Diagnostic Microbiology and Infectious Disease 84 (2016) 221–222

Contents lists available at ScienceDirect

Diagnostic Microbiology and Infectious Disease

journal homepage: www.elsevier.com/locate/diagmicrobio

Mycology

Schwanniomyces etchellsii: an unusual cause of fungemia in a patient with cholecystitis

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ARTICLE INFO

Article history:
Received 27 October 2015
Accepted 13 November 2015
Available online 14 November 2015

Keywords:
Schwanniomyces etchellsii
Fungemia
Blood culture
Cholecystitis

ABSTRACT

Schwanniomyces species are largely unrecognized as being pathogenic, and a paucity of published reports exist regarding their role as infectious agents. Here, for the first time, we describe a case of human infection caused by *Schwanniomyces etchellsii* in a patient with cholecystitis.

1. Case

A 35-year-old Caucasian male presented to an Indianapolis hospital emergency department (ED) with a 4-day history of symptoms that included nausea, vomiting, and fatigue secondary to worsening abdominal pain. The patient was afebrile and did not report hematemesis or diarrhea. Significant medical history obtained at the time of ED presentation included prior MRSA bacteremia associated with right upper extremity septic thrombophlebitis, a 4-year history of oxycodone and intravenous heroin abuse for which he received daily methadone treatments, a 1-pack-per-day cigarette smoking habit, and untreated hepatitis C. As part of the initial diagnostic workup, blood specimens, including 2 sets of blood cultures, were obtained for analysis.

A computed tomographic scan of the patient's abdomen and pelvis did not reveal acute abnormalities of the kidneys, bowel obstruction, or inflammatory changes of the bowel. However, dense material consistent with biliary sludge was noted within the gallbladder. Subsequent endoscopic retrograde cholangiopancreatography with sphincterotomy confirmed the presence of sludge within the gallbladder and the biliary tract. The patient continued to have abdominal pain and eventually underwent laparoscopic cholecystectomy.

A complete blood count demonstrated profound leukocytosis (36,000/mm^3) with a left shift and thrombocytopenia (67,000/mm^3), and serum biochemical analysis revealed both elevated liver enzymes (alkaline phosphatase, 137 U/L; alanine aminotransferase, 274 U/L; aspartate aminotransferase, 216 U/L) and renal function markers (bilirubin, 5.9 mg/dL; creatinine, 3.08 mg/dL; urea nitrogen, 51 mg/dL). Following 3 days of incubation in a continuous monitoring blood culture system (BACTEC™ 9240; BD Diagnostics, Sparks, MD, USA), the aerobic bottles (BD BACTEC™ Plus Aerobic/F) from both sets of blood cultures collected in the ED and an additional set of cultures collected on the day of cholecystectomy flagged positive. Gram stains of the blood culture broth revealed purple staining budding yeast that could not be identified by PNA FISH (Yeast Traffic Light® PNA FISH®; AdvanDx, Woburn, MA, USA).

Subcultures of the blood culture broth grew white, smooth, and creamy colonies measuring less than 1 mm after 24 h of incubation at 35 °C in ambient air on Sabouraud dextrose agar. After an additional 48 h of incubation, colonies measured on average 5 mm in diameter. Colonies on *Candida* chromogenic agar were colorless. Budding yeast cells measured 1.8–4 μm × 3.75–5 μm in greatest dimension (Fig. 1A), and a modified Kinyoun stain revealed ascospore production (Fig. 1B). The organism did not produce germ tubes in fetal bovine serum, was negative for rapid trehalose assimilation, and produced short pseudohyphae on cornmeal agar (Fig. 1C). An identification could not be rendered by repeat testing using the VITEK® 2 YST card (bioMérieux, Durham, NC, USA). Subsequent testing with the bioMérieux API® 20C AUX (summarized in Table 1) gave a profile number of 2576135. Possible species-level identifications included *Candida albicans* (75.9%), *Candida tropicalis* (22.6%), and *Candida parapsilosis* (1.0%) based on this profile. Triplicate analysis by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI Biotyper; Bruker Daltonic, Billerica, MA, USA) yielded an identification of *Debaryomyces*

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http://dx.doi.org/10.1016/j.diagmicrobio.2015.11.010
0732-8893/

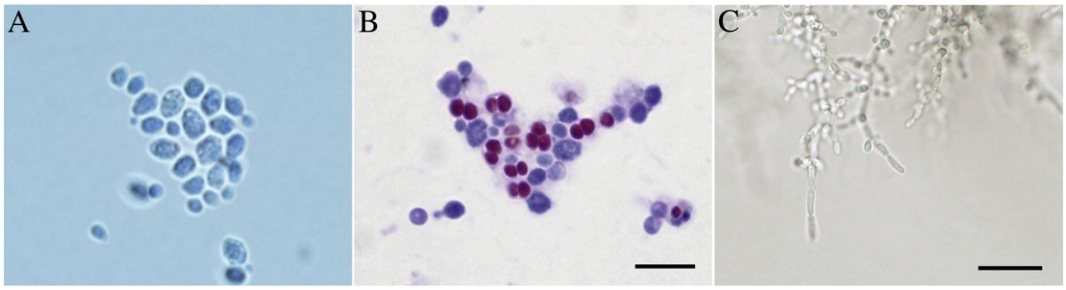

Fig. 1. (A) Lactophenol cotton blue–stained and (B) modified Kinyoun–stained smears of the patient isolate of *S. etchellsii*. The modified Kinyoun stain demonstrates ascospore production (red staining cells). (C) Pseudohyphae production demonstrated by growth on cornmeal agar for 24 h prior to photography. Bars: panels A and B, 10 μm; panel B, 20 μm.

(*Schwanniomyces*) *etchellsii* with score values >2.000 for each analysis. Dideoxy sequencing targeting the internal transcribed spacer (ITS1) and large ribosomal subunit (D1/D2) was performed at the University of Florida Interdisciplinary Center for Biotechnology Research (Gainesville, FL, USA) and the Fungus Testing Laboratory at the University of Texas Health Science Center at San Antonio. Assembled sequence reads indicated 100% identity across these regions between this isolate and the *S. etchellsii* type strain IFO 1283 (ATCC® 20126™). Results of antifungal susceptibility testing, performed using the Sensititre® YeastOne® YO-9 panel (TREK Diagnostic Systems, Cleveland, OH, USA), are presented in Table 1. Following the detection of yeast in the patient's blood cultures, he was started on a 2-week course of micafungin (100 mg/day). His condition improved, and subsequent blood cultures were negative. He was discharged to home without further complications.

Table 1
Substrate utilization and antifungal susceptibility analysis of the *S. etchellsii* clinical isolate.

Substrate utilization profile[a]	
Substrate	Reaction
D-Glucose	+
Glycerol	−
Calcium 2-ketogluconate	+
L-Arabinose	−
D-Xylose	+
Adonitol	+
Xylitol	+
D-Galactose	+
Inositol	−
D-Sorbitol	+
Methyl-αD-glucopyranoside	+
N-acetylglucosamine	+
D-Cellobiose	−
D-Lactose	−
D-Maltose	+
D-Saccharose	+
D-Trehalose	−
D-Melezitose	+
D-Raffinose	+
Antifungal susceptibility analysis[b]	
Drug	MIC
Anidulafungin MIC	0.12 μg/mL
Caspofungin MIC	0.06 μg/mL
Fluconazole MIC	4 μg/mL
5-Flucytosine MIC	≤0.06 μg/mL
Itraconazole MIC	≤0.015 μg/mL
Micafungin MIC	0.03 μg/mL
Posaconazole MIC	≤0.008 μg/mL
Voriconazole MIC	0.03 μg/mL

[a] From API 20AUX.
[b] From Sensititre® YeastOne® YO-9 panel.

Yeast belonging to the genus *Schwanniomyces* are perhaps best known for their biotechnological and industrial applications, including the use of *Schwanniomyces occidentalis* as a heterologous protein expression system (Janatova et al., 2003). Also, because this species is known to metabolize a number of carbon sources, it has been investigated for use in the fermentation industry (Wang et al., 1998). Currently, very little is known about the ecological niche of many members of this genus, including their role(s) in the human microbiome.

Schwanniomyces species are classified among the family Saccharomycetaceae, which includes a number of other yeast that are either not known to, or are rarely reported to, cause human disease. *S. etchellsii* (formerly *Debaryomyces etchellsii* and *Pichia etchellsii* (Motofumi and Kurtzman, 2011; Yamada et al., 1992)) is presumably of low pathogenicity, based partly on the uncomplicated disease course and clinical outcome of our patient. In addition, studies challenging cortisone-treated mice with *S. etchellsii* failed to generate gross or microscopic pathologic lesions (Khan et al, 1980). Related organisms, including *Debaryomyces hansenii*, *Pichia anomala*, and *Pichia angusta*, have been implicated in fungemia, endophthalmitis, and infections of immunocompromised (Bakir et al., 2004; Chakrabarti et al., 2001; McGinnis et al., 1980; Rao et al., 1991; St. Germain and Laverdière, 1986). It is unknown how the patient described herein acquired this infection, and, to the best of our knowledge, this is the first report of human infection associated with *S. etchellsii*.

Acknowledgments

The authors thank the IU Health Pathology Laboratory Division of Clinical Microbiology for help with initial isolation and characterization of the isolate.

References

Bakir M, Cerikcioglu N, Tirtir A, Berrak S, Ozek E, Canpolat C. *Pichia anomala* fungaemia in immunocompromised children. Mycoses 2004;47:231–5.
Chakrabarti A, Singh K, Narang A, Singhi S, Batra R, Rao KL, et al. Outbreak of *Pichia anomala* infection in the pediatric service of a tertiary-care center in northern India. J Clin Microbiol 2001;39:1702–6.
Janatova I, Costaglioli P, Wesche J, Masson J-M, Meilhoc E. Development of a reporter system for the yeast *Schwanniomyces occidentalis*: influence of DNA composition and codon usage. Yeast 2003;20:687–701.
Khan ZU, Misra VC, Randhawa HS, Damodaran VN. Pathogenicity of some ordinarily harmless yeasts for cortison-treated mice. Sabouraudia 1980;18(4):319–27.
McGinnis MR, Walker DH, Folds JD. *Hansenula polymorpha* infection in a child with chronic granulomatous disease. Arch Pathol Lab Med 1980;104:290–2.
Motofumi S, Kurtzman CP. *Schwanniomyces* (Chapter 67). In: Kurtzman CP, Fell JW, Buekhout T, editors. The yeasts: a taxonomic study. 5th ed. London, United Kingdom: Elsevier; 2011.
Rao NA, Nerenber AV, Forster DJ. *Torulopsis candida* (*Candida famata*) endophthalmitis simulating *Propionibacterium acnes* syndrome. Arch Ophthalmol 1991;109:1718–21.
St. Germain G, Laverdière M. *Torulopsis candida*, a new opportunistic pathogen. J Clin Microbiol 1986;24:884–5.
Wang Y, Liu H, Zhang S. Cloning of the alpha-amylase gene from *Schwanniomyces occidentalis* and expression in *Saccharomyces cerevisiae*. Sci China C Life Sci 1998;41(6):569–75.
Yamada Y, Maeda K, Banno I, van der Walt JP. An emendation of the genus *Debaryomyces* (Lodder Et Kreger-Van Rij) and the proposals of two new combinations, *Debaryomyces carsonii* and *Debaryomyces etchellsii* (*Saccharomycetaceae*). J Gen Appl Microbiol 1992;38:623–6.