Investigation into the COVID-19 Superspreading Potential and Generation Interval Differed by Settings Before Omicron Wave in Hong Kong

D. Chen[1,2,†], D.C. Adam[1,2,†], Y.C. Lau[1,2], D. Wang[1,2], F. Ho[1], H. Gao[1], W.W. Lim[1,2], T.K. Tsang[1,2], E.H.Y. Lau[1,2], P. Wu[1,2], D.K.M. Ip[1], B.J. Cowling[1,2,*], S.T. Ali[1,2]

[1] WHO Collaborating Centre for Infectious Disease Epidemiology and Control, School of Public Health, Li Ka Shing Faculty of Medicine, The University of Hong Kong, Hong Kong Special Administrative Region, China
[2] Laboratory of Data Discovery for Health Limited, Hong Kong Science and Technology Park, New Territories, Hong Kong Special Administrative Region, China

2 Dongxuan Chen (PhD)
Primary Supervisor: Prof Dennis K.M. Ip

Background

Understanding transmission heterogeneities of COVID-19 is crucial for effective outbreak prevention and control, however, few studies have investigated setting-specific transmission characteristics using empirical data. In this study, based on the line-list data from 9438 locally infected COVID-19 cases before the Omicron wave in Hong Kong, we categorized eight settings of our research interest: (i) households, (ii) care homes, (iii) restaurants, (iv) nosocomial, (v) blue-collar work, (vi) office work, (vii) close-social indoor activities (i.e. bars, dance clubs, gyms), or (viii) retail and leisure activities.

Objectives

We aimed to estimate and compare the reproduction number, generation intervals, and superspreading potential across these different outbreak settings of our research interest in Hong Kong between 2020 and 2021 prior to the emergence of Omicron, thus could provide insights for setting-specific intervention plans to mitigate future outbreaks.

Methods

The model that jointly estimates dispersion parameter and case reproduction number was based on a negative binomial framework that considered two probabilities [1]:

- Probability of each case being reported
- Probability of any reported case being successfully traced to their cluster and triggering an investigation identifying all related cluster members

The model that estimates setting-specific generation interval was revised from a previous work that used expectation maximization method to estimate parameters from mixture model [2]:

- We first infer infection times for all clustered cases based on symptom onset dates or report dates (if asymptomatic)
- Generate index-to-infection interval distribution within each cluster as first infected case to each successive case.
- Build a mixture model to infer the generation interval from infection interval distribution
- Mixture model assumes four potential paths within a cluster:
  I. co-primary infection
  II. primary to secondary infection (the natural generation interval)
  III. primary to tertiary infection
  IV. primary to quaternary infection.

Results

Based on the cluster size distribution of all clusters, our model estimated the overall dispersion parameter k was 0.59 with expected case reproduction number of 1.52. Household clusters had the lowest transmission heterogeneity indicating less likely superspreading potential. General consumption and leisure activity clusters had highest superspreading potential but the expected infection strength in this setting was weak. For all clusters, 28% of the cases were responsible for 80% secondary transmission, but such proportions differed across settings (Figure 1).

Longest generation intervals were found in nosocomial and care home settings, both with estimated mean around 7 days, while shortest generation interval was found in office work settings, with mean generation interval around 4.5 days (Figure 2).

Simulation results further found that more reduced realized generation interval from intrinsic setting was associated with smaller offspring size (Figure 3).

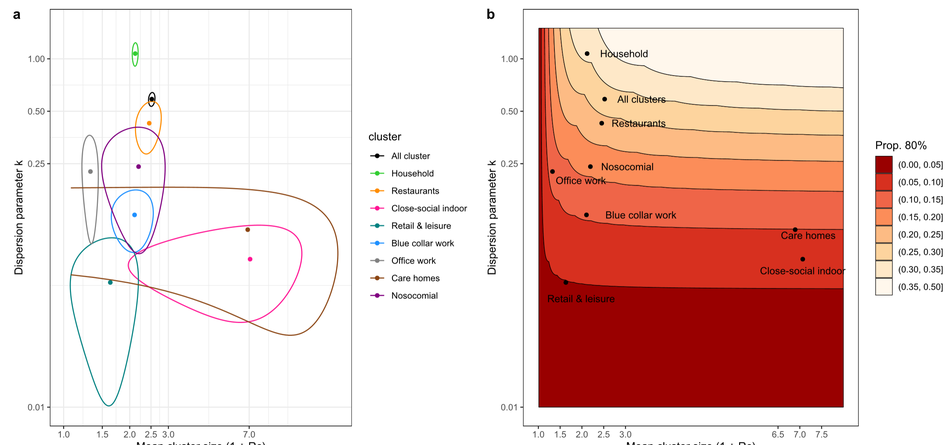

Figure 1. a. Visualization of superspreading potential and infection strength; b. Transmission heterogeneity across settings

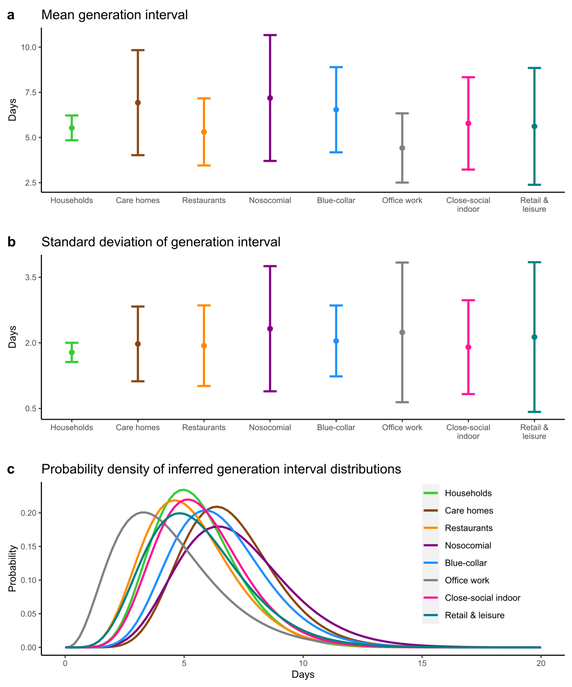

Figure 2. Generation interval distribution in different transmission settings

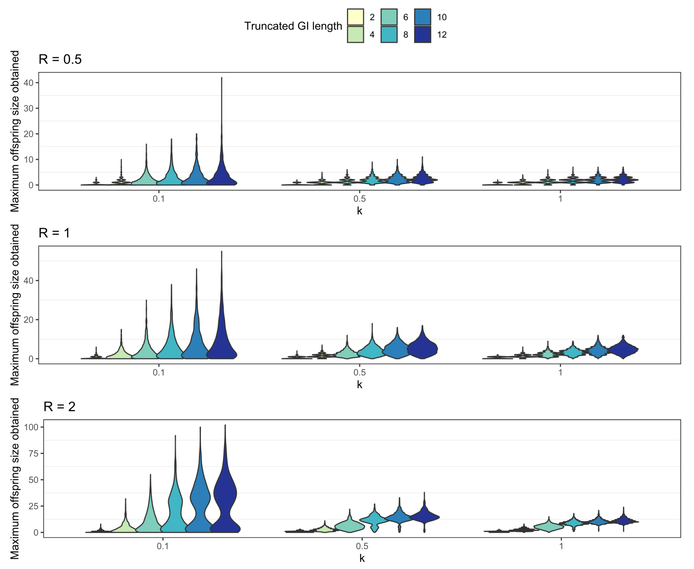

Figure 3. Realized generation interval reflects truncation and cutoff in maximum offspring

Conclusions

- Extreme transmission heterogeneity was observed across three particular cluster categories:
  - Care homes
  - Close-social indoor settings excluding restaurants (e.g. gyms and bars)
  - Retail and leisure settings such as shopping malls and supermarkets;
- Even if the infection strength was weak (i.e. Rc < 1 for retail setting), extreme transmission heterogeneity with relatively longer generation interval could still result in huge outbreak size (i.e. cluster size > 30);
- If NPIs and behavior changes could truncate the infectious period (as reflected by shorter realized GI), there would be more controllable outbreak size as indicated by both observation (i.e. office work setting) and simulation results.

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