JOURNAL OF CLINICAL MICROBIOLOGY, June 1992, p. 1541–1543
0095-1137/92/061541-03$02.00/0

Vol. 30, No. 6

Evaluation of the autoSCAN-W/A System for Rapid (2-Hour) Identification of Members of the Family *Enterobacteriaceae*

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Received 30 December 1991/Accepted 6 March 1992

We evaluated the ability of the Baxter autoSCAN-W/A System (MicroScan Division, Baxter Diagnostics, Inc., West Sacramento, Calif.) to use the rapid (2-h) gram-negative identification panel for accurate identification of members of the family *Enterobacteriaceae*. At 2 h, 353 of 467 (75.6%) strains in a challenge set of biochemically typical and atypical stock cultures were correctly identified to genus and species. Another 76 (16.3%) strains were correctly identified to genus and species after the performance of recommended additional biochemical testing. Thus, at 24 h, 91.9% of the 467 strains were correctly identified. Twenty-two strains (4.7%) were identified to the correct genus but the incorrect species, and 16 strains (3.4%) were misidentified. Of these 16 strains, 9 were incorrect at 2 h, and 7 were incorrect after the additional testing. Because the system is based on fluorogenic substrates, no conventional tests were readily available with which to compare aberrant reactions. These results suggest that the autoSCAN-W/A with its rapid gram-negative panels is acceptable for the identification of the *Enterobacteriaceae* in a clinical microbiology laboratory.

The MicroScan Division of Baxter Diagnostics, Inc. (West Sacramento, Calif.) historically has approached bacterial identification in several ways with their identification systems. These methods have included visual reading of biochemical test panels (with or without the touch-SCAN), semiautomated reading by using the autoSCAN-4, and the new automated reading system, the autoSCAN-W/A (WalkAway). Each of these approaches provides accurate results (2–8). The autoSCAN-W/A, the Vitek (Hazelwood, Mo.) AutoMicrobic System, and the ALADIN (Analytab Products, Inc., Plainview, N.Y.) constitute the available fully automatic bacterial identification instruments.

Advances in the use of fluorogenic substrates to recognize preformed-enzyme activity has allowed a more-rapid approach to organism identification. Coupled with computer-driven robotics, these instruments incubate, read, and interpret the tests, with virtually no additional manipulations after the instrument is loaded. By using this approach, 2- to 4-h identification and reporting times are common (3, 6).

Although the autoSCAN-W/A has been evaluated for its ability to accurately identify non-glucose-fermenting gram-negative rods (6) and has been tested against the Vitek AutoMicrobic System (3), the rapid panels have not been fully evaluated against standard *Enterobacteriaceae* reference procedures. We challenged the autoSCAN-W/A with 467 strains of the *Enterobacteriaceae* representing both common and rare clinical isolates in order to determine the limits of accuracy of the instrument under stringent test conditions.

MATERIALS AND METHODS

Culture collection. This study used 467 typical and atypical gram-negative fermenters taken from the stock culture collection of the Centers for Disease Control (Table 1).

All stock cultures were removed from storage at room temperature and passed once onto heart infusion agar (Difco Laboratories, Detroit, Mich.) with 5% sheep blood, once onto 5% sheep blood agar plates (TSA II; Becton Dickinson Microbiology Systems, Cockeysville, Md.), and then onto MacConkey's agar (Becton Dickinson) for inoculation of the Rapid Neg Combo Type 3 panels, which were provided by MicroScan. All plates were incubated at 35°C for 21 h. A bacterial suspension approximating a 0.5 McFarland standard was made in 0.4% saline with Pluronic D and used for inoculation of the identification portion of the Rapid Neg Combo Type 3 panel. The susceptibility portion of each panel was blanked with sterile water with Pluronic D, since this study did not evaluate susceptibility results. The decarboxylase base, lysine, and ornithine wells were overlaid with mineral oil, and user-generated bar code labels were applied to each panel. The panels were then inserted into the autoSCAN-W/A instrument as previously described (3, 6).

Identification results were available at 2 h and were compared for accuracy with identifications obtained with conventional biochemical tests as performed at the Centers for Disease Control (1). The indole test was performed only when prompted by the autoSCAN-W/A system for the completion of an identification or when necessary to differentiate between two possible species. Indole was not considered an additional test, since the test is performed by adding two drops of the indole reagent to the test panel. An additional test was defined as any test, such as a conventional biochemical test, which added 24 h to the time required for completion of an identification. Any additional biochemical tests required for completion of an identification by the autoSCAN-W/A were performed by Centers for Disease Control methods. Serologic tests required to confirm a *Salmonella* sp. or a *Shigella* sp. were also not considered additional tests. This evaluation utilized software version 17.02 of the MicroScan Data Management System.

The term "correct" is used here to mean that the identification was correct to the genus and species levels. "Correct to genus only" means that the identification was correct

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TABLE 1. autoSCAN-W/A identifications by category of accuracy

Strains		No. of identifications			
By genus	No. tested	Correct[a]		Correct to genus only	Error
		P, ≥85%	*P*, <85%		
Cedecea	19	17	2		
Citrobacter	30	27	3		
Edwardsiella	10	9			1
Enterobacter	70	43	22	3	2
Escherichia	60	46	5	1	8
Ewingella	10	8	2		
Hafnia	10	10			
Klebsiella	50	29	5	14	2
Kluyvera	10	7	3		
Koserella	10	7	3		
Morganella	10	10			
Proteus	30	22	8		
Providencia	28	24	4		
Salmonella	30	18	9	1	2
Serratia	60	52	5	2	1
Shigella	10	8	2		
Yersinia	20	16	3	1	
Totals (%)	467	353 (75.6)	76 (16.3)	22 (4.7)	16 (3.4)

[a] *P*, probability.

at the genus level but was incorrect at the species level when the manufacturer states that the autoSCAN-W/A can identify the organism to the species level. An "error" result indicates an incorrect genus identification, an unacceptable profile number, or a report of "very doubtful identification."

RESULTS AND DISCUSSION

Identifications rendered by the autoSCAN-W/A were grouped into four categories, i.e., those for which (i) the first identification listed was correct at ≥85% probability, (ii) the correct identification was listed among the possible choices at <85% probability but required additional biochemical tests for completion, (iii) the genus was correct but the correct species designation was not among the choices, or (iv) the correct identification was not among the choices (Table 1). At 2 h, 75.6% (353 of 467) of the strains were correctly identified at a probability of ≥85%; another 16.3% (76 of 467) required additional biochemical testing but were correctly identified at 24 h, even though the probability at 24 h was <85%. Most (16 of 22) of the strains that were correct to the genus level and incorrect to the species level were identified at 2 h. Of the 16 erroneous identifications, 9 were obtained at 2 h and 7 were obtained at 24 h.

Determinations for all misidentified strains were repeated twice to ensure that no technical error had occurred. Because the system is based on fluorogenic substrates, no conventional tests with which to compare aberrant reactions were readily available. For this reason, we were unable, in most cases, to determine why an incorrect answer was reported. No recurring problem areas were evident, with the exception of the genus *Escherichia* (Table 2). *Escherichia hermannii* and *Escherichia vulneris* were misidentified for 30% of the strains belonging to either of the two species. Of five atypical *Salmonella* strains, two were misidentified. One strain was identified as *Enterobacter gergoviae*, at a probability of 94.6%; the other was identified as *Escherichia coli*, at a probability of 99.9%. Because an optional identification of the *Salmonella* genus was not given for either strain, the need for a serologic test was not prompted.

TABLE 2. Misidentifications

Identification by:		Probability (%) of identification
Reference	autoSCAN-W/A	
Edwardsiella tarda, biogroup 1	*Salmonella typhi*	93.9
Enterobacter		
agglomerans	*Citrobacter freundii*	64.4
agglomerans	*Citrobacter freundii*	98.0
Escherichia		
coli (indole negative)	*Salmonella/Arizona*	87.0
fergusonii	*Citrobacter amalonaticus* or *diversus*	68.6
hermannii	*Citrobacter freundii*	8.7
hermannii	*Enterobacter agglomerans*	98.2
hermannii	*Klebsiella ozaenae*	0.2
vulneris	*Enterobacter sakazakii*	89.5
vulneris	*Citrobacter freundii*	22.0
vulneris	*Salmonella/Arizona*	99.9
Klebsiella		
ozaenae	*Citrobacter freundii*	65.7
rhinoscleromatis	*Enterobacter asburiae*	20.3
Salmonella		
enteritidis (atypical)	*Enterobacter gergoviae*	94.6
enteritidis (atypical)	*Escherichia coli*	99.9
Serratia rubidaea	*Enterobacter gergoviae*	93.8

Of the strains identified correctly to genus only, many were *Klebsiella ornithinolytica* (ornithine-positive *Klebsiella pneumoniae*). The error resulted because the panels were ornithine negative at 2 h. The manufacturer is aware of this problem. The low concentration of ornithine also adversely affected 3 of 10 of the *P. mirabilis* identifications. They required additional biochemical testing be-fore being correctly identified at the low probabilities of 13 to 16%.

These results suggest that the autoSCAN-W/A, with its rapid gram-negative panels, is acceptable for the identification of members of the family *Enterobacteriaceae*.

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