

Transmission of Omicron (B.1.1.529) - SARS-CoV-2 Variant of Concern in a designated quarantine hotel for travelers: a challenge of elimination strategy of COVID-19

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With the global evolution of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), the causative agent of coronavirus disease 2019 (COVID-19), for almost 2 years, various control strategies have been utilized around the world. While most of the western countries gradually lifted the border control and quarantine measures, elimination strategy aiming at “zero COVID-19” remains in place in Western Pacific Region such as mainland China and Hong Kong, where inbound travelers are required to undergo quarantine in designated quarantine hotels (DQHs) for up to 21 days. However, not designed for the purpose of quarantine, especially for infectious diseases with potential airborne spread, DQHs may be potential venues for COVID-19 transmission.¹ We recently reported an incident of community outbreak of imported SARS-CoV-2 beta variant due to possible intra-hotel transmission in a DQH.² Smoke tests in DQHs demonstrated that aerosols could leak out from guest rooms to the corridors, and guests in neighboring rooms may inhale the infectious aerosols when the doors were opened.³ We also conducted a serological survey of the hotel staff members in the implicated DQHs, which showed no serological evidence of guest-to-staff-to-guest transmission of COVID-19.⁴ This provides reassurance that our infection control training of hotel staff members, which was similar to the training of healthcare workers in hospitals and community treatment facilities, was effective at preventing intra-hotel transmission to staff.⁵ After this incident, portable air purifiers with high-efficiency particulate air filters were installed in the corridors of DQHs. Residents are

required to wear surgical mask for the purpose of mutual protection while opening the doors.

Despite these additional measures, another incident of SARS-CoV-2 transmission inside a DQH was reported.⁶ The asymptomatic index case (M/36), who had completed two doses of BNT162b2 mRNA COVID-19 vaccine (BioNTech) in June 2021, had anti-spike protein receptor-binding domain (anti-RBD) of 1142 AU/ml (14 November 2021). The secondary case (M/62) also completed two doses of BioNTech in May 2021. He developed respiratory symptoms on day 8 after arrival and clinically stable after hospitalization, with anti-RBD of 250 AU/ml (19 November 2021). Both cases had no chronic illness. Whole genome sequences of specimens collected from the two cases were different by only 1 nucleotide and belonged to the Omicron variant (B.1.1.529 lineage).⁶

To understand the mechanism of transmission, we performed smoke test during our on-site investigation on 22 November 2021. Smoke test demonstrated stagnant air in the corridor (width: 1.5 m; height: 2 m) adjoining the two rooms (index case: room A; secondary case: room B), and there was brief outward movement of air when the doors of the guest rooms were opened abruptly. Therefore, the virus-laden aerosol may escape into the guest room of the secondary case when the door was opened, either slightly or widely (Figure 1a and 1b). In fact, the index case did not wear mask or just wore cloth mask when opening the door to fetch food or discard garbage bags upon our direct questioning.

We also assess the extent of environmental contamination. Environmental swabs were taken from room B using methods described previously.⁷ One of 8 (12.5%) specimens collected from high-level non-reachable surfaces (wall or ceiling; 50 × 20 cm in size) on 22 November 2021 (3 days after transfer-out of the case) tested positive for SARS-CoV-2 by RT-PCR (cycle threshold

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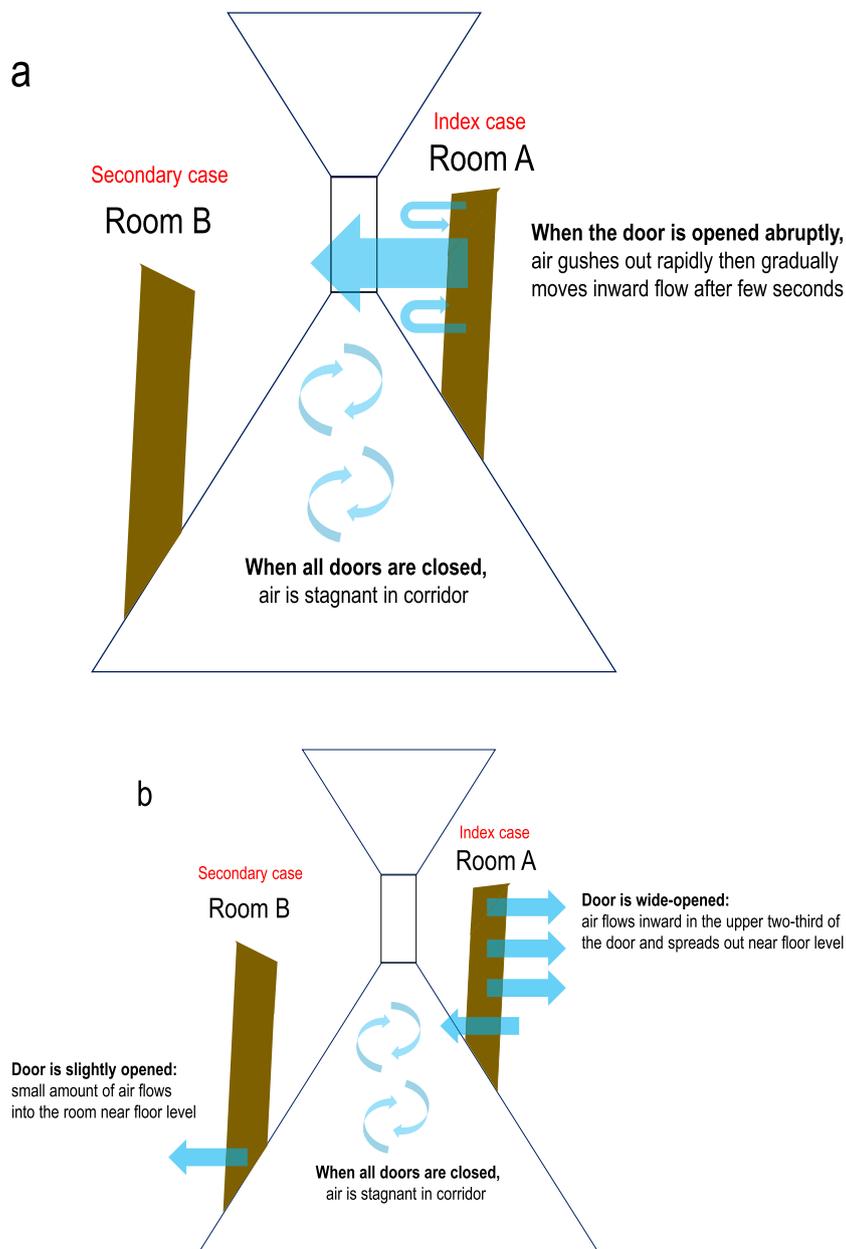


Figure 1. Schematic representation of smoke test to demonstrate the potential mechanism of airborne transmission of Omicron (B.1.1.529), SARS-CoV-2 Variant of Concern between the rooms in a designated quarantine hotel for travelers.

Figure 1a: To demonstrate the direction of airflow between the guest room and corridor when the door is opened abruptly. The windows were closed in the corridor.

Figure 1b: To demonstrate the direction of airflow between the guest room and corridor when the door is opened, either slightly or widely. When the door was widely opened, we demonstrated inward airflow in the upper two-third of the room door and outward airflow near the floor level. When the door was slightly opened, we also showed slightly inward airflow near the floor. The windows were closed in the corridor.

value: 39). Partial spike gene sequence of this environmental swab had a nucleotide identity of 100% with those from the cases, suggestive of air dispersal of Omicron variant. Furthermore, 21 of 39 (53.8%) commonly touched surfaces were positive in room B, with positive

rate 8 times higher than the contamination rate in quarantine rooms reported previously.⁸

SARS-CoV-2 B.1.1.529 was first identified in a specimen collected on 9 November 2021 and was reported to the World Health Organization on 24 November 2021.

Its emergence was associated with a steep increase of COVID-19 infections in South Africa.⁹ Potential air dispersal, extensive environmental contamination, and airborne transmission of Omicron variant have been demonstrated in this incident, which likely will pose a greater challenge to the “zero COVID” strategy in Hong Kong. Nosocomial transmission of COVID-19 can be prevented by the utilization of airborne infection isolation facilities in hospitals.¹⁰ For the DQHs, we may maximize the flow rate of air exhaust in guest rooms, further increase fresh air supply, and supplement with air purifiers in corridors, in addition to enhanced training of environment disinfection and use of personal protective equipment. Alternatively, quarantine camp with individual isolation unit and natural ventilation in the open area or more frequent testing may be considered for persons returning from high-risk areas with Omicron transmission.

Declaration of Competing Interest

All authors declare no conflict of interest.

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Author’s contribution

S-CW and VC-CC had roles in study design, data analysis, and writing up of the manuscript. S-CW, AK-WA, CH, DCL, K-YY, and VC-CC had roles in outbreak investigation. KK-WT and DCL had roles in whole genome sequencing and phylogenetic analysis. LX, AW-HC, JDI, W-MC, and H-WT had roles in laboratory work. S-CW, AK-WA, and LL-HY had roles in collection of environmental and clinical specimens. All authors reviewed and approved the final version of the manuscript.

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Data sharing

The partial spike gene sequence of the environmental swab collected from high-level non-reachable surface has been deposited into GISAID. The accession number is EPI_ISL_6841982-hCoV-19/Hong Kong/HKU-211129-003/2021.

Supplementary materials

Supplementary material associated with this article can be found in the online version at doi:[10.1016/j.lanwpc.2021.100360](https://doi.org/10.1016/j.lanwpc.2021.100360).

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