Short Communication

Catheter-Related Bloodstream Infection Due to *Lodderomyces elongisporus*

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SUMMARY: *Lodderomyces elongisporus* infrequently causes bloodstream infections and has been isolated from Asia and Mexico. We encountered a catheter-related bloodstream infection, which involved some risk factors, due to *L. elongisporus* masquerading as *Candida parapsilosis*. A 39-year-old man who received a total arch and thoracoabdominal aortic replacement was admitted with a diagnosis of aorto-esophageal fistula. After thoracic drainage for the aorto-esophageal fistula, a catheter-related bloodstream infection was diagnosed. Micafungin (100 mg/day) was successfully administered to treat the catheter-related bloodstream infection for 42 days in total. The bloodstream and catheter tip yeast was grown on Candida agar medium and produced dark green colonies indicating *Candida albicans*. We performed sequencing analysis using a GenBank BLAST search. The sequence of the internal transcribed spacer region differed, and we could not definitely identify the yeast or- ganism has frequently been technically mistaken for non-*albicans* *Candida* spp. Furthermore, the prognosis and risk factors of *L. elongisporus* infection remain unclear owing to the scarcity of reported cases. Catheter-related bloodstream infection caused by this organism has not been described to date.

A 39-year-old man who had undergone total arch and thoracoabdominal aortic replacement came to the hospital when he became febrile. He was admitted with a diagnosis of aorto-esophageal fistula according to his clinical presentation and computed tomography findings. After hospitalization, the patient received a central venous catheter and was started on total parenteral nutrition. Oral microfloras were detected in the blood sample taken upon admission, and antibiotic therapy was started with ampicillin-sulbactam (9 g/day). Because drug eruption was seen, the treatment was changed to cefazolin and clindamycin, which later triggered drug fever, and was eventually switched to levoflaxacin and clindamycin.

Eleven days after admission, thoracic drainage for the aorto-esophageal fistula was performed. Five days after the operation, the patient rapidly became febrile (38.6°C), and biochemical analysis showed elevated levels of C-reactive protein (5.1 mg/dL) and β-d-glucan (42.2 pg/mL). Since a catheter-related bloodstream infection (CRBSI) was suspected, 2 sets of blood cultures (Becton Dickinson, Franklin Lakes, NJ, USA) and a culture from the central venous catheter tip were taken. Two sets of the aerobic blood culture bottles yielded yeast growth after 48 h of incubation. The culture of the central venous catheter tip also yielded yeast growth on Candida agar medium (Nissui Pharmaceutical, Tokyo, Japan). We performed echocardiography to detect possible infective endocarditis at the time of admission and found no evidence of infective endocarditis. Therefore, we did not perform subsequent echocardiography or ophthalmoscopy. After the detection of yeast, micafungin (100 mg/day) was empirically administered to treat the suspected CRBSI. Following 10 days of micafungin administration, the patient became afebrile, and blood cultures taken 72 h after antifungal therapy were negative. Considering that the patient might have a device-related infection in addition to CRBSI, we administrated the micafungin for 42 days in total. The administration of micafungin was completed without an adverse event, and no recurrence was seen.

The bloodstream and catheter tip yeast was grown on Candida agar medium, and it produced dark green colonies indicating *Candida albicans*. Results of the germ tube formation test on the colony were negative, indicating non-*albicans* *Candida*. It is particularly indicated for white or cream color colonies on fungal culture, where a positive germ tube test is strongly indicative of *C. albicans*.

Further mycotic identification using the VITEK2 system (Sysmex bioMérieux, Tokyo, Japan) yielded a definitive identification of bloodstream yeast and catheter tip yeast as *Candida parapsilosis*. The concordance rate of this catheter tip *C. parapsilosis* was 99%. Because the results of the VITEK2 system and Candida agar medium differed, and we could not definitely identify this yeast, we performed molecular identification by PCR amplification and sequencing analysis of the internal transcribed spacer (ITS) region using DNA extracted from the isolates.

The universal primers ITS1 (5'-TCCGAGGTGAACTTCGCGG-3') and ITS4 (5'-TCTCTCGGTTGATTAAGTGC-3') were used as described previously (1). We performed sequencing analysis using the GenBank BLAST Database. The sequence of the ITS region was 99.9% identical (489 bp over the entire 490-bp fragment) with that of the type strain *Lodderomyces elongisporus*.

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The ascomycetous yeast *L. elongisporus* had long been considered a teleomorph of *C. parapsilosis* owing to various phenotypic similarities that they share (2). However, their genetic backgrounds are different, and they are presently classified as different genera of yeast (3). *L. elongisporus* forms turquoise blue colonies like *C. albicans* or *Candida tropicalis* on CHROMagar Candida medium (Nippon Becton Dickinson, Tokyo, Japan). On the other hand, this organism is identified as *C. parapsilosis* with a conventional identification kit such as VITEK2 and API 20C (Sysmex bioMérieux), indicating that the identification by phenotype is difficult; thus, genetic identification is mainly used (4).

Infectious disease caused by *L. elongisporus* has been reported primarily as a bloodstream infection. *L. elongisporus* is an unusual causative organism of bloodstream infections in humans and has been isolated from Asia and Mexico (4,5). *L. elongisporus* was also reported as the causative organism of endocarditis (6). CRBSI caused by this organism has been described in detail to date. *C. parapsilosis* has been isolated from bloodstream infections in humans and has been isolated from Asia and Mexico (4,5). *L. elongisporus* was also reported as the causative organism of endocarditis (6).

CRBSI caused by this organism has been described in detail to date. *L. elongisporus* shows similar biochemical characteristics to *C. parapsilosis*; however, its risk factors and disease prognosis are uncertain. Patients at risk for *C. parapsilosis* candidemia include neonatal patients, transplant recipients, patients with a history of antifungal therapy, and patients who received parenteral nutrition. Although the risk factors for *L. elongisporus* fungemia have not been described in detail to date, prior antibiotic therapy and parenteral nutrition were performed in this case, the same as for *C. parapsilosis* candidemia. The risk factors for *L. elongisporus* fungemia may closely resemble the risk factors for *C. parapsilosis* candidemia (7). We did not examine the colonization of *Candida* in sputum, stool, or urine. The common source of entry for developing candidemia induced by *L. elongisporus* and the risk of an intestinal colonization line by *C. albicans* are unclear owing to the scarcity of reported cases.

In previous reports, antifungal agents showed good potency against *L. elongisporus*. A summary of the MICs of some antifungal agents from previous reports are shown in Table 1 (4,8). There are no established breakpoint values for antifungal agents against *L. elongisporus*. However, the MICs of antifungal agents against *L. elongisporus* are well below the normally achieved plasma levels of these drugs. Furthermore, antifungal agent resistance mechanisms, such as the FKS gene mutation, in *Candida* species have not been reported. Micafungin was used successfully in this case on the argument that CRBSI due to *Candida* species was considered initially and the MIC of micafungin is low.

| Antifungal agent | MIC (µg/mL) |
|------------------|-------------|
| micafungin       | 0.015       |
| caspofungin      | —           |
| anidulafungin    | —           |
| voriconazole     | 0.015       |
| caspofungin      | —           |
| anidulafungin    | —           |

MIC, minimum inhibitory concentration.

CRBSI due to *Lodderomyces elongisporus* (ATCC11503, accession number HQ876042). We performed sequencing analysis again using the MycoBank Database, which revealed 100% sequence identity with that of the strain *L. elongisporus* from the first to 35th identification. The sequence of the D1/D2 regions was also 100% identical to that of the strain *L. elongisporus*. Based on the sequencing results, we identified the isolate as *L. elongisporus*.

In addition, antifungal susceptibility testing was performed according to the Clinical and Laboratory Standards Institute (CLSI M27-A3). The minimum inhibitory concentrations (MICs) (48 h of incubation) of micafungin, amphotericin B, flucytosine, fluconazole, itraconazole, voriconazole, and miconazole are shown in Table 1.

The crude death rate of candidemia is high, from 35% to 60%, and that of invasive candidiasis is from 40% to 50% (9,10). There have been 15 cases of *L. elongisporus* infections, of which 3 cases were fatal, reported to date (4–6,9,11). The prognosis of *L. elongisporus* infection remains unclear owing to the scarcity of reported cases. However, the death rate (3 out of 15) is not higher than that of candidemia. The clinical spectrum of *L. elongisporus* infection remains unclear.

*L. elongisporus* is identified as *C. albicans* or *C. tropicalis* on CHROMagar Candida medium and *C. parapsilosis* in the phenotypic identification. The phenotypic identification is different from the identification in CHROMagar Candida medium and *C. parapsilosis* in the phenotypic identification. The phenotypic identification is different from the identification in CHROMagar Candida medium; thus, the genetic identification is mainly used. *L. elongisporus* infections are underdiagnosed because many establishments consider the identification complete at the point of determining the colony color on CHROMagar Candida medium and phenotypic identification. Owing to the paucity of reported cases regarding pathogenicity and the clinical spectrum of *L. elongisporus*, the clinical importance of distinguishing *L. elongisporus* from *C. parapsilosis* is unclear, and further studies are required to clarify yeast infections.

**Conflict of interest** None to declare.

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