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# Public health interventions to control the spread of a directly transmitted human pathogen within and between Hong Kong and Guangzhou

## Key Messages

1. The ability to detect and differentiate between fast and slow spatial spread of infectious disease depends on the density of the surveillance network.
2. The results of this study suggest that more concentrated surveillance networks are required in Guangzhou compared with other regions, such as Thailand and Europe, as long-distance travel is less frequent.

## Background

The 2003 outbreak of severe acute respiratory syndrome (SARS) highlighted the social connectivity between mainland Chinese cities and Hong Kong. Epidemiological and molecular analyses suggest that the Hong Kong outbreak was seeded from Guangzhou. In future outbreaks of new or re-emerging directly transmitted infectious diseases, it would be desirable to quantify the pathogen-specific risk of transmission between these two city populations, based on the natural history of the disease and a detailed contact model of the populations involved.

Large-scale transmission models provide a versatile experimental structure for infectious disease epidemiology. Each host is usually represented explicitly in the model and is assigned a location in space. Typically, nodes may be susceptible, exposed but not yet infectious, infectious, or recovered. Infections occur either along arcs in the network or according to a spatial infection kernel. These models are used to investigate how patterns of spread are changed by public health interventions.

Properties of the network and transmission kernel are usually determined by surveillance data on how people travel to work. Reliable travel data are required to correctly parameterise large-scale transmission models. Previous modelling studies have used census-derived data to parameterise human movement. As part of an integrated study, we conducted a bespoke telephone questionnaire in order to generate data specific to our study population.

## Methods

This study was conducted from 1 October 2006 to 29 February 2008. A household-based telephone survey was conducted using random digit dialling in the metropolitan areas of Guangzhou, Foshan, and Hong Kong. The interviewer asked the respondent for the district in which the household was located, how many people lived in the household, and if anyone in the household had owned poultry in the past month. The next section of the questionnaire was on an individual basis. The respondent was asked to answer on behalf of any household members who were not present.

The origin and destination locations for each respondent (as described above) and fine-resolution population density estimates from the Landscan model of human population density was used to estimate a pair-wise choice kernel for each city within the survey. A static network model of an infectious disease outbreak of a novel respiratory pathogen was constructed and the model was parameterised using data from the travel questionnaire.

## Results

A total of 3318 households completed the questionnaires: 906 in Foshan, 1819 in Guangzhou, and 593 in Hong Kong. The total number of individuals was 3349 in

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Foshan, 5991 in Guangzhou, and 1854 in Hong Kong. The mean size of households was 3.7 persons in Foshan, 3.3 in Guangzhou, and 3.1 in Hong Kong.

An outbreak of pandemic influenza was simulated over the derived network, seeded within 10 km of the centre of Guangzhou. Due to the short generation time of pandemic influenza, the progression of the outbreak was rapid. For an outbreak seeded in Guangzhou, using the data from our telephone survey, local transmission dominated and no significant outbreaks were observed in nearby highly populated areas. This pattern contrasts sharply with predicted spatio-temporal dynamics for influenza in Thailand and Europe.

### **Conclusions**

A slower spatial spread of influenza in southern China has

public health implications, particularly for containment and surveillance. The slower the spatial spread for a given number of cases, the greater the requirement for surveillance. If the infection spreads rapidly, there is a much greater chance that it will be picked up by a sparse surveillance network. However, if the disease spreads slowly, then the number of cases that will occur before the disease appears on a sparse surveillance network will be much higher. Therefore, our results suggest that the surveillance network in China should be more intensive than in Thailand.

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