including New York (8 cases), Massachusetts, Pennsylvania, Connecticut, and Rhode Island (3 cases each) (1,2); single cases have been identified in Michigan, Ohio, North Carolina, Oklahoma, New Jersey, Louisiana, Florida, and California (1,2). Four other cases have been reported: 3 in South America (Colombia, Brazil, Peru) (3,7,8) and 1 in Africa (Ethiopia) (9). Only a few Brugia species have been identified, including B. leporis, found in rabbits in the northeastern United States (1,10); B. beaveri, found in raccoons and bobcats in the southern United States; and B. gyanensis, found in coatimundi and other vertebrates in South America (8). Definitive identification with molecular techniques will better identify causative species and help clarify many of the ecologic and epidemiologic questions surrounding zoonotic filarial infections.

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References


Address for correspondence: Alberto E. Paniz-Mondolfi, Yale–New Haven Hospital, Microbiology Laboratory (PS656), 55 Park St, New Haven, CT 06511, USA; email: albertopaniz@yahoo.com

Candida auris–Associated Candidemia, South Africa

To the Editor: We noted the report by Chowdhary et al. (1) and report Candida auris as a causative agent of candidemia in South Africa, with an estimated prevalence of 0.3% (N.P. Govender et al., unpub. data). First isolated in 2009, C. auris is an emerging species associated with clinical disease (2–6). We analyzed 4 isolates submitted to the National Institute for Communicable Diseases (Johannesburg, South Africa) from 4 patients with candidemia who had been admitted to different public- and private-sector hospitals from October 2012 through October 2013.

Identification of the isolates was undertaken by using ChromAgar Candida medium (Mast Diagnostics, Merseyside, UK), Vitek-2 YST (bioMérieux, Marcy l'Etoile, France), API 20C AUX (bioMérieux), and sequencing of internal transcribed spacer (ITS) and D1/D2 domains of the ribosomal RNA gene (7), followed by microbroth dilution susceptibility testing (8). All isolates were misidentified as C. haemulonii and Rhodotorula glutinis by Vitek-2 YST and API 20C AUX assays, respectively (Table).

Similar to the findings of Chowdhary et al., all isolates assimilated N-acetyl-glucosamine (1). With the use of the CBS-KNAW database, pairwise sequence alignment of ITS region showed 99% sequence homology to Kuwait isolates, and alignment of D1/D2 domain showed 98% homology to the Kuwait/India isolates (9). In a neighbor-joining phylogenetic tree based on ITS sequences, South Africa isolates formed a cluster with India and Kuwait isolates (online Technical Appendix Figure, http://wwwnc.cdc.gov/EID/article/20/7/13-1765-Techapp1.pdf).
Fluconazole MICs were high for all isolates (Table). Isolates 209 and 224 showed reduced voriconazole susceptibility with MICs of $1 \mu g/mL$ and $2 \mu g/mL$, respectively, which is above the epidemiologic cutoff value for $11$ Candida species (10). Isolates were susceptible to amphotericin B and echinocandins at low MICs. Clinical data were available for 1 patient (online Technical Appendix Table). Two C. haemulonii isolates were identified during laboratory-based sentinel surveillance for candidemia in South Africa; the ITS region of one isolate was sequenced and the isolate identified as C. auris (N.P. Govender, pers. comm.). In this study, C. auris was misidentified by routinely used tests and was accurately identified by sequencing, in keeping with previous findings (1,3,4,6).

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References


Address for correspondence: Nelesh P. Govender, National Institute for Communicable Diseases–Centre for Opportunistic, Tropical and Hospital Infections, Private Bag X4, Sandringham, 2132, South Africa; email: neleshg@nicd.ac.za

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Table. Identification and antifungal susceptibility results of 4 Candida auris isolates from 4 male patients with candidemia, South Africa, October 2012–October 2013

<table>
<thead>
<tr>
<th>Isolate ID</th>
<th>Patient age, y</th>
<th>Hospital unit</th>
<th>Vitek-2 YST†</th>
<th>API 20C AUX†</th>
<th>DNA sequence analysis‡</th>
<th>MIC AMB</th>
<th>FLX</th>
<th>VRC</th>
<th>POS</th>
<th>ITC</th>
<th>5FC</th>
<th>CAS</th>
<th>MFG</th>
<th>AFG</th>
</tr>
</thead>
<tbody>
<tr>
<td>208</td>
<td>85</td>
<td>High-care</td>
<td>C. haemulonii</td>
<td>Rhodotorula glutinis</td>
<td>Candida auris</td>
<td>1</td>
<td>&gt;256</td>
<td>0.5</td>
<td>0.03</td>
<td>0.12</td>
<td>0.12</td>
<td>0.25</td>
<td>0.06</td>
<td>0.25</td>
</tr>
<tr>
<td>209</td>
<td>60</td>
<td>Medical ICU</td>
<td>C. haemulonii</td>
<td>R. glutinis</td>
<td>Candida auris</td>
<td>0.5</td>
<td>&gt;256</td>
<td>1</td>
<td>0.06</td>
<td>0.12</td>
<td>0.12</td>
<td>0.12</td>
<td>0.06</td>
<td>0.12</td>
</tr>
<tr>
<td>224</td>
<td>73</td>
<td>Burn ICU</td>
<td>C. haemulonii</td>
<td>R. glutinis</td>
<td>Candida auris</td>
<td>1</td>
<td>&gt;256</td>
<td>2</td>
<td>0.06</td>
<td>0.25</td>
<td>0.12</td>
<td>0.12</td>
<td>0.25</td>
<td>0.12</td>
</tr>
<tr>
<td>293</td>
<td>27</td>
<td>Trauma ICU</td>
<td>C. haemulonii</td>
<td>R. glutinis</td>
<td>Candida auris</td>
<td>1</td>
<td>64</td>
<td>0.25</td>
<td>0.015</td>
<td>0.06</td>
<td>0.06</td>
<td>0.03</td>
<td>0.06</td>
<td>0.06</td>
</tr>
</tbody>
</table>

‡bioMérieux, Marcy l’Etoile, France.

†Sequence data for the 4 isolates have been deposited in GenBank, accession nos. KJ1236762–KJ126765 and KJ126758–KJ126761 for the internal transcribed spacer and D1/D2 regions, respectively.