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Evaluation of the DMS Rapid E System for Identification of Clinical Isolates of the Family *Enterobacteriaceae*

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A total of 387 unique clinical isolates of the family *Enterobacteriaceae* were examined with the new DMS Rapid E gram-negative identification system (DMS Laboratories, Inc., Flemington, N.J.) and the API 20E procedure (Analytab Products, Plainview, N.Y.). Altogether, 376 strains (97.2%) were correctly identified to species level within 4 h with the DMS Rapid E system; 366 strains (94.6%) were correctly identified with the API 20E after overnight incubation.

The identification of isolates of the family *Enterobacteriaceae* in the clinical laboratory may be accomplished by the use of conventional biochemical tests or a variety of commercially available miniaturized biochemical systems. These products usually consist of biochemical substrates in dehydrated form contained in plastic cupules, small tubes, or microtiter plates. Incubation times range from 4 to 24 h, and species identification is determined by the use of tables or codebooks supplied by the manufacturer. Both manual and automated systems are available.

Recently, a new 4-h biochemical micromethod, the DMS Rapid E system (DMS Laboratories, Inc., Flemington, N.J.), was introduced in the United States for purposes of determining the species identification of *Enterobacteriaceae* isolates. This system, which permits determination of 20 different biochemical characteristics within 4 h, was previously shown to accurately identify members of this family bacteria in two limited studies in France (5, 6).

The intent of the present study was to evaluate the DMS Rapid E system as a new means for the rapid identification of *Enterobacteriaceae* isolates routinely recovered from human clinical specimens. The results obtained with the DMS Rapid E system were compared with those obtained with the API 20E. Discrepancies between the two systems were arbitrated with a conventional biochemical identification schema.

A total of 387 strains of gram-negative bacilli resembling *Enterobacteriaceae* were selected consecutively from human clinical specimens other than stool submitted to the clinical microbiology laboratories of the University of Massachusetts Medical Center, Worcester, Mass., for analyses. Stool isolates were omitted since DMS Laboratories markets a separate product (the DMS-SST) specifically for the identification of enteric pathogens, such as *Salmonella* and *Shigella* species. The two procedures described below were performed with inocula prepared in the following manner. A single colony from a primary MacConkey agar plate was streaked to a 5% sheep blood agar plate and incubated overnight at 35°C in air. Growth from the sheep blood agar plate was used to inoculate both test systems and conventional biochemical tests, when necessary.

The DMS Rapid E system is a micromethod consisting of 20 biochemical substrates in dehydrated form incorporated into individual cupules attached to a paper strip. The following biochemical characteristics may be determined: production of beta-D-galactosidase, lysine, and ornithine decarboxylase; urease; phenylalanine deaminase; utilization of citrate and malonate; hydrolysis of esculin; production of indole and acetoin; fermentation of arabinose, xylose, adonitol, rhamnose, cellobiose, melibiose, sucrose, trehalose, raffinose, and glucose; and determination of the presence of cytochrome oxidase. After inoculation, strips were incubated for 4 h at 35°C in atmospheric air, reagents were added, and the results were interpreted according to the instructions of the manufacturer. An octal code profile was assigned based on the reaction pattern, and the identity of the isolate was ascertained by consulting the manufacturer's code compendium. Additional tests were performed when indicated in the codebook. Profile numbers not included in the identification codebook were referred to the manufacturer's computer service. Isolates which yielded no identification were tested a second time with the DMS Rapid E system with growth from an overnight 5% sheep blood subculture which had been prepared as a purity check from the original DMS inoculum suspension.

The API 20E (Analytab Products, Plainview, N.Y.) was used as described previously (8) according to the instructions of the manufacturer. After incubation of test strips overnight at 35°C at atmospheric air and the addition of reagents and interpretation of individual biochemical tests, an octal code profile was assigned, and the organism identity was determined by referring to the identification codebook supplied by the manufacturer. Additional biochemical tests were performed when indicated in the codebook. Isolates which were not identified by this procedure were tested a second time with the API 20E with growth from an overnight subculture on 5% sheep blood agar as the inoculum.

Conventional biochemical identification tests were performed on isolates which yielded no identification on one of the commercial systems or which were identified differently by the two systems. A single colony of test organism from an overnight 5% sheep blood agar culture was inoculated into 4.0 ml of tryptic soy broth and incubated at 35°C in atmospheric air until turbid. Two or three drops of this suspension was used to inoculate appropriate individual biochemical tests. After incubation for 24 or 48 h at 35°C and the addition of reagents where appropriate, organisms were identified according to conventional criteria (7).

The results of the species determinations of 387 clinical isolates of the family *Enterobacteriaceae* by the DMS Rapid E system and the API 20E are depicted in Table 1. The true identity of test organisms was considered to be that obtained with the DMS and API when concordance between the results of these two systems was achieved. When discrepan-

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TABLE 1. Comparison of the results of identification of *Enterobacteriaceae* isolates with the API 20E and the DMS Rapid E system

Organism (no.)	No. (%)[a] correctly identified to species level by:	
	API 20E (24 h)	DMS Rapid E (4 h)
Escherichia coli (205)	203 (99.0)	204 (99.5)
Klebsiella pneumoniae (49)	44 (89.8)	48 (98.0)
Klebsiella oxytoca (12)	12 (100)	12 (100)
Enterobacter aerogenes (18)	15 (83.3)	18 (100)
Enterobacter cloacae (15)	11 (73.3)	14 (93.3)
Proteus mirabilis (49)	49 (100)	48 (98.0)
Proteus vulgaris (4)	3 (75.0)	4 (100)
Proteus rettgeri (1)	1 (100)	1 (100)
Morganella morganii (10)	10 (100)	8 (80.0)
Providencia stuartii (7)	5 (71.4)	6 (85.7)
Serratia marcescens (8)	8 (100)	7 (87.5)
Citrobacter freundii (4)	4 (100)	3 (75.0)
Citrobacter diversus (4)	1 (25.0)	3 (75.0)
Citrobacter amalonaticus (1)	0 (0.0)	0 (0.0)

[a] Overall, API Z0E correctly identified 94.6%, and DMS Rapid E correctly identified 97.2%.

cies were noted, test strain identity was assigned based on the results of conventional biochemical tests.

A total of 376 isolates (97.2%) were correctly identified to species level by the DMS Rapid E system in 4 h. These results are consistent with the observations of Izard et al. (5, 6). One isolate of *Morganella morganii*, which yielded no identification upon initial testing, was correctly identified with repeat testing. Another strain of *M. morganii* required performance of a single additional biochemical test, mannose fermentation, for correct identification. This test, which was suggested by the DMS code compendium, resulted in a correct identification being achieved after 24 h. No identification was achieved with eight organisms, one strain each of *Escherichia coli*, *Klebsiella pneumoniae*, *Enterobacter cloacae*, *Providencia stuartii*, *Serratia marcescens*, *Citrobacter freundii*, *Citrobacter diversus*, and *Citrobacter amalonaticus*. Only a single organism was misidentified, a strain of indole-positive *Proteus mirabilis* which was identified as *M. morganii* due to a false-negative H_2S reaction.

The species identity of 366 isolates (94.6%) was correctly determined by the API 20E after overnight incubation. These results are similar to those previously reported by others after overnight incubation (1, 4, 9). Three strains required repeat testing for correct identification. In 12 cases, performance of additional biochemical tests was necessary to achieve complete species identification. These additional tests, all suggested by the API octal code profile index, resulted in a 1-day delay in identification. Three organisms, one strain of *K. pneumoniae* and two strains of *P. stuartii*, could only be identified to the genus level with the API 20E. A relatively large number of strains in this study, 15, required additional biochemical tests for correct species identification or could only be identified to the genus level, a result that has also been previously observed by others (1, 3, 4). No identification was obtained with single isolates of *E. coli* and *C. amalonaticus*. Only one organism was incorrectly identified, a strain of *Enterobacter aerogenes* which was identified as *Serratia liquefaciens*.

More *Enterobacteriaceae* strains were correctly identified to species level after 4 h with the DMS Rapid E system than with the API 20E after overnight incubation (376 versus 366, respectively). When isolates which required either repeat testing or performance of supplemental biochemical tests were included in the data analysis, a total of 378 and 381 strains were correctly identified by the DMS Rapid E system and the API 20E, respectively.

In conclusion, the DMS Rapid E system was found to be at least as accurate as the API 20E for identification of human clinical isolates of the family *Enterobacteriaceae* representative of those routinely encountered in clinical microbiology laboratories. The principal advantage of the DMS system is the provision of final identification results after 4 h. The utility of the DMS system for identification of less common *Enterobacteriaceae* species awaits further investigation.

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