

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. (Ann Clin Microbiol 2015;18:133-134)

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 *Cyberlindnera 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.*

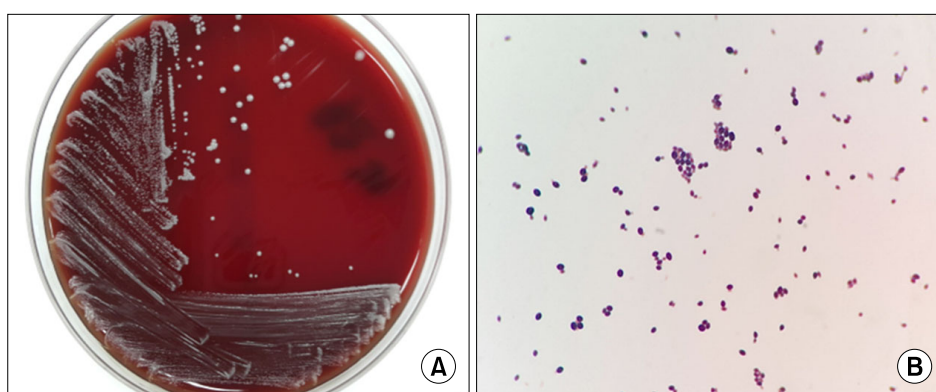


Fig. 1. Morphologic and microscopic features of *Cyberlindnera fabianii* colonies subcultured on blood agar plate. (A) Small white colony on blood agar plate. (B) Variable sized Gram-positive yeast-like cells (×1,000).

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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'-TCCGTAGGTGAACCTGCG G-3'; reverse ITS 4 5'-TCCTCCGCTTATTGATATGC-3'. The best match in ITS1/ITS4 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.

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=국문초록=

분자진단을 이용한 더 많은 침습성 *Cyberlindnera fabianii* 감염의 발견 가능성

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*Cyberlindnera fabianii*에 의한 진균혈증 1예가 Annals of Clinical Microbiology 최근 호에 보고되었다. 드물게 침습적 감염의 원인으로 보고되는 *C. fabianii*는 Vitek-2 YST ID (bioMérieux, USA)에서는 *Candida utilis*로, by API kit (bioMérieux, USA)에서는 *Candida pelliculosa*로 높은 확률로 동정될 수 있다. 최근 우리 또한 API 20C Aux (bioMérieux, USA)에서 *C. pelliculosa*로 오인된 *C. fabianii*에 의한 진균혈증을 경험하였다. 분자 동정이 더 보편화 됨에 따라 *C. fabianii*에 의한 감염은 더 자주 발견 될 수 있을 것으로 보인다. [Ann Clin Microbiol 2015;18:133-134]

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