



Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Elsevier hereby grants permission to make all its COVID-19-related research that is available on the COVID-19 resource centre - including this research content - immediately available in PubMed Central and other publicly funded repositories, such as the WHO COVID database with rights for unrestricted research re-use and analyses in any form or by any means with acknowledgement of the original source. These permissions are granted for free by Elsevier for as long as the COVID-19 resource centre remains active.



ELSEVIER

Contents lists available at ScienceDirect

Journal of Infection

journal homepage: www.elsevier.com/locate/jinf

Letter to the Editor

Comparative analysis of transmission and vaccine effectiveness in Omicron and Delta variant outbreaks in China

Dear editors

In this Journal, Yidun Zhang et al. compared Ct value difference between Omicron BA.1 and BA.2 variants and showed that Omicron BA.2 more transmissible than BA.1¹. Previous letter by Yue Yin et al. announced that inactivated COVID-19 vaccines (CoronaVac, Sinovac) is less effective against Omicron than against Delta, and its protection against Omicron². However, the transmission characteristics of infection in Delta and Omicron mutant strains have not been fully defined. The goal of this study is to examine the characteristics of Delta and Omicron variants, including transmission, Ct value, and effectiveness of vaccine, to provide additional information about the COVID-19 pandemic in China.

We examined three outbreaks caused by the different SARS-CoV-2 variants and located in Southern China (Fig. S1). A total of 202 infections due to SARS-CoV-2 variants in three outbreaks were included in our analysis. Of these infections, 33 (16.34%) were caused by the Omicron BA.2 variant, 38 (18.81%) were caused by the Omicron BA.1 variant, and 129 (63.86%) were caused by the Delta variant. The median age of infections for Omicron BA.2, Omicron BA.1 and Delta variant was varied (21.5 years vs. 31.0 years vs. 34.0 years), and 137 (67.82%) infections were in adults (19–64 years). 31 (88.57%) infections of Omicron BA.2 have been completed vaccine, higher than Delta (68.42%) and Omicron BA.1 (29.46%). In addition, the proportion of asymptomatic infections decreased from 15% in the Delta outbreak to 6%–8% in the Omicron outbreak (Table S1, Fig. 1A–C).

The distribution of epidemiological parameters was fitted to Gamma distribution, the Lognormal distribution and Weibull distribution were used as well and showed similar goodness-of-fit as measured by log-likelihood (Table S2, Fig. S2). Compared with the Delta variant, Omicron BA.2 and BA.1 variants were transmitted with a shorter serial interval (SI), (5.70 days vs. 2.24 days) (Fig. 1D), and incubation period (IP) (7.63 days vs. 4.35 days vs. 3.07 days) (Fig. 1E) in the outbreaks examined. Approximately 35.09% cases where SIs were shorter than IPs were recorded in individuals infected with Omicron BA.1; similarly, 70.98% cases were recorded in those infected with Omicron BA.2, and 75.00% cases in those infected by Delta (Fig. 1F). The estimation of generation time (GT) was based on a review of the exposed period and probable time of infection. Omicron BA.1 displayed a shorter GT than the Delta variant (1.76 days vs. 2.52 days), and a similar GT to Omicron BA.2 (2.93 days vs. 2.52 days). Transmission generation (TG) of variants, defined as the period between the positive test results of infector and infectee which did not rely on the recall of infectee, were also varied. Delta and Omicron BA.1 showed similar TG values (3.61 days vs. 3.56 days), and Omicron BA.2 displayed a

TG of 1.95 days (Fig. 1G–H). R_{eff} of Delta at increased stage was 1.93 (95% CI: 1.3–2.72), 2.94 (95% CI: 1.41–5.30) for Omicron BA.1, and 3.56 (95% CI: 1.20–7.94) for Omicron BA.2 (Fig. 1I). We also compared IP, SI, TG, and GT values between adults (older than 19 years) and children (0–18 years) and found that children had shorter IP in the Omicron BA.1 outbreak (4.00 days vs. 4.89 days) and shorter TG values in both the Omicron BA.1 (3.11 days vs. 4.14 days) and Delta (2.37 days vs. 4.06 days) outbreaks (Fig. S3). This may be related to a deficient vaccine coverage in children, in part (Fig. 1A–C). However, the difference between the epidemiological parameters of Omicron BA.2, as opposed to other variants, cannot be explained entirely by deficient vaccine coverage in children.

A total of 21,716 contacts were introduced by 202 infections and tracked by local CDC health workers (Table S3). Full vaccine coverage of contacts in Delta, Omicron BA.1, and BA.2 outbreaks was 44.33%, 79.77%, and 68.72%, respectively. Booster dose coverage was 40.84% and 29.62% in Omicron BA.1 and Omicron BA.2 outbreaks, respectively. Vaccine coverage of children (aged 0–18 years) and older adults (aged 65 years or older) was lower than that of younger adults (Fig. 2A–C). More than 99% of the vaccines received by contacts were produced by 5 manufacturers, including Sinovac Biotech Ltd., Sinopharm Group Co. Ltd., CanSino Biologics Inc., Anhui Zhifei Longcom Biopharmaceutical Co. Ltd., and Shenzhen Kangtai Biological Products Co., Ltd. The mixed vaccine strategy was also observed in each outbreak, but 98.27% of vaccinations were a dosing combination of CoronaVac (Sinovac Biotech Ltd.) and COVIL0 (Sinopharm Group Co. Ltd.) (Fig. 2D–F). Overall effectiveness of vaccine against the Delta variant in fully vaccinated individuals was 51.68% (95% CI: 28.90–67.16%) (Fig. 2G). In conditional logistic regression model, the vaccine effectiveness against Delta variant infection adjusted by age group was 67.87% (95% CI: 51.67–78.64%) (Fig. 2H). For Omicron BA.1 and BA.2, difference in vaccine effectiveness against infection was not observed, regardless of adjustment by age group.

Our findings imply that Omicron's transmissibility is 1.5–1.8 times higher than that of Delta in terms of viral transmission. This is lower than the value reported by other studies, which claim that Omicron has a transmissibility 2.5 to 4 higher than that of Delta^{3,4}. This might be attributable to the rising rate of fully vaccinated and booster-vaccinated people. Meanwhile, the geographic variability is also linked to inconsistencies in the implementation of COVID-19 prevention and control measures in different regions. We also saw that the transmissibility of the two Omicron sub-lineages differed, with Omicron BA.2 being 1.2 times more transmissible than BA.1, which is similar to the results of several studies that suggest that BA.2 is 30 to 40 percent more infectious than BA.1^{5–7}. In comparison to Delta, applying a dynamic zero-COVID policy for interrupting Omicron transmission may necessitate greater preventative and control efforts.

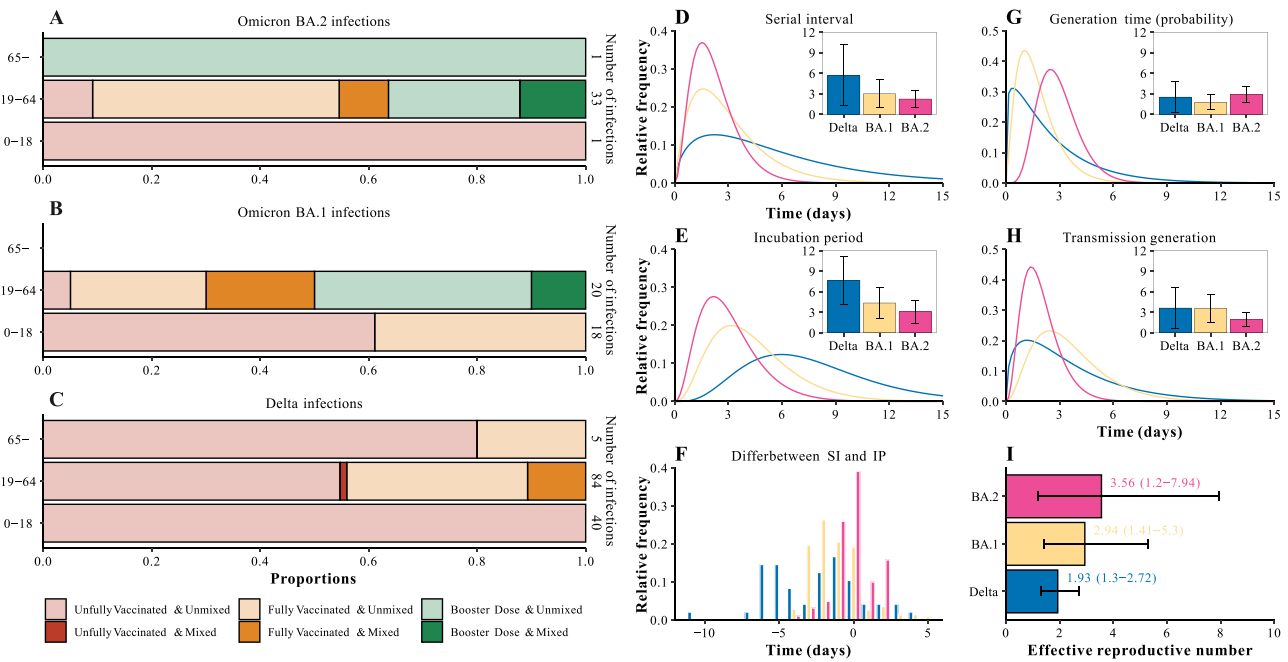


Fig. 1. Vaccination status and epidemiological parameters estimation of infections in COVID-19 outbreaks caused by Omicron BA.2, Omicron BA.1 and Delta. Vaccination status of infections from Omicron BA.2 (A), Omicron BA.1 (B) and Delta (C), respectively, and grouped by age. (D), Fitted serial interval (SI) distribution of paired cases of Delta ($n = 83$), Omicron BA.1 ($n = 31$) and BA.2 ($n = 19$). (E), Fitted incubation period (IP) distribution of cases of Delta ($n = 74$), Omicron BA.1 ($n = 35$) and BA.2 ($n = 33$). (F), The difference between IP and related SI of cases. (G), Fitted probability generation time (GT) distribution of infections of Delta ($n = 58$), Omicron BA.1 ($n = 33$) and BA.2 ($n = 20$). (H), Fitted transmission generation (TG) distribution of infections of Delta ($n = 90$), Omicron BA.1 ($n = 32$) and BA.2 ($n = 20$). (I), Effective reproductive number of difference outbreaks, estimated using R0 package.

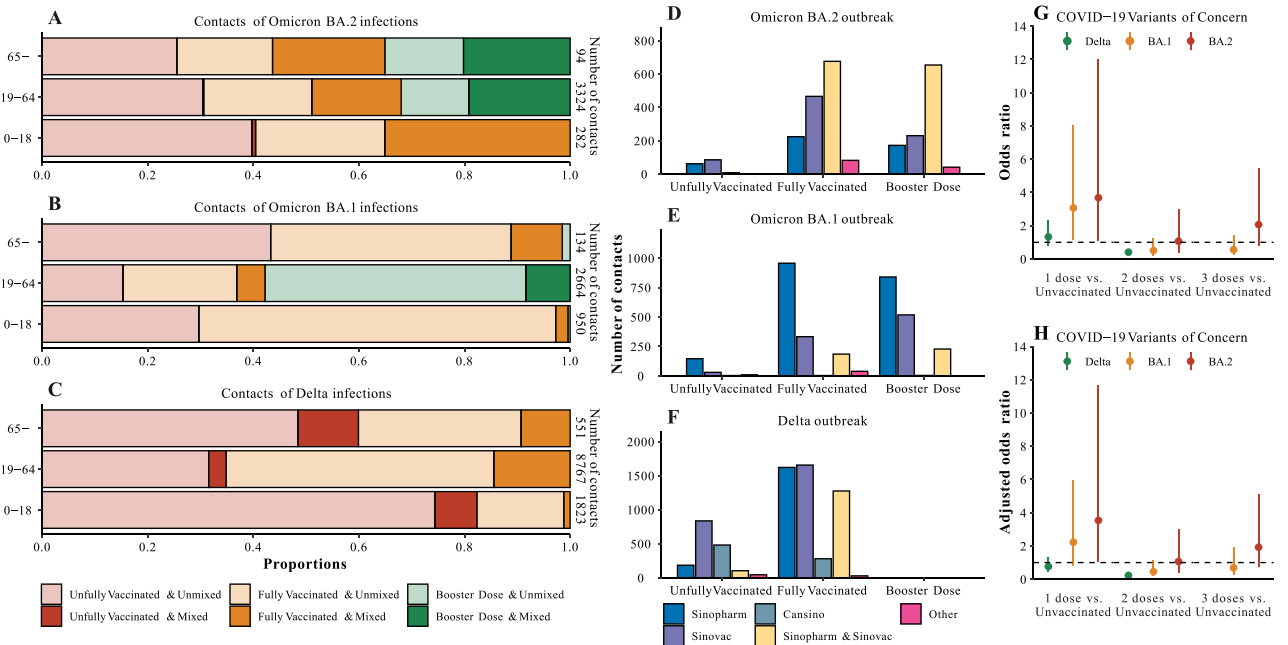


Fig. 2. Vaccination status of contacts and vaccine effectiveness against infections in COVID-19 outbreaks caused by Omicron BA.2, Omicron BA.1 and Delta. Vaccination status of contacts from Omicron BA.2 (A), Omicron BA.1 (B) and Delta (C), respectively, and grouped by age. Vaccine manufacturers with contacts in Omicron BA.2 (D), Omicron BA.1 (E) and Delta outbreaks (F), respectively. (G), Comparison of vaccine effectiveness against infection using a logistic regression model. (H), Comparison of vaccine effectiveness against infection using conditional logistic regression model, adjusted for age group.

Funding

This study was partly supported by the National Key Research and Development Program of China (2021YFC2301604), The Bill & Melinda Gates Foundation (Grant INV-005834 to T.C.) and Zhuhai Science and Technology Program (ZH22036302200077PWC).

Ethical statement

This study was approved by the institutional ethics committee of the Zhuhai Center for Disease Control and Prevention (CDC), Guangdong, China. Written consent was obtained from patients or their guardian(s) when samples were collected. The Hunan Provincial CDC, China and the Xiamen CDC, Fujian, China have a data-

sharing agreement of infections and contacts in 2021–10 Delta outbreaks and 2022–2 Omicron BA.2 outbreaks.

Author contributions

Conceptualization: TMC, FR, ZNG. Investigation: FR, XBZ, ZNG, XLY, WHM. Methodology: KGL, ZYZ, TMC. Software: KGL. Validation: TMC. Writing - original draft: ZYZ, KGL, SSY, ZMY, BA. Writing - review & editing: ZYZ, KGL, BA.

Data and source code availability

Source code and data of analysis procedure is accessible at GitHub repository (https://github.com/xmusphlkg/zuhai_omicron).

Declaration of competing interest

The authors declare no competing interests.

Acknowledgments

We thank staff at Zhuhai, Xiamen and Hunan Center for Disease Control and Prevention, China for accessing the various data sources. The opinions expressed are those of the authors and not necessarily the institutions to which they are affiliated.

Supplementary materials

Supplementary material associated with this article can be found, in the online version, at doi:[10.1016/j.jinf.2022.08.018](https://doi.org/10.1016/j.jinf.2022.08.018).

References

- Zhang Y, Li J, Jiang L, et al. Comparison of SARS-CoV-2 aerosol emission from patients with Omicron BA.1 or BA.2 subvariant infection. *J Infect* 2022;**85**(2) e37–e9. doi:[10.1016/j.jinf.2022.05.035](https://doi.org/10.1016/j.jinf.2022.05.035).
- Yin Y, Li X, Qian C, Cheng B, Lu F, Shen T. Antibody efficacy of inactivated vaccine boosters (CoronaVac) against Omicron variant from a 15-month follow-up study. *J Infect* 2022. doi:[10.1016/j.jinf.2022.06.018](https://doi.org/10.1016/j.jinf.2022.06.018).
- Nishiura H, Ito K, Anzai A, Kobayashi T, Piantham C, Rodriguez-Morales AJ. Relative Reproduction Number of SARS-CoV-2 Omicron (B.1.1.529) compared with delta variant in South Africa. *J Clin Med* 2021;**11**(1). doi:[10.3390/jcm11010030](https://doi.org/10.3390/jcm11010030).
- Liu Y, Rocklöv J. The effective reproduction number for the omicron SARS-CoV-2 variant of concern is several times higher than Delta. *J Travel Med* 2022. doi:[10.1093/jtm/taac037](https://doi.org/10.1093/jtm/taac037).

- Johnson H. New Omicron variant: symptoms of Covid subvariant BA.2, how contagious is it and does it cause severe illness? 2022. <https://www.nationalworld.com/health/new-omicron-variant-symptoms-of-covid-subvariant-ba2-how-contagious-is-it-and-does-it-cause-severe-illness-3612480> (accessed 15 April 2022).
- Skydsgaard N. Omicron subvariant BA.2 more infectious than 'original', Danish study finds. 2022. <https://www.reuters.com/business/healthcare-pharmaceuticals/omicron-subvariant-ba2-more-infectious-than-original-danish-study-finds-2022-01-31/> (accessed 30 January 2022).
- Kimball S. Omicron B.A. 2 subvariant is more contagious and can reinfect people, but isn't more severe, studies find. 2022. <https://www.cnn.com/2022/02/25/covid-transmissibility-severity-reinfection-of-omicron-bapoint2-subvariant.html> (accessed 25 January 2022).

Kangguo Li¹

State Key Laboratory of Molecular Vaccinology and Molecular Diagnostics, School of Public Health, Xiamen University, Fujian, China

Feng Ruan¹

Zhuhai Center for Disease Control and Prevention, Guangdong, China

Zeyu Zhao¹

State Key Laboratory of Molecular Vaccinology and Molecular Diagnostics, School of Public Health, Xiamen University, Fujian, China
CIRAD, Intertryp, Montpellier, France, IES, Université de Montpellier-CNRS, Montpellier, France

Zhinan Guo¹

Xiamen Center for Disease Control and Prevention, Fujian, China

Zimei Yang, Shanshan Yu, Buasiyamu Abudunaibi

State Key Laboratory of Molecular Vaccinology and Molecular Diagnostics, School of Public Health, Xiamen University, Fujian, China

Xuebao Zhang, Xiling Yin, Wenhua Mei*

Zhuhai Center for Disease Control and Prevention, Guangdong, China

Tianmu Chen*

State Key Laboratory of Molecular Vaccinology and Molecular Diagnostics, School of Public Health, Xiamen University, Fujian, China

*Corresponding authors.

E-mail addresses: 1297648405@qq.com (W. Mei),
13698665@qq.com (T. Chen)

¹ These authors contributed equally to this study.