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ORIGINAL ARTICLE

The Value of the VITEK 2 System in Routine Laboratory Identification of Non-*Candida albicans* Yeasts

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ABSTRACT

Background: **As fungal infections represent a growing global health concern, particularly among vulnerable populations, and antifungal susceptibility may vary even within the same genus or species complex, accurate and rapid diagnostic tools are increasingly essential. VITEK 2 is an automated identification system based on biochemical methods and widely used in microbiology laboratories, especially in developing countries. This study aimed to retrospectively evaluate the performance and accuracy of the VITEK 2 system in identifying yeasts, particularly rare and emerging species such as *Candida auris*.**
Methods: **Data of a total of 173 yeast isolates obtained from clinical specimens were evaluated, including 96 common non-*albicans Candida* species, 68 rare *Candida* species, and nine non-*Candida* yeasts.**
Results: **Overall, 111 (64.2%) isolates were accurately identified, eight (4.6%) were misidentified, and 54 (31.2%) were not identified. Accurate identification rates for common, rare, and non-*Candida* species were 73.9% (71/96), 57.3% (39/68), and 11.1% (1/9), respectively. Among 44 *C. auris* isolates, 36 (81.8%) were accurately identified, while three (6.8%) were misidentified (two isolates as *Cryptococcus laurentii* and one isolate as *Candida duobushaemulonii*), and five (11.4%) remained unidentified.**
Conclusions: **In conclusion, more studies evaluating the latest versions of the VITEK 2 system, with a greater number of isolates, particularly rare yeast species, are needed.**
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INTRODUCTION

Fungal infections represent a growing global health concern, particularly among immunocompromised individuals, intensive care unit (ICU) patients, and those undergoing invasive procedures or receiving immunosuppressive therapy. The rising incidence of invasive fungal diseases is further exacerbated by limited access to diagnostic tools and antifungal medication, especially in low- and middle-income countries, along with the growing problem of antifungal resistance. This resistance prolongs therapy, elevates healthcare costs, and contributes to increased mortality rates. Moreover, as the number of fungal species implicated in human infec-

tions continues to grow, the need for accurate and rapid diagnostic tools becomes increasingly critical. The multidrug-resistant *Candida auris* exemplifies these challenges by causing significant morbidity and mortality and persisting in healthcare settings despite rigorous infection control measures. Inadequate diagnostic capabilities have led to the underdiagnosis of *C. auris* in many developing countries. Furthermore, as antifungal susceptibility may vary even within the same genus or species complex, precise identification is essential for initiating timely and effective treatment. Early microbiological diagnosis, accurate species-level identification, and prompt antifungal therapy are vital for controlling fungal infections and reducing morbidity and mortality [1,2].

For nearly a century, microorganisms have been identified based on their phenotypic and biochemical characteristics, leading to an increasing demand for standardized, miniaturized, and automated biochemical testing methods. Today, automated techniques based on biochemical analysis are commonly used in microbiology laboratories. The use of these techniques significantly reduces the time required for yeast identification to approximately 6 - 12 hours [3]. Despite being time-consuming and less accurate, biochemical and morphological methods remain widely used in developing countries. However, these methods are not recommended for the identification of emerging fungal species such as *C. auris* [4].

Currently available manual systems for yeast identification include RapID Yeast Plus (ThermoFisher Scientific, USA), API Candida (bioMerieux, France), API 20C AUX (bioMerieux, France), AuxaColor 2 (BioRad, USA), and Integral System YEASTS Plus (Liofilchem, Italy). Examples of automated systems are VITEK 2 (bioMérieux, France), MicroScan (Beckman Coulter, USA), BD Phoenix (BD Diagnostics, USA), OmniLog (Biolog, USA), and Sherlock Microbial Identification System (MIDI, USA) [2-4]. Among these systems, VITEK 2 and API are particularly commonly used in microbiology laboratories, especially in resource-limited settings [5]. The effectiveness of any identification system largely depends on the comprehensiveness of its database and the ability of its algorithms to accurately match unknown organisms. Atypical or emerging organisms may not be reliably identified by commercial systems unless they are adequately represented in the database [3].

Matrix-assisted laser desorption ionization-time of flight mass spectrometry (MALDI-TOF MS), a proteomics-based method, is a cost-effective and reliable alternative that offers significantly faster identification compared to conventional automated biochemical systems widely used in microbiology laboratories. This technique has proven to be revolutionary in clinical microbiology. Using MALDI-TOF MS, both filamentous and yeast fungi can be identified from various solid and broth-based media. An additional advantage of this method is its potential to serve as a powerful tool and an alternative to gold-standard techniques, particularly for identifying less common or rare yeast species. Moreover, MALDI-TOF MS enables precise differentiation of species within *Candida* complexes, such as the *Candida glabrata* complex, *Candida parapsilosis* complex, and *Candida haemulonii* complex. The two most frequently used MALDI-TOF MS platforms are the MALDI Biotyper (Bruker Daltonics, USA) and VITEK MS (bioMérieux, France) [3-5].

In addition to MALDI-TOF MS, nucleic acid sequencing, which is a reference or gold standard for identifying pathogenic yeasts, is increasingly used for difficult-to-identify fungi either from isolates or directly from clinical specimens. Sequencing can be performed using either Sanger or next-generation sequencing technologies, with the latter utilizing targeted or shotgun approaches supported by dedicated informatics pipelines. Although relatively lower costs, simplified workflows, and advanced informatics pipelines have expanded its application in microbiology laboratories, it is not widely used in developing countries due to its high cost [2-4]. Nevertheless, it is crucial that clinically significant isolates that consistently fail to be identified through conventional methods are referred to a reference laboratory for MALDI-TOF MS analysis or DNA sequencing [6].

VITEK 2 (bioMerieux, France) is an automated identification system based on biochemical methods, comprising a reader/incubator and FlexPrep software installed on a separate computer station. This system utilizes fluorescence-based technology. It was the first automated identification system, initially introduced in 1980 under the name AutoMicrobic System by a different company, with the capability to identify a limited range of enteric Gram-negative bacteria. Currently various identification test cards are available for the VITEK 2, including those for Gram-positive, Gram-negative, and anaerobic bacteria, as well as coryneforms, yeasts, *Neisseria*, and *Haemophilus* species. The system demonstrates sensitivity and specificity rates above 95% for common *Candida* species [3,4]. However, misidentification has been reported for rare *Candida* species such as *C. auris*, *Candida guilliermondii*, *Candida orthopsilosis, Candida norvegensis, Candida africanum*, and *Candida duobushaemulonii* [5,7-11]. Over time, system updates have led to increased sensitivity and accuracy in the identification of yeasts, particularly emerging pathogens [4].

This study was designed to retrospectively evaluate the performance and accuracy of the latest version (database version 9.03.3) of the VITEK 2 system, one of the most widely used automated biochemical methods for yeast identification, particularly in identifying rare and emerging species.

MATERIALS AND METHODS

This study was approved by the Clinical Research Ethics Committee of Istanbul University, Istanbul Fac-

ulty of Medicine (date: 05-16-2025 and decision number: 2025/758).

In this study, data of a total of 173 non-*Candida albicans* yeast isolates, which were obtained from various clinical specimens submitted for fungal culture to the Mycology Laboratory of Istanbul University, Istanbul Faculty of Medicine, Department of Medical Microbiology, between July 2023 and March 2025, were evaluated retrospectively.

As a routine procedure, the isolates were subcultured on Sabouraud dextrose agar (BD Difco, USA) and incubated at 37°C for 24 - 48 hours prior to the experiments. Colony colors on Chromagar Candida (Chromagar, France), microscopic morphologies on cornmeal-Tween 80 agar, and India ink stain, if necessary, were examined [12]. Advanced identification was performed using the VITEK 2 YST system with the latest software update (bioMerieux, France, database version 9.03.3), following the manufacturer's recommendations. According to the VITEK 2 system procedure, identification result was reported as a qualitative value represented as a percentage, along with an interpretation such as “excellent”, “very good”, “good”, “acceptable” or “low discrimination”. The VITEK 2 identification profiles of the isolates were compared with the results obtained using the conventional methods mentioned above. The identification result was considered accurate when the identification percentage was ≥ 94%, accompanied by a comment of “excellent” or “very good”, and consistent with conventional methods. Isolates that yielded an “unidentified” result, those with a “low discrimination”, “acceptable” or “good” interpretation, or those with identification results inconsistent with conventional methods were re-identified using MALDI-TOF MS (VITEK MS, bioMérieux, France, database version 2.1.0), also according to the manufacturer's instructions. *C. albicans* ATCC 10231, *Candida glabrata* ATCC 2001, and *Candida krusei* ATCC 6258 were used as control strains [9, 13].

RESULTS

A total of 173 isolates included in this study were obtained from various clinical specimens, comprising 70 (40.4%) skin swabs, 33 (19.0%) oral swabs, 18 (10.3%) urine, 17 (9.7%) blood, 11 (6.3%) sputum, five (2.9%) pus, four (2.4%) bronchoalveolar lavage, four (2.4%) cerebrospinal fluid, three (1.8%) tissue biopsy, three (1.8%) transtracheal aspirations, two (1.2%) nail scrapings, and one sample (0.6%) each of corneal swab, pleural fluid, and bile fluid.

By using the VITEK 2 system, 111 (64.2%) isolates were accurately identified, eight (4.6%) were misidentified, and 54 (31.2%) were not identified. The identification results obtained with the VITEK 2 system are summarized in Table 1.

Out of the 173 isolates evaluated in this study, 96 were common *Candida* species, including *C. glabrata* (n = 77), *Candida parapsilosis* (n = 9), *Candida tropicalis* (n = 6), and *C. krusei* (n = 4), 68 were rare *Candida* species, and nine were non-*Candida* yeast species. By using the VITEK 2 system, 71 (73.9%) of the common *Candida* species were accurately identified, four (4.2%) were misidentified, and 21 (21.9%) were not identified. For the rare *Candida* species, 39 (57.3%) were accurately identified, four (5.9%) were misidentified, and 25 (36.8%) were not identified. A single isolate of *Candida viswanathii* among the rare *Candida* species could not be identified, as it is not present in the VITEK 2 system database. Out of the nine non-*Candida* yeasts tested, only one (11.1%) identification result was correct (*Geotrichum klebahnii*), while eight isolates (88.9%) were not identified.

A total of eight isolates were misidentified using the VITEK 2 system. Out of the 44 *C. auris* isolates, one (2.3%) was misidentified as *C. duobushaemulonii,* while two (4.6%) were misidentified as *Cryptococcus laurentii*. Misidentification occurred in two *C. parapsilosis* isolates, which were incorrectly identified as *C. guilliermondii* and *C. laurentii* (11.1% each). Additionally, two (33.3%) *C. tropicalis* isolates were misidentified as *C. laurentii*, and a *Candida blankii* isolate was misidentified as *Candida ciferrii* (Table 2).

DISCUSSION

The increasing diversity of fungal pathogens and their varying antifungal susceptibility profiles highlight the need for accurate species-level identification. However, high-accuracy methods such as MALDI-TOF MS and Sanger sequencing are often unavailable in developing countries, where slower and less specific phenotypic assays are more commonly used [2]. Conventional phenotypic and biochemical identification methods are often time-consuming, less reliable, and may lead to the misidentification or oversight of clinically significant species. VITEK 2 is a biochemically based automated system that is commonly used in routine microbiology laboratories, particularly in resource-limited settings. Its advantages include rapid same-day results, ease of use, and no requirement for mycology-specific expertise [5]. The effectiveness of semi-automated and fully automated systems used for the identification of microorganisms largely depends on the comprehensiveness of their databases, which continue to evolve and expand over time. As a result, these systems have progressively gained the ability to accurately identify a higher percentage of isolates with each new version. Therefore, in our opinion, it is not appropriate to directly compare earlier studies on the VITEK 2 system with more recent studies utilizing updated versions. Unfortunately, despite the widespread use of VITEK 2, there is a limited number of recent publications evaluating its current performance [8-10,14].

Posterero et al. [15] investigated the accuracy of the VITEK 2 system in their meta-analysis by evaluating 26

Table 1. Identification results of yeasts using VITEK 2.

Species	Total (n)	Correctly identified n (%)	Misidentified n (%)	Not identified n (%)
Common *Candida* species				
Candida glabrata	**77**	**70 (90.9)**	**-**	**7 (9.1)**
Candida parapsilosis	**9**	**1 (11.1)**	**2 (22.2)**	**6 (66.7)**
Candida tropicalis	**6**	**-**	**2 (33.3)**	**4 (66.7)**
Candida krusei	**4**	**-**	**-**	**4 (100)**
Total	**96**	**71 (73.9)**	**4 (4.2)**	**21 (21.9)**
Rare *Candida* species				
Candida auris	**44**	**36 (81.8)**	**3 (6.8)**	**5 (11.4)**
Candida kefyr	**12**	**2 (16.7)**	**-**	**10 (83.3)**
Candida inconspicua	**4**	**-**	**-**	**4 (100)**
Candida lusitaniae	**2**	**-**	**-**	**2 (100)**
Candida norvegensis	**1**	**-**	**-**	**1 (100)**
Candida spherica	**1**	**1 (100)**	**-**	**-**
Candida blankii	**1**	**-**	**1 (100)**	**-**
Candida lambica	**1**	**-**	**-**	**1 (100)**
Candida orthopsilosis	**1**	**-**	**-**	**1 (100)**
Candida wiswanathii	**1**	**-**	**-**	**1 (100)**
Total	**68**	**39 (57.3)**	**4 (5.9)**	**25 (36.8)**
Non-*Candida* yeasts				
Saprochaete clavata	**6**	**-**	**-**	**6 (100)**
Saprochaete capitata	**1**	**-**	**-**	**1 (100)**
Geotrichum klebahnii	**1**	**1 (100)**	**-**	**-**
Kloeckera apiculata	**1**	**-**	**-**	**1 (100)**
Total	**9**	**1 (11.1)**	**-**	**8 (88.9)**
Overall total	**173**	**111 (64.2)**	**8 (4.6)**	**54 (31.2)**

Table 2. Misidentification results using VITEK 2.

Species (n)	Misidentified as	n (%)
***Candida auris* (44)**	***Candida duobushaemulonii***	**1 (2.3)**
	Cryptococcus laurentii	**2 (4.6)**
***Candida parapsilosis* (9)**	***Candida guilliermondii***	**1 (11.1)**
	Cryptococcus laurentii	**1 (11.1)**
***Candida tropicalis* (6)**	***Cryptococcus laurentii***	**2 (33.3)**
***Candida blankii* (1)**	***Candida ciferrii***	**1 (100)**

studies conducted over a long period between 1993 and 2014. It was reported that, among the studies included, 2,616 out of 2,761 (94.7%) yeast isolates were correctly identified using the VITEK 2 system. Detailed results indicated correct identification rates of 96.1% (1970/2051) for common *Candida* species (*C. albicans*, *C. glabrata*, *C. krusei*, *C. parapsilosis*, and *C. tropicalis*), 89.8% (333/371) for rare *Candida* species, and 92.3% (313/339) for non-*Candida* species (*Cryptococcus neoformans*, other *Cryptococcus* spp., *Geotrichum candi-*

dum, *Geotrichum capitatum*, *Rhodotorula glutinis*, *Rhodotorula mucilaginosa*, *Trichosporon asahii*, *Trichosporon cutaneum*, *Trichosporon mucoides*, and *Saccharomyces cerevisiae*). Kord et al. [9] evaluated a total of 137 yeast isolates recovered from blood cultures using the VITEK 2 system and confirmed the identification results they obtained by sequence analysis of the internal transcribed spacer (ITS) region. Despite using an older version (version 3.0.1), 120 (87.6%) isolates were correctly identified, 14 (10.2%) were misidentified, and three (2.2%) remained unidentified. The correct identification rates were 92% for common and 50% for rare *Candida* species. Huang et al. [14] aimed to evaluate the accuracy of species-level identification of rare *Candida* isolates using VITEK 2 in a multi-center study. For confirmation of the VITEK results, they used MALDI-TOF MS and ITS sequencing. In their study, 22 out of 34 isolates (64.7%) were correctly identified, two (5.9%) were misidentified, and 10 (29.4%) were not identified. In the present study, using the VITEK 2 system, 111 (64.2%) out of 173 isolates were correctly identified, eight (4.6%) were misidentified, and no identification result was obtained for 54 isolates (31.2%). *C. albicans* isolates were not included in this study. Among the remaining common *Candida* species (*C. glabrata*, *C. parapsilosis*, *C. tropicalis*, and *C. krusei*), the correct identification, misidentification, and non-identification rates were 73.9% (71/96), 4.2% (4/96), and 21.9% (21/96), respectively. Out of 68 rare *Candida* isolates tested, 39 (57.3%) were accurately identified, four (5.9%) were misidentified, and 25 (36.8%) could not be identified. Among the nine non-*Candida* yeast isolates tested, only one (*G. klebahnii*) was accurately identified (11.1%), while the remaining eight (88.9%) could not be identified.

C. auris was identified as a novel species in 2009 and has since emerged as an increasingly reported cause of invasive opportunistic infections worldwide [16]. This species was isolated in Türkiye for the first time from the blood culture of an ICU patient in 2019 [17]. In 2022, the World Health Organization listed *C. auris* as the second most critical fungal pathogen, following *C. neoformans*, in its fungal priority pathogen list [1]. Recently in 2024, *C. auris* and related species have been reclassified under the newly proposed genus *Candidozyma*, and *C. auris* was renamed as *Candidozyma auris* [18]. *C. auris*, which has emerged as a multidrug-resistant species, can colonize the nasal cavity and skin of humans, as well as surfaces in healthcare settings, leading to outbreaks and cases of invasive candidiasis, particularly in ICUs. It represents a growing global health threat, necessitating its rapid and accurate identification in clinical specimens to ensure timely antifungal treatment and effective infection control [10]. Biochemical-based systems may fail to accurately identify this species [16]. The VITEK 2 system has also been reported to be unreliable for the identification of this emerging species. Although the VITEK 2 system can correctly identify some *C. auris* isolates, it fails to do so consistently across all isolates. Automated identification systems, including VITEK 2, often misidentify *C. auris* as *C. duobushaemulonii*, *Candida haemulonii*, *Candida famata*, *Candida lusitaniae,* or *R. glutinis*. In particular, distinguishing *C. auris* from closely related species such as *C. duobushaemulonii* and *C. haemulonii* remains challenging. Fortunately, in 2017, the VITEK 2 system was updated to version 8.01, which included *C. auris*, *C. duobushaemulonii*, *C. haemulonii* var. *vulnera*, and *Cryptococcus gattii* in its database. This updated version provided a reliable distinction between *C. auris* and *C. haemulonii*. However, the identification of *C. duobushaemulonii* using VITEK 2 version 8.01 has been reported to still require further confirmation to differentiate it from *C. auris* [10,11,16,19].

Ambaraghassi et al. [10] evaluated the performance of the VITEK 2 system in identifying *C. auris* and related species using a total of 44 isolates, including 35 *C. auris* strains from South American, African, East Asian, and South Asian clades, five *C. haemulonii*, and four *C. duobushaemulonii* isolates. The tests were conducted in three independent laboratories, and the final results were calculated by averaging the findings. Among the 35 *C auris* isolates, accurate identification was achieved in an average of 52% of the tested samples. Low-discrimination identifications, in which the system failed to distinguish between *C. auris*, *C. duobushaemulonii*, and *C. famata*, were observed in an average of 27% of samples. Incorrect identifications occurred in an average of 21% of cases, with the majority (91%) misidentified as *C. duobushaemulonii* and the remainder (9%) as *C. Lusitaniae*/*C. duobushaemulonii*. The performance of the VITEK 2 system varied significantly across different *C. auris* clades, demonstrating high accuracy for South American isolates but markedly lower accuracy for isolates from the East Asian and African clades. Clade-specific analysis revealed 100% correct identification of South American isolates (n = 8), in contrast to lower accuracies observed for the South Asian (74%, n = 13), African (7%, n = 10), and East Asian (0%, n = 4) clades. Importantly, none of the nine non-*auris Candida* isolates were misidentified as *C. auris*. All *C. haemulonii* isolates, and an average of 83% of *C. duobushaemulonii* isolates, were accurately identified. Tan et al. [8] evaluated the performance of the VITEK 2 system (version 8.01) in identifying *C. auris* using a total of seven *C. auris* isolates, comprising five from the South Asian, one from the South American, and one from the East Asian clades, along with five closely related *Candida* species, including two *C. haemulonii* and three *C. duobushaemulonii* isolates. Correct identification was achieved for four (57.1%) of the *C. auris* isolates, all of which belonged to the South Asian clade, as well as for all (100%) of the *C. duobushaemulonii* isolates. Misidentification as *C. duobushaemulonii* occurred in two *C. auris* isolates, one from the South Asian clade and one from the East Asian clade. Additionally, the VITEK 2 system failed to distinguish between *C. auris* and *C. duobushaemulonii* in the South American

isolate. Despite the low differentiation observed for both *C. haemulonii* isolates, they were correctly identified at the species level. In the present study, a total of 44 *C. auris* isolates with undetermined clades were tested. By using the VITEK 2 system, 36 (81.8%) isolates were accurately identified, which is a higher rate compared to similar studies. However, a total of three isolates (6.8%) were misidentified as *C. laurentii* (two isolates) and *C. duobushaemulonii* (one isolate), while five isolates (11.4%) could not be identified.

All *C. auris* isolates from the African clade displayed assimilation of L-rhamnose, whereas this feature was observed in only 0 - 4% of isolates from the other three clades in the study by Ambaraghassi et al. [10]. Similarly, Spruijtenburg et al. [20] reported that isolates from the African and South American clades assimilate L-rhamnose, unlike those from other clades. Chowdhary et al. [21] observed that *C. auris* isolates from the East Asian clade do not assimilate N-acetylglucosamine (NAG), whereas isolates from the South Asian clade do. Ambaraghassi et al. [10] also detected a lack of NAG assimilation in all isolates from the East Asian clade. Assimilation of NAG was observed in 100% of *C. auris* isolates from the African (31/31) and South Asian (31/31) clades, and in 94% (29/31) of isolates from the South American clade. They concluded that the biochemical differences between the East Asian clade and other clades could explain its high rate of misidentification [10]. In the present study, all misidentified (n = 3) and unidentified (n = 5) isolates were negative for L-rhamnose assimilation. Among the accurately identified isolates, only one isolate was L-rhamnose positive, while the remaining 43 isolates were negative. Regarding NAG assimilation, one of the misidentified and one of the unidentified isolates were negative and the remaining isolates were positive, whereas one of the accurately identified isolates was negative and 43 were positive. When evaluated based on L-rhamnose and NAG assimilation, the *C. auris* isolates in this study did not show a clear distribution pattern among correctly identified, misidentified, and unidentified groups, and therefore do not allow for definitive conclusions. However, the majority of *C. auris* isolates in this study were considered to belong to the South Asian clade based on their negative assimilation of L-rhamnose and positive assimilation of NAG. Notably, in the only study conducted on this subject in our country, Erturk Sengel et al. [22] identified *C. auris* isolates recovered from blood cultures of 10 patients as belonging to the South Asian clade through whole-genome sequencing analysis.

C. glabrata, one of the most commonly isolated non-*albicans Candida* species, generally exhibits reduced sensitivity to fluconazole, and a recent increase in the isolation of echinocandin-resistant strains has been reported [23,24]. For this reason, accurate identification of this species is essential. Kord et al. [9] reported that 27 out of 30 *C. glabrata* isolates (90%) were correctly identified using VITEK 2 in their study, while two (6.7%) were misidentified and one (3.3%) was not identified. In the meta-analysis by Posteraro et al. [15] 94.5% (463/490) of *C. glabrata* isolates were accurately identified. However, it was not specified whether the remaining 27 isolates (5.5%) were misidentified or yielded no identification result. In the present study, out of 77 *C. glabrata* isolates tested, 70 (90.9%) were correctly identified, while seven (9.1%) could not be identified. The correct identification rate is consistent with that reported in similar studies. It was determined that the biochemical profiles of the unidentified isolates varied from each other as well as from those of the correctly identified isolates.

There are several reports of yeast species being misidentified by the VITEK 2 system. Kord et al. [9] reported the misidentification of two *C. parapsilosis* isolates as *C. laurentii* (1/21; 4.7%) and *Debaryomyces hansenii* (1/21; 4.7%), two *C. orthopsilosis* isolates as *C. parapsilosis* (2/2; 100%), and one *C. norvegensis* isolate as *D. hansenii* (1/1; 100%). Similarly, Huang at al. [14] reported misidentification of *C. norvegensis* as *C. haemulonii*. In the present study, a total of eight isolates were misidentified, including three *C. auris* (3/44; 6.9%), two *C. parapsilosis* (2/9; 22.2%), two *C. tropicalis* (2/6; 33.3%), and one *C. blankii* (1/1; 100%). When yeast species are identified using biochemical-based commercial systems such as VITEK 2, it is important to evaluate the results alongside morphological characteristics and chromogenic media, as these methods serve as valuable tools for detecting discrepancies and ensuring accurate identification [6].

This study has some limitations, including the relatively small sample size and its retrospective design. Future studies including a larger number of rare yeast isolates, as well as isolates belonging to species complexes that are difficult to distinguish, and studies using a prospective approach will provide a better understanding of the performance of the VITEK 2 system in identifying yeasts.

CONCLUSION

VITEK 2, like other biochemical-based semi-automated and fully automated systems, is widely used in microbiology laboratories worldwide for the identification of yeasts and offers advantages over conventional methods in terms of time and workload. Since there are only a limited number of studies on the latest versions of the VITEK 2 system currently in use, more research is needed. Furthermore, the identification of certain rare yeast species, particularly *C. auris*, which currently poses a global health threat, can be challenging and misidentifications may occur. In such cases, additional confirmatory methods, such as microscopic examination on cornmeal-Tween 80 agar or investigation of capsule formation can be helpful in distinguishing biochemically similar yeast species. A result indicating *C. duobushaemulonii* with VITEK 2 requires further testing to rule out *C. auris*, as some *C. auris* isolates may be misiden-

tified as *C. duobushaemulonii* by this system, as in the present study. Biochemical variability among *C. auris* isolates from different clades contributes to differences in identification accuracy with biochemical-based systems such as VITEK 2. Further analyses of the biochemical characteristics within distinct *C. auris* clades would provide valuable information.

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References:

1. World Health Organization. WHO fungal priority pathogens list to guide research, development and public health action. World Health Organization: Geneva, 2022. https://iris.who.int/bitstream/handle/10665/363682/9789240060241-eng.pdf?sequence=1

2. Arastehfar A, Wickes BL, Ilkit M, et al. Identification of mycoses in developing countries. J Fungi (Basel) 2019 Sep 29;5(4):90. (PMID: 31569472)

3. Phillip R. Heaton, Micah M. Bhatti. Systems for identification of bacteria and fungi. In Manual of Clinical Microbiology, 13th ed.; Karen C. Carroll, Michael A. Pfaller, James A. Karlowsky, Eds.; ASM Press: Washington DC, 2023; pp. 101-122. (Book)

4. Morovati H, Kord M, Ahmadikia K, et al. A comprehensive review of identification methods for pathogenic yeasts: Challenges and Approaches. Adv Biomed Res 2023 Jul 25:12:187. (PMID: 37694259)

5. Jonani B, Kasule EC, Bwire HR, Mboowa G. Reported prevalence and comparison of diagnostic approaches for *Candida africana*: A systematic review with meta-analysis. Diag Prog Res 2024 Dec 5;8(1):16. (PMID: 39639364)

6. Andrew M. Borman, Elisabeth M. Johnson. *Candida*, *Cryptococcus*, and other yeasts of medical importance. In Manual of Clinical Microbiology, 13th ed.; Karen C. Carroll, Michael A. Pfaller, James A. Karlowsky, Eds.; ASM Press: Washington DC, 2023; pp. 2328-2359. (Book)

7. Alves J, Alonso-Tarrés C, Rello J. How to identify invasive candidemia in ICU -A narrative review. Antibiotics (Basel) 2022 Dec 12;11(12):1804. (PMID: 36551461)

8. Tan YE, Teo JQ, Rahman NBA, et al. *Candida auris* in Singapore: Genomic epidemiology, antifungal drug resistance, and identification using the updated 8.01 VITEK R®2 system. Int J Antimicrob Agents 2019 Dec;54(6):709-15. (PMID: 31600556)

9. Kord M, Salehi M, Khodavaisy S, et al. Epidemiology of yeast species causing bloodstream infection in Tehran, Iran (2015 - 2017); superiority of 21-plex PCR over the Vitek 2 system for yeast identification. J Med Microbiol 2020 May;69(5):712-20. (PMID: 32368996)

10. Ambaraghassi G, Dufresne PJ, Dufresne SF, et al. Identification of *Candida auris* by use of the updated Vitek 2 yeast identification system, version 8.01: A multilaboratory evaluation study. J Clin Microbiol 2019 Oct 23;57(11):e00884-19. (PMID: 31413079)

11. Dewaele K, Frans J, Smismans A, Ho E, Tollens T, Lagrou K. First case of *Candida auris* infection in Belgium in a surgical patient from Kuwait. Acta Clinica Belg 2020 Jun;75(3):221-8. (PMID: 30514182)

12. Lars F. Westblade, Eileen M. Burd, Shawn R. Lockhart, Gary W. Procop. Larone's medically important fungi, 7th ed.; ASM Press: Washington DC, 2023. (Book)

13. Karabıçak N, Uludağ Altun H, Karatuna O, et al. [Evaluation of common commercial systems for the identification of yeast isolates in microbiology laboratories: A multicenter study]. Mikrobiyol Bul 2015 Apr;49(2):210-20. (PMID: 26167821)

14. Huang YS, Wang FD, Chen YC, et al. High rates of misidentification of uncommon *Candida* species causing bloodstream infections using conventional phenotypic methods. J Formos Med Assoc 2021 May;120(5):1179-87. (PMID: 33250336)

15. Posteraro B, Efremov L, Leoncini E, et al. Are the conventional commercial yeast identification methods still helpful in the era of new clinical microbiology diagnostics? A meta-analysis of their accuracy. J Clin Microbiol 2015 Aug;53(8):2439-50. (PMID: 25994160)

16. Lockhart SR, Lyman MM, Sexton DJ. Tools for detecting a "superbug": Updates on *Candida auris* testing. J Clin Microbiol 2022 May 18;60(5):e0080821. (PMID: 34985980)

17. Kurt AF, Kuskucu MA, Balkan II, et al. *Candida auris* fungemia and a local spread taken under control with infection control measures: First report from Turkey. Indian J Med Microbiol 2021 Apr;39(2):228-30. (PMID: 33785243)

18. Liu F, Hu ZD, Zhao XM, et al. Phylogenomic analysis of the *Candida auris-Candida haemuli* clade and related taxa in the *Metschnikowiaceae*, and proposal of thirteen new genera, fifty-five new combinations and nine new species. Persoonia Aug:52: 22-43. (PMID: 39161632)

19. Centers for Disease Control and Prevention (CDC). *Candida auris*. Available online: https://www.cdc.gov/candida-auris/hcp/index.html (Accessed on 17 September 2025)

20. Spruijtenburg B, Badali H, Abastabar M, et al. Confirmation of fifth *Candida auris* clade by whole genome sequencing. Emerg Microb Infect 2022 Dec;11(1):2405-11. (PMID: 36154919)

21. Chowdhary A, Sharma C, Duggal S, et al. New clonal strain of *Candida auris* Delhi, India. Emerg Infect Dis Oct;19(10):1670-3. (PMID: 24048006)

22. Erturk Sengel B, Ekren BY, Sayin E, et al. Nosocomial infection of *C. auris* in COVID-19 intensive care unit in Türkiye and phylogenetic analysis of isolates. Mycopathologia 2023 Oct;188(5): 765-73. (PMID: 37542203)

23. Frías-De-León MG, Hernández-Castro R, Conde-Cuevas E, et al. *Candida glabrata* antifungal resistance and virulence factors, a perfect pathogenic combination. Pharmaceutics 2021 Sep 22;13-(10):1529. (PMID: 34683822)

24. Gülmez D, Sığ AK, Akar N, Duyan S, Arıkan Akdağlı S. [Changing trends in isolation frequencies and species of clinical fungal strains: What do the 12-years (2008 - 2019) mycology laboratory data tell about?] Mikrobiyol Bul 2021 Jan;55(1):53-66. (PMID: 33590981)