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Editorial: Advances in the diagnosis and genomic research of surveillance-response activities in emerging, re-emerging, and unidentified infectious diseases

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Editorial on the Research Topic

[Advances in the diagnosis and genomic research of surveillance-response activities in emerging, re-emerging, and unidentified infectious diseases](#)

Six pandemics of public health emergencies were announced as a global concern, causing numerous deaths and economic losses in this century (1). Strikingly, more than 3.5 million people died from COVID-19 in 2021, exceeding the combined number of deaths resulting from HIV, malaria, and tuberculosis in 2020 (2). The delayed diagnosis and inadequate surveillance of infectious diseases may indirectly lead to ineffective responses, making it harder to control the development of pandemics. Despite advances in health science, infectious diseases, including emerging, re-emerging, and unidentified infectious diseases, remain a major threat to human beings, particularly in low-resource settings.

Recent studies has been made in understanding infectious diseases transmission and dynamics (3). However, there are still gaps between diagnostic capacity and dynamic surveillance of infectious diseases. Nowadays, researchers have made significant efforts to optimize surveillance performance to emerging, reemerging, and unidentified infectious diseases, including diagnosis and genomic research (4, 5). However, increasing efforts are highly required to develop a more effective surveillance technique to continuously monitor, early warning and predict infectious diseases.

Therefore, we focused on the advances in the diagnosis and genomic research of surveillance-response activities in emerging, re-emerging, and unidentified infectious diseases in this Research Topic, which will contribute to infectious disease prediction and the effective decision making. Eleven papers were published worldwide, including opinion articles, original research, and case reports.

Apply metagenomics and molecular methods to combat infectious diseases

Currently, metagenomic surveillance provides an opportunity to improve the detection and prevention of pathogens by conducting epidemiological investigations (Zhang T. et al.), limiting clonal transmission of bacteria (Chen et al.), and ensuring the effectiveness of interventions (Zeng et al.). Padilla-Blanco et al. described a new variant of SARS-CoV-19 that emerged in Sicily in late 2020. It showed that continuous monitoring of SARS-CoV-2 variants is helpful in understanding virus evolution and provides timely information on sudden pathogen emergence, especially in times and places where epidemic virus pedigree is seldom explored. More importantly, monitoring viral variants by molecular biology technology can play a significant role in developing appropriate rapid detection tools and predicting potential vaccine escapes in emerging variants. For example, Feng et al. reported a case of *Parvimonas micra* pneumonia in a patient without obvious underlying disease and distal site of infection, expanding the etiology of pneumonia. It demonstrated that metagenomic sequencing allows rapid screening for rare pathogens, especially when regular strategy is ineffective. In addition, Tian et al. continuously monitored the changes in pathogenic bacteria by sequencing and drug sensitivity tests in a case of intracranial infection caused by multidrug-resistant *Acinetobacter baumannii*. As a complication of a series of invasive operations, the infection may seriously affect the prognosis of patients, in which it is necessary to monitor the pathogens in the patients' blood.

Data-based approaches to combat infectious disease

Rapid advances in Big Data and machine learning provide opportunities to collect and deeply utilize epidemiological data for combating infectious diseases (6–9). Hand-foot-and-mouth disease (HFMD) is a common infectious disease in children caused by a variety of enteroviruses. Yang et al. explored the interaction between multiple viruses and the regular patterns of HFMD in different regions using the susceptibility-exposure-infection-asymptomatic-rehabilitation (SEIAR) model. HFMD is a common infectious disease in children caused by a variety of enteroviruses. The results showed that the incidence of HFMD increased with temperature risk, and the interaction of different pathogens strongly depended on geographic locations. Compared with the transmission of only one major subtype, there was a dilution effect when multiple subtypes of pathogens were transmitted simultaneously. Andagalu et al. conducted a cohort study to evaluate the efficacy of two antimalarial drugs, artemether-lumefantrine (AL) and artesunate-mefloquine (ASAQ), while developing predictive models of treatment outcomes based on immune profile data. Using machine learning to assess humoral immunity to malaria to predict the effectiveness of treatment, the researchers found that ASAQ was more effective. The investigators applied computational methods for the first

time to show that serologic immune profiles differentially affect treatment outcomes based on artemisinin-based combination therapies (ACTs), providing an integrated approach to data integration, machine learning, and modeling.

Promote the diagnosis and response to infectious diseases

Some rapid testing techniques, which have the advantage of rapid, low-cost, and user-friendly, are suitable for epidemiologic studies and show the potential as high-throughput screening tools. A recent study evaluated the rapid detection of anti-*Trypanosoma cruzi* antibodies, providing recommendations balanced between sensitivity and operability for large-scale investigations (Iturra et al.). In addition, based on previous research, two opinion articles provided some optimization suggestions for antigen detection of SARS-CoV-2 (Zhang J. et al.), and discussed the methods to treat or alleviate the symptoms of infectious diseases (Aydemir and Ulu).

To effectively address the challenges from infectious disease outbreaks and public health emergencies, we need to strengthen surveillance on unexplained infectious diseases, improve the sensitivity and accuracy of diagnostic assessment, and enhance the capacity for *in situ* analysis and treatment. We expect that further studies on infectious diseases will lead to more cost-benefit programs that improve wellbeing and sustainability in diverse socio-ecological settings and ultimately throughout the world.

Thank all authors who contributed to this research theme, and we invite readers to explore the excellent articles in this compilation.

Author contributions

KY contributed to the original idea and conceived the paper. CW wrote the initial draft of the paper. The final version was reviewed by XF, JF, TC, and HC. All authors contributed to the article and approved the submitted version.

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References

1. Wilder-Smith A, Osman S. Public health emergencies of international concern: a historic overview. *J Travel Med.* (2020) 27:taaa227. doi: 10.1093/jtm/taaa227
2. World Health Organization. *WHO Director-General's Opening Remarks at the Media Briefing on COVID-19.* (2021). Available online at: <https://www.who.int/director-general/speeches/detail/who-director-general-s-opening-remarks-at-the-media-briefing-on-covid-19> (accessed December 22, 2021).
3. Chala B, Hamde F. Emerging and re-emerging vector-borne infectious diseases and the challenges for control: a review. *Front Public Health.* (2021) 9:715759. doi: 10.3389/fpubh.2021.715759
4. Robishaw JD, Alter SM, Solano JJ, Shih RD, DeMets DL, Maki DG, et al. Genomic surveillance to combat COVID-19: challenges and opportunities. *Lancet Microbe.* (2021) 2:e481–4. doi: 10.1016/S2666-5247(21)00121-X
5. Xie Y, Li H, Chen F, Udayakumar S, Arora K, Chen H, et al. Clustered regularly interspaced short palindromic repeats-based microfluidic system in infectious diseases diagnosis: current status, challenges, and perspectives. *Adv Sci.* (2022) 9:e2204172. doi: 10.1002/advs.202204172
6. Dolley S. Big data's role in precision public health. *Front Public Health.* (2018) 6:68. doi: 10.3389/fpubh.2018.00068
7. Simonsen L, Gog JR, Olson D, Viboud C. Infectious disease surveillance in the big data era: towards faster and locally relevant systems. *J Infect Dis.* (2016) 214:S380–5. doi: 10.1093/infdis/jiw376
8. Peiffer-Smadja N, Rawson TM, Ahmad R, Buchard A, Georgiou P, Lescure FX, et al. Corrigendum to 'machine learning for clinical decision support in infectious diseases: a narrative review of current applications' clinical microbiology and infection (2020) 584–595. *Clin Microbiol Infect.* (2020) 26:1118. doi: 10.1016/j.cmi.2019.09.009
9. Agany DDM, Pietri JE, Gnimpieba EZ. Assessment of vector-host-pathogen relationships using data mining and machine learning. *Comput Struct Biotechnol J.* (2020) 18:1704–21. doi: 10.1016/j.csbj.2020.06.031