Possibility of Frequent Detection of Invasive Cyberlindera fabianii Infection Using Molecular Method

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A case of fungemia caused by Cyberlindera fabianii was reported in the September issue of Annals of Clinical Microbiology. The C. fabianii that causes rare invasive infection can easily be misidentified as Candida utilis by Vitek-2 YST ID (bioMérieux, USA) and as Candida pelliculosa by API kit (bioMérieux, USA) with high probability. Recently, we also experienced a case of fungemia caused by C. fabianii that was misidentified as C. pelliculosa using API 20C Aux (bioMérieux, USA). As molecular identification is becoming more widespread, cases of C. fabianii infection are expected to be more frequently identified.

Key Words: Cyberlindera fabianii, Molecular biology species

We read an interesting case report by Lee et al. in the September issue of Annals of Clinical Microbiology titled “Successful treatment of fungemia caused by Cyberlindera fabianii with anidulafungin: a case report” [1]. Both two recent reports from Korea [1] and India [2] in 2015 describe misidentifications as Candida utilis using VITEK-2 YST ID card (bioMérieux, France) with high probability of 93% [1] and 97% [2], respectively. In other previous cases using rapid identification kit, C. fabianii was misidentified as Candida pelliculosa by API 32C kit (bioMérieux, Marcy l’Etoile, France) (%id 57.3; T 0.85) [3] and API 20C Aux (bioMérieux, Marcy l’Etoile, France) (%id not shown) [4]. Recently, we experienced a case of fungemia caused by C. fabianii from an intensive care unit (ICU) patient in neutropenic state with catheter insertion. Blood agar plate incubated for 24 hours under 35°C, 5% CO2 condition had small white colonies with Gram stain results almost identical to the previous report showing variable sized yeast-like cells (Fig. 1) [1].

Initial identification result using API 20C Aux (bioMérieux, France) was C. pelliculosa (%id 99.5; T 0.54). Isolation of C.
pelliculosa from blood is an uncommon finding at least in our institution. Therefore, a sequencing analysis was conducted on the internally transcribed spacer (ITS) region using primer pair of ITS1/ITS4: forward ITS 1 5′-TCCGTAGGTGAAGTCCTGCGG-3′; reverse ITS 4 5′-TCCTCCGCTTATTGTATATGC-3′. The best match in ITS1/IST4 region sequencing using BLASTn on the National Center for Biotechnology Information (NCBI) sequence database was C. fabianii (accession no. JQ342083.1, 600/600 100%) and the second match was Pichia mississippiensis (accession no. GQ340433.1, 584/593 98.5%).

According to a survey in Korea regarding the distribution of fungal species recovered from clinical specimen, both C. utilis and C. pelliculosa were rarely isolated with proportions of 0.1% (34/37,847) and 0.2% (74/37,847), respectively [5]. C. fabianii can easily be misidentified as C. utilis by Vitek-2 YST ID (bioMérieux) with high probability and as C. pelliculosa by API 20C AUX (bioMérieux) or API 32C (bioMérieux) because these commercial identification kit profiles do not include C. fabianii and its biochemical profile is similar to Candida species.

The case reports of C. fabianii causing various infections confirmed through molecular test have increased during the last few years. Fluconazole treatment for C. fabianii in literature was reported as ineffective due to higher minimal inhibitory concentration (MIC) while presumably a proportion of C. utilis and C. pelliculosa identified by commercial kits could actually be C. fabianii if molecular methods were used [6]. As molecular identification in clinical laboratories is becoming more widespread, cases of C. fabianii infection could be more frequently found. Also, C. pelliculosa or C. utilis isolated from critical specimens should be confirmed with molecular identification methods.

REFERENCES