1 **Title page**

2 **Full title**: Superspreading potential of SARS-CoV-2 Delta variants under intensive disease control

3 measures in China

4

5 Shi Zhao, MPhil[1,2,+], Zihao Guo, MSc[1,+], Marc Ka Chun Chong, PhD[1,2,*,#], Daihai He, PhD[4,*,#], and

6 Maggie H Wang, PhD[1,2,#]

7

8 **1** JC School of Public Health and Primary Care, Chinese University of Hong Kong, Hong Kong,

9 China

10 **2** CUHK Shenzhen Research Institute, Shenzhen, China

11 **3** Department of Applied Mathematics, Hong Kong Polytechnic University, Hong Kong, China

12

13 + SZ and ZG are joint first authors.

14 * Correspondence to: marc@cuhk.edu.hk (MKCC), and daihai.he@polyu.edu.hk (DH).

15 # MKCC, DH, and MHW are joint senior authors.

16

17 **Email addresses of all authors**

18 SZ: zhaoshi.cmsa@gmail.com; ZG: guozihao9602@163.com; DH: daihai.he@polyu.edu.hk; MKCC:

19 marc@cuhk.edu.hk; MHW: maggiew@cuhk.edu.hk.

20

21

22

23

24

25

26

27

28

29

30

31

32

35

36

37

38

39

40

41

42

43

44

45

46

47

48

49

Highlights

Given the heterogeneity in individual transmissibility, we estimated the superspreading potential of SARS-CoV-2 Delta variants. Using case series of Delta variants in Guangdong, China, we found 15% (95%CrI: 12, 19) of cases seeded 80% of offspring cases.

Keywords: COVID-19; superspreading; Delta variant; China; statistical modelling.

Main text

Characterizing the role of superspreading in infectious disease transmission is of public health importance for informing control strategies. Concerning the superspreading potentials of COVID-19 [1], these risks from different SARS-CoV-2 genetic variants remain unassessed. Under intensive disease control measures, the risk of outbreak may still not be eliminated despite self-limited transmission. In this work, we estimated the superspreading potential of Delta variants in China using a well-traced and -sequenced case series dataset.

From May to June December 2021, SARS-CoV-2 Delta variants, which were first reported in India, carrying novel genetic mutations including L452R, T478K, and P681R were detected in Guangdong, China, and rapidly resulted in a local outbreak, where most of cases could be traced back to one initial seed case. Among a total of 167 cases identified, 126 (75.4%) of them were sequenced, and with information of transmission link between each other, which was presented in [2]. We extracted the number of infectees associated each infector and obtained 126 observations for the offspring case distribution including 74 terminal cases, 10 sporadic cases, and 42 infectors having at least one infectees, see Fig 1A. By considering the disease transmission as a stochastic branching

2

process, the classic negative binomial model with likelihood-based estimating framework was employed to characterize the superspreading potentials of Delta variants infected COVID-19 cases [3].

We estimated reproduction number R of 0.91 (95%CrI: 0.63, 1.36) and dispersion parameter k of 0.26 (95%CrI: 0.16, 0.41), which is relatively smaller than the k estimates around 0.43 based on the contact tracing data in 2020 [1]. When given the basic reproduction number of Delta variants at 5, the superspreading threshold can be calculated as the 99-th percentile of Poisson (rate = 5) distribution [4], i.e., > 10, and thus we identified two (1.6%) superspreading events (SSE) across all 126 one-generation case clusters. Although SSE plays less of a role when there is widespread community transmission, SSEs could contribute to generate more source infectors during the early phase of an outbreak, which is less sensitive to the settings with intense public health measures at population scale. We estimated that 15% (95%CrI: 12, 19) of the most infectious cases seeded 80% of all offspring cases, which suggested a higher superspreading potential than the situations of early outbreaks in 2020 [4].

Although intensive COVID-19 control measure were implemented in mainland China as of 2020 [2], the variation in individual infectious history and in the properties of SARS-CoV-2 strains may still contribute to large case clusters dominated by SSEs [3]. With one seed case of Delta variant, there were 5% (95CrI: 1, 14) or 2% (95%CrI: 0, 12) of chance to have a cluster of cases with size > 30 or 100, respectively, see Fig 1B. As such, we recommend enforcing the intervention programs to monitor and limit COVID-19 transmission, especially regarding the contexts where SSEs are likely to occur, e.g., restaurants and entertainment sites. For the challenges from emerging Omicron variant against the global COVID-19 pandemic control, we urge concerns on the possible risks of superspreading when it invades places with low herd immunity in population or settings with large-scale congregations [5].

Declarations

Ethics approval and consent to participate

The COVID-19 number of cases and sequencing data are collected, and thus neither ethical approval nor individual consent is applicable.

Availability of materials

All data used in this work are publicly available via Li *et al* [2], and the computer codes used for statistical analysis may be available based on request to the authors.

Consent for publication

Not applicable.

Funding

Acknowledgements

None.

Conflict of interests

Authors' contributions

Conceptualization: SZ. Methodology: SZ, ZG, and MKCC. Software: SZ, and ZG. Validation: SZ, and ZG. Formal analysis: SZ. Investigation: SZ. Resources: SZ. Data Curation: SZ. Writing - Original Draft: SZ. Writing - Review and Editing: ZG, and MKCC, DH, and MHW. Visualization: SZ. Supervision: MKCC, and MHW. Project Administration: SZ. Funding acquisition: MKCC, and MHW. All authors critically read the manuscript, and gave final approval for publication.

References

1   Wang J, Chen X, Guo Z, et al. Superspreading and heterogeneity in transmission of sars, mers, and covid-19: A systematic review. Computational and Structural Biotechnology Journal 2021; 19(5039-5046.

2   Li B, Deng A, Li K, et al. Viral infection and transmission in a large, well-traced outbreak caused by the sars-cov-2 delta variant. Nature Communications 2022; 13(1):460.

3   Lim JS, Noh E, Shim E, Ryu S. Temporal changes in the risk of superspreading events of coronavirus disease 2019. Open Forum Infectious Diseases 2021; 8(7):ofab350.

4   Adam DC, Wu P, Wong JY, et al. Clustering and superspreading potential of sars-cov-2 infections in hong kong. Nat Med 2020; 26(11):1714-1719.

5   Mat NFC, Edinur HA, Razab MKAA, Safuan S. A single mass gathering resulted in massive transmission of COVID-19 infections in Malaysia with further international spread. J Travel Med. 2020; 27(3):taaa059.
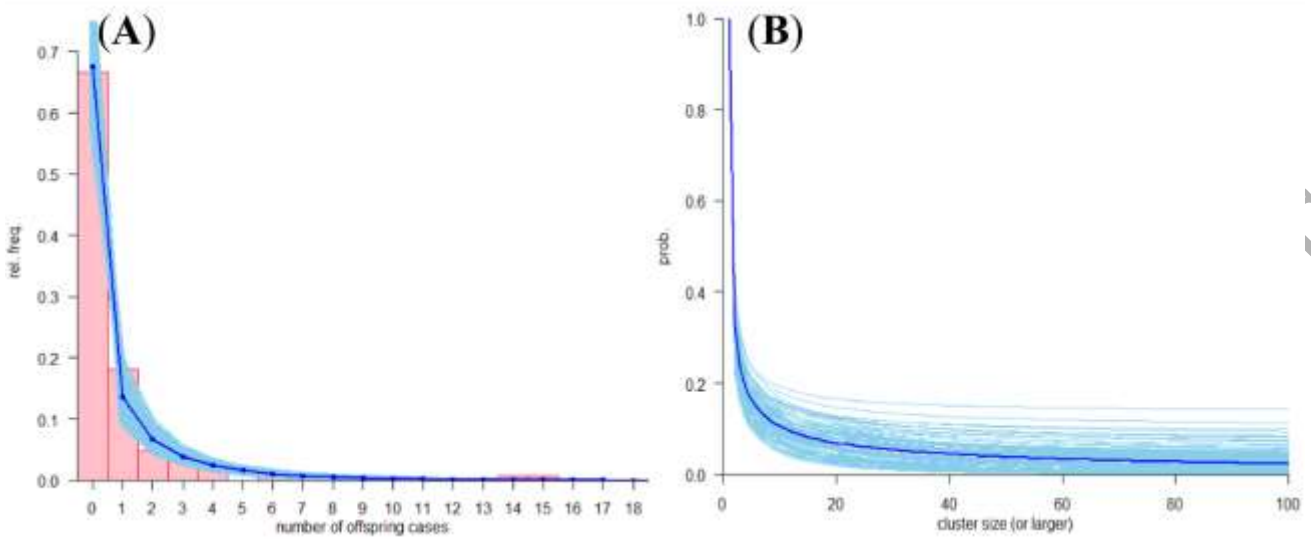
Figures

143

144   Figure 1.

145   The observed and fitted offspring cases distribution (A) and estimated probability of generating case

146   cluster with a given size (B). Panel (A) shows observed (in pink) and fitted (in blue) offspring cases

147   distribution. Panel (B) shows probability of observing a case cluster with a size equal to or larger

148   than a given number that is generated by one seed case. In both panels, the light blue curves are 100

149   posterior MCMC samples, and dark blue curve is the posterior median.

150

151   **Tables**

152   None.

153