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Evaluation of the Quantum II Yeast Identification System

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We compared three methods for identifying clinical yeast isolates: Abbott Quantum II, API 20C, and a modified BBL Minitek system. The API 20C and modified Minitek systems agreed on the identification of 243 of 245 yeasts (99.2%). The Quantum II system correctly identified 197 (80.4%), incorrectly identified 19 (7.8%), and did not identify 29 (11.8%) of the yeasts. Most of the misidentifications with the Quantum II occurred because assimilation or biochemical results were false-positive. Sixteen different species of yeasts and 16 different Quantum II substrates contributed to the discrepancies. On retesting with the Quantum II, 31% of the discrepant strains were correctly identified, while the remaining 69% were incorrectly identified or were not identified. Erroneous biochemical and assimilation results were also noted with yeasts that were correctly identified by the Quantum II system.

A new automated system for yeast identification was recently described (2). The system was developed with the Abbott MS-2 instrument and has been adapted for use with the Quantum II. We were interested in evaluating this system in a diagnostic microbiology laboratory that routinely identifies a large number of yeasts recovered from cultures from immunosuppressed patients (5, 10). This paper reports results of a comparison of Quantum II with two other yeast identification systems used in our laboratory: the API 20C and our reference method, which is a modification of the BBL Minitek yeast system.

MATERIALS AND METHODS

Organisms. A total of 245 yeast isolates were tested. Most strains were fresh clinical isolates. The remainder were stock isolates stored on silica gel (11) for less than 2 years. No species accounted for more than 30 of this total. Before testing, yeasts were subcultured onto Sabouraud glucose agar plates, and these were incubated at 30°C for 24 or 48 h.

Quantum II. The Quantum II system consists of a disposable plastic cartridge with 20 chambers containing lyophilized biochemical media. Included are tests for assimilations and urea and nitrate utilization. A list of substrates and a description of inoculum preparation has been reported (2). Cartridges were inoculated, incubated for 24 h at 30°C, and placed in the automated reader. A germ tube test, in which normal human serum incubated with the yeast for 3 h (12), was performed on all isolates, and the results were entered manually into the reader. The most likely identification, a list of additional tests required for identification, and a biotype code were automatically printed. The printout recorded the results of the biochemical tests and listed possible species identifications with a percent likelihood value for each. An isolate identification was considered final when the probability exceeded 80% or when additional tests suggested on the printout were completed.

API 20C. The API 20C system comprises 19 dehydrated substrates in a plastic strip (1, 6). The tests were performed as described in the instructions of the manufacturer, and results were recorded after the strips had been incubated at 30°C for 24, 48, and 72 h. Identification of the organisms was made with the aid of the API 20C analytical profile index which listed up to five species in descending order of likelihood. An isolate identification was considered final when the first choice listed was described as excellent, very good, or acceptable or when additional tests suggested in the index were completed.

Modified BBL Minitek reference system. A detailed description of the original auxanographic carbohydrate assimilation procedure has been reported (9). The turbidity of

TABLE 1. Identification of clinical yeast isolates by the Quantum II

Organism	No. of isolates tested	No. of correct results	No. of incorrect results	No. of isolates not identified
Candida albicans[a]	9	9		
Candida albicans[b]	8	5		3
Candida guilliermondii	10	7		3
Candida krusei	27	24	2	1
Candida lambica	1	1		
Candida lipolytica	2	2		
Candida lusitaniae	17	14	1	2
Candida parapsilosis	23	13	1	9
Candida pseudotropicalis	23	15	4	4
Candida rugosa	3	2	1	
Candida tropicalis	26	21	2	3
Candida stellatoidea	2	2		
Cryptococcus albidus	7	5	2	
Cryptococcus laurentii	8	7	1	
Cryptococcus neoformans	10	10		
Cryptococcus terreus	2	2		
Cryptococcus uniguttulattus	3	1	1	1
Geotrichum spp.	2	2		
Rhodotorula glutinis	2		2	
Rhodotorula minuta	1	1		
Rhodotorula rubra	5	5		
Saccharomyces cerevisiae	9	8	1	
Torulopsis candida	3		1	2
Torulopsis glabrata	30	30		
Trichosporon beigelii	12	11		1

[a] Germ tube-positive isolate.
[b] Germ tube-negative isolate.

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TABLE 2. Analysis of incorrect or incomplete identifications with the Quantum II system

Correct identification	Initial result	Discrepant tests[a]	Retest result
Candida albicans[b]	No ID	**CEL**	*Candida albicans*
Candida albicans[b]	No ID	**CEL**	*Candida albicans*
Candida albicans[b]	No ID	GAL, **CEL**, **LAC**, XYL, **ERY**	No ID
Candida guilliermondii	No ID	**LAC**, **ERY**, **INO**	No ID
Candida guilliermondii	No ID	**ERY**, **INO**	No ID
Candida guilliermondii	No ID	**ERY**, **INO**	*Cryptococcus neoformans*
Candida krusei	No ID	**LAC**, **INO**	*Candida lipolytica*
Candida krusei	*Trichosporon capitatum*	**GAL**	*Candida lipolytica*
Candida krusei	*Trichosporon capitatum*	**GAL**, **INO**	*Candida lipolytica*
Candida lusitaniae	*Trichosporon pullulans*	**URE**, **LAC**, **MEL**, **RAF**, **ARA**, **INO**, **NIT**	*Candida lusitaniae*
Candida lusitaniae	No ID	**ERY**, **DUL**, **INO**	No ID
Candida lusitaniae	No ID	**RAF**, **INO**	*Candida lusitaniae*
Candida parapsilosis	No ID	**ERY**, **INO**	*Candida tropicalis*
Candida parapsilosis	No ID	**ERY**, **DUL**, **INO**	No ID
Candida parapsilosis	No ID	**CEL**, **INO**	No ID
Candida parapsilosis	*Candida tropicalis*	ARA	No ID
Candida parapsilosis	No ID	**ERY**, **DUL**, **INO**	No ID
Candida parapsilosis	No ID	TRE, **INO**	No ID
Candida parapsilosis	No ID	**MEL**, **RAF**, **ERY**, **DUL**, **INO**	No ID
Candida parapsilosis	No ID	**ERY**, **DUL**, **INO**	No ID
Candida parapsilosis	No ID	**ERY**, **DUL**, **INO**	*Trichosporon pullulans*
Candida parapsilosis	No ID	TRE, **INO**	*Candida parapsilosis*
Candida pseudotropicalis	*Trichosporon beigelii*	**MEZ**, **RHA**, **ERY**, **INO**	*Trichosporon beigelii*
Candida pseudotropicalis	No ID	**MAL**, **TRE**, **MEL**, **MEZ**, **RHA**, **ERY**, **DUL**, **INO**	*Candida pseudotropicalis*
Candida pseudotropicalis	*Trichosporon beigelii*	RAF, **ERY**, **DUL**, **INO**	*Trichosporon beigelii*
Candida pseudotropicalis	*Trichosporon beigelii*	**MAL**, **TRE**, **ERY**, **INO**	*Candida pseudotropicalis*
Candida pseudotropicalis	*Torulopsis candida*	**MAL**, **TRE**, **MEL**, **INO**	*Trichosporon beigelii*
Candida pseudotropicalis	No ID	**MEZ**, **RHA**, **ERY**, **DUL**, **INO**	No ID
Candida pseudotropicalis	No ID	**MAL**, **TRE**, **MEL**, **MEZ**, **RHA**, **ERY**, **DUL**, **INO**	*Candida pseudotropicalis*
Candida pseudotropicalis	No ID	**MEZ**, **RHA**, **ERY**, **DUL**, INO	No ID
Candida rugosa	*Candida lipolytica*	GAL, **ERY**	*Candida lipolytica*
Candida tropicalis	*Trichosporon beigelii*	**LAC**, **ARA**, **RHA**, **ERY**, **INO**	*Candida tropicalis*
Candida tropicalis	*Candida lusitaniae*	**RHA**, **ERY**, **INO**	No ID
Candida tropicalis	No ID	**LAC**, **MEL**, **RAF**, **ARA**, **RHA**, **ERY**, **DUL**, **INO**	*Candida lusitaniae*
Candida tropicalis	No ID	**LAC**, **MEL**, **RAF**, **RHA**, **ERY**, **DUL**, **INO**	No ID
Candida tropicalis	No ID	CEL, **RHA**, **ERY**, **DUL**, **INO**	No ID
Cryptococcus albidus	*Cryptococcus laurentii*	**ERY**, **DUL**, NIT	*Cryptococcus albidus*
Cryptococcus albidus	*Cryptococcus uniguttulatus*	MEZ, NIT	*Candida krusei*
Cryptococcus laurentii	*Trichosporon pullulans*	LAC, DUL, **NIT**	*Cryptococcus laurentii*
Cryptococcus uniguttulattus	No ID	**RHA**	*Cryptococcus uniguttulatus*
Cryptococcus uniguttulattus	*Rhodotorula* sp.	MAL, ARA, INO, **NIT**	*Cryptococcus uniguttulatus*
Rhodotorula glutinis	*Rhodotorula rubra*	**INO**, NIT	*Rhodotroula rubra*
Rhodotorula glutinis	*Cryptococcus albidus*	GAL, **ERY**, **INO**	*Hansenula anomala*
Saccharomyces cerevisiae	*Torulopsis candida*	**MEL**, **MEZ**	*Saccharomyces cerevisiae*
Torulopsis candida	No ID	**INO**	*Candida guilliermondii*
Torulopsis candida	No ID	XYL	*Candida tropicalis*
Torulopsis candida	*Candida guilliermondii*	CEL	No ID
Trichosporon beigelii	No ID	**DUL**	*Trichosporon beigelii*

[a] Test abbreviations: ARA, arabinose; CEL, cellobiose; DUL, dulcitol; ERY, erythritol; GAL, galactose; INO, inositol; LAC, lactose; MAL, maltose; MEL, melibiose; MEZ, melezitose; NIT, nitrate; RAF, raffinose; RHA, rhamnose; TRE, trehalose; URE, urea; XYL, xylose; no ID, not identified by system. Discrepant tests that gave false-positive results are shown in boldface type; tests that gave false-negative results are shown in lightface type.

[b] Germ tube-negative isolate.

the yeast suspensions was adjusted to that of a MacFarland no. 5 nephlometry standard. These suspensions were used to inoculate portions of yeast nitrogen base in molten Noble agar, which were then poured into a sterile petri plate (150 by 15 mm). After the agar solidified, carbohydrate disks were placed on the surface. Our modification of the system consisted of using two sterile petri plates (150 by 15 mm) and 24 carbohydrate disks per isolate. Minitek disks included adonitol, arabinose, cellobiose, glucose, galactose, glycerol, inositol, lactose, maltose, mannitol, melibiose, raffinose, rhamnose, salicin, sorbitol, sucrose, trehalose, and xylose. Six additional substrate disks were prepared by saturating sterile BBL blank disks (0.25 in. [ca. 0.64 cm]) in sterile 3% water solutions of D-arabinitol, erythritol, melezitose, methyl-D-glucoside, sorbose, or starch. The disks were lyophilized and stored in a desiccator at 6°C. Twelve of the 24 disks were placed on each petri plate, plates were incubated at 30°C, and zones of growth around the substrate disks were noted after 24, 48, and 72 h. Results of a germ tube test and morphology on cornmeal-Tween 80 agar (12) were also noted. Organism identification was based on descriptions found in standard references (7, 8, 12).

Other identification tests. The following conventional tests were performed when initial test results were inconclusive: urease production on Christiansen urea agar (12), India ink (12), nitrate assimilation on auxanographic medium (3), chlamydospore and hyphae production on cornmeal-Tween 80 agar, ascospore formation (13), and fermentation of cellobiose, glucose galactose, lactose, maltose, raffinose, sucrose, and trehalose (4).

RESULTS

The API 20C and modified Minitek systems agreed on the identification of 243 of 245 yeasts (99.2%). One isolate of *Candida albicans* was initially not identified by API 20C but was correctly identified when retested, and an isolate of *Torulopsis candida* was identified initially and on repeat testing as *Candida guilliermondii* by the API 20C system.

Quantum II correctly identified 197 of the 245 yeasts (80.4%), incorrectly identified 19 (7.8%), and did not identify 29 (11.8%) on initial testing (Table 1). No single species accounted for more than 4 of the 19 incorrectly identified isolates. Twenty-five of the 29 yeasts that Quantum II did not identify were *Candida* spp. Three of these 29 were germ tube-negative strains of *Candida albicans*. Of the discrepant *Candida* strains, 50% were either *Candida parapsilosis* or *Candida pseudotropicalis*.

Table 2 lists the 48 yeasts that Quantum II incorrectly identified or did not identify, the individual results that probably contributed to the error, and the results obtained when yeasts were retested by the Quantum II system. Of the 152 discrepant tests involving 16 substrates, 132 (86.8%) were positive when a negative result was expected according to the results of the API 20C, modified Minitek systems, and conventional data. Discrepancies were most commonly seen with dulcitol, erythritol, inositol, or rhamnose as substrate. Many of the individual *Candida* spp. had several discrepant test results that could have contributed to the errors, whereas a false-positive nitrate test probably caused most of the *Cryptococcus* spp. and *Rhodotorula glutinis* misidentifications. When the 48 yeasts listed in Table 2 were retested by the Quantum II system, 15 were correctly identified, 16 were incorrectly identified, and 17 were not identified.

Yeasts that were initially identified correctly by the Quantum II system often had one or more individual substrate tests results that differed from results by conventional methods. Examples from nine different species are listed in Table 3. Included are several *Candida* spp. that gave more than one atypical result.

TABLE 3. Examples of unconventional assimilation results from yeasts correctly identified by the Quantum II system

Organism	Unconventional assimilation result[a]
Candida albicans (germ tube positive)	**LAC, MEL, RHA, ERY, DUL, INO**
Candida lusitaniae	**ERY, DUL, INO**
Candida parapsilosis	XYL, **INO**
Candida pseudotropicalis	CEL, ARA, RHA
Candida tropicalis	**NIT**
Candida stellatoidea	**MEL, RAF, MEZ, RHA, DUL, INO**
Cryptococcus neoformans	**NIT**
Cryptococcus uniguttulatus	MAL, INO
Saccharomyces cerevisiae	**CEL**

[a] Discrepant tests that gave false-positive results are shown in boldface type; tests that gave false-negative results are shown in lightface type. Test abbreviations are shown in footnote *a* of Table 2.

DISCUSSION

There was very good agreement between the results of the API 20C and modified Minitek systems. Identification to species correlated for 243 of 245 yeasts. These methods have compared favorably with standard identification systems (1, 6, 9).

Quantum II was not as accurate in identifying the yeasts, and many of the yeasts that were correctly identified had individual reaction results that differed from expected results. Twenty percent of the yeasts were not identified or were incorrectly identified by the Quantum II system. There was no obvious clustering of either misidentifications or individual test discrepancies; 16 different species of yeasts and 16 different test substrates contributed to the error.

Most of the discrepant identifications occurred because assimilation or biochemical tests with the Quantum II system were false-positive. The API 20C and modified Minitek systems required incubation for 48 or 72 h before some assimilation reactions were readable. Perhaps to make results available within 24 h with the Quantum II system, the media has a low pH threshold so that false-positive reactions can easily occur. We have listed the individual reactions that probably caused the discrepancies; however, knowledge of the software would be required for a specific explanation of the errors. In some instances discrepancies appeared to be overlooked by design. For example, all germ tube-positive *Candida albicans* isolates were correctly identified even though the same discrepant tests occurred as did for isolates that were germ tube negative. We feel that this identification system, which relies on conventional assimilation tests, should yield individual test results that generally correspond to conventional results.

We did not specifically compare the time to identification in the three systems. Each system sometimes required additional tests, including fermentations; time to final identification often exceeded 3 days. Although the manufacturers of the API 20C and Minitek systems recommend that assimilation results should be noted for 3 days, final identification was often available by days 1 or 2.

In summary, we have found that both the API 20C and modified-Minitek systems accurately identified a variety of clinical yeast isolates. Although 80% of the yeasts were correctly identified by the Quantum II system, a significant number were either misidentified or not identified. The Quantum II system for yeast identification appears to require hardware, substrate, or software-data base modifications to improve its accuracy.

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