results of studies conducted in other countries (5–7). None of the pregnant women were in critical condition and none died of pandemic (H1N1) 2009 infection during the surveillance period. The overall lower prevalence of pregnant women in Japan ($\approx 0.67\%$ of the total population) compared with that in other countries (8) might account for the low number of pregnant women hospitalized for pandemic (H1N1) 2009 virus in Japan.

Of all 12,702 patients, 4,420 (34.8%) had underlying medical conditions. In terms of age, 1,848 (32.6%) of 5,670 patients 5–9 years of age and 324 (81.0%) of 400 patients >70 years of age had underlying medical conditions. For those with underlying medical conditions, incidence of hospitalization was relatively higher for children than for adults; rates for hospitalized children were 814.1, 573.7, and 219.0 per 100,000 persons for those 5–9, 10–14, and 15-19 years of age, respectively; whereas, the rate for hospitalized adults 60-69 years of age was 6.7/100,000 persons. In all age categories, the incidence of hospitalization for pandemic (H1N1) 2009 virus infection was notably higher for patients with underlying medical conditions than for those without. The attributable risk for medical conditions associated with hospitalization for pandemic (H1N1) 2009 virus infection was highest among patients 5-9 and 10-14 years of age (744.7 and 549.6, respectively), whereas the risk was lowest (6.5) among patients 60-69 years of age. The relative risk associated with underlying medical conditions was comparatively higher for patients in age groups 15-19, 20-29, and 30-39 years (48.4, 54.9, and 48.4, respectively) than among those >70 years of age (17.9). In contrast to seasonal influenza (4), persons <20 years of age had higher risk for hospitalization for pandemic (H1N1) 2009 than did older age groups.

Considering our findings regarding the attributable risk for hospitalization, interventions that aim to control pandemic (H1N1) 2009 virus infection among children, especially those with underlying medical conditions, can be considered key for minimizing the strain (financial, staffing, space) on the healthcare system. Our findings justify prioritizing the treatment of children and young adults by vaccination and early prescription of antiviral drugs.

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Internet Search Limitations and Pandemic Influenza, Singapore

To the Editor: In the past few years, several publications have reported that Internet search queries may usefully supplement other, traditional surveillance programs for infectious diseases (*1*–*3*). The philanthropic arm of Google offers Flu Trends, a site that provides up-to-date estimates of influenza activity in 20 countries of the Pacific Rim and Europe (*4*) by using data mining techniques to find good predictors of historic influenza indicators (*1*).

This service has yet to be extended to other countries and other diseases because access to official surveillance data is required, among other reasons. However, another Google service, Insights for Search, enables users to find and download time-series data of relative counts of arbitrary searches for a

large number of countries (5). Pelat et al. have shown that a few, well-chosen searches on Google Insights provide data that closely correlate with French surveillance data for seasonal influenza, chickenpox, and gastroenteritis (3). Although Internet searches appear to be a promising tool for public health surveillance, our experience from using Google Insights in the context of pandemic (H1N1) 2009 in Singapore suggests it has important limitations.

In Singapore, the recent pandemic caused an outbreak that peaked at the start of August 2009; the first confirmed importation was at the end of May and first confirmed unlinked case was at the end of June. However, the number Google searches for "influenza," "H1N1," "swine flu," and similar terms (in English and Chinese), as well as symptoms associated with the disease, peaked much earlier than did the number of cases (Figure). The number of searches surged after newsworthy events but was low during the epidemic itself and had declined to about 20% of maximum search volume by the time of the actual peak, as shown by traditional surveillance. Furthermore, no discernible local maxima were observed that corresponded to the peak in case data. In contrast, alternative traditional measures of influenza incidence—prevalence of the novel strain among viral samples and general practice surveillance (6,7)—provide a consistent description of the outbreak.

This finding echoes a major point raised by Carneiro and Mylonakis (2), namely, that without adjusting for spikes driven by disease publicity rather than the disease itself, Internet searches may lose much of their value in supplementing traditional surveillance measures. Our experience is that using Google Insights to survey a disease may not work well for diseases with considerable media exposure, in particular, emerging diseases such as pandemic (H1N1) 2009 or severe acute respiratory syndrome. Such outbreaks may require the more sophisticated approach used by Flu Trends, should it be extended to other diseases and more corners of the globe. We agree with Pelat et al. (3) that Google Insights may work well for less-publicized infectious diseases. The dividing line between well-publicized and

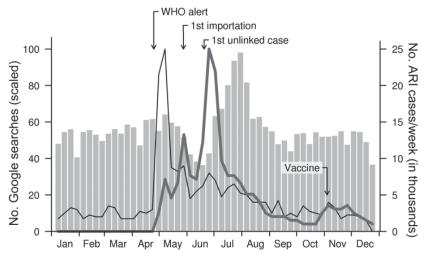


Figure. Number of Google searches conducted for "influenza" (black lines) and "H1N1" (gray lines) compared with number of acute respiratory infections (ARI, gray bars) reported in government clinics, Singapore, 2009. During the outbreak of pandemic (H1N1) 2009, Google search activity surged in response to newsworthy events (the World Health Organization [WHO] alert, first importation and unlinked local case, release of vaccine) but dropped substantially by the time most infections occurred in August. Other search patterns, such as for "swine flu" and simplified Chinese language terms for swine flu and influenza, were similarly disassociated with actual disease incidence.

unpublicized diseases may, however, remain ambiguous. Thus, to ensure that web search data reflect disease incidence requires validation against traditional surveillance, although in that situation, the availability of corroborating traditional methods of surveillance limits the value of webquery data.

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Body Lice, Yersinia pestis Orientalis, and Black Death

To the Editor: A scientific debate with public health implications wages: What caused the medieval European plague epidemics known as Black Death? Recent articles note inconsistencies between a rat fleaborne pandemic of Yersinia pestis (the bacterium that causes bubonic plague) and the documented characteristics of Black Death (1, among others). Ayyadurai et al. (2) acknowledge that a rat flea-only hypothesis does not fit Black Death observations, but they resolve theoretical transmission inconsistencies through a louse-borne hypothesis. Avvadurai et al. base their surety of fact-that medieval "plagues" were caused by Y. pestis infection—on a 2007 study (3) in which 5 of 36 teeth of "plague" victims, none of which were dated to the Black Death era (1347–1351), contained biological evidence of *Y. pestis*. The 3 locations in that study were all port cities: 2 on the Mediterranean Sea and 1 on the Rhone River. As Duncan and Scott (4) note, bubonic plague most likely existed endemically near ship-borne trade, unlike the fast-moving epidemic fronts exhibited by medieval "plagues." Moreover, Gilbert et al. (5) found no Y. pestis DNA in 61 skeletons from primarily nonport locations in England, France, and Denmark.

We do not dispute the authors' claim that Y. pestis might have been

present in some skeletons from port cities in France, or that body lice might, under certain circumstances, transmit the Orientalis biotype of Y. pestis; their work appears careful and considered. However, given the differences mentioned above and improved knowledge on the rapidity of virus mutation and worldwide transmission potential, we merely argue that the simplest explanation for medieval plagues has yet to be ruled out: that they may have resulted from a human-to-human transmitted virus. Adding complexity to an already complicated etiologic theory, and stating such as historical fact based on limited geography and sample size, does not seem congruent with Occam's razor.

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To the Editor: The letter of Ayyadurai et al. (1) reminded us of a littleknown paper (2) on rats and Black Death by our colleague and mentor David E. Davis. He researched and wrote in his retirement after years of research and reflection on rat ecology and rodent-borne diseases (3,4). Rattus rattus is commonly recognized as the vertebrate host of flea-borne plague that swept through Europe in the 1300s, killing >50% of the population. Davis believed this explanation did not fit what he knew of the ecologic requirements of fleas and black rats. He studied reports of archeologic excavations and reviewed poems, medieval bestiaries, and paintings and concluded that these rats were scarce during the Black Death era.

His theory, based on historical information and investigative trips to Europe, was that invasive rats, if present, mostly occurred in low densities in port areas, not in rural inland areas. He noted that the expected rodent die-offs with bubonic plague were not associated with human epidemics and that rodent fleas would not have been active during winter to transmit plague. Flea-borne transmission from rodents usually causes a few deaths per household, but deaths of entire households commonly occurred in the medieval epidemics. Human-tohuman transmission of pneumonic plague must have occurred, but as described by Ayyadurai et al., there was evidence of human bubonic plague, suggesting vector involvement. Davis did not present a viable reservoir/vector hypothesis for plague transmission; this and the later, well-known association of R. rattus and other rodents with plague throughout the world, may partially explain why his ideas received little attention. The finding that human body lice can be bubonic plague vectors suggests a mechanism for humanto-human transmission continuing during winter in inland areas and, as suggested by the authors, could also explain total deaths in households.