

## **A SARS-CoV-2 Delta variant outbreak on airplane: vaccinated air passengers are more protected than unvaccinated**

Qiuying Lv, PhD<sup>1</sup>†, Dongfeng Kong<sup>1</sup>†, MPH, Yaqing He<sup>2</sup>†, PhD, Yan Lu, PhD<sup>1</sup>, Long Chen, MA<sup>2</sup>, Jin Zhao, PhD<sup>3</sup>, Siyang Feng, MA<sup>3</sup>, Yixiong Chen, MPH<sup>4</sup>, Jia Wan, MMed<sup>1</sup>, Ying Wen, PhD<sup>1</sup>, Wei Gao, MMed<sup>1</sup>, Zhigao Chen, MMed<sup>1</sup>, Xiujuan Tang, Mphil<sup>1</sup>, Shujiang Mei, MMed<sup>1</sup>, Xuan Zou, MMed<sup>1</sup>\* and Tiejian Feng, MMed<sup>1</sup>\*

<sup>1</sup>Department of Communicable Diseases Control and Prevention, Shenzhen Center for Disease Control and Prevention, Shenzhen 518055, China, <sup>2</sup>Department of Pathogenic Biology, Shenzhen Center for Disease Control and Prevention, Shenzhen 518055, China, <sup>3</sup>Department of HIV/AIDS Control and Prevention, Shenzhen Center for Disease Control and Prevention, Shenzhen 518055, China, <sup>4</sup>Department of Communicable Diseases Control and Prevention, Shenzhen Boan District Center for Disease Control and Prevention, Shenzhen 518001, China.

\*To whom correspondence should be addressed. Prof. Tiejiang Feng, MMed.

Shenzhen Center for Disease Control and Prevention, 8 Longyuan Rd, Shenzhen

518055, China

fengtjcdc@163.com; These senior authors contributed equally to this article.

† Joint first authors.

**Key words:** SARS-CoV-2, Delta variant, inflight transmission, vaccine

**Highlight:** In-flight transmission of SARS-CoV-2 Delta variant could occur on airplane, and close contact is the main mode of transmission. Vaccination still protects against the Delta variant transmission.

UNCORRECTED MANUSCRIPT

An emerging variant of SARS-CoV-2, Delta (Pango lineage B.1.617.2) was labelled as one of the Variants of Concern (VOCs) on June, 2021 due to the increased transmissibility.<sup>1</sup> Other unaffected countries face increased risk of importation of the Delta-related cases. A local outbreak was resulted from the Delta variant imported cases from abroad in the cities of South China in May, of which the transmissibility was estimated to be increased by 100%.<sup>2</sup> International flights are undeniably a high-risk route for case importation.<sup>3</sup> It is essential to estimate the risk of the Delta variant associated transmission in flight.<sup>4</sup> We conducted a cohort study on the international airplane in order to understand the full course of transmission in flight.

An International airplane Flight CA868 with 203 passengers took off from South Africa on June 9 and arrived at Shenzhen, China on June 10. All passengers were required to have their negative PCR and IgM assays done at any two designated testing institutions (Pathcare, AMPATH, Lancet) within 48 hours before boarding (Supplementary Methods). Inbound passengers are mandatory to wear masks throughout the entire flight and on the way to the quarantine hotel. An online questionnaire survey was conducted among all passengers after the verbal consent (approved by the Medical Ethics Committee of Shenzhen Center for Disease Control and Prevention).

From the arrival of Flight CA868 on June 10 to the full 14 days of passenger quarantine, 39 passengers were tested positive for SARS-CoV-2 by RT-PCR. We successfully sequenced the viral RNA of 30 PCR-positive cases, and the rest 9 cases were undetectable due to low viral load. In terms of the phylogenetic analysis of genome sequence (Supplementary Methods), 27 cases were classified to the B.1.617.2 variant,

and the other 3 cases respectively belonged to B.1.1.7 variant (Seat No.52E), B.1.351 variant (Seat No.49E), and C.1.2 variant (Seat No.57C) based on the PANGO lineage (Supplementary Figure1).<sup>5</sup> Of the 27 Delta variant positive cases, three were tested positive on the day of entry (51C, 39A and 49H) and the other 24 were between 13 and 24 June. Thus, 6 PCR-positive cases (52E, 49E, 57C, 51C, 39A, 49H) were identified to be the primary cases (G1), who were likely to be infected in South Africa. The three B.1.617.2 variant G1 cases (51C, 39A and 49H) had the significant difference of mutation sites of viral sequence, while the 51C case had the highly homologous genome sequences of the other 24 cases with the B.1.617.2 variant (Supplementary Figure 2). Therefore we identified the 51C case to be the index case, and transmitted to 20 cases of the secondary generation (G2) during the flight and 4 cases of the third generation (G3) due to sharing rooms in the quarantine hotel (Figure 1). On June 14, when the number of PCR positive cases peaked at 22, a local custom officer in the airport of China was detected positive for PCR on the same day ([http://wjw.sz.gov.cn/yqxx/content/post\\_8864099.html](http://wjw.sz.gov.cn/yqxx/content/post_8864099.html)). He reported to have an investigation on the 51C case on June 10 upon entry. As the virus genome sequences of the custom officer and the 51C index case were same, it further justified the in-flight transmission from the index case in pre-symptomatic phase.

In the cohort study, 197 passengers were on risk of the 51C index case, and 33 flight-associated cases were reported during the quarantine. The multivariate logistic regression model (Supplementary Methods) suggested that, passengers sitting within three rows of the index case had a higher attack rate (30.9%,17/55), compared with that

of those located three rows away from the index case (11.3%,16/142) (risk ratio 4.22, 95% CI 1.55–11.50). The risk of contracting the virus was 9.41 (95% CI 2.87–30.79) times higher for passengers who shared rooms with others in quarantine hotels than those who were isolated alone. Use of hand sanitizer showed the significant protection in the multivariate regression model (risk ratio 0.24, 95% CI 0.09–0.66). Vaccination was suggested to have a protective effect (risk ratio 0.33, 95% CI 0.08–1.43), but not statistically significant in the multivariate analysis (Table 1).

Our study was one of the earliest to provide significant evidence that the B.1.617.2 variant led to an in-flight transmission. Our investigation found no clusters of cases in workplaces, tour groups or confined environments in the airport of South Africa, thus suggesting the limited likelihood of infection in South Africa. There were no cases reported in business class and among crew of flight, and 25 (64.1%) cases were located in Economy Class 3. A cluster of cases who were seated close to the index case (51C) on the Economy Class 3 were found, and this could be explained by the droplets or contact transmission, rather than the air conditioning filtration system (Figure 1).<sup>6</sup> It was considered that long-haul flights may increase the likelihood of passengers occasionally taking off their masks for reasons such as eating, drinking and uncomfortable breathing due to the long period of masking.<sup>7</sup> Our data showed that 87.3% (172/197) of travelers had ever taken off their masks during the flight. Occasional contact on flight or during the process of deplaning to transfer to the quarantine hotel possibly explained the cases seated in the Economy Class 1 and 2 cabins, t. We strongly recommend that passengers proceed in order on the plane as well as during the process

of deplaning to transfer to the quarantine hotel.

We are pleased to find that the vaccine is still effective against the Delta variant. In our study, vaccinated passengers were 74% less likely to be infected compared with those without vaccination. In general, 24.1% (49 /203) of the passengers reported a history of COVID-19 vaccination, while only a 10.2% (4/39) of the cases had the vaccination history. For those high-risk countries, increased risks of transmission might be associated with low vaccination rates in. Two United Kingdom studies reported vaccination could reduce symptomatic disease and hospitalization of the Delta variant.<sup>8</sup> With the gradual recovery of the global aviation industry, promotion of the vaccination would be beneficial to block the in-flight transmission.

### **Author's contribution**

Q.L., D.K. and Y.H. contributed equally to this article as the first author who conceived the idea and wrote the draft. T.F. and X.Z. contributed equally to this article as correspondence authors who worked collaboratively to edit and review the manuscript. L.C., J.Z., Y.L. and S.Y. conducted the data analysis. Y.C., J.W. and Y.W. drafted the figures. W.G., Z.C., X.T. and S.M. edited some parts of the manuscript.

### **Funding**

This work was supported by the Key Project of Shenzhen Science and Technology Innovation Commission (JCYJ20210324115411030), the Non-profit Central Research Institute Fund of Chinese Academy of Medical Sciences (2020-PT330-006), Shenzhen Key Medical Discipline Construction Fund (SZXK064), Shenzhen San-Ming Project of Medicine in Shenzhen (SZSM202011008), Shenzhen Municipal Technological Project (JSGG20200225152848007).

### **Acknowledgement**

The authors would like to thank Yingluan Zhang, Yuan Li, Lan Wei, Bin Cao, Huawei Xiong, Cong Cheng, Shule Xu, and Shitong Gao in Shenzhen Center for Disease Control and Prevention for their help in questionnaire design and data collection. The authors are also grateful to collaborating staff from the Baoan Center for Disease Control and Prevention for their field work. The authors are grateful to Dr. Huachun Zou and Dr. Shenglan Xiao for their comments on the questionnaire design and chart design.

**Conflicts of interest:** None declared.



## References

1. Campbell F, Arscher B, Laurenson-Schafer H et al. Increased transmissibility and global spread of SARS-CoV-2 variants of concern as at June 2021. *Euro surveillance : bulletin Europeen sur les maladies transmissibles = European communicable disease bulletin* 2021; **26**:2100509. doi:[10.2807/1560-7917.ES.2021.26.24.2100509](https://doi.org/10.2807/1560-7917.ES.2021.26.24.2100509).
2. Zhang M, Xiao J, Deng A, et al. Transmission Dynamics of an Outbreak of the COVID-19 Delta Variant B.1.617.2 — Guangdong Province, China, May–June 2021. *China CDC Weekly* 2021; **3**: 584-586.. doi: [10.46234/ccdcw2021.148](https://doi.org/10.46234/ccdcw2021.148).
3. Freedman DO, Wilder-Smith A. In-flight transmission of SARS-CoV-2: a review of the attack rates and available data on the efficacy of face masks. *J Travel Med* 2020; **27**: taaa178. <https://doi.org/10.1093/jtm/taaa178>.
4. Rosca EC , Carl H , Spencer EA , et al. Transmission of SARS-CoV-2 associated with aircraft travel: A systematic review. *J Travel Med*. 2021 Sep 3:taab133. doi: [10.1093/jtm/taab133](https://doi.org/10.1093/jtm/taab133). Online ahead of print. PMID: 34480171
5. Rambaut A, Holmes EC, O'Toole A, et al. A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. *Nat Microbiol* 2021; **6**: 415. doi: [10.1038/s41564-020-0770-5](https://doi.org/10.1038/s41564-020-0770-5).
6. Swadi T, Geoghegan JL, Devine T, et al. Genomic Evidence of In-Flight Transmission of SARS-CoV-2 Despite Predeparture Testing. *Emerg Infect Dis* 2021; **27**: 687-93. doi: [10.3201/eid2703.204714](https://doi.org/10.3201/eid2703.204714).
7. Khanh NC, Thai PQ, Quach HL, et al. Transmission of SARS-CoV 2 During

Long-Haul Flight. *Emerg Infect Dis* 2020; **26**: 2617-24.6.

8. COVID-19 Weekly Epidemiological Update. 22 June 2021.

[https://www.who.int/publications/m/item/weekly-epidemiological-update-on-covid-](https://www.who.int/publications/m/item/weekly-epidemiological-update-on-covid-19---22-june-2021)

[19---22-june-2021](https://www.who.int/publications/m/item/weekly-epidemiological-update-on-covid-19---22-june-2021), accessed 22 June 2021.

UNCORRECTED MANUSCRIPT

**Table 1 Risks for SARS-CoV-2 transmission among 197 exposed passengers on Flight CA868**

<b>Exposed factors</b>	<b>PCR- Positive, no. (%)†</b>	<b>PCR- Negative, no. (%)</b>	<b>Crude Risk ratio (95% CI)</b>	<b>Adjusted Risk ratio (95% CI)</b>
	<b>33(16.8)</b>	<b>164(80.8)</b>		
<b>Age (Mean±SD)</b>	41.76±14.91	36.82±14.06	1.03 (1.00-1.06)	1.03 (1.00-1.07)
<b>Gender</b>				
Male	24(72.7)	110(82.1)	1.31 (0.57-3.01)	2.81 (0.93-8.42)
Female	9(27.3)	54(32.9)		
<b>Vaccination</b>				
Vaccinated	3(9.1)	45(27.4)	0.26 (0.08-0.91)	0.33 (0.08-1.43)
Non-vaccinated	30(90.9)	119(72.6)		
<b>Seating location</b>				
Within three rows	17(51.5)	38(23.2)	3.52 (1.63-7.63)	4.22 (1.55-11.50)
Three rows away	16 (48.5)	126 (76.8)		
<b>Sharing room in quarantine hotel</b>				
Yes	13(39.4)	31(18.9)	2.79 (1.25-6.21)	9.41 (2.87-30.79)
No	20(60.6)	133(81.1)		
<b>Use of hand sanitizer*</b>				
Yes	14(51.9)	119 (74.4)	0.37 (0.16-0.85)	0.24 (0.08-0.66)
No	13(48.1)	41(25.6)		

† Six primary cases were excluded from the cohort.

\* 187 participants were available for the analyses of “Hand sanitizer”, 10 have missing data.

**Figure Legends:**

Table 1 Risks for SARS-CoV-2 transmission among 197 exposed passengers on Flight CA868

Figure 1 Spatial distribution of primary and secondary cases of SARS-CoV-2 aboard flight from Johannesburg, South Africa to Shenzhen, China, on June 10, 2021. The color of the seat fill represents the four generation cases. Red-primary case (G1); Yellow- the secondary case (G2), Purple- 3<sup>rd</sup> generation case (G3); Blue- the 4<sup>th</sup> generation case (G4). The shape of the seat filling represents the different strains of genetic sequencing. Solid box-the same Delta strains comparing the index case; Diamond, Triangle, Circle: Other type of strains; Dotted box- Failed to sequence due to low virus load; Blue Frame- Sinopharm Vaccine; Green Frame- Sinovac Vaccine; Red Frame – Other vaccine; L: Toilet; G: Workshop.

