Targeted mass testing and phylogenetic analysis is effective for preventing community transmission of SARS-CoV-2 beta variant

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Abstract

As of 9 September 2021, some areas of the Western Pacific region, such as China, Taiwan, and New Zealand, maintained their elimination strategy to minimize community incidence of SARS-CoV-2 infection. Even during the early vaccination phase of the pandemic, these areas had achieved suppression of the COVID-19 morbidity and mortality regardless of vaccine availability. On the other hand, the mitigation strategy with vaccination, which was employed by many other countries, has potential risk of a uncontrollable endemic of future variants with high resistance to vaccine-induced immunity. Thus, the “zero COVID” policy based on the elimination strategy would benefit public health by preventing community transmission of variants.

So how can local transmission of challenging variants be prevented in low incidence areas? Among the zero COVID areas, China has implemented rapid and extensive citywide mass testing by RT-PCR (reverse transcription-polymerase chain reaction), contact tracing, and quarantine as the most notable approach with only a few cases of community transmission. However, the effectiveness of this tactic needs validation for preventing community transmission of continuously challenging variants. Additionally, when only limited resources are available for mass testing, a focused design that targets particular persons may be needed.

In this issue of The Lancet Regional Health - Western Pacific, Chen and colleagues described their experience of successfully eliminating local transmission of SARS-CoV-2 beta variant by using RT-PCR testing, contact tracing, isolation, and rapid genome sequencing complemented by mass testing in Hong Kong, China. Initially, an inbound traveler with asymptomatic infection (the index case) was diagnosed nine days after 21 days of complete quarantine.

Only one secondary case was found by conventional contact tracing of 163 persons. This finding proves the limits of using conventional interviewing, which relies on the memory of the infected person. Cognitive bias (memory bias, false declaration, etc.) cannot be denied. Additionally, there are some people who do not cooperate with the survey for reasons of personal confidentiality. It may be difficult to enforce the survey due to ethical aspects (e.g., discrimination, social vulnerability).

When the case infected with the SARS-CoV-2 beta variant was identified in Hong Kong, they implemented rapid mass testing in the community for all people (0.47 million persons) who attended buildings, schools, malls, restaurants, and facilities where the confirmed cases had visited. Mass testing was also conducted for all unvaccinated or partially vaccinated foreign domestic helpers (FDH, 0.34 million persons tested within 9 days) because of the finding of one symptomatic FDH case with unknown epidemiological links but with the identical genome sequence of the index case by the phylogenetic analysis. Two more cases among the tested FDH were identified, and phylogenetic analysis again revealed that these two cases were linked. The mass testing was completed within one month. We believe that this could contribute to the early diagnosis and management, such as the use of medication and monoclonal antibody cocktails, in high-risk patients before the onset of illness.

While no cases were identified among mass testing for the general population, mass testing targeted on FDH identified two cases. Mass testing targeted to persons based on contact history of visiting the same premises, such as a marketplace, was used previously and showed effectiveness for identifying cases in China. This study reveals that mass testing is an effective measure for COVID-19 control in an early stage of endemic, even in a densely populated city with relatively low herd immunity. The phylogenetic analysis is also a powerful tool to identify infection roots and search hidden infected persons, but it is not easier than usual PCR tests given the needs of genome sequencing.

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the combination of mass testing and phylogenetic analysis is more useful in an early stage of an endemic.

Further studies are needed to confirm the effective testing strategies to targeted mass testing based on a specific group rather than mass testing for all citizens. The groups may include socially or economically vulnerable people with possible difficulty in employing infection prevention measures. Careful ethical consideration may be needed for selecting which group would be targeted for mass testing.

Mass testing in this study was conducted without citywide hard lockdown measures, like the early containment stage of Wuhan. Thus, the elimination strategy might be effective even without citywide hard lockdown. This is one of the benefits of employing zero COVID policy. Cost-effectiveness analysis may be required to estimate the total benefit of mass testing compared to cyclic lockdowns inhibiting social activities. This study also confirmed the higher clinical attack rate (including two infants cared for by FDHs) of close household contacts, indicating the necessity of rapid case identification and effective preventive measures among households.

The definition of close contacts did not include the lack of mask-wearing in this study. Different countries use different definitions of close contacts. For example, in Japan, close contacts are defined as persons who encounter an infectious patient within one-meter distance over 15-minutes without prevention measures for droplet infections or contagions, such as mask-wearing and hand sanitizing. A broader definition of contacts may be more helpful for identifying secondary cases.

The study by Chen and colleagues described that mass testing successfully prevented local transmission of the SARS-CoV-2 beta variant in Hong Kong. Another study in Guangdong, China, showed that approximately 30 million tests were performed in two weeks to find 167 cases of delta variant, and all cases could be epidemiologically or genetically traced back to the first index case. Therefore, mass testing seems essential for comprehensive searching in an early stage of infection control and enables aggressive epidemiological investigation or contact tracing.

Declaration of interests
None.

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