

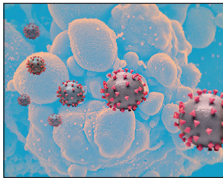


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Sustainability of surveillance systems for SARS-CoV-2



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Vaccines, variations in surveillance systems, virus testing, and a mix of measures to protect vulnerable groups keep SARS-CoV-2 case numbers at bay and avoid overburdening health systems. This process can be complex.

Whenever a new variant of SARS-CoV-2 emerges and is of concern, the scientific community races to understand its characteristics. Is this variant less or more transmissible? Can this variant evade immune responses to previous infection or vaccination? Does this variant cause less or more severe disease? Who is mostly affected, and which (sub)population is at the highest risk? These crucial parameters help estimate immediate response options and future responses and health-care needs.

Observational population-based data from different monitoring systems are the first available information to generate such evidence. Despite limitations, real-time and comprehensive surveillance data allow rapid assessment of the situation of any disease, during a pandemic or otherwise, underlined in the two country data analyses from Denmark and Scotland published in the *The Lancet Infectious Diseases* by Peter Bager and colleagues¹ and Aziz Sheikh and colleagues,² respectively. Both studies assess the risk of hospitalisation as a proxy for the severity of the SARS-CoV-2 omicron variant (B.1.1.529) by combining surveillance data across different health-care levels with mortality data and information on vaccination.

Both Denmark and Scotland rely on comprehensive data collection, which includes case-based data on outpatients and inpatients with confirmed SARS-CoV-2 infection, accompanied by detailed information about the patients, such as comorbidities, immunosuppression, previous SARS-CoV-2 infection, and vaccinations against COVID-19, as well as confirmation of the infecting variant virus through S-gene dropout analysis or variant-specific PCR, supplemented by extensive whole-genome sequencing programmes.

There are many challenges when investigating the severity of a newly emerging virus or virus variant. Over the course of the pandemic, younger age groups were infected before the virus reached older more at-risk populations, which influences the severity assessment over time. Both studies^{1,2} used hospitalisation as a proxy

of severity, covered a relatively early phase of the omicron wave, and had a short follow-up period, which could lead to underestimation of the true severity of the omicron variant.

In both studies,^{1,2} the rapid spread of the omicron variant within the population, with more than 150 000 cases in both studies over a very short period, provided the basis for robust analyses. Cox proportional hazards and log-linear Poisson regression approaches resulted in similar results, with risk ratios (RRs) of 0.32 (95% CI 0.19–0.52)² and 0.29 (0.21–0.39),¹ respectively, supporting results from South Africa^{3–5} and the UK⁶ of a lower risk of omicron causing severe disease requiring hospitalisation. The studies showed that the booster vaccine dose was associated with a 57% (54–60) reduction in the risk of symptomatic S-gene-negative infection relative to 25 weeks or more after the second vaccine dose,² and a RR for hospitalisation of 0.50 (95% CI 0.32–0.76) among those who received three vaccine doses.¹

High-quality data from various geographically different countries are of utmost importance in an international context for regional or global assessments. Tremendous efforts and investments into different surveillance systems have been made during the COVID-19 pandemic to enhance testing and genotyping capacity, data linking, and reporting. Both studies discussed here^{1,2} show that it is crucial to have solid data links between epidemiological and virological information in a timely manner. How long will countries be able to keep such comprehensive systems active for SARS-CoV-2 surveillance? Many countries in Europe are already reducing testing availability and limiting sequencing for various reasons, including availability of resources, as also already indicated in the Danish study.¹

How can we ensure that we will be able to identify, track, and assess the epidemiological situation for SARS-CoV-2, including new variants, with less comprehensive systems? Surveillance systems, testing, and sequencing efforts need to be representative and targeted, interlinked, robust, and detailed enough to establish rapid evidence for a situation overview. The balance between specific or marker PCRs accompanied by the right level of full genomic data needs to be found for the best cost-effectiveness and system sustainability.

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Expanding such a system to include diseases other than COVID-19 could benefit public health as a whole.

It is important to define the type and level of detail needed for data on a local, national, regional, and global level to be prepared for the next SARS-CoV-2 variant and subsequent pandemic threats.

We declare no competing interests.

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Modelling results on the impact of COVID-19 testing in schools



The COVID-19 pandemic has had widespread health, wellbeing, and economic impacts, both from the disease itself and from the measures put in place to try to control it. By mid-April, 2020, school closures had impacted 94% of the world's students, with the duration and impact of closures varying substantially by country.¹ As new variants rise and fall, it is vital to understand ways to minimise both educational and social disruption by keeping schools open while also reducing the spread of infection.

In *The Lancet Infectious Diseases*, Elisabetta Colosi and colleagues² report modelling results investigating the impact of different potential testing strategies in French primary (ages 6–11 years) and secondary (in this study comprising ages 17–18 years) schools. The results are informed by pre-pandemic data on contact patterns, collected via radio frequency identification tags (wearable sensors that detect proximity), and infection data from pilot screening trials in French primary and secondary schools. Colosi and colleagues use the infection data to estimate the effective reproductive number in schools during the alpha (B.1.1.7) and delta (B.1.617.2) variant waves, informing transmission in an individual-based model of infections that is structured according to the contact pattern data. They conclude that weekly asymptomatic testing could reduce both infections and the number of missed days of school due to reactive class closures.

How do these results compare with other models of school-based testing for COVID-19? Previous work

examining SARS-CoV-2 transmission among school pupils in the USA,³ Canada,⁴ and the UK^{5–7} found that asymptomatic testing can reduce school transmission. Similar results from a range of independent studies in different countries at different times can give some confidence of a sound conclusion. However, it is very difficult to quantify a reduction in transmission accurately and robustly. Comparisons between studies are further complicated by the implementation of different potential strategies. In addition, schools in different countries might be sufficiently different in setup that implemented measures might be reasonably expected to have different outcomes.

One aspect that reduces our ability to make robust quantifications in this area is the lack of comprehensive data to inform modelling. A strength of the study by Colosi and colleagues is their use of detailed data on school contact patterns, which allowed representative networks to be built using a data-driven basis. These data are one of the best sources of school contact patterns used in this type of study, and yet they still have inevitable drawbacks as they are, by necessity, from studies of particular schools and they represent pre-pandemic contact patterns. Another attempt to inform contact patterns has been made by Woodhouse and colleagues,⁵ who used structured expert judgement to construct their random contact networks. By contrast with the detailed contact pattern data available to Colosi and colleagues, Woodhouse and colleagues' data on school infections were sadly quite sparse (as they rightly



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