T.Didik,A.P-Y. Yau , H.L. Cheung , S-Y. Lee , N-H. Chan , Y-T. Wah ,H.K-H. Luk , G.K-Y. Choi , N.H-Y. Cheng , H. Tse , Y. Li , S.C.Y Wong ,D.C. Lung. (2023). Long-range air dispersion of Candida auris in a cardiothoracic unit outbreak in Hong Kong
doi:10.1016/j.jhin.2023.09.019

Long-range air dispersion of Candida auris in a cardiothoracic unit outbreak in Hong Kong

T.Didik
A.P-Y. Yau
H.L. Cheung
S-Y. Lee
N-H. Chan
Y-T. Wah
H.K-H. Luk
G.K-Y. Choi
N.H-Y. Cheng
H. Tse
Y. Li
S.C.Y Wong
D.C. Lung
Department of Pathology, Queen Elizabeth Hospital, Hong Kong Special Administrative Region, China
Department of Pathology, Hong Kong Children's Hospital, Hong Kong Special Administrative Region, China
Department of Respiratory Medicine, Kowloon Hospital, Hong Kong Special Administrative Region, China
Department of Cardiothoracic Surgery, Queen Elizabeth Hospital, Hong Kong Special Administrative Region, China
Infection Control Team, Queen Elizabeth Hospital, Hong Kong Special Administrative Region, China
Infection Control Team, Kowloon Hospital, Hong Kong Special Administrative Region, China
Department of Laboratory Medicine, Khoo Teck Puat Hospital, Singapore
Department of Mechanical Engineering, Faculty of Engineering, The University of Hong Kong, Hong Kong Special Administrative Region, China

Correspondingauthor.Address:DepartmentofPathology,QueenElizabethHospital/Hong KongChildren’sHospital,Hong Kong Special Administrative Region ,China.Tel.:þ85235066832.
E-mailaddress:lungdc@ha.org.hk(D.C.Lung).

Article history: Received 24 July 2023
Accepted 24 September 2023

Author Biographies

Tiffany DIDIK, a researcher in Department of Pathology, Queen Elizabeth Hospital, Hong Kong Special Administrative Region, China.

Anthony Pak-Yuen YAU, a researcher in Department of Respiratory Medicine, Kowloon Hospital, Hong Kong Special Administrative Region, China.

Hung Leong CHEUNG, a researcher in Department of Cardiothoracic Surgery, Queen Elizabeth Hospital, Hong Kong Special Administrative Region, China.

Suet-Yi LEE, a researcher in Infection Control Team, Queen Elizabeth Hospital, Hong Kong Special Administrative Region, China.

Nga-Han CHAN, a researcher in Infection Control Team, Queen Elizabeth Hospital, Hong Kong Special Administrative Region, China.

Yuen-Ting WAH, a researcher in Infection Control Team, Kowloon Hospital, Hong Kong Special Administrative Region, China.

Hayes Kam-Hei LUK, a researcher in Department of Pathology, Queen Elizabeth Hospital, Hong Kong Special Administrative Region, China.

Garnet Kwan-Yue CHOI, a researcher in Department of Pathology, Hong Kong Children's Hospital, Hong Kong Special Administrative Region, China.

Naomi Hua-Yin CHENG, a researcher in Department of Pathology, Queen Elizabeth Hospital, Hong Kong Special Administrative Region, China.

Herman TSE, a researcher in Department of Laboratory Medicine, Khoo Teck Puat Hospital, Singapore

Yuguo Li, PhD, is Chair Professor of Building Environment, Honorary Professor of School of Public Health, Associate Dean (Research) of Engineering. His research interests are in building environment engineering. His current research topics include city climate/environment, environment studies of infection and indoor environment.

Sally Cheuk-Ying WONG, a researcher in Department of Pathology, Queen Elizabeth Hospital, Hong Kong Special Administrative Region, China.

David Christopher LUNG, a researcher in Department of Pathology, Queen Elizabeth Hospital, Hong Kong Special Administrative Region, China.

Long-range air dispersion of Candida auris in a cardiothoracic unit outbreak in Hong Kong

Abstract

Background: Nosocomial outbreaks of Candida auris, a multidrug-resistant fungus, are increasingly reported worldwide; the mode of transmission has usually been reported to be via direct contact. Some studies previously suggested potential short-distance air dispersal during high-turbulence activities, but evidence on long-range air dispersal remains scarce.
Aim: To describe a C. auris nosocomial outbreak involving two wards (H7, 5E) in two local hospitals.
Methods: Samples were taken from patients, ward surfaces (frequently touched items and non-reachable surfaces) while settle plates were used for passive air sampling to investigate possible contributions by direct contact and air dispersal. Epidemiological and phylogenetic analyses were also performed on the C. auris isolates from this outbreak.
Findings: Eighteen patients were confirmed to have asymptomatic C. auris skin colonization. C. auris was expectedly identified in samplings from frequently touched ward items but was also isolated in two samples from ceiling supply air grilles which were 2.4 m high and inaccessible by patients. Moreover, one sample from a corridor return air grille as far as 9.8 m away from the C. auris cohort area was also positive. Two passive air samplings were positive, including one from a cubicle with no confirmed cases for four days, suggesting possible air dispersal of C. auris. Whole-genome sequencing confirmed clonality of air, environment, and patients' isolates.

(217 words)

Key words

Candida auris Multidrug-resistant candida Nosocomial outbreaks Air Ventilation Fungal outbreaks

Introduction

First reported in 2009, Candida auris is an emerging global health threat, due to the species' multidrug resistance and ability to cause outbreaks of colonization and infection in healthcare settings . Apart from asymptomatic colonization that can persist for months, C. auris can also cause fungaemia in susceptible hosts with mortality up to 40% . C. auris is mainly transmitted by contact with contaminated surfaces or colonized skin; however, disinfection of surfaces with usual disinfectants may be suboptimal due to biofilm formation . Previous reports of C. auris outbreaks have mainly demonstrated C. auris in environmental samples of the immediate patient surroundings, namely high-touch areas and low-touch areas such as window sills, and shared ward equipment . Presence of C. auris in air around bedside during high-turbulence activities (changing of bedding) has also been described, but evidence of long-range air dispersal remains scarce .

Candida auris clustering was first reported in Hong Kong in a local public hospital in 2019. Since then, nosocomial outbreaks have been reported in various other public hospitals within the territory. Here, we report an outbreak investigation in 2022 involving two hospitals in Hong Kong, including detailed epidemiological information, results of environmental sampling, and phylogenetic analysis based on wholegenome sequencing (WGS) of patients' and environmental strains. Samples were taken specifically from high-touch areas, areas of inaccessible heights, and from the ward ventilation system to study the possibility of air dispersal of this fungus, as this could have potential implications in infection control measures.

Methods

Settings

Queen Elizabeth Hospital (QEH) is a major acute hospital with more than 1800 beds. It is one of the three designated tertiary referral centres in Hong Kong for cardiothoracic surgeries (CTS). H7 ward is a 32-bedded male ward under the care of CTS, with four open cubicles and one two-bedded side room, with around 70 admissions per month. Its air handling unit (AHU) has a filter of 14 minimum efficiency reporting values (MERV), providing six air changes per hour (ACH) with a fresh air to recirculated air ratio of 1:2. Room air is recirculated into the AHU through returned air grilles in the corridor and is redistributed to each cubicle through ceiling supply air grilles. The patient toilet has direct exhaust air grilles (Figure 1) that create only a slight negative pressure for odour control with its door kept closed when not in use; therefore it would not cause significant disturbance to the ward's recirculation air flow (Supplementary Figure A1).

Postoperative stabilized cases from QEH H7 would either be discharged home or transferred to Kowloon Hospital (KH), a convalescent hospital, for rehabilitation. KH 5E is a multispecialty ward consisting of tuberculosis care unit, acute respiratory beds, and rehabilitation beds. It consists of 41 beds distributed among four cubicles and four single rooms e all in constant negative-pressure ranges from 5.5 to 21.2 kPa. Air in cubicles and single rooms is exhausted through AHU with highefficiency particulate air (HEPA) filter (Supplementary Figure A2).

Ethical approval was obtained from the Research Ethics Committee of the Kowloon Central/Kowloon East Cluster, Hospital Authority (HA) (Reference Number: KC/KE-22-0220/ ER-1).

Epidemiological investigation

On September 17th, 2022, an indwelling catheterized urine culture of a patient in H7 ward yielded C. auris. This patient had been an inpatient since July 11th, 2022 with multiple transfer between QEH H7 and KH 5E due to changes in clinical status. He had been in three different open cubicles (A, B, and C) in H7 and one general cubicle with closed door in 5E under standard precautions, before isolation in H7 ward side-room with additional contact precautions when the urine culture revealed C.auris.

Contact tracing and outbreak management

Immediate infection control measures and contact tracing were initiated on September 17th, 2022 according to the prevailing guideline of HA. A contact case was defined as a patient who stayed in the same ward as the index patient on or after July 11th, 2022 (admission date of the index patient), and who was identified through the Patient Administration Contact Tracing System of HA. Patient contacts who shared the same cubicle with the index patient were categorized as 'close contacts'; patients in the same ward but different cubicles were labelled as 'other contacts'. Screening for C. auris was performed by culture of nasal, axilla, and groin pooled swabs (Copan, Brescia, Italy) following the protocol of HA. Contact cases were under surveillance for 14 days e during which 'close contacts' were screened on days 1, 2, 7, 14, and 'other contacts' screened on days 1, 2, 3. Weekly screening of all contact cases for another four weeks was conducted following the last C. auris case identified in the outbreak. End of the outbreak was declared on October 20th, 2022.

Collection of environmental and air samples for Candida auris culture

Apart from frequently touched items of ward communal area, returned air grilles and high-level supply air grilles werealso sampled with flexible pre-moistened sterile polywipe sponge swabs (Medical Wire and Equipment, Corsham, UK) of 5 *10 cm in size. For passive air-sampling, tryptic soy agar (TSA) settle plates were exposed in the ward environment for 24 h, and on bed head trunking unit to ensure they were out of reach of patients (Figure 1).

<Figure 1>

Laboratory investigations

Patients' swabs were directly inoculated onto in-house PaganoeLevin Agar (PAGO) (Supplementary Text A1) and incubated for four days at 35° C ambient air. Patient swabs and environmental sponge swabs were submerged in Sabouraud dextrose broth (Oxoid CM0147; Thermo Fisher, Basingstoke,UK) with 10% NaCl, 50 mg/L chloramphenicol and 20 mg/L colistin for seven-day incubation at 40° C, ambient air. Both samples were examined daily and would be subcultured onto PAGO if turbidity were observed. In addition, routine subculture of inoculated broth onto PAGO on days 4 and 7 was performed for environmental sponge swabs. Colonial growth of any morphology on PAGO would be identified by matrixassisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS, IVD library version: DB-11758 MSP; Bruker, Bremen, Germany) with quality score 2.0 as correct speciation following direct on-plate extraction with 70% formic acid. TSA settle plates were incubated for seven days in 35 ° C ambient air and reviewed daily to look for any yeast-like colonies. Suspicious colonies were identified by MALDI-TOF MS as described above.

Whole-genome sequencing

Whole-genome sequencing on patients' and environmental isolates was performed. C. auris culture on Sabouraud agar (BD 211584; Becton Dickinson, Franklin Lakes, NJ, USA) was harvested into lysis buffer for two freezeethaw cycles to disrupt the cell wall and release genomic DNA . Genomic DNA was extracted using DNeasy

Blood & Tissue Kit (Qiagen, Hilden, Germany), followed by library preparation using DNA Prep kit (Illumina, San Diego, CA, USA). Sequencing of the pooled library was performed on iSeq or MiSeq sequencer (Illumina) to obtain paired-end 150 or 300 bp reads, which were processed with the programs and parameters described previously . Briefly, the low-quality bases in paired-end reads were filtered and trimmed using Trimmomatic v0.39; quality-trimmed reads were then de-novo assembled using SPAdes v3.15.3 and Ragout v2.3 for the reference-assisted scaffolding.

Single nucleotide polymorphism (SNP) analysis was performed using Snippy v4.60 (https://github.com/tseemann/ snippy). A maximum likelihood phylogeny was con structed from the SNP data using IQ-TREE v2.1.1 with a GTR F + I model with ascertainment bias correction. The whole-genome sequencing project has been deposited in GenBank under the accession number PRJNA990830.

Environmental decontamination and patient decolonization

Immediate change of curtains and twice-daily environmental disinfection using 5000 ppm sodium hypochlorite solution were implemented in involved wards. Sessions of terminal decontamination, whole ward ultraviolet C (UVeC) irradiation and hydrogen peroxide vapour (HPV) decontamination for equipment and ward were also conducted (Supplementary Table A1) . Decolonization of carriers was also performed (Supplementary Table A2).

Results

Contact tracing and outbreak management

H7 ward was enhanced to COVID-19 setup during the C. auris outbreak, when partitions and doors were installed at the entrance of open cubicles, and exhaust fans inside the cubicles were switched on (Figure 1). The modifications altered the airflow, which then directed from the corridor to cubicles and the outside (confirmed bysmoke tests), with no air recirculation from the cubicles back to the returned air grilles in the corridor. Air exchange rate has remained similar before and after the modifications. Single-patient-use devices (including blood-pressure cuffs, tourniquet, and thermometer) were already provided before this outbreak since September 2020 as per enhanced infection control practice under COVID-19 pandemic. Contact patients who remained hospitalized were physically segregated from other admitted patients, put under cohort nursing and contact precautions with cubicle doors kept closed at all times.

A total of 503 patients were identified from contact tracing with 176 and 327 patients categorized as ‘close contacts’ and ‘other contacts’, respectively. Only 28 ‘close contacts’ and 78 ‘other contacts’ were still hospitalized at the time of outbreak investigation.

Eighteen patients were positive for C. auris from screening samples (Supplementary Table A3); all were asymptomatic with no antifungals prescribed. Of those, 16 were from QEH H7, distributed across the four different open cubicles (Supplementary Figure A3), and three (P1, P3, P15) had been transferred to KH 5E before their C. auris colonization status was known. The remaining two patients (P6, P7) were directly admitted to KH 5E ward from other hospitals, and only one of them shared the same cubicle with the index patient (Supplementary Figure A2).

Sixteen patients with C. auris colonization received skin surface decolonization and six patients received an additional course of probiotic gut decontamination (Supplementary Table A4). There was no further follow-up in their carrier status by our team after their discharge from QEH and KH.

In QEH H7, confirmed patients were initially isolated in a side room during September 18th to 22nd, 2022. From September 23rd, 2022, patients with C. auris were cohorted in cubicle D due to the growing number of affected patients. On September 27th to 28th, 2022, six patients with C. auris were cohorted in cubicle D (Supplementary Figure A4). In KH, con- firmed cases were kept in side rooms or 5E2 cubicle.

Environmental samples and settle plates for C. auris culture

A total of 249 environmental samples and 39 settle plates were collected in QEH H7 ward from 19th September 2022 to 20th October 2022 (two weeks after the diagnosis of last C. auris patient). The environmental samples included 176 from frequently touched shared items, 10 from non-reachable high curtain rails in cubicles, three from returned air grilles, 18 from AHU bag filters, 26 from supply air grilles and 16 exhaust fans and grilles (Table II).

In ward communal areas, the extent of frequently touched item contamination by C. auris was 60%, 41.2%, and 35.3% on September 19th, 20th, and 27th, 2022 respectively, and remained at 0% since October 5th, 2022 upon implementation of environmental decontamination.

Settle plate passive air sampling revealed C. auris in two (5.1%) of 39 samples, both taken on September 27th, 2022, from cubicle D (positive case cohort area) and cubicle B. Notably, there were no patients with C. auris in cubicle B since September 23rd, 2022 (Table II).

<Table I >

Of the 36 high-level samples collected from supply air grilles and curtain rails, two (5.5%) from the supply air grilles were positive. They were both taken on September 26th, 2022, and were from cubicle D (positive case cohort area) and cubicle C. One (33.3%) of the three samples collected from returned air grilles was positive. The returned air grilles positive for C. auris were in the main corridor, 9.8 m away from all cubicles. The sample was taken on September 27th, 2022, when the highest number of C. auris-colonized patients (up to nine cases) were cohorted in H7 (Table II).

None of the six samples taken on two separate days from exhaust air grilles in the patient toilet was positive for C. auris (Table II).

A total of 20 environmental samples from frequently touched commonly shared items were collected in KH 5E ward on September 19th, 2022. None of the samples was positive for C. auris (Table II).

<Table II>

Whole-genome sequencing

All patient and environmental isolates belonged to clade I/ South Asia and formed a very closely related cluster with the C. auris isolates from the first local outbreak in 2019 (Cau 1915 and Cau 1919, ERR3503269 and ERR3503273) (Figure 2).

Discussion

.idence on possible spread by air dispersal is scarce. To our knowledge, four previous studies described potential air dispersal of C. auris with positive settle-plate sampling, two of which were demonstrated during high-turbulence activities (change of beddings) (Table I).

In our study, a passive air sampling method was used as it better reflects real-life settings where environmental contamination is caused by dust particles and skin squames . We demonstrated that C. auris was also detected in unreachable areas, namely the supply and extraction air grilles near the cubicle ceiling, and settle plates suggested likely spread by air dispersal.

Moreover, our study also shows that air dispersal of C. auris may be more extensive in terms of time and distance than previously thought, with contamination of 2.4 m high supply-air grilles and extraction-air grilles which were at least 9.8 m from the nearest cubicle entrance (Supplementary Figure A1). auris-containing particulates may continue to remain suspended in air for some time, as evidenced by air settle plates for C. auris remaining positive even in the absence of a con- firmed case in the cubicle at the time.

The role of transmission by air dispersal in this outbreak can be further substantiated by comparing the extent of outbreak and ward environment of the two main sites (QEH H7 and KH 5E). The former was a general ward with all cubicle air recirculated through the return air grilles in the corridor back to AHU. The latter, which also serves tuberculosis patients, was designed as an airborne infection isolation facility with all cubicles maintained at negative pressure with all effluent air directed to exhaust, thus preventing particulates from contaminating non-cubicle areas. We suspect that the difference in ventilation settings resulted in QEH H7 being associated with persistence and more extensive environmentalcontamination both inside and outside cubicles with more secondary positive cases despite implementation of other infection control measures. Moreover, all but one (P7) of the confirmed cases in KH

5E ward were in the same cubicle, whereas affected contacts in QEH H7 ward were distributed across the four different cubicles, suggesting the potential contribution of effective airborne precaution in limiting the spread of C. auris.

Contrary to previous reports, high-turbulence activity such as bed-making may not be the prerequisite for C. auris air dispersal. There were also no bedding changes during the settle-plate sampling period and within 48 h before sampling of supply air grilles in cubicles .

We postulate that C. auris air dispersion in the absence of high air-turbulence activity may be due to shedding of C. aurisladen skin squames carried by air current. This phenomenon has also been demonstrated in multidrug-resistant acinetobacter and meticillin-resistant Staphylococcus aureus . Soiling of ceiling air outlets as a result of air turbulence has been described . Air jet entrains molecules of air from its immediate surroundings to create a sleeve of low pressure (also known as Coanda effect), resulting in an upward airflow beneath the ceiling supply air jet. Human thermal plume may also contribute to this upward airflow by thermal buoyancy, driven by a density gradient between heat generated by human activity and cool air from the ceiling supply air grilles . C.auris-laden skin squames may thus be carried by this upward air flow to contaminate the supplied air grilles, dispersing around the cubicle through the supply air jet (Figure 3) and then further into the corridor by the recirculation airflow created by the ventilation setting of H7 ward. This is supported by positive culture from the extraction air grilles in the corridor of H7 ward. Although there is a possibility that C. auris has entered the AHU by recirculating air, none of the bag filter samples from inside the AHU were positive, and the MERV14 filter should have prevented C. auris from recirculating into the ward.

There are several limitations to this study. Air grille sampling or settle plates in KH were not performed. We were unable to compare the dynamics of air dispersal during different occasions, such as low- versus high-turbulence activities. Despite decolonization therapy, C. auris carrier status of confirmed cases was not screened if patients were discharged from hospital; therefore the optimal method of C. auris decolonization remains to be further explored.

<Figure 3>

Nevertheless, our findings demonstrated the potential longrange air dispersal of C. auris, which can be as far as 9.8 m in a conventionally designed ward, and suggested that ventilation precautions should be considered in C. auris outbreaks in addition to contact precautions alone. The use of HEPA grade filter may be considered if it is compatible with the AHU; otherwise upgrading ward AHU may be considered at the time of any future renovations. As temporary measures, portable air purifiers with HEPA filters may be used to augment the air exchange rate, helping to decrease the load of C. auris in the cubicles if higher grade HEPA filters such as MERV 17 filters cannot be accommodated by the ward AHU. Cubicle doors should be kept closed to prevent spreading of C. auris from affected cubicles. Air grilles, despite being unreachable to patients, may be contaminated and might act as a reservoir that contributes to air dispersion, hence should also be included in environmental disinfection. To prevent excessive interference of air recirculation, self-contained supply and exhaust ventilation systems should be considered in the long term for each

cohort cubicle. Inadequate removal of air-dispersed C. auris by contact precaution and environmental decontamination may be evidenced by positive settle-plate samplings on September 27th (Table II) despite relocation of all confirmed cases out of H7 since September 23rd and multi-modal environmental decontamination (UVeC and 5000 ppm sodium hypochlorite) just one day ago (Supplementary Table A1). This is likely due to the limitations of UV-C in disinfecting areas that are not in direct line-of-sight and sodium hypochlorite solution in removing C. auris on surfaces only. Therefore, ventilation measures should also be included to aid the removal of air-dispersed C. auris.

References

[1] Centers for Disease Control and Prevention. Recommendations for infection prevention and control for Candida auris. 2022. Available from: https://www.cdc.gov/fungal/candida-auris/c-auris-infection-control.html.

[2] Adams E, Quinn M, Tsay S, Poirot E, Chaturvedi S, Southwick K, et al. Candida auris in healthcare facilities, New York, USA, 2013–2017. Emerg Infect Dis 2018;24:1816.

[3] Centers for Disease Control and Prevention. Candida auris: information for laboratories and health professionals. Atlanta, GA: US Department of Health and Human Services; 2021.

[4] Rutala WA, Kanamori H, Gergen MF, Sickbert-Bennett EE, Weber DJ. Susceptibility of Candida auris and Candida albicans to 21 germicides used in healthcare facilities. Infect Control Hosp Epidemiol 2019;40:380–2.

[5] Ku TSN, Walraven CJ, Lee SA. Candida auris: disinfectants and implications for infection control. Front Microbiol 2018;9.

[6] Nett JE, Guite KM, Ringeisen A, Holoyda KA, Andes DR. Reduced biocide susceptibility in Candida albicans biofilms. Antimicrob Agents Chemother 2008;52:3411–3.

[7] Sansom S, Gussin GM, Singh RD, Bell PB, Jinai EB, Makhija, et al. Multicenter evaluation of contamination of the healthcare environment near patients with Candida auris skin colonization. Antimicrob Stewardsh Healthc Epidemiol 2022;2(Suppl 1):578–9.

[8] Kumar J, Eileston B, Cadnum JL, Whitlow CS, Jencson AL, Safdar N, et al. Environmental contamination with candida species in multiple hospitals including a tertiary care hospital with a candida auris outbreak. Pathog Immun 2019;4:260–70.

[9] Sexton DJ, Bentz ML, Welsh RM, Derado G, Furin W, Rose LJ, et al. Positive correlation between Candida auris skin-colonization burden and environmental contamination at a ventilator-capable skilled nursing facility in Chicago. Clin Infect Dis 2021;73:1142–8.

[10] Schelenz S, Hagen F, Rhodes JL, Abdolrasouli A, Chowdhary A, Hall A, et al. First hospital outbreak of the globally emerging Candida auris in a European hospital. Antimicrob Resist Infect Control 2016;5(1).

[11] Taori SK, Rhodes JJ, Khomyongwa K, Szendroi A, Smith M, Borman AM, et al. First experience of implementing Candida auris real-time PCR for surveillance in the UK: detection of multiple introductions with two international clades and improved patient outcomes. J Hosp Infect 2022;127:111–20.

[12] Tse H, Tsang AKL, Chu YW, Tsang DNC. Draft genome sequences of 19 clinical isolates of Candida auris from Hong Kong. Microbiol Resour Announc 2021;10(1).

[13] Harju S, Fedosyuk H, Peterson KR. Rapid isolation of yeast genomic DNA: bust n' grab. BMC Biotechnol 2004;4:8.

[14] Bolger AM, Lohse M, Usadel B. Trimmomatic: a flexible trimmer for Illumina sequence data. Bioinformatics 2014;30:2114–20.

[15] Nurk S, Bankevich A, Antipov D, Gurevich AA, Korobeynikov A, Lapidus A, et al. Assembling single-cell genomes and mini-metagenomes from chimeric MDA products. J Comput Biol 2013;20:714–37.

[16] Kolmogorov M, Armstrong J, Raney BJ, Streeter I, Dunn M, Yang F, et al. Chromosome assembly of large and complex genomes using multiple references. Genome Res 2018;28:1720–32.

[17] Minh BQ, Schmidt HA, Chernomor O, Schrempf D, Woodhams MD, Von Haessler A, et al. IQ-TREE 2: new models and efficient methods for phylogenetic inference in the genomic era. Mol Biol Evol 2020;37:1530–4.

[18] Kumar JA, Cadnum JL, Jencson AL, Donskey CJ. Are reduced concentrations of chlorine-based disinfectants effective against Candida auris? Am J Infect Control 2020;48:448–50.

[19] Abdolrasouli A, Armstrong-James D, Ryan L, Schelenz S. In vitro efficacy of disinfectants utilised for skin decolonisation and environmental decontamination during a hospital outbreak with Candida auris. Mycoses 2017;60:758–63.

[20] [20] Kean R, Sherry L, Townsend E, McKloud E, Short B, Akimbooka A, et al. Surface disinfection challenges for Candida auris: an in-vitro study. J Hosp Infect 2018;98:433–6.

[21] de Groot T, Chowdhary A, Meis JF, Voss A. Killing of Candida auris by UV-C: importance of exposure time and distance. Mycoses 2019;62:408–12.

[22] Kelly S, Schnugh D, Thomas T. Effectiveness of ultraviolet-C vs aerosolized hydrogen peroxide in ICU terminal disinfection. J Hosp Infect 2022;121:114–9.

[23] Maritta RM, Davis JH, Lottridge MM, Randive RV. Shining light on multi-drug resistant Candida auris: ultraviolet-C disinfection, wavelength sensitivity, and

prevention of biofilm formation of an emerging yeast pathogen. Microbiologyopen 2022;11(1).

[24] Yadav A, Singh A, Wang Y, Haren MH Van, Singh A, De Groot T, et al. Colonisation and transmission dynamics of Candida auris among chronic respiratory diseases patients hospitalised in a chest hospital, Delhi, India: a comparative analysis of whole genome sequencing and microsatellite typing. J Fungi 2021;7:1–16.

[25] Taori SK, Khomyongwa K, Hayden I, Athukorala GDA, Letters A, Fife A, et al. Candida auris outbreak: mortality, interventions and cost of sustaining control. J Infect 2019;79:601–11.

[26] Karigudar RM, Wavare SM, Kakhandki L, Bagali S, Kumar IH. Comparison of active and passive methods of air sampling to evaluate the microbial contamination of air in operation theaters. J Pure Appl Microbiol 2020;14:2691–7.

[27] Wong SC, Lam GKM, Chen JHK, Li X, Jr PTF, Yuen LLH, et al. Air dispersal of multidrug-resistant Acinetobacter baumannii: implications for nosocomial transmission during the COVID-19 pandemic. J Hosp Infect 2021;116:78–86.

[28] Wong SC, Chen JHK, Yuen LLH, Chan WMM, AuYeung CHY, Leung SSM, et al. Air dispersal of meticillin-resistant Staphylococcus aureus in residential care homes for the elderly: implications for transmission during the COVID-19 pandemic. J Hosp Infect 2022;123:52–60.

[29] Timmer H, Zeller M. Particle deposition near ceiling induction outlets. Int J Refrig 2004:248–54.

[30] Craven BA, Settles GS. A computational and experimental investigation of the human thermal plume. J Fluids Engng Trans ASME 2006;128:1251–8.

[31] Sun S, Li J, Han J. How human thermal plume influences near-human transport of respiratory droplets and airborne particles: a review. Environ Chem Lett 2021;19:1971–82.

Figure 1. Floor plan of Queen Elizabeth Hospital, H7 ward, to illustrate the collection of environmental and air samples. The ward has an open cubicle design with ceiling height of 2.6 m in each cubicle. Settle plates were placed at each corner of the cubicles.

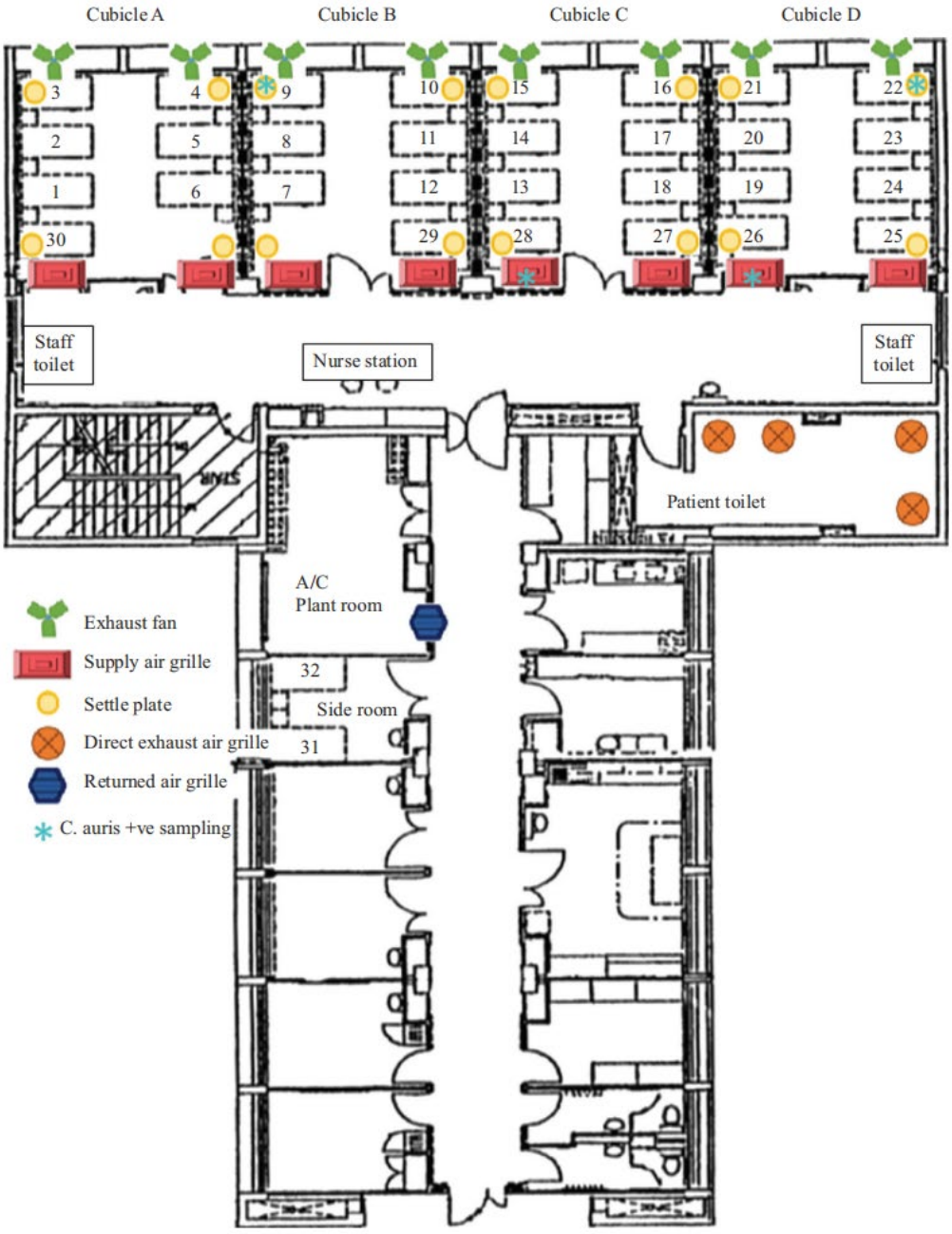

Figure 2. Phylogenetic tree of Candida auris isolates of patient and environmental samples, generated by single nucleotide polymorphism (SNP) analysis. A total of 25 C. auris isolates were selected for whole-genome sequencing including 17 patient isolates and eight environmental isolates. Isolate of P15 was not available as the patient was transferred to another hospital before diagnosis of C. auris colonization. The maximum number of pairwise SNP differences among the patient and environmental isolates is 14, indicating that they are highly genetically related and are transmitted recently.

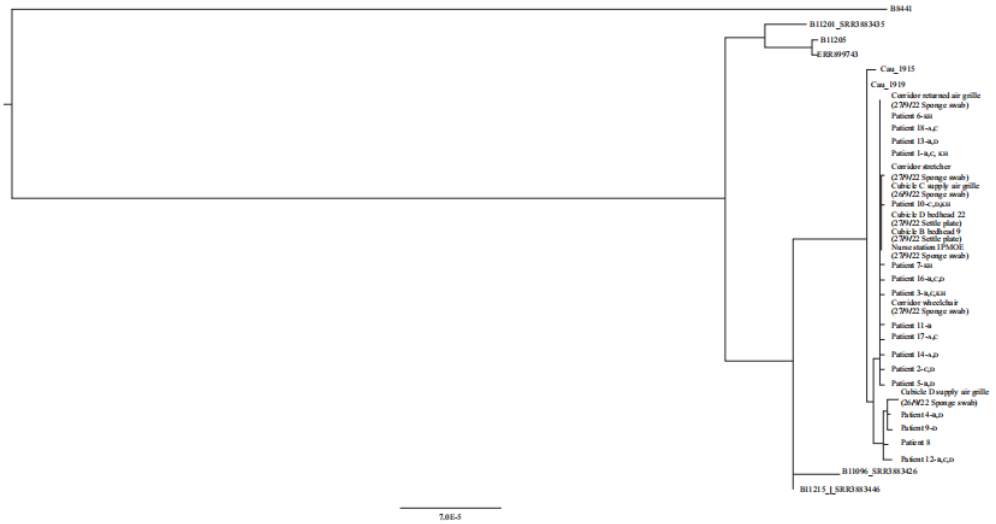

Figure 3. Schematic representation of cubicle air flow and the associated Candida auris air dispersion in Queen Elizabeth Hospital H7 ward. C. auris-laden skin squames are depicted as gold dots. Upward airflow (small blue arrows) is created by both the entrained air flow of supply air jet (dark blue arrow) and thermal plumes (orange arrows). C. auris-laden skin squames deposit onto the supply air grille by Coanda effect and are thus further dispersed around the cubicle through supply air jet and out of the cubicle into the corridor through recirculated air flow. In the background, warm air is shown as orange, cold air as blue.

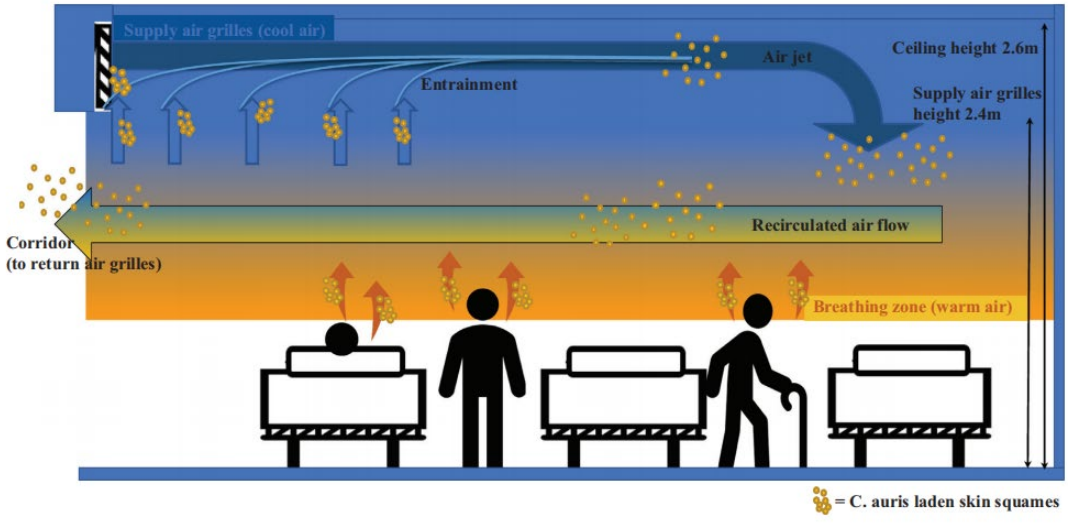

Table I Literature review on air dispersal of Candida auris in clinical settings

No.	Country (setting)	Study period	No. of *C. auris* +ve patients	Air sampling method	No. (%) of air samples +ve with *C. auris*	Distance of air sample from *C. auris* patient	Any high turbulence activity during sampling	Reference
1	UK (ward)	Apr 2015 to Jul 2016	50	Air sampler	Not mentioned	Bedside area	Yes	[10]
2	UK (ward)	Jul 2016 to Feb 2017	34	Settle plates	Not mentioned	3 m from patients' bed	No	[19]
3	UK (ward)	Jan 2018 to Mar 2019	21	Air sampler	Not mentioned	<1.5 m from patients' bed	Yes	[11]
4	India (ward)	Dec 2019 to May 2020	12	Swabs on air conditioner air wings	15.3%	Bedside area	No	[18]

Table IIa Environmental and air samples for Candida auris in cardiothoracic ward (Queen Elizabeth Hospital, H7 ward)

Types of sample	Location	No. of samples	% (no.) of positives	Date of collection	No. of *C. auris* +ve cases when sampling	Remarks
Frequently touched items by sponge swab. Items include:	Cubicle	5	20 (1/5)	Sep 19th, 2022	3	Oxygen and suction bed 19/22 (cubicle D)
– sinks – trolleys	Ward communal	15	60 (9/15)	Sep 19th, 2022	3	Keyboard, trolley, IPMOE, wheelchair
– blood pressure machine – computers – keyboards	Cubicle	8	37.5 (3/8)	Sep 20th, 2022	3	Oxygen and suction bed 19/22 (cubicle D), high chair and chest drain bed 13 (cubicle C)
– inpatient medication order entry devices	Ward communal	17	41.2 (7/17)	Sep 20th, 2022	3	Keyboard, trolley, wheelchair
– furniture – wheelchairs	Cubicle	9	33.3 (3/9)	Sep 27th, 2022	14	High chair bed 8/13 (cubicles B and C), bedhead 9/22 (cubicles B and D)
	Ward communal	17	35.3 (6/17)	Sep 27th, 2022	14	Keyboard, trolley, IPMOE, wheelchair, stretcher, linen room storage box
	Cubicle	3	0 (0/3)	Oct 5th, 2022	15	
	Ward communal	9	0 (0/9)	Oct 5th, 2022	15	
	Ward communal	2	0 (0/2)	Oct 7th, 2022	18	
	Cubicle	4	0 (0/4)	Oct 13th, 2022	18	
	Ward communal	16	0 (0/16)	Oct 13th, 2022	18	
	Cubicle	4	0 (0/4)	Oct 17th, 2022	18	
	Ward communal	42	0 (0/42)	Oct 17th, 2022	18	
	Cubicle	3	0 (0/3)	Oct 18th, 2022	18	
	Ward communal	8	0 (0/8)	Oct 18th, 2022	18	
	Cubicle	3	0 (0/3)	Oct 20th, 2022	18	
	Ward communal	11	0 (0/11)	Oct 20th, 2022	18	
	Cubicle	1	0 (0/1)	Nov 3th, 2022	18	
	Ward communal	5	0 (0/5)	Nov 3th, 2022	18	
Subtotal non-reachable surfaces at high levels by sponge swab	High curtain rails in cubicles	4	0 (0/4)	Oct 17th, 2022	18	
	High curtain rails in cubicles	2	0 (0/2)	Oct 18th, 2022	18	
	High curtain rails in cubicles	4	0 (0/4)	Oct 20th, 2022	18	
Subtotal air sample by settle plate	Corners of cubicle	7[a]	28.6 (2/7)	Sep 27th, 2022	14	Bed head of 9/22 (cubicles B and D)
	Corners of cubicle	16	0 (0/16)	Oct 15th, 2022	18	
	Corners of cubicle	8	0 (0/8)	Oct 19th, 2022	18	
	Corners of cubicle	8	0 (0/8)	Oct 20th, 2022	18	
Returned air grille by sponge swab	Corridor	1	100 (1/1)	Sep 27th, 2022	14	
	Corridor	1	0 (0/1)	Oct 7th, 2022	18	
	Corridor	1	0 (0/1)	Oct 17th, 2022	18	
Air handling unit by sponge swab	1st bag filter	12	0 (0/12)	Oct 10th, 2022	18	
	2nd bag filter	6	0 (0/6)	Oct 10th, 2022	18	
Supply air grilles by sponge swab	Cubicle A	2	0 (0/2)	Sep 26th, 2022	10	
	Cubicle B	2	0 (0/2)	Sep 26th, 2022	10	
	Cubicle C	2	50 (1/2)	Sep 26th, 2022	10	The one near bed 13
	Cubicle D	2	50 (1/2)	Sep 26th, 2022	10	The one near bed 19
	Side room (beds 31, 32)	1	0 (0/1)	Sep 26th, 2022	10	
	Cubicle A	2	0 (0/2)	Oct 7th, 2022	18	
	Cubicle B	2	0 (0/2)	Oct 7th, 2022	18	
	Cubicle C	2	0 (0/2)	Oct 7th, 2022	18	
	Cubicle D	2	0 (0/2)	Oct 7th, 2022	18	
	Side room (beds 31, 32)	1	0 (0/1)	Oct 7th, 2022	18	
	Cubicle A	2	0 (0/2)	Oct 17th, 2022	18	
	Cubicle B	2	0 (0/2)	Oct 17th, 2022	18	
	Cubicle C	2	0 (0/2)	Oct 17th, 2022	18	
	Cubicle D	2	0 (0/2)	Oct 17th, 2022	18	
Direct exhaust air grilles by sponge swab	Toilet	2	0 (0/2)	Oct 17th, 2022	18	
	Toilet	4	0 (0/4)	Oct 20th, 2022	18	
Exhaust fans by sponge swab	Cubicle A	1	0 (0/1)	Oct 17th, 2022	18	
	Cubicle B	1	0 (0/1)	Oct 17th, 2022	18	
	Cubicle C	1	0 (0/1)	Oct 17th, 2022	18	
	Cubicle D	1	0 (0/1)	Oct 17th, 2022	18	
	Cubicle A	1	0 (0/1)	Oct 18th, 2022	18	
	Cubicle B	1	0 (0/1)	Oct 18th, 2022	18	
	Cubicle A	1	0 (0/1)	Oct 20th, 2022	18	
	Cubicle B	1	0 (0/1)	Oct 20th, 2022	18	
	Cubicle C	1	0 (0/1)	Oct 20th, 2022	18	
	Cubicle D	1	0 (0/1)	Oct 20th, 2022	18	

[a] One of the corners was missed by staff and not placed with settle plates.

Table IIb Environmental and air samples for Candida auris in cardiothoracic ward (Kowloon Hospital, ward 5E)

Types of sample	Location	No. of samples	% (no.) of positive	Date of collection	No. of *C. auris* +ve cases when sampling	Remarks
Frequently touched items by sponge swab	Cubicle	3	0 (0/3)	Sep 19th, 2022	3	
	Ward, communal	17	0 (0/17)	Sep 19th, 2022	3	