

Letter to the Editor

Environmental contamination of a quarantine hotel via SARS-CoV-2 positive travellers

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Quarantine of international travelers at arrival, often in specialized quarantine centers or hotels, is a measure frequently used by many countries to reduce the risk of importation.^{1–3} Evidence of the risk for transmission by contaminated environment or fomites via infected travellers from such quarantine facilities is lacking. Here we report on the extent of environmental contamination of quarantine rooms via two SARS-CoV-2 VOCs positive travellers to China.

Two non-related Chinese female supermarket workers in Manila, Philippines, returned on the same flight to Qingdao, China on 23 March 2021; the nonstop flight lasted ~4 h. About 1 day before departure, nasopharyngeal swabs were sampled in the Philippines and both were negative by polymerase chain reaction (PCR) testing. On arrival at Qingdao airport, in line with routine procedures, a questionnaire was administered, body temperature was measured and nasopharyngeal swab sampling was done. As they had no fever and other symptoms on arrival, they were transferred to the designated hotel for 14-day quarantine while waiting for the results of nucleic acid testing of SARS-CoV-2.

As shown in [Figure 1](#), two whole-genome SARS-CoV-2 sequences were obtained and referred to as 2021QDCV-2672 from Case 1 and 2021QDCV-2665 from Case 2, respectively. By comparison of the assembled sequence with the published COVID-19 database, we obtained the phylogenetic relationship tree of the virus strains ([Figure 1](#)). 2021QDCV-2672 was a full-length SARS-CoV-2 sequence of 29 849 bp, with the characteristic mutation site (the mutations of the spike protein N501Y, A570D, D614G, P681H, T716I, S982A, D1118H) of the variant of concern B.1.1.7 first reported in the UK (Alpha variant). 2021QDCV-2665 was a full-length SARS-CoV-2 sequence of 29 842 bp, which contained the

characteristic mutation site (the mutations of the spike protein D80A, K417N, E484K, N501Y, D614G and A701V) of the variant strain B.1.351 (Beta variant).

The two travellers had stayed ~20 h in two separate quarantine rooms, before being transferred to the designated hospital for further monitoring and isolation once the PCR result came back as positive. Environmental surfaces from their quarantine rooms were sampled and tested for SARS-CoV-2, using the same methods as reported in a previous study.⁴

In total, 22 environmental samples collected from 11 sampling sites of each quarantine room were taken. As shown in [Figure 1](#), overall, 12 of 22 (54.5%) samples were tested positive for SARS-CoV-2. For Case 1, 7 of 11 samples (63.6%) were tested positive for SARS-CoV-2, and 5 of 11 (45.5%) samples were tested positive for Case 2. In the bathroom, the positivity rate of Case 1 was 100% (7/7) with the Ct values ranging from 29.08 to 39.95 (average value: 35.97), whilst the positivity rate for Case 2 in the bathroom was 71.4% (5/7) with Ct values ranging from 38.59 to 39.91 (average value: 39.29). Except for the television (TV) remote controller (Ct: 36.17), the rest of samplings from the two bedrooms were negative for both Case 1 and Case 2.

A telephone questionnaire survey was conducted with both travellers with regards to their hygiene measures such as face washing, hand washing, tooth brushing, bathing and excreting in the quarantine room were interviewed by telephone. Both cases had engaged in all the usual hygiene activities. Case 1 did not watch TV, whereas Case 2 did. While isolated in the quarantine room, they did not use hand disinfectants and did not wear face masks.

In conclusion, a high proportion of environmental samples from two quarantine rooms used by two asymptomatic

