Inferring influenza infection attack rate from seroprevalence data

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Date: 10 April 2013 (Wed)
Time: 10:30 am (Tea/Coffee service at 10:15 am)
Venue: B6619 (SEEM Conference Room)

Abstract

Seroprevalence studies were widely used to estimate infection attack rates (IARs) of 2009 pandemic influenza A/H1N1 (pdmH1N1). These studies entailed choosing a titer threshold for seropositivity (e.g. microneutralization [MN] 1:40) and assuming the proportion of infections seropositive (infection-seropositivity probability, ISP) was as observed among clinical cases. Different thresholds on the same seroprevalence data might give inconsistent IAR estimates if serologic responses of clinical cases was not representative (e.g. clinical cases had higher ISP). To illustrate this, we fitted a transmission model to pdmH1N1 hospitalization and seroprevalence data in Hong Kong and estimated that only 66%, 60% and 30% of infections among age 3-19, 20-29, 30-59 became MN1:40 seropositive, much lower than the 90%-100% observed among clinical cases. The fitted model was consistent with prevailing consensus on pdmH1N1 transmission characteristics: (i) the initial reproductive number and mean generation time were 1.28 and 2.4 days; (ii) intra-age-group mixing was reduced by 86% for age 3-12 during proactive school closure and by 59% and 23% for age 3-12 and 13-19 during summer holidays; (iii) the 3-12, 13-19 and 30-59 age groups were around 2-3, 1-1.6 and 0.5-0.7 times as susceptible as the 20-29 age group; and (iv) IAR was 52%, 49%, 25% and 13% for age 3-12, 13-19, 20-29, 30-59. Incidence of pdmH1N1
in Hong Kong and some other countries might have been previously underestimated, especially among adults, due to ISP overestimations. Influenza sero-surveillance should evaluate the robustness of IAR estimates by checking consistency between ISP adjustments and seroprevalence rises across different thresholds.

**About the Speaker**

His primary research focus is influenza pandemic preparedness and response. He develops mathematical models to assess the potential benefits and logistical requirement of different pandemic mitigation and surveillance strategies. Specific topics include household-based public health interventions, prioritized prepandemic vaccine allocation, multi-drug stockpiling for minimizing antiviral resistance, organized convalescent plasma therapy program, and serologic surveillance for real-time estimation of severity. Besides pandemic influenza modeling, his recent projects include (i) cost-effectiveness analysis of different strategies of HPV vaccination and cervical cancer screening in Hong Kong and (ii) field studies of influenza epidemiology.

He is a member of the Scientific Committee for the Center for Health Protection in Hong Kong. He is an affiliated faculty member of the Center for Communicable Diseases Dynamics (CCDD) at the Harvard School of Public Health. He is an associate editor of American Journal of Epidemiology.

He obtained a PhD in Operations Research from MIT in 2003 and a BS in Chemical Engineering from MIT in 1999. Before joining HKU, he was an assistant professor in the School of Industrial and Systems Engineering at Georgia Tech and a postdoc in the Theoretical Biology and Biophysics Group at Los Alamos National Laboratory.

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*All are welcome!*

SEEM Seminar 2012-2013/036