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. guyanensis*, 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 Investigaciónes Sanitarias, through the sixth national plan of research plus development plus innovation (2008–2011), Instituto de Salud Carlos III -General Sub-Direction of Networks and Centers for Collaborative Research (Red Temática de Investigación Cooperativa–Red de Investigación Cooperativa en Enfermedades Tropicales, grant no. RD12/0018/003).

Alberto Enrique Paniz-Mondolfi, Teresa Gárate, Christine Stavropoulos, Wen Fan, Luis Miguel González, Mark Eberhard, Fred Kimmelstiel, and Emilia Mia Sordillo

Author affiliations: Yale University School of Medicine, New Haven, Connecticut, USA (A.E. Paniz- Mondolfi); St. Luke's-Roosevelt Hospital Center of Columbia University College of Physicians and Surgeons, New York, New York, USA (A.E. Paniz-Mondolfi, C. Stavropoulos, W. Fan, F. Kimmelstiel, E.M. Sordillo); Servicio Autonomo Instituto de Biomedicina/Instituto Venezolano de los Seguros Sociales, Caracas, Venezuela (A. Paniz Mondolfi); Instituto de Salud Carlos III, Madrid, Spain (T. Gárate, L.M. González); and Centers for Disease Control and Prevention, Atlanta, Georgia, USA (M. Eberhard)

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

References

1. Orihel TC, Eberhard ML. Zoonotic filariasis. Clin Microbiol Rev. 1998;11:366–81.
2. Eberhard ML, DeMeester LJ, Martin BW, Lammie PJ. Zoonotic *Brugia* infection in western Michigan. Am J Surg Pathol. 1993;17:1058–61. http://dx.doi.org/10.1097/00000478-199310000-00012
3. Orihel TC, Beaver PC. Zoonotic *Brugia* infections in North and South America. Am J Trop Med Hyg. 1989;40:638–47.
4. Taylor MJ, Hoerauf A, Bockarie M. Lymphatic filariasis and onchocerciasis. Lancet. 2010;376:1175–85. http://dx.doi.org/10.1016/S0140-6736(10)60586-7
5. Schneider MC, Aguilera XP, Barbosa da Silva Junior J, Ault SK, Najera P, Martinez J, et al. Elimination of neglected diseases in Latin America and the Caribbean: a mapping of selected diseases. PLoS Negl Trop Dis. 2011;5:e964. http://dx.doi.org/10.1371/journal.pntd.0000964
6. Gutierrez Y. Diagnostic features of zoonotic filariae in tissue sections. Hum Pathol. 1984;15:514–25. http://dx.doi.org/10.1016/S0046-8177(84)80004-0
7. Kozek WJ, Reyes MA, Ehrman J, Garrido F, Nieto M. Enzootic *Brugia* infection in a two-year old Colombian girl. Am J Trop Med Hyg. 1984;33:65–9.
8. Baird JK, Neafie RC. South American brugian filariasis: report of a human infection acquired in Peru. Am J Trop Med Hyg. 1988;39:185–8.
9. Menéndez MC, Bouza M. *Brugia* species in a man from western Ethiopia. Am J Trop Med Hyg. 1988;39:189–90.
10. Beaver PC, Orihel TC. Human infection with filariae of animals in the United States. Am J Trop Med Hyg. 1965;14:1010–29.

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).

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

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

*AMB, amphotericin B; FLX, fluconazole; VRC, voriconazole; POS, posaconazole; ITC, itraconazole; 5FC, flucytosine; CAS, caspofungin; MFG, micafungin; AFG, anidulafungin.
†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.

Fluconazole 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 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*).

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.

Rindidzani E. Magobo, Craig Corcoran, Sharona Seetharam, and Nelesh P. Govender

Author affiliations: National Institute for Communicable Diseases, Johannesburg, South Africa (R.E. Magobo, N.P. Govender); National Health Laboratory Service, Johannesburg, South Africa (S. Seetharam); University of the Witwatersrand, Johannesburg (S. Seetharam, N.P. Govender); and Ampath National Reference Laboratory, Pretoria, South Africa (C. Corcoran)

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

References

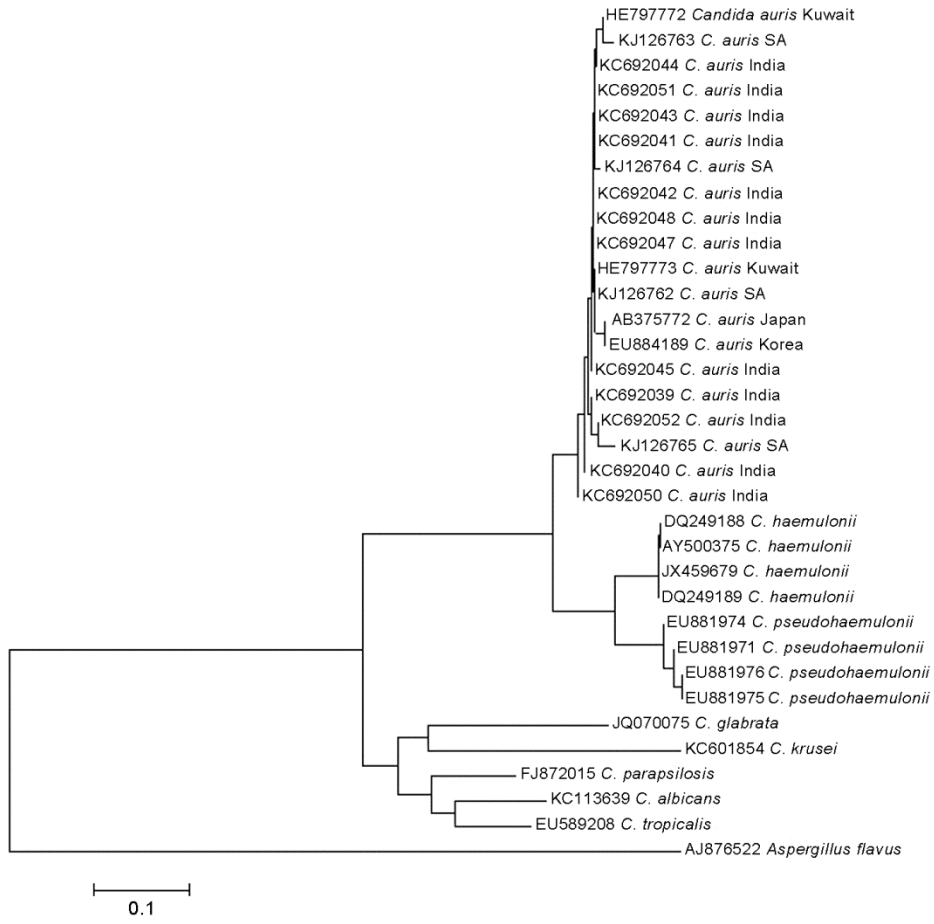
1. Chowdhary A, Sharma C, Duggal S, Agarwal K, Prakash A, Kumar Singh P, et al. New clonal strain of *Candida auris*, Delhi, India. Emerg Infect Dis.2013;19:1670–3. http://dx.doi.org/10.3201/ eid1910.130393
2. Satoh K, Makimura K, Hasumi Y, Nishiyama Y, Uchida K, Yamaguchi H. *Candida auris* sp. nov., a novel ascomycetous yeast isolated from the external ear canal of an inpatient in a Japanese hospital. Microbiol Immunol. 2009;53:41–4. http://dx.doi.org/10.1111/j.1348-0421.2008. 00083.x
3. Kim MN, Shin JH, Sung H, Lee K, Kim EC, Roy N, et al. *Candida haemulonii* and closely related species at 5 university hospitals in Korea: identification, antifungal susceptibility, and clinical features. Clin Infect Dis. 2009;48:e57–e61. http://dx.doi.org/10.1086/597108
4. Lee WG, Shin JH, Uh Y, Kang MG, Kim SH, Park KH, et al. First three reported cases of nosocomial fungemia caused by *Candida auris*. J Clin Microbiol. 2011;49:3139–42. http://dx.doi.org/10.1128/JCM.00319-11
5. Oh BJ, Shin JH, Kim MN, Sung H, Lee K, Joo MY, et al. Biofilm formation and genotyping of *Candida haemulonii*, *Candida pseudohaemulonii*, and a proposed new species (*Candida auris*) isolates from Korea. Med Mycol. 2011;49:98–102. http://dx.doi.org/10.3109/13693786.2010. 493563
6. Chowdhary A, Kumar VA, Sharma C, Prakash A, Agarwal K, Babu R, et al. Multidrug resistant endemic clonal strain of *Candida auris* in India. Eur J Clin Microbiol Infect Dis. 2013. Epub ahead of print. http://dx.doi.org/10.1007/s10096-013-2027-1
7. White TJ, Bruns T, Lee S, Taylor J. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis MA, Gelfand DH, Sninsky JJ, White TJ, editors. PCR protocols: a guide to methods and applications. San Diego: Academic Press; 1990. p. 315–22.
8. Clinical and Laboratory Standards Institute. Reference method for broth dilution antifungal susceptibility testing of yeasts; approved standard. 3rd ed. Wayne (PA): The Institute; 2008.
9. CBS-KNAW Fungal Biodiversity Centre. Pairwise sequence alignment tool [cited 2013 Nov 1]. http://www.cbs.knaw.nl/Collections/BioloMICSSequences.aspx?file=all.
10. Pfaller MA, Diekema DJ. Progress in antifungal susceptibility testing of *Candida* spp. by use of Clinical and Laboratory Standards Institute broth microdilution methods, 2010 to 2012. J Clin Microbiol. 2012;50:2846–56. http://dx.doi.org/10.1128/JCM.00937-12

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

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

Candida auris–Associated Candidemia, South Africa

Technical Appendix



Technical Appendix Figure. Phylogenetic relatedness of internal transcribed spacer region of the ribosomal RNA gene of *Candida auris* with closely related *Candida* species. Scale bar indicates nucleotide substitutions per site.

Technical Appendix Table. Clinical characteristics of a 73-year-old male patient with candidemia caused by *Candida auris*, South Africa

Isolate ID	Risk factor	Antifungal treatment	Outcome
224	Referred to a public-sector specialist burn unit from a private-sector hospital 40% third-degree burns with inhalational injury; required débridement, skin grafts, and tracheostomy In situ: central venous catheter/s, arterial line, urinary catheter Mechanically ventilated Multiple episodes of sepsis requiring broad-spectrum antimicrobial drugs, including β-lactams, colistin, linezolid, and vancomycin Renal failure requiring hemodialysis	Amphotericin B deoxycholate (received only 1 dose)	Died 35 d after admission to hospital