

Evaluation of the Sensititre® ARIS 2X and Vitek® 2 Automated Systems for Identification of Bacterial Pathogens Recovered from Veterinary Specimens

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REVISED ABSTRACT*

Background: Automated systems are commonly used for identification of bacterial pathogens seen in veterinary practice although performance limitations are recognized. We evaluated the accuracy of the Sensititre ARIS 2X (TREK Diagnostic Systems) and Vitek 2 (bioMérieux) systems compared with existing laboratory methods on a contemporary challenge collection.

Methods: Bacterial isolates (459 total) recovered in 2010 from companion and other animals were tested using Sensititre® GPID and GNID, and Vitek 2 GP and GN identification panels. Results were compared with existing biochemical algorithms. Consensus was defined as >=2 systems providing matching results; other results were considered discrepant.

Results: A total of 1377 identifications were analyzed (see Table). Overall, 93.5% and 85.1% of Vitek 2 identifications were correct at genus and species levels, respectively, compared with 93.5% and 83.4% for Sensititre ARIS 2X. Both systems provided acceptable (>= 95%) species-level identifications for *Escherichia coli*, *Klebsiella* spp., *Proteus mirabilis*, and *Enterococcus* spp. but performed less well for other Enterobacteriaceae, non-fermentative bacilli and staphylococci. Sensititre was inferior in identifying *P. aeruginosa* (86.8%) at the species level compared with Vitek 2 (97.4%).

Conclusions: The Sensititre ARIS 2X and Vitek systems produced a high level of accurate identification at the genus level (both systems 93.5%) but less well at the species level (83.4% and 85.1%, respectively). *Pasteurella/Actinobacillus* and non-fermentative bacilli other than *P. aeruginosa* were found to be problematic with both systems, a notable limitation for this important group of veterinary pathogens.

Species/Groups	n	% Agreement Genus/Species	
		Sensititre ARIS 2X	Vitek 2
Coagulase-positive staphylococci	63	95.2/82.5	98.4/87.3
Coagulase-negative staphylococci	27	85.2/40.7	96.3/51.9
<i>Enterococcus/Aerococcus</i> spp.	59	100/100	98.3/98.3
Enterobacteriaceae	194	95.4/85.6	98.4/85.6
<i>Pseudomonas aeruginosa</i>	38	97.4/86.8	97.4/97.4
Other non-fermentative bacilli	33	75.8/54.5	78.8/57.6
<i>Pasteurella/Actinobacillus</i> spp.	45	88.9/-	64.4/-
Totals	459	93.5/83.4	93.5/85.1

* Revised following additional analysis

INTRODUCTION

Automated instrumentation in the veterinary microbiology laboratory for the identification and susceptibility testing of bacterial pathogens is in widespread use due to convenience, accuracy and rapidity over that of traditional methods. Databases, database management and use of expert systems are common to most all systems and are periodically updated to expand identification abilities and for detection of newly emerging resistance profiles and mechanisms. Although no system is infallible, all should be reliable, especially with traditional pathogens, and minimize the number of repeat and off-line tests which may greatly lengthen time to reporting of results.

Clinical laboratories have the expectation that automated systems should be able to readily differentiate the most commonly occurring Enterobacteriaceae and non-fermentative species among Gram-negative bacilli, and among Gram-positive cocci, the commonly occurring species of staphylococci and enterococci. The over-arching goals of automation are to reduce turn-around times, increase efficiencies and, hopefully, reduce costs.

In addressing clinical needs, the primary goals of accurate bacterial identification are to provide veterinary practitioners with information that can be used to assist in selection of appropriate empiric therapy, assess prognosis and possible public health significance of the offending pathogen. Accurate identifications for the laboratorian allow us to properly interpret subsequent antimicrobial susceptibility testing results based upon consensus breakpoints.

Prior studies have demonstrated weaknesses in automated systems when identifying non-fermentative bacilli and certain Gram-positive cocci. In this study we evaluated the accuracy of the Sensititre ARIS 2X (TREK Diagnostic Systems) and Vitek 2 (bioMérieux) systems compared with existing laboratory methods on a contemporary (2010) challenge collection of Gram-positive and -negative pathogens recovered at a regional veterinary diagnostic laboratory. All isolates originated from specimens collected from domestic and exotic animals.

MATERIALS & METHODS

Bacterial isolates. Clinically significant veterinary pathogens (459 total) were recovered largely from domestic and exotic animals by a USA Midwest veterinary diagnostic laboratory in 2010 and included canine (76.5%), feline (17.4%), equine (2.2%), primate (1.5%), bovine (1.3%), mink (0.4%) and avian, caprine and porcine (each 0.2%). Groups and species of isolates included staphylococci (90), enterococci/aerococci (59), Enterobacteriaceae (194; including 71 *Escherichia coli* and 20 *Klebsiella* spp. and 33 *Proteus mirabilis*), *Pseudomonas aeruginosa* (38), other non-fermentative bacilli (33), *Pasteurella* (37) and *Actinobacillus* (8). Further details of species and numbers tested during this period are found in Table 1.

Identification test methods. All isolates were tested according to the manufacturers' recommendations using Sensititre GPID and GNID identification panels incubated and read by the ARIS 2X System; and Vitek 2 GP and GN identification panels incubated and read by the Vitek 2 instrument. Identification results were compared with existing laboratory biochemical algorithms (rapid spot tests, biochemical strip tests, traditional tube biochemicals and/or use of the Sherlock Microbial Identification system (MIS; MIDI, Inc.). Consensus was defined as two or three systems/methods providing matching results. Any system/method result discrepant from the other two was considered erroneous. Isolates for which no agreement was forthcoming were considered indeterminate.

Table 1. Identification summary for 459 animal-source bacterial isolates (all from year 2010) tested by two automated systems and the routine laboratory algorithm.

Isolate Species/Groups	n	Sensititre ARIS 2X % Agreement		Vitek 2 % Agreement		No Agreement Between Methods
		Genus	Species	Genus	Species	
Staphylococcus spp.	90	92.2	70.0	97.8	76.7	0
Coagulase-negative	27	85.2	40.7	96.3	51.9	0
Coagulase-positive	63	95.2	82.5	98.4	87.3	0
Enterococcus spp.	59	100	100	98.3	98.3	0
<i>Escherichia coli</i>	71	95.8	95.8	100	100	0
Klebsiella spp.	20	95.0	95.0	100	100	0
<i>Klebsiella oxytoca</i>	6	100	100	100	100	0
<i>Klebsiella pneumoniae</i>	14	92.9	92.9	100	100	0
Proteus mirabilis	33	100	100	97.0	97.0	0
Other Enterobacteriaceae	70	92.9	79.3	97.1	74.1	2
<i>Citrobacter</i> spp.	9	100	77.8	100	66.7	0
<i>Enterobacter</i> spp.	10	80.0	70.0	90.0	90.0	1
<i>Morganella morganii</i>	4	100	100	100	100	0
<i>Pantoea agglomerans</i>	9	77.8	77.8	100	33.3	0
<i>Salmonella</i> spp.*	12	100	-	100	-	0
<i>Serratia marcescens</i>	9	100	100	100	100	0
Pseudomonas aeruginosa	38	97.4	86.8	97.4	97.4	1
Other Non-fermentative GNB	33	75.8	54.5	78.8	57.6	7
<i>Bordetella bronchiseptica</i>	7	85.7	85.7	100	100	0
<i>Stenotrophomonas maltophilia</i>	6	100	100	100	100	0
Actinobacillus spp.	8	100	37.5	0.0	0.0	0
<i>Pasteurella</i> spp.*	37	89.2	-	83.8	-	1
Totals	459	93.5	83.4	93.5	85.1	11 (2.4%)

* *Salmonella* and *Pasteurella* spp. identified to genus level only by the standard lab methods

RESULTS

This evaluation generated a total of 1,377 identifications between the current laboratory testing algorithm (rapid spot tests, biochemical strip tests, traditional tube biochemicals, and use of the Sherlock MIS) and two automated systems (Sensititre GPID and GNID, and Vitek 2 GP and GN panels).

Agreement for methods at the genus and species levels was 93.5% and 83.4%, respectively, for the Sensititre system and 93.5% and 85.1% for the Vitek 2 system; lack of agreement between the three systems/methods occurred with 11 isolates (2.4% of the total; Table 1).

The Sensititre ARIS 2X and Vitek 2 systems provided very acceptable species-level identifications for *E. coli* (95.8% and 100%, respectively), *Klebsiella* spp. (95.0% and 100%), *P. mirabilis* (100% and 97.0%) and *Serratia marcescens*, *Morganella morganii* and *Stenotrophomonas maltophilia* (all 100%).

Table 2. Examples of identification errors by system.

Vitek 2

- Citrobacter* spp. misidentified at the species level (n=3; 33.3%)
- Pantoea agglomerans* not identified at species level (n=6; 66.7%)
- Actinobacillus equuli* misidentified at the genus level (n=7; 100%), including as *Sphingomonas paucimobilis* (n=4; 57.1%) or *Pasteurella pneumotropica* (n=2; 28.6%)
- Pasteurella* spp. misidentified at the genus level (n=6; 16.2%) as *Sphingomonas paucimobilis* (n=3; 8.1%)

Sensititre ARIS 2X

- Coagulase negative *Staphylococcus* not identified at the genus level (n=4, 14.8%)
- Citrobacter* spp. misidentified at the species level (n=2; 22.2%)
- E. coli* misidentified at the genus level (n=3; 4.2%) including as *Shigella sonnei* (n=2; 2.8%)
- Pantoea agglomerans* misidentified at the genus level (n=2; 22.2%)
- Actinobacillus equuli* misidentified at the species level (n=4; 57.1%)
- Pasteurella* spp. misidentified at the genus level (n=4; 10.8%)

All

No agreement of non-fermentative bacilli (n=7; 21.2%)

CONCLUSIONS

The Sensititre ARIS 2X and Vitek 2 systems produced an acceptable level of accurate identification overall at the genus level (both systems 93.5%) but less well at the species level (83.4% and 85.1%) when compared with each other and the standard laboratory identification algorithm (Table 1).

Lack of agreement between the three systems/methods occurred with 11 isolates (2.4% of the total).

The Sensititre ARIS 2X and Vitek 2 systems provided very acceptable species-level identifications for *E. coli* (95.8% and 100%, respectively), *Klebsiella* spp. (95.0% and 100%), *P. mirabilis* (100% and 97.0%) and *Serratia marcescens*, *Morganella morganii* and *Stenotrophomonas maltophilia* (all 100%).

Species identifications by Sensititre ARIS 2X and Vitek were most problematic for other Enterobacteriaceae (79.3% and 74.1%, respectively), non-fermentative bacilli (54.5 and 57.6%) and coagulase-negative staphylococci (40.7 and 51.9%; Tables 1 and 2).

Identifications of *Pasteurella/Actinobacillus* and non-fermentative bacilli other than *P. aeruginosa* were found to be problematic with both systems, a notable limitation for this important group of veterinary pathogens although the Sensititre ARIS 2X System was able to accurately identify *Actinobacillus* at the genus level (100%).

Limitations with each system were apparent and require consideration with implementation depending upon the animal population being served and prevalence of commonly occurring pathogens.

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