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Performance of Microflex LT Biotyper and VITEK MS for Routine Identification of Yeasts

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Dear Editor,

The epidemiology of yeast infections is rapidly evolving, leading to the emergence of uncommon yeasts [1]. Rapid identification, followed by appropriate antimicrobial therapy, is associated with lower mortality [2]. Conventional phenotypic methods cannot differentiate certain yeast species accurately [3]. Matrix-assisted laser desorption ionization-time of flight mass spectrometry (MALDI-TOF MS) has been introduced in clinical microbiology to facilitate rapid yeast identification [3]. MALDI-TOF MS for yeast identification requires special preparation, similar to that for *Mycobacterium* species and gram-positive bacteria [4]. We compared the yeast identification capabilities of two MALDI-TOF systems—the Microflex LT Biotyper (Bruker Daltonics, Leipzig, Germany) and the VITEK MS (bioMérieux, Marcy-l'Étoile, France)—with respect to different sample preparation methods.

We included 208 yeast isolates collected from clinical samples at Severance Hospital between 2012 and 2015: blood (N=169), catheter (N=19), urine (N=12), sputum (N=6), and pus (N=2). Yeasts were identified at isolation by conventional phenotypic methods, including the VITEK 2 YST card (bioMérieux, Durham, NC, USA). For the Biotyper analysis, on-plate formic acid extraction and in-tube formic acid/acetonitrile extraction were performed as previously described [5]. For the VITEK MS, only on-plate formic acid extraction was performed be-

cause the in-tube method is not recommended by the manufacturer. When the yeast identification results of the VITEK 2 YST card and the two MALDI-TOF systems were consistent, they were considered reference identification. However, when the commercial system failed to identify the species or in cases of discordant results between the two MALDI-TOF systems, internal transcribed spacer (ITS) region sequencing was performed. This study was approved by the Institutional Review Board of Severance Hospital (2017-2752-001).

The Biotyper identification results for the two sample preparation methods are shown in Table 1. With the on-plate method, 95.7% of the isolates were correctly identified at the species level. With the in-tube extraction method, all isolates were correctly identified at the species level, consistent with previous reports [5-8]. The difference could be attributed to the ineffective lysis of the encapsulated yeast by the incomplete on-plate extraction method [9].


The Biotyper provides a species log score. A score ≥ 2.0 indicates excellent identification at the species level. However, the data demonstrated correct identification of isolates with cut-off scores < 2.0 as well. We derived an optimal cut-off score of ≥ 1.7 for the Biotyper, using a ROC curve. This cut-off score demonstrated a sensitivity of 100.0% (95% confidence interval [CI] 86.3–100.0%) and a specificity of 99.5% (95% CI 98.1–99.9%).

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Table 1. Microflex LT Biotyper identification scores using the on-plate and in-tube formic acid extraction methods

Reference ID* (N tested)	N (%) of isolates with Biotyper score									
	On-plate method					In-tube extraction method				
	≥2.0	1.9–<2.0	1.8–<1.9	1.7–<1.8	<1.7	No ID	≥2.0	1.9–<2.0	1.8–<1.9	1.7–<1.8
<i>Candida</i> spp.										
<i>Candida albicans</i> (65)	34 (52.3)	25 (38.5)	3 (4.6)	3 (4.6)			65 (100)			
<i>Candida tropicalis</i> (38)	8 (21.1)	15 (39.5)	11 (28.9)	1 (2.6)		3 (7.9)	35 (92.1)	3 (7.9)		
<i>Candida glabrata</i> (37)	28 (75.7)	4 (10.8)	3 (8.1)	1 (2.7)	1 (2.7)		37 (100)			
<i>Candida parapsilosis</i> (29)	4 (13.8)	9 (31)	10 (34.5)	4 (13.8)		2 (6.9)	15 (51.7)	8 (27.6)	4 (13.8)	2 (6.9)
<i>Candida krusei</i> (9)	7 (77.8)	1 (11.1)				1 (11.1)	7 (77.8)	2 (22.2)		
<i>Candida lusitaniae</i> (7)	4 (57.1)	2 (28.6)	1 (14.3)				6 (85.7)	1 (14.3)		
<i>Candida guilliermondii</i> (5)	3 (60)	2 (40)					4 (80)	1 (20)		
<i>Candida dubliniensis</i> (3)	1 (33.3)	2 (66.7)					2 (66.7)	1 (33.3)		
<i>Candida kefir</i> (2)	2 (100)						2 (100)			
Non- <i>Candida</i> spp.										
<i>Cryptococcus neoformans</i> (6)	3 (50)		1 (16.7)			2 (33.3)	6 (100)			
<i>Trichosporon asahii</i> (4)	3 (75)					1 (25)	4 (100)			
<i>Cryptococcus gattii</i> (1)	1 (100)						1 (100)			
<i>Cyberlindnera fabianii</i> (1)	1 (100)						1 (100)			
<i>Saccharomyces cerevisiae</i> (1)	1 (100)						1 (100)			
Total (208)	100 (48.1)	60 (28.8)	29 (13.9)	9 (4.3)	1 (0.5)	9 (4.3)	186 (89.4)	16 (7.7)	4 (1.9)	2 (1)
Cumulative Total	100 (48.1)	160 (76.9)	189 (90.8)	198 (95.2)	199 (95.7)	208 (100)	186 (89.4)	202 (97.1)	206 (99.0)	208 (100)

*If the identifications of the three methods were consistent, the result was considered a reference identification. When any of the results varied, ITS region sequencing was performed.

Abbreviation: ID, identification.

Table 2. Identification of clinical yeast isolates using the Microflex LT Biotyper, VITEK MS, and VITEK 2

Reference ID (N, ITS-tested N)	Microflex LT Biotyper		VITEK MS		VITEK 2	
	Correct IDs at the species level	Discordant IDs	Correct IDs at the species level	Discordant IDs	Correct IDs at the species level	Discordant IDs
<i>Candida albicans</i> (65, 1)	65 (100)		65 (100)		64 (98.5)	1 (1.5)
<i>Candida tropicalis</i> (38, 1)	37 (100)		37 (100)		37 (97.4)	1 (2.6)
<i>Candida glabrata</i> (37, 0)	37 (100)		37 (100)		37 (100)	
<i>Candida parapsilosis</i> (29, 3)	29 (100)		29 (100)		24 (82.8)	5 (17.2)
<i>Candida krusei</i> (9, 1)	9 (100)		9 (100)		7 (77.8)	2 (22.2)
<i>Candida lusitaniae</i> (7, 2)	7 (100)		7 (100)		5 (71.4)	2 (28.6)
<i>Candida guilliermondii</i> (5, 3)	5 (100)		5 (100)		1 (20.0)	4 (80.0)
<i>Candida dubliniensis</i> (3, 1)	3 (100)		3 (100)		2 (66.7)	1 (33.3)
<i>Candida kefir</i> (2, 0)	2 (100)		2 (100)		2 (100)	
<i>Cryptococcus neoformans</i> (6, 1)	6 (100)		6 (100)		5 (83.3)	1 (16.7)
<i>Trichosporon asahii</i> (4, 1)	4 (100)		4 (100)		3 (75.0)	1 (25.0)
<i>Cryptococcus gattii</i> (1, 1)	1 (100)		0 (0)	1 (100)		1 (100)
<i>Cyberlindnera fabianii</i> (1, 1)	1 (100)		1 (100)			1 (100)
<i>Saccharomyces cerevisiae</i> (1, 0)	1 (100)		1 (100)		1 (100)	
Total (208, 20)	208 (100)		207 (99.5)	1 (0.5)	188 (90.4)	20 (9.6)

Values are presented as N (%).

Abbreviations: ID, identification; ITS, internal transcribed spacer; MS, mass spectrometry.

When this cut-off was applied, 94.7% of the isolates were correctly identified at the species level using the Biotyper system with the on-plate method. This rate increased to 100% using the same system with the in-tube method. With this cut-off, the yeast identification ability of the Biotyper was comparable with that of VITEK MS. The final identification rates were 100.0% and 99.5% for the Biotyper and VITEK MS, respectively (Table 2). VITEK MS provided correct identification at the species level for all 208 isolates, except *Cryptococcus gattii*, which is not included in the VITEK MS database. The correct identification rate of the VITEK 2 system with the YST card was 90.4%.

Previous studies have suggested various cut-off values <2 [3, 10], and we found that the laboratory-validated cut-off value yielded a higher identification rate without compromising accuracy. Lee *et al* [5] reported correct identification rates of 91.4% and 97.8% using the Biotyper (≥ 1.7) and the VITEK MS, respectively, with the on-plate method. Their results included 37 uncommon yeast species, which might explain why their correct identification rates were slightly lower than ours (94.7% and 99.5%).

The on-plate method is preferred to in-tube extraction method. The latter method is time-consuming and laborious, although, traditionally, it has provided better identification results in the clinical laboratory. Lower cut-off scores using the on-plate method have resulted in greater consistency between the results of the two methods, except for *C. neoformans*. Moreover, the on-plate method may reduce the time and labor required to perform retests that are often required with the in-tube method or other complementary tests, such as ITS region sequencing.

In summary, the Biotyper and VITEK MS platforms demonstrated comparable performance for routine identification of clinically common yeasts (100% vs 99.5%, respectively). VITEK MS yields accurate results using the simple on-plate method. The Biotyper requires the in-tube extraction method to reach a score ≥ 2.0 ; however, with the application of a flexible cut-off value (≥ 1.7), the on-plate method is sufficient to achieve a correct identification rate of >95%.

Authors' Disclosure of Potential Conflict of Interest

No potential conflicts of interest relevant to this article were reported.

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