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Paper Poster Session
Fungal diagnosis: from culture to molecular techniques

Identification of uncommon Candida species by commercial identification systems: consider the distribution of Candida species in the specimen type and the region

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Background: Recently, several studies have revealed that commercial microbial identification systems did not accurately identify the uncommon causative species of candidiasis including *C. famata*, *C. guilliermondii*, and *C. auris.* we investigated the accuracy of species-level identification in a collection of clinical isolates previously identified as *C. famata, C. guilliermondii,* and *C. lusitaniae* by the Vitek 2 system, using other conventional phenotypic method, two matrix-assisted laser desorption ionization-time of flight mass spectrometry (MALDI-TOF MS) systems, and the internal transcribed space (ITS) regions or 26S rRNA gene D1/D2 domain (D1/D2) sequencing.

Material/methods: A total of 55 clinical isolates, from individual patients, previously identified as *C. famata* (N=38)*, C. lusitaniae* (N=12)*,* and *C. guilliermondii* (N=5) by the Vitek 2 system. All 55 isolates were analyzed by the Phoenix system (Becton Dickinson Diagnostics, Sparks, MD, USA), two MALDI-TOF MS analyzers, Vitek MS (BioMérieux) and Bruker Biotyper (Bruker Daltonik, Fremont, CA), and ITS or D1/D2 sequencing.

Results: Among 38 isolates initially identified as *C. famata* by the Vitek 2 system, there was no *C. famata* and the majority (27/38 isolates, 71.1%) was identified as *C. tropicalis* (20 isolates) or *C. albicans* (7 isolates), by ITS sequencing. Among 20 isolates that were identified as *C. tropicalis*, 17 isolates (85%) were isolated from urine. And the two isolates that were finally identified as *C. auris* by ITS sequencing were from ear discharge. The Phoenix system did not accurately identify *C. lusitaniae, C. krusei, and C. auris.* The correct identification rates for 55 isolates were 92.7% (51/55 isolates) for the Vitek MS and 94.6% (52/55 isolates) for the Bruker Biotyper compared to those of the ITS sequencing.

Conclusions: These results suggested that *C. famata* is very rare in Korea as previously thought and specimen type and region should be considered in identification of uncommon *Candida* species.