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Comparison of the MicroScan WalkAway and VITEK 2 Compact systems for the identification and susceptibility of clinical Gram-positive and Gram-negative bacteria

Comparación de los sistemas MicroScan WalkAway y VITEK 2 Compact para la identificación y susceptibilidad de bacterias Gram-positivas y Gram-negativas de aislados clínicos

Melissa Hernández-Durán,* Luis E López-Jácome,* Claudia A Colín-Castro,* Guillermo Cerón-González,* Silvestre Ortega-Peña,* E Samuel Vanegas-Rodríguez,* Jaime A Mondragón-Eguiluz,* Rafael Franco-Cendejas*

* Laboratorio de Infectología, Centro Nacional de Investigación y Atención a Quemados (CENIAQ), Instituto Nacional de Rehabilitación (INR), Mexico City, Mexico.

Mailing address:
Rafael Franco Cendejas M.D., MSc.
División de Infectología, CENIAQ,
Instituto Nacional de Rehabilitación
«Luis Guillermo Ibarra Ibarra».
Av. México-Xochimilco Núm. 289,
Col. Arenal de Guadalupe,
14389, Del. Tlalpan,
Ciudad de México, México.
Phone: (+52) (55) 5999 1000,
ext. 14801
Fax: (+52) (55) 5603 9127
E-mail: raffcend@yahoo.com

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Abstract

Introduction: The accuracy and fastness in bacterial identification and antimicrobial susceptibility are essentials in the management of the hospitalized patients with infectious diseases. **Methodology:** This study compares the usefulness of the semi-automated VITEK 2® Compact system vs. against the MicroScan WalkAway® SI system for bacterial identification and antimicrobial susceptibility. We included 54 bacterial strains isolated from hospitalized patients, 20 were Gram-positive cocci, 34 Gram-negative rods and 13 reference strains. **Results:** Of these strains, 89.5% were successfully identified at the species level by both systems. Concordance in susceptibility was 90.2% for Gram-negative and 96.3% for Gram-positive bacteria. Median delay time in obtaining the results of susceptibility testing was 6.5 h for VITEK 2 and 12.5 h for MicroScan. The MicroScan system presented a longer delay in obtaining results and greater difficulty in the correct identification of Gram-negative bacteria, **Conclusions:** Identification systems are a necessary tool in microbiological laboratories. Prompt and correct identification of clinical isolates aids in appropriate antimicrobial treatment.

Resumen

Introducción: *La precisión y rapidez en la identificación bacteriana y la susceptibilidad antimicrobiana son esenciales en el manejo de los pacientes hospitalizados con enfermedades infecciosas.* ***Metodología:*** *Este estudio compara la utilidad del sistema semi-automatizado VITEK 2® Compact contra el sistema MicroScan WalkAway® SI para la identificación bacteriana y la susceptibilidad antimicrobiana. Se incluyeron 54 cepas bacterianas aisladas de pacientes hospitalizados, 20 fueron cocos Gram-positivos, 34 bacilos Gram-negativos y 13 cepas de referencia.* ***Resultados:*** *De estas cepas, el 89.5% fueron identificadas con éxito a nivel de especie por ambos sistemas. La concordancia en la susceptibilidad fue de 90.2% para Gram-negativos y 96.3% para bacterias Gram-positivas. El tiempo medio de demora en la obtención de los resultados de la prueba de susceptibilidad fue de 6.5 h para VITEK 2 y 12.5 h para MicroScan.* ***Conclusiones:*** *Los sistemas de identificación son una herramienta necesaria en los laboratorios de microbiología. La identificación rápida y correcta de los aislamientos clínicos ayuda en el tratamiento antimicrobiano apropiado.*

Introduction

Clinical laboratories manage semi automated systems for the identification and bacterial susceptibility that is associated with the increased volume at hospitals, in addition to offering a cost reduction and linking with the laboratory interfaces or hospitalary informatics systems.[1] Each system possesses its strengths and weaknesses; however, correct bacterial identification of patients with an infectious process and its corresponding result of susceptibility in vitro constitute a basic tool for accurate treatment of the patient; without correct bacterial identification, morbimortality and health-system costs increase.[2] Rapidity in the diagnosis and treatment of the infections is not solely reflected in the patient's health, but also in the emergence of strains resistant to multiple antibiotics. The well-aimed, rapid, and timely identification of Multi Drug-Resistant (MDR) clinical isolates in the nosocomial ambit permits the prompt application of precautionary measures to delimit and avoids the propagation of bacteria with these patterns of resistance.[3] The grounds for semi automated systems is based on different analytical methods, such as colorimetry, turbidimetry, or fluorometry, in which bacterial development is detected in micro panels containing different substrates to achieve the identification and serial dilutions of different antibiotics, which in turn allows for establishing minimum inhibitory concentrations (MIC).[4] The VITEK 2® Compact system utilizes colorimetric technology accompanied by the employment of three wave longitudes in order to provide the general profiles of clinically important organisms. Antimicrobial susceptibility is performed by means of test cards containing standardized dilutions of distinct antibiotics corresponding to susceptibility cut-off points established by the Clinical and Laboratory Standards Institute (CLSI).[5,6] Species identification by this system is completed in a median of 3 hours, but can last from 5–7 hours in slow-growth or problematic microorganisms. Susceptibility results can take up to 15 hours, with a mean of around 9 hours.[3,6] On the other hand, the MicroScan WalkAway® SI (MicroScan) system utilizes fluorescent technology. MicroScan panels are conventional, 96-well microdilution plates. Bacteria can be determined within an average of 4 hours, but can be 6-42 hours in slow-growth bacteria. The results of susceptibilities can be obtained in 20 hours, within a range of 16.8-27.8 hours, depending on the bacteria.[3,6] Comparative studies have been conducted between both equipments;[7-9] however, there are few studies that compare multiple clinical isolates.[9,10] The objective of this study was to compare the results of the identification and bacterial susceptibility of clinical samples and strains of the American Type Culture Collection (ATCC); comparison of the susceptibility tests by the MIC method were conducted according to CLSI recommendations,[11] as well as times for obtaining the results procured by the VITEK 2 and the MicroScan systems.

Material and methods

Clinical isolates and reference strains: fifty four clinical isolates were analyzed during the months of July and August 2011, in a simultaneous and comparative manner, of Gram-negative bacilli and Gram-positive cocci associated with infectious processes deriving from hospitalized patients; the reason for employing clinical isolates was to manifest a current and real situation of the systems in the clinical laboratory. We also utilized 13 reference strains, which included 9 genuses and 11 species, such as the following: *Pseudomonas* (1 isolate); *Stenotrophomonas* (1 isolate); *Escherichia* (2 isolates); *Enterobacter* (1 isolate); *Proteus* (1 isolate); *Staphylococcus* (2 isolates); *Enterococcus* (3 isolates); *Streptococcus* (1 isolate), and *Listeria* (1 isolate) *(Table I)*.

Identification methods: In all of the strains, Gram staining was carried out in order to classify these according to the staining characteristics conferred by the walls of the bacteria; fast biochemical tests were carried out, which consisted of the fast indole and oxidase reaction for Gram-negative bacilli, while in the case of Gram-positive cocci, catalase and coagulase tests were conducted. For identification and susceptibility by the VITEK 2 system (bioMérieux, Marcy d'Etoile, France), Gram-negative (GN) bacterial and identification test cards were used, which contains 47 substrates and AST-N087, which contains 12 antibiotics. For Gram-positive microorganisms, we utilized Gram-positive (GP) test cards, which contain 43 substrates, and AST-GP67, which has 14 antibiotics. A bacterial concentration at 0.5 in McFarland standards was employed for bacterial identification. A bacterial load of 6.9 × 106 Colony-Forming Units (CFU)/mL was used in Gram-positives and one of 1.2 × 107 CFU/mL Gram-negatives for the susceptibility analysis, and MPI Library ver. 04.02 software was utilized.

For evaluation of the MicroScan WalkAway SI system (Siemens Healthcare Diagnostics, West Sacramento, CA, USA), we utilized Neg 44 Combo panels that contain 33 substrates and 26 antibiotics for Gram-negatives in the same panel, and the Pos 33 Combo panel, which contains 27 substrates and 14 antibiotics for Gram-positives in the same panel.

Table I. Clinical and reference strains used in the study.

Microorganism		n
Clinical isolates	*Acinetobacter baumannii*	9
	Pseudomonas aeruginosa	9
	Aeromonas hydrophila	3
	Burkholderia cepacia	1
	Escherichia coli	6
	Citrobacter koseri	1
	Citrobacter freundii	1
	Serratia marcescens	1
	Klebsiella oxytoca	1
	Enterobacter cloacae	2
	Staphylococcus aureus	3
	Staphylococcus epidermidis	2
	Staphylococcus conhii	1
	Staphylococcus haemolyticus	1
	Enterococcus faecalis	9
	Enterococcus faecium	2
	Enterococcus casseliflavus	1
	Streptococcus pneumoniae	1
ATCC strains	*Staphylococcus aureus* ATCC 29213	1
	Staphylococcus sciuri ATCC29061	1
	Enterococcus casseliflavus ATCC700327	1
	Enterococcus faecalis ATCC 29212	1
	Enterococcus faecalis ATCC 51299	1
	Listeria monocytogenes ATCC BAA-751	1
	Escherichia coli ATCC 25922	1
	Escherichia coli ATCC 35218	1
	Proteus vulgaris ATCC 6380	1
	Enterobacter cloacae ATCC 7003323	1
	Stenotrophomonas maltophilia ATCC1766	1
	Pseudomonas aeruginosa ATCC 27853	1
	Streptococcus pyogenes ATCC 19615	1
Total		67

LabPro ver. 2.0 software was utilized. Identifications were accepted with a level of ≥ 90%. For susceptibility, we evaluated the MIC reported for each system.

Confirmatory methods: for correct identification of discordant strains, we utilized the conventional biochemical identification schemas according to Murray and colleagues,[3] according to each case. For susceptibility, results were proven by MIC, according to CLSI criteria for the corresponding microorganism.[5]

The antibiotics that were compared by both methods were the following for Gram-negatives: ampicillin; amikacin; gentamicin; ciprofloxacin; cefepime; ceftazidime; ertapenem (except for *Pseudomonas aeruginosa*); imipenem; meropenem; piperacillin/tazobactam; trimethoprim-sulfamethoxazole, and tigecycline. For Gram-positives, the antibiotics were as follows: ampicillin; ciprofloxacin; erythromycin; linezolid; oxacillin (only for *Staphylococcus spp.*); rifampicin (except for *Enterococcus spp.*); quinupristin/dalfopristin; trimethoprim-sulfamethoxazole; teicoplanin; vancomycin; high-concentration gentamicin, and high-concentration streptomycin (the latter two only for *Enterococcus spp.*), according to the case. Discordant results were confirmed by MIC, which were classified as errors depending on the results in the following manner: serious error, when result was resistant due to the confirmation method but susceptible due to the system utilized; major error, when the result was susceptible to the confirmation method but resistant to the system utilized, and minor error, when the result was sensitive or resistant to the conformation method but intermediate to the system utilized. Times were compared in the emission of the definitive results of identification and susceptibility obtained for both methods, considering delay time as well as time necessary in hours for emitting the results of identification and antimicrobial susceptibility.

Statistical analysis: to determine whether there were differences in the identification rates between both systems, we utilized χ^2 statistical test. The result of each identification result with VITEK 2 system and the MicroScan system was marked as «correct» or «incorrect» in each aspect of genus and species.

Comparison of median time was carried out with the Mann-Whitney U test, considering $p < 0.05$ as a significant value. The STATA ver.12.0 statistical software program was employed.

Results

The 54 clinical isolates corresponded to 34 Gram-negative bacilli and to 20 Gram-positive cocci *(Table I)*.

One hundred percent (100%) identification was achieved for Gram-negative bacilli and for Gram-positive cocci by the VITEK 2 system; however, 31 (91%) Gram-negative bacilli and 18 (90%) Gram-positive cocci were identified by the MicroScan system. Of the 67 isolates, concordance was obtained in bacterial identification at the genus level in 61 (91%) and at the species level in 60 (89.5%) isolates *(Table II)*. The discordant strains included 4 Gram-positive cocci and 3 Gram-negative bacilli, with the MicroScan system, which only presented discordant strains in 6 clinical isolates *(Table III)*. For ATCC strains (n = 13), 100% reproducibility was obtained in the results for the two systems for Gram-negative bacilli and Gram-positive

Table II. Identification results comparison between VITEK 2 and MicroScan systems.

Microorganisms	VITEK 2		MicroScan		Concordance (%)
	Genus	Species	Genus	Species	
No *Enterobacteriaceae* (n)					
A. baumannii	9	9	8	8	89
P. aeruginosa	9	9	9	9	100
A. hydrophila	3	3	3	3	100
B. cepacia	1	1	0	0	0
P. aeruginosa ATCC 27853	1	1	1	1	100
S. maltophilia ATCC 1766	1	1	1	1	100
Subtotal n (%)	24 (100)	24 (100)	22 (90.9)	22 (90.9)	
Enterobacteriaceae (n)					
E. coli	6	6	5	5	83.30
C. freundii	1	1	1	1	100
C. koseri	1	1	1	1	100
S. marcescens	1	1	1	1	100
K. oxytoca	1	1	1	1	100
E. cloacae	2	2	2	2	100
E. coli ATCC 25922	1	1	1	1	100
E. coli ATCC 35218	1	1	1	1	100
E. cloacae ATCC 700323	1	1	1	1	100
P. vulgaris ATCC 6380	1	1	1	1	100
Subtotal n (%)	16 (100)	16 (100)	15 (91.6)	15 (91.6)	
Staphylococcus sp.					
S. aureus	3	3	3	3	100
S. epidermidis	2	2	2	2	100
S. conhii	1	1	1	1	100
S. haemolyticus	1	1	0	0	0
S. aureus ATCC 29213	1	1	1	1	100
S. sciuri ATCC 29061	1	1	1	1	100
Subtotal n (%)	9 (100)	9 (100)	8 (88.8)	8 (88.8)	

Continuous Table II. Identification results comparison between VITEK 2 and MicroScan systems.

Microorganisms	VITEK 2		MicroScan		Concordance (%)
	Genus	Species	Genus	Species	
Enterococcus sp.					
E. faecalis	9	9	9	9	100
E. faecium	2	2	2	2	100
E. casseliflavus	1	1	1	0	50
E. faecalis ATCC 29212	1	1	1	1	100
E. faecalis ATCC 51299	1	1	1	1	100
E. casseliflavus ATCC 700327	1	1	1	1	100
Subtotal n (%)	15 (100)	15 (100)	15 (100)	14 (92.3)	
Streptococcus					
S. pneumoniae	1	1	0	0	0
S. pyogenes ATCC 19615	1	1	1	1	100
Subtotal (%)	2 (100)	2 (100)	1 (50)	1 (50)	
Others					
L. monocytogenes ATCC BAA-751	1	1	0	0	0
Total n (%)	67 (100)	67 (100)	61 (91)	60 (89.5)	

Table III. Seven discordant identified isolates between VITEK 2 and MicroScan systems.

	Identification by conventional biochemical tests*	Identification by biochemical tests between systems	
		VITEK 2	MicroScan
No *Enterobacteriaceae*	*B. cepacia* *A. baumannii*	*B. cepacia* *A. baumannii*	*A. xylosoxidans* *E. brevis*
Enterobacteriaceae	*E. coli*	*E. coli*	*C. freundii*
Enterococcus sp.	*E. casseliflavus* *S. pneumoniae*	*E. casseliflavus* *S. pneumoniae*	*E. gallinarum* *E. faecalis*
Staphylococcus sp.	*S. haemolyticus*	*S. haemolyticus*	*R. mucilaginosa*
ATCC strains	*L. monocytogenes* ATCC BAA-751	*L. monocytogenes*	N/I

cocci, and only *Listeria monocytogenes* ATCC BAA-751 was unable to be identified by the MicroScan system. There was a significant difference between the capacity of identification between the two systems (p = 0.013).

In susceptibility studies for the clinical samples, 49 discordant results were found between both methods, with 40 discordant results of Gram-negative bacilli in the following antibiotics: amikacin; aztreonam; ceftazidime; ciprofloxacin; cefepime; gentamicin; imipenem; meropenem; piperacillin/tazobactam, and 9 discordant results of Gram-positive cocci in the following: ciprofloxacin; erythromycin; linezolid;

penicillin, and tetracycline. With ATTC strains, we obtained 10 discordances in susceptibility as follows: 8 in Gram-negative bacilli and 2 in Gram-positive cocci *(Tables IV and V)*. The concordance obtained between these two systems was 89.9% for Gram-negative bacilli and 96.2% for Gram-positives. The 59 discordant results were classified by error: the VITEK 2 system did not demonstrate serious errors, 8 errors (13.5%) were major and 4 (6.8%), minor, obtaining a greater amount of errors in Gram-negative bacilli; for the MicroScan system, 2 (3.4%) serious errors were obtained, in addition to 14 (23.8%) major errors and 31 (52.5%) minor errors, obtaining serious errors in Tetracycline for Gram-positive cocci.

Median time for final identification of Gram-negative *Enterobacteriaceae* was 5.1/12.33 hours and for non-*Enterobacteriaceae* of 6.8/26.7 hours, and in Gram-positive cocci, *Staphylococcus spp.*, of 5.6/19.92 hours and *Enterococcus spp.*, of 9.6/16.8 hours for the VITEK 2/MicroScan systems, respectively. The difference between global times between both equipments had a p of < 0.0005.

Discussion

Due to that clinical microbiology laboratories have become increasingly dependent on automated systems, the accuracy of these can be evaluated with clinical as well as with reference samples. In the present study, final concordance of genus and species, as well as the susceptibility tests of different strains between two of the most utilized systems in the hospital environment, were tested. Distinct studies have evaluated the performance of these systems for the bacterial identification and antimicrobial susceptibility of specific isolates;[7-9] however, there are few studies with diverse clinical samples. With the advent of MultiDrug-Resistant (MDR) microorganisms, clinical laboratories must provide a result with respect to the causal microorganism and to the susceptibility that these microorganisms possess as soon as possible, these results being reliable for adequate infectious treatment and for maintaining adequate epidemiological vigilance. In this study, the VITEK 2 system demonstrated better performance in terms of strain identification in comparison with the MicroScan system in genus (100 vs. 91%) and species levels (100 vs. 89.5%). Gram-negative bacilli presented more errors of identification, as has been observed in previous reports, in which non-fermenter microorganisms had a higher proportion of identification.[12] It has also been suggested that for slow-metabolism bacteria, such as collection strains stored under ultrafreezing, for non-fermenter bacteria, a sufficiently long, 24-h incubation period is recommended in commercial kits or conventional means with the purpose of better identification.[12]

With respect to identification of Gram-positive cocci, it was observed that there were better results regarding Gram-negative bacilli, but the MicroScan system failed in three identifications, one of these of the genus *Enterococcus*. It was reported by Moore et al.[13] that the VITEK 2 and MicroScan systems correctly identify 72 and 80% of the genus Enterococcus at the species

Table IV. Percentage of susceptibility concordance between VITEK 2 and MicroScan systems.

Gram negative bacilli n = 34	AK	AZT	CAZ	CIP	FEP	GM	ERT	IMP	MRP	TZP	SXT	TIG	
	76.5	76.5	91.2	97	91.2	91.2	100	94.2	97	67.7	100	100	
ATCC strains n = 6	100	50	66.7	75	100	100	100	100	100	66.7	100	100	
Gram positive cocci n = 19	AM	CIP	E	LZD	OXA	P	RIFA	SYN	SXT	TE	VA	GN S	ST S
	100	89.5	94.8	89.5	100	89.5	100	100	100	89.5	100	100	100
ATCC strains n = 5	100	80	100	100	100	100	100	100	100	80	100	100	100

AK = amikacin; AM = ampicillin; AZT = aztreonam; CAZ = ceftazidime; CIP = ciprofloxacin; FEP = cefepime; GM = gentamicin; ERT = ertapenem; IMP = imipenem; MRP = meropenem; TZP = piperacillin/tazobactam; SXT = trimethoprim-sulfamethoxazole; TIG = tigecycline; LZD = linezolid; OXA = oxacillin; P = penicillin; RIFA = rifampicin, SYN = quinupristin-dalfoprintin; TE = tetracycline; VA = vancomycin; GN S = high concentration gentamicin; ST S = high concentration streptomycin.

Table V. Percentage in susceptibility concordant results comparison between VITEK 2 and MicroScan systems and broth microdilution test.

Microorganism	n	Percentage of concordance with BMD	
		VITEK 2	MicroScan
Gram negative bacilli	40	73.65%	19.6%
Clinical strains			
Amikacin	8	100	0
Aztreonam	8	75	25
Ciprofloxacin	1	100	0
Cefepime	3	66.7	0
Ceftazidime	3	100	0
Gentamicin	3	66.7	33.3
Imipenem	2	100	0
Meropenem	1	0	100
Piperacillin/ tazobactam	11	54.5	18.1
ATCC strains	8	100%	0%
Aztreonam	3	100	0
Ceftazidime	2	100	0
Ciprofloxacin	1	100	0
Piperacillin/ tazobactam	2	100	0
Gram positive cocci	9	80%	20%
Clinical strains			
Tetracycline	2	100	0
Ciprofloxacin	2	100	0
Erythromycin	1	100	0
Linezolid	2	100	0
Penicillin	2	0	100
ATCC strains	2	100%	0%
Tetracycline	1	100	0
Ciprofloxacin	1	100	0

BMD = broth microdilution.

level, respectively; however, in the study of Won-Young et al.,[9] something different was reported, in that the VITEK 2 and MicroScan systems identified 92.3 and 76.9%, respectively, of the genus *Enterococcus* at the species level these differences in both studies can be attributed to the discrepancy between the organisms evaluated. In the case of identification of the *Staphylococcus* genus, this has, to our knowledge, only been reported in an article with a comparison between both systems utilizing 120 clinical samples of *Staphylococcus* coagulase-negatives, finding correct identification in 87.5 vs. 82.5%, in the VITEK 2 system vs. the MicroScan system.[14] In our study of 11 clinical isolates, one *Staphylococcus haemolyticus* was not identified by the MicroScan system, without observing errors in ATCC strains. *Staphylococcus* coagulase-negatives are increasingly identified in medical complications, such as their association with medical devices. Thus, clinical laboratories should correctly identify these microorganisms at the species level by means of reliable and reproducible methods. The MicroScan system could not identify a Gram-positive bacillus corresponding to a ATCC strain (*Listeria monocytogenes*), the latter probably due to that the VITEK 2 system possesses a greater spectrum of microorganisms in its database with respect to the MicroScan system, and to that there can be differences in the software utilized in the equipment of both systems, as has been reported in other studies;[15] however, the genus *Listeria* has been previously compared utilizing the MicroScan vs. the conventional VITEK system,[16] employing food-transmitted pathogens, and sensitivity and specificity for 100% identification was observed of the former in comparison with 97.5% of the latter, which is not in agreement with the results that we obtained.

The accuracy and reproducibility of antimicrobial susceptibility are dependent on the skill and experience of the clinical laboratory staff; thus, the report should be corroborated and validated by the staff members themselves.[17] The development of expert automated-equipment systems has allowed for an increase in reproducibility and in the veracity of susceptibility results; unfortunately, numerous studies have reported various errors in these systems when diverse combinations of antimicrobials are evaluated.[18-20] *Enterobacteriaceae* family isolates of nosocomial samples present different mechanisms of resistance to multiple antibiotics, and this has become a general public health problem;[21-23] thus, adequate reporting of susceptibility is obligatory. In this study, both systems exhibited adequate correlation in the majority of the

antibiotics; however, this was < 90% for Gram-negative bacilli of clinical isolates and ATCC strains in amikacin, aztreonam, ceftazidime, and piperacillin/tazobactam when these were compared with MIC with a greater percentage of major (MicroScan) and minor (VITEK 2) errors in this latter antibiotic between both systems, which can imply a lack in identification of resistant strains. The correlation of susceptibility is considered adequate when this is < 10%, with < 1.5% serious errors and < 3% major errors and when total agreement with respect to MIC is > 90% 2. Commercial systems can identify producer strains of Extended-Spectrum Beta Lactamases (ESBL) and/or AmpC strains; however, there is poor capacity for differentiating these with carbapenemase producers, which should be a global priority due to that an increase in the number of these has been registered.[21,24,25] For total Gram-positive cocci strains, there was a discordance in ciprofloxacin and teicoplanin; additionally, the clinical isolates were discordant in penicillin and linezolid, which was reported previously in other studies.[26] With the emergence of methicillin-resistant strains, adequate identification of this susceptibility for the genus *Staphylococcus* is required. These systems have been individually and comparatively evaluated in various studies,[15,27-30] exhibiting adequate results with respect to the susceptibility of oxacillin, which is in agreement with our clinical results. We consider that the results found in bacterial identification equipment should be corroborated according to a microbiological verdict with some other test, above all when its therapeutic importance could be relevant. Both systems presented errors in terms of susceptibility, with the MicroScan system presenting two serious errors, 24 major errors, and 31 minor errors, and the VITEK 2 system, 8 major and 4 minor errors. These differences can be due to the lack of standardization of the inoculum, in that the MicroScan system does not possess a constant inoculum. It is of utmost importance that commercial cases maintain updated software programs for adequate interpretation of susceptibility tests in that there can be errors in their final interpretation. In the present study, we corroborated MIC and not interpretation to avoid this bias. Rapidity in obtaining identification as well as susceptibility is one of the most important characteristics for users; in this study, global time was less than that in the VITEK 2 system, with a global median of 6 h (range, 2.75–18 h), presenting a delay in identification of *Enterococcus* spp. The MicroScan system demonstrated a greater delay in all of the genuses with a median of 18 hr (range, 8–72 h), this greater in the non-*Enterobacteriaceae*, because the system's equipment requires more time for correct growth of the microorganism.

With the advent of novel identification methods, such as systems with technology utilizing mass spectrometry, greater rapidity is promoted in identification,[31-33] which has advantages in providing timely treatment; however, the procedures are costly and are not accessible at all hospital units and, at the same time, do not solve the problem inherent in the identification of bacteria highly related in species with similar molecular weights and in susceptibility tests still under development.[33] In the present study, accuracy in MicroScan- and VITEK 2-system identification could be influenced by the differences in the number and distribution of the species of organisms tested, the software version, and the aptitude of the users. The performance of the two systems can also be related with the number of bacterial species tested by the systems' manufacturers and enumerated in the systems' databases. There are some differences in the number of bacterial species between the two systems' identification kit databases tested in this study, because the number of bacterial species of Gram-negative and -positive bacteria in the databases were 143 and 115 for VITEK 2 and 34 and 58 for MicroScan, respectively. There is no system that can achieve 100% identification of the microorganisms. In addition, the combination of both systems has been recommended, in that this considerably increases the efficiency of microbiological diagnoses; however, it also increases costs.[9] The result of the present study is useful for demonstrating the behavior of two common system equipments during daily performance at a hospital unit. One limitations of this study comprises the amount of clinical isolates employed; however, these represent the microorganisms of the population of this institution, which reflect the present findings in habitual clinical situations. In conclusion, bacterial identification systems are useful for increasing efficiency in clinical laboratories. The VITEK 2 system appears to possess better performance in antimicrobial identification and susceptibility, including study finalization time.

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