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**Candida haemulonii and C. auris, Tel Aviv, Israel**

Ronen Ben-Ami, Judith Berman, Ana Novikov, Edna Bash, Yael Shachor-Meyouhas, Shiri Zakin, Yasmin Maor, Jalal Tarabia, Vered Schechner, Amos Adler, Talya Finn

**Learning Objectives**

Upon completion of this activity, participants will be able to:

1. Assess the phylogenetic analysis of *Candida auris* and *C. haemulonii* in the current study
2. Analyze patient characteristics among infections with *C. auris* and *C. haemulonii*
3. Distinguish the pattern of antifungal resistance in infections with *C. auris* and *C. haemulonii*
4. Evaluate the pathologic potential of *C. auris* and *C. haemulonii*

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*Candida auris* and *C. haemulonii* are closely related, multidrug-resistant emerging fungal pathogens that are not readily distinguishable with phenotypic assays. We studied *C. auris* and *C. haemulonii* clinical isolates from 2 hospitals in central Israel. *C. auris* was isolated in 5 patients with nosocomial bloodstream infection, and *C. haemulonii* was found as a colonizer of leg wounds at a peripheral vascular disease clinic. Liberal use of topical miconazole and close
contact among patients were implicated in *C. haemulonii* transmission. *C. auris* exhibited higher thermotolerance, virulence in a mouse infection model, and ATP-dependent drug efflux activity than *C. haemulonii*. Comparison of ribosomal DNA sequences found that *C. auris* strains from Israel were phylogenetically distinct from isolates from East Asia, South Africa and Kuwait, whereas *C. haemulonii* strains from different countries were closely interrelated. Our findings highlight the pathogenicity of *C. auris* and underscore the need to limit its spread.

**Candida** species are leading causes of bloodstream infection (BSI) in hospitalized patients, particularly those in intensive care units who are exposed to broad-spectrum antimicrobial drugs, indwelling vascular catheters, parenteral nutrition, abdominal surgery, and immunosuppressive agents (1,2). High rates of attributable death have been associated with delayed initiation of appropriate antifungal treatment (3,4). This problem is compounded by the emergence of drug-resistant **Candida** species, notably *C. glabrata*, in many hospitals (5).

*C. auris* is an emerging opportunistic pathogen, first reported in 2009 as an isolate from the external ear of an inpatient at a hospital in Japan (6). It has since been identified as a cause of nosocomial BSI in numerous countries in East Asia, the Middle East, Africa, and Europe (7–11). *C. auris* might be resistant to multiple classes of antifungal agents and apparently has a potential for person-to-person transmission, challenging clinicians and infection control teams (12). *C. auris* often is misidentified by traditional microbiological methods as *C. haemulonii*, a phylogenetically related drug-resistant *Candida* species that also is increasingly reported in healthcare facilities worldwide (13).

We report on the detection of multidrug-resistant *C. auris* and *C. haemulonii* in clinical specimens in Tel Aviv, Israel, and specifically on the emergence of *C. auris* as a cause of nosocomial BSI. We highlight distinct clinical and epidemiologic characteristics of these 2 species and present experimental evidence for differences in their virulence.

**Materials and Methods**

We undertook this study after *C. auris* BSI was detected in 4 patients during May–October 2014 at the Tel Aviv Sourasky Medical Center (TASMC), a tertiary-level hospital in Tel Aviv. An additional *C. auris* bloodstream isolate was recovered in April 2015 from a patient at the Wolfson Medical Center in Holon (southern Tel Aviv metropolitan area). No additional *C. haemulonii* or *C. auris* isolates were identified through inquiries at additional clinical microbiology laboratories in Israel.

The TASMC Institutional ethics committee approved this study. Need for informed consent was waived because of the observational and anonymous nature of the study.

**Clinical Candida isolates**

*Candida* isolates recovered from clinical specimens were identified at the TASMC Clinical Microbiology Laboratory by growth characteristics on CHROMagar Candida (CHROMagar, Paris, France) and the Vitek 2 YST ID system (bioMérieux, Marcy-l’Étoile, France). The Vitek 2 database does not include *C. auris*, and this species is routinely misidentified as *C. haemulonii* (13). We therefore reviewed all isolates identified as *C. haemulonii* during January 2009–August 2015. Isolates recovered during May 2014–August 2015 were stored at -20°C and subjected to further analyses. We assessed thermotolerance by plating serial dilutions of yeast culture on Sabouraud dextrose agar (SDA) plates and assessing growth after 24 h incubation at 35°C–42°C.

**Sequence-Based Species Identification**

*Candida* isolates were streaked on SDA plates to ensure purity. We extracted DNA by using PrepMan Ultra solution (Applied Biosystems, Foster City, CA, USA) according to the manufacturer’s instructions and amplified and sequenced the internal transcribed spacer (ITS) and D1/D2 large subunit (LSU) ribosomal DNA segments by using primer pairs ITS1/ITS4 and LSU1/LSU2 (14), respectively. PCR was performed in 0.2-mL tubes with 0.4 μmol/L or 0.2 μmol/L of each primer for ITS and LSU, respectively; 10 μL Larova Red Load Taq Master Mix (5×) (Larova, Jena, Germany); and ≈25 ng of template. PCR conditions were 95°C for 4.5 min (denaturation), 40 cycles of 95°C for 30 s (denaturation), 55°C (ITS) or 48°C (LSU) for 30 s (annealing), 72°C for 1 min (extension), and a final extension stage of 72°C for 7 min. PCR products were resolved on 0.7% agarose gel and stained with SERVA DNA stain clear G (Tamar, Mevaseret Zion, Israel). Products were cleaned with QIAquick PCR purification kit (QIAGEN, Hilden, Germany) and sequenced at Hy-Labs (Rehovot, Israel). We then aligned ITS and LSU sequences with the matching type strain sequences for CBS5149T (**C. haemulonii**), CBS7798T (**C. duboshaeumulonii**), CNM-CL7239T (**C. haemulonii** var. *vulnera*), CBS10099T (**C. pseudohaemulonii**), and CBS10913T (**C. auris**). A similarity score of >98% in both ITS and LSU sequences was required for species-level identification. All new sequences were deposited in GenBank (Table 1, https://wwwnc.cdc.gov/EID/article/23/2/16-1486-T1.htm).

**Phylogenetic Analyses**

We aligned ITS and LSU sequences of *C. haemulonii* and *C. auris* isolates by using MUSCLE (15) and generated phylogenetic trees with the neighbor-joining method (16), using the Kimura 2-parameter method to compute evolutionary distances (17). We tested phylogeny with the bootstrap method (500 replicates) and used *Schizosaccharomyces pombe* strains ATCC 38366 and CBS 356 as outgroups. Evolutionary analyses were performed in MEGA7 (18).
Patient Characteristics
We retrospectively reviewed the medical records of patients from whom Vitek-identified *C. haemulonii* was recovered from any site and recorded patient demographics, hospital unit, co-morbidities, medications, and clinical characteristics by using a structured form. We found 40 patient-specific *C. haemulonii* isolates, 20 (50%) of which originated from patients receiving care at an outpatient peripheral vascular disease clinic (clinic A). We therefore conducted an investigation at clinic A, which included review of patient treatment protocols, observed patient care, and surveillance mycologic cultures from environmental surfaces, wound irrigation solutions, dressings, and the hands of medical staff. To define risk factors for *C. haemulonii* colonization, we conducted an unmatched case–control study using 40 noncolonized patients followed at clinic A as controls.

Antifungal Susceptibility Testing
We determined MICs of fluconazole, itraconazole, voriconazole, posaconazole, amphotericin B, anidulafungin, micafungin, caspofungin, and fluconosine by broth microdilution using Clinical and Laboratory Standards Institute methods (19). Results were read after 48 h for azoles, amphotericin B, and flucytosine and after 24 h for echinocandins.

Rhodamine 6G Efflux
To assess ABC-type drug transporter activity, we determined glucose-induced efflux of rhodamine 6G, as described previously (20,21). We grew *Candida* isolates to log-phase in liquid yeast extract glucose at 35°C. We then collected yeast cells by centrifugation, transferred 10⁴ cells to 20 mL fresh yeast extract glucose, and incubated them at 27°C for an additional 2 h. Next, we collected yeast cells by centrifugation, washed them twice in phosphate-buffered saline (PBS), and added 10 mL PBS containing 15 μM rhodamine 6G without glucose to the pellets. Suspensions were vortexed and incubated at 27°C for 90 min to enable rhodamine 6G uptake under carbon source–depleted conditions. We then collected cells by centrifugation, washed them twice in PBS, and suspended them in 750 μL PBS in microfuge tubes. To start rhodamine 6G efflux, we added 250 μL PBS with 8 mmol/L glucose. We prepared control tubes with glucose-free PBS, removed them after 5, 15, and 25 min of incubation at 35°C, and measured fluorescence in 200-μL aliquots of supernatant by using a spectrophotometer at excitation 527 nm and emission 555 nm (Synergy HT, BioTek, Winooski, VT, USA).

Mouse Model of Disseminated Candidiasis
To assess the relative virulence of *C. haemulonii* and *C. auris*, we determined the lethality and tissue fungal loads of representative strains in a mouse model of hematogenous disseminated candidiasis. Experiments were approved by the TASMC Institutional Animal Care and Use Ethics Committee. We used cyclophosphamide (150 mg/kg intraperitoneally) to immunosuppress 6-week-old female BALB/c mice weighing 16–20 g (Harlan, Rehovot, Israel) 3 days before and on the day of infection. *Candida* cells were collected from log-phase culture on the day of infection and washed twice in sterile PBS. Mice were infected in groups of 10 with *C. haemulonii* strain TA001-14, *C. auris* strain TA005-14, and *C. albicans* strain CBS 8837. We injected 100 μL of PBS containing 7 × 10⁷ yeast cells intravenously into the lateral tail vein of each animal. A control group received intravenous injection of cell-free PBS. Death was assessed over 30 days. Kidney tissue fungal loads were determined in separate experiments where mice were similarly immunosuppressed and infected intravenously with 4 × 10⁷ yeast cells/100 μL PBS. Seven days after infection, mice were killed by CO₂ inhalation, and kidneys were excised aseptically, weighed, and homogenized in a TissueLyser (QIAGEN). Homogenates were serially diluted 10- to 1,000-fold in sterile saline and plated on SDA. We calculated fungal loads (CFU per gram of tissue) from colony counts after 48 h incubation at 35°C.

Statistical Analyses
We compared continuous variables between case and control patients using the Student t test for normally distributed variables and the Wilcoxon rank-sum test for non–normally distributed variables. We compared dichotomous variables using Fisher’s exact test. Rhodamine 6G efflux, expressed as relative fluorescence units, was computed for each control group receiving intravenous injection of cell-free PBS. Death was assessed over 30 days. Kidney tissue fungal loads were determined in separate experiments where mice were similarly immunosuppressed and infected intravenously with 4 × 10⁷ yeast cells/100 μL PBS. Seven days after infection, mice were killed by CO₂ inhalation, and kidneys were excised aseptically, weighed, and homogenized in a TissueLyser (QIAGEN). Homogenates were serially diluted 10- to 1,000-fold in sterile saline and plated on SDA. We calculated fungal loads (CFU per gram of tissue) from colony counts after 48 h incubation at 35°C.

Results
Sequence-Based Identification
We identified 40 patient-specific *Candida* strains as *C. haemulonii* by the Vitek-2 YST ID system during January 2009–July 2015. Isolates were recovered from wounds (n = 24), urine (n = 9), blood (n = 5), and central venous catheter tips (n = 2). Of these, 9 isolates recovered during May 2014–May 2015 were available for analysis; we identified 6 (including the 5 blood isolates) as *C. auris* and 3 as *C. haemulonii* by ITS and LSU sequencing (Table 1). Sequences were 100% identical among strains of each species. *C. auris* strains from Israel shared 98.6% and 98.3% similarity of ITS and LSU sequences, respectively, with the...
C. auris type strain CBS10913®. C. haemulonii strains were 100% identical to C. haemulonii CBS5149® on the basis of ITS and LSU sequences.

Phylogenetic trees based on ITS and LSU sequences showed that the C. auris isolates from Tel Aviv are distinct from other isolates from East Asia, Africa, and the Middle East. Specifically, isolates from Israel showed 98.6% similarity of ITS and LSU sequences with the India clone, represented by CBS12768, 96.2% similarity with the South Korea clone, and 96.7% similarity with strain CH1 from Kuwait. In contrast, ITS and LSU sequences from Israel C. haemulonii strains were 100% homologous with C. haemulonii from South Korea, Brazil, and Kuwait, suggesting worldwide predominance of a single C. haemulonii clone (Figure 1).

**Clinical Features**

Eight of 9 patients with sequence-validated isolates were hospitalized at TASMC (Table 1). An additional patient with C. auris infection was hospitalized at the Wolfson...
isolates had fluconazole 50 and C. haemulonii to 2 mg/L for (MIC of other azoles were also elevated: itraconazole, 0.25 to MICs >8 mg/L (range 16–64 mg/L; MIC C. glabrata. C. haemulonii and C. auris strains exhibited robust rhodamine 6G efflux activity when glucose (8 mM) was present in the medium, consistent with ABC-type transport. Rhodamine 6G efflux of C. auris strains was significantly greater than that of C. glabrata strains (14.4-, 10-, and 6.7-fold higher at 5, 15, and 25 min, respectively; p<0.0001) and C. haemulonii (3.8-, 3.8-, and 3.6-fold higher at 5, 15, and 25 min, respectively; p<0.0001). C. haemulonii showed greater rhodamine 6G efflux than C. glabrata (3.8-, 2.7-, and 1.9-fold higher at 5, 15, and 25 min, respectively (p<0.0001) (Figure 2).

Thermotolerance
Survival and growth at physiologic temperature are prerequisites for microbial invasion and pathogenicity. C. haemulonii isolates grew well at 35°C, but growth at 37°C was poor or absent, and no growth occurred at 40°C and 42°C. In contrast, growth of C. auris isolates at 37°C and 40°C was similar to that of C. albicans, and 4 of 6 isolates grew at 42°C (Figure 3).

Virulence in a Mouse Model of Disseminated Candidiasis
We compared the virulence of C. auris and C. haemulonii isolates in a mouse model of hematogenous disseminated candidiasis. C. haemulonii was completely nonvirulent in this model; 100% of mice survived 12 days after inoculation with no visible signs of illness. In contrast, inoculation with C. auris resulted in rapid death and only 20% survival 5 days after infection (p = 0.0002, log-rank test). Death of mice infected with C. auris was significantly less rapid than that of mice infected with C. albicans (median survival 4 d

### Antifungal Susceptibility
All C. haemulonii and C. auris isolates had fluconazole MICs >8 mg/L (range 16–64 mg/L; MIC50 32 mg/L). MICs of other azoles were also elevated: itraconazole, 0.25 to >16 mg/L (MIC50 0.5 mg/L); voriconazole, 0.25–1 mg/L (MIC50 0.5 mg/L); and posaconazole, 0.06 to >8 mg/L (MIC50 0.25 mg/L). Amphotericin B MIC ranged from 1 to 2 mg/L for C. auris isolates and from 2 to 8 mg/L for C. haemulonii isolates. All isolates appeared susceptible to anidulafungin (MIC 0.03 mg/L) and all isolates except 1 C. haemulonii were susceptible to micafungin (MIC 0.12–0.5 mg/L; MIC50 0.12 mg/L). Caspofungin MIC was 0.5 mg/L for all isolates. All isolates except 1 C. auris were susceptible to flucytosine (Table 3).

### Rhodamine 6G Efflux
Rhodamine 6G is a substrate of ATP binding cassette (ABC) type efflux pumps responsible for multiazole resistance in C. glabrata. C. haemulonii and C. auris strains exhibited robust rhodamine 6G efflux activity when glucose (8 mM) was present in the medium, consistent with ABC-type transport. Rhodamine 6G efflux of C. auris strains was significantly greater than that of C. glabrata strains (14.4-, 10-, and 6.7-fold higher at 5, 15, and 25 min, respectively; p<0.0001) and C. haemulonii (3.8-, 3.8-, and 3.6-fold higher at 5, 15, and 25 min, respectively; p<0.0001). C. haemulonii showed greater rhodamine 6G efflux than C. glabrata (3.8-, 2.7-, and 1.9-fold higher at 5, 15, and 25 min, respectively (p<0.0001) (Figure 2).

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### Table 2. Comparison of colonized and noncolonized patients with Candida haemulonii, clinic A, Tel Aviv Sourasky Medical Center, Tel Aviv, Israel

<table>
<thead>
<tr>
<th>Variable</th>
<th>Cases, n = 20</th>
<th>Controls, n = 40</th>
<th>Odds ratio (95% CI)</th>
<th>p value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Median age, y (range)</td>
<td>77.5 (44–91)</td>
<td>63.0 (43–94)</td>
<td>NA</td>
<td>0.015</td>
</tr>
<tr>
<td>Male sex</td>
<td>18 (90)</td>
<td>23 (57.5)</td>
<td>6.65 (1.26–65.0)</td>
<td>0.017</td>
</tr>
<tr>
<td>Median time in clinic A, mo (range)</td>
<td>40 (8–228)</td>
<td>48 (9–192)</td>
<td>NA</td>
<td>0.44</td>
</tr>
<tr>
<td>eGFR, ml/min/1.73m², mean ± SEM</td>
<td>47.7 ± 5.56</td>
<td>62.9 ± 3.61</td>
<td>NA</td>
<td>0.022</td>
</tr>
<tr>
<td>Chronic kidney disease, stage 3–4</td>
<td>13 (65)</td>
<td>15 (37.5)</td>
<td>3.05 (0.88–11.2)</td>
<td>0.057</td>
</tr>
<tr>
<td>Dialysis</td>
<td>6 (30)</td>
<td>4 (10)</td>
<td>3.85 (0.76–21.0)</td>
<td>0.069</td>
</tr>
<tr>
<td>Ischemic heart disease</td>
<td>13 (65)</td>
<td>10 (25)</td>
<td>5.5 (1.51–21.1)</td>
<td>0.003</td>
</tr>
<tr>
<td>Diabetes mellitus</td>
<td>13 (65)</td>
<td>19 (47.5)</td>
<td>2.05 (0.59–7.37)</td>
<td>0.27</td>
</tr>
<tr>
<td>Peripheral vascular disease</td>
<td>17 (85)</td>
<td>35 (87.5)</td>
<td>0.80 (0.13–5.84)</td>
<td>1.00</td>
</tr>
</tbody>
</table>

*Values are no. (%) patients except as indicated. eGFR, glomerular filtration rate, estimated using the Modification of Diet in Renal Disease (MDRD) equation (22); NA, odds ratio is not applicable for continuous variables.
and 1 d, respectively; p = 0.01; Figure 4, panel A). Kidney tissue fungal load correlated with survival rates. Specifically, we recovered no viable yeast cells from kidneys of mice inoculated with \( C. \) haemulonii, whereas infection with \( C. \) auris and \( C. \) albicans yielded median tissue loads of \( 5.9 \times 10^4 \) CFU/g and \( 7.1 \times 10^4 \) CFU/g, respectively (p<0.0001; Figure 4, panel B). Histopathologic analysis showed yeast cell aggregates in kidneys of \( C. \) auris–inoculated mice, distinct from tissue invasive hyphae observed in \( C. \) albicans–infected kidneys (Figure 4, panel C).

**Discussion**

Concern about the international emergence and spread of \( C. \) auris as a cause of invasive infection in hospitals stems from 3 characteristics of this opportunistic pathogen (12,13): 1) resistance to multiple antifungal drugs and possibly to all major classes of systemic antifungal drugs; 2) horizontal transmission among hospitalized patients, leading to nosocomial outbreaks (8,10,11,13); and 3) high associated death rates (7,8,10). \( C. \) auris and \( C. \) haemulonii are phylogenetically related species in the Metschnikowia clade that share a propensity for multidrug resistance. We identified \( C. \) auris and \( C. \) haemulonii in 2 hospitals in Israel and highlighted clinical and experimental evidence for differences in the drug-susceptibility patterns, drug efflux activity, pathogenicity, and global phylogenetics of these 2 species.

In our study, \( C. \) auris and \( C. \) haemulonii had high MICs of azoles and amphotericin B. Echinocandin MICs were within the susceptible range. An amphotericin B epidemiologic cutoff value of 2 mg/L previously was established (23), but clinical correlation between amphotericin B MIC and treatment outcomes is lacking (24). Compared with \( C. \) auris, \( C. \) haemulonii isolates had higher amphotericin B MICs. The relevance of these resistance patterns to treatment strategies remains to be determined.

ABC-type efflux activity, as evidenced by Rhodamine 6G transport, was significantly greater among \( C. \) auris than \( C. \) glabrata isolates. This observation provides a mechanistic basis for the intrinsic resistance of \( C. \) auris to azoles and is consistent with the identification of multiple putative transporter-encoding genes belonging to the ABC and major facilitator gene families in the \( C. \) auris genome (25).

![Figure 2. Comparison of rhodamine 6G efflux over time among Candida isolates from Tel Aviv, Israel.](image-url)

**Table 3. Antifungal susceptibility profiles of Candida haemulonii and C. auris isolates, Tel Aviv, Israel**

<table>
<thead>
<tr>
<th>Isolate ID</th>
<th>Species</th>
<th>FLZ</th>
<th>ITZ</th>
<th>VRZ</th>
<th>PSZ</th>
<th>AMB</th>
<th>ANF</th>
<th>MCF</th>
<th>CSF</th>
<th>FC</th>
</tr>
</thead>
<tbody>
<tr>
<td>TA001–14</td>
<td>C. haemulonii</td>
<td>16</td>
<td>&gt;16</td>
<td>0.25</td>
<td>&gt;8</td>
<td>2</td>
<td>0.03</td>
<td>0.5</td>
<td>0.5</td>
<td>0.12</td>
</tr>
<tr>
<td>TA001–15</td>
<td>C. haemulonii</td>
<td>64</td>
<td>1</td>
<td>0.5</td>
<td>0.5</td>
<td>8</td>
<td>0.03</td>
<td>0.12</td>
<td>0.5</td>
<td>0.12</td>
</tr>
<tr>
<td>TA004–15</td>
<td>C. haemulonii</td>
<td>16</td>
<td>0.25</td>
<td>1</td>
<td>0.06</td>
<td>8</td>
<td>0.03</td>
<td>0.12</td>
<td>0.5</td>
<td>0.12</td>
</tr>
<tr>
<td>TA003–14</td>
<td>C. auris</td>
<td>32</td>
<td>0.5</td>
<td>0.5</td>
<td>0.5</td>
<td>1</td>
<td>0.03</td>
<td>0.12</td>
<td>0.5</td>
<td>0.12</td>
</tr>
<tr>
<td>TA002–14</td>
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<td>64</td>
<td>0.5</td>
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<td>0.03</td>
<td>0.12</td>
<td>0.5</td>
<td>0.5</td>
</tr>
</tbody>
</table>

*AMB, amphotericin B; ANF, anidulafungin; CSF, caspofungin; FC, flucytosine; FLZ, fluconazole; ITZ, itraconazole; MCF, micafungin; PSZ, posaconazole; VRZ, voriconazole.*
Of Vitek-identified *C. haemulonii* isolates at TASMC, 50% were wound cultures from patients cared for at clinic A. That most of these isolates were not available for sequencing is a limitation of our study. However, we identified the 2 *Candida* isolates from clinic A patients that were available by ITS and LSU sequencing as *C. haemulonii*, and all 3 sequence-identified *C. haemulonii* isolates were recovered from leg ulcers of patients with peripheral vascular disease. Colonization of patients treated in close proximity in 1 room strongly suggests person-to-person transmission and supports interim guidelines for contact isolation (26). However, we were unable to identify an environmental reservoir of *C. haemulonii*. We suggest that topical application of miconazole to wounds most likely caused selective pressure and facilitated the overgrowth of *C. haemulonii*. After this investigation and termination of routine topical azole use, no additional cases of *C. haemulonii* were detected in clinic A during April 2015–July 2016.

We recovered 5 of 6 sequence-identified *C. auris* isolates from patients with nosocomial BSI. In contrast, all *C. haemulonii* isolates were cultured from superficial wounds. This observation reflects the global epidemiology of these species. *C. haemulonii* has been isolated from chronic leg ulcers of patients in India and Brazil (27,28). *C. auris* has caused outbreaks of BSI in the United Kingdom (13), India (8), Kenya (11), South Africa (9), and South Korea (29), whereas reports of *C. haemulonii* as an agent of BSI have been infrequent (27,29–32). Moreover, *C. auris* fungemia is associated with high death rates (8,10), contrasting with reports of patients surviving prolonged *C. haemulonii* fungemia (31). Fatal *C. haemulonii* fungemia, although rare, has been reported in neonates and in patients with cancer and neutropenia (27,32).

In our study, *C. auris*, but not *C. haemulonii*, grew at 37°C–42°C and exhibited lethality and tissue invasion in a mouse model of invasive candidiasis only slightly less than those of *C. albicans*, the prototypical pathogenic *Candida* species. Both *C. auris* and *C. haemulonii* are unable to form hyphae, which contribute to virulence in *C. albicans*. Formation of large aggregates resulting from failure of budding yeast to separate has been noted in some *C. auris* isolates (33). We observed distinct yeast cell aggregates in the kidneys of mice with lethal *C. auris* infection, which suggests that aggregation might be a mode of immune evasion and persistence in tissue. The *C. auris* genome
contains *C. albicans* gene orthologs, such as secreted proteinases and mannosyl transferases, which might have roles in pathogenesis (25). However, *C. auris* has a genome that is highly divergent from those of other *Candida* species, and most of its genes have not yet been characterized (25).

Ribosomal DNA sequences were identical among *C. haemulonii* strains from Israel, Kuwait, East Asia, South America, and the United States. In contrast, the global phylogenetics of *C. auris* demonstrate distinct clones for each country, indicating greater genomic diversity for this species. Further study is needed to establish whether the divergence of *C. auris* clones translates into country-specific patterns of invasiveness, virulence, and drug resistance. Our findings affirm the need for intensified vigilance and mobilization of infection control measures to limit the spread of *C. auris*.

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References


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