**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
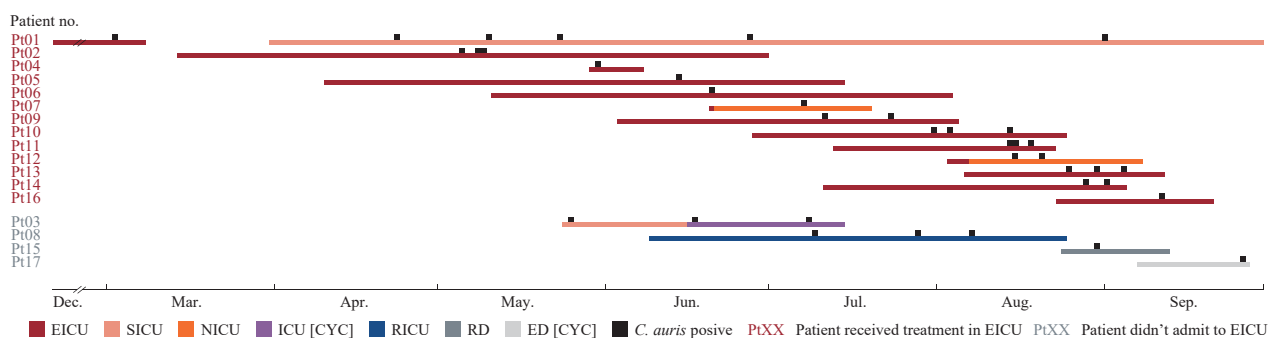
FIGURE 1. Epidemiological timeline of *Candida auris* (*C. auris*)–positive cases identified in the CY Hospital.
Note: This timeline tracked the hospitalization duration and specific clinical wards for each patient and the *C. auris* culture–positive timepoints. Pt01 was admitted to the Emergency Intensive 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*
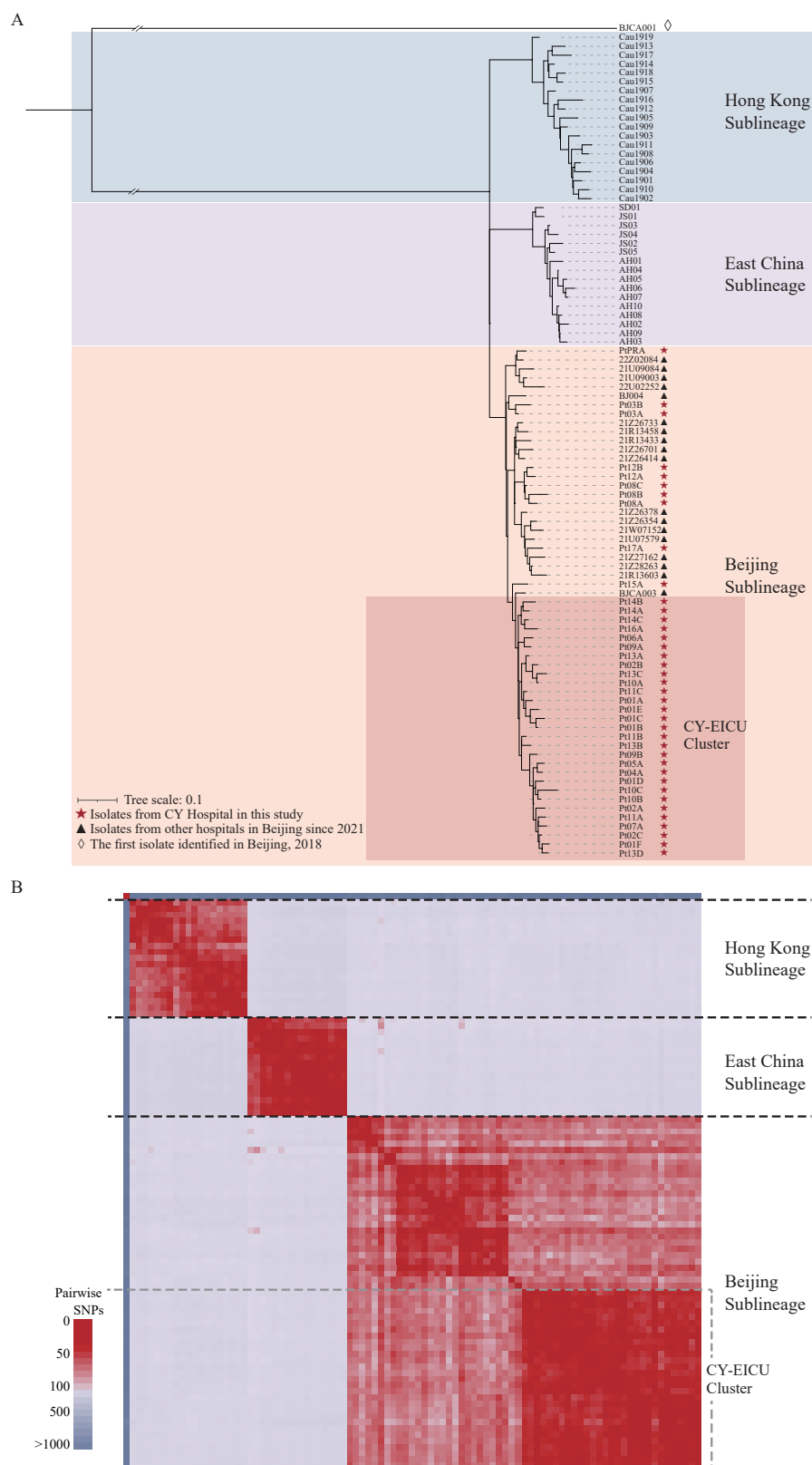
FIGURE 2. Analysis of Clade I *Candida auris* (*C. auris*) isolates in China based on whole-genome sequencing. (A) Phylogenetic tree of *C. auris* Clade I isolates. (B) Heatmap based on genome-wide pairwise SNP analysis, with the order of strains in rows (from top to bottom) and the order in the phylogenetic 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.

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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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