplies and continuous financial investments. Consequently, continuous investment and support from internal organizations, agencies, and developed countries are vital for long‐term maintenance. Besides, it is essential to build an interconnected network among centers located in global hotspots and local governments to guard against zoonotic‐derived outbreaks in the future.

<span id="page-1-0"></span>TABLE 1 Prominent spillover of pathogens from animals to humans over the past 20 years.



Abbreviations: MERS‐CoV, Middle East respiratory syndrome coronavirus; SARS, severe acute respiratory syndrome; SARS‐CoV, SARS‐associated coronavirus; SARS‐CoV‐2, severe acute respiratory syndrome coronavirus 2.

### CONFLICT OF INTEREST STATEMENT

The authors declare no conflict of interest.

## DATA AVAILABILITY STATEMENT

Data sharing is not applicable to this article as no datasets were generated or analyzed during the current study. All relevant data are included in this published article.

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