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Two Parameters Characterizing 2009 H1N1 Swine Influenza Epidemic in Different Countries/Regions of the World

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The worldwide epidemic of the new H1N1 swine influenza virus that emerged in Mexico in April 2009 could present an opportunity to study how the virus spreads while changing its niche and its virulence. To monitor such events, we need good parameters. I found that the log-log plot of cumulative numbers of infected and the killed persons could at least partly satisfy such a need.

The plot is shown in Fig. 1, where the cumulative number of H1N1 swine-infected persons is plotted on the *x* axis and the cumulative number of persons killed by the virus is plotted on the *y* axis. The data from April 30 to July 6, 2009 were obtained from the website of the Infectious Disease Surveillance Center, National Institute of Infectious Diseases, Japan (http://idsc.nih.go.jp/index-j.html [in Japanese]). The last plot of each curve is the plot of July 6, 2009 (data thereafter are currently unavailable).

All the plots gave near straight lines, i.e., $\log Y = k\log X + L$, where X and Y respectively indicate the numbers of infected and killed persons, and k and L are constants. Let X be N_0 when the first fatal case appears (i.e., Y = 1). Then, $0 = k\log N_0 + L$. As $L = -k\log N_0$, the original equation becomes $\log Y = k\log X - k\log N_0$, which can be rewritten as $Y = (X/N_0)^k$.

If the mortality rate among the infected persons remains unchanged throughout the epidemic, the coefficient k equals 1 (irrespective of the level of mortality, either 1% or 20%, for example). However, if the mortality rate among the infected persons increases or decreases as the epidemic progresses, k will become larger or smaller accordingly.

N_0 is the value obtained by extrapolation of the line to the *x* axis. It is the "estimated" cumulative number of infected persons up to which point the epidemic progressed without causing mortality.

It is clear from Fig. 1 that the epidemic pattern in Mexico was entirely different from that of the other countries or regions.

First, countries or regions other than Mexico will be considered. Clearly, the basic pattern of the plot was the same for all in this group. Irrespective of N_0, the epidemic switched from the entirely flat line to the abruptly ascending line at the point $X = N_0$. The slope or the coefficient k of the ascending line was in the same range (~2.8 for Argentina and ~1.8 for the others). N_0 was ~6,000 for non-American continents; ~1,000 for USA, Canada, Latin America and the Caribbean (LAC) excluding Mexico and Argentina; and 500 for Argentina. The switch from the flat line to the ascending line is, among other possibilities, most probably due to the change in the niche, i.e., the virus found, by chance, a niche where the mortality becomes high. As the coefficient k was almost

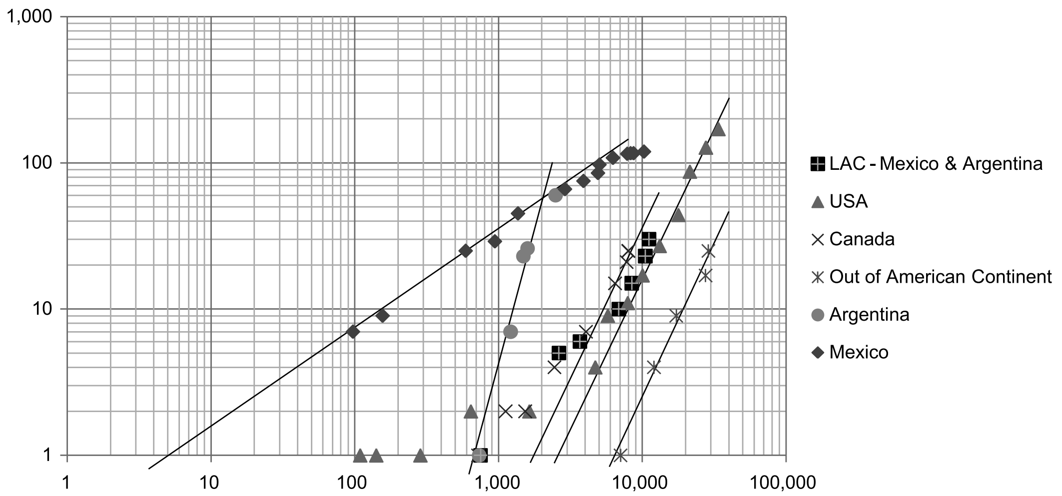

Fig. 1. Log-log plot of the cumulative numbers of infected and killed persons in the 2009 H1N1 swine epidemic. Horizontal axis, cumulative number of the infected; vertical axis, cumulative number of the killed.

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invariable among countries or regions, such a niche should be present in any countries or regions. It could be a highly vulnerable group of persons, such as aged persons, infants, or sick persons in hospitals or institutions. This interpretation is consistent with the observation that N_0 was highest for the group of non-American countries, where the virus could have been imported by occasional travelers to sparsely distributed places; such a situation requires more infections to reach the niche. $k = 2 \sim 3$ means that mortality increased with the progress of the epidemic.

For Mexico, k was about 0.65 and N_0 was $4 \sim 5$. $N_0 = 4 \sim 5$ indicates that the virus started to kill persons from the start of the epidemic without requiring a special niche, i.e., unlike in other regions, in Mexico the virus killed otherwise healthy people. This hypothesis is consistent with the low k value, because healthy people are far more resistant than people in the hospital or similar facilities, and the susceptible population decreases by acquiring immunity as the epidemic progresses.

If this reasoning is correct, the inevitable conclusion is that the influenza virus that killed Mexicans was different from the virus that spread to other countries. If so, the question is, Where has the Mexican strain gone? So far, no known mutations responsible for high virulence have been found in the new H1N1 swine isolates (1). Monitoring of the further progress of the epidemic and the molecular dissection of isolates will reveal the real face of the new H1N1 swine flu virus.

Though the two parameters, k and N_0, appear useful for characterizing the influenza epidemic, the log-log plot has one drawback. As the cumulative numbers of infections and fatalities do not increase exponentially, after sometime the plots will become clogged towards the end and the whole picture will remain overrepresented by the initial data. Therefore, it is important to reset the plot regularly. This is also necessary to identify possible new epidemic trends.

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