

SYNOPSIS

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Review of “Probable transmission of SARS-CoV-2 Omicron variant in quarantine hotel, Hong Kong, China, November 2021”

Article citation: Gu H, Krishnan P, Ng DYM, Chang LDJ, Liu GYZ, Cheng SSM, et al. Probable transmission of SARS-CoV-2 Omicron variant in quarantine hotel, Hong Kong, China, November 2021. *Emerg Infect Dis.* 2021 Dec 03 [Epub ahead of print]. Available from: <https://doi.org/10.3201/eid2802.212422>

One-minute summary

- The authors report detection of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) Omicron (B.1.1.529) variant of concern (VOC) in an asymptomatic, fully-vaccinated traveller (case A) in a quarantine hotel in Hong Kong, China, along with potential transmission to a fully vaccinated traveller in a room across the corridor (case B).
- Case A arrived in Hong Kong on November 11, 2021 from South Africa, and case B arrived on November 10, 2021 from Canada. Both cases were previously fully vaccinated with two doses of the Pfizer BioNTech Comirnaty COVID-19 vaccine, and both had tested negative by reverse transcription polymerase chain reaction (RT-PCR) within 72 hours before arrival to the Hong Kong airport and quarantine hotel.
- Case A was asymptomatic, tested positive for SARS-CoV-2 on November 13, 2021 and was hospitalized and isolated the next day. Case B had mild symptoms develop on November 17, 2021, tested positive for SARS-CoV-2 on November 18, 2021 and was hospitalized on the same day. No other guests on the hotel floor and no hotel staff tested positive in the subsequent study period.
- Hotel closed-circuit television footage confirmed neither case left their rooms during the quarantine period, and only opened their doors to pick up meals delivered to their rooms. No other persons entered either room and no items were shared between rooms. RT-PCR tests were conducted at 3-day intervals and, due to different arrival dates, the two cases were not likely tested on the same days.
- Viral sequencing confirmed both cases were the Omicron VOC, and sequencing between cases differed by only one nucleotide. Authors suggest airborne transmission across the corridor is the most probable mode of transmission.

Additional information

- Omicron was designated as a VOC by the World Health Organization (WHO) on November 25, 2021, and as of December 9, 2021 the Global Initiative on Sharing All Influenza Data (GISAID) reported 42 countries have shared 1,292 Omicron genome sequences.¹
- The cycle threshold (C_t) values for cases are reported: case A, C_t value=18; case B, C_t value=19. Authors report these C_t values indicate high viral loads.
- Viral sequencing was conducted from respiratory swab samples collected from cases A and B at the WHO laboratory at the University of Hong Kong.
- Authors compare Omicron's sequencing profile, which revealed a large number of mutations ($n=57$), with other VOCs and variants of interest (VOIs). Of the 35 mutations found on Omicron's spike protein, 43% were also identified in other VOCs and VOIs, and 31% were found only in VOCs (Alpha, $n=6$; Beta, $n=4$; Gamma, $n=5$; Delta, $n=4$). Several of the 22 non-spike protein mutations identified are not novel and have been identified in other SARS-CoV-2 variants.
- It is reported that the large number of mutations may theoretically impact RT-PCR tests results, virus antigenicity, transmissibility, replication, disease severity or immune escape. However, more evidence is needed to know any true impact of the Omicron VOC on these virus and disease characteristics.

PHO reviewer's comments

- This report provides a brief overview of two cases of Omicron VOC identified in a quarantine hotel; however, additional details would be beneficial to better understand the potential mechanisms of transmission. For example, closed-circuit television camera footage was used to confirm no direct contact or shared items between the cases and more information on timing between door openings, and distance between their respective hotel room doors would have been of interest. Airflow direction and ventilation within the hotel hallway would also have been of interest.
- The authors report that the viral genomes differed by only 1 nucleotide; however, 6 unrelated sequences from Africa in the appendix also only differ by 1-2 nucleotides. Given the short time frame and lack of genetic heterogeneity of Omicron, genetic sequencing cannot rule out that case B acquired their infection in Canada. However, the author's conclusion are the most likely explanation. Details of the travellers' movements and experiences (e.g., on their flights) prior to arrival at the quarantine hotel are not reported. While it is reported no cases were identified among other hotels guests or staff, the follow up period and testing strategy are not described. Findings from this report should be interpreted within the limitations of a brief case report.
- PHO's recent report on the Omicron VOC reported it has over 50 mutations,² which is consistent with Gu et al.'s (2021) investigation identifying 57 mutations. Also consistent between reports is discussion around the need for more evidence to determine with certainty if and how Omicron mutations will impact transmissibility, disease severity, or vaccine effectiveness.

Additional references

1. GISAID. Tracking of variants [Internet]. Munich: Freunde von GISAID; 2021 [cited 2021 Dec 09] Available from: <https://www.gisaid.org/hcov19-variants/>
2. Ontario Agency for Health Protection and Promotion (Public Health Ontario). COVID-19 variant of concern Omicron (B.1.1.529): risk assessment [Internet]. Toronto, ON: Queen's Printer for Ontario; 2021 Nov 29 [cited 2021 Dec 06]. Available from: https://www.publichealthontario.ca/-/media/documents/ncov/voc/2021/11/covid-19-omicron-b11529-risk-assessment.pdf?sc_lang=en.

Citation

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