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## Letter to the Editor

## Superspreading potential of infection seeded by the SARS-CoV-2 Omicron BA.1 variant in South Korea



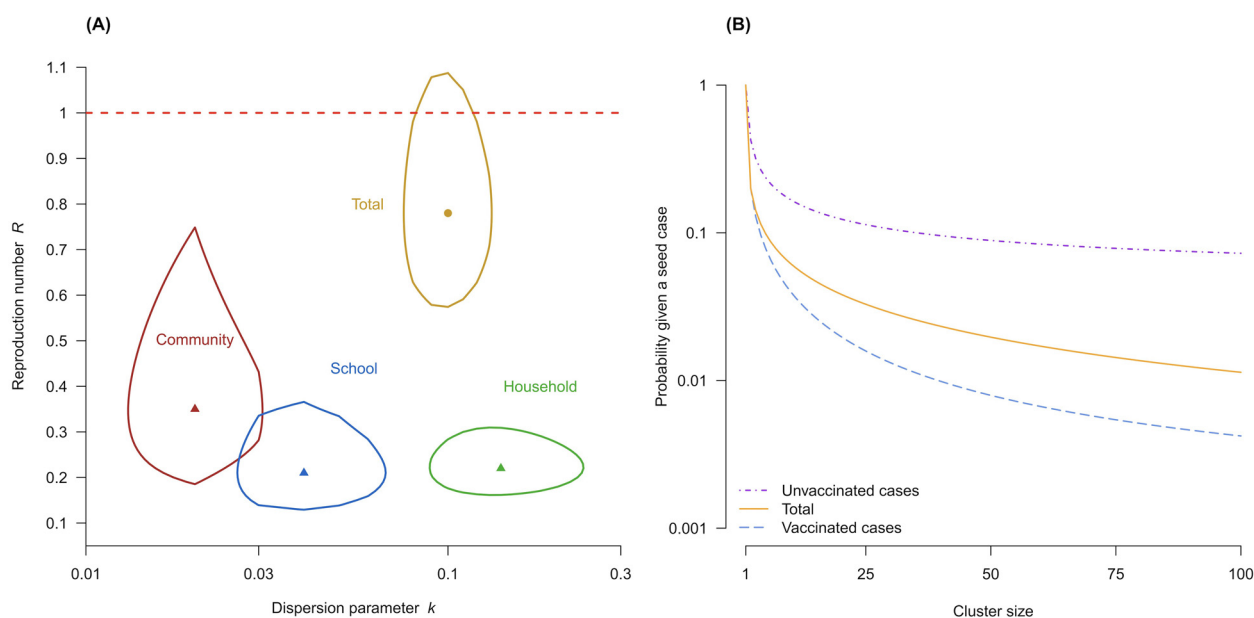
Dear Editor,

As a distinct feature of the COVID-19 transmission, superspreading<sup>1–2</sup> plays an essential role for fueling the disease transmissions in the outbreaks caused by the recent SARS-CoV-2 (B.1.1.529) Omicron variant. In South Korea, superspreading events (SSEs) frequently occurred and thus posed considerable challenges for controlling COVID-19 outbreak through contact tracing.<sup>3</sup> Assessing the potential of superspreading could provide insight into the transmissibility of the emerged variant. Here, we used line-list epidemiological contact tracing data that collected during an Omicron outbreak in South Korea to estimate the superspreading potential of the Omicron BA.1 variant.

We obtained data of 427 laboratory-confirmed cases infected by the Omicron BA.1 variant from 25 November to 31 December 2021 in South Korea<sup>4</sup>. We extracted the contact tracing information and vaccination history for each case. Their contact settings were classified into household, community (including infectious contact

occurred within churches, restaurants, workplaces, and social contacts), and school. Case clusters infected by the same infector were identified to construct a negative binomial model governed by the reproduction number ( $R$ ) and dispersion ( $k$ )<sup>5</sup>, a parameter to characterize the heterogeneity in individual transmissibility. Technical details of the statistical models and parameter estimations were described in the Supplementary material.

Of the 427 cases, 85 (19.9%) cases led to at least one secondary cases (Fig. S1), with one case directly seeded 78 cases in the community setting (Fig. S2). Of the 156 cases with known vaccine status, 84 (53.8%), 2 (1.3%), and 70 (44.9%) of them were unvaccinated, received one dose, and two doses, respectively. The  $R$  and  $k$  were estimated at 0.78 (95% confidence interval (CI): 0.58–1.08) and 0.10 (95% CI: 0.08–0.13), respectively. We inferred that 80% of all transmissions were generated by 9% of the most infectious cases. Community settings had a higher transmission risk and superspreading potential than household and school (lower  $k$  value compared to household and school) (Fig. 1A and Table 1). Furthermore, unvaccinated cases had a higher potential in seeding SSEs. The probability of an unvaccinated case seeding an outbreak with  $\geq 100$  cases was 7%, as compared to 0.4% for that of a vaccinated case (Fig. 1B).



**Fig. 1.** (A) Joint estimations of the reproduction number,  $R$ , and dispersion,  $k$ , for cases infected with SARS-CoV-2 Omicron BA.1 variant. The estimates were based on total case clusters data (yellow) and case clusters observed in community (red), school (blue) and household (green) settings. The circle and triangle points denoted maximum likelihood estimations, and the coloured solid lines represented 95% confidence intervals. The red dashed line indicated that  $R$  equals to one. (B) The probability of observing a transmission cluster of a given size or greater seeded by one BA.1 variant case. The probabilities were computed by total case clusters (orange solid line), and case clusters seeded by vaccinated (purple dot-dash line) and unvaccinated cases (blue dashed line), integrating over the full parameter space during the estimations.

**Table 1**  
Estimated reproduction number (*R*), dispersion (*k*), and superspreading potential by contact settings and vaccination status.

		Reproduction number (95%CI)	Dispersion (95%CI)	Expected Proportion of seed cases generating 80% of transmission,%
Contact Settings	Household ( <i>n</i> = 427)	0.22 (0.17–0.30)	0.14 (0.09–0.23)	8%
	Community ( <i>n</i> = 427)	0.35 (0.19–0.74)	0.02 (0.02–0.03)	2%
	School ( <i>n</i> = 427)	0.21 (0.13–0.36)	0.04 (0.03–0.06)	4%
Vaccination status	Vaccinated ( <i>n</i> = 72)	0.47 (0.24–1.10)	0.13 (0.06–0.28)	10%
	Unvaccinated ( <i>n</i> = 84)	1.26 (0.88–1.87)	0.44 (0.26–0.75)	22%
Total ( <i>n</i> = 427)		0.78 (0.58–1.08)	0.10 (0.08–0.13)	9%

Our findings suggest that the transmission of the BA.1 variant had high potential of superspreading, which is higher than the Delta variants<sup>6</sup>, and other historical SARS-CoV-2 strains<sup>7</sup>. The BA.1 variant appeared more transmissible with a higher risk of superspreading within community settings than in household and school settings. In addition to contact settings, vaccination status was also a potential risk modifier.

Given a generally larger scale favoring the social contacts, the transmissibility and superspreading potential of the BA.1 variant were high in community settings. As shown in Figure S2, large SSEs within the community occurred at the edge of the transmission chain, which offers greater opportunity for continuously spreading. The overdispersion feature of the case-cluster distributions across different contact settings could result in a lower effectiveness of population-wide control measures<sup>5</sup> because of the heterogeneity in individual transmissibility, that is, only a few cases generated majority of the infections. As such, public health interventions that are developed to trim the “long-tailed events” (i.e., SSEs) of the case-cluster distributions would disproportionately reduce the virus transmissibility and thereby suppress the outbreak. Given the behavioral and biological factors including social gatherings and high viral load within the host are well-established key drivers of SSEs, enforcement of the monitoring and physical distancing in high-risk settings (e.g., churches, restaurants, and health care facilities)<sup>8</sup>, accompanied by timely identification and isolation of highly infectious cases should be the focal points for controlling the Omicron outbreaks.

Additionally, given that vaccinated cases had a diminished transmissibility and a lower superspreading potential than unvaccinated cases, we speculated that T cells induced by the vaccine may lower the infectivity of the Omicron cases. During the study period, three types of COVID-19 vaccine, including mRNA, viral vector, and subunit vaccine were used in South Korea. Despite a relatively low effectiveness of these vaccines against the Omicron infection due to immune escape, immunization should be promoted to lower the transmissibility and mitigate the outbreak size.

Because only self-limited case clusters were observed, our findings may only serve as preliminary results for assessing the superspreading potential of the ongoing epidemics in South Korea. Nevertheless, we highlighted the importance of monitoring the superspreading potential under different settings and for other emerging variants. While two doses of vaccination may significantly contribute to reducing the transmissibility of cases infected with the BA.1 variant, administration of the booster dose is warranted given that the protection from vaccination would wane over time.

## Funding

This research was supported by Health and Medical Research Fund [grant numbers COVID190105, INF-CUHK-1], National Natural Science Foundation of China [71974165], Group Research Scheme from The Chinese University of Hong Kong, Guangdong-

Hong Kong-Macau Joint Laboratory of Respiratory Infectious Disease [grant numbers 20191205], and visiting scientist scheme from Lee Kong Chian School of Medicine, Nanyang Technological University, Singapore.

## Declaration of Competing Interest

None.

## Acknowledgements

None.

## Supplementary materials

Supplementary material associated with this article can be found, in the online version, at [doi:10.1016/j.jinf.2022.05.041](https://doi.org/10.1016/j.jinf.2022.05.041).

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