Outbreak Reports

Emergence of a New Sublineage of *Candida auris* Causing Nosocomial Transmissions — Beijing Municipality, China, March–September 2023

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Summary

What is already known about this topic?

Candida auris (*C. auris*) is an emerging multidrug-resistant fungal pathogen classified as a global public health threat with notable mortality and nosocomial transmission capacity. In China, the first *C. auris* case was reported from Beijing in 2018. However, large cases of nosocomial transmission have rarely been identified in this municipality.

What is added by this report?

During March–September 2023, *C. auris* was isolated from 17 patients admitted to CY Hospital in Beijing. All strains were resistant to fluconazole and amphotericin B. In addition, three isolates were resistant to echinocandins. Whole-genome sequencing (WGS) analysis revealed that all strains found in this hospital belonged to *C. auris* Clade I. These strains were genetically closely related to the *C. auris* strains reported in two other hospitals in Beijing since 2021, forming a new sublineage different from the Clade I strains causing previous outbreaks in the Eastern Provincial-level administrative divisions and Hong Kong Special Administrative Region.

What are the implications for public health practice?

The dissemination of *C. auris* has become an increasing threat to healthcare facilities in China. The WGS analysis indicates the spread of a unique sublineage of *C. auris* Clade I isolates in Beijing. Further, enhanced surveillance and hospital infection control of *C. auris* are warranted to resolve the public health challenge.

Candida auris (*C. auris*) has emerged as a significant global public health threat, leading to its classification as a Critical Priority pathogen by the World Health Organization (WHO) (*1*). Outbreaks of *C. auris* have been reported in several provincial-level administrative divisions (PLADs) in China, including Liaoning, Anhui, and Guangdong (*2*). This study identified 17 nosocomial cluster cases of *C. auris* at a teaching hospital in Beijing Municipality between March and September 2023. Whole-genome sequencing revealed a novel *C. auris* sublineage responsible for this outbreak, highlighting its dissemination within the city.

INVESTIGATION AND RESULTS

This outbreak was identified at CY Hospital, a tertiary teaching hospital in Beijing with 2,500 inpatient beds. The first *C. auris* case was identified on March 2, 2023, from the urine sample of a 78-year-old male patient (Pt01). Pt01 was admitted to the emergency intensive care unit (EICU) due to coronavirus disease 2019 (COVID-19), followed by severe bacterial pneumonia. He underwent a tracheotomy and was discharged on day 6 after the first positive *C. auris* culture. However, Pt01 was readmitted on March 31, 2023, due to an influenza A infection. During his second hospital stay, *C. auris* was cultured 4 times from the patient's urine samples and once from his central venous catheter (Figure 1 and Supplementary Table S1, available at https://weekly.chinacdc.cn/).

Between March and September 2023, *C. auris* isolates were detected in an additional 16 patients (Pt02 to Pt17) at this hospital (Figure 1 and Supplementary Table S1). A total of 38 *C. auris* strains were collected from the 17 patients (Figure 2 and Supplementary Table S2, available at https://weekly.chinacdc.cn/). The hospital's microbiology laboratory and infection prevention team conducted a retrospective study to investigate transmission. A review of patient medical records indicated that of the 17 patients, 82.4% (14/17) were male, and 88.2% (15/17) were older than 65 years. Moreover, 82.4% (14/17) were critically ill. Notably, 76.5% (13/17) of patients had confirmed *C. auris* infections, including

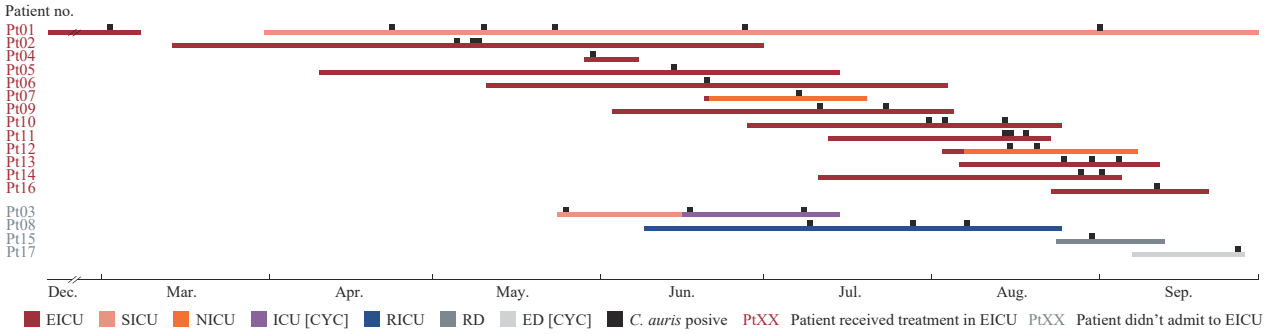

FIGURE 1. Epidemiological timeline of *Candida auris* (*C. auris*)–positive cases identified in the CY Hospital.
Note: This timeline tracked the hospitalization duration and specific clinical wards for each patient and the *C. auris* culture–positive timepoints. Pt01 was admitted to the Emergency Intensive Care Unit of the hospital on December 23, 2022, and the first *C. auris* was isolated from Pt01 on March 2, 2023. Till September 30, 2023, 17 *C. auris*–positive patients were identified in total.

29.4% (5/17) with candidemia and 23.5% (4/17) with *C. auris* colonization. Additionally, 70.6% (12/17) of patients had ≥1 positive urine culture (Supplementary Table S1).

The median duration from patient admission to the first isolation of *C. auris* isolates was 31 days, with an interquartile range of 16–45 days. To better understand the characteristics of *C. auris* nosocomial transmission at the hospital, the investigation team summarized the hospitalization timelines and associated department associations for the 17 positive patients. The investigation revealed that 76.5% (13/17) of patients had a documented history of receiving treatment in the EICU ward, indicating that the EICU may potentially mediate the spread of *C. auris* in the hospital (Figure 1). However, 168 culture-based environmental microbiologic surveillance cultures from the EICU ward, including samples collected before routine ward disinfections, yielded no positive results for *C. auris*. The team also conducted an on-site evaluation focused on infection prevention and control practices in the unit, including the use of personal protective equipment, hand hygiene, processing of reusable medical equipment, and environmental cleaning and disinfection. In general, healthcare personnel adhered to infection control regulations. However, the investigators also observed potential opportunities for contamination of mobile medical devices during patient care and that equipment surface disinfection was sometimes not properly done, which may facilitate the transmission of *C. auris*.

To provide more credible evidence, whole-genome sequencing (WGS) was performed on all 38 isolates using the Illumina Nova 6000 platform in PE150 (150-bp paired-end) sequencing mode (Beijing Novogene Bioinformatics Technology Co., Ltd., China). Additionally, the genomes of 54 Clade I *C. auris* isolates previously reported in China were acquired from the public database (Supplementary Table S3, available at https://weekly.chinacdc.cn/). Single nucleotide polymorphism (SNP) calling and phylogenetic analysis based on WGS data were performed as described previously using the genome of *C. auris* B8441 (GCA_002759435.2_Cand_auris_B8441_V2) as the reference. Detailed laboratory investigation methods are provided in Supplementary Material (available at https://weekly.chinacdc.cn/) (*3*).

WGS analysis revealed that all *C. auris* strains from CY Hospital during this period belonged to Clade I, with 15 to 100 pairwise SNPs between strains (Figure 2). For isolates from the same patient, pairwise SNPs were consistently ≤50. Compared with the genomes of *C. auris* Clade I strains previously reported in China, the strains in this study were genetically similar to those identified from 2 other hospitals in Beijing after 2021 (pairwise SNPs ≤100) but significantly divergent from the first *C. auris* Clade I case reported in Beijing in 2018 (pairwise SNPs >1,000) (Figure 2B). The strains from CY Hospital were also phylogenetically distant from the sublineage of *C. auris* Clade I isolates from the eastern China region (Anhui, Jiangsu, and Shandong provinces) and the outbreak strains recorded in Hong Kong Special Administrative Region (SAR), China, in 2019. Additionally, the strains isolated from 12 of the 13 patients who received treatment in the EICU exhibited more conserved genomic features (pairwise SNPs ≤50) compared with phylogenetic variations against strains from other departments in CY Hospital and other hospitals in Beijing (Figure 2). This molecular evidence further suggests that the rapid dissemination of *C. auris*

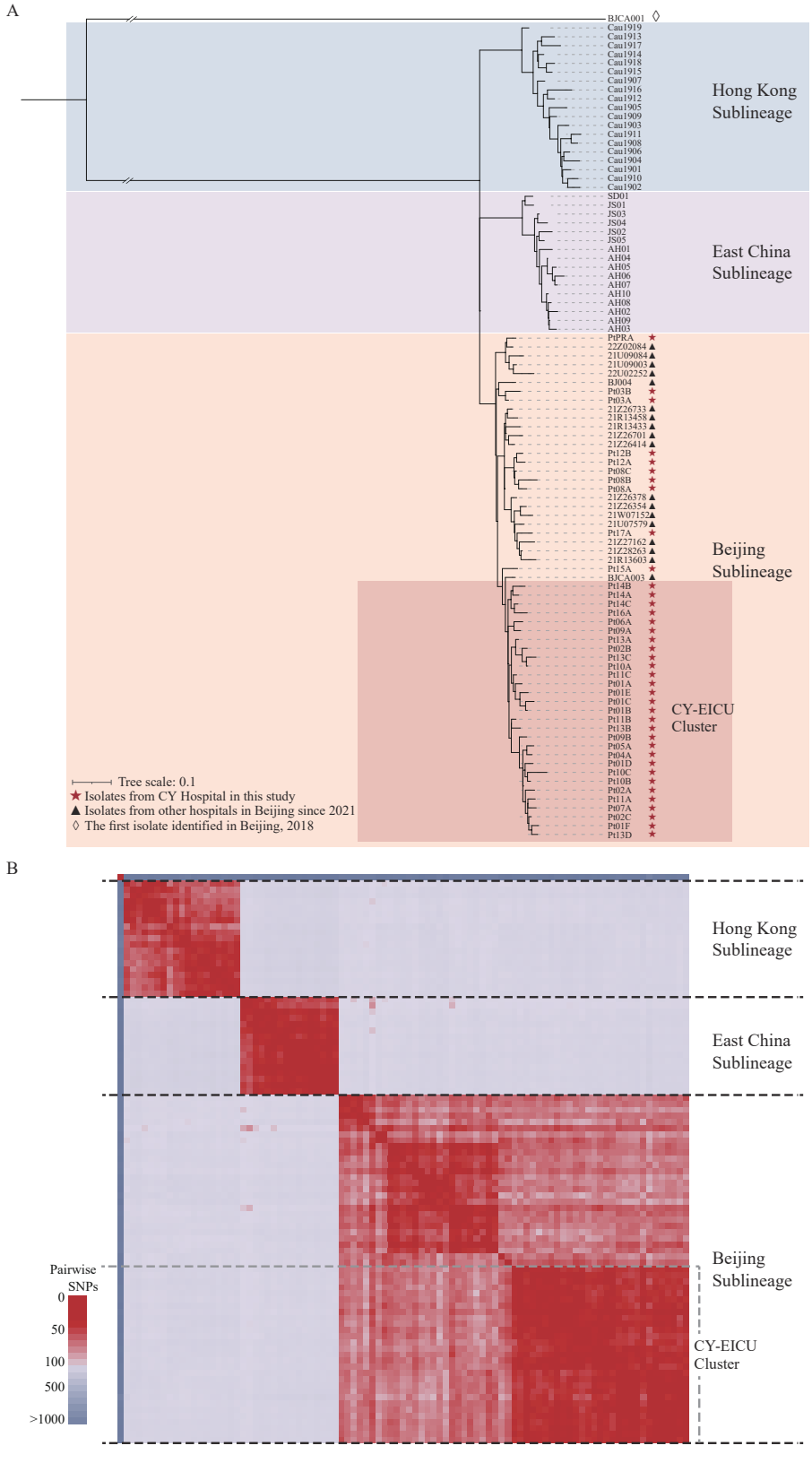

FIGURE 2. Analysis of Clade I *Candida auris* (*C. auris*) isolates in China based on whole-genome sequencing. (A) Phylogenetic tree of *C. auris* Clade I isolates. (B) Heatmap based on genome-wide pairwise SNP analysis, with the order of strains in rows (from top to bottom) and the order in the phylogenetic tree in columns (from left to right).
Note: The first *C. auris* Clade I strain reported in Beijing (BJCA001) was used as root of the phylogenetic tree.

within the EICU may facilitate nosocomial transmission.

Antifungal susceptibility testing suggested that all isolates from CY Hospital were resistant to fluconazole and amphotericin B, according to US CDC tentative breakpoints (Supplementary Table S2). Moreover, WGS analysis revealed that all strains carried the amino acid substitutions Y132F on Erg11 and A583S on Tac1b, both of which are presumed to be associated with azole resistance (*4*–*5*). Of note, the Erg11 Y132F substitution was present in 100% of strains from the Beijing and eastern China sublineages, and 84.2% of strains from the Hong Kong SAR sublineage carried this substitution. In contrast, the Tac1b A583S substitution was found exclusively in the Beijing sublineage and was absent in both the eastern China and Hong Kong sublineage isolates. Additionally, 3 strains from different patients (strains Pt03B, Pt04A, and Pt17A) were echinocandin-resistant, and a key substitution, S639F, on Fks1 (*6*) was observed in 2 of these 3 strains. The overall outcome for these 17 patients was poor, with 35.3% (6/17) of patients dying in the hospital and 29.4% (5/17) showing no improvement before discharge (Supplementary Table S1).

DISCUSSION

C. auris is an emerging multidrug-resistant fungal pathogen that causes life-threatening diseases and nosocomial outbreaks. The crude mortality of invasive infections caused by *C. auris* has exceeded 40%, and the pathogen has rapidly spread to approximately 50 countries worldwide since it was first reported in 2008 (*7*). Notably, the incidence of *C. auris* cases has increased significantly in China since 2023, with several outbreak events reported (*2*). However, most *C. auris* cases reported in Beijing occurred as sporadic events (*2*,*4*–*5*).

In this nosocomial transmission event, 17 *C. auris*-positive patients admitted to the same hospital in Beijing during a 7-month period in 2023 were identified. More than 76% of the cases were confirmed to be *C. auris* infections, and all patients had typical *Candida* infection/colonization risk factors, for example, elderly age or underlying critically ill conditions (*8*–*9*). Patient medical records revealed that >76% of *C. auris*-positive patients received medical management in the EICU ward. As a nosocomial pathogen, *C. auris* has a predilection for colonizing patient skin and can survive on the surface of medical equipment for more than 1 month (*8*). Of note, >70% of patients at CY Hospital had at least one positive urine culture for *C. auris*, with >80% having undergone urinary catheterization. Additionally, on-site investigations in the EICU ward revealed lapses in infection control precautions, such as insufficient disinfection of medical devices and environmental surfaces, which may facilitate the transmission of *C. auris* within the hospital.

WGS is a powerful tool widely used for geographic epidemiology studies and outbreak investigations of microbial pathogens, including fungi. To date, six *C. auris* clades have been categorized globally (Clades I–VI) by WGS (*7*,*10*). In China, *C. auris* Clade I isolates were responsible for several outbreaks that occurred in East China (Anhui, Jiangsu) and Hong Kong SAR, China. In contrast, Clade III isolates caused independent outbreak events in northeastern China (Liaoning Province) and southern China (Guangdong Province) (*2*). As WGS has distinctive discriminatory power, it can provide further insights into the temporal and spatial spread of *C. auris*. In this report, WGS results revealed that the *C. auris* strains isolated in CY Hospital belonged to an emerging sublineage of Clade I, which comprised strains previously found in two other hospitals in Beijing since 2021. This Beijing sublineage had >100 bp SNP differences compared with the Clade I outbreak sublineage in East China and the sublineage spread in Hong Kong SAR. These results indicated that city-wide dissemination of a new *C. auris* sublineage was ongoing in Beijing. Additionally, sporadic cases caused by *C. auris* Clades II and III strains have also been detected in Beijing (*2*), suggesting multiple introductions of diverse lineages of *C. auris* from various sources into the city. As Beijing is a major medical hub receiving patients nationwide for medical services, enhanced surveillance of *C. auris* in the city's healthcare facilities is warranted.

Globally, *C. auris* is highly resistant to fluconazole (>80%) and moderately resistant to amphotericin B (8%–35%) (*1*). Of note, 100% of the strains identified in CY Hospital, as well as strains of the same sublineage in Beijing, were resistant to fluconazole, and all these strains carried substitutions Y132F on Erg11 and A583S on Tac1b (*4*–*5*). In particular, Tac1b A583S represents a unique genomic feature of the Beijing sublineage isolates, distinguishing them from strains of the eastern China and Hong Kong SAR sublineages. Additionally, all but one isolate within the sublineage were amphotericin B resistant. However,

the molecular mechanism responsible for amphotericin B resistance in *C. auris* remains to be investigated. Considering the high possibility of fluconazole and amphotericin B resistance among *C. auris* strains, treatment with echinocandins is currently the preferred method, and echinocandin resistance is rare (*1*). However, in this nosocomial transmission event, we further identified echinocandin-resistant isolates from 3 different patients, and a key substitution, S639F, was found on the hotspot region of Fks1 in 2 of these patients (*6*). Both of these echinocandin-resistant isolates were cultured from urine samples. Their concentration was significantly lower (<1.5%) in urine than in plasma due to the inherent nature of echinocandin-class agents. Consequently, the development of echinocandin resistance in *C. auris* could have been induced by the subtherapeutic low echinocandin concentrations present in urine during treatment (*6*).

A global consensus has emerged recognizing the significant challenges *C. auris* poses to healthcare facilities and public health. This consensus highlights the potential need for more aggressive strategies, including comprehensive surveillance, active case findings, and enhanced infection control measures (*1*). Currently, infection control strategies for *C. auris* generally adhere to standard prevention protocols for other multidrug-resistant organisms. These protocols include routine hand hygiene, environmental disinfection, and contact precautions (*9*). However, the efficacy of these strategies requires further evaluation.

This study has several limitations. First, all environmental samples from the EICU ward were negative for *C. auris*, which limited investigation of potential transmission pathways. These negative results may be due to the limited sensitivity of traditional culture-based methods; molecular tools will be incorporated in future screening efforts. Additionally, healthcare personnel and personal protective equipment have not yet been screened for *C. auris*. Overall, infection control investigations in this case require further enhancement.

In conclusion, as stated in this report, an emerging sublineage of multidrug-resistant Clade I *C. auris* disseminated in Beijing, which was responsible for nosocomial transmission in 17 patients. WGS assays can provide insights into the dynamics of *C. auris* transmission in addition to resistance mechanisms.

Conflicts of interest: No conflicts of interest.

Acknowledgements: The WGS results of *C. auris* isolates in this study are deposited at the NCBI Sequence Read Archive under BioProject ID: PRJNA906339.

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SUPPLEMENTARY MATERIAL

METHODS

Antifungal Susceptibility Testing

Minimum inhibitory concentrations (MICs) of nine antifungal agents were measured using Sensititre YeastOne^{TM} YO10 methodology (Thermo Scientific, Cleveland, OH, United States) for all *Candida auris* (*C. auris)* isolates collected in this study. The nine antifungal agents tested included four azoles (fluconazole, voriconazole, itraconazole and posaconazole), three echinocandins (caspofungin, micafungin and anidulafungin), 5-flucytosine and amphotericin B. Current available US CDC tentative breakpoints were applied (https://www.cdc.gov/fungal/candida-auris/c-auris-antifungal.html) for interpretation of susceptibility results. The quality-control strains were *Candida parapsilosis* ATCC 22019 and *Candida krusei* ATCC 6258.

Whole Genome Sequencing and Phylogenetic Analysis

All the isolates collected in this study were subjected to whole genome sequencing (WGS) using Illumina Nova 6000 platform in PE150 (150 bp paired-end) sequencing mode at Beijing Novogene Bioinformatics Technology Co., Ltd. Trimmomatic (version 0.36) was used to remove the adapters and low-quality reads from raw sequencing data (*1*). For each isolate, the reads were mapped to the *C. auris* Clade I strain B8441 (GCA_002759435.2_Cand_auris_B8441_V2) with the Burrows–Wheeler Aligner (BWA version 0.7.7) (*2*). SAMtools (version 1.6) coupled with Genome Analysis Toolkit (GATK version 4.3.0.0) were used for single nucleotide polymorphism (SNP) and indel calling (*3*–*4*). IQ-TREE (version 1.6.12) was used to generate a maximum likelihood (ML) tree of all *C. auris* isolates studied using the 2,373 confident SNPs and 1,000 ultrafast bootstrap replicates (*5*). The script "vcf2phylip.py" (https://github.com/edgardomortiz/vcf2phylip) was used to generate a FASTA for calculating inter-strain pairwise SNPs.

SUPPLEMENTARY TABLE S1. Information on 17 *C. auris*–positive patients from the CY Hospital.

Patient no.	Gender	Age (years)	Critical condition	Experienced treatment in EICU	Infection or colonization	Outcome	Date admitted to the hospital	Hospitalization days to first isolation of *C. auris*	No. of *C. auris* isolates cultured from						
									Total	Urine	Blood	CVC	Drainage	Pus	BALF
Pt01	Male	78	Yes	Yes	Infection	Not improved	2022/12/23	70	6	5		1			
Pt02	Female	86	Yes	Yes	Infection	Dead	2023/3/14	53	3	1		1	1		
Pt03	Male	71	Yes	No	Infection	Improved	2023/5/24	2	2	2					
Pt04	Female	79	Yes	Yes	Colonization	Not improved	2023/5/29	2	1	1					
Pt05	Male	26	Yes	Yes	Infection	Not improved	2023/4/10	66	1					1	
Pt06	Female	86	Yes	Yes	Infection	Improved	2023/5/11	41	1			1			
Pt07	Male	67	Yes	Yes	Infection	Improved	2023/6/20	18	1					1	
Pt08	Male	67	Yes	No	Colonization	Dead	2023/6/9	31	3	3					
Pt09	Male	78	Yes	Yes	Infection	Improved	2023/6/3	39	2	2					
Pt10	Female	82	Yes	Yes	Infection	Improved	2023/6/28	34	3	3					
Pt11	Male	81	Yes	Yes	Infection	Dead	2023/7/13	33	3	1	1				1
Pt12	Female	74	Yes	Yes	Infection	Not improved	2023/8/3	13	2		2				
Pt13	Male	52	Yes	Yes	Infection	Dead	2023/8/6	20	4	1	1	1			
Pt14	Female	83	Yes	Yes	Infection	Dead	2023/7/11	49	3	1	2				
Pt15	Female	84	No	No	Colonization	Improved	2023/8/24	7	1	1					
Pt16	Female	75	Yes	Yes	Infection	Not improved	2023/8/23	20	1		1				
Pt17	Male	74	No	No	Colonization	Not improved	2023/9/7	21	1	1					

Abbreviation: *C. auris* =*Candida auris*; BALF=bronchoalveolar lavage fluid; CVC=central venous catheter.

SUPPLEMENTARY TABLE S2. Information on *C. auris* isolates identified from the CY Hospital.

Strain no.	Patient no.	Department of isolation	Date of sampling	Specimen type	Antifungal susceptibility (minimum inhibitory concentration, mg/L)*									Genome accession no.	Key substitutions	
					Fluconazole	Voriconazole	Itraconazole	Posaconazole	Amphotericin B	Caspofungin	Micafungin	Anidulafungin	5-Flucytosine		Erg11	Fks
Pt01A	Pt01	EICU	2023/3/2	Urine	***128***	0.5	0.12	0.03	***4***	0.12	0.12	0.12	0.12	SRR29824987	Y132F	
Pt01B	Pt01	SICU1	2023/4/23	Urine	***256***	0.5	0.12	0.03	***4***	0.5	0.12	0.25	0.12	SRR29824986	Y132F	
Pt01C	Pt01	SICU1	2023/5/10	Urine	***256***	0.5	0.25	0.06	***2***	0.25	0.12	0.25	<0.06	SRR29824972	Y132F	
Pt01D	Pt01	SICU1	2023/5/23	Urine	***256***	0.5	0.25	0.03	***2***	0.5	0.12	0.25	0.12	SRR29824961	Y132F	
Pt01E	Pt01	SICU1	2023/6/27	Urine	***128***	0.5	0.12	0.03	***2***	0.5	0.12	0.25	0.12	SRR29824951	Y132F	
Pt01F	Pt01	SICU1	2023/9/2	CVC	***256***	0.5	0.12	0.06	***2***	0.5	0.12	0.25	0.12	SRR29824950	Y132F	
Pt02A	Pt02	EICU	2023/5/5	Drainage	***128***	0.5	0.12	0.03	***4***	0.12	0.12	0.25	0.06	SRR29824949	Y132F	
Pt02B	Pt02	EICU	2023/5/8	Urine	***128***	0.25	0.06	0.03	***2***	0.12	0.12	0.12	0.12	SRR29824983	Y132F	
Pt02C	Pt02	EICU	2023/5/9	CVC	***128***	0.5	0.12	0.03	***4***	0.12	0.12	0.12	0.12	SRR29824982	Y132F	
Pt03A	Pt03	SICU2	2023/5/25	Urine	***256***	0.5	0.12	0.03	***4***	0.12	0.12	0.12	0.12	SRR29824981	Y132F	
Pt03B	Pt03	ICU2 [CYC]	2023/6/17	Urine	***128***	0.25	0.06	0.03	***4***	***8***	***>8***	***>8***	<0.06	SRR29824985	Y132F	S639F
Pt04A	Pt04	EICU	2023/5/30	Urine	***128***	0.5	0.06	0.03	***2***	***4***	***>8***	***4***	0.12	SRR29824984	Y132F	S639F
Pt05A	Pt05	EICU	2023/6/14	Pus	***256***	1	0.12	0.06	***4***	0.12	0.12	0.12	0.12	SRR29824980	Y132F	
Pt06A	Pt06	EICU	2023/6/20	CVC	***128***	0.5	0.12	0.03	***4***	0.12	0.12	0.12	0.12	SRR29824979	Y132F	
Pt07A	Pt07	NICU	2023/7/7	Pus	***256***	1	0.25	0.06	***2***	0.25	0.25	0.25	0.12	SRR29824978	Y132F	
Pt08A	Pt08	RICU	2023/7/9	Urine	***>256***	1	0.25	0.06	***2***	0.12	0.12	0.12	<0.06	SRR29824977	Y132F	
Pt08B	Pt08	RICU	2023/7/28	Urine	***>256***	1	0.25	0.12	***4***	0.12	0.12	0.12	0.12	SRR29824976	Y132F	
Pt08C	Pt08	RICU	2023/8/7	Urine	***>256***	1	0.12	0.06	***2***	0.12	0.12	0.12	<0.06	SRR29824975	Y132F	
Pt09A	Pt09	EICU	2023/7/11	Urine	***128***	0.25	0.12	0.03	***2***	0.06	0.12	0.12	<0.06	SRR29824974	Y132F	
Pt09B	Pt09	EICU	2023/7/23	Urine	***128***	0.25	0.06	0.03	***2***	0.12	0.12	0.12	0.06	SRR29824973	Y132F	
Pt10A	Pt10	EICU	2023/7/31	Urine	***128***	0.5	0.06	0.03	***4***	0.12	0.12	0.12	0.12	SRR29824971	Y132F	
Pt10B	Pt10	EICU	2023/8/3	Urine	***256***	1	0.25	0.06	***4***	0.25	0.12	0.25	0.12	SRR29824970	Y132F	
Pt10C	Pt10	EICU	2023/8/14	Urine	***256***	2	0.25	0.06	***2***	0.25	0.12	0.25	0.12	SRR29824969	Y132F	
Pt11A	Pt11	EICU	2023/8/14	Urine	***128***	0.25	0.06	0.03	***4***	0.06	0.12	0.12	0.06	SRR29824968	Y132F	
Pt11B	Pt11	EICU	2023/8/15	BALF	***256***	1	0.12	0.12	***4***	0.12	0.12	0.12	0.12	SRR29824967	Y132F	
Pt11C	Pt11	EICU	2023/8/18	Blood	***128***	0.5	0.12	0.03	***4***	0.12	0.12	0.12	0.12	SRR29824966	Y132F	

Continued

Strain no.	Patient no.	Department of isolation	Date of sampling	Specimen type	Antifungal susceptibility (minimum inhibitory concentration, mg/L)*									Genome accession no.	Key substitutions	
					Fluconazole	Voriconazole	Itraconazole	Posaconazole	Amphotericin B	Caspofungin	Micafungin	Anidulafungin	5-Flucytosine		Erg11	Fks
Pt12A	Pt12	NICU	2023/8/15	Blood	***>256***	0.5	0.12	0.03	***4***	0.25	0.25	0.12	<0.06	SRR29824965	Y132F	
Pt12B	Pt12	NICU	2023/8/20	Blood	***256***	1	0.25	0.06	***2***	0.5	0.12	0.25	0.12	SRR29824964	Y132F	
Pt13A	Pt13	EICU	2023/8/25	Blood	***256***	0.5	0.12	0.03	***4***	0.12	0.12	0.12	0.12	SRR29824963	Y132F	
Pt13B	Pt13	EICU	2023/8/25	CVC	***128***	0.5	0.12	0.03	***4***	0.12	0.12	0.12	0.12	SRR29824962	Y132F	
Pt13C	Pt13	EICU	2023/8/30	Wound	***256***	0.5	0.12	0.03	***4***	0.12	0.12	0.12	0.12	SRR29824960	Y132F	
Pt13D	Pt13	EICU	2023/9/4	Urine	***256***	0.5	0.12	0.03	***4***	0.12	0.12	0.12	0.12	SRR29824959	Y132F	
Pt14A	Pt14	EICU	2023/8/28	Blood	***128***	0.5	0.12	0.03	***4***	0.12	0.12	0.12	0.12	SRR29824958	Y132F	
Pt14B	Pt14	EICU	2023/9/1	Urine	***256***	0.5	0.12	0.03	***4***	0.12	0.12	0.25	0.12	SRR29824957	Y132F	
Pt14C	Pt14	EICU	2023/9/1	Blood	***256***	0.5	0.25	0.06	***2***	0.25	0.12	0.25	0.12	SRR29824956	Y132F	
Pt15A	Pt15	RD2	2023/8/30	Urine	***128***	0.5	0.12	0.06	***4***	0.12	0.12	0.12	0.12	SRR29824955	Y132F	
Pt16A	Pt16	EICU	2023/9/11	Blood	***128***	0.5	0.12	0.03	***4***	0.12	0.12	0.12	0.06	SRR29824954	Y132F	
Pt17A	Pt17	ED [CYC]	2023/9/26	Urine	***>256***	8	0.5	0.25	***4***	***>8***	***2***	***2***	0.12	SRR29824953	Y132F	
PtPRA[†]	PtPR	RD4	2022/3/2	Urine	***>256***	8	0.5	0.25	***8***	0.5	0.25	0.25	0.25	SRR29824952	Y132F	

Abbreviation: *C. auris*=*Candida auris*; ED=emergency department; RD=respiratory department; ICU=intensive care unit; EICU=emergency ICU; NICU=neurology ICU; RICU=respiratory ICU; SICU=surgical ICU; BALF=bronchoalveolar lavage fluid; CVC=central venous catheter.

* Resistant results for fluconazole, amphotericin B and echinocandin agents interpreted per US CDC tentative breakpoints (https://www.cdc.gov/fungal/candida-auris/c-auris-antifungal.html) were marked in italic bold font.

[†] Strain PtPRA was isolated from a patient admitted to the hospital one year before the study period. This patient had been described in another report during treatment at a different hospital (Chen XF et al. 2024), and was not included in the 17 cases reported in this study.

SUPPLEMENTARY TABLE S3. Published *Candida auris* Clade I genomes used in this study.

Genome accession no.	Isolate	Provincial-level administrative divisions	Reference
SRR9316737	BJCA001	Beijing	6
ERR3503255	Cau1901	Hong Kong	7
ERR3503256	Cau1902	Hong Kong	7
ERR3503257	Cau1903	Hong Kong	7
ERR3503258	Cau1904	Hong Kong	7
ERR3503259	Cau1905	Hong Kong	7
ERR3503260	Cau1906	Hong Kong	7
ERR3503261	Cau1907	Hong Kong	7
ERR3503262	Cau1908	Hong Kong	7
ERR3503263	Cau1909	Hong Kong	7
ERR3503264	Cau1910	Hong Kong	7
ERR3503265	Cau1911	Hong Kong	7
ERR3503266	Cau1912	Hong Kong	7
ERR3503267	Cau1913	Hong Kong	7
ERR3503268	Cau1914	Hong Kong	7
ERR3503269	Cau1915	Hong Kong	7
ERR3503270	Cau1916	Hong Kong	7
ERR3503271	Cau1917	Hong Kong	7
ERR3503272	Cau1918	Hong Kong	7
ERR3503273	Cau1919	Hong Kong	7
SRR20980354	BJCA003	Beijing	8
SRR26035613	BJ004	Beijing	9
SRR26035602	SD01	Shandong	9
SRR26035601	JS01	Nanjing	9
SRR26035600	JS02	Nanjing	9
SRR26035599	JS03	Nanjing	9
SRR26035598	JS04	Nanjing	9
SRR26035597	JS05	Nanjing	9
SRR26035596	AH08	Anhui	9
SRR26035623	AH09	Anhui	9
SRR26035622	AH10	Anhui	9
SRR26035621	AH04	Anhui	9
SRR26035620	AH05	Anhui	9
SRR26035619	AH06	Anhui	9
SRR26035618	AH07	Anhui	9
SRR26035617	AH01	Anhui	9
SRR26035616	AH02	Anhui	9
SRR26035615	AH03	Anhui	9
SRR29536503	21U07579	Beijing	10
SRR29536500	21Z28263	Beijing	10
SRR29536497	22Z02084	Beijing	10
SRR29536494	21Z26378	Beijing	10

Continued

Genome accession no.	Isolate	Provincial-level administrative divisions	Reference
SRR29536491	21Z26701	Beijing	10
SRR29536488	21W07152	Beijing	10
SRR29536501	21Z27162	Beijing	10
SRR29536498	21U09084	Beijing	10
SRR29536495	21R13433	Beijing	10
SRR29536492	21Z26414	Beijing	10
SRR29536489	21Z26733	Beijing	10
SRR29536502	21Z26354	Beijing	10
SRR29536499	21U09003	Beijing	10
SRR29536496	22U02252	Beijing	10
SRR29536493	21R13458	Beijing	10
SRR29536490	21R13603	Beijing	10

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