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Comparison of the API Candida System with the AUXACOLOR System for Identification of Common Yeast Pathogens

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Two commercial systems for the identification of yeasts were evaluated by using 159 clinical isolates that had also been identified by conventional biochemical and morphological methods. The API Candida system correctly identified 146 isolates (91.8%), and the AUXACOLOR system correctly identified 145 isolates (91.2%). However, of the 146 isolates identified by the API Candida system, 23 required supplemental biochemical tests or morphological assessment to obtain the correct identification. The AUXACOLOR system gave no identification in 13 cases (8.2%), while the API Candida system gave an unreadable profile in only one case. Incorrect identifications were more common with the API Candida system (12 isolates; 7.5%) than with the AUXACOLOR system (1 isolate; 0.6%).

The incidence of serious yeast infections has increased in recent years, particularly in immunocompromised and debilitated patients (1, 18). Although *Candida albicans* remains the most common cause of human candidiasis, the proportion of infections attributed to other members of the genus is increasing (16, 20). This shift in species distribution has been attributed, at least in part, to changes in antifungal drug-prescribing practices. These changes are believed to have contributed to an increase in infections caused by organisms, such as *Candida glabrata* and *Candida krusei*, that are often much less susceptible to treatment with azole antifungal agents (11, 14). As a result of these factors, it has become more important to determine the species of the organisms as soon as possible after commencing treatment.

The increasing incidence of yeast infections has stimulated the development of both manual and automated commercial systems for the identification of these organisms. The API 20C system (bioMerieux, Marcy-l'Etoile, France) was one of the first commercial systems to be introduced for the purpose of yeast identification (3, 13) and is now considered a reliable, proven system with which others are to be compared (4–7, 10, 19). However, even though it is faster than classical assimilation and fermentation methods, the API 20C system is still time-consuming to set up and read, requires up to 72 h of incubation, and gives results that are often difficult to interpret.

Unlike the API 20C yeast identification system, the AUXACOLOR (Sanofi Diagnostics Pasteur, Paris, France) and API Candida systems (bioMerieux) are intended to identify only a limited range of taxa, comprising the most commonly encountered clinical pathogens. The AUXACOLOR system, it is claimed, is capable of identifying 26 species, while the API Candida system can identify 15 species, with or without additional tests. Both systems have been reported to provide a simple, rapid, and accurate means of identifying clinical yeast isolates (4, 8, 9, 19). The object of this evaluation was to compare the performance of the API Candida system with that of the AUXACOLOR system. We selected for testing only those isolates that our traditional tests identified as falling within the identification range of both commercial systems.

Test isolates. A total of 159 isolates, representing 12 species, were tested (Table 1). Among these, 94 were clinical isolates submitted to the Mycology Reference Laboratory (Bristol, United Kingdom) for identification and 65 were obtained from the United Kingdom National Collection of Pathogenic Fungi, held at the Mycology Reference Laboratory. All isolates were coded before being passed to us for identification. Their identities were unknown until the final results were examined. Isolates were retrieved from storage in liquid nitrogen and subcultured twice on plates of Oxoid Sabouraud dextrose agar (Unipath Limited, Basingstoke, England) (supplemented with 0.5% [wt/vol] chloramphenicol) to ensure optimal growth. Prior to testing, subcultures on Sabouraud dextrose agar were incubated at 35°C for 24 h.

API Candida system. All tests were performed according to the manufacturer's instructions. The API Candida system consists of a single-use disposable plastic strip with 10 wells to perform 12 colorimetric biochemical tests: five sugar assimilation tests (for glucose, galactose, sucrose, trehalose, and raffinose) and seven enzymatic tests (for β-maltosidase, α-amylase, β-xylosidase, β-glucuronidase, urea hydrolysis, *N*-acetyl-β-glucosaminidase, and β-galactosidase). Inoculation of the wells was performed by adding a yeast suspension to the dehydrated substrates. The results were read after incubation for 18 to 24 h at 35°C. A four-digit numerical profile was generated for each isolate depending upon the reactions it produced. Identifications were made by referring to the list of numerical profiles and a computer program provided by the manufacturer.

AUXACOLOR system. All tests were performed according to the manufacturer's instructions. The AUXACOLOR system consists of a disposable plastic microplate containing 16 wells. The first well is a negative control, while the other 15 wells perform colorimetric biochemical tests: 13 sugar utilization tests (for glucose, maltose, sucrose, galactose, lactose, raffinose, inositol, cellobiose, trehalose, adonitol, melezitose, xylose, and arabinose), a test for cycloheximide (actidione) resistance, and a test for the detection of the enzyme phenoloxidase.

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TABLE 1. Identification of 159 yeast isolates with the API Candida and AUXACOLOR systems

Organism	Total no. of isolates	No. of isolates identified by:					
		API Candida			AUXACOLOR		
		Correctly[a]	Incorrectly	Not	Correctly	Incorrectly	Not
Candida albicans	22	22 (1)	0	0	20	1	1
Candida glabrata	24	24	0	0	24	0	0
Candida guilliermondii	11	7	4	0	9	0	2
Candida krusei	20	20	0	0	20	0	0
Candida lusitaniae	9	6 (1)	3	0	5	0	4
Candida parapsilosis	19	18 (5)	1	0	19	0	0
Candida tropicalis	20	17 (7)	3	0	19	0	1
Cryptococcus neoformans	19	19 (9)	0	0	19	0	0
Saccharomyces cerevisiae	8	7	1	0	5	0	3
Trichosporon beigelii	7	6	0	1	5	0	2

[a] Figures in parentheses are the numbers of isolates that required further tests for correct identification.

Inoculation of the wells was performed by adding a yeast suspension to the dehydrated substrates. The results were read after incubation for 24 and 48 h at 30°C. A five-digit numerical profile was generated for each isolate depending upon the reactions it produced. Two further digits were then added to the profile number depending upon the growth characteristics of the isolate in morphological tests (see below). Identifications were made by referring to the list of numerical profiles provided by the manufacturer.

Conventional identification method. Liquid media in test tubes were used to determine the assimilation of glucose, maltose, sucrose, lactose, rhamnose, and trehalose and the fermentation of glucose, maltose, sucrose, and lactose (12). The tubes were incubated at 30°C and examined for growth after 7 and 14 days. Nitrate assimilation was tested in broth medium, by using α-naphthylamine and sulfanilic acid reagents (12). Urease production was determined on Philpot's urea agar (15). Results were recorded after incubation at 30°C for 7 and 14 days.

Morphological characteristics, essential for both the traditional method and for the AUXACOLOR profiles and of supplemental importance for the API Candida system, of organisms grown on Oxoid cornmeal agar, supplemented with 1% Tween 80, were studied; a sterile coverslip was placed over a single streak of the isolate. The results were recorded after 2 to 3 days of incubation at 30°C.

Results. If we assume that the traditional method gave the correct results, the API Candida system correctly identified 146 isolates (91.8%) and the AUXACOLOR system correctly identified 145 isolates (91.2%) (Table 1). However, of the 146 isolates correctly identified by the API Candida system, 23 required additional tests to obtain the correct identification. Incorrect identifications were more common with the API Candida system (12 isolates; 7.5%) than with the AUXACOLOR system (one isolate; 0.6%). The AUXACOLOR system gave no identification in 13 cases (8.2%), while the API Candida system gave an unreadable profile in only one case.

The species of 23 of the 36 isolates that were not initially identified by the API Candida system were determined after additional tests. In most cases, an examination of morphology by Dalmau plate culturing to establish the presence or absence of mycelia or pseudomycelia, chlamydospores, and arthrospores was sufficient to make a final identification. In some instances, however, additional biochemical tests were also required.

Twelve isolates (7.5%), belonging to five different species (*Candida guilliermondii*, *Candida lusitaniae*, *Candida parapsilosis*, *Candida tropicalis*, and *Saccharomyces cerevisiae*), were misidentified with the API Candida system. Three of 11 isolates of *C. guilliermondii* were identified as *S. cerevisiae* (good identification), and one of them was identified as either *Candida famata* or *C. parapsilosis*. Of nine *C. lusitaniae* isolates tested, one was identified as *C. albicans* (very good identification) and two were identified as *C. famata* (good identification). Of 19 *C. parapsilosis* isolates, one was identified as *C. lusitaniae* (doubtful profile), but with a stated probability of 99.2% most laboratories would have accepted this identification. Of the 20 *C. tropicalis* isolates tested, two were identified as *C. albicans* (excellent identification) and one as *C. famata* (good identification). The eight *S. cerevisiae* isolates included one which was identified as *C. guilliermondii* (doubtful profile, with a probability of 99.9%) with *C. lusitaniae* as the next choice.

The AUXACOLOR system gave no identification in 13 cases (8.1%). These comprised four isolates of *C. lusitaniae*, three of *S. cerevisiae*, two of *C. guilliermondii*, two of *Trichosporon beigelii*, and one each of *C. albicans* and *C. tropicalis*. The only incorrect result obtained with this system was a *C. albicans* isolate that was identified as *C. tropicalis*.

Discussion. Our results demonstrate that the two commercial systems were almost identical in terms of the proportions of isolates correctly identified (API Candida, 91.2%; AUXACOLOR, 91.8%). Moreover, both systems were similar with respect to the ease of inoculation and reading. The AUXACOLOR system was able to provide the correct identification for almost all the isolates tested after 48 h of incubation, because it also incorporated the results of a morphological assessment. Other work in this laboratory has demonstrated that it is also able to exclude isolates without providing identifications when the taxa were not included in the database (3a). The API Candida system permitted many isolates to be identified within 24 h. Others, however, required a morphological assessment or additional biochemical tests (assimilation of *N*-acetylglucosamine, sorbitol, melezitose, or sorbose). In practice, the need for supplemental tests means retesting isolates with the API 20C or ID 32C systems, increasing the cost and the time needed for identification to 72 or 96 h.

Many laboratories now use commercial identification systems to determine the physiological profiles of yeast isolates. Some of these systems offer extensive databases, capable of identifying a wide range of taxa, but others are much more limited in scope. In either case, a morphological assessment of isolates remains essential to avoid errors in the identification of organisms with identical biochemical profiles. This is of par-

ticular importance when identification is to be based on systems with a limited range of biochemical tests. Unlike the AUXACOLOR system, which requires the morphological characteristics of isolates to be taken into account when determining the profile, the API Candida system allows a profile to be generated without the need for a morphological assessment. This feature helps to account for the small but worrisome number of incorrect identifications obtained with this system in this and other evaluations (2, 8). For instance, three pseudomycelium-forming *Candida* spp. (*C. guilliermondii*, *C. lusitaniae*, and *C. tropicalis*) were misidentified as *C. famata* during this evaluation. Likewise, Fricker-Hidalgo et al. (8) noted the misidentification of *C. tropicalis* as *C. famata* and described the misidentification of *C. famata* as *C. guilliermondii* and of *S. cerevisiae* as *C. parapsilosis*.

In conclusion, we found the AUXACOLOR yeast identification system to be suitable for use in routine clinical microbiology laboratories, due to its ease of setting up and reading, the cost per test, and its performance with taxa of medical importance. The API Candida system is a promising product, but occasional errors in identification could be avoided if morphological characteristics were taken into account within the numerical profile.

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