

Will the SARS epidemic recur?

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SARS is the first severe and readily transmissible disease emerged in the 21st century. It has a unique capacity of spreading quickly in hospitals and clinics affecting thousands of health care workers in a short period of time. The booming of international air travel in recent decades has also empowered the infection to be quickly spread across the continents. In March 2003, one infected tourist from China checked into a hotel in Hong Kong and spread the infection to eight countries within 2 weeks. By July 2003, 32 countries were involved and 8439 patients were infected around the world. Although WHO has announced that the initial crisis is over, we should not be complacent. There is, in my personal view, a high possibility that the epidemic will come back during the winter. This prediction is based on 3 reasons. First, despite much efforts contributed by virologists and molecular biologists, we are still not sure the source of the infection. Early reports suggested that SARS-CoV resembled the bovine coronavirus or mouse hepatitis virus. Yet, after the sequence of the whole viral genome was completed, it becomes clear that the SARS-CoV is a distinctly new pathogenic strain that does not arise from a simple recombination of known existing strains [1]. But, we are still not sure where it comes from. Second, serological studies have reviewed that asymptomatic or subclinical infection of SARS-CoV is uncommon. We examined 674 health care workers at the Prince of Wales Hospital, where the first hospital outbreak occurred in Hong Kong, among them 43% had direct contact with SARS patients. None of them had IgG antibody to SARS-CoV [2]. Similar studies conducted in China confirmed that asymptomatic carriers are few. This implies that immunity to SARS-CoV in the community will develop slowly. Third, although RNA viruses are known to mutate more readily than DNA viruses, genomic studies of SARS-CoV including strains isolated from Singapore, Hong Kong, Guangdong and Beijing showed a remarkable genetic conservation of the virus since the outbreak was first started in November 2002 [3]. Unlike most other infectious agents transmitted by direct person-to-person contact, the SARS-CoV is unlikely to mutate to a benign infection and attenuated symptoms. Without herd immunity and attenuation of the virus, when the next

epidemic comes, one would still expect to have large-scale outbreak with severe symptoms. What can we do to prepare for the come back? It would be a while before vaccine can be developed, if it could ever be developed. We should continue to search the source of the virus and study the mode of transmitting the disease. We should maintain our high vigilance of the infection. When we see suspected cases, we should implement isolation, quarantine and cohorting measures. Developing a rapid diagnostic test, probably PCR-based, which can differentiate SARS from other atypical pneumonia at an earliest possible stage of the disease would be instrumental in applying these measures successfully. Don't let down your guards, the battle is not over yet!

1. Marra MA, Jones SJM, Astell CR et al. The genome sequence of the SARS-associated coronavirus. Published online May 1, 2003.
<http://www.sciencemag.org/cgi/rapidpdf/1085953v1.pdf>.
2. Chan PKS, Ip M, Ng KC et al. Sero-prevalence of severe acute respiratory syndrome (SARS)-associated coronavirus infection among health care workers after a major outbreak of SARS in a regional hospital *Emerging Infect Dis* (in press)
3. Ruan Y, Wei CL, Ee LA et al. Comparative full-length genome sequence analysis of 14 SARS coronavirus isolates and common mutations associated with putative origins of infection. *Lancet* 2003; 361:1779-1785.