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Collaborative Evaluation of the Abbott Yeast Identification System

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The Abbott yeast identification system (Abbott Laboratories, Diagnostics Division, Irving, Tex.) is a 24-h, instrumental method for identifying medically important yeasts, based on matrix analysis of 19 biochemical reactions and the germ tube test. The system was evaluated in two clinical laboratories by using 179 coded isolates, which included a high percentage of the less frequently encountered species. Based upon results with these coded isolates and from previously obtained laboratory data, the system software was adjusted and accuracy of the yeast identification system was further evaluated with 378 isolates from clinical sources. Of the 378 clinical yeast isolates tested, 364 (96%) were correctly identified with the Abbott system. Isolates were deliberately selected so that germ tube-positive isolates made up less than 10% of the clinical isolates tested.

The mycology section of most clinical laboratories produces results with an inherent slowness that can be generally attributed to the growth rates of the various fungi being studied. However, with the increase in awareness of the morbidity and mortality (1, 2, 5, 9, 10, 12, 17) associated with opportunistic infections caused by yeasts, it has become important to investigate rapid and automated methods for the rapid and specific diagnosis of these infections. The toxic medications that are necessary for treating invasive infections caused by yeasts are used only when necessary by prudent physicians. For this reason, it is important to rapidly detect and identify pathogenic yeasts so that the decision to use an antimycotic drug can be made while the pathological process caused by an invasive infection is still reversible.

With this in mind, it has been of interest to investigate the feasibility of using the Abbott MS-2 instrument (MS-2) for performing biochemical tests for identifying clinical yeast isolates. The MS-2 has previously been evaluated for identifying enteric bacteria and was shown to yield reliable results (15). Automated approaches to performing biochemical tests for identifying yeasts that have previously been described have used the Autobac 1 (18, 21) or the AutoMicrobic system Yeast Biochemical Card (11, 19). Biochemical tests with these two instruments could be completed in 12 h with the Autobac 1 and in 24 h with the AutoMicrobic system.

Conventional methods for identifying clinical yeast isolates can require as long as 14 to 28 days for completion of biochemical tests (14, 20, 22). The newer miniaturized systems such as the API 20C, the BBL Minitek Yeast system, and Uni-Yeast-Tek provide biochemical testing in 3 to 7 days with an acceptable level of reliability (3, 4, 7, 13, 16).

In this report, we describe the development and clinical testing of the Abbott yeast identification system (Abbott IDS). Preliminary developmental studies with this system have been reported previously (6; B. H. Cooper, S. Prowant, D. Brunson, and R. Vannest, Abstr. Annu. Meet. Am. Soc. Microbiol. 1982, C274, p. 317).

MATERIALS AND METHODS

Protocol and organisms. These studies were carried out in two phases. Phase 1 consisted of testing 179 previously identified and coded yeast isolates obtained from culture collections at Baylor University Medical Center and the North Carolina Memorial Hospital. These coded cultures were submitted as unknowns to the participants for identification. Phase 2 consisted of testing fresh clinical isolates obtained in the participating centers along with some isolates submitted from other laboratories. These clinical isolates were first screened by the germ tube test (20). The number of germ tube-positive (i.e., *Candida albicans*) isolates tested was restricted to less than 10% of the clinical isolates tested. A total of 378 yeast isolates were evaluated in this phase. The Abbott IDS results were compared with findings obtained by each clinical laboratory by using their current identification method. When a discrepancy was observed between an Abbott IDS identification and the routine lab test result, morphology data and conventional reference testing with the Wickerham broth carbohydrate assimilation media, nitrate assimilation, a test for phenol oxidase activity, and Christensen urea agar were used to establish identification. When necessary, fermentation tests were also used to verify an identification.

Abbott IDS. The MS-2 system modules have been described previously (15). The Abbott yeast identification cartridge is a single-use disposable plastic unit consisting of 20 chambers containing lyophilized biochemical media. The active substrates in the cartridge are as follows: urea, *p*-hydroxybenzoic acid and protocatechuic acid, negative control, glucose, galactose, sucrose, maltose, cellobiose, trehalose, lactose, melibiose, raffinose, melizitose, xylose, arabinose, rhamnose, erythritol, dulcitol, inositol, and nitrate. With the exception of the test for assimilation of the mixture of *p*-hydroxybenzoic acid and protocatechuic acid, the biochemical tests utilized are those routinely employed in conventional identification systems (14, 20, 22). The utility of a test for *p*-hydroxybenzoic acid utilization, as an aid to identification of *Candida parapsilosis* and certain other yeasts, has already been described (8).

Well-isolated yeast colonies from Sabouraud agar plates, incubated for 24 to 48 h at 30°C, were used to prepare the inocula. Colonies of a test organism were selected and, by using a sterile inoculating loop or cotton-tipped applicator, were suspended in 0.05% Noble agar to prepare a slightly turbid suspension which visually matched the turbidity of a 0.5 McFarland standard. The suspension was mixed on a vortex mixer, and 0.2-ml portions were delivered into each

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chamber of the Abbott IDS cartridge. The cartridge was then sealed with a polyester film to eliminate any adverse effects that volatile metabolic end products might have on adjacent reactions. An initial reading of the optical density of each reaction chamber in the cartridge was taken with the MS-2, and these data were automatically stored in the computer memory. Cartridges were then incubated off-line at 30°C for 22 to 25 h, after which they were reinserted into the MS-2 for a final reading. After the final reading, results of several morphological tests and additional test results were entered via computer keyboard to provide a comprehensive record of these studies. These tests included morphological observations for detecting hyphae, chlamydospores, arthroconidia, germ tube formation, and capsules and for measuring growth at 37°C and phenol oxidase activity. Such determinations were made by conventional methodology (14, 20) and were set up at the time the isolates were subcultured, before inoculation of the cartridge. These ancillary tests were read before the final reading of the yeast cartridges. It was subsequently determined that only the germ tube test results were needed as ancillary input. The MS-2 data printout included a record of the positive and negative biochemical reactions, the identity of the yeasts (with up to five species listed in descending order of likelihood), and a percent likelihood value for each species listed.

Laboratory identification procedures. In these studies, each collaborating laboratory used its current routine methodology for identifying clinical yeast isolates. The Abbott IDS results were compared with those identifications. Routine methods were predominantly API 20C (Analytab Products, Plainview, N.Y.) or Uni-Yeast-Tek (Flow Laboratories, Inc., MacLean, Va.), used in accordance with the instructions of the manufacturer. As noted previously, any discrepant results were resolved by testing with classical reference methodology (14, 20, 22).

Data evaluation. Accuracy of the Abbott IDS results with coded isolates was analyzed initially in two ways: (i) by considering both cartridge biochemical results and all morphological tests (germ tube formation, capsules, chlamydospores, hyphae, and arthroconidia); and (ii) by considering only the biochemical and germ tube test data. Results obtained with coded isolates were also used to make adjustments to the MS-2 analytical program before final analysis of results with clinical isolates. Data from clinical isolates were analyzed with only the biochemical and germ tube test results. Abbott IDS results were considered correct if they agreed with either the initial routine laboratory identification, or, in the case of a discrepancy, the result of subsequent extensive reference testing.

RESULTS

Abbott IDS accuracy with the collection of coded isolates is shown in Table 1. The values shown reflect results with either only the MS-2 cartridge data and germ tube results or all morphology data included in the computer-calculated results. When used, morphological data were weighed equally with any single biochemical test result. The Abbott IDS results shown in all tables reflect results with final software modifications in place. The coded isolate collection was limited to contain only 5% (8 of 179) *C. albicans*, but did include 10% (18 of 179) *Geotrichum* and *Trichosporon* spp. The remaining 153 isolates were distributed among the remaining species as shown in Table 2. Considering only biochemical and germ tube test results, the accuracy of the Abbott IDS in the two laboratories was, respectively, 93 and 89%. In this initial phase, species that were most difficult to identify in both laboratories included *Trichosporon beigelii*, *Geotrichum spp.*, *Candida famata*, and *Candida humicola*.

TABLE 1. Accuracy of identification of coded isolates by Abbott IDS with germ tube test results and with corn meal morphology

Laboratory	Method	No. correct (%)	No. incorrect (%)
1	IDS and germ tube test	166 (93)	13 (7)
	IDS and corn meal morphology	169 (94)	10 (5)
2	IDS and germ tube test	159 (89)	20 (11)
	IDS and corn meal morphology	165 (92)	14 (8)

Combined results from 378 clinical strains isolated in the two participating laboratories and from other sources in phase 2 of the study are shown in Table 3. Correct identifications were obtained with 364 (96%) of these isolates with the

TABLE 2. Accuracy of Abbott IDS with coded isolates

Species	No. of isolates tested	No. of correctly identified isolates at laboratory:	
		1	2
Candida			
albicans	9	8	9
famata	3	1	1
glabrata	10	10	10
guilliermondii	9	9	7
humicola	3	0	0
krusei	10	9	7
lambica	1	1	1
lipolytica	4	3	4
lusitaniae	5	5	4
parapsilosis	12	11	11
pseudotropicalis	4	4	4
rugosa	3	3	3
stellatoidea	5	5	5
tropicalis	15	15	15
utilis	3	3	2
Cryptococcus			
albidus	8	8	8
laurentii	7	7	7
luteolus	4	4	4
neoformans	12	12	12
skinneri	1	1	1
terreus	5	5	5
uniguttulatus	4	4	4
Geotrichum capitatum	6	5	2
Geotrichum spp.	8	6	7
Hansenula anomala	1	1	1
Rhodotorula			
glutinis	1	1	1
minuta	1	1	0
pilimanae	2	2	2
rubra	12	12	12
Saccharomyces cerevisiae	7	7	7
Trichosporon beigelii	4	3	3

TABLE 3. Accuracy of Abbott IDS with clinical isolates[a]

MS-2 identification \ Clinical identification	*Candida albicans*	*famata*	*glabrata*	*guilliermondii*	*krusei*	*lambica*	*lipolytica*	*lusitaniae*	*parapsilosis*	*pseudotropicalis*	*rugosa*	*stellatoidea*	*tropicalis*	*Cryptococcus albidus*	*laurentii*	*neoformans*	*Geotrichum capitatum*	*Geotrichum* spp.	*Hausenula anomala*	*Rhodotorula graminis*	*rubra*	*Saccharomyces cerevisiae*	*Trichosporon beigelii*	Total
Candida albicans	32	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
Candida famata	—	0	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
Candida glabrata	—	—	96	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
Candida guilliermondii	—	—	—	11	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
Candida krusei	—	—	—	—	4	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
Candida lambica	—	—	—	—	—	1	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
Candida lipolytica	—	—	—	—	1	—	3	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
Candida lusitaniae	—	1	—	—	—	—	—	1	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
Candida parapsilosis	—	—	—	—	—	—	—	—	61	—	—	—	2	—	—	—	—	—	—	—	—	—	—	—
Candida pseudotropicalis	—	—	—	—	—	—	—	—	—	6	—	—	—	—	—	—	—	—	—	—	—	—	—	—
Candida rugosa	—	—	—	—	—	—	—	—	—	—	4	—	—	—	—	—	1	3	—	—	—	—	—	—
Candida stellatoidea	—	—	—	—	—	—	—	—	—	—	—	5	—	—	—	—	—	—	—	—	—	—	—	—
Candida tropicalis	—	—	—	—	—	—	—	—	—	—	—	—	82	—	—	—	—	—	—	—	—	—	—	—
Cryptococcus albidus	—	—	—	—	—	—	—	—	—	—	—	—	—	4	—	—	—	—	—	—	—	—	—	—
Cryptococcus laurentii	—	—	—	—	—	—	—	—	—	—	—	—	—	—	1	—	—	—	—	—	—	—	1	—
Cryptococcus neoformans	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	16	—	—	—	—	—	—	—	—
Geotrichum capitatum	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	1	—	—	—	—	—	—	—
Geotrichum spp.	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	3	—	—	—	—	—	—
Hansenula anomala	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	1	—	—	—	—	—
Rhodotorula graminis	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	1	—	—	—	—
Rhodotorula rubra	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	2	—	—	—
Saccharomyces cerevisiae	—	—	—	—	—	—	—	—	—	—	—	—	1	—	—	—	—	—	—	—	—	12	—	—
Trichosporon beigelii	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	17[b]	—
Not identified	—	—	—	—	—	—	—	—	—	—	—	—	1	—	—	—	—	—	—	—	—	—	—	—
Total	32	1	96	11	5	1	3	1	61	6	4	5	86	4	1	16	2	6	1	1	2	12	21	378
No. correct	32	0	96	11	4	1	3	1	61	6	4	5	82	4	1	16	1	3	1	1	2	12	17	364
Accuracy (% correct)	100	0	100	100	80	100	100	100	100	100	100	100	95	100	100	100	50	50	100	100	100	100	81	96

[a] Deviations from the diagonal line of correlating results represent MS-2 discrepancies.
[b] Two misidentified as *C. humicola*, one misidentified as *C. terreus*.

Abbott IDS. Of the 14 discrepancies, 8 (57%) were accompanied by a warning message indicating a low likelihood of correct identification (less than 80%). Conversely, of those isolates correctly identified by the Abbott IDS, only eight (2%) were accompanied by a low-likelihood statement indicating the advisability of additional testing. Of the 16 total low-likelihood situations encountered, 11 (69%) would have been effectively resolved by morphological observation alone.

DISCUSSION

The data presented here illustrate the capability of the Abbott IDS for performing biochemical tests used in identifying medically important yeasts. Reliable results were obtained, and the tests were completed in just 20 to 24 h. A high level of agreement with conventional test results (96%) was achieved by using only the germ tube test results and biochemical tests with clinical isolates in phase 2 of the study. The more time-consuming studies of microscopic morphology on corn meal agar were not necessary with most isolates. Even clinical isolates belonging to the genera *Trichosporon* and *Geotrichum* could frequently be identified without morphological observations. However, it should be pointed out that isolates belonging to those two genera present a significant challenge to any identification system. It is desirable to have available morphological test results along with biochemical test results for identifying such clinical yeast isolates, when using the Abbott IDS system on a routine basis.

The overall agreement with conventional test results was somewhat lower (91%) in phase 1 of the study, in which blind-coded isolates were identified, than in phase 2, which involved routine clinical isolates. Two important factors contributed to this difference. First, the spectrum of isolates tested in phase 1 included a number of rare and unusual isolates. This wide range of organisms was deliberately selected to challenge the system at a maximum level. Some isolates were included that have not been reported to cause human disease and are rarely encountered in clinical laboratories. Secondly, the results obtained in phase 1 were used to further refine the data matrix so that more accurate results could be obtained. This factor contributed significantly to the improved correlation observed with conventional test results and clinical isolates in phase 2.

The availability of a means for rapid, automated identification of yeasts significantly expands the capabilities of the Abbott IDS system. The ability to complete biochemical tests within 20 to 24 h after the test initiation offers a significant saving of time compared with both conventional tube tests and currently available manual systems. More rapid identification of pathogenic species of yeasts is a significant step toward the goal of diagnosing invasive yeast infections in sufficient time to enable effective treatment to be administered before the pathological process becomes irreversible.

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