

## Integrated pneumonia surveillance: pandemics and beyond



Nov 12, 2022, marks the third annual World Pneumonia Day since SARS-CoV-2 came to worldwide attention. As we continue to confront new SARS-CoV-2 variants, we also need to anticipate and prepare for the emergence of other potential respiratory epidemics and pandemics. The previous 2 years have shown the importance of timely disease surveillance to detect cases and track the emergence of new variants of SARS-CoV-2. The COVID-19 pandemic revealed global and regional gaps in reliable testing and reporting of cases and deaths, and has led to calls for increased attention and investment in resilient surveillance systems for respiratory viruses of pandemic potential that leverage existing platforms towards more coordinated approaches to inform public health decision making.<sup>1</sup> To ensure early warning and to better understand and track viral variants and their specific genetic changes and characteristics, WHO have established an integrative forum and global risk-monitoring framework based on a multidisciplinary approach that uses in-silico, virological, clinical, and epidemiological data.<sup>2</sup>

Given that not all deadly respiratory pathogens result in pandemics and that the burden of, and mortality from, pneumonia remain unacceptably high, insights gained from COVID-19 highlight the need for improved and integrated disease surveillance for the leading causes of pneumonia-related mortality globally, including *Streptococcus pneumoniae* and respiratory syncytial virus. Integrated surveillance that incorporates patient testing, pathogen genomic sequencing, population serosurveillance, and mortality tracking is essential for epidemic preparedness and should become routine, including for the most common pneumonia-causing pathogens.

Existing sentinel platforms, such as WHO's Global Influenza Surveillance and Response System (GISRS), a mechanism of worldwide surveillance, preparedness, and response for seasonal, pandemic, and zoonotic influenza and an alert system for novel influenza viruses, have been leveraged for the testing and genomic sequencing of SARS-CoV-2 and respiratory syncytial virus in select countries. This integrated surveillance approach should be expanded and adapted to routinely include these pathogens and leveraged for emerging pathogens when needed—something WHO is already calling for in the envisioned GISRS-Plus platform.<sup>3</sup> The use of genomic

surveillance could also be expanded more broadly to infectious respiratory pathogens, including those for which vaccine escape is a considerable risk.<sup>4</sup> The application of genomics to *S pneumoniae* surveillance was crucial in the identification of pneumococcal serotype replacement caused by homologous recombination events in the capsular locus genes that can allow the emergence of serotypes that are not preventable by existing pneumococcal conjugate vaccines.<sup>5</sup> These kinds of data, especially when linked to systems to measure vaccine effectiveness, are crucial to informing vaccine-related policy decisions.

In addition to pathogen genomic surveillance, seroepidemiology is a key surveillance component to measure population immunity to a pathogen and to understand the potential for vaccine escape. The ability to multiplex serological assays allows real-time assessment of population immunity, and, in longitudinal surveys, could allow for the detection of circulating strains through their immunological signatures. For SARS-CoV-2, population-based seroprevalence data from sub-Saharan Africa suggest that case counts in this region were under-reported, perhaps due to low testing capacity and a high prevalence of asymptomatic infections.<sup>6,7</sup> Seroepidemiology has hence greatly enhanced our understanding of the COVID-19 epidemic in the African context. In terms of other pathogens, longitudinal assessment of pneumococcal capsular serotype-specific antibodies has been used to detect serotype-specific pneumococcal carriage and to derive correlates of protection for each serotype, and, similarly, longitudinal serosurveillance of Vi capsular antibodies has been used to estimate exposure to typhoid fever.<sup>8,9</sup>

Presented with the urgency of a deadly global pandemic, unprecedented action was taken to develop diagnostics, therapeutics, and vaccines. Beyond pandemics, can we expand this urgency to other respiratory pathogens? In 2019, before COVID-19, 2.5 million people died from pneumonia, of whom almost a third were children. Pneumococcus has remained the leading infectious cause of childhood deaths. In children younger than 5 years in 2019, 33 million episodes and 101 400 deaths were attributable to respiratory syncytial virus.<sup>10</sup> To address pneumonia-related mortality, pneumonia pathogens regarded as routine or usual will

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require enhanced and integrated surveillance, including sentinel serosurveillance, mortality surveillance, and genomic surveillance. The same sense of urgency should be brought to respiratory pathogens other than SARS-CoV-2, particularly for children living in low-income and middle-income countries. In turn, surveillance platforms can then be leveraged for better pandemic preparedness. Enhancing global sequencing capabilities, targeting increased coverage, particularly to geographical and population blind spots, and building consensus towards integrated and coordinated surveillance are instrumental to ensuring that we are prepared for the current and evolving COVID-19 pandemic, for any future respiratory virus of pandemic potential, and, perhaps most importantly, for our ongoing deadly respiratory epidemics.

We declare no competing interests.

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- 1 WHO. Global strategic framework “crafting the mosaic”: resilient surveillance systems for respiratory viruses of pandemic potential; May 10–12, 2022.
- 2 Subissi L, von Gottberg A, Thukral L, et al. An early warning system for emerging SARS-CoV-2 variants. *Nat Med* 2022; **28**: 1110–15.
- 3 WHO. Integrated sentinel surveillance of influenza and SARS-CoV-2 and the development of the Global Influenza Surveillance and Response System Plus: virtual meeting, 12–14 October 2021. 2022. <https://apps.who.int/iris/handle/10665/356310> (accessed Sept 9, 2022).
- 4 Excler JL, Saville M, Berkley S, Kim JH. Vaccine development for emerging infectious diseases. *Nat Med* 2021; **27**: 591–600.
- 5 Lo SW, Mellor K, Cohen R, et al. Emergence of a multidrug-resistant and virulent *Streptococcus pneumoniae* lineage mediates serotype replacement after PCV13: an international whole-genome sequencing study. *Lancet Microbe* 2022; **3**: e735–43.
- 6 Idoko OT, Usuf E, Okomo U, et al. Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in Africa: current considerations and future projections. *Clin Infect Dis* 2022; **75** (suppl 1): S136–40.
- 7 Madhi SA, Kwatra G, Myers JE, et al. Population immunity and COVID-19 severity with omicron variant in South Africa. *N Engl J Med* 2022; **386**: 1314–26.
- 8 Voysey M, Fanshawe TR, Kelly DF, et al. Serotype-specific correlates of protection for pneumococcal carriage: an analysis of immunity in 19 countries. *Clin Infect Dis* 2018; **66**: 913–20.
- 9 Phillips MT, Meiring JE, Voysey M, et al. A Bayesian approach for estimating typhoid fever incidence from large-scale facility-based passive surveillance data. *Stat Med* 2021; **40**: 5853–70.
- 10 Li Y, Wang X, Blau DM, et al. Global, regional, and national disease burden estimates of acute lower respiratory infections due to respiratory syncytial virus in children younger than 5 years in 2019: a systematic analysis. *Lancet* 2022; **399**: 2047–64.