The European Research Journal 2020;6(2):154-162 Original Article

DOI: 10.18621/eurj.469655 *Clinical Microbiology*

Early bacterial identification and carbapenemase detection from positive blood culture by mass spectrometry and Blue-Carba test

María Eugenia Cattani, Sandra Cogut, Sara C. Kaufman

Sección Microbiología Clínica, División Laboratorio, Hospital Juan A.Fernández, Ciudad Autónoma de Buenos Aires, Argentina

ABSTRACT

Objectives: In this study, we evaluated a rapid and simple protocol for direct identification of microorganisms with Matrix-Assisted Laser Desorption/Ionization Time of Flight, Mass Spectrometry (MALDI-TOF MS) after a short incubation in solid medium (3 to 5h).

Methods: We have examined a total of 1101 positive blood culture bottles from 782 patients.

Results: We obtained a correct identification in 1037 (94.18%); 190 (98.44%) were *Staphylococcus aureus*, and 386 (98.44%) *Enterobacteriaceae*. Both are the most frequent etiological agents of sepsis. A total of 1004 bottles were monomicrobial (96.81%) and 33 (3.18%), polimicrobial. In the latter we identified at least one species. Two hundred eighty (27.00%) organism isolated were considered skin contaminant. Carbapenemase tests were performed with Blue-Carba test in 140 patinas from Gram negative bacilli, we have detected earlier 27 of 29 positive (93.10%).

Conclusions: Mass spectrometry by MALDI-TOF MS is very useful to quickly identify the microbial agent and Blue-Carba contribute to adapt the antibiotic therapy to obtain a correct clinical management of the patient with bacteremia.

Keywords: MALDI-TOF MS, rapid identification, blood culture, carbapenemase, short incubation

Sepsis is associated with high mortality rate in adults and children worldwide. Blood cultures continue to be the gold standard for the etiological diagnostic. Considering the emerging resistance mechanisms and the diverse spectrum of organisms, the rapid microbiological identification and the fast resistance mechanisms detection are crucial for optimal management of these infections [1]. Also, it is important to know the local resistance patterns to optimize the empirical treatment. We carry out this work for giving a quick response that allows adequate management of the bacteremic patient, and a decrease in morbidity and mortality associated with these serious infections. Techniques to decrease turnaround time to identify the causative agents are imperative for the reduction of mortality due to sepsis. A standard protocol for microbial identification is based on phenotypic aspect and biochemical patterns. Complete identification is routinely achieved within 18 to 48h, but may require more time for fastidious or atypical organisms. Introduction of Matrix-Assisted Laser Desorption/Ionization Time of Flight, Mass Spectrometry (MALDI-TOF MS) changed the general workflow in the clinical microbiology laboratories, had increased speed and

Received: *October 11, 2018;* ***Accepted:*** *November 26, 2019;* ***Published Online:*** *January 15, 2020*

How to cite this article: *.Cattani ME, Cogut S, Kaufman SC. Early bacterial identification and carbapenemase detection from positive blood culture by mass spectrometry and Blue-Carba test. Eur Res J 2020;6(2):154-162. DOI: 10.18621/eurj.469655*

Address for correspondence: *Sara C. Kaufman, MD., Hospital Juan A.Fernández, Sección Microbiología Clínica, División Laboratorio, Ciudad Autónoma de Buenos Aires, Argentina, E-mail: sarackaufman@gmail.com*

e-ISSN: 2149-3189

accuracy of microbiological results. In a few minutes, MALDI-TOF MS can allows the analysis of proteins, mainly ribosomal type, for the exact identification of bacteria, mycobacteria and yeasts through the creation of a mass spectrum specific for each microorganism. The mass spectra of test isolates are sequentially compared with those in a reference, database for identification. Depending on the MALDI-TOF MS score, the genus and species identification for an organism may be accurate. Individual mass peaks are used for microorganism identification and provide valuable information for the fingerprinting of bacteria. This technology generates fast and reliable identifications, and has the ability to analyze a large number of isolates simultaneously [2-4].

MALDI-TOF MS could be applied directly to blood cultures. In prospective studies, using different protocols such as Sepsityper (Bruker, Germany) or in-house procedures for bacterial extraction followed by lysis centrifugation and washing, it is possible to identify almost 72 to 80% of the microorganisms of positive blood cultures [2, 5, 6].

The marked increase in the incidence of infections due to antibiotic-resistant Gram-negative bacilli in recent years is of great concern, as patients infected by those isolates might initially receive antibiotics that are inactive against the pathogens [1, 7].

The objective of this study is to validate the bacterial identification from patinas obtained from short solid incubation of positive blood cultures, compared to overnight incubation and the rapid carbapenemase detection in Gram-negative bacilli that has clinical and epidemiological implications.

METHODS

Between 6/1/2014 and 12/31/2016 from 7 am to 2 pm, except weekends, a total of 1101 positive blood culture bottles, aerobic plus/F, anaerobic plus/F and pediatric plus/F, from BACTEC FX (Becton Dickinson, USA) were included. A total of 50 µl of broth was taken from the positive bottles and inoculated onto Columbia sheep blood agar plate (bio-Merieux, Marcy-l´Ètoile, France) and incubated in a 5% CO2 environment at 35º C. Simultaneously, the Gram stain was done and if structures compatible with anaerobic bacteria were seen, we added other plate in anaerobic condition of incubation. Three hours later, the presence of bacterial growth as patina was controlled and, if it was positive, the MALDI-TOF MS (Bruker Daltonic, Germany) typing was performed; otherwise, the plaque was reincubated and it was observed after 2 h. If the grow was visible, it was proceeded to study. The processing of the patina consisted in transferring an amount of the bacterial patina to a spot of the reusable plate with a wooden stick. One µl of 100% formic acid (Fluka, Germany), and then 1 µl of alpha-cyano-4-hydroxycinnamic acid matrix solution (HCCA, Bruker Daltonik, Bremen, Germany) was added. Calibration was performed using a BTS calibrator following the instructions given in the procedure manual; data was entered according to the software.

Criteria for successful identification were achieved according to manufacturer and international literature [8-10]. The Maldi Biotyper Software version 3.1 (Bruker Daltonik) was used to process the data. The results were compared with the routine identification procedures, including MALDI-TOF MS from overnight incubation in all cases of preliminary acceptable identification.

To classify in true bacteriemia or contamination we rely on medical records according to the criteria of the CDC/NHSN [11].

One hundred and forty gram negative bacilli patinas of hospitalized patients were tested against the Blue-Carba Test (BCT) [7, 12]. This method is based on the hydrolysis of imipenem in a bromothymol blue solution, in order to detect the presence of bacteria producing carbapenemases. The phenotypic confirmation of the presence of carbapenemases was made through the sensitivity profile and the use of different inhibitors (APB, EDTA, DCM-Brit) [13-15]. The carbapenemases isolates, other than *Klebsiella pneumoniae* carrying KPC, were confirmed molecularly by PCR / DNA sequencing.

RESULTS

The results are summarized in Table 1. From 1101 positive blood cultures bottles; a valid identification was obtained in 1037 (94.18%). Two hundred and eighty patinas (27%) were considered skin contaminants. A total of 1004 bottles were

Table 1. Results of the bottles studied

Bottles studied	1101	100,00%
Positive Identification	1037	94.18%
No Score	64	5.82%
Polymicrobials	33	3.18%
Monomicrobials	1004	96.81%
Contaminated	280	27.00%

monomicrobial (96.81%) and 33 (3.18%), polimicrobial. In the latter we identified at least one species.

Table 2, shows the groups of microorganisms by gender and species, followed by the total number of these and their percentage of positivity identification, and also the average score of each goup of them.

From 1037 blood cultures bottles, were identified 563 Gram-positive cocci, 453 Gram-negative bacilli, and 21 Gram-positive bacilli. Within this last category, 11 were anaerobes; 7, belonged to the genus *Corynebacterium*; 3 were included in the other categories *(Bacillus cereus and Lactococcus lactis)*. The remaining 64 (5.81%) patinas showed no results. No yeasts results were obtained between 3 and 5 hours of incubation of the solid media. Whichever the reason was, we did not achieve reliable results or visible patinas.

Of all the patinas studied, more reliable scores were observed in the Gram-negative bacilli, and *Staphylococcus aureus* since these showed an average score of 2.00. On the other hand, Gram-positive cocci showed an average score of 1.80 (between coagulase negative staphylococci and streptococci).

Table 3 shows the bottles in which microorganisms were considered contaminant. Out of the 140 patinas tested by BCT, 29 were positive, and no false positive ones were obtained. There were two

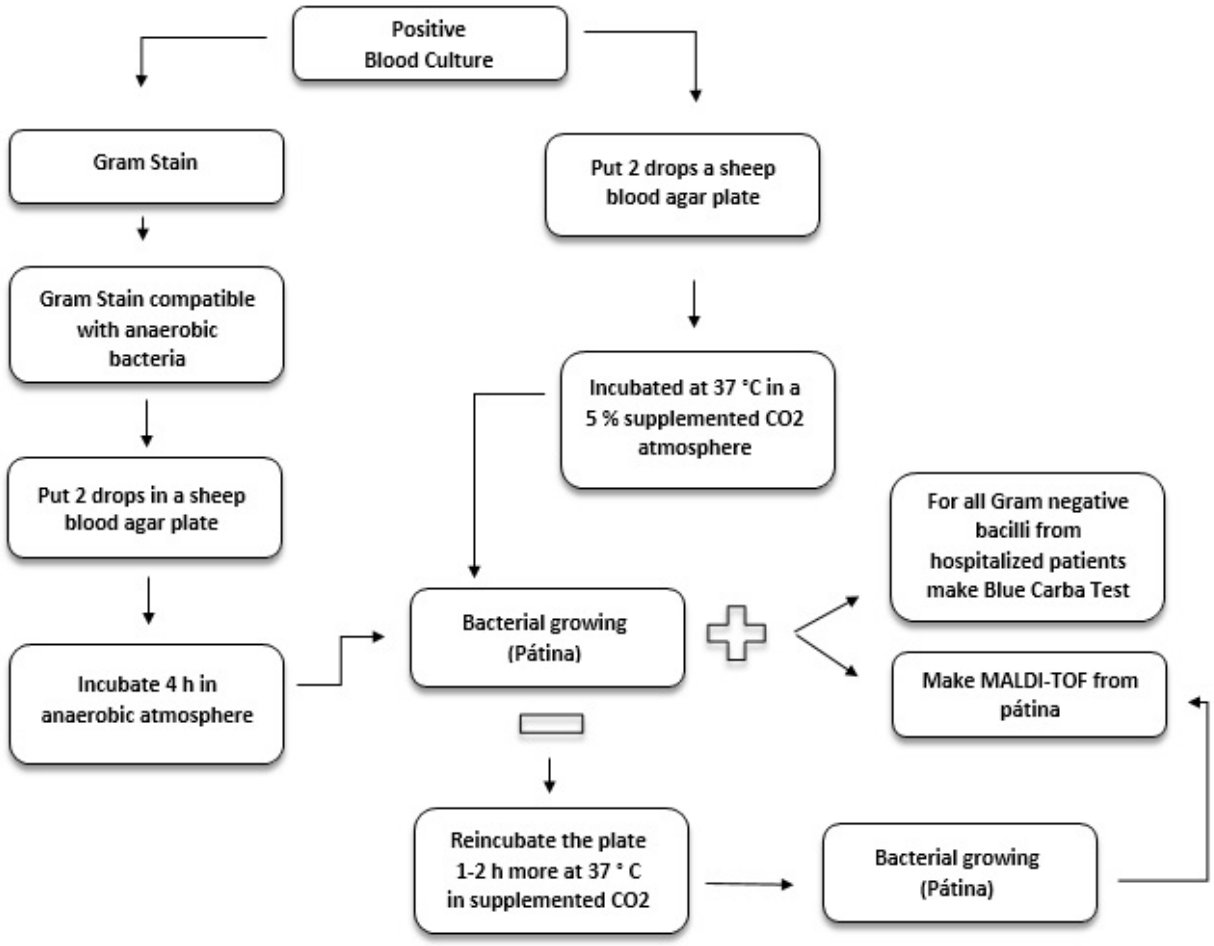

Fig. 1. Workflow diagram.

Table 2. MALDI-TOF MS identification results at 3 and 5 h-incubation time on solid medium at genus and species levels with average score and % of identification

Microorganisms	Number	% of isolates	Id.	No Id.	Average score	% of Id.
Gram-positive cocci	**610**		**563**	**47**		**92.29**
Staphylococcus aureus	193		190	3	2.01	98.44
Coagulase Negative Staphylococcus (CNS)	302		262	40		86.75
Staphylococcus capitis	10		8	2	1.86	
Staphylococcus caprae	1		1			
Staphylococcus cohnii	2		2		1.7	
Staphylococcus epidermidis	188		162	26	1.83	86.17
Staphylococcus haemolyticus	38		35	3	1.79	
Staphylococcus hominis	48		36	12	1.92	
Staphylococcus saprophyticus	1		1		1.82	
Staphylococcus lugdunensis	4		4		2.33	
Staphylococcus simulans	3		3		1.99	
Staphylococcus schleiferi	1		1		1.68	
Staphylococcus xylosus	3		3		1.98	
Staphylococcus pseudintermedius	2		2		1.98	
Staphylococcus pettenkoferi	1		1		1.75	
***Enterococcus* spp.**	**49**		**48**	**1**		**97.96**
Enterococcus faecalis	35		34	1	2.05	97.14
Enterococcus faecium	13		13		1.9	
Enterococcus casseliflavus	1		1		2.24	
***Streptococcus* spp.**	**52**		**51**	**1**		**98.07**
Streptococcus pneumoniae	20		19	1	2.17	
Streptococcus anginosus	4		4		1.92	
Streptococcus oralis	6		6		1.92	
Streptococcus constellatus	1		1		2.14	
Streptococcus gallolyticus	2		2		1.91	
Streptococcus gordonii	1		1		2.04	
Streptococcus lutetiensis	1		1		2.18	
Streptococcus parasanguinis	3		3		1.95	
Streptococcus salivarius	7		7		1.99	
Streptococcus agalactiae	3		3		2.31	
Streptococcus pyogenes	4		4		2.42	
Other Gram-positive cocci	**14**		**12**			
Aerococcus viridans	6		4	2	1.73	
Micrococcus luteus	5		5		1.85	
Rothia mucilaginosa	3		3		1.91	
Gram-negative bacilli	**461**		**453**	**8**		**98.26**
Enterobacteriaceae	386		380	6		98.44
Citrobacter freundii	3		3		2.19	
Citrobacter koseri	1		1		1.98	
Enterobacter cloacae	24		23	1	2.07	
Enterobacter kobei	2		2		2.23	
Enterobacter aerogenes	6		6		2.02	
Enterobacter asburiae	2		2		2.13	
Escherichia coli	129		128	1	2.13	99.22

Table 2 continued.

Klebsiella pneumoniae	160	156	4	2.12	97.50
Klebsiella oxytoca	4	4		2.07	
Kluyvera ascorbata	1	1		1.98	
Leclercia adecarboxylata	3	3		1.99	
Morganella morganii	5	5		2.29	
Proteus mirabilis	17	17		2.10	
Providencia stuartii	3	3		2.13	
Raoultella ornithinolytica	8	8		2.13	
Salmonella sp	5	5		1.94	
Serratia marcescens	12	12		2.08	
Aeromonas caviae	1	1		2.10	
Non fermenters Gram-negative bacilli	**67**	**66**			**98.50**
Acinetobacter baumannii	31	31		1.94	
Acinetobacter nosocomialis	3	3		1.92	
Acinetobacter pittii	3	3		2.12	
Achromobacter xylosoxidans	1		1	no peaks	
Burkholderia vietnamiensis	1	1		2.05	
Comamonas kerstersii	1	1		1.84	
Pseudomonas aeruginosa	15	15		2.09	
Pseudomonas oryzihabitans	3	3		1.84	
Pseudomonas putida_Group	5	5		1.93	
Stenotrophomonas maltophilia	4	4		1.98	
Gram negative cocobacilli	**6**	**6**			
Haemophilus influenzae	3	3		1.79	
Neisseria meningitidis	3	3		1.75	
Other gram negative bacilli	**1**		**1**		
Capnocytophaga sputigena	1		1	no peaks	
Gram positive bacilli	**12**	**10**	**2**		
Corynebacterium jeikeium	1	1		1.98	
Corynebacterium striatum	4	4		1.75	
Corynebacterium imitans	2	2		1.99	
Bacillus cereus	2	2		2.11	
Brevibacterium ravenspurgense	1		1	no peaks	
Lactococcus lactis	1	1		2.33	
Listeria monocytogenes	1		1	no peaks	
Anaerobes	**13**	**11**	**2**		**84.61**
Clostridium perfringens	6	6		2.04	
Fusobacterium mortiferum	1	1		2.16	
Peptostreptococcus anaerobius	1	1		1.95	
Propionibacterium acnes	5	3	2	1.76	
Yeasts	**5**		**5**		
Candida albicans	3		3	no peaks	
Candida tropicalis	1		1	no peaks	
Candida parapsilosis	1		1	no peaks	
	1101		**1037**		

Id = Identification

false negative patinas corresponding to 2 *Enterobacter cloacae* with OXA 163. The carbapenemases detected by the BCT were 24 KPC from 22 *Klebsiella pneumoniae*, one *Escherichia coli*, one *Serratia marcescens;* 3 MBL from two *Acinetobacter baumannii* with NDM and one *Pseudomonas putida* with VIM. The average turnaround time of BCT for the detection of KPC was 10 minutes and 1.30 h for

Table 3. **Microorganisms that were consider contaminants**

Microorganisms	Number	% of isolates	Id	No Id	Average score	% of identification
Staphylococcus capitis	10		8	2	1.86	
Staphylococcus caprae	1		1		1.7	
Staphylococcus cohnii	2		2		1.7	
Staphylococcus epidermidis	143		130	13	1.83	90.9
Staphylococcus haemolyticus	36		32	4	1.79	88.8
Staphylococcus hominis	44		36	12	1.92	81.8
Staphylococcus saprophyticus	1		1		1.82	
Staphylococcus lugdunensis	4		4		2.33	
Staphylococcus simulans	3		3		1.99	
Staphylococcus schleiferi	1		1		1.68	
Staphylococcus xylosus	3		3		1.98	
Staphylococcus pseudintermedius	2		2		1.98	
Staphylococcus pettenkoferi	1		1		1.75	
Streptococcus salivarius	7		7		1.99	
Aerococcus viridans	6		4	2	1.73	
Micrococcus luteus	5		5		1.85	
Rothia mucilaginosa	3		3		1.91	
Bacillus cereus	2		2		2.11	
Brevibacterium ravenspurgense	1			1	no peaks	
Propionibacterium acnes	5		3	2	1.76	
Total	280		248			88.8

Id = Identification

MBL. In 27 (93.10%) microorganisms we have detectet earlier the carbapenemase resistance. The specificity and sensitivity of BCT were 100% and 93.55%, respectively, linking molecular method, and the positive and negative predictive values were respectively 100% and 98.23% comparing with molecular routine. These results are showed in Table 4. Based on the data obtained, we propose the flow chart shown in Fig. 1.

DISCUSSION

The results of positive blood cultures should be quickly or promptly available to guide the treatment of critically ill patients. Conventional diagnoses are based on isolated colonies of 24h solid media. Species identification could be accelerated by the use of MALDI-TOF MS if short growth patinas in solid medium are used [16]. These results are usually not

Table 4. Carbapenemases in 29 hospitalized patients

Resistance mechanism	Microorganism	N
KPC	*Klebsiella pneumoniae*	22
KPC	*Escherichia coli*	1
KPC	*Serratia marcecens*	1
MLB	*Acinetobacter baumanii* (NDM)	2
MLB	*Pseudomonas putida* (VIM)	1
OXA 163	*Enterobacter cloacae* (False Negative)	2

used to initiate antibiotic therapy, but rather to assess whether the initial empirical therapy was accurate and otherwise to adjust it [17]. In general, blood culture identification techniques take one day of incubation, and although subsequent staining of Gram can be performed in several minutes, the result of this technique alone does not provide enough information to properly administer adequate antibiotic therapy. Therefore, additional testing should be performed in order to properly identify the pathogen causing the disease, leading to an increase in time to initiate appropriate antibiotic therapy [18].

Previous work has shown that the identification obtained with MALDI-TOF MS from subcultures of very few hours of incubation is concordant with that obtained with the conventional technique of identification from subcultures of 18-24h [19-23].

In order to reduce identification times, different extraction techniques have been attempted, which are performed directly from the positive blood culture bottles. So, as to obtain a sample suitable for identification with the MALDI-TOF MS, it should not be forgotten that the proper proteins of the blood can interfere with the identification [17]. These procedures take time and are laborious, and in some cases, the identification is not achieved [2]. In a study that we have done in our hospital comparing Sepsytiper with an in-house procedure, we have obtained better results with the later procedure, compared to most of extraction procedures, commercially, and in-house [2, 3, 22-24].

In a study of 925 positive blood cultures bottles (representing 470 bacteremic episodes), Verroken *et al*. [25] obtained a correct identification in 727 (81.1% of the 896 monomicrobial blood cultures), In Gram-positive cocci 85.6% and in 92.7% of the enterobacteria and in 94.1% of the non-fermenters Gram-negative bacilli; with failure being mostly observed with anaerobes and yeasts. Bazzi *et al*. [20] evaluated 4 methods of blood culture procedures, and in one of them, the pellet of the extraction tubes was cultured in blood agar plates, which were incubated during 90-180 min, obtaining the identification of 94.5% of the microorganisms. Curtoni *et al*. [4] also evaluated the growth of short-incubation patinas obtaining about 92.2% of the Gram-positive cocci; 93.1% of the Gram-negative bacilli and 66.7% of the non-fermenters. Hong *et al*. [26] analyzed 175 microbial blood cultures evaluating bacterial growth between 4-6 h, of which 50.9% were Gram-positive and 49.1% were Gram-negative bacteria. They achieved a concordance of 98.9% at the gender level compared to conventional biochemical tests. Finally, Kohlmann *et al*. [27] reached similar percentages by performing tests on short incubation subcultures.

Regarding *Enterobacteriaceae*, the percentage of identification in our study was high 98.44% and the bacterial grow as patina has been seen in 4h or less. About the non fermenting Gram-negative bacilli, it took 5 h for the observation of the patina, and the identification success was 98.5%.

With the Gram-positive cocci we obtained identification in 92.30% of the microorganisms; 86.75% in coagulase negative staphylococci (CNS) and 98.44% in *Staphylococcus aureus*. There was a great difference between CNS and Staphylococcus aureus identification times. In CNS the growth of the patina was much slower and we have to incubate them at least 5h. The early identification of the CNS in one of two blood cultures, allows us to foresee the possibility of skin contaminants. In our study we considered skin contaminated (280) 27.00% of the 1037 bottles. Thus we contributed to reduce time and costs and avoided the use of unncessary antibiotic therapy.

In the polimicrobial blood culture bottles, the concomitant presence of two different bacteria could be anticipated in some instances by Gram staining.
We must highlight that the correct interpretation of the Gram staining from the positive blood culture bottles has a great impact on the microorganisms' identification, in this way, we were able to obtain

anaerobic identifications in 4h since they were incubated in an anaerobic atmosphere.

The BCT for 140 blood cultures from hospitalized patients with Gram-negative bacilli allowed re-evaluating or initiating the antibiotic approach in the presence of carbapenemase-producing bacteria. As for the isolated bacteria tested, we obtained 29 carbapenemase resistant (20.71%); 27 were detectet quickly with the BCT (93.10%); the majority of them came from the intensive unit therapy, wich is our hospital epidemiology. We believe that the performance of MALDI-TOF MS identification after short-term subculture is directly related to the sufficient growth of microorganisms.

The quickly bacterial identification from the patinas has the advantage of performing no previous treatments on the sample; it is an easy method and greatly reduces the time and material used. It can be used together with local antibiotic resistance data in order to optimize the empiric antimicrobial treatment. BCT is an early diagnostic tool to guide an appropriate treatment in order to reduce the mortality associated with the infections caused by these multi-resistant bacteria.

CONCLUSION

The use of patina for BCT and early identification by MALDI-TOF MS, is a powerful tool that shortens time and helps select appropriate antibiotic therapy. This benefits the patient. Limitation of the patina MALDI-TOF MS identification was also observed for mixed bloodstream infection, where only one bacterium could be identified.

In conclusion, the application of MALDI-TOF MS identification to rapid growth microorganism obtained from positive blood culture allows an early identification of the most important microorganisms growing in blood culture such as Staphylococcus aureus and Eenterobacteriaceae which is important for the management of nosocomial and community bloodstream infections. Laboratory automation and work flow optimization may play an important role in reducing the microbiology results turnaround time.

Conflict of interest

The authors disclosed no conflict of interest during the preparation or publication of this manuscript.

Financing

The authors disclosed that they did not receive any grant during conduction or writing of this study.

Acknowledgements

We are grateful to Tamara Posse and Luis Aquino for their technical assistance.

REFERENCES

1. Kang CI, Kim SH, Park WB, Lee KD, Kim HB, Kim EC, et al. Bloodstream infections caused by antibiotic-resistant gram-negative bacilli: risk factors for mortality and impact of inappropriate initial antimicrobial therapy on outcome. Antimicrob Agents Chemother 2005;49:760-6.
2. Cattani ME, Posse T, Hermes R, Kaufman S. [Rapid identification of microorganisms by mass spectrometry in a blood culture system. Comparison of two procedures]. Rev Argent Microbiol 2015;47:190-5. [Article in Spanish]
3. Prod'hom G, Bizzini A, Durussel C, Bille J, Greub G. Matrix-assisted laser desorption ionization-time of flight mass spectrometry for direct bacterial identification from positive blood culture pellets. J Clin Microbiol 2010;48:1481-3.
4. Curtoni A, Cipriani R, Marra Barbui AM, Cavallo R, Costa C. Rapid identification of microorganisms from positive blood culture by MALDI-TOF MS after short-term incubation on solid medium. Curr Microbiol 2017;74:97-102.
5. Prod'hom G, Bizzini A, Durussel C, Bille J, Greub G. Matrix-assisted laser desorption ionization-time of flight mass spectrometry for direct bacterial identification from positive blood culture pellets. J Clin Microbiol 2010;48:1481-3.
6. Stevenson L, Drake S, Murray P. Rapid identification of bacteria in positive blood culture broths by matrix-assisted laser desorption ionization-time of flight mass spectrometry. J Clin Microbiol 2010;48:444-7.
7. Cogut S, Errecalde L, Cattani M, Kaufman S. Desempeño del ensayo colorimétrico Blue Carba Test en la detección de bacterias portadoras de carbapenemasas. ALAM-CAM, 2016, Poster JU-1062, Rosario, Santa Fe, Argentina.
8. Clark A, Kaleta E, Arora A, Wolk D. Matrix-assisted laser desorption ionization time of flight mass spectrometry: a fundamental shift in the routine practice of clinical microbiology. Clin Microbiol Rev 2013;26:547-603.
9. De Bel A, Wybo I, Vandoorslaer K, Rosseel P, Lauwers S, Piérard D. Acceptance criteria for identification results of Gram-negative rods by mass spectrometry. J Med Microbiol 2011;60:684-6.
10. Vlek A, Boten M, Boel C. Direct matrix-assisted laser desorptionionization time-of-flight mass spectrometry improves appropriateness of antibiotic treatment of bacteremia. PloS One 2012;7:e32589.
11. Centers for Disease Control and Prevention/National

Healthcare Safety Network (CDC/NHSN) (2014) CDC/NHSN surveillance definitions for specific types of infections. Available online at: http:// www.cdc.gov/nhsn/pdfs/pscmanual/17 pscnosinfdef_current.pdf. Accessed 19 June 2014
12. Pasteran F, Veliz O, Lucero C, Rapoport M, Ceriana P, Corso A. Blue-Carba Test (BCT) for Rapid Detection of Carbapenemases in Gram-negative Species: Performance against a Panel of Challenging Carbapenemases. 54th ICAAC, Abstract 963; 2014.
13. Pasteran F, Veliz O, Ceriana P, Lucero C, Rapoport M, Albornoz E, et al.; ReLAVRA Network Group. Evaluation of the Blue-Carba test for rapid detection of carbapenemases in gram-negative bacilli. J Clin Microbiol 2015;53:1996-8.
14. Pasteran F, Mendez T, Guerriero L, Rapoport M, Corso A. Sensitive screening tests for suspected class A car bapenemase production in species of Enterobacteriaceae. J Clin Microbiol 2009;47:1631-9.
15. Pasteran F, Veliz O, Lucero C, Guerriero L, Ceriana P, Cogut S, et al. Evaluación de un equipo comercial de discos combinados de meropenem (DCM-brit) para la detección de KPC, MBL y OXA basado en innovadoras combinaciones de inhibidores. XIII Congreso Argentino de Microbiologia, Ciudad de Buenos Aires, 23 al 26 de septiembre 2013.
16. Köck R, Wüllenweber J, Horn D, Lanckohr C, Becker K, Idelevich E. Implementation of short incubation MALDITOF MS identification from positive blood cultures in routine diagnostics and effects on empiric antimicrobial therapy. Antimicrob Resist Infect Control 2017;6:12.
17. Köck R, Kipp F, Ellger B. [Blood culture diagnostic-challenge or routine standard of care?]. Anasthesiol Intensivmed Notfallmed Schmerzther 2015;50:124-31. [Article in German]
18. Loonen AJ, Jansz AR, Stalpers J, Wolffs PF, van den Brule AJ. An evaluation of three processing methods and the effect of reduced culture times for faster direct identification of pathogens from BacT/ALERT blood cultures by MALDI-TOF MS. Eur J Clin Microbiol Infect Dis 2012;31:1575-83.
19. Ballestero-Téllez M, Recacha E, de Cueto M, Pascual Á. Identification and antimicrobial susceptibility testing of positive blood culture isolates from briefly incubated solid medium cultures. Enferm Infecc Microbiol Clin 2017;35:582-5.
20. Bazzi AM, Rabaan AA, El Edaily Z, John S, Fawarah MM, Al-Tawfiq JA. Comparison among four proposed direct blood culture microbial identification methods using MALDI-TOF MS. J Infect Public Health 2017;10:308-15.
21. Bhatti MM, Boonlayangoor S, Beavis KG, Tesic V. Rapid identification of positive blood cultures by matrix-assisted laser desorption ionization-time of flight mass spectrometry using prewarmed agar plates. J Clin Microbiol 2014;52:4334-8.
22. Köck J, Thomas L, Olma T, Chen S, Iredell J. Identification of bacteria in blood culture broths using matrix-assisted laser desorption-ionization Sepsityper and time of flight mass spectrometry. PloS One 2011;6:e23885.
23. Idelevich EA, Schüle I, Grünastel B, Wüllenweber J, Peters G, Becker K. Rapid identification of microorganisms from positive blood cultures by MALDITOF mass spectrometry subsequent to very short-term incubation on solid medium. Clin Microbiol Infect 2014;20:1001-6.
24. La Scola B, Raoult D. Direct identification of bacteria in positive blood culture bottles by matrix-assisted laser desorption ionisation time-of-flight mass spectrometry. PloS One 2009;4:e8041.
25. Verroken A, Defourny L, Lechgar L, Magnette A, Delmée M, Glupczynski Y. Reducing time to identification of positive blood cultures with MALDI-TOF MS analysis after a 5-h subculture. Eur J Clin Microbiol Infect Dis 2015;34:405-13.
26. Hong SK, Chang BK, Song SH, Kim EC. Use of MALDI-TOF MS technique for rapid identification of bacteria from positive blood cultures. Indian J Med Microbiol 2014;32:419-22.
27. Kohlmann R, Hoffmann A, Geis G, Gatermann S. MALDI-TOF mass spectrometry following short incubation on a solidmedium is a valuable tool for rapid pathogen identification from positive blood cultures. Int J Med Microbiol 2015;305:469-79.