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Evaluation of Sensititre Plates Read on the Automated Incubation and Reading System (ARIS 2X®) with Comparison to Vitek Legacy, Pasco Frozen Microdilution Panels, and E-test Strips for Determining Susceptibility Profiles of Commonly Encountered Bacteria

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ABSTRACT

The TREK Automated Reading and Incubation System (ARIS 2X©) has been tailored to automate the reading of Sensititre susceptibility and identification plates with data archiving and report generation via data management software. This study focused on verifying the accuracy of Sensititre MIC trays incubated and read automatically by the ARIS 2X© for a variety of clinical isolates. Susceptibility results were compared to those obtained with either the Vitek Legacy, Pasco frozen microdilution panels, the E-test gradient diffusion method, or combinations of these methods for 401 clinical isolates comprising multiple genera and antimicrobial resistant patterns. Gram-negative identifications were evaluated using Sensititre GNID panels. In general the ARIS 2X© performed well demonstrating an overall agreement of 98% with the other methods. A total of 26 categorical errors were noted with the ARIS 2X©, including 19 (0.5%) minor errors, 1 (0.03%) major error, and 6 (0.8%) very major errors. The ARIS 2X©-Sensititre platform can be used to accurately determine susceptibility profiles of most clinical isolates, including fastidious bacteria,thus eliminating the need to maintain multiple ancillary susceptibility methods.

INTRODUCTION

Susceptibility studies remain among the most important functions performed in the clinical microbiology laboratory; however, mounting resistance, coupled with sometimes novel mechanisms, continue to challenge the ability of commercial antimicrobial susceptibility testing (AST) systems to accurately detect some resistant phenotypes (7, 10, 13, 14, 15). Indeed, for some organisms, microdilution methods with full 18-24 hours of incubation yield the most accurate phenotypic results (6, 9, 10, 11). This has forced many laboratories to maintain multiple AST methodologies to generate reliable results for different clinical isolates, which adds cost to overall laboratory operations.

The ARIS 2X© has been designed to incubate and then auto-read Sensititre microdilution susceptibility and identification plates. Sixty-four plates can be incubated in each ARIS 2X©, with up to four modules (256 plate capacity) being linked to a single computer. Inventory is tracked using barcode information present on each plate. A temperature controlled, and timed incubation is maintained within the instrument, after which, robotics are used to transport plates to the reading unit. Hydrolysis of a fluorogenic substrate by the bacterial isolate is used to measure growth in each well and determine MIC endpoints. Appealing features of Sensititre plates include a traditional doubling dilution format, a large selection of antimicrobics, and the ability to test both fastidious and non-fastidious bacteria using a single AST system.

This study focused on verifying the accuracy of Sensititre MIC trays incubated and read automatically by the ARIS 2X© for a variety of clinical isolates. Susceptibility results were compared to those obtained with either the Vitek Legacy (bioMerieux, Marcy L'Etoile, France), Pasco frozen microdilution panels (Becton Dickinson, Sparks, Md.), the E-test gradient diffusion method (AB Biodisk, Solna, Sweden), or combinations of these methods for 401 clinical isolates comprising multiple genera and antimicrobial resistant patterns. Gram-negative identifications were evaluated using Sensititre GNID panels. The ability to consolidate multiple AST methods currently used in our laboratory onto the ARIS 2X© platform was also explored.

MATERIALS & METHODS

Organisms. A total of 401 clinical isolates were tested against clinically appropriate antibiotics. Bacterial isolates included a "defined" collection of 318 strains (200 gram-negative and 118 gram-positive) collected up to 90 days prior to the start of the study. These isolates were maintained frozen at -70°C until testing, and were selected for species diversity and phenotypic resistant patterns. An additional 83 (69 gram-negative and 14 gram-positive) organisms were tested concurrently with the Vitek Legacy (Table 1). No duplicate isolates were tested.

Gram negative identifications. Identifications using Sensititre GNID panels were compared with those obtained using Vitek GNI Plus cards (V1311) for 205 gram-negative isolates. Discrepant identifications were settled using an additional commercial identification kit, Crystal ID (Becton Dickinson), API 20 NE strips (bioMerieux), and/or conventional tubed biochemical media (Remel, Inc). Isolates included both patient and laboratory stock cultures (Table 2).

Quality control. Reference strains, including three gram-negative isolates, *Escherichia coli* ATCC 25922, *Escherichia coli* ATCC 35128, *Pseudomonas aeruginosa* ATCC 27853, and three gram-positive isolates, *Staphylococcus aureus* ATCC 29213, *Enterococcus faecalis* ATCC 29212, *Streptococcus pneumoniae* ATCC 49619 (Remel, Inc.) were included each day of testing.

Precision testing. In addition to quality control organisms, the reproducibility of the ARIS 2X© was further evaluated with repeated testing of 16 different isolates, comprised of both gram-negative and gram-positive organisms. All were selected specifically based on the organism's identification and antibiogram. Each isolate was tested for 5 consecutive days (inter-run precision), and in triplicate on one of the 5 testing days (intra-run precision). These plates were also read visually on a light box (SensiTouch, TREK Diagnostics Systems) to confirm the accuracy of the automated, fluorescent read performed by the ARIS 2X©.

Testing format. Comparison studies were completed by testing the "defined" collection of clinical isolates (n=318) on Sensititre plates, followed by direct comparison of MIC's and interpretations to those already determined and reported. All discrepant results were arbitrated. In addition, parallel testing was performed for 5 consecutive days by simultaneously running ARIS 2X© and Vitek susceptibility panels on newly recovered clinical isolates (n=83), with direct comparison of MIC's and interpretations.

Susceptibility setup and workflow. Fresh, 24 hour old cultures were used for all susceptibility studies. Frozen isolates were sub-cultured twice prior to testing. For the ARIS 2X©-Sensititre system, a suspension equal to a 0.5 McFarland turbidity standard, verified by nepheloметry, was prepared in 5 ml of sterile demineralized water (gram-negative bacteria, staphylococci, and enterococci) or 5 ml of cation-adjusted Mueller-Hinton broth (pneumococci and viridans streptococci) using isolated colonies. For gram-negative (GN1F) and gram-positive (GPN2F) Sensititre plates, a disposable plastic bacteriologic loop was used to transfer 10 *u*l of the 0.5 McFarland suspension to a tube containing 11 ml of cation-adjusted Mueller-Hinton broth; plates were then dosed with 50 *u*l per well of the inoculated Mueller-Hinton broths using the Autoinoculator; final concentration range 5 x 10^4 – 5 x 10^5 cfu/mL. For fastidious organisms, 100 *u*l of the 0.5 McFarland suspension was transferred using a precision pipette to a tube containing 11 ml of Mueller-Hinton broth supplemented with laked horse blood (LHB) and plates (STP3F) were dosed similarly, but with 100 *u*l per well; final concentration 1-5 x 10^5 cfu/mL. Colony counts were performed and recorded for each Sensititre plate by sampling the positive growth control well using a 0.001 *u*l loop and sub-culture on a blood agar plate; colonies were counted after 18-24 hours of incubation. Inoculated plates were incubated in the ARIS for 18 (gram-negative isolates) or 24 (gram-positive isolates) hours, followed by automated reading and generation of a susceptibility report via data management software (SWIN 3.08).

Vitek card GPS-105 (V4334) was used to test all staphylococci and enterococci, while two card types, GNS-122 (V4354) and GNS-123 (V4355) were used for gram-negative isolates. Vitek cards were inoculated and incubated in the Vitek Legacy in accordance with guidelines outlined by the manufacturer.

Pasco panels (Gram-positive MIC, #26945; Gram-negative MIC, #269461; Gram-negative MIC/ID, #269441) were inoculated using the Director Inoculation System (Becton Dickinson). Briefly, this involved sampling 2-4 similar colonies with a wand-type device that was then placed in a 25 ml water diluent with 0.02% polysorbate and mixed. The prepared inoculum was poured into a seed tray and a lid containing plastic pins was used to sample the suspension and deliver 5*u*l of inoculum to each well of a thawed MIC panel. All panels were incubated in ambient air at 35C for either 18 hours (gram-negative isolates) or 24 hours (gram-positive isolates) followed by visual reading of MIC's.

Mueller-Hinton or Mueller-Hinton agar plates supplemented with 5% sheep blood, for streptococci (Remel Inc.) were inoculated following guidelines described by the National Committee for Clinical Laboratory Standards (NCCLS) for disk-diffusion testing. E-test strips (up to six strips/plate) were applied as directed by the manufacturer, and plates were incubated following NCCLS recommendations for the isolate, followed by visual reading.

Data evaluation and discrepant testing. Results and categorical interpretations for drugs recommended by NCCLS as appropriate for the isolates were evaluated. The MIC's determined for each isolate were assessed for essential agreement, defined as being within 1 doubling dilution, and categorical agreement (sensitive, intermediate, or resistant). Categorical errors were determined to be minor (ARIS 2X© intermediate vs. a susceptible or resistant result), major (ARIS 2X© resistant vs. a true susceptible result), or very major (ARIS 2X© susceptible vs. a true resistant result). Calculations of major and very major errors were done as previously described by Jorgensen, using as the denominator the total number of susceptible isolates or the total number of resistant isolates respectively (8). Minor error calculations utilized the total number of organism-antimicrobial agent combinations as the denominator, but were not tallied if the MIC's were in essential agreement (1 dilution), but the interpretation revealed a minor categorical error. When MIC's failed to demonstrate essential, or categorical agreement, all susceptibility studies were repeated. Discrepant results that did not resolve after repeat testing were refereed, using either Pasco frozen microdilution panels, E-test strips, or as blinded samples submitted to TREK Laboratory Services for testing using the NCCLS M7-A6 microdilution procedure (11).

RESULTS

Both the Sensititre GNID panels and Vitek GNI Plus cards were able to accurately identify the majority of the gram-negative isolates included in the challenge set. Of 205 gram-negative bacilli tested, 199 (97%) were correctly identified using Sensititre GNID panels and 202 (99%) were correctly identified with Vitek GNI Plus cards (Table 2).

Precision measured by the repeated testing of ATCC quality control reference strains as defined by the NCCLS was satisfied during the present testing of the ARIS 2X© system. Additional strains used to challenge the ARIS also showed a high degree of reproducibility (Table 3).

Two vancomycin resistant strains of enterococci (VRE) were included in the precision testing runs. An isolate of *E. faecium* expressing probable *vanA* resistance (MIC of >256 *u*g/ml) repeatedly tested resistant using Sensititre plates read on the ARIS 2X© (MIC >32 *u*g/ml). However, a second VRE strain, *E. faecalis* ATCC 51299 expressing *vanB* resistance, was missed, and consistently yielded vancomycin MIC's of 4 *u*g/ml on Sensititre plates read by the ARIS 2X©; these endpoints were verified with visual readings. The same isolate yielded resistant interpretations, and MIC's of >16 *u*g/ml when tested on Vitek or Pasco, and 24 *u*g/ml with E-test strips. The isolate also grew on BHI agar supplemented with 6 *u*g of vancomycin. While growth medium has been identified as an integral component for accurate detection of *vanB* resistance in enterococci, using the Vitek system, similar findings for Sensititre have not been reported, but may warrant investigation (7).

Essential agreement (1 dilution) of 98% between the ARIS 2X© and the other AST methods was calculated following discrepant analysis of the results generated for 318 isolates (4029 organism-antimicrobial agent combinations). A total of 26 categorical errors were noted with the ARIS 2X©, including 19 (0.5%) minor errors, 1 (0.03%) major error, and 6 (0.8%) very major errors. All of the major and very major errors occurred between the Vitek and ARIS 2X©, and all six of the ARIS 2X© very major errors occurred with three different antibiotics (Table 4). The ARIS 2X© failed to detect cefazolin resistance in three strains of *Citrobacter freundii* and oxacillin-resistance in two strains of *S. aureus.* However, 22 strains of MRSA and 10 additional cefazolin resistant strains of *C. freundii,* included in the culture set correctly tested resistant on Sensititre plates.

Twenty-six additional categorical errors resolved in favor of the ARIS, resulting in 15 minor errors, 5 major errors and 6 very major errors for the Vitek Legacy (Table 4).

The LHB Sensititre plate proved to be very versatile, accurately detecting beta-lactam and macrolide resistance expressed in clinical isolates of pneumococci, correlating 100% with E-test generated MIC's. While not yet FDA approved for this application, the LHB panel was also used to test nine strains of viridans streptococci recovered from systemic sites, and again, 100% agreement with E-test MICs was observed.

The one week of direct parallel testing involved a smaller, and less diverse collection of 83 organisms, including 64 *Enterobacteriaceae* (43 – *E. coli,* 14 – *Klebsiella* spp., 4 – *Enterobacter* spp., 2 – *Proteus* and 1- *Serratia* spp.), 4 strains of *P. aeruginosa* and a single isolate of *Acinetobacter* spp., and 14 isolates of staphylococci (6 *S. aureus* [1 MRSA] and 8 CoNS). An essential agreement of 97.4% was obtained with this collection, with no major or very major categorical errors noted

TABLE 1. Isolates evaluated in susceptibility studies

Organism	No. tested
Gram-negative isolates	
Acinetobacter spp.	8
Citrobacter spp.	16
Enterobacter spp.	22
Escherichia coli	84
Klebsiella spp.	56
Proteus spp.	22
Pseudomonas aeruginosa	33
Serratia marcescens	10
Stenotrophomonas maltophilia	5
Miscellaneous Gram negative bacilli	13[a]
Sub-total	**269**
Gram-positive isolates	
Enterococcus faecalis	18
Enterococcus faecium	5
Enterococcus spp., NOS	1
Staphylococcus aureus (oxacillin susceptible)	31
Staphylococcus aureus (oxacillin resistant)	22
Staphylococcus spp. (coagulase negative)	26
Streptococcus pneumoniae (penicillin susceptible)	12
Streptococcus pneumoniae (penicillin resistant)	8
Viridans streptococci	9
Sub-total	**132**
TOTAL	**401**

[a]Includes *Aeromonas sobria* (n=1), *B. cepacia* (n=1), *Morganella morgani* (n=2), *Pantoea agglomerans* (n=1), *Providencia stuartii* (n=2), *Pseudomonas luteola* (n=1), *Pseudomonas fluorescens* (n=1), *Ralstonia picketti* (n=1), *Salmonella* spp. (n=2), *Serratia* spp. (n=1).

TABLE 2. Gram-negative isolates evaluated for correct identification

Isolate	No. of strains
Aeromonas hydrophila	1
Aeromonas sobria	1
Acinetobacter spp.	7
Alcaligenes faecalis	1
Burkholderia cepacia	1
*Citrobacter freundii**	13
*Citrobacter koseri**	3
*Enterobacter aerogenes**	4
Enterobacter cloacae	16
*Escherichia coli**	43
Klebsiella pneumoniae	38
Klebsiella oxytoca	4
*Pseudomonas aeruginosa**	29
Proteus mirabilis	19
Proteus vulgaris	1
Providencia stuartii	2
Salmonella spp.	3
Salmonella typhi	1
Serratia marcescens	10
Serratia liquifaciens	1
Shigella flexneri	1
Sphingobacterium multivorum	1
Stenotrophomonas maltophilia	5
TOTAL	**205**

*Discrepant gram-negative identifications:

Correct Identification	Vitek GNI Plus identification	Sensititre GNID identification
Citrobacter freundii	*Citrobacter freundii*	*Klebsiella pneumoniae*
Citrobacter koseri	*Citrobacter koseri*	*Citrobacter amalonaticus*
Enterobacter aerogenes	*Enterobacter aerogenes*	*Citrobacter koseri*
Enterobacter aerogenes	*Serratia marcescens*	*Enterobacter aerogenes*
Escherichia coli	*Escherichia hermanii*	*Escherichia coli*
Proteus vulgaris	*Proteus penneri*	*Proteus vulgaris*
Pseudomonas aeruginosa	*Pseudomonas aeruginosa*	*Pseudomonas putida*
Pseudomonas aeruginosa	*Pseudomonas aeruginosa*	*Pseudomonas fluorescens*
Pseudomonas aeruginosa	*Pseudomonas aeruginosa*	*Pseudomonas mendocina*

RESULTS cont.

TABLE 3. Reproducibility of selected isolates tested repeatedly on the ARIS 2X©

Isolate	Phenotype	Precision Data		
		Inter-run[a]	Intra-run[a]	Phenotype[b]
E. coli 9336	Aminoglycoside resistant Fluoroquinolone resistant	98%	100%	100%
E.coli 51953	Cefazolin, Cefuroxime resistant Cephamycin resistant Fluoroquinolone resistant	98%	100%	100%
C. freundii 710702	Cephamycin resistant	98%	100%	100%
K. pneumoniae 19240	Cefazolin resistant Cephamycin resistant SXT[c] resistant	98%	100%	93%
P. aeruginosa 40638	Carbapenem resistant	77%	100%	100%
P. aeruginosa 180350	Aminoglycoside resistant Fluoroquinolone resistant	95%	100%	100%
S. maltophilia 999111	SXT[c] resistant	90%	96%	100%
S. aureus D12	Oxacillin resistant Fluoroquinolone resistant Macrolide & lincosamide resistant	100%	98%	100%
S. aureus 972616	Macrolide resistant Fluoroquinolone resistant	90%	98%	100%
S. aureus 240104	Oxacillin resistant Macrolide resistant	98%	96%	100%
E. faecalis ATCC 51299	Vancomycin resistant High-level aminoglycoside resistant	98%	100%	67%
E. faecium 2200926	Vancomycin resistant Ampicillin resistant	98%	96%	100%
E. faecalis 2033007	Ampicillin susceptible Vancomycin susceptible	87%	96%	100%
S. pneumoniae 27	Penicillin intermediate Ceftriaxone resistant	94%	100%	100%
S. pneumoniae 87	Penicillin intermediate Ceftriaxone susceptible	99%	100%	100%
S. pneumoniae 160	Penicillin resistant Ceftriaxone resistant	96%	98%	100%

[a] Inter- and intra-run precision calculations based on total antimicrobial-organism combinations (Gr. Negative = 660 drug/organism combinations, Gr. Positive = 705 drug/organism combinations)
[b] Phenotype precision indicates reproducibility in detecting known antibiogram for the isolate
[c] Trimethoprim / sulfamethoxazole

TABLE 4. Discrepant analysis for isolates with major or very major errors[a]

Antimicrobic	Organism	Sensititre	Vitek	Pasco	E-test	Trek[b]	Error classification[b]
Ampicillin	*Enterobacter cloacae*	8	>32	8	10	--	Vitek Major
	Coagulase negative staph	<=0.12	>16	0.25	--	--	Vitek Major
Ampicillin/ Sulbactam	*Enterobacter cloacae*	32	<=4	>16/8	--	--	Vitek Very major
Cefazolin	*Citrobacter freundii*	<=4	>32	>16	--	64	ARIS 2X© Very Major
	Citrobacter freundii	8	>32	>16	--	64	ARIS 2X© Very Major
	Citrobacter freundii	8	>32	>16	--	64	ARIS 2X© Very Major
	Enterobacter aerogenes	<=4	>32	8	--	4	Vitek Major
	Escherichia coli	8	>32	16	--	8	Vitek Major
Erythromycin	*Staphylococcus aureus*	>8	<=0.5	>4	8	--	Vitek Very Major
Oxacillin	*Staphylococcus aureus*	<=0.25	>8	>4	--	>4	ARIS 2X© Very Major
	Staphylococcus aureus	0.5	>8	>4	--	>4	ARIS 2X© Very Major
Piperacillin	*Pseudomonas aeruginosa*	128	16	>64	96	--	Vitek Very Major
	Enterobacter cloacae	128	<=8	>64	>256	--	Vitek Very Major
Piperacillin/ tazobactam	*Escherichia coli*	<=16	64	>64/4	>256		ARIS 2X© Very Major
Streptomycin	*Enterococcus faecium*[d]	>1000	<2000	>1000	--	--	Vitek Very Major
Tetracycline	Coagulase negative staph	>16	2	<=2	--	--	ARIS 2X© Major
SXT[c]	*Escherichia coli*	4	<=0.5/9.5	>38/2	--	--	Vitek Very Major

[a] Major error indicates "false" resistance; very major error indicates "false" susceptibility
[b] Results for isolates submitted to TREK Diagnostics for testing using NCCLS M7-A6 broth microdilution method
[c] Trimethoprim / sulfamethoxazole
[d] Also resistant when tested for HLAR by disk diffusion screening; NCCLS M2-A8

DISCUSSION

The ARIS 2X© system was developed in the 1980s, however, its' widespread use in the clinical arena has been limited. Improved panel design, instrumentation, and data management software support the need for direct comparisons of the ARIS 2X© to other available instruments and AST methods. Our evaluation compared the ARIS 2X© automated susceptibility and identification system, to results obtained with Vitek Legacy, Pasco frozen microdilution panels, and E-test strips for a number of clinically significant isolates, including fastidious bacteria. We also evaluated the use of Sensititre-GNID panels incubated and read on the ARIS 2X© and they proved reliable for identifying commonly encountered gram-negative bacilli.

An essential agreement of 98%, after discrepant analysis, was obtained between the ARIS 2X© and the AST methods evaluated. Categorical error rates obtained with the ARIS 2X© were within accepted limits, and a very major error rate of <1.5%, was similar to recent studies evaluating the ARIS 2X©-Sensititre and MicroScan System (3, 4). However, significant resistant phenotypes, with both clinical and epidemiological implications, were not consistently detected on Sensititre plates in our evaluation. Of concern were two MRSA strains that repeatedly and inaccurately tested susceptible to oxacillin on Sensititre plates. Both isolates were correctly characterized as oxacillin resistant on Vitek, Pasco microdilution panels, and MRSA Screening Agar. Both of these strains were also found oxacillin resistant when tested by the NCCLS reference microdilution procedure at TREK Laboratory Services (Table 4). In addition, both isolates were positive for *mecA* by PCR, and for PBP2a using the Oxoid PBP2a Latex assay, supporting the need to include supplemental testing for MRSA.

The repeated misclassification of *E. faecalis* ATCC 51299, used in precision testing, as vancomycin susceptible on Sensititre plates was also troubling. Interestingly, when plate inoculation procedures were modified, and a precision pipette was used in place of a bacteriologic loop to deliver the 10 *u*l of inoculum to the Mueller-Hinton broth used for plate inoculation, vancomycin MIC's of 16 *u*g/ml were visibly observed on three consecutive Sensititre plates inoculated with this organism (data not shown). However the ARIS 2X© automated reading failed to correctly read these vancomycin MIC endpoints. A similar finding has been noted when vancomycin resistant strains of *S. aureus* were tested on Sensititre plates (J. Lorbach, Trek Diagnostics, personal communication). Since growth was clearly visible in the wells containing higher concentrations of vancomycin, adjustments to the fluorescent growth algorithms may correct this problem. The misclassification of three cefazolin resistant strains of *C. freundii* as susceptible was also observed. While this was noteworthy, it did represent an unexpected phenotype, and Expert rules included with the data management software correctly alerted the user of the unusual result.

Currently many laboratories are forced to maintain multiple AST methods in order to accurately detect antibiotic resistance expressed by the multiple bacterial genera encountered in the clinical setting. An attractive feature of the ARIS 2X©-Sensititre system is the potential to consolidate susceptibility testing onto a single platform. In the current study, all susceptibility studies, including those for fastidious organisms, were completed on the ARIS 2X© using just three different susceptibility panels. Inoculation and incubation procedures are basically the same for all Sensititre plates further streamlining workflow. In contrast, three separate Vitek cards, three different Pasco panel configurations, and multiple E-test strips were necessary to complete the same work. Adapting to an 18-24 hour incubation time for susceptibilities may also seem problematic, given data that supports improved patient outcome when rapid susceptibility results are made available to clinicians (1, 5). However, rapid phenotypic susceptibility testing of gram-positive organisms presents problems, and may not accurately detect beta-lactam or glycopeptide resistance (2, 7, 12, 13, 14). While combining genotypic and phenotypic susceptibility methods help in addressing this issue, at present, phenotypic susceptibility studies for gram-positive cocci require a full 24 hours of incubation (6, 9, 10).

Unlike Vitek cards, Sensititre plates can be incubated off-line and read visually with results entered directly into the data management software for report generation, computer interface transmission, and statistical archiving; this virtually eliminates instrument down-time. The 96-well microtiter format, number of approved antimicrobials and testing dilutions, coupled with automated panel inoculation procedures lend flexibility to the system and create the potential for unique enhancements to Sensititre plate design. Possibilities include reconfiguring the LHB panel to allow testing of two different isolates per plate. Similarly, a urine susceptibility panel could be designed that would accommodate three isolates per plate, testing limited antimicrobials relevant for urinary tract infections. This would conserve instrument capacity and reduce reagent costs.

This study was performed to verify the performance of the ARIS 2X© automated susceptibility and identification system for routine use in the clinical microbiology laboratory. The ARIS 2X©-Sensititre performed well, and offers a reliable and accurate means to perform routine susceptibility testing of rapidly growing bacteria frequently encountered in the clinical laboratory. The ARIS 2X© also addresses the difficulty of maintaining multiple AST methods in the laboratory with the ability to consolidate most susceptibility testing onto a single platform. Instrument design, capacity, and capability to link multiple units to a single computer further support the ARIS as a suitable automated susceptibility and identification system worthy of consideration.

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