Original Article

Air dispersal of severe acute respiratory coronavirus virus 2 (SARS-CoV-2): Implications for hospital infection control during the fifth wave of coronavirus disease 2019 (COVID-19) due to the SARS-CoV-2 omicron variant in Hong Kong

Shuk-Ching Wong MNurs1, Veronica Wing-Man Chan MPH1, Lithia Lai-Ha Yuen MNurs1, Christine Ho-Yan AuYeung MNurs1, Jessica Oi-Yan Leung MNurs1, Chi-Kuen Li MNurs1, Monica Oi-Tung Kwok BNurs1, Simon Yung-Chun So MSc2, Jonathan Hon-Kwan Chen PhD2, Anthony Raymond Tam MBBS3, Ivan Fan-Ngai Hung MD3, Kelvin Kai-Wang To MD4, Janice Yee-Chi Lo FRCPA5, Kwok-Yung Yuen MD4 and Vincent Chi-Chung Cheng MD1,2

1Infection Control Team, Queen Mary Hospital, Hong Kong West Cluster, Hong Kong Special Administrative Region, China, 2Department of Microbiology, Queen Mary Hospital, Hong Kong Special Administrative Region, China, 3Department of Medicine, Li Ka Shing Faculty of Medicine, The University of Hong Kong, Hong Kong Special Administrative Region, China, 4Department of Microbiology, Li Ka Shing Faculty of Medicine, The University of Hong Kong, Hong Kong Special Administrative Region, China and 5Centre for Health Protection, Department of Health, Hong Kong Special Administrative Region, China

Abstract

We obtained 24 air samples in 8 general wards temporarily converted into negative-pressure wards admitting coronavirus disease 2019 (COVID-19) patients infected with severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) omicron variant BA.2.2 in Hong Kong. SARS-CoV-2 RNA was detected in 19 (79.2%) of 24 samples despite enhanced indoor air dilution. It is difficult to prevent airborne transmission of SARS-CoV-2 in hospitals.

(Received 1 August 2022; accepted 24 September 2022)

Since the emergence of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) omicron variant in November 2021, it became the dominant variant circulating globally. The evolving SARS-CoV-2 omicron sublineages from (BA.1 to BA.2 to BA.4 to BA.5) have demonstrated progressively increased transmissibility,1 leading to explosive outbreaks in the community.2 Whether the SARS-CoV-2 omicron variant increased the risk of coronavirus disease 2019 (COVID-19) transmission in the healthcare setting remains uncertain. Recent studies have shown that the universal use of surgical respirators as a component in infection prevention contributed to the rapid control of SARS-CoV-2 omicron transmission in the hospital.3 Universal use of surgical respirators in the healthcare setting was also advocated when the infection rate of COVID-19 in community was high.4 The preliminary findings of surgical respirator use in the SARS-CoV-2 omicron era may provide an indirect implication of airborne transmission of SARS-CoV-2 omicron variant in the clinical areas.

Demonstration of air dispersal of the SARS-CoV-2 omicron variant may further support the use of surgical respirators by healthcare workers (HCWs) in general wards. Based on our previous experience in performing air sampling to detect SARS-CoV-2 RNA in the airborne infection isolation room (AIIR) of hospitals and community treatment facilities during the COVID-19 pandemic5–7 we performed air sampling to assess the air dispersal of SARS-CoV-2 in general wards that were temporarily converted into negative-pressure wards (NPWs) for COVID-19 patients during the surge of SARS-CoV-2 omicron cases in the fifth wave of COVID-19 in Hong Kong. These findings may have implications for infection control.

Methods

Collection of air samples for SARS-CoV-2 RNA in wards

To assess the air dispersal of SARS-CoV-2, air samples were collected in Queen Mary Hospital using an AerosolSense Sampler (Thermo Fisher Scientific, MA) as previously described.5,8 The air sample was collected through an omnidirectional inlet and directed toward the collection substrate through an accelerating slit impactor at a flow rate of 200 L per minute for a total of 1–6 hours, resulting in 12,000 L to 72,000 L of air per sample. The air sampler was placed outside the nursing station, which was located at the center of the ward (Fig. 1).

Author for correspondence: Vincent Chi-Chung Cheng, E-mail: vcccheng@hku.hk
Cite this article: Wong S-C, et al. (2022). Air dispersal of severe acute respiratory coronavirus virus 2 (SARS-CoV-2): Implications for hospital infection control during the fifth wave of coronavirus disease 2019 (COVID-19) due to the SARS-CoV-2 omicron variant in Hong Kong. Infection Control & Hospital Epidemiology, https://doi.org/10.1017/ice.2022.258

© The Author(s), 2022. Published by Cambridge University Press on behalf of The Society for Healthcare Epidemiology of America.
Viral load assessment of air samples and respiratory specimens

The collection substrate of each air sample was immersed in 2 mL viral transport medium, and 1 mL medium was used for total nucleic acid extraction using the eMAG extraction system (bioMérieux, Marcy-l’Etoile, France) following the manufacturer’s instructions. Quantification of SARS-CoV-2 RNA was performed by reverse-transcription polymerase chain reaction (RT-PCR) as previously described. For clinical specimens, total nucleic acid extraction was performed using 250 μL of the specimen and was subjected to RT-PCR as described above.

Whole-genome sequencing of respiratory specimens

Whole-genome sequencing (WGS) and determination of viral lineage were performed using the Oxford Nanopore MinION device (Oxford Nanopore Technologies) and Nanopore protocol, that is, the PCR tiling of COVID-19 (version PTC_9096_v109_revH_06Feb2020), respectively, as we described previously. This study was approved by the Institutional Review Board of The University of Hong Kong/Hospital Authority Hong Kong West Hospital Cluster.

Statistical analysis

Univariate analysis and multiple linear regression were used where appropriate. All reported P values were 2-sided. A P value of <.05 was considered statistically significant. Computation was performed using SPSS version 15.0 software for Windows (IBM, Armonk, NY).

Results

Analysis of air samples for SARS-CoV-2 RNA in wards

For this study, 24 air samples were collected in 8 NPWs (Supplementary Table online). The median number of patients in each NPW was 19 (range, 8–37) at the time of air sampling. SARS-CoV-2 RNA was detected at a cycle threshold (Ct) value of 39.1 ± 2.3 in 19 (79.2%) of 24 air samples. Univariate analysis revealed that detectable SARS-CoV-2 RNA in air samples was significantly associated with more COVID-19 patients in the ward, lower mean Ct value of clinical specimens, longer duration of air sampling, and timing of air sampling. Multivariable analysis with multiple linear regression showed that the duration of air sampling was negatively correlated with the Ct value of air samples (B = −0.929; P = .006) (Table 1).

Analysis of WGS of respiratory specimens

Of 495 RT-PCR–positive respiratory specimens collected from COVID-19 patients in 8 NPWs, 41 (8.3%) were randomly selected for WGS, of which 3 (6.7%) of 45 specimens were collected from ward A2, 7 (10.1%) of 69 from ward B2, 2 (3.5%) of 57 from ward B3, 6 (15.4%) of 39 from ward D4, 10 (15.4%) of 65 from ward D6, 6 (7.0%) of 86 from ward E4, 3 (2.9%) of 102 from E6, and 4 (12.5%) of 32 from ward K13N. All sequences were identified to be SARS-CoV-2 omicron sublineage BA.2.2.

Discussion

We have consistently demonstrated the phenomenon of air dispersal of SARS-CoV-2 RNA in almost 80% of air samples collected in the NPWs caring for patients infected with SARS-CoV-2 omicron.
Infection when transitioning from the pandemic to endemicity.

is the key to protect patients and HCWs from developing severe
SARS-CoV-2 in hospitals. Promulgation of COVID-19 vaccination
Therefore, it is difficult to prevent airborne transmission of
of MMHUs could not eliminate the virus, as shown in our study.

over time with continual respirator use at work,9 making universal
dispersal from infected HCWs. However, discomfort would increase
was negatively correlated with the Ct value of air samples. The
our multivariable analysis in which the duration of air sampling
increased risk of infection. This factor was indirectly implied in
breaks. Prolonged exposure to COVI9-19 patients may have an
impact on hospital infection control, especially in general wards or
the windows to improve the indoor air dilution (Fig. 1).

The finding of SARS-CoV-2 dispersal in the NPWs may have an
impact on hospital infection control, especially in general wards or
other clinical areas where the indoor air dilution is not as good as
AIIRs or NPWs. Asymptomatic COVID-19 patients may spread
the virus in these areas via airborne route, which may result in out-
breaks. Prolonged exposure to COVID-19 patients may have an
increased risk of infection. This factor was indirectly implied in
our multivariable analysis in which the duration of air sampling
was negatively correlated with the Ct value of air samples. The
use of surgical respirators by HCWs may protect them from acquisi-
tion of SARS-CoV-2 and may minimize the risk of SARS-CoV-2
dispersal from infected HCWs. However, discomfort would increase
time over with continual respirator use at work,9 making universal
use of surgical respirator not practical, especially during a nonout-
break period. In addition, it is impossible to eliminate the risk of
SARS-CoV-2 dispersal from infected patients. Although surgical
masks can be provided to all patients, compliance may not be
100%.30 The MMHUs cannot be installed at all wards because of
its large size. Enhancement of indoor air dilution by installation of
MMHUs could not eliminate the virus, as shown in our study.
Therefore, it is difficult to prevent airborne transmission of
SARS-CoV-2 in hospitals. Promulgation of COVID-19 vaccination
is the key to protect patients and HCWs from developing severe
infection when transitioning from the pandemic to endemicity.

Table 1. Univariate and Multivariable Analysis on the Results of SARS-CoV-2 RNA in Air Samples

<table>
<thead>
<tr>
<th>Variable</th>
<th>Univariate Analysis*</th>
<th>Multiple Linear Regression Model Predicting the Ct Value of All Air Samples b</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Air Samples With</td>
<td>Air Samples Without</td>
</tr>
<tr>
<td></td>
<td>Detectable SARS-CoV-2 RNA (n=19)</td>
<td>Detectable SARS-CoV-2 RNA (n=5)</td>
</tr>
<tr>
<td></td>
<td>P Value</td>
<td>Unstandardized Coefficient B</td>
</tr>
<tr>
<td>COVID-19 patients in ward during air sampling, mean no. ± SD</td>
<td>22.6±18.5</td>
<td>13.2±3.3</td>
</tr>
<tr>
<td>Age of COVID-19 patients per ward, mean y ± SD</td>
<td>79.0x4.6</td>
<td>78.6±4.4</td>
</tr>
<tr>
<td>Ct value of COVID-19 patients, mean ± SD</td>
<td>25.8±2.1</td>
<td>28.7±1.0</td>
</tr>
<tr>
<td>Time interval between the clinical and air samples, mean d ± SD c</td>
<td>2.9±1.0</td>
<td>2.2±0.1</td>
</tr>
<tr>
<td>Duration of air sampling, mean h ± SD</td>
<td>4.3±1.8</td>
<td>2.2±1.1</td>
</tr>
<tr>
<td>Timing of air sampling, mean d ± SD d</td>
<td>10.4±6.4</td>
<td>14.4±2.5</td>
</tr>
</tbody>
</table>

Note. COVID-19, coronavirus disease 2019; Ct, cycle threshold; NA, not applicable; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2; SD, standard deviation.

*Student t test was used for 2-group comparison of continuous variables.

†Variables that were considered as statistically significant in univariate analysis were subjected to multivariable analysis using multiple linear regression to determine whether there is any correlation between Ct value of air samples and each variable. Any negative air samples were assigned with a Ct value of 45 for statistical analysis.

‡Clinical sample of COVID-19 patients included deep throat saliva, combined nasal and throat swab, or nasopharyngeal swab.

§Timing of air sampling was defined as day of air sampling counting from the start of the study.

This study had several limitations. We did not perform WGS for the air samples due to low viral load. However, the WGS of our hospitalized patients confirmed the presence of SARS-CoV-2 omicron sublineage BA.2.2, which was also the predominant sublineage during the fifth wave of COVID-19 in Hong Kong.2 We did not report the details of COVID-19 transmission in wards. Given the finding of air dispersal of SARS-CoV-2 RNA, nosocomial transmission of COVID-19 would be possible. We did not perform virus isolation for the air samples. The low level of RNA detected may not directly translate to an infective dose. Nevertheless, our results provide an alert to support continued vigilance against nosocomial airborne transmission of COVID-19.

Supplementary material. To view supplementary material for this article, please visit https://doi.org/10.1017/ice.2022.258

Acknowledgments. We thank Dr. Kelvin Hei-Yeung Chiu, Department of Microbiology, Queen Mary Hospital, for advice on the statistical analysis during revision of manuscript.

Financial support. This study was partially supported by the Health and Medical Research Fund (HMRF) Commissioned Research on Control of Infectious Disease (Phase IV), CID-HKU1-16, Food and Health Bureau, Hong Kong SAR government.

Conflict of interest. All authors report no conflicts of interest relevant to this article.

References


