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Original Research Article

Comparative performance of biofire pneumonia panel and standard culture-based methods for diagnosing pneumonia in critically ill patients: Impact on antibiotic stewardship

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ABSTRACT

Introduction: Lower respiratory tract infections (LRTIs) are a common cause of morbidity and mortality worldwide. Accurate identification of the pathogens causing LRTIs is crucial for ensuring of diagnostic and antibiotic stewardship. The Biofire Pneumonia Panel (BFPP) is a molecular diagnostic test that allows rapid detection of various bacterial and viral pathogens. In this study, we compared the performance of BFPP with standard culture methods for the detection of pathogens.

Materials and methods: Respiratory samples from 70 patient with suspected LRTIs were tested using both BFPP and standard culture methods. The distribution of isolated bacterial pathogens was analyzed, and the sensitivity and specificity of BFPP were calculated. Additionally, the performance of BFPP in detecting antimicrobial resistance genes was evaluated. The results were compared with those obtained from VITEK-2 antimicrobial susceptibility testing and culture-based methods.

Results: Among the suspected LRTI cases, BFPP identified a single pathogen in 32.8% of cases and multiple pathogens in 40% of cases. The standard culture method detected a single pathogen in 47.1% of cases. BFPP showed a sensitivity of 93.9% and a specificity of 45.9% for the total sample. The performance of BFPP in detecting antimicrobial resistance genes varied for different pathogens with overall sensitivity of 40.1% and specificity of 95.9%.

Conclusion: The Biofire Pneumonia Panel (BFPP) demonstrated high sensitivity for several bacterial pathogens, indicating its potential as a rapid diagnostic tool. However, its performance varied for different microorganisms, and it had limitations in detecting certain pathogens and antimicrobial resistance genes for which still required more further studies to explore different resistance gene mechanism that can be incorporated in this panel in future. The BFPP can complement standard culture methods as a rapid tool in the diagnosis of LRTIs.

1. Introduction

Lower respiratory tract infections (LRTIs), particularly pneumonia cases, are a significant global cause of mortality among intensive care unit (ICU) patients. With the ongoing COVID-19 pandemic, all-cause mortality rates associated with pneumonia are estimated to exceed 70% [1]. Hospital-Acquired Pneumonia (HAP) occurs globally at an annual incidence rate of 5–10 cases per 1000 hospital admissions in adults, while Ventilator-Associated Pneumonia (VAP) affects 10–25% of all mechanically ventilated patients. HAP is the second most common hospital-acquired infection, following urinary tract infections, and VAP leads among nosocomial infections and ICU-related fatalities. HAP risk is elevated in immunocompromised individuals, post-surgical patients, and the elderly. In the United States, VAP occurs at a rate ranging from 2 to 6 cases per 1000 ventilator-days, and non-ventilator-associated HAP has an incidence rate of approximately 3.63 cases per 1000 patient-days. A 2018 systematic review from 22 Asian countries reported an overall VAP incidence rate of 15.1 cases per 1000 ventilator-days [2]. These infections lead to morbidity, financial burden, and challenges in microbiological diagnosis, primarily due to difficulties in obtaining reliable lower respiratory tract specimens non-invasively [3]. The wide range of potential pathogens, emergence of multidrug-resistant (MDR)

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bacteria [4], and time-consuming culture-based methods further complicate accurate identification of causative agents [5,6]. Timely and accurate microbiological identification is crucial for guiding empirical antibiotic regimens and prescribing appropriate treatment [7]. Rapid molecular diagnostic tools are urgently needed to provide timely and accurate identification of respiratory pathogens and antimicrobial sensitivity patterns in HAP patients.

The BioFire FilmArray Pneumonia Panel plus (BFPP), developed by BioMerieux, has emerged as a promising molecular diagnostic tool. This multiplex polymerase chain reaction (PCR) assay can simultaneously detect 27 clinically relevant pneumonia-associated pathogens and 7 antibiotic-resistant targets within 1 h. The panel covers 15 typical bacteria, 3 atypical bacteria, and 9 viruses, demonstrating superior sensitivity and specificity compared to conventional methods [8]. It also offers semi-quantitative detection of typical bacteria and qualitative detection of other bacteria and respiratory viruses, aiding in distinguishing between infection and colonization states for improved clinical outcomes. Despite FDA approval, limited data are available on the BFPP's utility in swiftly identifying complex microbial etiologies of pneumonia infections. There is a scarcity of data to inform clinical decision-making regarding the effectiveness of rapid diagnostic tests (RDTs) in low- and middle-income countries (LMICs) like India [9].

2. Aims and objective

1) To compare the performance of the Biofire Pneumonia Panel (BFPP) with standard culture methods in the detection of pathogens in suspected LRTIs. 2) To determine the sensitivity and specificity of BFPP for the identification of bacterial and viral pathogens in respiratory samples. 3) To analyze the distribution and prevalence of isolated bacterial pathogens using BFPP and standard culture methods. 4) To evaluate the performance of BFPP in detecting antimicrobial resistance genes and compare the results with VITEK-2 antimicrobial susceptibility testing and culture-based methods.

3. Material and methods

A cross-sectional observational study conducted in the Department of Microbiology after taking proper ethical clearance from the IEC (Institutional Ethical Committee). All the mentioned sample like Endotracheal secretions (ET), Tracheostomy tube secretions (TT), Brochoalveolar lavage fluid (BAL) & sputum from suspected pneumonia clinically and radiologically critically ill patients admitted in the hospital during the study period for 7 months collected after the proper consent were included and excluded those not given consent, and lack of proper clinical and radiological evidence of pneumonia; then processed in the microbiology lab for pathogen identification processed for Biofire pneumonia panel (BFPP) along with conventional standard culture methods from the same sample and identified the isolates with Vitek-2 along with MIC based antimicrobial susceptibility testing [10]. Results were analyzed as True Positives (TP): The number of cases where the pathogen was detected by both BFPP and standard microbiological methods, False Negatives (FN): The number of cases where the pathogen was detected by standard microbiological methods but not by BFPP, False Positives (FP): The number of cases where the pathogen was detected by BFPP but not by standard microbiological methods, True Negatives (TN): The number of cases where the pathogen was not detected by either BFPP or standard microbiological methods,

Positive Predictive Agreement (PPA): The proportion of cases where the pathogen was detected by BFPP that were actually positive for the pathogen, Negative Predictive Agreement (PPA): The proportion of cases where the pathogen was not detected by BFPP that were actually negative for the pathogen & Concordance:Among culture positive, those not detected by BFFP panel.

SOC testing: Standard-of-care testing involved the inoculation of a portion of the BAL fluid into selective and differential growth media, such as blood agar, chocolate agar, and MacConkey agar, following established SOP. Using calibrated loops as per local protocols, plates were streaked to achieve a semiquantitative culture result, and the inoculated media were incubated at 35 °C in a 5% CO2 atmosphere, with daily examination for bacterial growth. Identification of bacterial colonies was primarily performed using VITEK-2 ID, supplemented with VITEK 2 ASTcard when necessary, all in accordance with local protocols. Results, indicating potential pathogens and normal flora, were reported semiquantitatively in CFU per milliliter, employing descriptors like "rare," "mild," "moderate," or "many." For sputum, TT and ET specimens, quality assessment involved examining Gram stains for bacteria, leukocytes, and epithelial cells, with Q-score criteria determining quality. Specimens were inoculated on blood agar, chocolate agar, and MacConkey agar plates, incubated at 35 °C in a 5% CO2 incubator, and observed at 18–24 h, with an additional 2 days of incubation before reporting as negative for bacterial growth [10].

4. Results

In this study, out of a total of 70 cases, 47 (67.1%) had suspected LRTI alone, while 23 (32.9%) had suspected LRTI with co-morbidities. The mean age was 44.5 years for LRTI alone and 49.8 years for LRTI with co-morbidities & the male to female ratio was approximately 4:1 for both groups, not found statistically significant. Even regarding pathogen identification, mortality association there were no statistically significant differences observed between the two groups (Table 1).

Fig. 1 shows the isolates distribution pattern detected by both the tests, according to the BFPP results, 14 (20%) of cases showed the presence of a single bacterial pathogen, 27 (38.5%) of cases exhibited the presence of two or more bacterial pathogens, 6 (8.6%) of cases were positive for viral pathogens, 14.3% of cases showed the presence of both bacterial and viral pathogens & 10 (18.6%) of cases shows no pathogens. In contrast, when using the standard culture method, 33 (47.1%) of cases indicated the presence of a single bacterial pathogen. However, no cases detected multiple bacterial pathogens or viral pathogens using this method. In particular, BFPP was more likely to detect pathogen when compared with standard culture seems to be statistically significant ($p < 0.0001$).

Fig. 2 shows the BFPP demonstrated superior pathogen detection capabilities compared to standard culture methods. Among the bacterial isolates, Acinetobacter calcoaceticus had the highest detection rate, with 23 (2.86%) detected by BFPP and 9 (12.86%) detected by standard culture methods. *Klebsiella pneumoniae* followed closely behind with 15 (21.43%) detected by BFPP and 11 (15.71%) by standard culture methods. Haemophilus influenza was detected in 12 (17.14%) of samples by BFPP, but none were detected by standard culture methods. *Pseudomonas aeruginosa* was detected in 12 (17.14%) of samples by BFPP and 6 (8.57%) by standard culture methods.

Among viral isolates, Human Rhinovirus had the highest detection rate, with 6 (8.57%) detected by BFPP. Adenovirus, Coronavirus, and Parainfluenza virus were also detected by BFPP, with detection rates of 1 (1.43%), 3(4.29%), and 3 (4.29%) respectively, while standard culture methods did not detect any of these viruses.

Table 2 shows the BFPP demonstrated high performance for several bacterial pathogens. It achieved a PPA of 100% for Acinetobacter calcoaceticus baumannii complex, *Escherichia coli*, and *Klebsiella pneumoniae* group and pseudomonas, indicating accurate detection of these pathogens. Regarding the NPA, the BFPP showed variable performance. Acinetobacter calcoaceticus baumannii complex had an NPA of 80.3%, indicating that it had a relatively higher false-positive rate in ruling out the absence of this pathogen. *Enterobacter cloacae* complex, on the other hand, had an NPA of 95.7%, suggesting a lower false-positive rate for this pathogen. *Escherichia coli* and *Pseudomonas aeruginosa* both had an NPA of 87.5%, indicating a moderate ability to rule out their absence. Overall, when considering the PPA and NPA for all microorganisms collectively, the BFPP demonstrated a high PPA of 92% & NPA was

Table 1
Clinico-demographic characterstics of patients from suspected LRTI with and without co-morbidities.

Clinicodemographic characterstics		Suspected LRTI alone		Suspected LRTI with co-morbidities*		Total		p-value
Sample proportion positive/tested by each method	**Type of sample**	**BFPP**	**SCM**	**BFPP**	**SCM**	**BFPP**	**SCM**	
	ET(n-34)	**22/23**	**11/23**	**8/11**	**5/11**	**30/34**	**16/34**	
	TT(n-01)	**0/0**	**0/0**	**1/1**	**0/1**	**01/01**	**00/01**	
	Sputum(n-20)	**14/14**	**8/14**	**3/6**	**1/6**	**17/20**	**9/20**	
	BAL(n-15)	**5/10**	**3/10**	**4/5**	**3/5**	**9/15**	**6/15**	
Mean Time of sampling from the patients admission(in days)		5		4		4.5		
No.of Cases(n)		47 (67.1%)		23 (32.9%)		70		
Mean(age in yrs)		44.5		49.8		46.3		0.66
M:F		4.2:1		3.6:1		4:1		0.79
Biofire isolates	**Single pathogen**	17 (24.2%)		6 (8.6%)		23 (32.8)		0.3
	Multiple pathogen	19 (27.1%)		9 (12.9%)		28 (40)		
	Not detected	11 (15.7%)		8 (11.4%)		19 (27.1)		
Standard culture method based	**Single pathogen**	22 (31.4%)		11 (15.7%)		33 (47.1%)		0.9
	Multiple pathogen	0		0		0		
	Not detected	25 (35.7%)		12 (17.1%)		37 (52.8%)		
Mortality	**Cured**	25 (35.7%)		14 (20%)		39 (55.7%)		0.3
	Expired	14 (20%)		4 (5.7%)		18 (25.7%)		
	LAMA	13 (18.6%)		10 (14.2%)		23 (32.8%)		

Co-morbidities* includes CKD(Chronic kidney disease),CVA(Cerebrovascular accident),Ca(Cancer),CHF(Congestive heart failure),ILD(Interstitial lung disease),ARDS (Acute respiratory distress syndrome),COPD(Chronic obstructive pulmonary disease).
Endotracheal secretions(ET), Tracheostomy tube secretions(TT), Brochoalveolar lavage fluid(BAL), Biofire pneumonia panel(BFPP), Standard Culture methods(SCM).

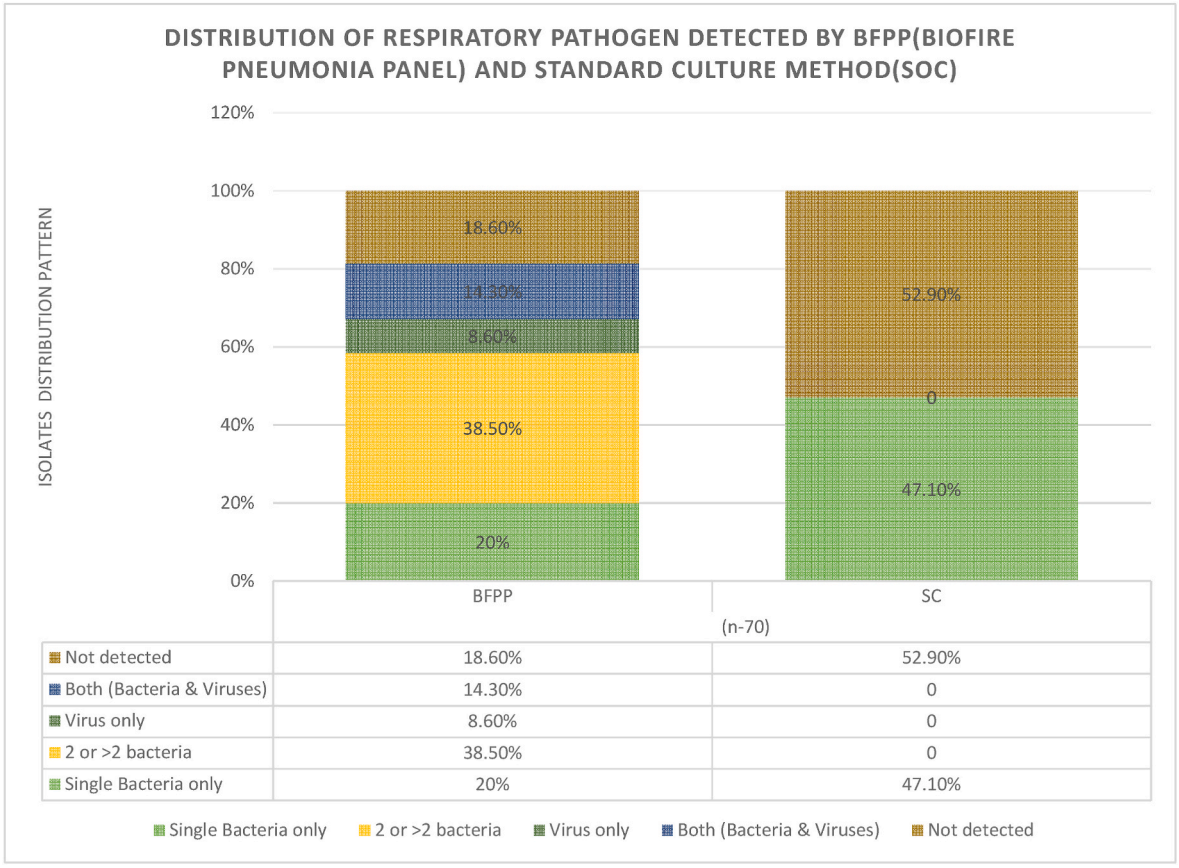

Fig. 1. Distribution of respiratory pathogen detected by BFPP(Biofire Pneumonia Panel) and standard culture method.

92.3%.

For carbapenemase-producing Gram-negative bacteria, the BFPP showed varying performance in detecting specific resistance genes. The PPA for each gene was as follows: IMP (4.7%), KPC (31.8%), NDM (76.2%), OXA-48 (61.9%), and VIM (22.7%). The NPA ranged from 91.8% to 97.9% for these resistance genes. When considering all carbapenemase producers together, the overall PPA was 39.2%, and the NPA was 95.88%. In the case of ESBL (Extended-Spectrum Beta-Lactamase) producing bacteria, the BFPP had a PPA of 50% for detecting the CTX-M gene, indicating moderate performance. The NPA for this gene was 98.2%. For Methicillin-resistant *Staphylococcus aureus* (MRSA), the BFPP did not detect any cases with the MecA/C and MREJ genes, resulting in a PPA of 0%. The NPA for MRSA resistance genes was 94.2%.Overall, when considering all the detected resistant genes, the

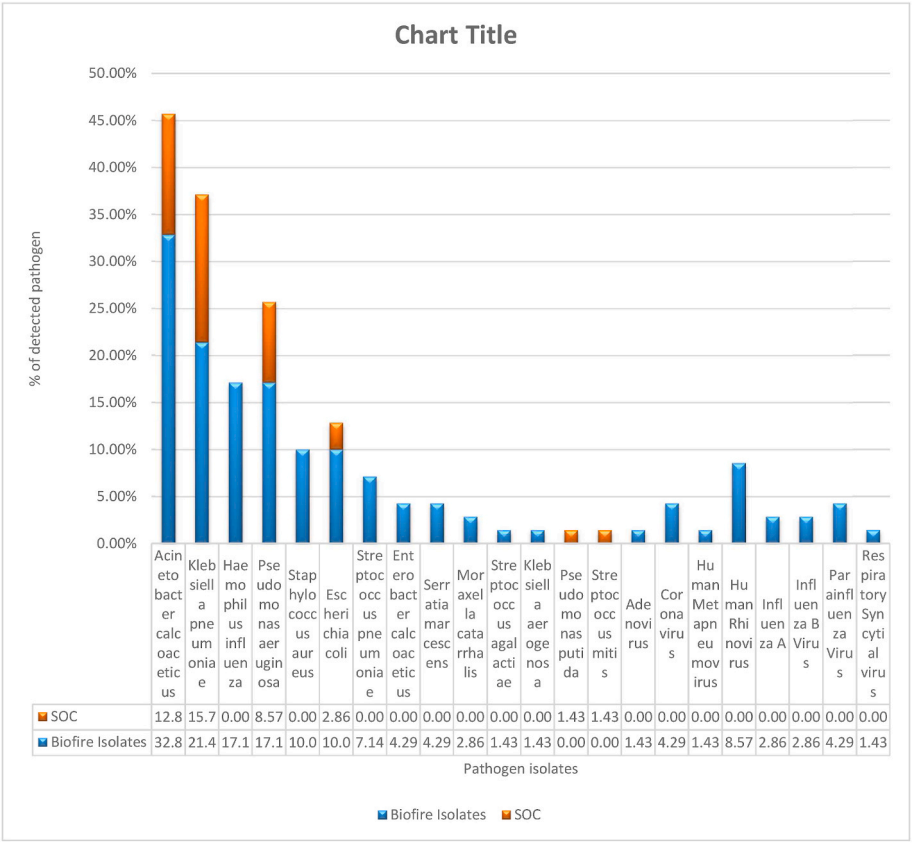

Fig. 2. Summary of the percentage of detected pathogens by BioFire Pneumonia Panel plus (BFPP) and standard culture methods (n-70).

BFPP had an overall PPA of 40.1% and an NPA of 95.9% (Table 3).

Table 4 presents the quantitative agreement of bacterial targets based on the Pn panel detection and SOC culture results. In the "Not detected" category, exhibited a high concordance rate of 92.4%. The "10^3 (Mild)" category the concordance was lower at 33.3% (1 out of 3 samples). Similarly, in the "10^4(Moderate)" category, the Pn panel detected moderate bacterial presence in one sample, resulting in a concordance rate of 14.3% (1 out of 7 samples). The "$>10^5$ (Many)" category showed the concordance of 100% (15 out of 15 samples). Concordance between BFPP and culture quantification among all positive cultures was 68%. (17/25).

Table 5 shows moderate agreement between the two diagnostic tests the BFPP and SC(standard culture) indicated by a correlation coefficient of 0.44. The Table 6 show the association of pathogen detection by BFPP with Fungal and Mycobacterium Tuberculosis (MTB) isolated from conventional culturte methods seems statistically significant with p value of 0.0412.

5. Discussion

This study's findings indicate that while there are some differences in age, pathogen isolation, and mortality rates between patients with suspected LRTI alone and those with co-morbidities, these differences are not statistically significant. These results underscore the complex nature of LRTI and suggest that co-morbidities may not be the sole determinant of patient outcomes or pathogen isolation complexity in cases of LRTI. However, it's important to consider other variables and factors that may influence these outcomes and to interpret these findings in the context of the study's limitations.

In this study, BFPP outperformed standard culture methods in pathogen detection. Specifically, BFPP detected pathogens in 82.0% of cases, while standard culture methods only identified pathogens in 47.1% of cases. This substantial difference in detection rates aligns with previous research findings, which have consistently shown that molecular diagnostic methods like BFPP provide rapid and accurate results compared to traditional culture methods [11–14] might be due to inabiltiy to cultivate the viruses and atypical bacteria in conventional standard culture methods.

Pathogen Distribution: The study's findings regarding the distribution of pathogens in cases are in line with previous research. Gram-negative bacteria (GNB) such as Acinetobacter baumannii complex, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa* were the most commonly detected pathogens, with detection rates of 32.8%, 21.4%, and 17.1% by BFPP, respectively. While Standard culture methods had lower detection rates for these pathogens, at 12.8%, 15.7%, and 8.5%, respectively. These results emphasize the clinical relevance of BFPP in identifying key pathogens associated with pneumonia within a short span of time [15]. The BFPP method has successfully identified specific opportunistic bacterial targets, including *Staphylococcus aureus* and Streptococcus pneumoniae, which were not originally detected in our culture results. Additionally, it has pinpointed various other Gram-negative bacteria that possess the potential to induce pneumonia in critically ill patients [16].

Poly-microbial Infections: The study revealed that BFPP detected multiple bacterial pathogens in 38.5.0% of cases and co-detected bacteria and viruses in 14.3% of cases among the 70 specimens. This highlights the prevalence of polymicrobial infections in HAP cases, which is consistent with other studies that have reported similar findings [11–14]. BFPP's ability to identify these complex infections underscores its importance in comprehensive pathogen detection.

Viral Detection: BFPP demonstrated its capability to detect only viral pathogens in 8.6% of cases. Specifically, rhinovirus/enterovirus were detected in 8.57% of cases, and; coronaviruses and parainfluenza virus in 4.29% each cases. Viral infections can contribute to secondary

Table 2
Summary on the performance of BFPP and standard microbiological methods to detect the bacterial pathogens.

	TP	FN	FP	TN	PPA	NPA
Acinetobacter calcoaceticus baumannii complex	9	0	12	49	100%	80.3%
Enterobacter cloacae complex	0	0	3	67	NA	95.7%
Escherichia coli	2	0	7	61	100%	87.1%
Haemophilus influenzae	0	0	11	59	NA	84.2%
Klebsiella pneumoniae group	8	0	4	58	100%	93.5%
Moraxella catarrhalis	0	0	2	68	NA	97.1%
Proteus spp.	0	0	0	70	NA	100%
Pseudomonas aeruginosa	4	2	8	56	100%	87.5%
Serratia marcescens	0	0	3	67	NA	95.7%
Staphylococcus aureus	0	0	6	64	NA	91.4%
Streptococcus agalactiae	0	0	1	69	NA	98.5%
Streptococcus pneumoniae	0	0	5	65	NA	92.8%
Total bacterial pathogen	23	2	62	753	92%	92.3%

True Positives (TP): The number of cases where the pathogen was detected by both BFPP and standard microbiological methods.
False Negatives (FN): The number of cases where the pathogen was detected by standard microbiological methods but not by BFPP.
False Positives (FP): The number of cases where the pathogen was detected by BFPP but not by standard microbiological methods.
True Negatives (TN): The number of cases where the pathogen was not detected by either BFPP or standard microbiological methods.
Positive Predictive Agreement(PPA): The proportion of cases where the pathogen was detected by BFPP that were actually positive for the pathogen.
Negative Predictive Agreement (NPA): The proportion of cases where the pathogen was not detected by BFPP that were actually negative for the pathogen.

bacterial or fungal co-infections in critically ill patients, highlighting the clinical significance of viral detection by BFPP [17,18]. However, the absence of SARS-CoV-2 in the panel is noteworthy, and the potential for future updates to include it in the panel is mentioned.

Our study results demonstrated that BFPP achieved an overall Positive Percent Agreement (PPA) of 92% and Negative Percent Agreement (NPA) of 92.3% for detecting bacterial targets included in our panel. These findings are in line with other studies, such as those conducted by Edin et al. (PPA = 100%, NPA = 73.2%), Ginocchio et al. (PPA = 93%, NPA = 96%), and Lee et al. (PPA = 90%, NPA = 97.4%), which have also reported strong performance by BFPP in identifying microbial etiology in HAP patients [19–21].

Although BFPP demonstrated enhanced sensitivity (PPA) and specificity (NPA) in determining the microbial causes of pneumonia when compared to standard microbiological methods, it's important to note that our study had a relatively small sample size of respiratory specimens.

BFPP's accuracy in detecting antimicrobial resistance genes was a crucial aspect of the study. It showed varied agreement with VITEK-2 in identifying these resistance genes specifically when compared to VITEK-2 breakpoints, with PPA(39.2%,50%, NA) and NPA(95.88%, 98.2% and

Table 4
Quantitative agreement of bacterial targets detected by BFPP and Standard culture method.

BFPP detected	No. of samples with SOC culture result (CFU/ml)			
	ND	10^3 (Mild)[a]	10^4(Moderate)[b]	$>10^5$ (Many)[c]
Not detected	753	1	1	0
10^4	24	0	0	0
10^5	17	0	1	1
10^6	13	1	2	2
$>10^7$	8	1	3	12
%	92.4 (753/	33.3 (1/3)	14.3 (1/7)	100 (15/15)
Concordant	815)			

Concordance* between the PN panel and culture quantitation among all positive cultures was 68% (17/25).
[a] Growth up to the first quadrant of the plate.
[b] Growth up to the second quadrant of the plate.
[c] Growth up to the third or fourth quadrant of the plate.

Table 5
Kappa agreement between performance of BFPP and standard microbiological methods (n-70).

	Culture +	Culture -
Biofire +	41	16
Biofire -	1	12
	k-0.44[a]	

[a] Shows moderate agreement between the BFPP and SC(standard culture).

Table 6
Association of BFPP pathogen detection with conventional cultural Fungal and Mycobacterium Tuberculosis (MTB) isolates.

	Fungal&MTB +	Fungal&MTB -	Total
Biofire isolates +	2	55	57
Biofire isolates -	3	10	13
	p-0.0412[a]		

[a] Statistically significant.

Table 3
Correlation between BFPP and VITEK-2 antimicrobial phenotype AST pattern for determination of antimicrobial resistance genes (n-70).

BFPP Target Organisms		Specimens [No. of Results for BFPP/VITEK2 AST phenotype Pattern flagged]					
Antimicrobial Resistance Genes		TP	FN	FP	TN	PPA	NPA
Carbapenamses producing GNB	IMP	1	20	0	49	4.7%	100%
	KPC	7	15	3	45	31.8%	93.7%
	NDM	16	5	2	47	76.2%	95.9%
	OXA-48	13	8	4	45	61.9%	91.8%
	VIM	5	17	1	47	22.7%	97.9%
	Total carbapenamase producers	42	65	10	233	39.2%	95.88%
ESBL producing bacteria	CTX-M	7	7	1	55	50%	98.2%
Methicillin Resistant*Staphylococcus aureus*	MecA/C and MREJ	0	1	4	65	NA	94.2%
	Total no of detected resistant genes	49	73	15	353	40.1%	95.9%

94.2%) for carbapenamases produces, ESBLs and MRSA respectively. The overall PPA for all detected resistant genes was 40.1%, and the NPA was 95.9% [21–24]. Our study revealed significant disparities in identifying antimicrobial resistance genes. It's important to note that the absence of a resistance gene doesn't necessarily indicate susceptibility to the corresponding antibiotic, given the various genetic variations and resistance mechanisms. Likewise, the existence of a particular genetic marker cannot be directly tied to the detected pathogen. Therefore, it is crucial to conduct comprehensive culture and susceptibility testing for each potential case, following the recommended guidelines [25].

The study also discussed BFPP's ability to quantify the microbiological load of bacterial DNA targets. It found that BFPP's estimated values were approximately 1 log10 higher than culture results, which is consistent with previous studies. Among all the positive cultures, the concordance rate between culture quantification and BFPP quantification was 68% (17/25), which is almost consistent to previous studies shows 47.4%, 43.6% and 53.6% [21,26,27]. This relatively low concordance rate in quantification could be attributed to BFPP's ability to detect both viable and non-viable organisms, whereas culture methods are restricted to viable cells only.

5.1. Limitations

The study acknowledges certain constraints, primarily the limited sample size due to resource and cost limitations associated with the BFPP test. Nevertheless, it provides valuable insights into BFPP's diagnostic performance. Another limitation is antibiotic intake history prior to sampling not assessed might impacted the comparative performance of the results too. A notable limitation is that among the 70 specimens tested, approximately 5.7% displayed multiple resistance genes in bacteria identified by BFPP but were categorized as sensitive by the VITEK-2 phenotypic test. This incongruity implies that these resistance genes may not be actively expressed or functional, potentially complicating treatment decisions for clinicians who receive conflicting genetic and phenotypic testing information.

Another limitation emerged when comparing the results of fungal and TB cultures with both the BFPF and standard methods. It was observed that samples testing negative in the BFPF method were more likely to yield positive results in fungal and TB cultures, a statistically significant finding. This suggests a potential need to incorporate specific primers for detecting *Mycobacterium tuberculosis* and common fungal pathogens such as candida and aspergillus in pneumonia cases.

6. Conclusion

In conclusion, our study emphasizes the practical implications of PN panel results on reporting compared to standard culture tests, highlighting the need for careful interpretation due to heightened sensitivity and quantification variations. Clinician sensitization is vital for successful integration, emphasizing result evaluation in conjunction with other laboratory findings. Education on interpreting genotypic resistance, considering positive and negative predictive values, is crucial for effective antibiotic stewardship.

Negative results should not dismiss potential phenotypic resistance through alternative mechanisms. Maximizing PN panel impact may require additional resources, such as direct gram staining correlation and interpretive comments in reports. Involving an active antimicrobial stewardship team further enhances the utility of PN panel results. Designed as a complement, not a replacement, for routine culture, the PN panel rapidly identifies pathogens in lower respiratory tract infections, facilitating definitive diagnosis and contributing positively to infection prevention and antibiotic stewardship efforts.

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Ethical statement

All the participants were involved in this study after proper ethical approval from Institutional Ethics Committee (ICMR Reg No. EC/NEW/INST/2022/UA/0152), with approval letter no. SRHU/HIMS/RC/2023/196; dated:September 05, 2023.

Declaration of competing interest

The authors declare the following financial interests/personal relationships which may be considered as potential competing interests:

Dr. Rajender Singh reports administrative support and statistical analysis were provided by Swami Rama Himalayan University. If there are other authors, they declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.ijmmb.2024.100564.

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