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/(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, 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 (x 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, 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: twwong@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 ≤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 probabiltiy that ≤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

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 τ. 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.

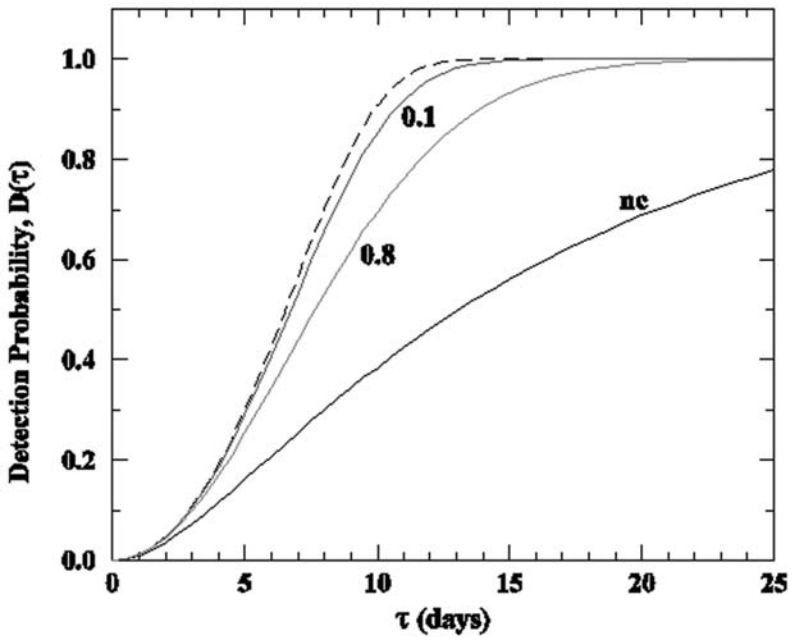

Figure. Probability of attack detection delay for a contagious agent. Dashed line represents the early approximation, solid lines the full solution (where the numbers represent the fraction p of the population initially infected)*, and the symbol "nc" stands for noncontagious agent ($R_0 = 0$). The parameters are as follows: blood donation rate k = 0.05 per person per year, screening mean window period ω = 3 days, mean duration of infectiousness 1/r = 14 days, basic reproductive number $R_0 = 5$, and the initial attack size Np = 500. Note that the exposed populations are therefore 5,000 and 625 for p = 0.1 and p = $(R_0 - 1)/R_0 = 0.8$, respectively.

Consequently, the resulting probability of attack detection [noted $D_{es}(\tau)$] is dependent only upon the initial size of the release I_0, the basic reproductive number R_0 (the mean number of secondary cases per initial index case), and other variables (the blood screening window ω, the mean number k of blood donations per person and per unit of time, and the mean duration of infectiousness 1/r) (see online Appendix at: http://www.cdc.gov/ncidod/EID/vol10no8/03-1044.htm). Early approximation can lead to unreliable results because it is valid only at earlier stages of the epidemics and in the limit where the proportion p of initially infected is much smaller than the intrinsic steady proportion $(R_0-1)/R_0$ of the epidemics (online Appendix). Relaxing this approximation and using the full solution for the progression of the number of infected persons leads to the probability D(τ) that takes into account the size of the exposed population (online Appendix). The latter is important because, in contrast to $D_{es}(\tau)$ that leads to the same conclusion, $D(\tau)$ indicates that the probabilities of detecting an attack within two exposed populations of different sizes, but with the same numbers of initially infected, are not identical. As illustrated in the Figure, when the other variables are fixed, d$D(\tau)$ ecreases as the proportion p of initially infected increases because the epidemic size decreases as p approaches the threshold $(R_0-1)/R_0$. These subtleties of a simple epidemic model are even less reliable when using the blood screening to detect a bioterror attack with agents that cause diseases of very short incubation period.

Nonetheless, detecting a bioterror attack is very similar to detecting the response of pathogen-specific immunoglobulin M antibodies (as an indicator of recent contact of hosts with pathogens) within a population of hosts by using serologic surveys. Therefore, the reasoning developed for a bioterror attack can be extended and applied to detect and time the invasion or early circulation of certain pathogens within a population. In that perspective, it might be useful to develop an analysis that includes more details of the epidemic progression within this framework.

Dominique J. Bicout*

*Ecole National Veterinaire Lyon, Marcy L'Etoile, France

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Address for correspondence: D. J. Bicout, Unité Biomathématiques et Epidémiologie, ENVL-INRA, 1 avenue Bourgelat, B.P. 83, 69280 – Marcy-l'Etoile, France; fax: +33-476-88-24-16; email: bicout@ill.fr

In Reply: As stated and argued throughout our article (1), we conducted a best-case analysis under assumptions that favored blood-donor screening to detect bioterror attacks; if such an analysis fails to justify donor screening, no analysis will. Bicout (2) is concerned about our assumption of exponential infection growth after attack; however, this assumption was one of several we made deliberately as part of our best-case scenario (1).

Bicout's calculations actually reinforce rather than refute our analysis. By relaxing our assumption of exponential infection growth and using the well-known logistic solution to the basic epidemic model (equation 1 in

Bicout's letter), Bicout shows that more time is required to detect a bioterror attack than when exponential infection growth is assumed (Figure accompanying Bicout's letter). The number of persons infected over time under the logistic model will be fewer than the number of persons infected if exponential growth is assumed; therefore, screening blood donors to detect a bioterror attack is even less attractive than using our best-case assumptions. The take-home message from our article was and is: It makes little sense to screen blood donors to detect a bioterror attack.

Edward H. Kaplan*
and Lawrence M. Wein†

*Yale School of Management, New Haven, Connecticut, USA; and †Stanford University, Stanford, California, USA

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Address for correspondence: Edward H. Kaplan, Yale School of Management, 135 Prospect Street, New Haven, CT 06511-3729, USA; fax: 203-432-9995; email: edward.kaplan@yale.edu

Aeromonas spp. and Infectious Diarrhea, Hong Kong

To the Editor: Vila et al. reported the prevalence of *Aeromonas* spp. associated with traveler's diarrhea in Spain (1). Some of the patients described in this study had traveled to countries in Asia, such as Thailand and India. This report details the prevalence of this pathogen in patients with acute infectious diarrhea who were treated in emergency department settings in Hong Kong.

Over a 12-month period, we retrospectively studied all adult patients who showed clinical features of acute infectious diarrhea, were treated as outpatients with or without observation in the emergency department, and had a positive stool culture (2–4). Our data were collected at an urban university-affiliated hospital with 1,400 beds and an emergency department with an annual census of 190,000 patient visits. *Aeromonas* spp. were isolated from stool samples by standard culture procedures, which included introduction onto xylose lysine desoxycholate agar plate and thiosulphate citrate bile sucrose plate, and subsequent screening by triple iron sugar slant (acid butt with no H_2S), positive oxidase, negative urease, fermentation of mannitol but not dulcitol and inositol, resistance to vibriostatic agent 0/129, and ability to grow at 0% NaCl. The main species of *Aeromonas* were identified by the differential biochemical reactions of gas production from D-glucose, arginine dihydrolase, ornithine and lysine decarboxylase; esculin hydrolysis; Voges Proskauer reaction; fermentation from arabinose, sucrose, mannitol, salacin, and D-sorbitol; and citrate and glycerol utilization (5).

Of 130 patients with positive stool cultures, *Aeromonas* spp. were isolated in 9 patients (6.9%), including *A. caviae* in 4 patients, *A. hydrophila* in 2 patients, and *A veronii* in 3 patients. The cases were not epidemiologically linked. In one of these isolates (*A. caviae*), another enteropathogen (*Vibrio parahemolyticus*) was also isolated. None of the patients reported recent travel abroad or to mainland China before treatment.

Our review of the clinical features of these nine patients found that the mean highest body temperature at the time of treatment or during the patient's stay in the emergency department was 37.4°C (95% confidence interval [CI] 36.9–38.0). Two patients (both with *A. caviae* isolated) had temperatures >37.5°C. Bloody diarrhea was present in two patients (one with *A. veronii* and one with *A. caviae*). The mean number of unformed stools per day was 8.6 (95% CI 4.0–13.2). Abdominal pain in eight patients and vomiting in four patients was reported. Five patients required admission to the emergency department's observation unit before discharge. Of these, four patients needed intravenous fluid therapy. Empiric ciprofloxacin was given to one patient with a temperature of 38.3°C. Stool culture results were available within 3 days for positive isolation of *Aeromonas*. All A*eromonas* strains were susceptible to ciprofloxacin, cefotaxime, cotrimoxazole, and chloramphenicol, while two of nine isolates (one *A. caviae* strain and one *A. hydrophila* strain) were susceptible to ampicillin. All patients had recovered satisfactorily by the time stool culture results were available, and antimicrobial therapy was not necessary, except for the patient who was given ciprofloxacin empirically.

In conclusion, *Aeromonas* spp. are responsible for a small proportion of cases of bacterial gastroenteritis encountered in an urban emergency department setting in Hong Kong. Patients affected do not necessarily have a history of travel to a nonindustrialized region. In a substantial proportion of cases, the symptoms are severe enough to require intravenous fluid therapy and observation. However, symptoms generally would have resolved by the time the pathogen was isolated from stool culture. In contrast to the report of Vila et al., persistent diarrhea is uncommon, and antimicrobial therapy is usually unnecessary in our particular setting. *Aeromonas* spp. are susceptible to a wide range of antimicrobial drugs, except ampicillin. Whether empiric antimicrobial drugs given at the time of treatment would

Appendix

Following Kaplan et al. (1), the probability $D(\tau)$ of finding at least one positive blood donation and detecting the attack within time τ, after a single bioterror attack initially infecting a proportion p of an exposed population of size N, is given by $D(\tau) = 1 - \exp\left\{-kN\int_0^{\tau}\pi(t)dt\right\}$, where k is the mean number of blood donations per person and per unit of time and $\pi(t)$ is the probability that, within the blood screening window period of ω days, a randomly selected member of the population would test positive t days after the attack, $\pi(t) = p\left[1-e^{-\omega t}\right] + (rR_0/N)\int_0^t\left[1-e^{-\omega(t-u)}\right]I(u)du$. As cited (1), the progression of the number of infected persons $I(t)$ is described using the differential equation (2), $dI/dt = (rR_0/N)(N-I) - rI$, with the initial condition $I(0) = I_0 = Np$. From this, we have,

$$I(t) = \frac{I_0(R_0-1)}{pR_0 + (R_0 - 1 - pR_0)\exp\{-(R_0-1)rt\}} \qquad [1]$$

When $R_0 > 1$, this logistic function increases, remains constant or decreases from the initial value $I(0) = I_0$ towards the steady state $I(t\to\infty) = I_\infty = (R_0-1)N/R_0$ for $I_0 < I_\infty$, $I_0 = I_\infty$, or $I_0 > I_\infty$, respectively. In particular, in the limit of $p << (R_0-1)/R_0$, this expression reduces to the early approximation solution, $I_{es}(t) = I_0\exp\{-(R_0-1)rt\}$, and the resulting probability $D_{es}(\tau)$ of attack detection is instead,

$$D_{es}(\tau) = 1 - \exp\{-I_0[af(\tau/\omega) - bf[(R_0-1)r\tau]]\} \qquad [2]$$

where the function, $f(x) = x - 1 + \exp(-x)$, and the constants are, $a = k\omega[1 - r\omega(2R_0-1)]/[1-r\omega(R_0-1)]$ and $b = kR_0/\{r(2R_0-1)^2[1-r\omega(R_0-1)]\}$. This $D_{es}(\tau)$ increases when any of the parameters increase.