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Major Article

Investigation of air dispersal during a rhinovirus outbreak in a pediatric intensive care unit

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Background: While airborne transmission of rhinovirus is recognized in indoor settings, its role in hospital transmission remains unclear.
Methods: We investigated an outbreak of rhinovirus in a pediatric intensive care unit (PICU) to assess air dispersal. We collected clinical, environmental, and air samples, and staff's surgical masks for viral load and phylogenetic analysis. Hand hygiene compliance and the number of air changes per hour in the PICU were measured. A case-control analysis was performed to identify nosocomial rhinovirus risk factors.
Results: Between March 31, 2023, and April 2, 2023, three patients acquired rhinovirus in a cubicle (air changes per hour: 14) of 12-bed PICU. A portable air-cleaning unit was placed promptly. Air samples (72,000 L in 6 hours) from the cohort area, and outer surfaces of staff's masks (n = 8), were rhinovirus RNA-negative. Hand hygiene compliance showed no significant differences (31/34, 91.2% vs 33/37, 89.2%, $P = 1$) before and during outbreak. Only 1 environmental sample (3.8%) was positive (1.86×10^3 copies/mL). Case-control and next-generation sequencing analysis implicated an infected staff member as the source.
Conclusions: Our findings suggest that air dispersal of rhinovirus was not documented in the well-ventilated PICU during the outbreak. Further research is needed to better understand the dynamics of rhinovirus transmission in health care settings.

BACKGROUND

Rhinovirus is a common cause of upper respiratory tract infections in both children and adults, and it is responsible for a significant burden of morbidity and health care costs worldwide. In pediatric populations, rhinovirus infections can be particularly severe, especially in vulnerable patients such as those with underlying medical conditions or immunocompromised status. In recent years, several outbreaks of rhinovirus infections have been reported in pediatric settings.[1–3] These outbreaks can pose a significant challenge to health care professionals, as the infected cases can result in prolonged hospital stays, increased health care costs, and even mortality.

The transmission of rhinoviruses occurs primarily through respiratory droplets that are released when an infected person coughs or sneezes. These droplets can enter another person's body through inhalation or by touching a surface contaminated with the virus and then touching their eyes, nose, or mouth.[4] However, previous studies have suggested that aerosolized rhinovirus could be detected by air sampling via Teflon filters in an experimental setting.[5] Rhinovirus was also detected in the air samples collected in the indoor area with low outdoor air supply.[6] Individuals with symptomatic respiratory viral infections including rhinovirus had shown to produce both large and small particles carrying viral RNA on coughing and breathing.[7]

During the coronavirus disease 2019 (COVID-19) pandemic, the potential for airborne transmission of respiratory viruses has been revisited.[8] Our recent study demonstrated the phenomenon of air dispersal of respiratory viruses, including rhinovirus, in patients isolated in airborne infection isolation rooms (AIIRs).[9] Indeed, a recent systematic review suggested the possibility that the major route of rhinovirus in many indoor settings is through airborne transmission.[10]

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However, the clinical significance of air dispersal of these respiratory viruses in non-AIIR settings and their propensity to cause hospital outbreaks remains uncertain. In this study, we report an incident of nosocomial transmission of rhinovirus in a pediatric intensive care unit (PICU) and investigate whether airborne dispersal contributes to rhinovirus transmission.

METHODS

Setting

This study was conducted in the PICU of Queen Mary Hospital, a university-affiliated teaching hospital with a capacity of 1,700 beds in Hong Kong. The PICU shared the same ward with the Special Care Baby Unit. The PICU contains 12 beds arranged as 2 single-bed AIIRs, one 7-bed (PICU area 1), and one 3-bed (PICU area 2) cubicles with no pressure difference between the cubicles and the common area (Fig 1). In area 1 and area 2, the air supply is located far away from the common area while the air exhaust is located outside the open cubicle. The AIIR is prioritized to care for patients aged ≤17 and infected with pathogens of airborne transmission, such as severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), measles virus, varicella-zoster virus, and *Mycobacterium tuberculosis*. Other patients who are aged ≤17 and have fever and respiratory symptoms may also be admitted to the AIIRs, depending on the availability of beds. Appropriate respiratory specimens were collected from patients based on their clinical presentation and the hospital's standard protocols for infection control. The infection control precautions and use of personal protective equipment during patient care practice depend on the microbiological diagnosis of the patients. During the nosocomial transmission of rhinovirus, a portable air-cleaning unit is placed in area 1 in order to reduce the risk of airborne transmission. An ad hoc measurement of the air ventilation system in the PICU was performed. The data on hand hygiene opportunities and compliance in the PICU were retrieved from the infection control team. The opportunity and compliance of hand hygiene audit are performed by infection control nurses as per the World Health Organization protocol.[11] A case-control analysis was conducted to investigate the risk factors associated with rhinovirus transmission in the PICU. This study was approved by the Institutional Review Board of The University of Hong Kong/Hospital Authority Hong Kong West Hospital Cluster (IRB reference number: UW 23-373).

Microbiological diagnosis of a patient with respiratory symptoms

To facilitate rapid microbiological diagnosis, the nasopharyngeal aspirates (NPA) collected in viral transport medium (VTM) were simultaneously tested for 23 pathogens using the BIOFIRE Respiratory

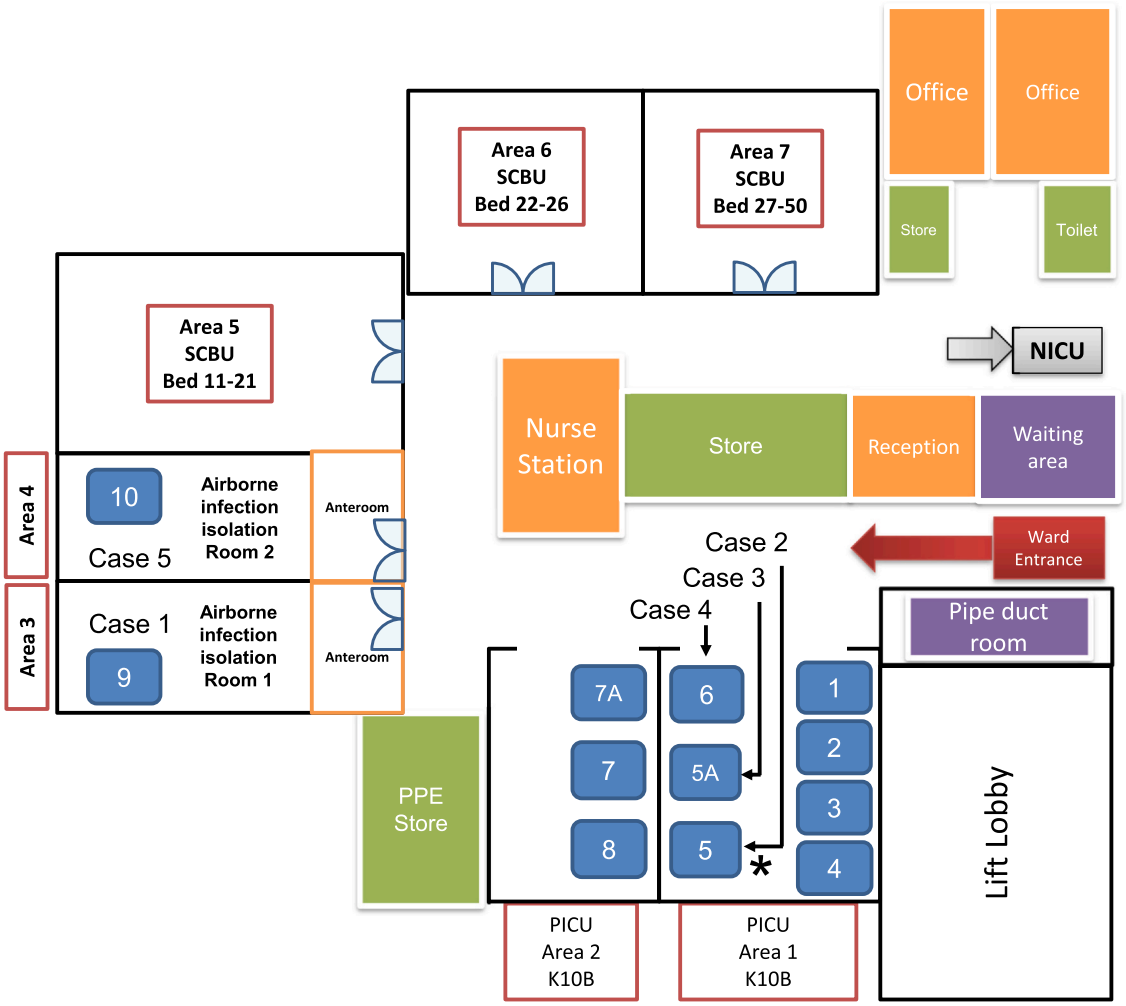

Fig. 1. Floor plan of pediatric intensive care unit and special care baby unit shared ward: layout and spatial configuration. PICU, pediatric intensive care unit; NICU, neonatal intensive care unit; SCBU, special care baby unit. PICU areas 1 and 2 are open cubicles without doors. * indicates the position of the portable air-cleaning unit, which was placed adjacent to Case 2 (bed 5 of PICU area 1).

2.1 *plus* Panel (bioMérieux). The panel targets 19 viruses, including adenovirus, coronavirus 229E, coronavirus HKU1, coronavirus OC43, coronavirus NL63, Middle East respiratory syndrome coronavirus, SARS-CoV-2, human metapneumovirus, human rhinovirus/enterovirus, influenza A/H1, A/H1–2009, A/H3, and B, as well as parainfluenza viruses 1 to 4 and respiratory syncytial virus. In addition, the panel targets 4 bacteria: *Bordetella pertussis, Bordetella parapertussis, Chlamydophila pneumoniae*, and *Mycoplasma pneumoniae*. Samples positive for human rhinovirus and enterovirus were confirmed by real-time reverse transcription polymerase chain reaction (RT-PCR) specific for rhinovirus.[12]

Collection of environmental and air samples for rhinovirus

Swab samples were collected from the patient's bedside environment, including the nurse area, ventilator, vital sign monitor, and bed, in 7 beds from PICU area 1. Additionally, commonly used items such as the nurse station, injection cart, medication cart, table for milk preparation, and computer on wheels were swabbed using the previously described method.[13]

To assess the air dispersal of rhinovirus RNA, air sample was collected using an AerosolSense Sampler (Thermo Fisher Scientific) as previously described.[14,15] A single-use sampling cartridge containing a 1-inch polycarbonate filter was installed into the sampler. 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/minute for a total of 6 hours, resulting in 72,000 L of air per sample. After the sampling cycle of 6 hours, the sample cartridge was removed and sent to the microbiology laboratory within 30 minutes for further processing. The air sampler was placed inside PICU area 1, adjacent to the first recognized hospital-acquired rhinovirus case.

Collection of surgical masks from staff for rhinovirus detection

To evaluate the presence of rhinovirus on surgical masks worn by staff, the masks were collected immediately at the end of the work shift. The masks were dissected into specific pieces, as outlined in a previously published method.[16] The method involved dividing the mask into various sections, including the right and left sides, the nose area, and the mouth area, each with specific dimensions. For masks with multiple layers, these sections were further subdivided into inner, middle, and outer layers as appropriate, based on the previously described dimensions of each section. The dissected mask pieces were then submerged into 2 mL VTM for subsequent analysis.[12]

Viral load assessment of environmental, air, and mask samples and respiratory specimens

For the environmental samples, each swab sample in VTM was vortexed and centrifuged at 13,000 × g for 1 minute, and 1 mL of the supernatant was used for nucleic acid extraction. For the air sample, the collection substrate of the air sample was immersed in 2 mL of VTM, and 1 mL of the medium was used for total nucleic acid extraction. For the mask samples, 1 mL of the VTM was used for total nucleic acid extraction using the eMAG extraction system (bioMérieux) following the manufacturer's instructions. Quantification of rhinovirus RNA was performed by RT-PCR as previously described.[12,17] For the clinical specimens, total nucleic acid extraction was performed using 250 µL of the specimen and subjected to RT-PCR as described above. The laboratory protocol of rhinovirus whole-genome sequencing is shown in the Supplementary File.

Statistical analysis

The Fisher's exact test and t test were used as appropriate. A P value of < .05 was considered statistically significant.

RESULTS

Nosocomial transmission of rhinovirus in PICU

On March 23, 2023, Case 1 was confirmed to have symptomatic rhinovirus 4 days after being transferred from another pediatric hospital, which had ongoing rhinovirus transmission. Case 1 was pre-emptively isolated in the AIIR (bed 9) upon admission (Fig 1). Case 2 (area 1, bed 5) was confirmed to have symptomatic rhinovirus infection on March 31, 2023, and a portable air-cleaning unit was placed adjacent to Case 2. Eight patients in area 1 were considered exposed cases and underwent medical surveillance for fever and respiratory symptoms. Environmental disinfection using sodium hypochlorite 1,000 ppm was performed twice daily for 3 consecutive days. Directly observed hand hygiene once every 2 hours was performed as one of the proactive infection control measures, as described previously.[18–21] Of the 8 patients who underwent medical surveillance, 2 additional cases, Case 3 (area 1, bed 5A), and Case 4 (area 1, bed 6) were confirmed to have symptomatic rhinovirus infection 2 days later on April 2, 2023, resulting in a total of three hospital-acquired rhinovirus infections (cases 2-4) (Table 1).

The overall hand hygiene compliance among staff just before the nosocomial transmission of rhinovirus was not significantly different from that during and after the transmission (31/34, 91.2% vs 33/37, 89.2%, $P = 1$).

Area 1 in the PICU was supplied with air from 4 diffusers. The average air velocity from each diffuser was measured twice during the nosocomial transmission of rhinovirus. The air change per hour in area 1 was calculated based on the flow rate of air supply and the volume of the area. The result was 14.86 (Supplementary Table).

Retrospective analysis revealed that a nurse (staff A), who did not care for Case 1, reported being sick with a cough and running nose on March 27, 2023. Staff A then resumed duty and cared for Case 2 (area 1, bed 5) and Case 3 (area 1, bed 5A) on 28 March and March 29, 2023, respectively. Staff A also cared for all patients in area 1 during the night shift on March 30, 2023. The NPA of staff A was positive for rhinovirus by RT-PCR with a viral load of 5.23×10^7 copies/mL. A case-control analysis of 3 infected patients and 6 exposed but non-infected cases showed that being under the care of the infected staff was the only significant risk factor for hospital-acquired rhinovirus infection (3/3, 100% vs 1/6 17%, $P = .048$) (Table 2).

Environmental, air, and mask samples for rhinovirus

In view of the newly diagnosed cases of 3 hospital-acquired rhinovirus, samples were collected from the environment, air, and masks for detection of rhinovirus RNA. A total of 26 environmental samples were collected, including 21 samples from the bedside environment (3 samples per bed) and 5 samples from commonly used items collected before routine environmental disinfection. Only 1 sample (3.8%) collected from the ventilator and vital sign monitor (bed 5 of Case 2) was positive for rhinovirus by RT-PCR, with a viral load of 1.86×10^3 copies/mL (Table 3). The air sample was negative for rhinovirus RNA.

Eight staff working in area 1 submitted their used surgical masks at the end of their 8-hour work shift. No detectable rhinovirus RNA was found in the middle and outer layers of any of the surgical masks. However, one mask tested positive for rhinovirus RNA in the inner layer. Specifically, the inner nose area had 1.22×10^3 copies/mL, while the inner mouth area had 4.92×10^3 copies/mL.

Table 1
Line listing of patients with rhinovirus infection in pediatric intensive care unit

Case	Sex/ age	Underlying disease*	Nature	Admission date	Symptom onset	Symptoms	Viral load (copies/ mL)	Outcome†
1.	F/3y	DiGeorge syndrome‡	Transfer-in§	March 19, 2023	March 23, 2023	Pneumoperitoneum, shock	7.60×10^5	Recovered and transferred back on April 11, 2023‡
2.	F/3y	Multiple congenital anomalies	HAI	March 14, 2020**	March 31, 2023	Fever, cough, RN	1.21×10^7	Recovered
3.	F/7m	Short gut syndrome	HAI	November 29, 2022	April 2, 2023	RN	1.90×10^8	Recovered
4.	M/9m	NEC	HAI	June 21, 2022	April 2, 2023	Fever	7.41×10^7	Recovered
5.	F/15y	Asthma	CAI	April 2, 2023	April 2, 2023	Cough, RN, status asthmaticus	4.72×10^7	Recovered

CAI, community-acquired infection; *HAI*, hospital-acquired infection; *NEC*, necrotizing enterocolitis; *RN*, running nose.
*Predominant diagnosis.
†14 days after the last laboratory-confirmed case of rhinovirus.
‡Incomplete manifestation of DiGeorge syndrome.
§Transferred from and back to a pediatric rehabilitation center when clinical condition is stabilized.
**Born in hospital.

Table 2
Risk factor for acquisition of rhinovirus during hospitalization in pediatric intensive care unit

	Case (n = 3)	Control (n = 6)	*P* value
Age (months) ± SD	17 ± 16	84 ± 88	.248
Sex (female)	2 (66%)	3 (50%)	1
Presence of			
Central line	1 (33%)	3 (50%)	1
Endotracheal tube	0	2 (33%)	.500
Feeding tube	2 (66%)	4 (66%)	1
Requiring of			
NIPPV caring	1 (33%)	3 (50%)	1
Napkin changing	3 (100%)	5 (83%)	1
Wound dressing	2 (66%)	5 (83%)	1
Exposure to infected staff*	3 (100%)	1 (17%)	.048

NIPPV, noninvasive positive pressure ventilation; *SD*, standard deviation.
*The duties of a nurse (staff A) concerned in the pediatric intensive care unit are assigned to the A, P, and N shifts, with patient care times as follows: A shift (7:00 AM to 2:36 PM), P shift (12:45 PM to 9:33 PM), and N shift (9:05 PM to 7:05 AM). Each staff member is assigned to a specific list of patients. The period of exposure is defined as the time from when the staff member resumed duty after sick leave to the onset of the first hospital-acquired case of rhinovirus infection.

Table 3
Environmental contamination by rhinovirus in pediatric intensive care unit

Category	Items	Viral load (copies/mL)
Bedside environment	Nurse area (bed 1)	ND
	Ventilator and vital sign monitor (bed 1)	ND
	Bed (bed 1)	ND
	Nurse area (bed 2)	ND
	Ventilator and vital sign monitor (bed 2)	ND
	Bed (bed 2)	ND
	Nurse area (bed 3)	ND
	Vital sign monitor (bed 3)*	ND
	Bed (bed 3)	ND
	Nurse area (bed 4)	ND
	Ventilator and vital sign monitor (bed 4)	ND
	Bed (bed 4)	ND
	Nurse area (bed 5)	ND
	Ventilator and vital sign monitor (bed 5)	1,860
	Bed (bed 5)	ND
	Nurse area (bed 5A)	ND
	Ventilator & vital sign monitor (bed 5A)	ND
	Bed (bed 5A)	ND
	Nurse area (bed 6)	ND
	Vital sign monitor (bed 6)*	ND
	Bed (bed 6)	ND
Commonly used items	Nurse area	ND
	Injection cart	ND
	Medication cart	ND
	Table for milk preparation	ND
	Computer on wheel	ND

ND, Not detected
*Ventilator was not available in bed 3 and bed 6.

Phylogenetic analysis of rhinovirus

The phylogenetic analysis showed that the staff A and patients with hospital-acquired rhinovirus (cases 2, 3, and 4) belonged to rhinovirus C1 and clustered together by whole-genome sequencing (Fig 2). Case 1 was phylogenetically distinct from the three hospital-acquired cases. Although Case 5 was also clustered together with 3 hospital-acquired cases, it is epidemiologically unrelated.

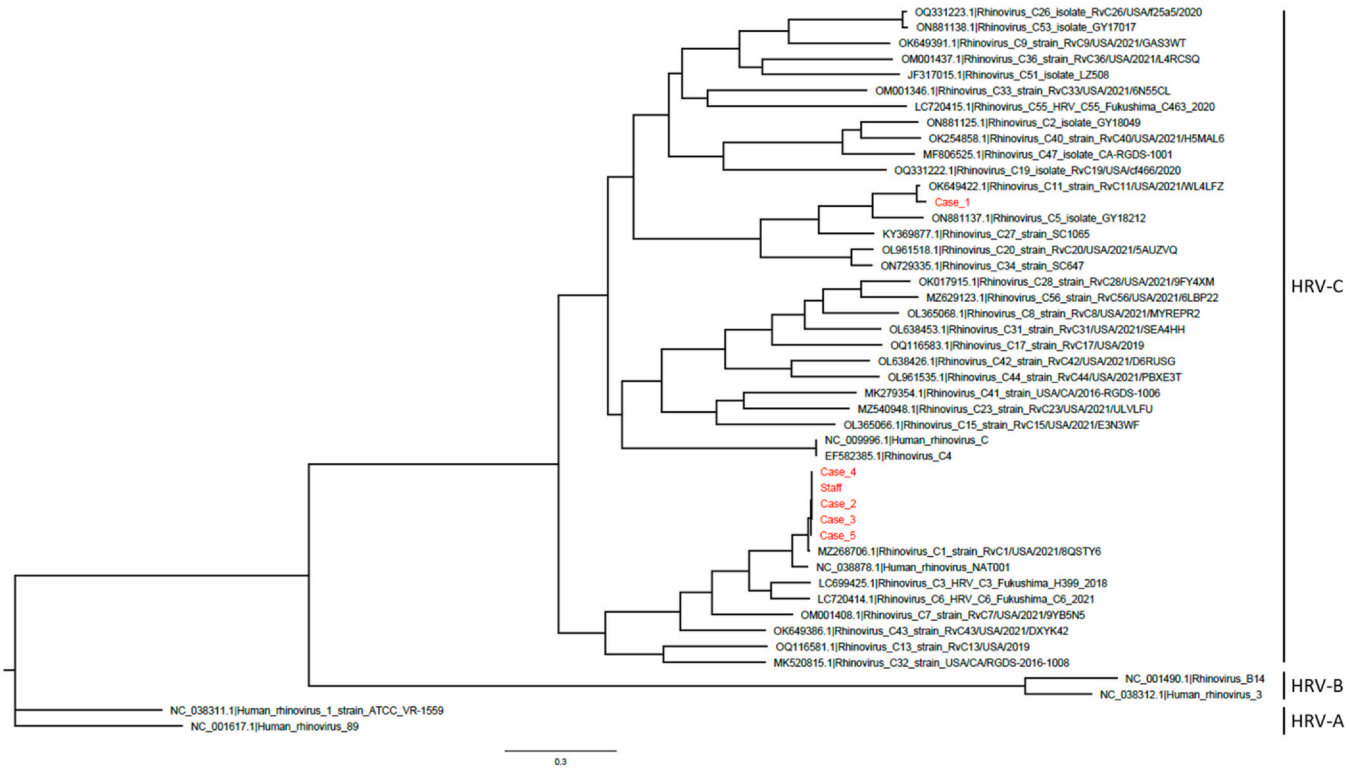

Fig. 2. Whole-genome phylogenetic analyses of the rhinovirus genomes sequenced in this study. The whole-genome phylogenetic tree was constructed using IQ-TREE2.

DISCUSSION

Previous studies have suggested that airborne transmission, either via large or small aerosols, is a significant route of rhinovirus transmission in real-life indoor settings.[5] However, our study suggests that airborne transmission may not have played a significant role in the nosocomial transmission of rhinovirus in the PICU. This is supported by the fact that the air sample collected during the outbreak, where 3 hospital-acquired rhinovirus cases were cohorted together, tested negative for rhinovirus RNA. Despite having high viral loads of 10^7 to 10^8 copies/mL in their nasopharyngeal specimens and not wearing surgical masks by pediatric patients of 3 years or less, the negative air sample may be attributed to the early placement of a portable air-cleaning unit in the cubicle (area 1), immediately when the first case of hospital-acquired rhinovirus infection was diagnosed. Portable air-cleaning units have been shown to be most effective when placed close to the source of aerosols to reduce exposure.[22] Recent study also found that an air-cleaning unit considerably reduced airborne particulate matter levels in a hospital ward, indicating its potential as an effective intervention to reduce the risk posed by infectious airborne particles.[23] Additionally, the calculated air changes per hour (ACH) in the cubicle (area 1), based on real-time measurements of air velocity from air supply diffusers, was up to 14, which was significantly higher than the usual requirement of at least 6 ACH.[24] The number of ACH was usually set higher than the minimal requirement but was not intentionally increase further during the outbreak. The higher number of ACH enhanced the dilution of infectious respiratory particles in the air.

Therefore, it is not surprising to find that the outer surface of surgical masks worn by our staff, collected at the end of the work shift, did not reveal rhinovirus RNA. In fact, a previous study has shown that contamination of respiratory viruses on the outer surface of masks used by hospital health care workers was 10%. However, the contamination might be due to self-inoculation, as well as deposition of respiratory viruses by airborne route.[25] It is interesting to note that 1 out of 8 surgical masks had detectable rhinovirus RNA on the inner surface at a viral load of about 10^3 copies/mL. This surgical mask was worn by the infected staff, who had a viral load of 10^7 copies/mL in their nasopharyngeal specimen. The difference in viral load between the nasopharyngeal specimen and the inner surface of the surgical mask, as observed in our study, is also consistent with the findings from 45 paired samples of nasopharyngeal swabs and masks obtained from patients infected with SARS-CoV-2, with a difference of approximately 1,000 RNA copies/mL.[16]

The absence of detectable rhinovirus RNA on the outer surface of the surgical mask worn by the infected staff indicates that self-inoculation of the virus did not take place. This finding suggests that the staff may have been aware of the importance of infection control measures, especially hand hygiene practices, after touching their face, particularly after the onset of nosocomial transmission of rhinovirus in the PICU. Touching the eyes and nose is a subconscious behavior that has been linked to self-inoculation of rhinovirus.[26] A prospective study evaluated the facial touching behavior of 134 medical students over a 15-minute observation period, finding that 66% of the participants touched either their mask area (38%), eyes (38%), or other parts of their face (49%) at least once. On average, the number of touches recorded per hour was approximately 12.[27] Subsequent studies have demonstrated that there are no significant differences in the frequency of facial touching between patients and health care workers, regardless of whether they are wearing surgical masks.[28,29] Patients have been observed to touch their face up to 13 to 15 times per hour.[28] In contrast, wearing masks has been found to significantly reduce mucosal touches among health care workers.[29] However, a single episode of lapses in infection control practices may lead to the transmission of rhinovirus from infected staff to patients, as may have occurred in our case.

Phylogenetic analysis of the whole-genome sequencing revealed an almost identical sequence between the infected staff and 3 patients who had acquired rhinovirus infection in the hospital. Based

on the chronology of symptom onset and the case-control analysis, it is likely that the infected staff was the source of transmission, rather than the first rhinovirus case (Case 1) in the PICU. Molecular epidemiology using whole-genome sequencing analysis can aid in outbreak investigations and help to identify the source of transmission.[30] As far as we understand, this is the first report of a rhinovirus outbreak in the PICU using whole-genome sequencing to investigate the molecular epidemiology of rhinovirus transmission.

Although a staff member is epidemiologically implicated as the source of the infection, the persistent implementation of infection control measures, particularly hand hygiene practices, universal masking by health care workers, and environmental disinfection during the COVID-19 pandemic,[31–33] helped to limit the spread of rhinovirus in the PICU. The overall compliance with hand hygiene among staff was approximately 90% just before and during the nosocomial transmission of rhinovirus. In addition, only 1 out of 26 environmental samples were found to be contaminated with rhinovirus RNA, indicating a high standard of infection control practices in the PICU. The clinical attack rate of our nosocomial rhinovirus infection was 25% (3 cases out of a fully occupied 12-bed PICU). Given the absence of published rhinovirus outbreaks in PICUs, we observed rhinovirus outbreaks in the neonatal intensive care unit.[1,34,35] We compared the corresponding data reported in neonatal intensive care units, where 38% (3 out of 8 infants),[1] and 64% (7 out of 11 infected infants)[35] acquired rhinovirus infections during their hospital stay, respectively. The prevalence of rhinovirus infection upon admission to PICU among patients with respiratory tract infection (8.5%-48.8%), and bronchiolitis (~25%) remains a significant burden (Supplementary Table 2). It is important to enforce infection control measures to minimize the risk of nosocomial transmission of rhinovirus in intensive care settings.

There are several limitations in this study. First, we did not perform air sampling before the use of portable air-cleaning units, which means that detectable rhinovirus RNA may have been missed. Nevertheless, the use of portable air-cleaning units has already been shown to reduce airborne particulate matter levels in clinical areas.[23] Second, the absence of rhinovirus RNA detection in the air sample may be attributed to the possibility that the peak phase of exhaled aerosol viral shedding had already passed by the time the air sample was collected. However, it is noteworthy that the viral loads in their nasopharyngeal specimens remained consistently high, ranging from 10^7 to 10^8 copies/mL, throughout the collection of air samples. This may suggest that the extent of air dispersal of rhinovirus RNA may be limited by the low tidal volume observed in pediatric patients aged 3 years or younger.

CONCLUSIONS

Given that rhinovirus is known to be transmitted through airborne route[36] and has persisted throughout the COVID-19 pandemic despite infection control and public health measures implemented against COVID-19,[37–39] further studies are warranted to investigate the role of airborne transmission in the spread of rhinovirus in health care settings, and to identify effective infection control measures to prevent nosocomial transmission.

CREDIT AUTHORSHIP CONTRIBUTION STATEMENT

Shuk-Ching Wong: Conceptualization, Data curation, Formal analysis, Investigation, Methodology, Project administration, Writing – original draft, Writing – review & editing. **Cyril Chik-Yan Yip:** Data curation, Formal analysis, Writing – original draft, Writing – review & editing. **Jonathan Hon-Kwan Chen:** Data curation, Formal analysis, Writing – original draft, Writing – review & editing. **Lithia Lai-Ha Yuen:** Investigation. **Christine Ho-Yan AuYeung:** Investigation. **Wan-Mui Chan:** Investigation. **Allen Wing-Ho Chu:** Investigation. **Rhoda Cheuk-Ying Leung:** Investigation. **Jonathan Daniel Ip:** Investigation. **Simon Yung-Chun So:** Data curation, Formal analysis. **Kwok-Yung Yuen:** Funding acquisition, Supervision. **Kelvin Kai-Wang To:** Formal analysis, Investigation, Methodology, Writing – review & editing. **Vincent Chi-Chung Cheng:** Conceptualization, Data curation, Formal analysis, Investigation, Methodology, Project administration, Supervision, Writing – original draft, Writing – review & editing. All authors have read and agreed to the published version of the manuscript.

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APPENDIX A. SUPPORTING INFORMATION

Supplementary data associated with this article can be found in the online version at doi:10.1016/j.ajic.2023.11.003.

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