Evaluation of the Enteric Analyzer, an Instrument to Aid in the Identification of *Enterobacteriaceae*

DON J. BRENNER* AND ALBERT BALOWS

Center for Disease Control, Atlanta, Georgia 30333

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This study evaluated the Enteric Analyzer, an instrument designed to identify *Enterobacteriaceae*, with data obtained from the Modified r/b Enteric Differential System, other rapid identification systems, or conventional identification systems. It is programmed for 19 reactions with data obtained from Center for Disease Control publications. The instrument is very simple to use. Typical strains from 25 of 28 species were unequivocally identified. With the other three species, two choices were given. A switch allows the user to identify all species possibilities where a given biochemical pattern occurs in more than 1% of the strains or more than 10% of the strains. The instrument is useful both in the clinical laboratory and for teaching purposes.

The significant increases in nosocomial infections, in multiple drug-resistant bacteria, and in bacteria that are biochemically atypical due to the presence of plasmid-mediated metabolic genes are but some of the reasons why more laboratories tend to speciate *Enterobacteriaceae*. The policy in individual laboratories with regard to identification at the species level is contingent upon cost, time, and space requirements, as well as the number of personnel and their level of competence.

A number of kits or systems are now commercially available for the rapid identification of *Enterobacteriaceae*. These systems have been evaluated in a number of laboratories (11-16) and also have been found to be practical from a cost-accounting point of view. By properly using these systems and properly interpreting results, trained personnel are better able to speciate organisms. The use of these systems helps to eliminate errors and variations in results caused by using different media, reagents, tests, or differences in quality control. The ability to compare results obtained from different laboratories should now be substantially increased.

With the availability of these systems, a major remaining problem is how best to apply the data to speciation. Various approaches have been recommended including relying on the expertise of the bacteriologist, providing flow sheets for identification, and providing either biochemical profile analysis keys or a computer analysis of biochemical data.

Diagnostic Reasearch, Inc., has developed an instrument called the Enteric Analyzer. This instrument is programmed according to percent-

ages published by Ewing et al. (2-9) to identify *Enterobacteriaceae* based on 18 biochemical reactions and motility.

As seen in Fig. 1, the keyboard has switches for each reaction. Each switch has a positive, neutral, and negative position. Above the keyboard are 28 red lights, each corresponding to an enteric species or group of species. As positive or negative reactions are entered, the red lights are extinguished as species are eliminated. Also on the keyboard is a switch with two positions labeled 90 and 99%. In the 90% mode a species is eliminated when the test strain exhibits a positive or negative reaction seen in less than 10% of the strains of that species. In the 99% mode, a species is eliminated only when a given reaction is seen in less than 1% of its strains.

The Enteric Analyzer is designed for use with the Modified r/b Enteric Differential System. The manufacturer states that it can also be used with any other rapid identification system or a conventional identification system which includes the reactions covered by the instrument. In the present study this instrument was evaluated with data obtained from approximately 1,000 gram-negative, oxidase-negative, fermentative strains that had been previously identified as *Enterobacteriaceae* by conventional biochemical methods.

MATERIALS AND METHODS

Bacteria. The species used in this study are listed in Table 1, along with the corresponding designations on the Enteric Analyzer. They were pure cultures isolated from clinical specimens including stools, sputa, urines, blood, and wounds.

FIG. 1. The Enteric Analyzer. The keyboard contains an On/Off switch, 90% mode or 99% mode, and 19 switches for entering reactions. The reaction switches have a positive, neutral, and negative position. The display has 28 boxes each with a species name and a red light emitting diode.

Evaluation. The data used to evaluate the Enteric Analyzer had previously been obtained by conventional biochemical tests (1–10) on approximately 1,000 gram-negative, oxidase-negative, fermentative strains. Representatives of all of the genera and/or species covered by the instrument were included. In most cases all reactions coded by the instrument were used. These were phenylalanine deaminase, hydrogen sulfide production, gas production from glucose, lysine decarboxylase, lactose fermentation, indole production, ornithine decarboxylase, motility, citrate utilization, rhamnose fermentation, deoxyribonuclease, raffinose fermentation, sorbitol fermentation, arabinose fermentation, malonate utilization, urease, inositol fermentation, adonitol fermentation, and esculin utilization. All reactions were read at 24 and 48 h. Any reaction that became positive after 48 h was deemed negative. Specific comments usually apply to strains exhibiting only one atypical reaction. An attempt was made to include strains exhibiting each atypical reaction occurring in from 1 to 10% of the total strains of a given species.

RESULTS

Use of the Enteric Analyzer. The Enteric Analyzer is designed for use with the Modified r/b Enteric Differential System. The manufacturer states that it can also be used with any other rapid identification system or conventional identification system. The instrument is extremely simple to operate. The instruction booklet is clearly and concisely written. Examples are included to help the user learn to operate the instrument, which can be accomplished within 15 min. With practice, the data can be easily entered and the result obtained in 30 s to 1 min.

When only one species is indicated no interpretation of results is necessary. When all species are ruled out in both the 90 and 99% modes, the culture can be presumptively reported as unidentified. In these cases the users are directed to various publications listed in the in-

TABLE 1. *Species studied and Enteric Analyzer designations*

Species	Enteric Analyzer designation ^a
<i>Arizona hinshawii</i>	<i>Arizona</i> sp. (typical)
<i>Citrobacter diversus</i>	
<i>C. freundii</i>	
<i>Edwardsiella tarda</i>	
<i>Enterobacter aerogenes</i>	
<i>E. agglomerans</i>	
<i>E. cloacae</i>	
<i>E. hafniae</i>	
<i>Escherichia coli</i>	
<i>Klebsiella ozaenae</i>	
<i>K. pneumoniae</i>	
<i>K. rhinoscleromatis</i>	
<i>Proteus mirabilis</i>	
<i>P.morganii</i>	
<i>P. rettgeri</i>	
<i>P. vulgaris</i>	
<i>Providencia alcalifaciens</i>	
<i>P. stuartii</i>	
<i>Salmonella choleraesuis</i>	<i>Salmonella</i> sp. (typical)
<i>S. enteritidis</i>	
<i>S. enteritidis</i> ser paratyphi A	<i>Salmonella paratyphi</i> A
<i>S. typhi</i>	
<i>Serratia rubidaea</i>	<i>Shigella</i> sp. (typical)
<i>Shigella boydii</i>	
<i>S. dysenteriae</i>	
<i>S. flexneri</i>	
<i>S. sonnei</i>	
<i>Yersinia enterocolitica</i>	<i>Yersinia pseudotuberculosis</i>
<i>Y. pseudotuberculosis</i>	

^a Only listed when different from designation in the lefthand column.

struction manual for guidance in the identification. When more than one species possibility exists in either the 90 or 99% mode the user must choose between the possibilities or decide what additional tests are required because: (i) there is no indication as to which of the choices has a greater probability of being the correct one; and (ii) there are no guidelines for which additional tests, if any, should be carried out.

Identification of typical strains. For purposes of evaluation, a typical strain exhibits the reaction shown by more than 50% of all strains included in the Center for Disease Control tables for the 19 tests programmed in the Enteric Analyzer (1-10). Ideally, in the 90% mode, the Enteric Analyzer should unequivocally identify every typical strain. Twenty-five of the 28 species are identified in the 90% mode. The exceptions are as follows: (i) *Enterobacter cloacae*

cannot be distinguished from *Citrobacter freundii*. The addition of the methyl red and Voges-Proskauer tests would allow differentiation of these species. (ii) *Yersinia pseudotuberculosis* cannot be distinguished from *Enterobacter agglomerans*. The addition of Voges-Proskauer, sucrose, and motility tests at 22 C would allow differentiation of these species. (iii) *Shigella sonnei* is not distinguished from *Shigella* sp. (typical). *S. sonnei* is ornithine positive, whereas strains of other shigellae are 98% or more ornithine negative. Therefore, *S. sonnei* can be distinguished from other shigellae without any additional tests. This appears to be a programming error.

Identification of atypical strains. Any strain of a species exhibiting a reaction shown by less than 10% of the total strains of that species is eliminated in the 90% mode. If the reaction occurs in less than 1% of the strains, the atypical strain is also eliminated at 99%. Of particular interest are atypical strains that exhibit reactions shared by 1 to 10% of the total strains of a species. These are identified at 99%, but a choice often must be made between two or more possibilities. As shown in Table 2, this type of strain is encountered in almost every species. The instrument gives no indication of which possibility is more likely. Furthermore, a strain that exhibits one atypical reaction (occurring in 1 to 10% of strains in a given species) is not distinguished from a strain exhibiting as many as six or more atypical reactions.

In each case, additional reactions are necessary to choose between possible species. Some of these reactions are shown in Table 3. In some cases these are commonly used tests such as methyl red, Voges-Proskauer, KCN, arginine, and maltose. In other instances the reactions such as corn oil, gelatin, α -methyl glucoside, mucate, and tartrate are less commonly used.

Possible programming errors. There are several cases where a strain is not identified in the 90% mode or the 99% mode even though the atypical reaction occurs in more than 1 or 10% of the total strains (Table 4). There are also instances when a strain exhibiting a reaction shared by less than 10% of the total strains is identified in the 90% mode (Table 4). These reactions are most likely the result of errors in programming the Enteric Analyzer.

Delayed reactions. Rapid identification systems are usually designed to be read between 18 and 24 h. Conventional systems may be read anywhere from 18 h to two weeks or longer. There is no mention of delayed reactions in the instruction manual. Some examples of com-

TABLE 2. Identification of atypical strains of enteric bacteria by use of the Enteric Analyzer in the 99% mode

Species	Reaction ^a	Choices
<i>Klebsiella ozaenae</i>	orn ⁺ (2%) mal ⁺ (6%) ado ⁻ (1%)	<i>K. ozaenae</i> , <i>E. aerogenes</i> , <i>S. liquefaciens</i> <i>K. ozaenae</i> , <i>E. aerogenes</i> , <i>E. agglomerans</i> <i>K. ozaenae</i> , <i>E. aerogenes</i> , <i>E. agglomerans</i>
<i>K. pneumoniae</i>	gas ⁻ (3.5%) lys ⁻ (3%) lac ⁻ (2%) ind ⁺ (6%) cit ⁻ (2%) mal ⁻ (7.5%) ure ⁻ (5.5%) ino ⁻ (2%)	<i>K. pneumoniae</i> , <i>K. ozaenae</i> , <i>E. aerogenes</i> , <i>S. rubidaea</i> <i>K. pneumoniae</i> , <i>K. ozaenae</i> , <i>E. aerogenes</i> , <i>E. cloacae</i> , <i>E. agglomerans</i> , <i>S. rubidaea</i> <i>K. ozaenae</i> , <i>E. aerogenes</i> <i>K. pneumoniae</i> , <i>S. rubidaea</i> <i>K. pneumoniae</i> , <i>K. ozaenae</i> , <i>E. aerogenes</i> , <i>S. rubidaea</i> <i>K. pneumoniae</i> , <i>K. ozaenae</i> , <i>E. aerogenes</i> , <i>S. rubidaea</i> <i>K. pneumoniae</i> , <i>K. ozaenae</i> , <i>E. aerogenes</i> , <i>S. rubidaea</i> <i>K. pneumoniae</i> , <i>K. ozaenae</i> , <i>E. aerogenes</i> , <i>S. rubidaea</i>
<i>Enterobacter aerogenes</i>	lys ⁻ (1%) mot ⁻ (3%)	<i>E. aerogenes</i> , <i>E. cloacae</i> <i>E. aerogenes</i> , <i>K. ozaenae</i>
<i>E. cloacae</i>	orn ⁻ (4%) mot ⁻ (5.5%) raf ⁻ (3%) sor ⁻ (5.5%)	<i>E. cloacae</i> , <i>E. aerogenes</i> , <i>E. agglomerans</i> , <i>C. freundii</i> , <i>S. rubidaea</i> <i>E. cloacae</i> , <i>E. aerogenes</i> , <i>K. ozaenae</i> , <i>C. freundii</i> <i>E. cloacae</i> , <i>E. aerogenes</i> , <i>C. freundii</i> <i>E. cloacae</i> , <i>E. aerogenes</i> , <i>C. freundii</i>
<i>E. hafniae</i>	ure ⁺ (3%) esc ⁺ (6%) mot ⁻ (7%)	<i>E. hafniae</i> , <i>E. aerogenes</i> <i>E. hafniae</i> , <i>E. aerogenes</i> <i>E. hafniae</i> , <i>E. aerogenes</i> , <i>K. ozaenae</i>
Anaerogenic <i>E. agglomerans</i>	ado ⁺ (3%)	<i>E. agglomerans</i> , <i>E. cloacae</i> , <i>E. aerogenes</i>
<i>Serratia marcescens</i>	mot ⁻ (1%) cit ⁻ (1%)	<i>S. marcescens</i> , <i>S. liquefaciens</i> <i>S. marcescens</i> , <i>S. liquefaciens</i>
<i>S. liquefaciens</i>	mot ⁻ (7%) esc ⁻ (5%)	<i>S. liquefaciens</i> , <i>K. ozaenae</i> <i>S. liquefaciens</i> , <i>Salmonella</i> sp. (typical)
<i>Salmonella typhi</i>	H ₂ S ⁻ (6%)	<i>S. typhi</i> , <i>Salmonella</i> sp. (typical)
<i>Salmonella</i> sp. (typical)	H ₂ S ⁻ (8%) lys ⁻ (5%) rha ⁻ (10%) raf ⁺ (3%) sor ⁻ (6%)	<i>Salmonella</i> sp. (typical), <i>E. aerogenes</i> , <i>S. liquefaciens</i> <i>Salmonella</i> sp. (typical), <i>C. freundii</i> <i>Salmonella</i> sp. (typical), Arizona <i>Salmonella</i> sp. (typical), Arizona <i>Salmonella</i> sp. (typical), Arizona
<i>Shigella sonnei</i>	lac ⁺ (2%)	<i>S. sonnei</i> , <i>C. freundii</i> , <i>E. coli</i> , <i>K. ozaenae</i> , <i>E. aerogenes</i> , <i>S. liquefaciens</i>
<i>Shigella</i> sp. (typical)	gas ⁺ (2%)	<i>Shigella</i> sp. (typical), <i>Salmonella</i> sp. (typical), <i>E. agglomerans</i>
<i>Escherichia coli</i>	gas ⁻ (8%) lac ⁻ (8%) ind ⁻ (1.5%) ado ⁻ (6%)	<i>E. coli</i> , <i>S. liquefaciens</i> <i>E. coli</i> , <i>S. liquefaciens</i> <i>E. coli</i> , <i>E. aerogenes</i> , <i>S. liquefaciens</i> <i>E. coli</i> , <i>S. liquefaciens</i>
<i>Providencia alcalifaciens</i>	phe ⁻ (3%)	<i>P. alcalifaciens</i> , <i>E. agglomerans</i>
	mot ⁻ (4%) cit ⁻ (2%)	<i>P. alcalifaciens</i> , <i>E. agglomerans</i> <i>P. alcalifaciens</i> , <i>E. agglomerans</i>
<i>P. alcalifaciens</i>	ado ⁻ (5%)	<i>P. alcalifaciens</i> , <i>P. vulgaris</i> , <i>P. mirabilis</i> , <i>E. agglomerans</i>
<i>P. stuartii</i>	phe ⁻ (6%) lac ⁻ (4%) cit ⁻ (4%) raf ⁺ (6%) sor ⁺ (4%) ara ⁺ (5%) ado ⁺ (4%) ino ⁻ (2.5%)	<i>P. stuartii</i> , <i>E. agglomerans</i> <i>P. stuartii</i> , <i>E. agglomerans</i> <i>P. stuartii</i> , <i>E. agglomerans</i> <i>P. stuartii</i> , <i>E. agglomerans</i> <i>P. stuartii</i> , <i>E. agglomerans</i> <i>P. stuartii</i> , <i>E. agglomerans</i> <i>P. stuartii</i> , <i>E. agglomerans</i> <i>P. stuartii</i> , <i>E. agglomerans</i> <i>P. stuartii</i> , <i>P. alcalifaciens</i> , <i>P. mirabilis</i> , <i>P. vulgaris</i> , <i>E. agglomerans</i>
<i>Proteus mirabilis</i>	orn ⁻ (1%)	<i>P. mirabilis</i> , <i>P. vulgaris</i>
<i>P. vulgaris</i>	H ₂ S ⁻ (5%)	<i>P. vulgaris</i> , <i>P. rettgeri</i>

TABLE 2—Continued

Species	Reaction ^a	Choices
<i>P. rettgeri</i>	phe ⁻ (2%) lac ⁺ (9%) mot ⁻ (6%) cit ⁻ (4%) raf ⁺ (9.5%) ino ⁻ (7%)	<i>P. rettgeri</i> , <i>E. agglomerans</i> <i>P. rettgeri</i> , <i>E. agglomerans</i> <i>P. rettgeri</i> , <i>E. agglomerans</i> <i>P. rettgeri</i> , <i>E. agglomerans</i> <i>P. rettgeri</i> , <i>E. agglomerans</i> <i>P. rettgeri</i> , <i>E. agglomerans</i>
<i>P. morganii</i>	mal ⁺ (5%) ure ⁻ (2%) phe ⁻ (5%) orn ⁻ (3%)	<i>P. morganii</i> , <i>P. mirabilis</i> <i>P. morganii</i> , <i>P. mirabilis</i> <i>P. morganii</i> , <i>S. liquefaciens</i> <i>P. morganii</i> , <i>P. mirabilis</i> , <i>P. rettgeri</i> , <i>P. vulgaris</i> , <i>E. agglomerans</i>
<i>Yersinia enterocolitica</i>	gas ⁻ (1.3%) rha ⁺ (1.3%) DNase ⁺ (3%) raf ⁺ (7%)	<i>K. ozaenae</i> , <i>S. liquefaciens</i> <i>C. freundii</i> , <i>K. ozaenae</i> , <i>E. aerogenes</i> , <i>S. liquefaciens</i> <i>Y. enterocolitica</i> , <i>K. ozaenae</i> , <i>S. liquefaciens</i> <i>Y. enterocolitica</i> , <i>K. ozaenae</i> , <i>S. liquefaciens</i>

^a The numbers in parentheses are the percentages of strains of a given species exhibiting the listed reaction.

TABLE 3. Additional tests of value in identifying atypical strains of enteric bacteria

Species	Reactions
<i>Klebsiella ozaenae</i> from <i>K. rhinoscleromatis</i>	Sucrose, starch, α -methylglucoside
<i>K. ozaenae</i> from <i>K. pneumoniae</i>	Methyl red, Voges-Proskauer
<i>K. ozaenae</i> from <i>Enterobacter aerogenes</i>	Methyl red, Voges-Proskauer
<i>K. ozaenae</i> from <i>E. agglomerans</i>	α -Methyl glucoside, gelatin
<i>K. pneumoniae</i> from <i>E. aerogenes</i>	Gelatin
<i>K. pneumoniae</i> from <i>E. cloacae</i>	Arginine, gelatin
<i>K. pneumoniae</i> from <i>E. agglomerans</i>	Tartrate, α -methyl glucoside
<i>K. pneumoniae</i> from <i>Serratia rubidaea</i>	Corn oil, gelatin
<i>E. aerogenes</i> from <i>E. cloacae</i>	Arginine, gelatin
<i>E. cloacae</i> from <i>Citrobacter freundii</i>	Methyl red, Voges-Proskauer
<i>E. hafniae</i> from <i>E. aerogenes</i>	Methyl red, sucrose, salicin
<i>E. hafniae</i> from <i>K. ozaenae</i>	Voges-Proskauer, salicin
<i>E. agglomerans</i> from <i>E. aerogenes</i>	Methyl red, Voges-Proskauer, KCN, tartrate
<i>E. agglomerans</i> from <i>E. cloacae</i>	Methyl red, arginine, α -methyl glucoside
<i>E. agglomerans</i> from <i>S. rubidaea</i>	Mucate, corn oil, tartrate
<i>E. agglomerans</i> from <i>C. freundii</i>	Methyl red, Voges-Proskauer, arginine
<i>S. marcescens</i> from <i>S. liquefaciens</i>	Methyl red, Voges-Proskauer, xylose
<i>S. liquefaciens</i> from <i>K. ozaenae</i>	Voges-Proskauer, xylose
<i>S. liquefaciens</i> from <i>Salmonella</i> sp. (typical)	KCN, sucrose, gelatin
<i>S. rubidaea</i> from <i>K. ozaenae</i>	Methyl red, Voges-Proskauer, gelatin, corn oil
<i>Salmonella typhi</i> from <i>Salmonella</i> sp. (typical)	Dulcitol, mucate, sodium acetate
<i>Salmonella</i> sp. (typical) from <i>Arizona hinshawii</i>	Gelatin, dulcitol, tartrate
<i>Salmonella</i> sp. (typical) from <i>C. freundii</i>	KCN, tartrate, β -galactosidase
<i>Salmonella</i> sp. (typical) from <i>E. aerogenes</i>	Methyl red, Voges-Proskauer, KCN, sucrose
<i>C. freundii</i> from <i>E. aerogenes</i>	Methyl red, Voges-Proskauer
<i>Edwardsiella tarda</i> from <i>S. liquefaciens</i>	KCN, sucrose, xylose, mannitol
<i>E. tarda</i> from <i>Salmonella</i> sp. (typical)	Arginine, dulcitol, xylose, mannitol
<i>Shigella sonnei</i> from <i>Escherichia coli</i>	Dulcitol, salicin, mucate
<i>S. sonnei</i> from <i>Salmonella</i> sp. (typical)	Dulcitol, xylose, mucate
<i>S. sonnei</i> from <i>C. freundii</i>	KCN, xylose, mucate
<i>S. sonnei</i> from <i>K. ozaenae</i>	KCN, salicin
<i>S. sonnei</i> from <i>E. aerogenes</i>	Methyl red, Voges-Proskauer, KCN
<i>S. sonnei</i> from <i>S. liquefaciens</i>	KCN, gelatin, corn oil
<i>Shigella</i> sp. (typical) from <i>Salmonella</i> sp. (typical)	Xylose, maltose, tartrate, mucate
<i>Shigella</i> sp. (typical) from <i>E. agglomerans</i>	Voges-Proskauer, sucrose, xylose
<i>Shigella</i> sp. (typical) from <i>E. coli</i>	Xylose, mucate, tartrate
<i>Shigella</i> sp. (typical) from <i>K. ozaenae</i>	Methyl red, Voges-Proskauer, salicin

TABLE 3—Continued

Species	Reactions
<i>Shigella</i> sp. (typical) from <i>K. rhinoscleromatis</i>	Methyl red, Voges-Proskauer, sucrose
<i>Shigella</i> sp. (typical) from <i>Proteus morganii</i>	KCN, tartrate
<i>Shigella</i> sp. (typical) from <i>Providencia alcalifaciens</i>	KCN, tartrate
<i>Shigella</i> sp. (typical) from <i>P. stuartii</i>	KCN, tartrate
<i>E. coli</i> from <i>S. liquefaciens</i>	KCN, gelatin, mucate
<i>E. coli</i> from <i>Arizona hinshawii</i>	Gelatin, tartrate
<i>E. coli</i> from <i>E. aerogenes</i>	Methyl red, Voges-Proskauer, KCN
<i>E. coli</i> from <i>S. rubidaea</i>	Methyl red, Voges-Proskauer
<i>E. coli</i> from <i>E. agglomerans</i>	Methyl red, Voges-Proskauer, arginine, tartrate
<i>P. alcalifaciens</i> from <i>P. vulgaris</i>	Sucrose, maltose, xylose, gelatin, corn oil
<i>P. alcalifaciens</i> from <i>P. mirabilis</i>	Gelatin, corn oil, xylose
<i>P. alcalifaciens</i> from <i>E. agglomerans</i>	Voges-Proskauer, tartrate, xylose, maltose
<i>P. stuartii</i> from <i>P. alcalifaciens</i>	Trehalose, sodium acetate
<i>P. stuartii</i> from <i>P. mirabilis</i>	Gelatin, corn oil, xylose
<i>P. stuartii</i> from <i>P. vulgaris</i>	Gelatin, sucrose, corn oil, xylose
<i>P. stuartii</i> from <i>E. agglomerans</i>	Voges-Proskauer, maltose, xylose, tartrate
<i>P. mirabilis</i> from <i>P. vulgaris</i>	Sucrose, maltose, salicin
<i>P. vulgaris</i> from <i>P. rettgeri</i>	Sucrose, maltose, xylose
<i>P. rettgeri</i> from <i>E. agglomerans</i>	Voges-Proskauer, maltose, xylose, gelatin
<i>P. morganii</i> from <i>P. rettgeri</i>	Mannitol, glycerol, erythritol
<i>P. morganii</i> from <i>P. mirabilis</i>	Xylose, gelatin, corn oil
<i>P. morganii</i> from <i>P. vulgaris</i>	Sucrose, gelatin, corn oil, maltose
<i>P. morganii</i> from <i>S. liquefaciens</i>	Sucrose, xylose, salicin, gelatin
<i>P. morganii</i> from <i>E. agglomerans</i>	Voges-Proskauer, gelatin, maltose, tartrate
<i>Yersinia enterocolitica</i> from <i>K. ozaenae</i>	Motility (22 C), KCN, corn oil
<i>Y. enterocolitica</i> from <i>S. liquefaciens</i>	Motility (22 C), KCN, gelatin
<i>Y. enterocolitica</i> from <i>C. freundii</i>	Motility (22 C), KCN, sucrose
<i>Y. enterocolitica</i> from <i>E. aerogenes</i>	Motility (22 C), KCN, methyl red, Voges-Proskauer
<i>Y. enterocolitica</i> from <i>Salmonella</i> sp. (typical)	Motility (22 C), arginine, sucrose, dulcitol
<i>Y. enterocolitica</i> from <i>Shigella</i> sp. (typical)	Motility (22 C), corn oil, cellobiose
<i>Y. enterocolitica</i> from <i>E. coli</i>	Motility (22 C), corn oil, mucate, cellobiose
<i>Y. pseudotuberculosis</i> from <i>E. agglomerans</i>	Motility (22 C), Voges-Proskauer, sucrose
<i>Y. pseudotuberculosis</i> from <i>K. ozaenae</i>	Motility (22 C), KCN, salicin, cellobiose
<i>Y. pseudotuberculosis</i> from <i>E. aerogenes</i>	Motility (22 C), methyl red, Voges-Proskauer
<i>Y. pseudotuberculosis</i> from <i>P. rettgeri</i>	Motility (22 C), KCN, mannitol, maltose

mon, delayed reactions that will result in misidentification on the Enteric Analyzer are lactose or citrate for *Enterobacter hafniae*, lactose or raffinose for *S. sonnei*, esculin for *Citrobacter diversus*, and sorbitol for *Providencia stuartii*. The user should be cautioned that reactions turning positive after 24 h are programmed as negative in the Enteric Analyzer.

Flexibility and service. The instruction manual states that all repairs and adjustments must be made by the manufacturer. We have had no malfunction during 7 months of use and therefore cannot comment on the time involved or cost of repairs. Since the user cannot make adjustments, any updating in percentages, changes in reactions, or in recognized species will have to be carried out by the manufacturer.

DISCUSSION

The Modified r/b Enteric Differential System is considered to be "highly satisfactory as a system for identification of Enterobacteriaceae" (12). The Enteric Analyzer is designed for use with this system; however, it is programmed with data obtained from conventional biochemical tests performed at the Center for Disease Control. This data was obtained at 24 and 48 h and should be perfectly compatible with the data programmed in the instrument and valid for purposes of evaluation. Some variation in test results among various rapid identification systems and between these systems and conventional biochemical methods is to be expected. We have not yet attempted to evaluate the Enteric Analyzer with data obtained from any

TABLE 4. Possible programming errors in the present Enteric Analyzer

Species	Reaction ^a	Enteric Analyzer identification	
		90% mode	99% mode
<i>Klebsiella ozaenae</i>	raf ⁺ (12%)	—	—
<i>K. pneumoniae</i>	lac ⁻ (2%)	—	—
<i>Enterobacter hafniae</i>	lac ⁺ (<1%)	—	+
	cit ⁺ (<1%)	—	+
	raf ⁺ (<1%)	—	+
	glu ⁻ (<1%)	—	+
	ara ⁻ (4%)	—	—
<i>Serratia marcescens</i>	lac ⁺ (2%)	—	—
	raf ⁺ (2%)	—	—
<i>S. rubidaea</i>	esc ⁻ (10%)	—	—
<i>Arizona hinshawii</i>	ara ⁻ (2%)	—	—
<i>Salmonella</i> sp. (typical)	lac ⁺ (1%)	—	—
	ind ⁻ (1%)	—	—
	rha ⁻ (10%)	—	—
<i>Citrobacter freundii</i>	cit ⁻ (10%)	—	—
<i>Edwardsiella tarda</i>	glu ⁻ (1%)	—	—
	ind ⁻ (1.5%)	—	—
<i>Escherichia coli</i>	ino ⁺ (1%)	—	—
<i>Providencia stuartii</i>	mal ⁺ (1%)	—	—
	ado ⁺ (4%)	+	—
<i>Proteus mirabilis</i>	raf ⁺ (1%)	—	—
<i>P. rettgeri</i>	sor ⁺ (1%)	—	—
	mal ⁺ (1%)	—	—
<i>Yersinia enterocolitica</i>	glu ⁻ (1%)	—	—
	rha ⁺ (1%)	—	—

^a The numbers in parentheses are the percentages of strains of a given species exhibiting the listed reaction.

rapid system. However, previous reports detail our evaluation of the r/b system (12, 16). On balance, the Enteric Analyzer is a very useful adjunct for rapid conversion of biochemical test results to identification at an acceptable level.

When more than one species fits the biochemical profile, the user must have a considerable degree of competence to choose between them. There is no way provided to assess either absolute or relative probabilities of possible species. For instance, a *Klebsiella pneumoniae* strain that is citrate negative (2% of *K. pneumoniae* are citrate negative) is listed in the 99% mode. The same is true for a hypothetical strain of *K. pneumoniae* that does not produce gas from glucose (3.5% of strains), is citrate negative (2% of strains), lysine negative (3% of strains), indol positive (6% of strains), urease negative (5.5% of strains), and inositol negative (2% of strains). Assuming that these traits are not linked, the probability of the second strain is about 10⁻⁸.

In most cases additional reactions will resolve the instances where more than one species is possible. The reactions felt to be useful are listed in Table 3. A flow sheet diagram for some of these additional reactions in the identification of enteric bacteria is given in reference 12. Taxonomy of *Enterobacteriaceae* is a dynamic field. Until 2 or 3 years ago H₂S-positive *Escherichia coli* were not recognized. Now they are more frequently isolated. Newer species designations include *Serratia rubidaea*, *E. agglomerans*, and *C. diversus*. The instrument correctly identified these, but will have to be periodically updated as new groups are recognized and changes occur in reaction frequency. For instance, urease-positive *E. coli*, KCN-positive *E. coli*, *Pectobacterium*, and *Erwinia* may have to be included in the future. *Yersinia pestis* is not included. The instrument has no built-in flexibility. This may become a serious drawback if updating cannot be carried out quickly and at low cost.

The presence of the Enteric Analyzer has stimulated our personnel to compare, check, and discuss their results. Used either individually or by groups the instrument is an extremely useful teaching and reference tool for both students and technicians. The effect of any given reaction or group of reactions on a genus or species can rapidly be determined. Atypical or hypothetical strains can be entered at will and then discussed. Again it must be noted that not all useful tests are programmed, and that other sources must be consulted for problem organisms.

The following recommendations are made in an effort to increase the overall effectiveness of the Enteric Analyzer. (i) The nomenclature used is that recommended by Ewing (2-10). For consistency, *Arizona* sp. (typical) should be changed to *Arizona hinshawii*, and *Salmonella paratyphi* A should be changed to *Salmonella enteritidis* ser *paratyphi* A. (ii) *Klebsiella rhinoscleromatis* is extremely rare. Perhaps this species should be combined with *Klebsiella ozaenae*. *Klebsiellae* would then occupy two slots: *K. pneumoniae* and *Klebsiella* sp. (iii) *Enterobacter agglomerans* should perhaps be subdivided into aerogenic and anaerogenic biotypes. These two groups differ in several reactions. The two categories would frequently make *E. agglomerans* easier to eliminate from consideration. (iv) The programming error found with typical *S. sonnei* and those apparent programming errors listed in Table 4 should be corrected. (v) Additional tests as outlined in Table 3 are advisable, particularly methyl red, Voges-Proskauer, and KCN. In the absence of

additional tests, the user should be provided with guidelines as to which additional tests are useful in differentiating between pairs of organisms. (vi) It would be extremely beneficial to have some indication of the relative probability of species. This could be accomplished by either having a bright or dim setting for the light next to each species, by having two or three different colored lights next to each species, or by providing a table of relative probabilities. (vii) There is no indication given as to the number of strains of a species used as the data base. This can vary substantially. For example, the following numbers of strains were used in the references cited: 616 strains of *C. freundii* and 137 strains of *C. diversus* (3); 371 strains of *Salmonella* (4), only 16 of which are *S. typhi*, and 16, *S. enteritidis* ser *paratyphi* A (4, 7); 1021 strains of *E. coli* (2); and 5166 strains of shigellae (2). The user should be aware of these variations in numbers and in the difference in significance between data based on 16 strains and 5,000 strains.

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