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. lepasi, found in rabbits in the southeastern United States (1,10); B. beaveri, found in raccoons and bobcats in the southern United States; and B. guayanesis, 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.

This work was supported by the Instituto de Salud Carlos III, Fondo de Investigaciones Sanitarias, through the sixth Networks and Centers for Collaborative Research (Red Temática de Investigación Cooperativa–Red de Investigación Cooperativa en Enfermedades Tropicales, grant no. RD12/0018/003).

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DOI: http://dx.doi.org/10.3201/eid2007.131654

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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).

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Emerging Infectious Diseases • www.cdc.gov/eid • Vol. 20, No. 7, July 2014
Flucconazole MICs were high for all isolates (Table). Isolates 209 and 224 showed reduced voriconazole susceptibility with MICs of 1 µg/mL and 2 µg/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. Clindamycin showed reduced susceptibility with MICs of 1 µg/mL. Isolates 209 and 208 were identified as Candida 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).

Acknowledgments

We thank Serisha Naicker for technical assistance.

The work was supported by the National Institute for Communicable Diseases. N.P.G. has received honoraria from MSD (Pty) Ltd South Africa (Merck) and Pfizer for speaking engagements and has received a research grant from Pfizer South Africa.

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DOL: http://dx.doi.org/10.3201/eid2007.131765

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