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Original Article

Application of a multiplex molecular pneumonia panel and real-world impact on antimicrobial stewardship among patients with hospital-acquired and ventilator-associated pneumonia in intensive care units

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KEYWORDS
Critically ill;
Intensive care unit;
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Abstract *Background:* The optimal timing for applying the BioFire FilmArray Pneumonia Panel (FAPP) in intensive care unit (ICU) patients with hospital-acquired pneumonia (HAP) or ventilator-associated pneumonia (VAP) remains undefined, and there are limited data on its impact on antimicrobial stewardship.
Methods: This retrospective study was conducted at a referral hospital in Taiwan from November 2019 to October 2022. Adult ICU patients with HAP/VAP who underwent FAPP testing

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Ventilator-associated pneumonia;
Multiplex polymerase chain reaction;
Antimicrobial stewardship

were enrolled. Patient data, FAPP results, conventional microbiological testing results, and the real-world impact of FAPP results on antimicrobial therapy adjustments were assessed. Logistic regression was used to determine the predictive factors for bacterial detection by FAPP.
Results: Among 592 respiratory specimens, including 564 (95.3%) endotracheal aspirate specimens, 19 (3.2%) expectorated sputum specimens and 9 (1.5%) bronchoalveolar lavage specimens, from 467 patients with HAP/VAP, FAPP testing yielded 368 (62.2%) positive results. Independent predictors for positive bacterial detection by FAPP included prolonged hospital stay (odds ratio [OR], 3.14), recent admissions (OR, 1.59), elevated C-reactive protein levels (OR, 1.85), Acute Physiology and Chronic Health Evaluation II scores (OR, 1.58), and septic shock (OR, 1.79). Approximately 50% of antimicrobial therapy for infections caused by Gram-negative bacteria and 58.4% for Gram-positive bacteria were adjusted or confirmed after obtaining FAPP results.
Conclusions: This study identified several factors predicting bacterial detection by FAPP in critically ill patients with HAP/VAP. More than 50% real-world clinical practices were adjusted or confirmed based on the FAPP results. Clinical algorithms for the use of FAPP and antimicrobial stewardship guidelines may further enhance its benefits.

Introduction

Severe pneumonia is one of the leading causes of morbidity and mortality in intensive care units (ICUs), and delayed antibiotic administration is a significant indicator of hospital mortality.[1—3] Rapid diagnosis and early antibiotic treatment are essential in the management of critically ill patients, contributing to reduced morbidity and mortality.[4]

The incidence of drug-resistant pathogens in ICUs is increasing.[5] However, conventional microbiological techniques for detecting bacterial infections often lack sensitivity, and the turnaround time for antimicrobial susceptibility testing following microbiological sampling typically exceeds 48 h.[6] Consequently, empirical treatment based on clinical presentation and risk factors remains the preferred approach in most cases according to international guidelines.[2,7] Patients admitted to an ICU, due to the severity of their condition and the potential risk of acquiring multidrug-resistant organisms (MDROs), often receive broad-spectrum antibiotics as empirical treatment. This increases the probability of inappropriate antibiotic usage and contributes to the heightened prevalence of MDROs.[8]

The BioFire FilmArray Pneumonia Panel (FAPP) (BioFire Diagnostics, LLC, Salt Lake City, UT) is a multiplex polymerase chain reaction (mPCR) panel capable of detecting 15 bacteria, providing semiquantitative estimates of bacterial load, and identifying 7 antibiotic resistance genes, including those encoding carbapenemases (bla_{IMP}, bla_{KPC}, bla_{NDM}, bla_{OXA-48}, bla_{VIM}), extended-spectrum β-lactamase (ESBL) (bla_{CTX-M}), and methicillin resistance (*mec*A/C and MREJ). It also offers qualitative assessment for viral and atypical bacterial targets. Recently, more studies have focused on the impact of the syndromic mPCR test on pneumonia management, including shortening the turnaround time, increasing pathogen detection rates, and providing antimicrobial resistance markers,[9,10] all of which offer the potential for early detection of MDROs in the ICU and a decreased duration of inappropriate antimicrobial therapy.[11]

However, the optimal timing for utilizing this technique in ICU patients with hospital-acquired pneumonia (HAP) and ventilator-associated pneumonia (VAP) remains undefined, and there are limited data available regarding eligible candidates for its application. For these reasons, we conducted a retrospective study to evaluate suitable patients with HAP and VAP in the ICU for FAPP testing and to assess real-world clinical impact after receiving FAPP results.

Materials and methods

Patients and study design

This single-centre retrospective observational study was conducted in a tertiary referral hospital (China Medical University Hospital [CMUH]) in central Taiwan. Adult (aged ≥18 years) patients admitted to the ICU with a diagnosis of HAP or VAP who underwent FAPP testing for pathogen identification between November 2019 and October 2022 were enrolled. The study adhered to the Declaration of Helsinki and followed the Strengthening the Reporting of Observational Studies in Epidemiology (STROBE) guidelines. The institutional review board of CMUH waived the requirement for written informed consent because the study involved minimal risk to the patients (IRB number: CMUH112-REC3-041).

Definitions and data collection

Pneumonia was defined as the presence of new lung infiltrate on chest imaging with clinical evidence that the infiltrate was of an infectious origin, which included the new onset of fever, purulent sputum, leucocytosis, and a decline in oxygenation. HAP was defined as pneumonia occurring 48 h or more after admission. VAP was defined as pneumonia occurring 48 h or more after endotracheal intubation.[2]

The variables recorded retrospectively from electronic medical records included patient characteristics, comorbidities, and the results of standard-of-care investigations and FAPP for pneumonia pathogen survey. Pneumonia-related complications, including acute respiratory distress syndrome (ARDS) and septic shock, as well as the utilization of organ support, were also recorded.

Microbiological testing

Microbiological testing was performed upon the diagnosis of pneumonia in all patients. Specimens obtained from expectorated sputum, endotracheal aspirate (ETA), or bronchoalveolar lavage (BAL) were used for microbiological testing. During the study period at CMUH, FAPP was indicated for pathogen surveys in hospitalized patients with pneumonia requiring invasive mechanical ventilation (IMV) or vasopressor use, as well as those with a poor response to initial treatment. FAPP was performed in accordance with the manufacturer's instructions in the clinical microbiology laboratory at CMUH with panel turnaround time about 1 h.

The conventional culture method included Gram staining and quantitative culture. Isolated colonies were identified using matrix-assisted laser desorption ionization-time of flight mass spectrometry, and antimicrobial susceptibility testing was performed using an automatic Phoenix system (Becton—Dickinson Microbiology Systems, Sparks, MD, USA).

Laboratory tests for other pathogens, such as *Pneumocystis jirovecii* (PJ), cytomegalovirus (CMV), severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), and *Aspergillus* species, were also conducted when clinically suspected.

Performance measures of FAPP

The culture results for bacterial analytes, as the standard of care, were used as the gold standard and reference method. An FAPP result was classified as true positive or true negative when it matched the standard-of-care investigation result. A positive FAPP result when the culture result was negative was considered a false positive, whereas a negative FAPP result when the culture result was positive was considered a false negative. The FAPP results were considered concordant when they were consistent with the results of the conventional culture.

Clinical behaviour following receipt of FAPP results

Patients received empirical antimicrobial therapy from the treating physician. Clinicians tailored antimicrobial regimens based on the results of FAPP and conventional cultures for detecting pathogens or antimicrobial resistance, in accordance with treatment guidelines.[2,7,12] The impact of FAPP results on pneumonia treatment decisions was retrospectively assessed by three independent intensivists through chart reviews. Antibiotic de-escalation was defined as (i) replacing carbapenem with another β-lactam antibiotic, (ii) withdrawing antipseudomonal agents due to negative *Pseudomonas aeruginosa* results, (iii) narrowing the antibiotic spectrum due to negative genetic markers for Gram-negative bacteria (GNB) antimicrobial resistance, and (iv) discontinuing methicillin-resistant *Staphylococcus aureus* (MRSA) coverage upon negative *S. aureus* or *mec*A/C and MREJ gene results.[13,14] Antibiotic escalation was defined as broadening the antibiotic spectrum according to the FAPP results. Antibiotic continuation[6,15] was defined as no change in the antimicrobial regimen after receiving the FAPP results.

The real-world clinical behaviour regarding antimicrobial therapy adjustments after obtaining the FAPP results was documented. Potential mPCR-guided antimicrobial therapy adjustments based on the FAPP results were classified as (i) could be de-escalated, (ii) could be continued, or (iii) could be escalated. The rationale for antimicrobial therapy adjustments according to the FAPP results was also recorded. If the antimicrobial regimens remained unchanged after obtaining the FAPP results, it was categorized as "undetermined reason". Antibiotics targeting GNB or Gram-positive bacteria (GPB) were recorded separately.

Statistical analysis

All statistical analyses were conducted using SAS 9.4 software (SAS Institute, Cary, North Carolina, USA). Logistic regression models were developed to assess the probability of obtaining a positive FAPP result for bacterial detection, with odds ratios (ORs) and 95% confidence intervals (CIs) reported. Generalized linear models with generalized estimating equations, adjusted for patient characteristics and significant interactions, were used to model multiple test data. For practical purposes, continuous variables or data that had a maximal Youden's index were dichotomized before regression analysis according to clinically meaningful thresholds. All tests were two-tailed, and statistical significance was indicated by a p value < 0.05.

Results

Demographic characteristics

This study included a total of 592 respiratory specimens, including 564 (95.3%) ETA specimens, 19 (3.2%) expectorated sputum specimens and 9 (1.5%) BAL specimens, from 467 patients diagnosed with HAP/VAP (Fig. S1). Of the 467 patients, 303 (64.9%) were male, and the mean age was 67.9 years (standard deviation [SD], 14.3). The median Acute Physiology and Chronic Health Evaluation (APACHE) II score was 24.0 (IQR, 10.0), and 232 (49.7%) patients had an APACHE II score exceeding 25 (Table 1). ARDS developed in 208 (44.5%) patients, while 203 (43.5%) patients experienced septic shock. IMV was needed in 462 (98.9%) patients.

Microbiological outcomes

FAPP findings

The median time from sample collection to obtaining FAPP results was 6 h (Fig. S2). Among all respiratory specimens, the FAPP yielded 368 (62.2%) positive results. The most frequently identified pathogens were the *Acinetobacter calcoaceticus-baumannii* complex (n = 168), *P. aeruginosa*

Table 1 Demographic data of patients with hospital-acquired pneumonia/ventilator-associated pneumonia undergoing the FilmArray® Pneumonia Panel for pathogen identification in the intensive care unit.

Characteristic	n = 467
Age (years), mean (SD)	67.9 (14.3)
Age ≥65 years, n (%)	292 (62.5)
Sex, male, n (%)	303 (64.9)
BMI ≥25 kg/m^2, n (%)	154 (33.0)
Pneumonia type, n (%)	
HAP	166 (35.5)
VAP	301 (64.5)
Hospital LOS before FAPP (days), median (IQR)	10.0 (5.0–21.0)
0–14 days, n (%)	304 (65.1)
15–28 days, n (%)	81 (17.3)
>28 days, n (%)	82 (17.6)
Charlson comorbidity index, median (IQR)	6.0 (4.0–8.0)
Comorbidities, n (%)	
Chronic lung disease	83 (17.8)
Active cancer	168 (36.0)
Immunocompromised[a]	56 (12.0)
Diabetes mellitus	215 (46.0)
Renal failure	
End stage renal disease	58 (12.4)
Acute renal failure	49 (10.5)
History of hospital admission within 90 days, n (%)	151 (32.3)
Intravenous antibiotic(s) exposure within 90 days, n (%)	121 (25.9)
History of RCU[b] admission within 30 days, n (%)	139 (29.8)
CRP (mg/L), median (IQR)	14.2 (6.3–21.3)
CRP >6.6 mg/L, n (%)	327 (74.5)
APACHE II score, median (IQR)	24.0 (20.0–30.0)
APACHE II score ≥25, n (%)	232 (49.7)
ARDS, n (%)	208 (44.5)
Septic shock, n (%)	203 (43.5)
Invasive mechanical ventilation, n (%)	462 (98.9)
Continuous renal replacement therapy, n (%)	81 (17.3)

[a] Chronic steroid use (prednisolone 5 mg/day or equivalent >1 month or >30 mg/day) or other immunosuppressive therapy for diseases such as connective tissue disease, rheumatic disease or solid organ transplantation.
[b] RCU, respiratory care unit, including respiratory care centres and respiratory care wards.
APACHE II, Acute Physiology and Chronic Health Evaluation II; ARDS, acute respiratory distress syndrome; BMI, body mass index; CI, confidence interval; CRP, C-reactive protein; FAPP, FilmArray® Pneumonia Panel; ICU, intensive care unit; LOS, length of stay; OR, odds ratio; SD, standard deviation.

(n = 139), and *Klebsiella pneumoniae* group (n = 130) (Fig. 1). Antimicrobial resistance genes were detected in 157 (26.5%) specimens (Fig. S3). Enterobacterales were the most common GNB (n = 211), and 54% of specimens had detected resistance genes (Fig. 2). Specifically, $bla_{CTX\text{-}M}$ was detected in 17.1%, carbapenemase genes were detected in 36.9% of the bacterial isolates. Furthermore, metallo-β-lactamases (MBLs) accounted for 30.9% of all carbapenemase genes. In *S. aureus* detected by FAPP, *mec*A/C and MREJ genes were found in 52.1% of samples (Fig. 2).

Conventional culture findings

Among all respiratory specimens, the conventional bacterial culture yielded 200 (33.8%) positive results (Fig. 3A). The most frequently detected bacteria were the *A. calcoaceticus-baumannii* complex (n = 46), *P. aeruginosa* (n = 36), and *K. pneumoniae* (n = 32). Bacteria and other pathogens that were not detectable by the FAPP are shown in Fig. 3B.

Performance of FAPP

The culture results from the standard-of-care investigation were used as the gold standard and reference method. The sensitivity for detecting GNB exceeded 80% for all strains except *Serratia marcescens* (71%). The sensitivity of *S. aureus* detection was 75%, and conventional culture failed to detect GPB other than *S. aureus*. Overall, the concordance rate of FAPP with conventional culture exceeded 90%, with the exceptions of *P. aeruginosa* (82.8%), the *K. pneumoniae* group (82.3%), and the *A. calcoaceticus-baumannii* complex (78.9%) (Table S1).

Clinical factors predicting bacterial detection by FAPP

Logistic regression analysis revealed that a hospital length of stay (LOS) exceeding 28 days (OR, 3.14; 95% CI, 1.73–5.69), history of hospital admission within 90 days (OR, 1.59; 95% CI, 1.04–2.45), C-reactive protein (CRP) level >6.6 mg/L (OR, 1.85; 95% CI, 1.19–2.86), APACHE II score ≥25 (OR, 1.58; 95% CI, 1.03–2.40), and septic shock (OR, 1.79; 95% CI, 1.18–2.71) were independent predictors for positive bacterial detection by FAPP (Table 2).

Patients with active cancer and ARDS showed a negative association with bacterial detection by FAPP (Table 2). In a subgroup analysis of FAPP-negative pneumonia cases (Fig. S4A), a significantly higher rate of detecting other pathogens was observed among patients with ARDS compared to those without ARDS (48.0% vs. 18.3%) (Fig. S4B). Patients with active cancer also showed a higher rate of other pathogens detection than those without active cancer (40.4% vs. 29.1%) (Fig. S4C).

Real-world clinical behaviour following receipt of FAPP results

After excluding 5 patients who died within 24 h of the FAPP test, antimicrobial therapy adjustments were retrospectively reviewed in 587 pneumonia episodes.

Fig. 4A illustrates the real-world clinical antimicrobial therapy adjustments for GNB according to the FAPP results. In 25.4% of cases (n = 149 out of 587 pneumonia episodes), antibiotic escalation occurred due to the detection of GNB (n = 87) and the identification of antimicrobial resistance genes (n = 62) by FAPP. Additionally, FAPP confirmed 19.8%

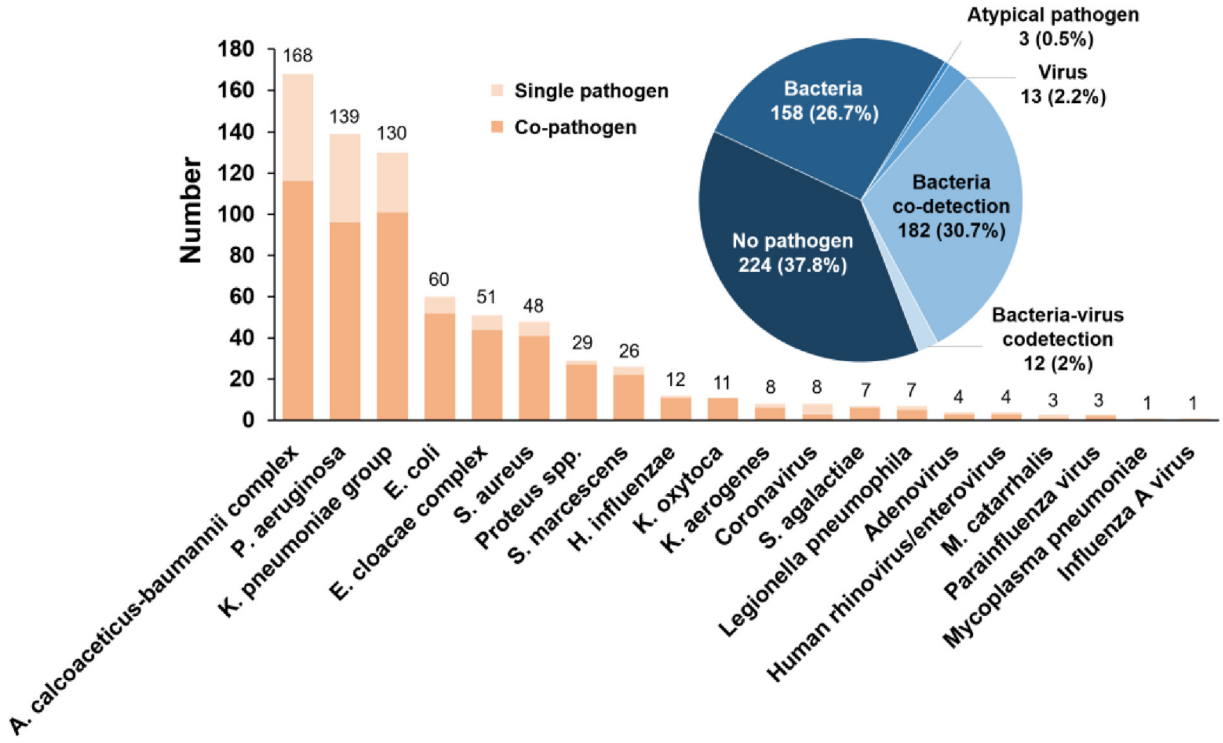

Figure 1. Pathogens detected by FilmArray® Pneumonia Panel among 592 respiratory specimens from 467 critically ill patients diagnosed with HAP/VAP. A single pathogen is indicated in light orange; copathogens are indicated in a deeper colour. Pathogens detected in a single patient are represented in their respective bars. HAP, hospital-acquired pneumonia; VAP, ventilator-associated pneumonia.

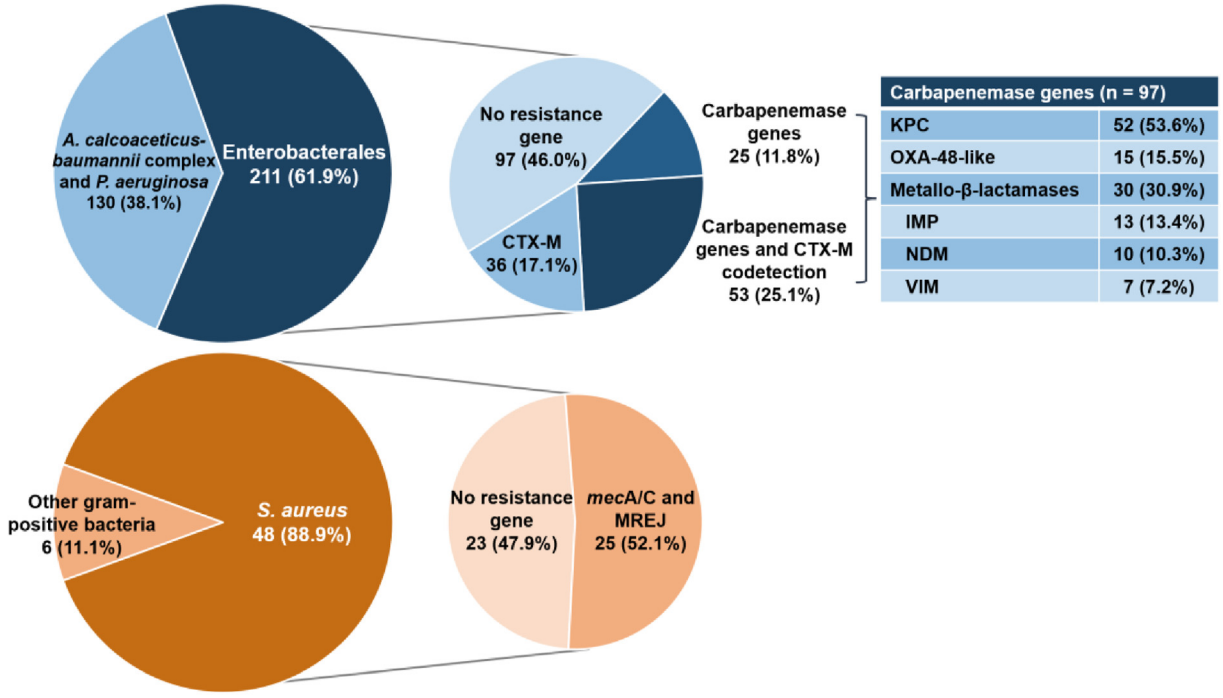

Figure 2. The relationship of resistance genes in different bacterial strains, with a focus on Enterobacterales and *S. aureus*.

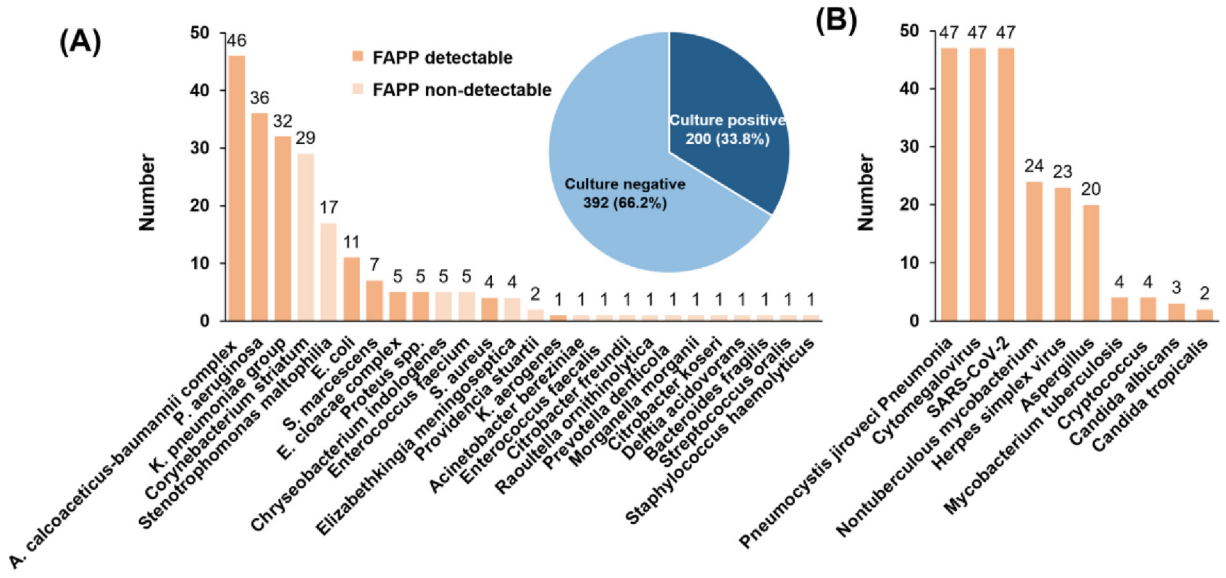

Figure 3. Pathogens detected by conventional microbiological testing. (A) Bacterial pathogens. (B) Other pathogens. FAPP, FilmArray® Pneumonia Panel; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

Table 2 Logistic regression model for evaluation of clinical factors predicting bacterial detection using the FilmArray® Pneumonia Panel.

	OR (95% CI)	*P* value
Age ≥65 years	1.38 (0.88—2.17)	0.1562
Male	1.42 (0.94—2.14)	0.0968
BMI ≥25 kg/m^2	0.79 (0.51—1.22)	0.2868
Pneumonia type		
HAP	Reference	—
VAP	0.99 (0.65—1.49)	0.9542
Hospital LOS before FAPP		
0—14 days	Reference	—
15—28 days	1.18 (0.69—2.01)	0.5369
>28 days	3.14 (1.73—5.69)	0.0002
Charlson comorbidity index	0.97 (0.89—1.06]	0.5196
Comorbidities		
Chronic lung disease	0.90 (0.54—1.52)	0.7004
Active cancer	0.58 (0.35—0.94)	0.0263
Immunocompromised	1.08 (0.62—1.90)	0.7862
Diabetes	1.43 (0.95—2.17)	0.0896
Renal failure		
End stage renal disease	0.80 (0.39—1.64)	0.5419
Acute renal failure	0.65 (0.30—1.39)	0.2640
History of hospital admission within 90 days	1.59 (1.04—2.45)	0.0337
History of RCU[a] admission within 30 days	1.50 (0.96—2.34)	0.0785
CRP >6.6 mg/L	1.85 (1.19—2.86)	0.0059
APACHE II ≥ 25	1.58 (1.03—2.40)	0.0347
ARDS	0.46 (0.30—0.70)	0.0003
Septic shock	1.79 (1.18—2.71)	0.0059
Continuous renal replacement therapy	1.81 (0.95—3.44)	0.0697

[a] RCU, respiratory care unit, including respiratory care centres and respiratory care wards.
ARDS, acute respiratory distress syndrome; BMI, body mass index; CI, confidence interval; CRP, C-reactive protein; FAPP, FilmArray® Pneumonia Panel; HAP, hospital-acquired pneumonia; ICU, intensive care unit; LOS, length of stay; OR, odds ratio; SD, standard deviation; VAP, ventilator-associated pneumonia.

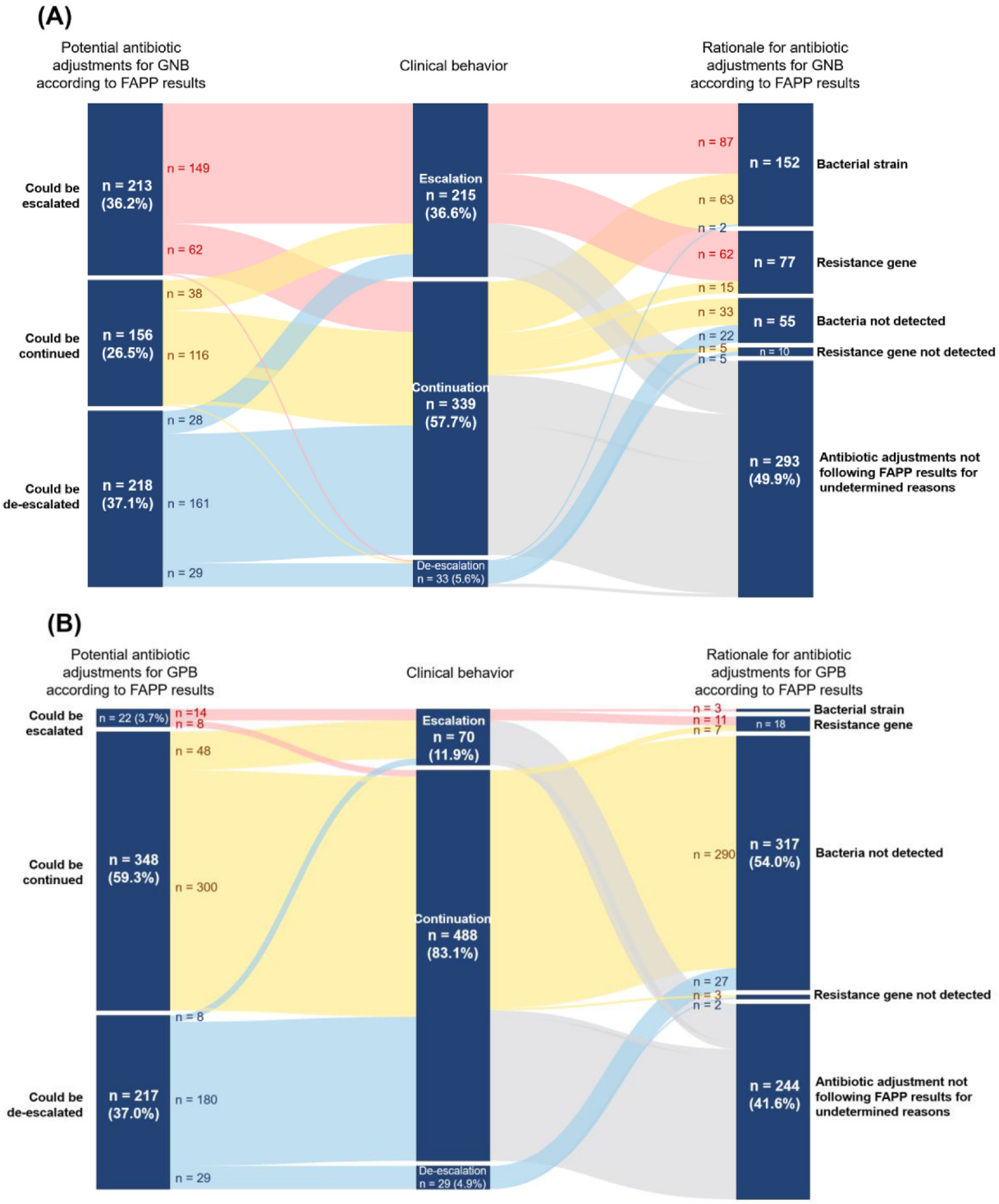

Figure 4. Sankey diagram of potential antibiotic adjustment and the real-world clinical behaviour following FilmArray® Pneumonia Panel results. (A) Gram-negative bacteria (GNB). (B) Gram-positive bacteria (GPB). The first column is the potential antibiotic adjustment according to the FAPP result. The second column is the real-world clinical behaviour following the FAPP result. The third column is the rationale of the antibiotic adjustment according to the FAPP result. Blue indicates antibiotic de-escalation, red indicates antibiotic escalation, and yellow indicates current antibiotic continuation. Grey represents switches not attributed to FAPP results, with reasons undetermined due to the retrospective design.

(n = 116) of empirical antimicrobial regimens. This confirmation was based on the detection of bacterial strains (n = 63), identified resistance genes (n = 15), the absence of bacteria requiring antimicrobial therapy adjustment (n = 33), and the absence of resistance genes (n = 5). A total of 29 patients underwent antibiotic de-escalation due to either the negative detection of bacteria or the absence of resistance genes. Furthermore, 343 (58.4%) antimicrobial regimens for GPB were confirmed or adjusted based on the FAPP results (Fig. 4B).

Discussion

This study is the first to focus on clinical factors predicting bacterial detection by FAPP in patients with HAP and VAP in the ICU. It is also the largest real-world study to date regarding clinical behaviour following FAPP results, including the rationale for antimicrobial therapy adjustment according to the detection of pathogens and resistance genes.

Our results showed that a hospital LOS exceeding 28 days, a history of hospital admission within 90 days, CRP level >6.6 mg/L, APACHE II score ≥25, and septic shock were independent predictors for bacterial detection by FAPP in patients with HAP and VAP in the ICU. Due to the severity of patients and the potential acquisition of MDROs, the use of rapid techniques such as FAPP is recommended because of the urgent necessity to initiate quick and appropriate antibiotic treatment in the ICU.[7,8] The IDSA Diagnostics Committee suggests that multiplex bacterial pneumonia panels may be most valuable in patients with deteriorating lung infiltrates, severe illness, prior use of empirical antibiotics before culture collection, or a risk of MDROs.[16] Previous studies have shown positive correlation between serum inflammatory markers and the detection of bacterial pathogens by FAPP.[17,18] However, no study has discussed the optimal timing for utilizing FAPP in the ICU according to patient risk factors and disease severity. Our findings provide a clearer understanding of the appropriate timing for the effective utilization of FAPP for bacterial detection in patients with HAP and VAP in the ICU.

Active cancer and ARDS were identified as negative predictors for bacterial detection by FAPP. These findings were unexpected based on the IDSA recommendations.[16] Subgroup analysis revealed a notably high presence of other pathogens in patients with ARDS and active cancer (Fig. S4B, S4C). This finding indicates that if FAPP yields a negative result, other pathogens, including PJ and CMV, may still play a significant role in infection in patients with active cancer and ARDS. In this context, negative FAPP results are still valuable in preventing the inappropriate use of broad-spectrum antibiotics. It is worth noting that these results could be influenced by selection bias, as clinical physicians may have conducted more extensive pathogen detection, including the use of FAPP, in these two patient groups.

We found that more than half Enterobacterales carried resistance genes and nearly 40% exhibited carbapenem resistance. Furthermore, among all the detected carbapenemase genes, 30% were MBLs. Although *S. aureus* was less frequently identified, over 50% of samples carried *mec*A/C and MREJ genes. The emergence of antimicrobial-resistant bacterial pathogens has led to an increasing health care burden.[19,20] While multiple factors assist clinicians in broad-spectrum antimicrobial therapy decisions, none are completely accurate, and fear of resistance drives excessive antibiotic use.[4] The mPCR tool FAPP addresses this challenge by targeting commonly encountered bacteria in HAP and VAP and antimicrobial resistance genes in clinical settings, including ESBL strains, carbapenem-resistant Enterobacterales, and MRSA. Although mPCR does not predict susceptibility or resistance to all antibiotics, the identification of the microorganism and resistance genes, along with knowledge of local epidemiology and information on resistance genes and the local genotype—phenotype correlation of common pathogens, can help guide semi-targeted antimicrobial therapy promptly. This approach reduces the initial reliance on empirical treatments for respiratory bacterial infections.[4,5,21,22]

Our data demonstrate that over half of the antimicrobial regimens were adjusted or confirmed based on the FAPP results. Previous studies have shown that mPCR could lead to antibiotic changes in 66—77% of cases, early initiation or escalation of effective antibiotics in 21—22% of cases, and antibiotic de-escalation or discontinuation in 39—48% of cases.[6,13,14] However, some of these studies did not classify pneumonia cases according to admission history. Additionally, none of these studies reported whether antimicrobial therapy adjustments were made based on the detection of pathogens or resistance genes by FAPP, which offers limited information for patients with HAP and VAP in the ICU. In this study, the majority of antimicrobial therapy adjustments for GNB following FAPP consisted of escalations (n = 149). These escalations were attributed to the detection of bacterial strains (n = 87) or resistance genes (n = 62). Importantly, these benefits were achieved in a shorter time compared to conventional pathogen surveys. In the case of GPB, the majority of antimicrobial regimens were confirmed by the absence of bacterial pathogen and resistance genes through FAPP, thus avoiding the unnecessary addition of antibiotics to cover drug-resistant GPB. This reveals that FAPP could provide valuable information for clinicians, increasing their confidence in confirming the empirical antimicrobial therapy. According to a previous study, negative FAPP results strongly correlated with the presence of normal flora in culture, and when combined with a thorough clinical assessment, they could offer clinicians valuable insights for potential antibiotic de-escalation or discontinuation.[23,24] However, it is essential to note that when considering de-escalation, the absence of detected resistance genes should not always be interpreted as phenotypic susceptibility.[6]

It is worth noting that in our study, the antimicrobial regimens remained unchanged after obtaining the FAPP results in 49.9% of GNB cases and 41.6% of GPB cases, respectively, even in the absence of detected bacteria or resistance genes. Several reasons may explain these observations. The disease severity and clinical instability of patients in the ICU are the main concerns. Additionally, a lack of knowledge and confidence in the test,[15] and the absence of antimicrobial stewardship guidelines in combination with FAPP, are also issues. This highlights the need for multidisciplinary team collaboration and local

antimicrobial treatment guidelines based on FAPP results, to assist clinical physicians in antimicrobial stewardship guided by FAPP. We provide insights into clinical algorithms (Fig. S5) for utilizing FAPP for HAP and VAP, with local antimicrobial resistance epidemiology, to maximize its benefits.

This study has several limitations. First, because it is a retrospective single-centre study, our findings may not be generalizable to other hospitals. Second, the researchers did not influence clinicians regarding antibiotic use; instead, antibiotic behaviours were retrospectively assessed through chart review, introducing the possibility of bias. Third, there were missing data concerning inflammatory markers other than CRP. This limitation hindered our ability to estimate the role of these markers in the context of FAPP usage. Fourth, we did not record the time from pneumonia symptom onset to respiratory sample collection, and the duration from sample collection to FAPP execution, but focused on determining how long clinical physicians take to receive the test results after submitting the clinical samples.

Conclusion

In conclusion, prolonged hospital stays, recent admissions, elevated CRP levels, high APACHE II scores, and septic shock were independent predictors of positive bacterial detection by FAPP. Rapid identification of the pathogen and resistance genes in patients with HAP/VAP can facilitate the prompt guidance of semi-targeted antimicrobial therapy in the ICU. More than 50% real-world clinical practices were adjusted or confirmed based on the FAPP results. Clinical algorithms for the use of FAPP and antimicrobial stewardship guidelines may further enhance its benefits.

Ethics statement

The institutional review board of China Medical University Hospital waived the requirement for written informed consent because the study involved minimal risk to the patients (IRB number: CMUH112-REC3-041).

Authors' contributions

CLC, HYT, YCL and PRH participated in study conception and design. CLC, HYT, WCC, and SJL participated in the acquisition of data. CLC, HYT, WCC, SJL, CYT, YCL and PRH participated in data analysis and interpretation. CLC, HYT, YCL, and PRH drafted the manuscript, with all authors revising it critically for intellectual content. All authors have read and approved the final version of the manuscript.

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Data availability statement

The data of this study are available on request from the corresponding author.

Declaration of competing interest

No conflicts exist for the specified authors.

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None.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.jmii.2024.02.010.