

Population Factors Affecting Initial Diffusion Patterns of H1N1

Poh-Chin Lai, PhD, MA,¹ Chun Bong Chow, MBBS(HK), FHKAM(Paed), FHKCPaed, FRCPC, FRCP, DCH(Lond),²
Ho Ting Wong, PhD, MPhil,³ Kim Hung Kwong, PhD, MPhil,³
Yat Wah Kwan, MBBS(HK), MRCP (UK), FHKCPaed, MRCPCH (UK), MSc(AE)CUHK,⁴
Shao Haei Liu, MBBS(HK), MRCP(UK), MHA(NSW),⁵ Wah Kun Tong, RN, PhD, FHKAN(Med),⁶
Wai Keung Cheung, RN, MN, MScAE, MScPH,⁷ and Wing Leung Wong, PStat, CStat, CSc⁸

THE RAPID TRANSMISSION of H1N1 influenza that started in Mexico in March 2009 and spread to more than 11 countries within a month caused worldwide significant social and economic impacts. Therefore, researchers have suggested mathematical/epidemiological and simulation models to emulate disease surveillance or even to predict disease spread. It has been argued that the performance of such predictive models likely would improve with better heuristics (experience-based techniques for problem solving) as opposed to a pure data-driven approach. Research into identifying factors that influence the spread of a disease is regarded as necessary and becoming more important. It has been shown that various epidemiological parameters (including basic reproduction number, cumulative attack rate, and peak daily incidence rates) depend heavily on sociodemographic factors (eg, household size, percent worker population, percent student population).¹

Applying spatial statistics and geographic information systems to visualize patterns of disease clustering and dispersion can provide stimuli for formulating hypotheses of disease outbreaks.² Because human-to-human transmission of influenza is through close contact, factors affecting population behavior (including variation in demographic and environmental characteristics) would be useful in developing predictive models for disease risk assessment. Of notable concern is that results of spatiotemporal prediction would vary according to geographic scales.³

We are pleased to report that based on residential locations of a sample of 548 confirmed H1N1 patients from May 1 to July 8, 2009, our spatial models reported 4 of the 6 population-related factors to be significantly correlated with disease incidence at different grid resolution: percentage of elderly population (aged 65+ years), percentage of cross-district work population, net residential density, and population density. The data were aggregated into 3 geographic levels (200mx200m, 400mx400m, and 1000mx1000m) with population density emerging as the only factor bearing a consistent

relationship with disease incidence at different spatial resolution ($r=0.245, 0.290, 0.373$ for the respective cell sizes; $P<0.01$). Indeed, the effect size of the correlation coefficients also was the largest among the selected variables in the analysis. Disease incidence within the elderly population or cross-district work population exhibited significant relationships but their effect sizes were relatively small. Even though the younger population made up the largest proportions of reported H1N1 cases, the insignificant relationship likely was confounded by better hygiene and control measures at the school level and the fact that the majority of infection occurred among school-age children attending the same school.

The process of disaggregating map units to the finer grid cell level has proven effective in 2 aspects. First, the gridded data are easy to manipulate in an automated setting. Second, the grid format seems to ameliorate the Modifiable Areal Unit Problem.⁴ Our study demonstrated successfully that the grid cell approach not only was able to mask individual identity but also to extract relationships hidden by larger aggregated spatial units. Besides, the exclusion of country parks (with no population) and non-diseased grid cells offered additional discriminating powers to isolate salient factors in disease relationships. However, a higher spatial resolution or a smaller cell size does not necessarily mean improved associative relationships because of more data scattering and diminished health effects related to insufficient explanatory powers, especially when disease cases in the earlier phases of an infection outbreak were few. Even though the grid format may be useful for analysis, it must be reconstituted into some preset administrative units to draw references to area-based socioeconomic measures and for the implementation of broad policies. Our study showed that results would vary in accordance with spatial resolution. Errors and false alarms could be prevented or minimized by choosing the proper data resolution.

These findings have practical implications given that the census statistics are readily available from official sources.

¹Department of Geography, The University of Hong Kong, Hong Kong SAR, China.

²Formerly Hospital Authority Infectious Disease Centre, Princess Margaret Hospital, Hong Kong SAR, China.

³Formerly at the Department of Geography, The University of Hong Kong, Pokfulam Road, Hong Kong SAR, China.

⁴Department of Paediatrics & Adolescent Medicine, Princess Margaret Hospital, Hong Kong SAR, China.

⁵Hospital Authority, Kowloon, Hong Kong.

⁶Princess Margaret Hospital, Hong Kong SAR, China.

⁷School of Nursing, The University of Hong Kong, Hong Kong SAR, China.

⁸City University of Hong Kong, Hong Kong SAR, China.

The established relationships inform public health officials of the target population groups and pertinent locations to strategize intervention measures or to tighten public health practices. One limitation in relying on risk factors based on local census for disease modeling is the inability to account for a sudden upsurge in disease occurrences arising from external sources. Although the 4 factors would still be useful in simulating disease transmission, additional variables such as the occupancy rate of hotels within an area would be useful to estimate the potential of imported cases.

Acknowledgment

This letter is the result of research collaboration among Princess Margaret Hospital, Hospital Authority, and Department of Geography at the University of Hong Kong.

Author Disclosure Statement

The authors declared no conflicts of interest with respect to the research, authorship, and/or publication of this letter. The project is funded by the Research Fund for the Control of Infectious Diseases administered by the Food and Health Bureau and the Hong Kong SAR Government.

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Address correspondence to:
Poh-Chin Lai, PhD, MA
Department of Geography
The University of Hong Kong

E-mail: pclai@hku.hk