

Review Article

Characteristics and management of SARS-CoV-2 delta variant-induced COVID-19 infections from May to October 2021 in China: post-vaccination infection cases

Boqi Xiang^{1,2*}, Yunhua Zhang^{3*}, Qiong Ling⁴, Zhenrong Xie⁵, Na Li¹, Duozhi Wu¹

¹Department of Anesthesiology, Hainan General Hospital, Haikou 570311, Hainan, China; ²School of Public Health, Rutgers University, New Brunswick, NJ, United States; ³Hubei Provincial Hospital of Traditional Chinese Medicine; Clinical Medical College of Hubei University of Chinese Medicine; Hubei Province Academy of Traditional Chinese Medicine, Wuhan 430061, China; ⁴Department of Anesthesiology, The Second Affiliated Hospital of Guangzhou University of Chinese Medicine, Guangzhou, China; ⁵Department of Anesthesiology, The Seventh Affiliated Hospital of Sun Yat-sen University, Shenzhen 518107, China. *Equal contributors.

Received February 25, 2022; Accepted May 11, 2022; Epub June 15, 2022; Published June 30, 2022

Abstract: SARS-CoV-2 variants have shown increased transmission capabilities and pandemic to an extent with severe presentation and mortality. The delta variant has been declared as an emerging variant of concern (VOC) by the World Health Organization (WHO) on May 10, 2021. This review summarizes the post-vaccination infection events related to SARS-CoV-2 delta variant outbreaks in many areas of China. The characteristics and measures of delta variant-induced COVID-19 infections from May 2021 to October 2021 were reported. We compared the delta variant with the omicron from the latest literature review.

Keywords: COVID-19 disease, SARS-CoV-2 delta variant, variant B.1.617.2, scientific protective measures

Introduction

It is known that the generation of novel coronavirus variants occur through accumulation of viral genome mutations in host defense against emerging pathogens [1]. SARS-CoV-2 pandemic, concerning the rapid spread of many viruses transmitted by respiratory droplets and fomites, has reminded us that the host immune status and different responses have played the fundamental role in virus mutation and ongoing pandemic of SARS-CoV-2. The delta variant has been signed as an emerging variant of concern (VOC) by the World Health Organization (WHO) on May 10, 2021. Delta variants had addressed worldwide attention. Host immune responses to current delta variants is unclear and needs further elucidation.

Several studies have shown that SARS-CoV-2 virus has owned many progressive changes and becomes mutated with the rising infection and is more lethal for human beings than ever before [2-4]. SARS-CoV-2 virus B.1.617 lineage

was a special variant conferring advantage to rapidly become dominant lineages [5]. It is known that the variant B.1.617.2 (SARS-CoV-2 delta variant) was first detected in India in October 2020. It has contributed to the current wave of infection ravaging the Southern Asia subcontinent due to its apparent increased transmissibility. Variant B.1.617.2 (SARS-CoV-2 delta variant) was designated a variant of concern (VOC) by the World Health Organization (WHO) and had been reported in more than 80 countries on June 20, 2021 [6]. Delta variant B.1.617.2 was the most widespread VOC in 2021 [5]. With the role of imported visitors and commodities in the transmission of COVID-19 [7-11], the objectives of the review summarize current characteristics and management measures of delta variant-induced sporadic COVID-19 outbreaks from June to October 2021 in China. These results will offer key information to other countries at this important stage of the pandemic COVID-19 induced by the delta variant.

Post-vaccination infection by delta variant

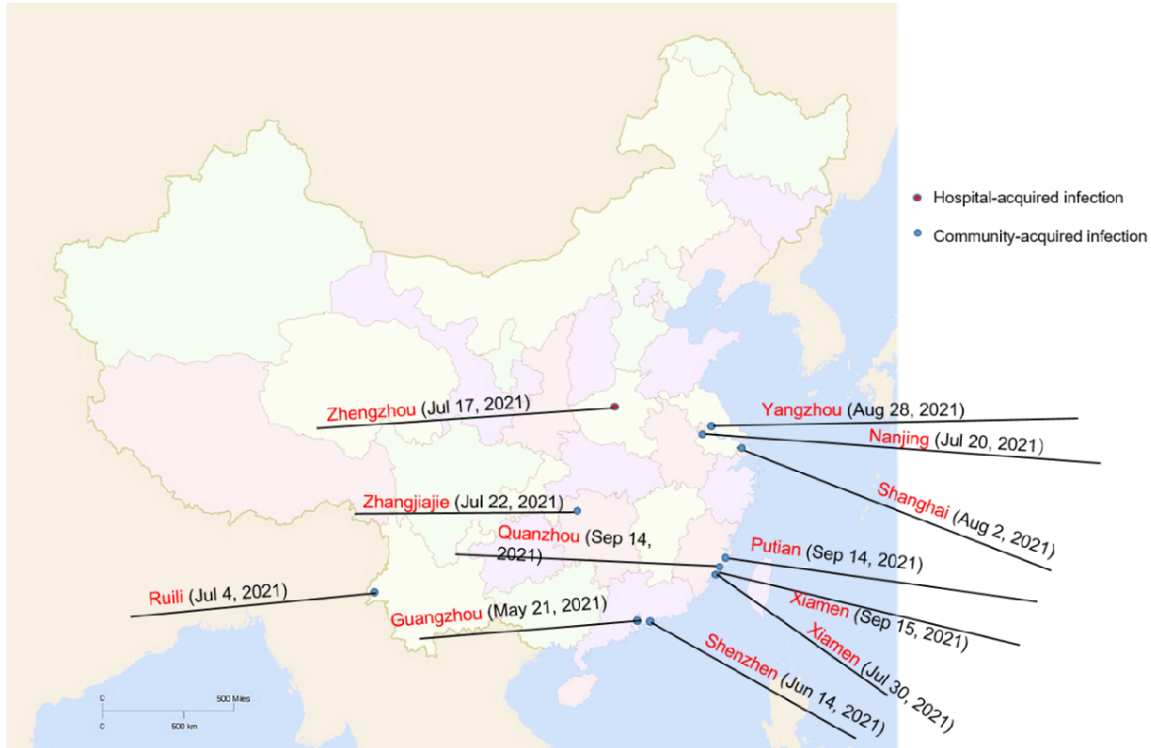


Figure 1. Geographical epidemiological characteristics of the 12 cities during the sporadic COVID-19 outbreaks induced by the imported virus strain B.1.617.2 (delta) in China. Nanjing, Guangzhou, Shenzhen, and Shanghai are aviation hub cities. Ruili is border city.

Methods

We collected the delta variant-induced COVID-19 epidemic data from the Chinese CDC and the local Municipal Health Commissions every day and summarized a descriptive analysis of the characteristics and measures of delta variant-related sporadic COVID-19 outbreaks (from May to October 2021). We searched the literature by the PubMed and SCOPUS database from October 2020 to December 31, 2021. Suitable keywords or terms included ‘SARS-CoV-2 delta variant’, ‘post-vaccination SARS-CoV-2 infection’, ‘COVID-19’, ‘B.1.617.2 variant’, and ‘vaccine’. We also assessed Chinese epidemiology and trends of delta variant-related infection and SARS-CoV-2-related post-vaccination infection.

Results

Geographical distribution of different cities during the sporadic COVID-19 outbreaks

From May to October 2021, geographical distribution of different cities delta mutant strain-induced COVID-19 pandemic is shown in **Figure**

1. Nanjing, Guangzhou, Shenzhen, Xiamen, and Shanghai are aviation hub cities. Ruili is a border city. Nanjing epidemic-associated cities included Zhangjiajie and Yangzhou. Putian epidemic-associated cities included Xiamen (15 Sep.) and Quanzhou.

Epidemiological characteristics of different cities during the sporadic COVID-19 infections

Characteristics of sporadic SARS-CoV-2 outbreak is presented in **Table 1** and **Figure 2**. Discovering the source of COVID-19 infection is critical in seeking new SARS-CoV-2 infection regions. Infection cases with COVID-19 in Nanjing, Shanghai, and Shenzhen were reported by routine nucleic acid testing for airport staff. COVID-19 infection cases in Zhengzhou were found by routine nucleic acid testing for patients and hospital staff. Infection cases in Yangzhou, Putian, Zhangjiajie, Xiamen, and Quanzhou were discovered by nucleic acid testing for close contacts of people with infection cases.

Identifying the transmission chain is especially important to implement prevention strategies for COVID-19 infection. Main infection chains of

Post-vaccination infection by delta variant

Table 1. Epidemiological characteristics of sporadic COVID-19 infections by imported virus strain B.1.617.2 (Delta) Lineage

Date	City	Infection cases	How to discover the source of infection	Classification of infection	Main infection chain	Database
21 May	Guangzhou	153	Routine nucleic acid testing	Community-acquired infection	close contact contagion chain	Link 1
14 Jun.	Shenzhen	4	Routine nucleic acid testing	Community-acquired infection	close contact contagion chain	Link 2
18 Jun.	Dongguan	4	Nucleic acid testing for close contacts	Community-acquired infection	close contact contagion chain	Link 3
20 Jul.	Nanjing	238	Regular screening for airport staffs	Community-acquired infection	International airport contagion chain	Link 4
22 Jul.	Zhangjiajie	72	Nucleic acid testing for close contacts of people with infection cases	Community-acquired infection	Drama-audience contagion chain	Link 5
28 Jul.	Yangzhou	54	Nucleic acid testing for close contacts of people with infection cases	Community-acquired infection	Chess room infection chain	Link 6
30 Jul.	Zhengzhou	63	Regular screening for medical staff	hospital-acquired infection	nosocomial infection	Link 7
31 Jul.	Xiamen	4	Routine nucleic acid testing	Community-acquired infection	close contact contagion chain	Link 8
2 Aug.	Shanghai	1	Routine nucleic acid testing	Community-acquired infection	close contact contagion chain	Link 9
10 Sep.	Putian	261	Nucleic acid testing for close contacts of people with infection cases	Community-acquired infection	family, factory, and school contagion chains	Link 10
14 Sep.	Quanzhou	24	Nucleic acid testing for close contacts of people with infection cases	Community-acquired infection	close contact contagion chain	Link 11
15 Sep.	Xiamen	235	Nucleic acid testing for close contacts of people with infection cases	Community-acquired infection	close contact contagion chain	Link 12

Link 1 <https://www.jiemian.com/article/6459847.html>; Link 2 <https://zhuanlan.zhihu.com/p/383289593>; Link 3 <https://zhuanlan.zhihu.com/p/383289593>; Link 4 https://mbd.baidu.com/newspage/data/landingsuper?context=%7B%22nid%22%3A%22news_10065293164295960897%22%7D&n_type=1&p_from=4; Link 5 <http://cs.bendibao.com/news/2021728/76896.shtm>; Link 6 <https://www.cn-healthcare.com/article/20210802/content-558140.html>; Link 7 <https://www.cn-healthcare.com/article/20210802/content-558161.html>; Link 8 <http://fj.people.com.cn/n2/2021/0731/c181466-34846905.html>; https://www.sohu.com/a/480645422_162758; Link 9 <https://baijiahao.baidu.com/s?id=1707212055810820390&wfr=spider&for=pc>; Link 10 https://www.163.com/dy/article/GL0C54V605521AFD.html?f=post2020_dy_recommends; <https://news.sina.com.cn/c/2021-10-07/doc-iktzscy8242990.shtml>; Link 11 <https://www.yf-zs.com/zixun/62818.html>; Link 12 <https://epaper.xkb.com.cn/view/1189400>.

Post-vaccination infection by delta variant

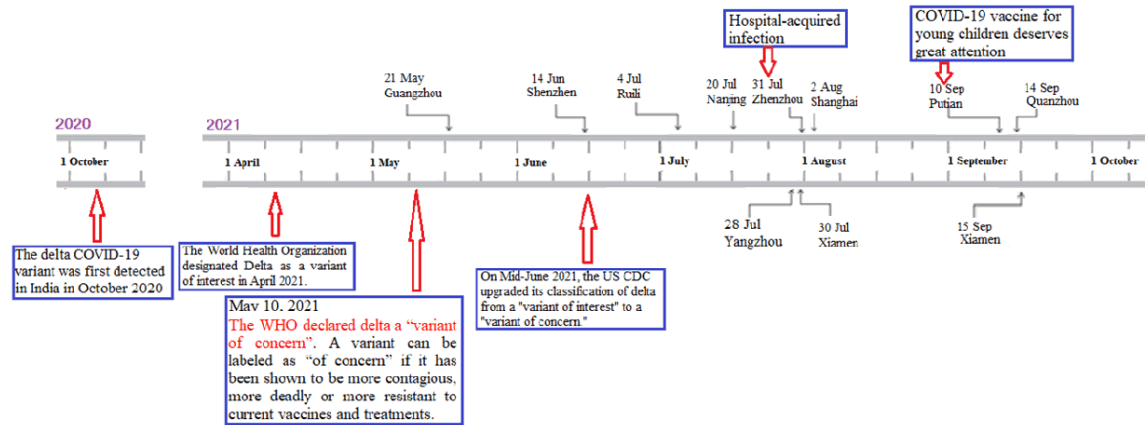


Figure 2. Graph's x-axis (dates from October 1, 2020, to October 1, 2021) is used as a timeline of key events and dynamic profile of imported virus strain B.1.617.2 (delta) transmission during sporadic COVID-19 outbreaks in China. The delta COVID-19 variant was first detected in India in October 2020. The WHO declared the delta variant a "variant of concern" on May 10, 2021. On Mid-June 2021, the US Centers for Disease Control and Prevention upgraded its classification of delta from a "variant of interest" to a "variant of concern".

Guangzhou, Nanjing, Zhangjiajie, and Yangzhou cases were associated with tearoom infection chain, international airport contagion chain, drama-audience contagion chain, chess room infection chain, respectively. Infection chain of Zhengzhou cases was mainly involved in nosocomial infection. Infection chains of Putian cases included family, factory, and school contagion chains. There was the superspreading phenomenon in many cities, for example, Putian, Guangzhou, Nanjing, Zhangjiajie, and Yangzhou.

Discussion

This study provided novel insights into the vital role of SARS-CoV-2 delta variant in the process of sporadic outbreaks with SARS-CoV-2 infections in China from May to October 2021. Our findings were as follows: (1) Routine nucleic acid testing for susceptible populations, including immigrants, international airport staff, is crucial to seeking new imported sporadic outbreak regions in China. (2) Genomic epidemiology study for COVID-19 cases is important to provide insights of the transmission dynamic. (3) The delta variant of SARS-CoV-2 is even more contagious than the older variants. (4) Post-vaccination SARS-CoV-2 infection by delta variant has attracted great attention.

Last year, the delta variant-induced pandemic COVID-19 circulated across most of the globe. The importation of the SARS-CoV-2 virus vari-

ant had posed a significant threat to Chinese epidemic prevention and control. Since inbound travelers and imported goods can carry the virus variant B.1.617.2, the Chinese government had taken strict measures to seeking new imported sporadic outbreak regions through routine nucleic acid testing for susceptible populations over the past few months. These populations included immigrants (Fujian cases), international airport staff (Shenzhen and Nanjing cases) and designated COVID-19 hospital staff (Zhengzhou cases). Our data offers key information to the global community at this important stage of the delta variant-induced COVID-19 pandemic.

The SARS-CoV-2 pandemic induced by the delta variant has forced various countries to make important decisions to repress their spread. In order to uncover the initial spread of this virus delta variants into other countries or regions, health authorities across the world conducted a genomic epidemiology study [12-16]. Page et al. [17] suggested that large-scale SARS-CoV-2 genome sequencing from one region allowed informative epidemiological investigation and strengthened the management of local epidemics. Borisova et al. [1] found that the delta strain appeared in the Moscow region in May 2021, and became prevalent in June, partially displacing other strains. Our data indicated that SARS-CoV-2 delta variant-induced COVID-19 infection had dramatically impacted Chinese regions, partic-

Post-vaccination infection by delta variant

ularly in the Guangzhou, Shenzhen, and Nanjing communities. Genomic epidemiology results from Guangzhou, Shenzhen, and Nanjing cities provided key insights which were involved in the transmission dynamic in these regions and reported important information to pursue strategies to curtail the spread of the delta variant in the Chinese population.

According to the WHO's definition, SARS-CoV-2 variant B.1.617 had three sublineages, including B.1.617.1 sublineage, B.1.617.2, and B.1.617.3. The B.1.617.2 sublineage is known to bear receptor binding domain mutations L452R and T478K [5, 18]. The B.1.617.2 variant has been reported a higher rate of transmission than other variants [19]. The role of the most widespread VOC all over the world in the spread of COVID-19 highlights the importance of researching virus variant B.1.617 transmission through the air. Adenaiye et al. [20] showed that the delta variant circulating now is even more contagious than the alpha variant, suggesting that the delta variants are evolving to be better at becoming airborne. Lam-Hine et al. [21] reported the school outbreak of SARS-CoV-2 B.1.617.2 (delta) variant in May-June 2021, suggesting the delta variant had rapidly spread in unvaccinated populations. High community vaccination populations reduced further transmission of the delta variant. Dougherty [19] addressed the facility outbreak induced by B.1.617.2 (delta) variant in April-May 2021, and found that the B.1.617.2 variant was highly transmissible in indoor sports settings and within households.

Post-vaccination SARS-CoV-2 infection cases by the delta variant was reported in many countries [2, 3, 22-24]. It is known that vaccination is a leading strategy against SARS-CoV-2 during the COVID-19 pandemic all over the world [19, 21]. A report from Israel indicated that delta variant-related hospitalizations and severe disease were mainly reduced after vaccination [22]. Antonelli et al. [2] reported the characteristics of post-vaccination SARS-CoV-2 infection, and discovered that almost all symptomatic cases were vaccinated individuals. The findings of Lam-Hine [21] addressed that the current SARS-CoV-2 vaccines with FDA approval were effective to prevent the delta variant transmission in vaccinated communities. Our post-vaccination delta infection cases,

including cases from Nanjing and Putian, supported the vaccine effectiveness during the post-vaccination era.

Since the SARS-CoV-2 outbreak in 2019, it has evolved rapidly into new variants [25, 26], posing a significant threat to public health. There is the fast transmission of the omicron infection that is now spread all over the world. Compared to the previous delta variant infection, the omicron-induced COVID-19 outbreak was much larger. Although it showed the high transmissibility of the omicron variant, the fatality rate of omicron was lower than that of the delta variant [27]. Multipronged strategies, including human scientific protective behavior and vaccination, are effective to reduce imported SARS-CoV-2 delta variant and omicron variant-related morbidity.

In conclusion, our results showed that the imported SARS-CoV-2 delta variants were easily transmissible in many Chinese cities. Understanding determinants of delta variant transmission, including discovering the source of COVID-19 infection and identifying the transmission chain, is crucial to developing prevention strategies for the COVID-19 outbreak.

Acknowledgements

This project was supported by the Hainan Province Clinical Medical Center and the Key Research and Development Program of Hainan Province (ZDYF2021SHFZ087).

Disclosure of conflict of interest

None.

Address correspondence to: Boqi Xiang, School of Public Health, Rutgers University, New Brunswick, NJ 08901, United States. E-mail: bx67@sph.rutgers.edu; Duozi Wu and Na Li, Department of Anesthesiology, Hainan General Hospital, Haikou 570311, Hainan, China. E-mail: 13976674619@163.com (DZW); 33293996@qq.com (NL)

References

- [1] Borisova NI, Kotov IA, Kolesnikov AA, Kaptelova VV, Speranskaya AS, Kondrasheva LY, Tivanova EV, Khafizov KF and Akimkin VG. Monitoring the spread of the SARS-CoV-2 (coronaviridae: coronavirinae: betacoronavirus; sarbecovirus) variants in the Moscow region using targeted

Post-vaccination infection by delta variant

- high-throughput sequencing. *Vopr Virusol* 2021; 66: 269-278.
- [2] Antonelli M, Penfold RS, Merino J, Sudre CH, Molteni E, Berry S, Canas LS, Graham MS, Kläser K, Modat M, Murray B, Kerfoot E, Chen L, Deng J, Österdahl MF, Cheetham NJ, Drew DA, Nguyen LH, Pujol JC, Hu C, Selvachandran S, Polidori L, May A, Wolf J, Chan AT, Hammers A, Duncan EL, Spector TD, Ourselin S and Steves CJ. Risk factors and disease profile of post-vaccination SARS-CoV-2 infection in UK users of the COVID symptom study app: a prospective, community-based, nested, case-control study. *Lancet Infect Dis* 2022; 22: 43-55.
- [3] Graham MS, Sudre CH, May A, Antonelli M, Murray B, Varsavsky T, Kläser K, Canas LS, Molteni E, Modat M, Drew DA, Nguyen LH, Polidori L, Selvachandran S, Hu C, Capdevila J; COVID-19 Genomics UK (COG-UK) Consortium, Hammers A, Chan AT, Wolf J, Spector TD, Steves CJ and Ourselin S. Changes in symptomatology, reinfection, and transmissibility associated with the SARS-CoV-2 variant B.1.1.7: an ecological study. *Lancet Public Health* 2021; 6: e335-e345.
- [4] Jain VK, Iyengar KP, Garg R and Vaishya R. Elucidating reasons of COVID-19 re-infection and its management strategies. *Diabetes Metab Syndr* 2021; 15: 1001-1006.
- [5] Liu C, Ginn HM, Dejnirattisai W, Supasa P, Wang B, Tuekprakhon A, Nutalai R, Zhou D, Mentzer AJ, Zhao Y, Duyvesteyn HME, López-Camacho C, Slon-Campos J, Walter TS, Skelly D, Johnson SA, Ritter TG, Mason C, Costa Clemens SA, Gomes Naveca F, Nascimento V, Nascimento F, Fernandes da Costa C, Resende PC, Pauvolid-Correa A, Siqueira MM, Dold C, Temperton N, Dong T, Pollard AJ, Knight JC, Crook D, Lambe T, Clutterbuck E, Bibi S, Flaxman A, Bittaye M, Belij-Rammerstorfer S, Gilbert SC, Malik T, Carroll MW, Klenerman P, Barnes E, Dunachie SJ, Baillie V, Serafin N, Dittse Z, Da Silva K, Paterson NG, Williams MA, Hall DR, Madhi S, Nunes MC, Goulder P, Fry EE, Mongkolsapaya J, Ren J, Stuart DI and Screaton GR. Reduced neutralization of SARS-CoV-2 B.1.617 by vaccine and convalescent serum. *Cell* 2021; 184: 4220-4236, e13.
- [6] Delta COVID-19 variant is now in more than 80 countries. <https://www.goodmorningamerica.com/news/story/delta-covid-19-variant-now-80-countries-78339159>.
- [7] Feng M, Ling Q, Xiong J, Manyande A, Xu W and Xiang B. Geographical and epidemiological characteristics of sporadic coronavirus disease 2019 outbreaks from June to december 2020 in China: an overview of environment-to-human transmission events. *Front Med (Lausanne)* 2021; 8: 654422.
- [8] Feng M, Ling Q, Xiong J, Manyande A, Xu W and Xiang B. Occupational characteristics and management measures of sporadic COVID-19 outbreaks from June 2020 to January 2021 in China: the importance of tracking down “patient zero”. *Front Public Health* 2021; 9: 670669.
- [9] Han S and Liu X. Can imported cold food cause COVID-19 recurrent outbreaks? A review. *Environ Chem Lett* 2022; 20: 119-129.
- [10] Feng M, Li Z, Xiong J, Xu W and Xiang B. Geographical and epidemiological characteristics of 3,487 confirmed cases with COVID-19 among healthcare workers in China. *Front Public Health* 2021; 8: 586736.
- [11] Xiang B, Li P, Yang X, Zhong S, Manyande A and Feng M. The impact of novel coronavirus SARS-CoV-2 among healthcare workers in hospitals: an aerial overview. *Am J Infect Control* 2020; 48: 915-917.
- [12] Ballesteros N, Muñoz M, Patiño LH, Hernández C, González-Casabianca F, Carroll I, Santos-Vega M, Cascante J, Angel A, Feged-Rivadeneira A, Palma-Cuero M, Flórez C, Gomez S, van de Guchte A, Khan Z, Dutta J, Obla A, Alshammary HA, Gonzalez-Reiche AS, Hernandez MM, Sordillo EM, Simon V, van Bakel H, Paniz-Mondolfi AE and Ramírez JD. Deciphering the introduction and transmission of SARS-CoV-2 in the Colombian Amazon Basin. *PLoS Negl Trop Dis* 2021; 15: e0009327.
- [13] Simmonds P. Pervasive RNA secondary structure in the genomes of SARS-CoV-2 and other coronaviruses. *mBio* 2020; 11: e01661-20.
- [14] Chen L, Zody MC, Di Germanio C, Martinelli R, Mediavilla JR, Cunningham MH, Composto K, Chow KF, Kordalewska M, Corvelo A, Oschwald DM, Fennessey S, Zetkalic M, Dar S, Kramer Y, Mathema B, Germer S, Stone M, Simmons G, Busch MP, Maniatis T, Perlin DS and Kreiswirth BN. Emergence of multiple SARS-CoV-2 antibody escape variants in an immunocompromised host undergoing convalescent plasma treatment. *mSphere* 2021; 6: e0048021.
- [15] Genome Canada Canadian COVID-19 Genomics Network (CanCOGeN) and the Canadian Public Health Laboratory Network CanCOGeN Working Group. Canadian national COVID-19 genomics surveillance priorities for existing and emerging variants of concern. *Can Commun Dis Rep* 2021; 47: 139-141.
- [16] Marquitti FMD, Coutinho RM, Ferreira LS, Borges ME, Portella TP, Silva RLPD, Canton O, Poloni S, Franco C, Coelho V, Barberia L, Bolle M, Boing AC, Donalisio MR, Boing AF, Silva AAMD, Prado PI, Veras MASM and Kraenkel RA. Brazil in the face of new SARS-CoV-2 variants: emergencies and challenges in public health. *Rev Bras Epidemiol* 2021; 24: e210022.

Post-vaccination infection by delta variant

- [17] Page AJ, Mather AE, Le-Viet T, Meader EJ, Alikhan NF, Kay GL, de Oliveira Martins L, Aydin A, Baker DJ, Trotter AJ, Rudder S, Tedim AP, Kolyva A, Stanley R, Yasir M, Diaz M, Potter W, Stuart C, Meadows L, Bell A, Gutierrez AV, Thomson NM, Adriaenssens EM, Swingler T, Gilroy RAJ, Griffith L, Sethi DK, Aggarwal D, Brown CS, Davidson RK, Kingsley RA, Bedford L, Coupland LJ, Charles IG, Elumogo N, Wain J, Prakash R, Webber MA, Smith SJL, Chand M, Dervisevic S and O'Grady J, The Covid-Genomics UK Cog-UK Consortium. Large-scale sequencing of SARS-CoV-2 genomes from one region allows detailed epidemiology and enables local outbreak management. *Microb Genom* 2021; 7: 000589.
- [18] WHO narrows in on Delta COVID variant. June 2, 2021. <https://medicalxpress.com/news/2021-06-narrows-covid-delta-variant.html>.
- [19] Dougherty K, Mannell M, Naqvi O, Matson D and Stone J. SARS-CoV-2 B.1.617.2 (delta) variant COVID-19 outbreak associated with a gymnastics facility - Oklahoma, April-May 2021. *MMWR Morb Mortal Wkly Rep* 2021; 70: 1004-1007.
- [20] Adenaiye OO, Lai J, de Mesquita PJB, Hong F, Youssefi S, German J, Tai SS, Albert B, Schanz M, Weston S, Hang J, Fung C, Chung HK, Coleman KK, Sapoval N, Treangen T, Berry IM, Mullins K, Frieman M, Ma T and Milton DK; University of Maryland StopCOVID Research Group. Infectious SARS-CoV-2 in exhaled aerosols and efficacy of masks during early mild infection. *Clin Infect Dis* 2021; [Epub ahead of print].
- [21] Lam-Hine T, McCurdy SA, Santora L, Duncan L, Corbett-Detig R, Kapusinszky B and Willis M. Outbreak associated with SARS-CoV-2 B.1.617.2 (delta) variant in an elementary school - Marin County, California, May-June 2021. *MMWR Morb Mortal Wkly Rep* 2021; 70: 1214-1219.
- [22] Haas EJ, Angulo FJ, McLaughlin JM, Anis E, Singer SR, Khan F, Brooks N, Smaja M, Mircus G, Pan K, Southern J, Swerdlow DL, Jodar L, Levy Y and Alroy-Preis S. Impact and effectiveness of mRNA BNT162b2 vaccine against SARS-CoV-2 infections and COVID-19 cases, hospitalisations, and deaths following a nationwide vaccination campaign in Israel: an observational study using national surveillance data. *Lancet* 2021; 397: 1819-1829.
- [23] He Z, Xiang H, Manyande A, Xu W, Fan L and Xiang B. Epidemiological characteristics of sporadic nosocomial COVID-19 infections from June 2020 to June 2021 in China: an overview of vaccine breakthrough infection events. *Front Med (Lausanne)* 2021; 8: 736060.
- [24] Huang Y, Ling Q, Manyande A, Wu D and Xiang B. Brain imaging changes in patients recovered from COVID-19: a narrative review. *Front Neurosci* 2022; 16: 855868.
- [25] Sun Y, Lin W, Dong W and Xu J. Origin and evolutionary analysis of the SARS-CoV-2 omicron variant. *J Biosaf Biosecur* 2022; 4: 33-37.
- [26] Liu C, Xiang H, Manyande A, Xu W, Fan L, Zhang Y and Xiang B. Epidemiologic characteristics and differential management strategies of seven case series with COVID-19 outbreaks caused by asymptomatic carriers from June 2020 to May 2021 in China. *Am J Transl Res* 2022; 14: 2244-2255.
- [27] Zhao Y, Huang J, Zhang L, Lian X and Wang D. Is the omicron variant of SARS-CoV-2 coming to an end? *Innovation (Camb)* 2022; 3: 100240.