**Background**

- Candida is a common and deadly hospital infection; the majority of cases is due to invasion of the bloodstream by the opportunistic fungus, *Candida albicans*.
- Recently, *Candida haemulonii* and the closely-related, and phenotypically-indistinguishable species, *Candida auris* and *Candida pseudohaemulonii*, have emerged as opportunistic pathogens causing outbreaks.
- Importantly, these species are relatively resistant to fluconazole with elevated minimum inhibitory concentrations (MICs).
- *C. auris*, an unusual species, was first reported in Japan in 2009 and can only be reliably identified using sequence analysis of the ribosomal RNA gene.

**Objectives**

- To describe the identification and antifungal susceptibility profile of *C. auris* isolated from four South African patients with candidemia.
- To describe the phylogenetic relatedness of these isolates to those from other geographic locations.

**Methods**

- We analyzed four isolates submitted to the National Institute for Communicable Diseases, from four patients with candidemia admitted to different public- and private-sector hospitals. Patient demographic and clinical data were collected, where possible.
- Phenotypic identification: ChromAgar Candida medium (Mast Diagnostics, Merseyside, UK), Vitek-2 YST (bioMérieux Inc, Marcy l’Etoile, France) and API 20C AUX (bioMérieux Inc, Marcy l’Etoile, France).
- Molecular identification: Sequencing of internal transcribed spacer (ITS) region of the ribosomal RNA gene.
- Antifungal susceptibility testing: Microbroth dilution testing was performed for nine antifungal agents based on recommendations from the Clinical Laboratory Standards Institute (CLSI) (M27-A3). There are no clinical breakpoints for *C. auris*.

**Results**

- All isolates were misidentified as *C. haemulonii* and *Rhodotorula glutinis* using Vitek-2 YST and API 20C AUX assays (Table 1). All isolates assimilated N-acetyl-glucosamine.
- All isolates had high fluconazole MICs (Table 1). Isolates 209 and 224 showed reduced voriconazole susceptibility with MICs of 1 µg/ml and 2 µg/ml, above the epidemiologic cut-off value for 11 *Candida* species. *Amphotericin B* and echinocandins showed good activity.
- Using the CBS-KNAW database, pairwise sequence alignment of ITS region showed 99% sequence homology to Kuwaiti isolates and alignment of D1/D2 domain showed 98% homology to Kuwaiti/Indian isolates.
- In a neighbor-joining phylogenetic tree based on ITS sequences, South African isolates formed a cluster with Indian and Kuwaiti isolates (Figure 1).
- Clinical data were only available for one patient:
  - A 74-year-old male. Referred to a public-sector specialist burns unit from a private-sector hospital; 40% third degree burns with inhalational injury (required debridement, skin grafts and tracheostomy); in-ITU: central venous catheter/s, arterial line, urinary catheter, mechanically ventilated; multiple episodes of sepsis (requiring broad-spectrum antibiotics including beta-lactams, colistin, linezolid and vancomycin); renal failure (required hemodialysis).
  - **Treatment**: amphotericin B deoxycholate (only received 1 dose).
  - **Outcome**: died 35 days after first admission to hospital.

**Discussion**

- This is the first description of candidemia due to *C. auris* in South Africa.
- All isolates were misidentified by routine diagnostic platforms and eventually identified using sequence analysis.
- *C. auris* should be suspected in the clinical laboratory when a white yeast with reduced susceptibility to fluconazole is cultured and biochemical tests indicate *C. haemulonii* or *R. glutinis*.

![Phylogenetic relatedness of internal transcribed spacer (ITS) region of the ribosomal RNA gene of *C. auris* with closely-related *Candida* species.](image-url)

<table>
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<th>Table 1: Identification and antifungal susceptibility results of four <em>Candida auris</em> isolates from four patients with candidemia</th>
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<td><strong>Strain</strong></td>
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**Abbreviations**: AMB: amphotericin B; FLU: fluconazole; VRC: voriconazole; POS: posaconazole; ITC: itraconazole; FC: flucytosine; CAS: caspofungin; MFG: micafungin; AFG: anidulafungin. Sequence data for the four isolates have been deposited in the National Center for Biotechnology Information (NCBI). The allocated accession numbers are KJ1236782 to KJ1236785 and KJ1236786 to KJ1236789 for the ITS and D1/D2 regions.