

No SARS transmission was shown among contacted passengers seated in close proximity to the index patient; these results suggest that in-flight transmission of SARS is not common. These results are consistent with other studies that assessed the risk for in-flight transmission of SARS (5,6). The results also suggest that SARS-CoV is not efficiently transmitted, as reflected in its basic reproduction number  $R_0$  (range 2–4) (7). The SARS-infected patient on the indicated flights was in his first week of illness; infectivity is greatest in the second week (8). Therefore, the likelihood of SARS transmission on the indicated flights was not high. These results are further supported by the fact that all contacts were asymptomatic 13 days after their last contact with the SARS patient. No information was available on health-care contacts. Although we did not observe any SARS transmission, we cannot rule out the possibility that it may have occurred. We had no contact information on 56% of the passengers on the indicated flights and, therefore, had to exclude them from the investigation. Obtaining complete contact information from the remaining passengers was difficult, which severely impeded the investigation. Similarly, we were unable to contact crew members and had to exclude them. Recent studies have documented SARS transmission to passengers seated more than four rows away from an index patient (5,9); thus, studying the passenger proximity to the patient may not be sufficient. Because of these limitations, our final sample size was small and probably biased. Since we did not observe any evidence to indicate in-flight transmission of SARS, we were unable to assess the importance of seat assignment proximity as a risk factor.

The study shows that the roles of public health authorities and the aviation industry should be to “harmonise the protection of public health without the need to avoid unnecessary disruption

of trade and travel” in public health emergencies such as global SARS transmission (10). We recommend strengthening the collaboration between national health authorities and the airline industry. Furthermore, the International Air Transport Association should establish procedures to ensure that complete contact information is available for all passengers and that rapid notification can be accomplished in case of potential exposure to infectious diseases.

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**J. Gabrielle Breugelmans,\*  
Phillip Zucs,\* Klaudia Porten,\*  
Susanne Broll,\* Matthias Niedrig,\*  
Andrea Ammon,\*  
and Gérard Krause\***

\*Robert Koch-Institut, Berlin, Germany

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Address for correspondence: Gérard Krause, Robert Koch Institute Department of Infectious Disease Epidemiology, Seestrasse 10, 13353 Berlin, Germany; fax: +49-30-4547-3533; email: [KrauseG@rki.de](mailto:KrauseG@rki.de)

## Estimating SARS Incubation Period

**To the Editor:** In a recent article, Meltzer described a simulation method to estimate the incubation period for patients infected with SARS with multiple contact dates (1). In brief, he assumed a uniform distribution of all possible incubation periods derived from these contact dates for each patient and randomly selected an incubation period from all contact dates for each patient to obtain a distribution of the incubation period for all 19 patients. The process is

repeated 10,000 times to obtain an overall frequency distribution of the incubation period.

Instead of using this cumbersome iterative approach, the same results can be obtained by a simple method. When a uniform distribution is assumed for all possible incubation periods, the expected frequency for a day  $x$  as the incubation period is either 0 or  $1/(\text{total number of possible days})$ . Taking the first patient (Canada 1) in (1) as an example, the expected frequency for 1, 2, 3, ..., 18 days is 0, 1/11, 1/11, 1/11, 1/11, 1/11, 1/11, 1/11, 1/11, 1/11, 1/11, 0, 0, ..., 0. The expected frequencies for the other patients are available online from: <http://www.cdc.gov/ncidod/EID/vol10no8/04-0284.htm#table>.

The total expected frequency for each day is the sum of the expected frequencies for all patients for that day. Therefore, the frequency distribution of the incubation period is given by dividing each total expected frequency by the sum of the total expected frequencies ( $\times 100\%$ ) and is 7.6, 22.1, 14.2, 9.0, 6.5, 11.5, 4.6, 3.7, 3.7, 6.4, 3.7, 1.7, 1.1, 1.1, 0.7, 0.7, 0.7. This is identical to the frequency distribution shown in Figure 1 of the paper by Meltzer (1).

#### Tze-wai Wong\* and Wilson Tam\*

\*The Chinese University of Hong Kong, Hong Kong

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Address for correspondence: Tze-wai Wong, Department of Community and Family Medicine, The Chinese University of Hong Kong, 4/F, School of Public Health, Prince of Wales Hospital, Shatin, NT, Hong Kong, China; fax: 852-2606-3500; email: [tw Wong@cuhk.edu.hk](mailto:tw Wong@cuhk.edu.hk)

**In Reply:** Drs. Wong and Tam (1) are correct in stating that their method of calculating mean frequencies of possible incubation periods for patients with severe acute respiratory syndrome (SARS) is simpler than the method that I presented (2). However, their method cannot replicate the confidence intervals shown in Figure 1 in my article. Their suggested methodology can only replicate Figure 2 in my article, which shows the cumulative distribution of the mean frequencies of individual incubation periods.

The comparative complexity of my method provides data that are essential for making public health decisions. For example, public health officials need to know incubation periods to determine appropriate periods of quarantine and isolation and how long to conduct intensive (and expensive) surveillance after the last clinical case has been reported. To reduce costs and to enhance public support, public health officials may keep quarantine and isolation periods to a minimum. They also need to know the risk for failure of such interventions attributable to patients with relatively long incubation periods. Both Figure 2 in my article and Drs. Wong and Tam's data show that approximately 95% of the mean incubation period will be  $\leq 12$  days (i.e., 5% will incubate for 13 to 18 days). By summing the 95th percentiles for days 13 through 18 from my Figure 1, it can be seen that there is a probability that  $\leq 30\%$  of patients will have incubation periods  $> 12$  days (the actual probability of any given percentage incubating for  $> 12$  days can be easily calculated by using the spreadsheet which is an appendix to my article). Public health officials need to understand the degree of variability associated with any data used to make public health policies. Sole reliance on the mean incubation periods (or mean frequencies) will hide more than is shown, which increases the probability of failed public health interventions.

#### Martin I. Meltzer\*

\*Centers for Disease Control and Prevention, Atlanta, Georgia, USA

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Address for correspondence: Martin I. Meltzer, Centers for Disease Control and Prevention, 1600 Clifton Road, Mailstop D59, Atlanta, GA 30333, USA; fax: 404-371-5445; email: [MMeltzer@cdc.gov](mailto:MMeltzer@cdc.gov)

## Detecting Bioterror Attack

**To the Editor:** In a recent article (1), Kaplan et al. addressed the problems in detecting a bioterror attack from blood-donor screening. The main point of this comment is the "early approximation" used by Kaplan et al. to derive the probability of detecting an attack. The simplification used by Kaplan et al. leads to a probability that does not account for the size of the exposed population and can lead to incorrect results and misinterpretations.

Consider a single bioterror attack that infects a proportion  $p$  of an exposed population of size  $N$  at time  $\tau = 0$ , such that the initial number of infected is  $I_0 = Np$ . The quantity of interest is the probability  $D(\tau)$  of finding at least one positive blood donation and detecting the attack within time  $\tau$ . For attacks conducted with contagious agents that could lead to an epidemic, Kaplan et al. used the early approximation solution of the classic epidemic models (2) to describe the progression of the number of infected persons.