

Superspreading potential of COVID-19 outbreak seeded by Omicron variants of SARS-CoV-2 in
Hong Kong

Superspreading potential of the SARS-CoV-2 Omicron variants

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Highlights

Using two early transmission chains in Hong Kong, the estimated R and k were 1.34 (95%CrI: 0.94-2.19) and 0.33 (95%CrI: 0.17-0.62) respectively, inferring 20.3% (95%CrI: 12.7%-29.6%) cases were responsible for 80% of the transmissions of the Omicron epidemic. Compared with Omicron BA.1, Omicron BA.2 had a greater superspreading potential.

Keywords: SARS-CoV-2; Omicron variants; superspreading events; transmission heterogeneity.

Main text

Although COVID-19 transmission dynamics are often heterogeneous, that is, only a small fraction of cases can generate unusual large outbreaks (i.e., superspreading), little is known about the superspreading potential of Omicron variant. We assessed the superspreading potential of COVID-19 outbreak seeded by the Omicron variants, using two observed transmission chains in Hong Kong.

Two case clusters involving 234 cases were reported by the Hong Kong Government from 2 to 21 January 2022¹. Both clusters were traced back to single initial cases who were sequenced as Omicron BA.1 and BA.2 variants' infections. We reconstructed the transmission process of these two case clusters into transmission chains, and jointly estimated the reproduction number (R) and a dispersion parameter (k), which quantifies the transmission heterogeneity, using Negative Binomial models (**Appendix**).

Of the 67 epidemiologic linked cases, forty-three cases led to no secondary case, and one case initiated a transmission cluster comprising 167 cases was linked to the Omicron BA.2 chain (Figure 1A). Twenty-three out of 67 infectors generated at least one secondary cases, with one case infected 12 people (Figure 1B). The estimated R and k were 1.34 (95% credible interval (CrI): 0.94-2.19) and 0.33 (95% CrI: 0.17-0.62), respectively. We inferred that 20.3% (95%CrI: 12.7%-29.6%) of cases generated 80% of all transmissions during the initial phase of Omicron epidemic in Hong Kong. The risk of observing more than three generations of infections in the current epidemic is 20.7% (**Figure S1A in Appendix**), with a risk of observing a large outbreak (≥ 100 cases) seeded by one case as 12.3% (**Figure S1B in Appendix**). The probabilities of observing superspreading events seeded by Omicron BA.1 and Omicron BA.2 are 4.9% (95%CrI: 1.4%-8.7%) and 6.4% (95%CrI: 3.5%-8.5%), respectively.

Our study showed the outbreak seeded by the Omicron variant exhibited high superspreading potential with sustained transmissibility even though stringent public health interventions including border control (e.g., compulsory testing and quarantine for travelers upon arrivals), physical

distancing (e.g., closure of bars or pubs, prohibition on gatherings of >4 persons in public places), and contact tracing (e.g., quarantine of close contacts) have been in place with moderately high immunization coverage (i.e., 75% two-dose vaccination rate) in January 2022¹. The estimated transmission heterogeneity is higher than the wild strains that prevailed in 2020, which had a larger k of 0.43². Our findings suggested that effective control of Omicron epidemic remains huge challenge because of not only the higher transmissibility and immune escape³, but also the superspreading potential. Transmission surveillance models that considered the effect of superspreading could better quantify the uncertainty surround estimated transmissibility and improve the prediction⁴. Low prevalence on boosted immunity provided by the mRNA vaccines, and limited natural immunity in local population due to “zero COVID-19 policies” may contribute to the community vulnerability to the superspreading. Hence, the concerns on superspreading potential should be addressed when Omicron or other circulating SARS-CoV-2 variants invades in the contexts of low herd immunity and exposure in settings with larger scale gatherings⁵, where the enforcement of intervention to limit COVID-19 transmission would need to be strategically developed.

Declarations

Ethics approval and consent to participate

The data used in this study are publicly available, and thus neither ethical approval nor individual consent is applicable.

Availability of materials

All data used in this work are publicly available and the computer codes used for statistical analysis may be available based on request to the authors.

Consent for publication

Not applicable.

Funding

KCC is supported by Health and Medical Research Fund [grant numbers COVID190105, 19181132], Collaborative Research Fund of University Grants Committee [grant numbers C4139-20G], and National Natural Science Foundation of China (NSFC) [71974165]. MHW is supported by Health and Medical Research Fund [INF-CUHK-1, COVID190103], CUHK grant [PIEF/Ph2/COVID/06, 4054456], and partially supported by the National Natural Science Foundation of China (NSFC) [31871340].

Acknowledgements

None.

Conflict of interests

MHW is a shareholder of Beth Bioinformatics Co., Ltd. Other authors declared no competing interests. The funding agencies had no role in the design and conduct of the study; collection, management, analysis, and interpretation of the data; preparation, review, or approval of the manuscript; or decision to submit the manuscript for publication.

Authors' contributions

ZG, SZ, KCC designed the study, ZG and JW collected the data, ZG built the model and carried out the analysis, ZG write the original draft, KCC, SZ, SSL, CKPM gave critical revisions of the manuscript with important intellectual content. EKY, MHW, NSW, KMJ, JW, CHKY and TYC contributed to the revision of the manuscript. All authors read and approved the final manuscript.

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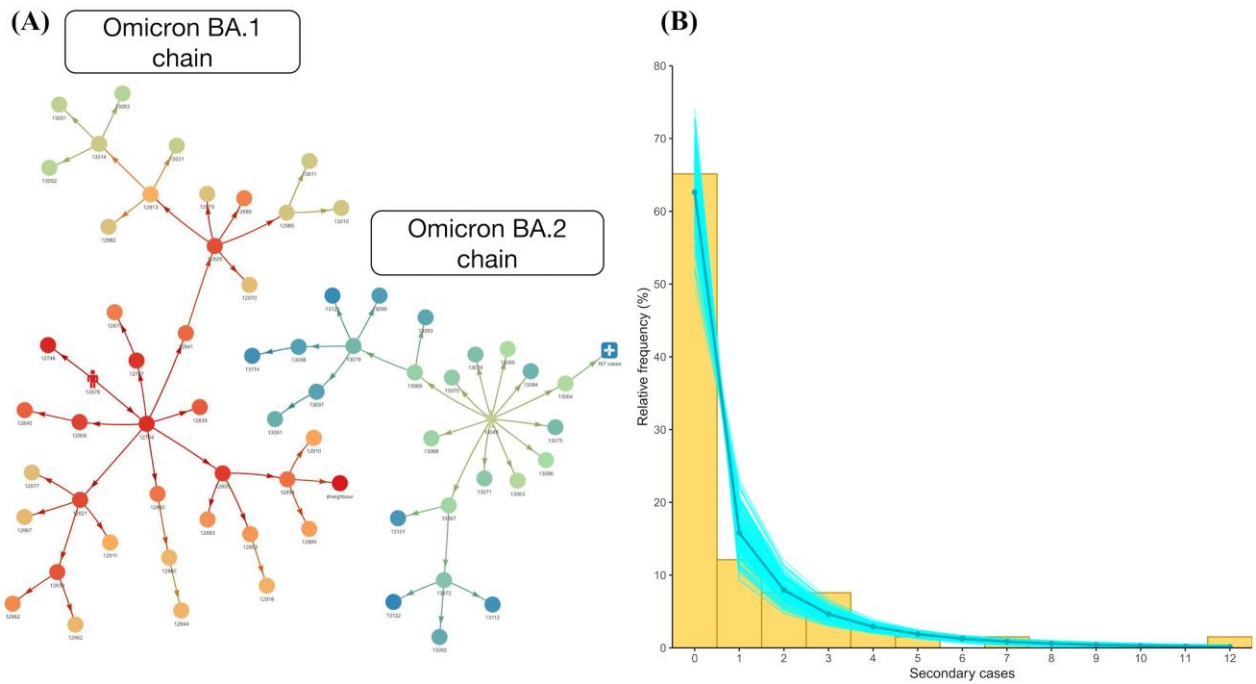


Figure 1. (A) Two observed transmission chains during the initial phase of the Omicron epidemic in Hong Kong. Man-shaped nodes represent initiators of the two chains and solid circles denote the subsequent cases. The solid square with plus sign inside denotes the transmission chain with unknown number of generations. The arrows are the direction of the transmissions from the infectors to the infectees. The numbers under the nodes represent unique id numbers recorded by the Department of Health for each case. The node marked with “#neighbour” haven’t been matched to an identifier. The different colors set for each node are only for aiding visualization. (B) The observed offspring distribution with fitted curves for the transmission chains. Dotted dark blue curve were the posterior median and the cyan curves were 200 posterior MCMC samples.