

# Impact of Adding Rapid Polymerase Chain Reaction-based Blood Culture Identification Panel to Antimicrobial Stewardship Program: Initial Experience

Rajalakshmi Arjun<sup>1</sup>, Vettakkara Kandy Muhammed Niyas<sup>2</sup>, Kalpana Elizabeth John<sup>3</sup>, Ashalatha Nair<sup>4</sup>, Febeena Hussain<sup>5</sup>

Received on: 25 July 2022; Accepted on: 20 August 2022; Published on: 30 September 2022

**Keywords:** Antibiotic stewardship, Bacteremia, Blood culture identification, Blood culture identification 2, Multiplex polymerase chain reaction. *Indian Journal of Critical Care Medicine* (2022): 10.5005/jp-journals-10071-24329

In patients with bacteremia, time delay to effective therapy is associated with poor outcome.<sup>1</sup> Rapid diagnostic tests can help to improve the time to targeted therapy by coupling with an antimicrobial stewardship program (ASP).<sup>2</sup> In the era of antimicrobial resistance, the choice of appropriate therapy depends not only on the phenotype (carbapenem resistance) but also on the genotype (type of resistance gene) of the organism.<sup>3</sup> Phenotypic identification and susceptibility results require at least 48–72 hours using conventional methods. This time gap in targeted antimicrobial therapy could result in inappropriate therapy, result in poor patient outcomes, adverse effects, induce antimicrobial resistance, and the cost associated with the use of broad-spectrum antibiotics.

In this context, we assessed the impact of adding a multiplex polymerase chain reaction (PCR) FilmArray blood culture identification 2 (BCID2) panel (bioMe'rieux Company, Salt Lake City, UT, USA) in overcoming the delay in conventional culture methods, in a hospital with a robust ASP. The BCID2 panel is run with blood from culture positive bottles. It detects organisms specified in the panel and also identifies the resistance genes for gram-negative bacteria (GNB) including *CTX-M*, *NDM*, *VIM*, *IMP*, *KPC*, and *OXA-48*-like; colistin resistance is detected as well. Resistance genes for gram-positive cocci (GPC) detected are *mecA/C*, *MREJ* for MRSA, and *van A/B* for enterococci. The turn-around time for pathogen and resistance gene identification by the BCID2 panel is 1 hour.

Culture positive blood from critically ill patients were tested with the panel, as decided by the treating team and infectious disease (ID) physician. The results of the BCID2 were reported to the ASP team and antibiotic changes were suggested to the treating team. The antibiotic regimen was reassessed after obtaining the conventional blood culture, where bacterial identification and susceptibility were done using VITEK® 2 system (bioMe'rieux Company, Salt Lake City, UT, USA). A total of 23 patients who underwent BCID2 test from January 2022 to May 2022 were included; the median age was 53 years [interquartile range (IQR): 45–63], 11 were males and the rest were females (Table 1). The median time from blood culture flag to identification and susceptibility result by the conventional method was 43.3 hours (IQR: 36–52) and the lead time to result by BCID2 panel (difference in time between BCID2 and conventional method)

<sup>1,2,5</sup>Department of Infectious Diseases, KIMSHEALTH, Thiruvananthapuram, Kerala, India

<sup>3,4</sup>Department of Laboratory Medicine, KIMSHEALTH, Thiruvananthapuram, Kerala, India

**Corresponding Author:** Rajalakshmi Arjun, Department of Infectious Diseases, KIMSHEALTH, Thiruvananthapuram, Kerala, India, Phone: +91 9447151920, e-mail: dr.a.rajalakshmi@gmail.com

**How to cite this article:** Arjun R, Niyas VKM, John KE, Nair A, Hussain F. Impact of Adding Rapid Polymerase Chain Reaction-based Blood Culture Identification Panel to Antimicrobial Stewardship Program: Initial Experience. *Indian J Crit Care Med* 2022;26(10): 1155–1157.

**Source of support:** Nil

**Conflict of interest:** None

was 25.25 hours (IQR: 18.3–44.3). Nineteen isolates were GNB and four were GPC, *Klebsiella pneumoniae* being the commonest isolate. The concordance in organism identification between the 2 methods was 100%. Concordance in antibiotic susceptibility by conventional method and presence of genes for resistance enzymes in BCID2 panel was also 100%. *CTX-M* was the commonest resistance enzyme identified and noted in 10 isolates either alone or in combination with carbapenemases. *OXA-48*-like was noted in 6 and was the commonest carbapenemase and in 1, combination of *OXA-48*-like and *NDM* was noted.

Time to targeted therapy ranged between 3 and 11 hours from the release of BCID2 panel result and was due to delay in communication of the result to ID physician or the primary physician who wanted to wait for stabilization of the patient. Antibiotic revisions were recommended as follows: escalated, in 5 patients; de-escalated, in 10 patients; stopped in 1 patient; and no change in 7 patients.

In this study, we found that multiplex PCR that we used, the BCID2 panel, correctly identified the pathogen and resistance pattern ahead of the conventional method by 25.25 hours. The time to targeted therapy noted in our study can be further shortened by establishing rapid communication between the treating team, ID physicians, and microbiologists. Future studies should focus on the effect of rapid diagnostics on cost savings and outcome.<sup>4,5</sup>

Table 1: Details of BCID2 panel and conventional culture and susceptibility results

Case	BCID report	Resistance genes	Blood culture organism	Susceptibility pattern	Concurrence in organism between BCID2 and conventional culture	Concurrence in susceptibility profile between BCID2 and conventional culture	Comments
1	<i>K. pneumoniae</i>	CTX-M, OXA 48-like	<i>K. pneumoniae</i>	CR	Yes	Yes	CAZ-AVI susceptible
2	<i>K. pneumoniae</i> , <i>Escherichia coli</i>	CTX-M	<i>K. pneumoniae</i> , <i>E. coli</i>	ESBL	Yes	Yes	
3	<i>K. pneumoniae</i>	CTX-M	<i>K. pneumoniae</i>	ESBL	Yes	Yes	
4	<i>Staphylococcus aureus</i>	mecA/C, MREJ	<i>S. aureus</i>	MRSA	Yes	Yes	
5	<i>Streptococcus</i> spp.	Nil	<i>Streptococcus galloyticus</i>	Nil	Yes	Yes	
6	<i>Stenotrophomonas maltophilia</i>	Nil	<i>S. maltophilia</i>	Nil	Yes	Yes	
7	<i>K. pneumoniae</i>	CTX-M, OXA 48-like	<i>K. pneumoniae</i>	CR	Yes	Yes	CAZ-AVI susceptible
8	None	NA	<i>Burkholderia cepacia</i>	No resistance	Organism not in the panel	NA	Organism not in the panel
9	<i>E. coli</i>	CTX-M, NDM, OXA 48-like	<i>E. coli</i>	CR	Yes	Yes	CAZ-AVI resistant, synergy with ATM was noted
10	<i>K. pneumoniae</i>	CTX-M, OXA 48-like	<i>K. pneumoniae</i>	CR	Yes	Yes	CAZ-AVI susceptible
11	<i>K. pneumoniae</i>	CTX-M, OXA 48-like	<i>K. pneumoniae</i>	CR	Yes	Yes	CAZ-AVI susceptible
12	<i>Streptococcus pneumoniae</i>	Nil	<i>S. pneumoniae</i>	Nil	Yes	NA	No resistance genes for this organism in the panel
13	<i>S. maltophilia</i> , <i>Staphylococcus</i> spp.	Nil	<i>S. maltophilia</i> , <i>S. haemolyticus</i>	Nil	Yes	Yes	
14	<i>K. pneumoniae</i>	Nil	<i>K. pneumoniae</i>	Nil	Yes	Yes	
15	<i>Staphylococcus epidermidis</i>	mecA	<i>S. epidermidis</i>	MR CONS	Yes	Yes	
16	<i>K. pneumoniae</i>	Nil	<i>K. pneumoniae</i>	Nil	Yes	Yes	
17	<i>Staphylococcus</i> spp.	Nil	<i>Staphylococcus haemolyticus</i>	Nil	Yes	Yes	
18	<i>Pseudomonas aeruginosa</i>	Nil	<i>P. aeruginosa</i>	Nil	Yes	Yes	
19	<i>E. coli</i>	CTX-M	<i>E. coli</i>	ESBL	Yes	Yes	
20	<i>K. pneumoniae</i>	CTX-M, OXA 48-like	<i>K. pneumoniae</i>	CR	Yes	Yes	CAZ-AVI susceptible
21	None	Nil	<i>Acinetobacter lwoffii</i>	Nil	NA	NA	The organism is not in the panel
22	<i>E. coli</i>	Nil	<i>E. coli</i>	Nil	Yes	Yes	
23	<i>E. coli</i>	CTX-M	<i>E. coli</i>	ESBL	Yes	Yes	

ATM, aztreonam; CAZ-AVI, ceftazidime-avibactam; CR, carbapenem resistant; ESBL, extended spectrum beta-lactamase pattern; MR CONS, methicillin-resistant coagulase-negative staphylococcus; MRSA, methicillin-resistant *Staphylococcus aureus*

**ORCID**

Rajalakshmi Arjun  <https://orcid.org/0000-0002-4838-183X>

Vettakkara Kandy Muhammed Niyas  <https://orcid.org/0000-0002-7255-6257>

Kalpna Elizabeth John  <https://orcid.org/0000-0002-6355-8170>

Ashalatha Nair  <https://orcid.org/0000-0001-6369-9160>

Febeena Hussain  <https://orcid.org/0000-0002-4563-2971>

**REFERENCES**

1. Vadala R, Princess I. Antimicrobial stewardship program in critical care: Need of the Hour. *Indian J Crit Care Med* 2020;24(9):847. DOI: 10.5005/10071-23557.
2. Ramanathan YV, Arjun R, Krishna V, Tarigopula A, Gopalakrishnan R. Multiplex polymerase chain reaction (PCR) for rapid bacterial identification from blood cultures: ready for prime time in India? *J Contem Clin Pract* 2019;5(1):24–31. <https://link.gale.com/apps/doc/A590126267/HRC?u=anon~4535d173&sid=google Scholar&xid=7e304d4f>.
3. Satlin MJ, Chen L, Gomez-Simmonds A, Marino J, Weston G, Bhowmick T, et al. Impact of a rapid molecular test for *Klebsiella pneumoniae* carbapenemase and ceftazidime-avibactam use on outcomes after bacteremia caused by carbapenem-resistant enterobacterales. *Clin Infect Dis* 2022; ciac354. DOI: 10.1093/cid/ciac354.
4. Yin M. Rapid diagnostics for antibiotic resistance: Urgent need for strong clinical evidence. *Clin Infect Dis* 2022; ciac358. DOI: 10.1093/cid/ciac358.
5. Porwal R, Gopalakrishnan R, Rajesh NJ, Ramasubramanian V. Carbapenem-resistant gram-negative bacteremia in an Indian intensive care unit: A review of the clinical profile and treatment outcome of 50 patients. *Indian J Crit Care Med* 2014;18(11):750. DOI: 10.4103/0972-5229.144021.