Clinical Laboratory Evaluation of the AutoMicrobic System for Rapid Identification of *Enterobacteriaceae*

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The capability of the AutoMicrobic system (Vitek Systems, Inc., Hazelwood, Mo.) has been expanded to identify members of the family *Enterobacteriaceae* with the use of a sealed, disposable accessory card (the *Enterobacteriaceae* Biochemical Card) containing 26 biochemical tests. To judge the accuracy of the AutoMicrobic system's identification in a hospital laboratory, 933 *Enterobacteriaceae* isolates were studied. The AutoMicrobic system provided the correct identification for 905 of the isolates (97%). For *Enterobacteriaceae* excluding *Escherichia coli* (533 isolates not *E. coli*), 506 isolates were correctly identified (94.9%). The AutoMicrobic system integrates well into the clinical microbiology laboratory, providing a simple, accurate, and efficient automated system for the rapid identification of *Enterobacteriaceae*.

Within the past decade a variety of manual commercial systems have gained acceptance in clinical microbiology laboratories for the identification of bacteria of the family *Enterobacteriaceae* to the genus and species level. Many of the commercially available systems offer accuracy, reproducibility, convenience, and ease of storage. Perhaps the most desirable departure from conventional tube media use in the clinical microbiology laboratory is the provision by the commercial kit systems of standardized material which provides greater assurance of intra- and interlaboratory reproducibility in identification.

An alternative to the manual commercial kits has been introduced whereby standardized objective readings of biochemical tests are provided by automated and computerized systems. The AutoMicrobic system (AMS) (Vitek Systems, Inc., Hazelwood, Mo.) is one such system and consists of five modules, the diluent-dispenser, the filling module, the reader-incubator module, and computer control module with data terminal, which have been described in detail elsewhere (1). Plastic disposable cards consisting of microcuvettes containing dehydrated media are inoculated and incubated in the AMS. An optical system monitors light transmission changes in the microcuvettes of each card and transmits the optical measurements to a computer which analyzes the results and provides a final report. The first card developed for use in the AMS, the Urine Identification Card, by which certain microorganisms in urine are detected, enumerated, and identified, has been evaluated (1, 5-8). Recently, the AMS has been expanded to identify *Enterobacteriaceae* iso-

lates from clinical specimens. The *Enterobacteriaceae* Biochemical Card (EBC) (Vitek), when used in conjunction with the AMS, is purported to identify 30 species of *Enterobacteriaceae* from pure culture. The EBC consists of 30 microcuvettes containing 26 biochemicals, one positive broth control, and three empty wells for future application. Although preliminary results may be obtained after 4 h, final identification is determined after 8 h.

This study evaluates the performance of the EBC in the final identification of routine *Enterobacteriaceae* isolates in a hospital clinical microbiology laboratory.

MATERIALS AND METHODS

Microorganisms. Of the 933 microorganisms identified, 803 were consecutively collected from fresh clinical isolates and 130 were selectively collected. These microorganisms represented 22 species of the family *Enterobacteriaceae* (Table 1) and were from a wide variety of clinical specimens (Table 2).

During the course of the study, the taxonomic nomenclature of Edwards and Ewing (3) as recently revised by the Centers for Disease Control (2) was used.

Identification methods. Oxidase-negative, gram-negative rods, grown on 5% sheep blood agar (BBL Microbiology Systems, Cockeysville, Md.) or eosin methylene blue (BBL) agar plates incubated at 37°C for 18 to 24 h, were studied. A total of 938 microorganisms were collected during this study. Identification was made by using the API 20E test strip (Analytab Products, Plainview, N.Y.). On isolates that were questionably identified by API 20E and on isolates where API 20E identification differed from EBC identification, other tests were performed. These other tests were the Enterotube II (Roche Diagnostics, Nutley,

TABLE 1. Summary of 933 clinical isolates of *Enterobacteriaceae* identified in this study

Organism	No. of isolates identified
<i>Escherichia coli</i>	400
<i>Shigella sonnei</i>	10
<i>S. flexneri</i>	4
<i>Shigella</i> species	1
<i>Klebsiella pneumoniae</i>	129
<i>K. oxytoca</i>	5
<i>K. ozaenae</i>	1
<i>Enterobacter cloacae</i>	63
<i>E. aerogenes</i>	24
<i>E. sakazakii</i>	1
<i>E. agglomerans</i>	6
<i>Hafnia alvei</i>	3
<i>Serratia marcescens</i>	26
<i>Salmonella</i> species	36
<i>Citrobacter freundii</i>	18
<i>C. diversus</i>	8
<i>Proteus mirabilis</i>	138
<i>P. vulgaris</i>	15
<i>Morganella morganii</i>	20
<i>Providencia stuartii</i>	15
<i>P. alcalifaciens</i>	3
<i>P. rettgeri</i>	7

TABLE 2. Sources of isolates listed in Table 1

Specimen	No. of isolates found
Urine	440
Wound	120
Sputum	101
Stool	72
Vagina	62
Blood	40
Abdominal cavity	31
Ulcer	22
Ear	15
Throat	11
Bone	5
Nasopharynx	4
Surgical tissue	4
Eye	4
Gallbladder	2

N.J.), the Micro-ID (General Diagnostics, Morris Plains, N.J.), and conventional biochemical media. Five isolates could not be confirmed and were not considered in the study.

Description and use of the EBC. The EBC incorporates a series of tests which are performed during the 8 h of incubation in the AMS reader-incubator module. Most of these biochemical tests are conventional; however, three nonconventional tests have been included to provide more accurate identification of some species of the family *Enterobacteriaceae*. Two of the nonconventional tests are based on glucose fermentation in the presence of specific inhibitors, whereas the third test is based on the formation of a unique compound from a D-glucoside group which forms a black, indigo blue precipitate in the presence of oxygen.

Five lots of EBC were used in this study (lots D 1072679, D 1080879, D 1052379, D 1091779, and D 1100579) which were stored at 2 to 8°C. Each lot was tested by the quality control organisms that were recommended by Vitek. In accordance with manufacturer's instructions, a bacterial suspension equivalent to the McFarland no. 1 standard was prepared in the card injector. Card microcuvettes were simultaneously filled within 4.5 min by negative pressure in the filling module. The cards were next detached from the injectors and inspected to verify that each card was properly filled. Cards were placed in the AMS 120 reader-incubator module (120-card capacity) at a temperature of 35.5°C. The programmed computer determined when a biochemical test in a microcuvette became positive based on the attenuation of light measured by the optical system. The biochemical patterns were analyzed and stored automatically by the computer. At the completion of the 8-h incubation cycle, the data terminal printed a final status report for each card in the reader-incubator module. Each final status report contained a laboratory accession number that had been marked on the card at the beginning of the test cycle, the time and date of test completion, and a final identification with probability; the probability expressed is the likelihood of correct identification in accordance with the biochemical patterns incorporated into the data base of the computer.

RESULTS

Identification of microorganisms by the EBC. The accuracy of the EBC in the identification of 933 microorganisms to the genus and species level is shown in Table 3. Nine of 11 genera (*Escherichia*, *Klebsiella*, *Shigella*, *Hafnia*, *Serratia*, *Salmonella*, *Proteus*, *Morganella*, and *Providencia*) identified by the EBC showed a 95% or greater correct identification to the genus level. For the two remaining genera studied, *Enterobacter* and *Citrobacter*, there was between 90 and 95% agreement of identification to the genus level. At the species level, 905 of 933 isolates were correctly identified. An agreement of 95% or greater was seen with the following organisms: *E. coli*, *S. sonnei*, *S. flexneri*, *K. pneumoniae*, *E. aerogenes*, *E. agglomerans*, *H. alvei*, *S. marcescens*, *Salmonella* species, *C. diversus*, *P. mirabilis*, *M. morganii*, *P. stuartii*, *P. alcalifaciens*, and *P. rettgeri*. Of clinical significance, no *Shigella* or *Salmonella* species were missed with the EBC. A 93.3% correlation was seen with *P. vulgaris*. Less agreement with the final identification was seen with *E. cloacae* (88.9%), *C. freundii* (88.9%), *E. sakazakii* (0%), *K. ozaenae* (0%), and *K. oxytoca* (0%). It should be noted that Vitek does not claim that the EBC identifies *E. sakazakii* or *K. oxytoca*. In the case of the latter, this is due to the absence of an indole test in the EBC. Thus, for all *Enterobacteriaceae*, 97% were cor-

TABLE 3. Accuracy of identification by the EBC

Organism	Total of no. isolates	No. of isolates identified by EBC	Correct identification (%)
<i>Escherichia coli</i>	400	398	99.5
<i>Shigella</i>	15	15	100
<i>S. sonnei</i>	10	10	100
<i>S. flexneri</i>	4	4	100
<i>Shigella</i> species ^a	1	1	100
<i>Klebsiella</i>	135	129	95.5
<i>K. pneumoniae</i>	129	125	96.9
<i>K. oxytoca</i> ^b	5	0	0
<i>K. ozaenae</i>	1	0	0
<i>Enterobacter</i>	94	87	92.5
<i>E. cloacae</i>	63	56	88.9
<i>E. aerogenes</i>	24	23	95.8
<i>E. sakazakii</i> ^b	1	0	0
<i>E. agglomerans</i>	6	6	100
<i>Hafnia alvei</i>	3	3	100
<i>Serratia marcescens</i>	26	26	100
<i>Salmonella</i> species	36	36	100
<i>Citrobacter</i>	26	24	92.3
<i>C. freundii</i>	18	16	88.9
<i>C. diversus</i>	8	8	100
<i>Proteus</i>	153	149	97.4
<i>P. mirabilis</i>	138	134	97.1
<i>P. vulgaris</i>	15	14	93.3
<i>Morganella morganii</i>	20	20	100
<i>Providencia</i>	25	25	100
<i>P. stuartii</i>	15	15	100
<i>P. alcalifaciens</i>	3	3	100
<i>P. rettgeri</i>	7	7	100
Total <i>Enterobacteriaceae</i> isolates (No. of <i>Enterobacteriaceae</i> isolates excluding <i>E. coli</i>)	933 (533)	905 (506)	97 (94.9)

^a Typed as *alkalescens-dispar* group.^b Not included in the AMS data base.

rectly identified by the EBC. For *Enterobacteriaceae* excluding *E. coli* (533 isolates not *E. coli*) a 94.9% correct identification was observed.

Misidentifications by the EBC. Incorrect identifications made by the EBC (28 of 933 isolates) are listed in Table 4. Isolates misidentified by the EBC were repeated twice to ascertain whether misidentification was a trial error or a repetitive problem. With evident misidentification problems, an effort was made to determine whether biochemical failure(s) or inadequacy of the data base was at fault. As seen in Table 4, correct identification with both of the EBC repeat tests was observed in 10 of 28 iso-

lates (35.7%) originally misidentified; correct identification was seen only in one of two repeat EBC tests for 6 of 28 isolates (21.4%). No shift to correct identification was observed with 12 of 28 isolates (42.9%); however, it should be noted that of the 12 isolates in which no shift to correct identification was observed, 6 were not included in the AMS data base (1 *E. sakazakii* and 5 *K. oxytoca* isolates).

The AMS data base (3 August 1979) was examined to determine key biochemicals upon which the identification of bacteria are dependent; for example, 95% of *E. aerogenes* are ornithine positive. The EBC biochemical failures which exerted influence on final identification are noted in Table 4.

Each laboratory sets criteria for the adequacy of identification before issuing a final report; Vitek has provided such a guide for the EBC identification. In an attempt to verify the adequacy of this guide, the data of Table 5 have been included as a comparison between correct identification and the probability of such identification as given by the AMS. Of the 905 isolates correctly identified by the EBC, 94.2% showed a probability greater than 0.9, whereas of the 28 isolates incorrectly identified, only 32.1% showed a probability this high.

DISCUSSION

Automation has developed more slowly in clinical microbiology than it has in other medical laboratory services (for example, in clinical chemistry or serology), because bacteriological techniques and data interpretation have not lent themselves easily to past technology. The AMS is an automated system with the potential of detecting, enumerating, identifying, and performing drug susceptibility testing of microorganisms. We have evaluated one aspect of the present capabilities of the AMS identification of *Enterobacteriaceae* with the use of the EBC.

In addition to its present high degree of accuracy in identification (Table 3), the EBC provides a variety of advantages over commonly used identification systems. The system offers time savings for the technologist in terms of the following. Minimal set-up time is required, in comparison with that required for other identification systems. Time spent reading biochemical reactions and interpreting biochemical profiles is eliminated, since the optical system reads the cards, the computer analyzes the data, and the automatic printer reports the results. Unlike some identification systems, the EBC requires no additional reagents to perform tests, and in most cases it requires no additional biochemical tests to make an identification. This system rap-

TABLE 4. *Microorganisms (28 of 933 isolates) incorrectly identified by the EBC: results of repeat tests*

Organism	EBC identification: initial test plus two repeat tests	Probability of correct identification indicated by the AMS	No. of correct identifications on two repeat tests	Biochemical(s) responsible for initial incorrect identification ^a
1. <i>Escherichia coli</i>	<i>Salmonella choleraesuis</i> <i>Salmonella choleraesuis</i> <i>Escherichia coli</i>	0.4851 0.4851 0.9974	1	False-negative ONPG
2. <i>Escherichia coli</i>	<i>Yersinia enterocolitica</i> <i>Escherichia coli</i> <i>Escherichia coli</i>	0.9142 0.6216 0.9874	2	False-positive urease
3. <i>K. pneumoniae</i>	<i>Enterobacter aerogenes</i> <i>Klebsiella pneumoniae</i> <i>Enterobacter aerogenes</i>	0.9958 0.8859 0.9958	1	False-positive ornithine
4. <i>K. pneumoniae</i>	<i>Enterobacter aerogenes</i> <i>Klebsiella pneumoniae</i> <i>Klebsiella pneumoniae</i>	0.9930 0.9300 0.9300	2	False-positive ornithine
5. <i>K. pneumoniae</i>	<i>Enterobacter aerogenes</i> <i>Klebsiella pneumoniae</i> <i>Klebsiella pneumoniae</i>	0.7774 0.9960 0.9960	2	False-positive ornithine
6. <i>K. pneumoniae</i>	<i>Enterobacter cloacae</i> <i>Klebsiella pneumoniae</i> <i>Klebsiella pneumoniae</i>	0.8428 0.9958 0.9958	2	False-positive arginine, false-positive RX2
7. <i>K. oxytoca</i> ^b	<i>Klebsiella pneumoniae</i> <i>Enterobacter aerogenes</i> <i>Klebsiella pneumoniae</i>	0.9293 0.9851 0.9300	0	
8. <i>K. oxytoca</i> ^b	<i>Klebsiella pneumoniae</i> <i>Klebsiella pneumoniae</i> <i>Klebsiella pneumoniae</i>	0.9960 0.8859 0.9934	0	
9. <i>K. oxytoca</i> ^b	<i>Enterobacter aerogenes</i> <i>Klebsiella pneumoniae</i> <i>Klebsiella pneumoniae</i>	0.7774 0.9960 0.9960	0	False-positive ornithine
10. <i>K. oxytoca</i> ^b	<i>Klebsiella pneumoniae</i> <i>Klebsiella pneumoniae</i> <i>Klebsiella pneumoniae</i>	0.9300 0.9300 0.9300	0	
11. <i>K. oxytoca</i> ^b	<i>Klebsiella pneumoniae</i> <i>Klebsiella pneumoniae</i> <i>Klebsiella pneumoniae</i>	0.9960 0.9960 0.9960	0	
12. <i>K. ozaenae</i>	<i>Escherichia coli</i> <i>Escherichia coli</i> <i>Escherichia coli</i>	0.9546 0.9546 0.9983	0	
13. <i>E. cloacae</i>	<i>Serratia liquefaciens</i> <i>Serratia liquefaciens</i> <i>Serratia liquefaciens</i>	0.6583 0.6583 0.6583	0	False-negative arginine
14. <i>E. cloacae</i>	<i>Serratia liquefaciens</i> <i>Serratia liquefaciens</i> <i>Serratia liquefaciens</i>	0.6583 0.6583 0.6583	0	False-negative arginine
15. <i>E. cloacae</i>	<i>Serratia liquefaciens</i> <i>Serratia liquefaciens</i> <i>Serratia liquefaciens</i>	0.6583 0.6583 0.6583	0	False-negative arginine

TABLE 4—Continued

Organism	EBC identification: initial test plus two repeat tests	Probability of correct identification indicated by the AMS	No. of correct identifications on two repeat tests	Biochemical(s) responsible for initial incorrect identification ^a
16. <i>E. cloacae</i>	<i>Serratia liquefaciens</i> <i>Serratia liquefaciens</i> <i>Serratia liquefaciens</i>	0.6583 0.6583 0.6583	0	False-negative arginine
17. <i>E. cloacae</i>	<i>Serratia liquefaciens</i> <i>Enterobacter cloacae</i> <i>Serratia liquefaciens</i>	0.9658 0.9558 0.9658	1	False-negative arginine
18. <i>E. cloacae</i>	<i>Serratia liquefaciens</i> <i>Enterobacter cloacae</i> <i>Serratia liquefaciens</i>	0.9658 0.9490 0.9658	1	False-negative arginine
19. <i>E. cloacae</i>	<i>Enterobacter aerogenes</i> <i>Enterobacter cloacae</i> <i>Enterobacter cloacae</i>	0.8967 0.9310 0.9304	2	False-negative arginine, false-positive inositol
20. <i>E. aerogenes</i>	<i>Serratia liquefaciens</i> <i>Enterobacter cloacae</i> <i>Enterobacter aerogenes</i>	0.8890 0.6876 0.7086	1	
21. <i>E. sakazakii</i> ^c	<i>Enterobacter cloacae</i> <i>Enterobacter cloacae</i> <i>Enterobacter cloacae</i>	0.7556 0.7556 0.7556	0	
22. <i>C. freundii</i>	<i>Serratia liquefaciens</i> <i>Citrobacter freundii</i> <i>Citrobacter freundii</i>	0.5363 0.9999 0.9999	2	
23. <i>C. freundii</i>	<i>Serratia liquefaciens</i> <i>Yersinia enterocolitica</i> <i>Yersinia enterocolitica</i>	0.9883 0.6430 0.6430	0	
24. <i>P. mirabilis</i>	<i>Morganella morganii</i> <i>Proteus mirabilis</i> <i>Proteus mirabilis</i>	0.8626 0.9999 0.9999	2	False-negative H ₂ S, false-negative TDA, false-positive RX1
25. <i>P. mirabilis</i>	<i>Morganella morganii</i> <i>Proteus mirabilis</i> <i>Proteus mirabilis</i>	0.9251 0.6993 0.9356	2	False-negative TDA, false-negative RX2
26. <i>P. mirabilis</i>	Glucose negative <i>Proteus mirabilis</i> <i>Morganella morganii</i>	0.5086 0.9968	1	False-negative glucose
27. <i>P. mirabilis</i>	Glucose negative <i>Proteus mirabilis</i> <i>Proteus mirabilis</i>	0.9999 0.9999	2	False-negative glucose
28. <i>P. vulgaris</i>	<i>Proteus mirabilis</i> <i>Proteus vulgaris</i> <i>Proteus vulgaris</i>	0.9683 0.9989 0.9989	2	False-positive ornithine

^a ONPG, *o*-Nitrophenyl- β -D-galactopyranoside; H₂S, hydrogen sulfide; TDA, tryptophan deaminase; RX1 and RX2, AMS proprietary nonconventional tests.

^b *K. oxytoca* is not in the AMS data base.

^c *E. sakazakii* is not in the AMS data base.

TABLE 5. Identification versus probability as given by the AMS

Probability	No. of organisms correctly identified	% ^a	No. of organisms incorrectly identified	% ^b
>0.9	852	94.2	9	32.1
Between 0.8 and 0.9	23	2.5	4	14.3
<0.8	30	3.3	15	53.6

^a Percent of total correctly identified organisms.^b Percent of total incorrectly identified organisms.

idly identifies *Enterobacteriaceae*, providing final identification at 8 h and presumptive identification as early as 4 h. Also, use of the sealed plastic cards reduces the risk of contamination of work areas. (At present, our cost of disposables, at \$2.70 per isolate, is somewhat higher than that of conventional and commercial kit identification systems.)

Biochemical test failures were responsible in part for incorrect identifications by the EBC. These biochemical failures were determined by noting which biochemical(s) in the AMS data base was responsible for a shift from incorrect to correct identification and by noting which biochemicals were key to the identification scheme. Although there is evidence that the results of a single biochemical failure in these instances caused misidentification, it is felt that the enlargement and the maturation of the AMS data base, with the resultant refinement of the computer program, will give improved identification performance. Single biochemical failures which affected final identification were seen primarily with two biochemicals, ornithine decarboxylase and arginine dihydrolase. False-positive ornithine decarboxylase results accounted for five misidentifications. Ornithine decarboxylase was falsely positive by the EBC, as confirmed by conventional tube media, on three occasions for *K. pneumoniae* (no. 3–5, Table 4). On all three occasions *K. pneumoniae* was incorrectly identified as *E. aerogenes* because of this single biochemical failure. There was one instance each in which a false-positive ornithine decarboxylase reaction accounted for a *P. vulgaris* (no. 28, Table 4) being misidentified as a *P. mirabilis*, and a *K. oxytoca* (no. 9, Table 4) being misidentified as an *E. aerogenes*. False-negative arginine dihydrolase reactions by the EBC were seen with 15 of 63 *E. cloacae* isolates. Of these 15 *E. cloacae* isolates, 6 were misidentified as *S. liquefaciens* (no. 13 and 18, Table 4), whereas the other 9 were correctly identified. This indicates that a false-negative for this bio-

chemical is insufficient by itself to cause incorrect identification; however, in combination with a negative rhamnose and negative malonate reaction, incorrect identification has occurred. Other variations in single or multiple biochemical determinations, which accounted for sporadic misidentifications, can be seen in Table 4. Air bubbles in the EBC which could have affected biochemical readings by the optical systems were probably not responsible for the majority of biochemical variations that affected final identification. All isolates were run by the EBC protocol by the same technologist and were checked for air bubbles in the EBC before placement of the card into the reader-incubator module. Varying inoculum concentrations (McFarland no. 0.5, 1, and 2 standards) were tested for misidentified isolates with single biochemical determination failures, with no biochemical fluctuation seen that affected final identification. Inoculum concentration not equivalent to the recommended McFarland no. 1 standard was, therefore, not responsible for these single biochemical failures.

Inherent weaknesses in the AMS data base and programming were evident with several of the misidentifications. The new taxonomic designations of *E. sakazakii* (no. 21, Table 4) and *K. oxytoca* (no. 7–11, Table 4) were not included in the AMS data base. To differentiate *K. pneumoniae* from *K. oxytoca*, a spot indole test with a bacterial suspension from the positive control microcuvette of the card is recommended by Vitek for all *K. pneumoniae* strains identified by the EBC. A *K. ozaenae* isolate (no. 12, Table 4) was misidentified as an *E. coli* on all three EBC tests.

Major technical problems associated with the use of the EBC in the AMS 120 included defective card fills due to card tube assemblies, and electrostatic printer breakdowns. About 7% of the card fills resulted in the failure of the bacterial suspension to be drawn into the card, resulting in incomplete filling of all microcuvettes of the card. These defective card fills were due to the design of the injector tube card assemblies and not to deficiencies of the filling module. Currently, Vitek is reimbursing for defective card fills. (A new transfer tube system for filling cards is presently undergoing clinical trials at our institution and, thus far, results are promising.) In addition to this persistent problem, electrostatic printer failure was experienced on numerous occasions. Results at the end of several 8-h test cycles were not automatically printed due to insufficiently moist paper or due to mechanical paper jams. However, results were still manually retrievable in all instances, since the

AMS retains in its computer memory each card's results until the card is removed from the reader-incubator module. A new printer, recently installed in our laboratory, has proven to be relatively trouble free, providing dry-copy printouts that are easily read and stored. No major problems were encountered with the other modules. Routine maintenance of the AMS requires no more than 5 min daily, and should anything go wrong during the test cycle, the AMS audibly and visibly alerts the operator to the problem.

In conclusion, use of the EBC with the AMS is a valuable adjunct for a clinical microbiology laboratory that identifies large numbers of *Enterobacteriaceae* isolates daily or that has problems staffing the laboratory with skilled technologists or both. A recent multi-center study (4) has favorably evaluated the EBC, finding it to have an identification accuracy of 97.8%. It was shown in the study presented here that the EBC when used in conjunction with the AMS in a hospital clinical microbiology laboratory is a simple, accurate, and efficient automated system for the rapid identification of *Enterobacteriaceae*. Identification thus obtained showed a high degree of accuracy, with 905 of 933 *Enterobacteriaceae* isolates correctly identified for an overall agreement with a final identification of 97%. For organisms other than *E. coli* (533 isolates not *E. coli*), there was an agreement of 94.9%. The AMS is an extremely flexible instrument with the capabilities of wider applications in the clinical microbiology laboratory.

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