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Premarket Evaluation of IDS RapID SS/u System for Identification of Urine Isolates

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A total of 170 fresh clinical urine isolates were tested with a premarket configuration of the RapID SS/u system (Innovative Diagnostic Systems, Inc., Atlanta, Ga.), a qualitative micromethod for the identification of selected organisms commonly isolated from urine specimens. Results were compared with those obtained with conventional methods of identifying gram-positive isolates and with the AutoMicrobic system (Vitek Systems, Inc., Hazelwood, Mo.), utilizing Gram-Negative Identification cards for the identification of gram-negative rods. Organisms representing 12 taxa were included in the study. Of the 170 isolates, 163 (95.9%) were correctly identified. A total of 144 strains (84.7%) were correctly identified without additional testing, whereas 19 isolates (11.2%) required further testing. Seven isolates (4.1%) were incorrectly identified. The SS/u system required minimal hands-on time to inoculate and interpret reactions. Discrepancies most often occurred with regard to misinterpretation of *Escherichia coli* and *Enterobacter* sp. as *Citrobacter* sp. The IDS RapID SS/u system may indeed prove valuable for the rapid manual identification of urine isolates.

Urine cultures comprise a major portion of the clinical microbiology laboratory workload. Therefore, rapid yet cost-effective methods for the identification of urine isolates is desirable in the management of urinary tract infections.

Currently, several manual (1, 3, 5, 7) and automated (2, 6, 8) systems offer same-day identification of a large spectrum of *Enterobacteriaceae* as well as gram-positive organisms, but they are not designed specifically for urine isolate identification. The AutoMicrobic system Urine Identification-3 Card (Vitek Systems, Inc., Hazelwood, Mo.) detects, enumerates, and selectively identifies the most common gram-positive and gram-negative urine isolates directly from urine specimens within 13 h (4). However, the AutoMicrobic system may not fulfill the needs of many laboratories limited in space or funding. Thus, a premarket evaluation of the RapID SS/u system (Innovative Diagnostic Systems, Inc. [IDS], Atlanta, Ga.), was undertaken to assess its ability to identify common urine isolates.

(This report was presented in part at the annual meeting of the American Society for Microbiology, Washington, D.C., 24 to 28 March 1986 [D. G. Halstead, M. Hoffert, and G. Colasante, Abstr. Annu. Meet. Am. Soc. Microbiol. 1986, C-120, p. 348].)

MATERIALS AND METHODS

Organisms. A total of 170 fresh clinical urine isolates from our hospital laboratory were tested. Gram-negative rods were identified by using the AutoMicrobic system in conjunction with Gram-Negative Identification cards. Staphylococci were identified by using the Gram stain and Staphyloslide (BBL Microbiology Systems, Cockeysville, Md.). Bile esculin, salt tolerance (Scott Laboratories, Inc., Fiskeville, R.I.), and Streptex (Wellcome Diagnostics, Dartford, England) tests were used to identify *Enterococcus* species. Germ tube testing was carried out to aid in the identification of yeasts.

Organisms were isolated on 5% sheep blood agar (Scott) or MacConkey agar (BBL) after 18 to 48 h of incubation at 35 to 37°C and tested for oxidase activity (Marion Scientific, Div. Marion Laboratories, Inc., Kansas City, Mo.) when appropriate.

RapID SS/u system. Two premarket configurations of the RapID SS/u panels were used in the study and contained the following 11 tests: ONPG (β,D-galactosidase); G1, G2, and G3 (glycosidases); PHS (phosphatase); URE (urease); GMS, A1, A2, and A3 (aminopeptidases); and IND (indole formation).

A suspension of each isolate was prepared in IDS RapID Inoculation Fluid to be equivalent to at least a MacFarland no. 1 turbidity standard. The suspensions were mixed thoroughly and introduced into the RapID SS/u panels within 15 min of preparation. The suspensions were carefully added through the inoculation ports of the panels by using a diSPo pipet (American Scientific Products, McGaw Park, Ill.). After the ports were resealed, the panels were slowly tilted forward, allowing the inoculum to flow along the partitions into each of the 10 front reaction cavities. The panels were gently tapped to remove small bubbles and then incubated aerobically for 1 or 2 h at 35 to 37°C. Eight isolates incorrectly identified after 1 h of incubation were subcultured and retested in panels incubated for 2 h.

Reactions were scored on the basis of visual color changes within the panel test cavities. Cavities containing GMS, ONPG, G1, G2, G3, PHS, and URE did not require reagent addition for color detection. Color development in three aminopeptidase tests and in the indole test required 2 drops of IDS RapID SS/u Reagent or indole reagent, respectively.

A four-digit microcode was derived from the 11 test scores and the oxidase test. Interpretations of the resulting four-digit microcodes were done by using the IDS computer-assisted identification program. RapID SS/u identifications were based on the probability and biofrequency of a given isolate having a particular microcode.

RESULTS

Two incubation times for panels were studied. A total of 102 isolates were incubated for 2 h, and 68 isolates were incubated for 1 h. Eight isolates initially tested with a 1-h

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TABLE 1. Identification of urine isolates by the RapID SS/u system

Organism	No. tested	No. correctly identified		No. incorrectly identified
		Without additional testing	With additional testing	
E. coli	66	58	6	2
Proteus sp.	19	19	0	0
Klebsiella sp.	14	14	0	0
Enterobacter sp.	9	6	0	3
Providencia sp.	4	2	2	0
Serratia sp.	2	2	0	0
Citrobacter sp.	2	1	1	0
Pseudomonas sp.	16	16	0	0
Enterococcus sp.	14	13	0	1
Staphylococcus sp.	13	10	3	0
Candida albicans	6	3	3	0
Yeasts (other)	3	0	3	0
Streptococci (non-group D)[a]	2	0	1	1

[a] Not included in the RapID SS/u data base.

incubation were reevaluated; five were correctly identified with a 2-h incubation.

Because results obtained after 1 h of incubation closely paralleled those obtained after 2 h of incubation, all results were combined (Table 1). A total of 163 of 170 isolates (95.9%) were identified by the system: 144 of 170 isolates (84.7%) were correctly identified without additional testing, and 19 of 170 isolates (11.2%) required additional testing. With the exception of two isolates, one strain of *Citrobacter diversus* and one viridans group streptococcus, the IDS RapID SS/u Code Compendium listed the reference method identification as one of the choices when a probability overlap was encountered. Additional characteristics were listed in the compendium under these conditions; therefore, even the two exceptions were not assigned an incorrect identification. Seven isolates (4.1%) were incorrectly identified (Table 2).

Of 132 gram-negative rods, 127 (96.2%) were correctly identified to the species or genus level; 118 of 132 (89.4%) did not require additional testing for identification, whereas 9 of 132 (6.8%) required additional testing for complete identification. Of the 132 gram-negative isolates, 5 (3.8%) were incorrectly identified. Of 38 gram-positive isolates, including yeasts, 36 (94.7%) were correctly identified; 26 of 38 (68.4%) did not require additional testing for identification, whereas 10 of 38 (26.3%) required additional testing for complete identification. Of the 38 gram-positive isolates, 2 (5.3%) were incorrectly identified.

TABLE 2. Discrepant results obtained with the RapID SS/u system

Reference identification	Microcode	Rapid SS/u identification	Probability level
E. coli	3040	*C. freundii*	Satisfactory
E. coli	3040	*C. freundii*	Satisfactory
Enterobacter agglomerans	1000	*Klebsiella pneumoniae*	Adequate
E. aerogenes	3041	*C. freundii*	Implicit
E. cloacae	3360	*Serratia* sp.	Satisfactory
Viridans group streptococcus	2000	*Staphylococcus* sp.	Satisfactory
Enterococcus sp.	0001	*Staphylococcus* sp.	Implicit

DISCUSSION

The IDS RapID SS/u system rapidly identifies the vast majority of microorganisms commonly encountered in urine, including gram-negative rods, gram-positive cocci, and yeasts, in a single test kit. The incorrect identifications encountered in our study closely resembled those found by DeGirolami et al. (P. C. DeGirolami, J. S. Siegel, L. Sigmund, and R. A. Eichelberger, Abstr. Annu. Meet. Am. Soc. Microbiol. 1986, C-119, p. 347). Whereas we found *Escherichia coli* incorrectly identified as *Citrobacter freundii*, they found *Citrobacter* sp. incorrectly identified as *E. coli*. Our sample size of *Citrobacter* sp. was too small to establish a reliable error rate. Furthermore, the assessment of error rates was complicated by differences between the API 20E (24 h) system used by DeGirolami et al. and the AutoMicrobic system used by us (6).

In our experience, three elements of the test procedure must be followed closely to avoid aberrant results: (i) suspensions used as inocula should be minimally equivalent to a MacFarland no. 1 turbidity standard; (ii) the inoculum should be well mixed; and (iii) panels should be incubated for a full 2 h. In our study, five isolates identified incorrectly initially were correctly identified upon retesting when the manufacturer's instructions for suspension preparation and incubation were adhered to closely.

Since the RapID SS/u system identifies both gram-positive and gram-negative organisms, we explored the possibility of using only blood agar for plating urine specimens to decrease the cost of materials (MacConkey agar plates) and labor in initial specimen processing. An attempt was made to selectively use isolates growing on blood agar from 133 cultures. However, in several instances were found the need to select colonies from MacConkey agar (37 isolates) because of the better separation of colonies in a mixed culture, particularly those containing swarming *Proteus mirabilis*. Additionally, elimination of the MacConkey agar plate reduced the ability to use lactose fermentation as an aid in presumptively screening isolates.

The RapID SS/u system was found to be a rapid and accurate 2-h system for the identification of significant urine isolates. Overall, 95.9% of the isolates studied were correctly identified. Among the strains identified, 11.2% required simple additional testing for complete identification. The system required minimal hands-on time to inoculate and interpret reactions, but close attention to inoculum density and mixing were necessary.

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