

One Flu for One Health

To the Editor: The emergence and spread of influenza A pandemic (H1N1) 2009 virus from the animal reservoir to humans raise questions about the future approach to influenza virus infections. The scientific community has evidence demonstrating that influenza virus genes migrate across continents and animal species and assemble themselves in combinations that are a threat to animal and human health, resulting in panzootics like that caused by influenza A virus (H5N1) or pandemics like that caused by pandemic (H1N1) 2009 virus. The latter virus emerged from the animal reservoir, containing a unique combination of genes donated by viruses originating from 3 species and 2 hemispheres. In a globalized environment, mapping gene movement across species and national borders and identifying mutations and gene constellations with pandemic potential or virulence determinants are essential to enact prevention and control strategies at a global level. This conclusion is in agreement with, and possibly the best example of, the One Health (<http://un-influenza.org/node/2341>) vision: a multidisciplinary collaborative approach to improving the health of humans, animals, and the environment. One Health is endorsed by the United Nations Food and Agriculture Organization, the World Organisation for Animal Health, and the World Health Organization.

Vast improvements in capacity building have been achieved as a result of the influenza A (H5N1) global crisis. Thousands of viral isolates with zoonotic potential have been obtained through surveillance efforts, although the genetic information has not been exploited fully. In addition, investigating how influenza viruses circulate in certain species, including dogs, pigs, and horses, has been neglected. This neglect is evidenced by the fact that, at the time of this writing, GenBank

contained 4,001 full genome sequences of influenza viruses isolated from humans, 2,590 of viruses isolated from birds, and only 325 from swine, 85 from horses, 2 from mink, 4 from dogs, 2 from cats, 2 from tigers, and 3 from seals.

We invite donors and international agencies to invest in a novel approach to influenza virus infections, to abandon prefixed compartments linked to geographic origin or species of isolation, and to analyze the influenza gene pool as one entity. We propose capitalizing on existing achievements and investments to develop an international network and a permanent observatory, which will improve our understanding of the dynamics of the influenza virus gene pool in animals and humans. A greater understanding will generate important information to support both public and animal health. Ideally, a small consortium, including representatives of major international organizations, could take leadership and liaise with major institutions involved in influenza surveillance and research to develop a feasibility study and roadmap to achieve this goal. The One Flu initiative could result in international synergies, the bridging of gaps between medical and veterinary scientists, permanent monitoring of virus evolution and epidemiology, and the best exploitation of investments in capacity building. Above all, this collaboration could be a challenge and opportunity to implement the One Health vision, and possibly act as a model for other emerging zoonotic diseases.

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Pandemic (H1N1) 2009 Risk for Nurses after Trivalent Vaccination

To the Editor: We report results of the effect of inactivated seasonal influenza vaccination on risk of pandemic (H1N1) 2009 in a cohort of nurses in Canada who participated in a recent randomized controlled trial that compared the effectiveness of surgical masks with that of N95 respirators in preventing influenza (1). From September 23, 2008, through December 8, 2008, a total of 446 nurses from 8 hospitals in the province of Ontario were enrolled. They were then randomly assigned an intervention; 225 were assigned to wear surgical masks, and 221 were assigned to wear the N95 respirator. The mean age of participants was 36.2 years; 94% were women. A total of 128 (30.3%) received the trivalent influenza vaccine. Vaccination status was similar between the groups: 68 (30.2%) persons in the surgical mask group and 62 (28.1%) persons in the N95 respirator group had received the 2008–2009 trivalent inactivated influenza vaccine. The nurses were monitored from January 12, 2009, through April 23, 2009.

Blood specimens for serologic analysis were obtained before enrollment and at the end of the follow-up period. End-of-study serum samples were collected from April 23 through May 15, 2009. Serologic infection

was defined by a ≥ 4 -fold increase in influenza-specific hemagglutinin inhibition assay titer between baseline and convalescent-phase serum samples by using turkey erythrocytes and A/TN/1560/2009(H1N1), a representative pandemic influenza virus.

Of the 422 nurses included in the analysis, 42 (10.0%) showed seroconversion to pandemic (H1N1) 2009. Of 128 nurses who received the trivalent influenza vaccine, 9 (7.0%) showed seroconversion vs. 33 (11.2%) of those that did not (relative risk 0.63, 95% confidence interval 0.31–1.27, $p = 0.19$).

Although the point estimate was protective, the confidence interval is wide and does not exclude an increase in risk. Our sample size limits inferences that can be drawn. Heterotypic antibodies may have contributed to the relatively high rate of seroconversion. A rise in antibody titer is considered by some as an outcome associated with bias, unlike virus identification. Nevertheless, these data suggest a possible positive effect of seasonal influenza vaccine reducing risk of infection with pandemic (H1N1) 2009.

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Patients with Pandemic (H1N1) 2009 in Intensive Care Units, Israel

To the Editor: We report results of an active surveillance system established by the Tel Aviv District Health Office in Israel. This surveillance system monitors the daily status of patients with laboratory-confirmed pandemic (H1N1) 2009 virus infection in each of the district's intensive care units (ICUs), including pediatric ICUs.

Follow-up is maintained by daily phone conversations with medical staff until disease outcome is concluded by discharge, transfer to a long-term rehabilitation facility, or death. Medical records, as well as daily laboratory reports, are collected to confirm or to rule out pandemic (H1N1) 2009 infection.

During July 10–October 10, 2009, our prospective cohort included 17 patients with pandemic (H1N1) 2009 laboratory-confirmed infection who were residents of the district; 12 (70.6%) were male patients. The median age was 44 years (interquartile range 13–72 years). By October 10, 2009, six patients had been discharged, 7 had died, 2 had been transferred to long-term rehabilitation facilities, and 2 remained hospitalized.

Twelve (70.6%) patients had an underlying medical condition, mainly chronic lung disease (6 patients) or chronic cardiovascular disease (5 patients). Two patients were morbidly obese (body mass index ≥ 35), and 1

patient was pregnant. Additionally, 3 patients (17.6%) were infected while hospitalized.

Thirteen patients (76.5%) had acute respiratory distress syndrome caused by diffuse viral pneumonitis. Other notable manifestations were acute renal failure (6 patients), sepsis/septic shock (5 patients), and neurologic complications such as Guillain-Barré syndrome, encephalitis, and seizures (3 patients).

Documented nosocomial sepsis, often of multiple gram-negative bacteria (9 patients), was the most frequent complication during the course of the disease. Other frequent characteristics were the use of high positive end-expiratory pressure during mechanical ventilation (4 patients) and the need for tracheostomy (5 patients).

Average time from disease onset to hospital admission was 3 days. Time from hospital admission to ICU admission for those patients who died was longer than for those who survived, with a median of 2 days compared with 0.5 day, respectively, albeit not significant ($p = 0.26$). Average hospitalization was 23.4 days; average length of stay in the ICU was 16.7 days (71.4% of the average hospitalization time).

As mentioned previously, 7 patients (41.2%) died; 5 (71.4%) were male, similar to their cohort's proportion. One significant difference ($p = 0.02$) was found between the age of survivors (mean 26.0 years, 95% confidence interval 7.6–44.3) and the age of nonsurvivors (mean 59.3 years, 95% confidence interval 39.6–79.0). The most prominent case-fatality rate was for elderly patients, >65 years of age (3 of 4 patients) followed by patients between 20 and 64 years of age (4 of 9 patients); these subgroups constituted 23.5% and 52.9% of the cohort, respectively.

Estimated incidence rate was 13.8 patients and 5.7 deaths in ICUs per million residents in the Tel Aviv district. Again, the elderly subgroup was