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CONTRIBUTION OF SYNDROMIC MULTIPLEX PCR FOR RESPIRATORY TRACT INFECTIONS AND MENINGOENCEPHALITIS: A RETROSPECTIVE STUDY FROM A MOROCCAN TERTIARY CARE CENTER

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ABSTRACT

Background: Syndromic multiplex polymerase chain reaction (PCR) assays provide rapid etiological orientation in infectious syndromes with non-specific clinical presentations. This study assessed the contribution of the BioFire FilmArray system to the diagnosis of respiratory tract infections and suspected meningitis/encephalitis in a Moroccan tertiary care center. **Methods:** This retrospective descriptive study included 299 FilmArray panels performed at the microbiology laboratory of the International University Hospital Cheikh Zaid, Rabat, between March 2020 and April 2022. Respiratory, pneumonia and meningitis/encephalitis panels were reviewed together with available conventional microbiological, biological and radiological data. **Results:** Among 218 respiratory panels, 62 were positive. Human rhinovirus/enterovirus was the leading respiratory pathogen, followed by SARS-CoV-2, respiratory syncytial virus and parainfluenza virus. Among 45 pneumonia panels, 17 were positive and most positive specimens were polymicrobial. Bacterial targets predominated over viral detections, mainly Staphylococcus aureus, Klebsiella pneumoniae and Haemophilus influenzae. Culture was performed in 14 positive FA-PN cases and recovered a bacterial pathogen in six. Resistance determinants were identified in several positive pneumonia panels, mainly CTX-M. Among 36 meningitis/encephalitis panels, nine were positive, with HSV-1, Listeria monocytogenes and Streptococcus pneumoniae as the main detections. **Conclusion:** FilmArray syndromic testing provided rapid broad-range pathogen detection and clinically useful resistance information. Its results, however, require careful clinicobiological interpretation and correlation with conventional microbiology.

KEYWORDS: BioFire FilmArray; syndromic diagnosis; multiplex PCR; respiratory tract infections; pneumonia panel; meningitis/encephalitis panel.

INTRODUCTION

Respiratory tract infections and central nervous system infections remain frequent diagnostic and therapeutic challenges in hospital practice. Their initial clinical presentation is often non-specific, and empirical antimicrobial therapy is commonly started before etiological confirmation. Conventional culture and antimicrobial susceptibility testing remain indispensable for bacterial infections, but they require technical expertise and usually take 24-72 h before a complete microbiological result is available. Their diagnostic yield may also be reduced by previous antimicrobial exposure, fastidious organisms or viral etiologies.

Syndromic multiplex PCR assays were developed to shorten this diagnostic interval by detecting several pathogens from a single specimen. The BioFire FilmArray platform combines nucleic acid extraction, amplification and detection in a closed automated system, with results generally available in about one hour. The respiratory panel targets pathogens involved in upper respiratory tract infections; the pneumonia panel is designed for lower respiratory tract specimens and includes selected resistance determinants; and the meningitis/encephalitis panel detects major viral, bacterial and fungal causes of acute central nervous system infection.

The FilmArray Pneumonia Panel has been evaluated in several clinical studies. Yoo et al. reported high sensitivity for bacterial detection and useful identification of resistance markers in sputum and endotracheal aspirates, with semi-quantitative bacterial loads helping interpretation.[1] Caméléna et al. also found high agreement between FilmArray Pneumonia Panel Plus and culture in intensive-care respiratory samples, while emphasizing that interpretation depends on specimen type and bacterial load thresholds.[2] Data from North African tertiary care settings remain scarce. This study therefore aimed to describe the real-world contribution of FilmArray syndromic panels to the diagnosis of upper respiratory tract infections, lower respiratory tract infections and meningoencephalitis in a Moroccan tertiary care center.

MATERIALS AND METHODS

Study design and setting

This retrospective descriptive study was conducted in the microbiology laboratory of the International University Hospital Cheikh Zaid (HUICZ), Rabat, Morocco. The study period extended from March 2020 to April 2022.

Study population and specimens

A total of 299 FilmArray tests were reviewed, including 218 FilmArray Respiratory Panels (FA-RP), 45 FilmArray Pneumonia Panels (FA-PN) and 36 FilmArray Meningitis/Encephalitis Panels (FA-ME). FA-RP was performed mainly on upper respiratory tract specimens. FA-PN was performed on lower respiratory tract samples, including bronchoalveolar lavage and distal protected respiratory samples. FA-ME was performed on cerebrospinal fluid specimens from patients with suspected meningitis or encephalitis.

Molecular testing

Testing was performed using BioFire FilmArray panels according to manufacturer recommendations and routine laboratory procedures. FA-RP detects respiratory viruses and atypical bacteria. FA-PN detects typical bacteria with semi-quantitative reporting in bins of approximately 10^4, 10^5, 10^6 and >=10^7 copies/mL for selected bacterial targets, in addition to respiratory viruses, atypical bacteria and resistance genes. FA-ME detects selected bacterial, viral and fungal pathogens responsible for central nervous system infections.

Conventional microbiology and biological data

Conventional culture, Gram stain, cytological examination, inflammatory markers and radiological data were reviewed when available. For FA-PN, culture results were compared with molecular detection and bacterial load whenever culture had been performed. For FA-ME, CSF cytology, proteinorachia, glycorrhachia, C-reactive protein, Gram stain, culture, procalcitonin and brain imaging findings were analyzed when available.

Statistical analysis

Descriptive statistics were used. Counts and percentages are provided in tables, while the text focuses on the main microbiological patterns. Quantitative variables are presented as means, medians and standard deviations when available from the original dataset. Because the number of positive results for individual organisms was limited, robust sensitivity, specificity and predictive values could not be calculated per pathogen.

RESULTS AND DISCUSSION

Results

Overall distribution of FilmArray panels

During the study period, 299 FilmArray panels were analyzed. FA-RP accounted for most tests, followed by FA-PN and FA-ME. The respiratory-panel cohort covered a wide age range, from infancy to 98 years, with a median age of 37 years and a slight male predominance. The pneumonia-panel cohort also showed a slight male predominance. FA-ME testing was performed in patients aged from 2 months to 85 years; most were hospitalized either in intensive care or medical wards, while a small number were external patients without available hospital records.

Table 1: Distribution and positivity of FilmArray panels included in the study.

Panel	n	Positive, n (%)	Negative, n (%)
FA-RP	218	62 (28.44%)	156 (71.55%)
FA-PN	45	17 (37.77%)	28 (62.23%)
FA-ME	36	9 (25.0%)	27 (75.0%)

FilmArray Respiratory Panel findings

Among the respiratory panels, 62 were positive. Positive FA-RP results were mostly observed in a community-acquired context, with only a small number classified as nosocomial. Pediatric patients accounted for the majority of positive panels, whereas adult positive results were comparatively uncommon. This distribution reflects the high burden of viral respiratory infections in children and the frequent use of multiplex respiratory testing in pediatric hospital practice.

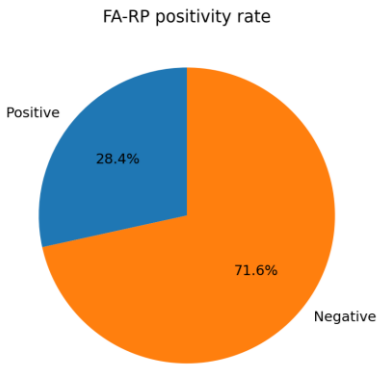

Figure 1: Positivity rate of the FilmArray Respiratory Panel (FA-RP).

Overall, 82 viral detections were recorded among positive FA-RP results, together with one atypical bacterial detection corresponding to Mycoplasma pneumoniae. Human rhinovirus/enterovirus (HREV) was the predominant pathogen and represented nearly half of all viral detections. SARS-CoV-2, respiratory syncytial virus (RSV) and parainfluenza virus followed, whereas adenovirus and influenza virus were less frequent. These findings indicate that the respiratory panel mainly documented viral etiologies, with HREV as the dominant pathogen throughout the cohort.

Table 2: Pathogens detected by the FilmArray Respiratory Panel.

Pathogen	n	Proportion among viral detections
Human rhinovirus/enterovirus	39	47.56%
SARS-CoV-2	12	14.63%
Respiratory syncytial virus	11	13.41%
Parainfluenza virus	10	12.19%
Adenovirus	7	8.53%
Influenza virus	3	3.63%

The distribution of respiratory pathogens differed substantially across age groups. Children younger than two years showed the highest diagnostic yield of the FilmArray Respiratory Panel, whereas positivity progressively declined with increasing age and reached its lowest level among adults. HREV predominated across all age categories and represented the largest share of detections in young children, confirming its major contribution to acute respiratory tract infections encountered in routine clinical practice. RSV was detected mainly in pediatric patients, particularly among children younger than five years, in keeping with its recognized role as a leading cause of respiratory morbidity and hospitalization in infancy. Adenovirus and parainfluenza virus were also mainly identified in children, whereas influenza virus remained relatively uncommon throughout the study period. SARS-CoV-2 displayed a distinct age distribution, with detections distributed across pediatric and adult groups in the context of the COVID-19 pandemic. Only sporadic detections of atypical bacterial pathogens were observed. Overall, the age-stratified analysis highlights the higher burden of respiratory viral infections in pediatric patients and the particularly high diagnostic yield of multiplex respiratory testing in this population.

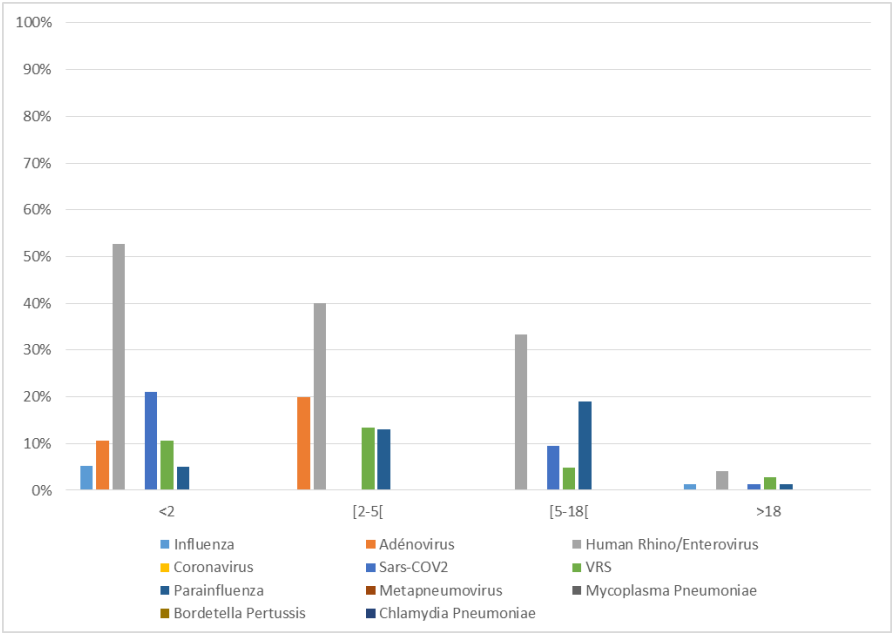

Figure 2: Distribution of respiratory pathogens per age group.

Table 3: Age-stratified FA-RP positivity and infection pattern.

Age group	Panels, n	Positive, n (%)	Negative, n (%)	Mono-infection	Co-infection
<2 years	38	30 (78.9%)	8 (21.1%)	73.3% of positives	26.7% of positives
[2-5[years	15	8 (53.3%)	7 (46.7%)	4/8	4/8
[5-18[years	21	9 (42.9%)	12 (57.1%)	6/9	3/9
>=18 years	144	15 (10.4%)	129 (89.6%)	14/15	1/15

Infection patterns also varied according to age. Mono-infections predominated across all age groups; however, co-infections were more frequent among pediatric patients. Children younger than two years and those aged 2-5 years showed the greatest proportion of co-detections, whereas multiple-pathogen detection became progressively less common with increasing age and was exceptional among adults. In parallel, the proportion of negative respiratory panels increased steadily across age categories, rising from approximately one fifth of tests in children younger than two years to nearly 90% among adults. This progressive increase in negative results was accompanied by a decline in both mono-infections and co-infections, confirming the much higher diagnostic yield of FA-RP in children. The difference observed between children younger than two years and those aged 2-5 years reached statistical significance ($p = 0.002$), whereas no significant difference was observed between the 2-5-year and 5-18-year groups ($p = 0.53$). The comparison between adolescents and adults showed a trend toward significance ($p = 0.082$). These findings suggest that younger children are not only more frequently infected by respiratory pathogens, but are also more likely to harbor multiple viral agents simultaneously.

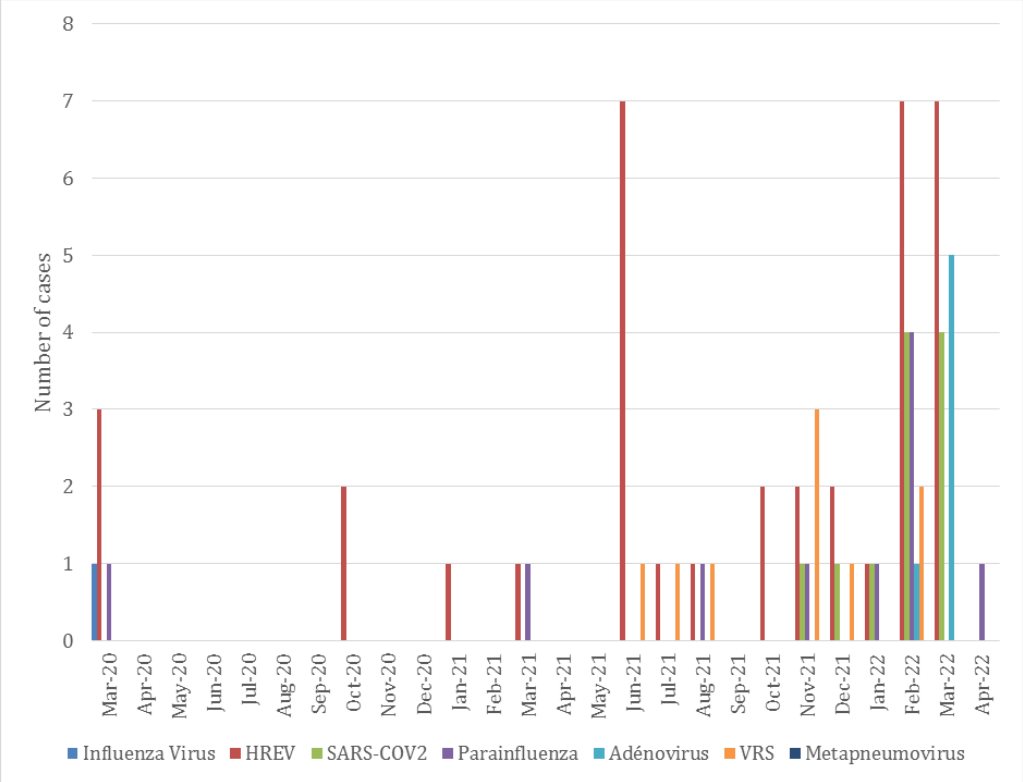

Figure 3: Distribution of respiratory pathogens detected by FA-RP between March 2020 and April 2022.

The temporal distribution of FA-RP detections showed sustained HREV circulation over the study period, with several peaks during summer and late winter months. Adenovirus detections were concentrated mainly in February, while RSV showed peaks in November and February, with occasional lower-level detections outside the usual winter period. This pattern illustrates the epidemiological value of the respiratory panel beyond individual diagnosis, as it allowed visualization of local viral circulation over time. Co-infections represented an important component of positive FA-RP results. HREV was present in all co-infected specimens, most frequently in association with parainfluenza virus, followed by RSV and adenovirus. The predominance of HREV in co-detections suggests that it may act as a frequent background respiratory virus in pediatric respiratory illness, although the clinical contribution of each pathogen must be interpreted according to symptoms, viral load when available and associated radiological findings.

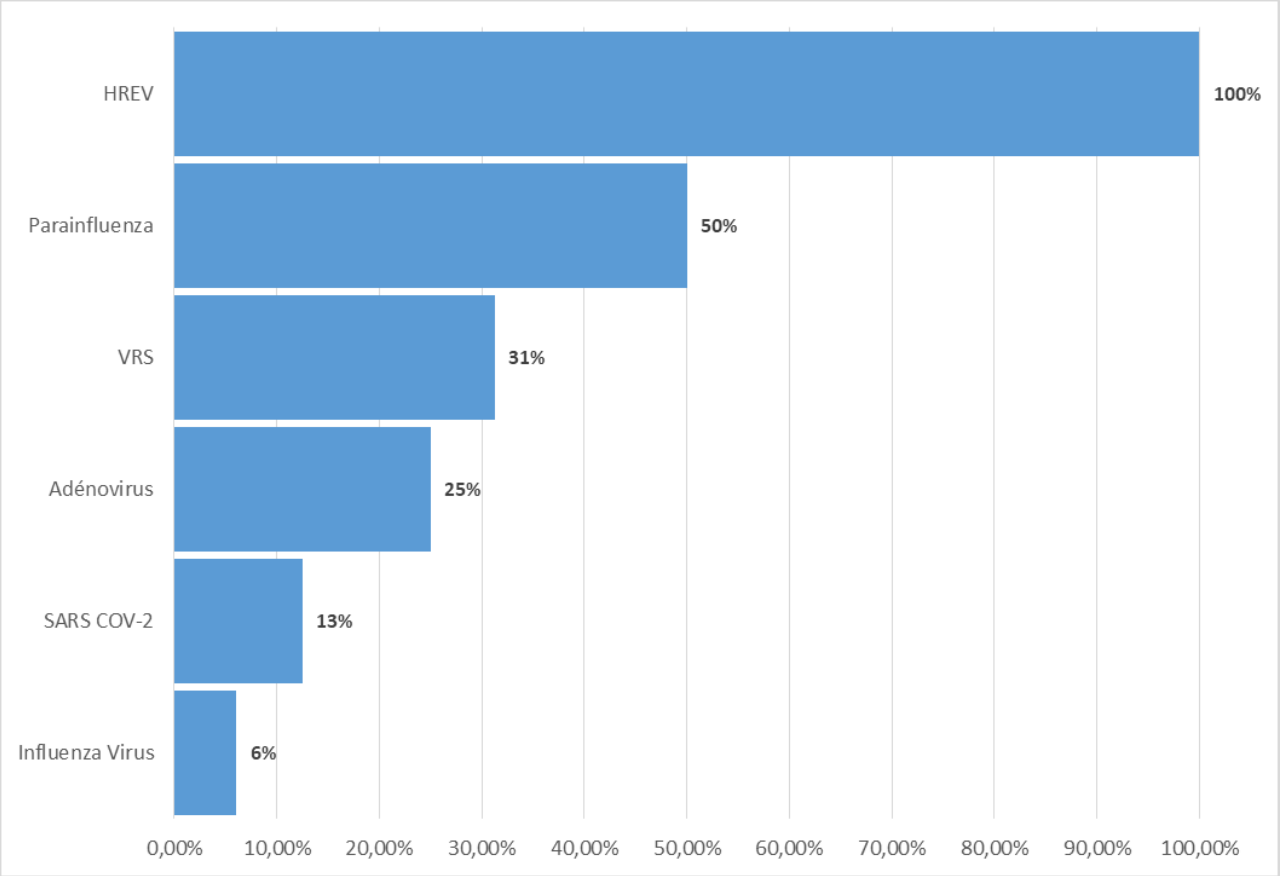

Figure 4: Frequency of pathogens involved in FA-RP co-infections.

Table 4: Pathogens involved in FA-RP co-infections.

Pathogen involved in co-infection	n	Proportion among co-infections, %
HREV	16	100.00%
Parainfluenza virus	8	50.00%
RSV	5	31.25%
Adenovirus	4	25.00%
SARS-CoV-2	2	12.50%
Influenza virus	1	6.25%

Available clinical data supported the respiratory relevance of many positive FA-RP results. Chest imaging was performed in 28 positive cases, and most examinations showed abnormalities compatible with pulmonary involvement. Ground-glass opacities were reported in several abnormal examinations, while the remaining abnormal imaging results were described as other signs of pneumopathy. C-reactive protein was available in 31 positive cases and was elevated in more than half of them.

Complete blood count was available in 32 positive cases. Hyperleukocytosis was observed in most of these patients and was usually associated with neutrophilic predominance. These findings emphasize that, although FA-RP mainly detected viral pathogens, positive results frequently occurred in patients with inflammatory or radiological abnormalities. The molecular result should therefore be interpreted as part of a broader clinicobiological assessment rather than as an isolated virological finding.

The distribution of requesting departments reflected the population in which FA-RP was most clinically useful. Pediatric departments accounted for most positive requests, particularly the pediatric cardiovascular surgery unit. Adult intensive care units, medical wards, COVID isolation and outpatient requests represented smaller proportions. This distribution likely contributed to the strong pediatric signal observed in the FA-RP results and should be considered when interpreting the overall viral epidemiology of the cohort.

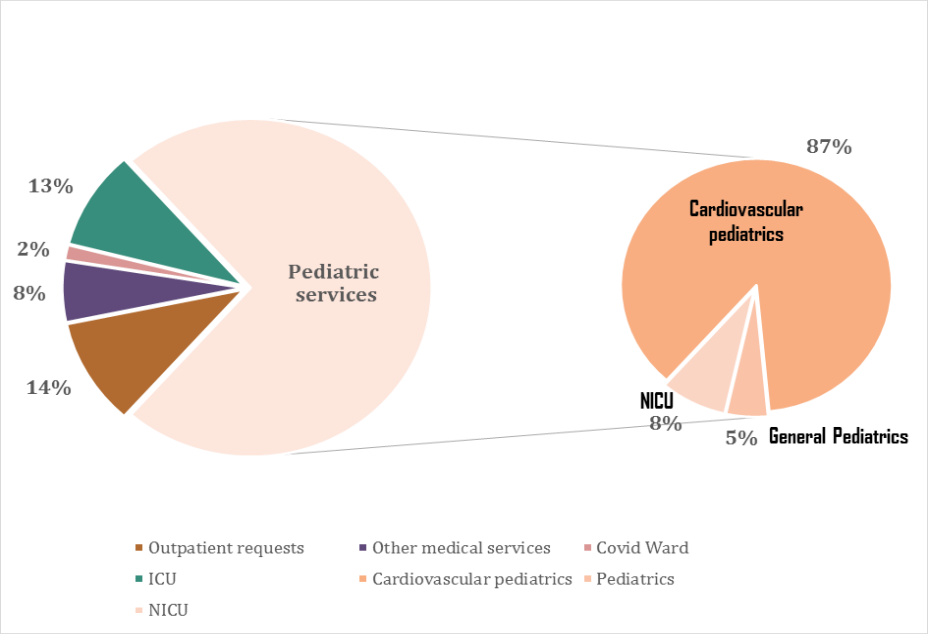

Figure 5: Distribution of positive FA-RP requests according to hospital department.

Table 5: Positive FA-RP requests according to hospital department.

Department category	Positive requests, n	Proportion
Pediatric departments	39	63%
Adult intensive care units	8	13%
Medical wards	5	8%
COVID isolation unit	1	2%
Outpatient requests	9	14%

FilmArray Pneumonia Panel findings

Forty-five lower respiratory tract specimens were analyzed using FA-PN. Seventeen specimens yielded at least one target. Most positive specimens were polymicrobial, whereas only a minority were monomicrobial. This pattern is common in lower respiratory tract samples from hospitalized or intensive-care patients, but it also complicates interpretation because molecular detection may reflect true infection, colonization or residual nucleic acid after antimicrobial exposure.

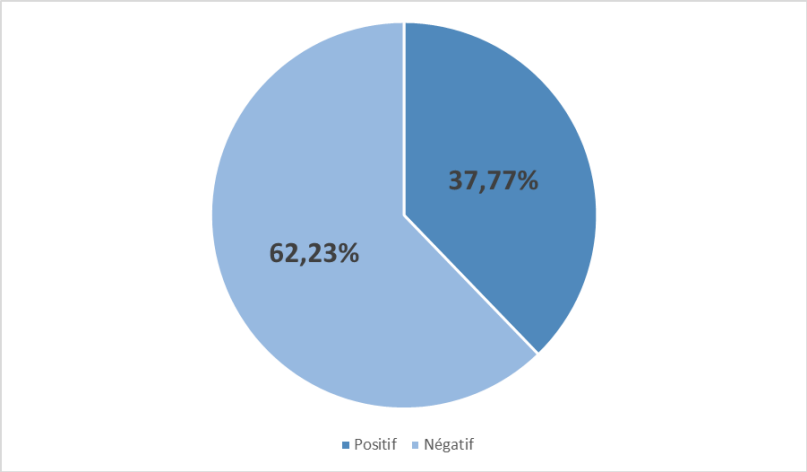

Figure 6: Positivity rate of the FilmArray Pneumonia Panel (FA-PN).

FA-PN identified 44 organisms overall. Bacterial targets predominated over viral detections. Staphylococcus aureus was the most frequent bacterial target, followed by Klebsiella pneumoniae and Haemophilus influenzae. Serratia marcescens, Acinetobacter baumannii complex, Escherichia coli, Pseudomonas aeruginosa, Moraxella catarrhalis, Enterobacter cloacae complex and Streptococcus pyogenes were also detected. This distribution differs from ICU-focused studies in which Pseudomonas aeruginosa or Acinetobacter baumannii

may predominate, underlining the influence of local epidemiology, sample type and patient recruitment on syndromic molecular findings.

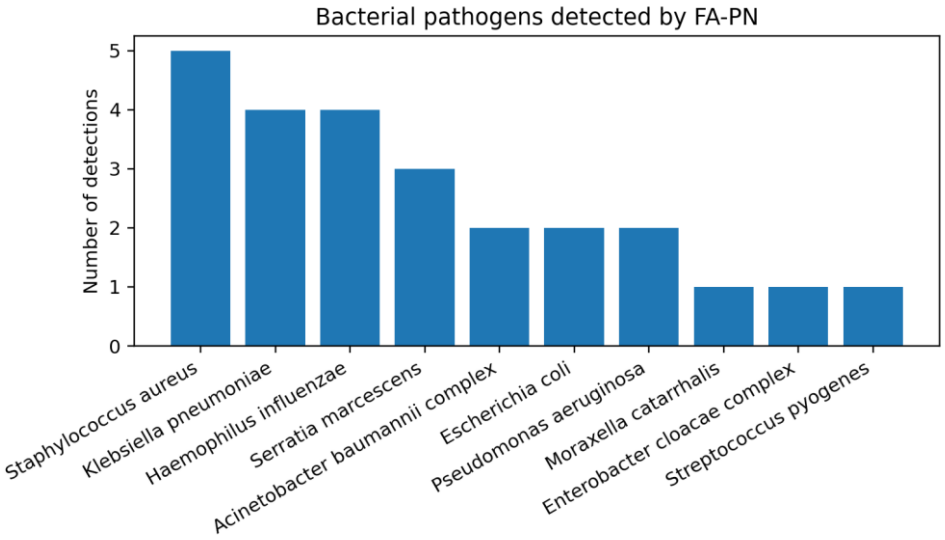

Figure 7: Bacterial pathogens detected by FA-PN.

Table 6: Bacterial pathogens detected by FA-PN.

Bacterial pathogen	n	Proportion among bacteria, %
Staphylococcus aureus	5	20.00%
Klebsiella pneumoniae	4	16.00%
Haemophilus influenzae	4	16.00%
Serratia marcescens	3	12.00%
Acinetobacter baumannii complex	2	8.00%
Escherichia coli	2	8.00%
Pseudomonas aeruginosa	2	8.00%
Moraxella catarrhalis	1	4.00%
Enterobacter cloacae complex	1	4.00%
Streptococcus pyogenes	1	4.00%

Viral detections by FA-PN were led by HREV, followed by human metapneumovirus, adenovirus and parainfluenza virus. Non-SARS-CoV-2 coronavirus, RSV and influenza virus were detected only sporadically. The presence of respiratory viruses in lower respiratory tract specimens highlights the value of syndromic testing in patients with severe respiratory presentations, where viral and bacterial etiologies may overlap or coexist.

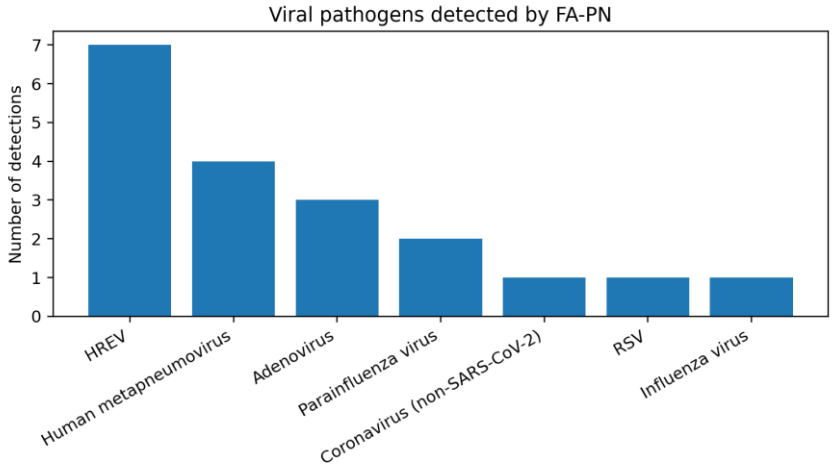

Figure 8: Viral pathogens detected by FA-PN.

Table 7: Viral pathogens detected by FA-PN.

Viral pathogen	Detections, n	Proportion among viruses
HREV	7	36.84%
Human metapneumovirus	4	21.05%
Adenovirus	3	15.79%
Parainfluenza virus	2	10.53%
Coronavirus (non-SARS-CoV-2)	1	5.26%
RSV	1	5.26%
Influenza virus	1	5.26%

Conventional culture was performed in most positive FA-PN cases and recovered a bacterial pathogen in six. The lower culture positivity compared with molecular detection is clinically relevant. It may reflect previous antimicrobial exposure, low bacterial burden, fastidious organisms or detection of non-viable bacteria. Conversely, culture remains indispensable because it confirms viable pathogens and provides phenotypic antimicrobial susceptibility testing.

Table 8: Correlation between positive FA-PN bacterial detections and culture results.

Targets and FA-PN bacterial load	Culture	Organism(s) found on culture
Klebsiella pneumoniae 10^5; Serratia marcescens 10^4	Positive	Klebsiella pneumoniae
Enterobacter cloacae 10^6; Moraxella catarrhalis 10^5	Positive	Enterobacter cloacae
Klebsiella pneumoniae 10^4	Positive	Klebsiella pneumoniae
Acinetobacter baumannii 10^7	Positive	Acinetobacter baumannii
Acinetobacter baumannii 10^7	Positive	Acinetobacter baumannii
Staphylococcus aureus 10^7	Positive	Staphylococcus aureus
Serratia marcescens 10^5	Negative	None
Escherichia coli 10^5; Enterobacter cloacae 10^4	Negative	None
Haemophilus influenzae 10^5; Staphylococcus aureus 10^5; Klebsiella pneumoniae 10^4	Negative	None

Semi-quantitative bacterial load was closely related to culture positivity. All bacteria detected at the highest molecular loads grew in culture, whereas culture positivity decreased markedly for detections at 10^4 and 10^5 copies/mL. Mean and median copy numbers were also higher in culture-positive than in culture-negative cases. These findings support the use of bacterial load as an interpretative aid, while confirming that no molecular threshold can define infection independently of clinical, radiological and microbiological context.

Table 9: Culture positivity according to FA-PN semi-quantitative bacterial load.

FA-PN bacterial load	Bacterial detections, n	Culture-positive, n/N	Culture positivity
>=10^7 copies/mL	3	3/3	100%
10^6 copies/mL	1	1/1	100%
10^5 copies/mL	5	1/5	20%
10^4 copies/mL	4	1/4	25%

Table 10: Distribution of FA-PN quantification according to culture result.

Culture result	n	Mean copies/mL	Median	Standard deviation	p-value
Culture-positive bacteria	6	5.18 x 10^6	5.50 x 10^6	5.29 x 10^6	0.063
Culture-negative bacteria	8	55,000	55,000	48,107	0.035

Resistance determinants were identified in several positive FA-PN specimens. CTX-M was the most frequent marker and was mainly associated with Klebsiella pneumoniae detections; available culture and antimicrobial susceptibility testing confirmed an ESBL phenotype in corresponding isolates. mecA was detected with Staphylococcus aureus and was phenotypically consistent with methicillin-resistant S. aureus. NDM and OXA-48-like carbapenemase markers were also detected. These findings illustrate the potential value of early molecular resistance detection, particularly in settings where multidrug-resistant organisms may compromise empirical therapy. Nevertheless, resistance markers should always be interpreted together with culture and **Antimicrobial Susceptibility Testing** whenever possible.

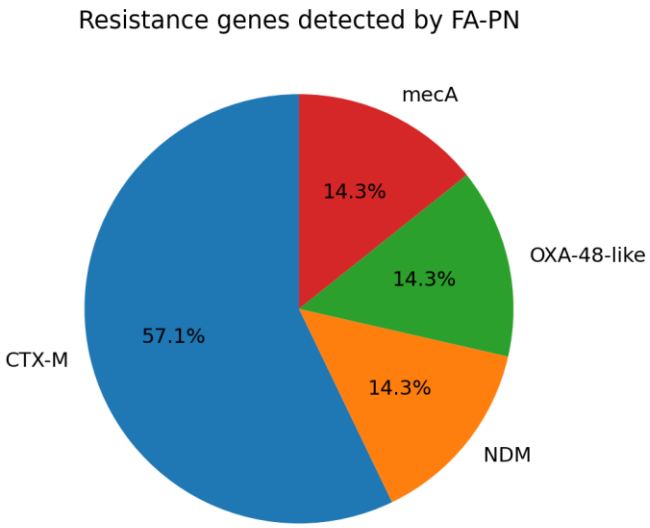

Figure 9: Resistance genes detected by FA-PN.

Table 11: Antimicrobial resistance genes detected by FA-PN.

Resistance gene	Detections, n	Proportion among resistance genes
CTX-M	4	57.14%
NDM	1	14.28%
OXA-48-like	1	14.28%
mecA	1	14.28%

Pulmonary imaging was available for a subset of patients who underwent FA-PN testing. Most available examinations showed abnormalities compatible with pulmonary involvement, indicating that FA-PN was generally requested in clinically meaningful respiratory presentations. However, the presence of normal imaging in some patients reinforces the need to interpret molecular results in relation to clinical probability and radiological findings.

FilmArray Meningitis/Encephalitis Panel findings

Thirty-six CSF specimens were analyzed using FA-ME, and nine panels were positive. Positive detections included both viral and bacterial pathogens. Viral pathogens slightly predominated, with HSV-1 as the leading viral target, followed by HHV-6, enterovirus and varicella-zoster virus. Among bacterial detections, Listeria monocytogenes and Streptococcus pneumoniae were each identified in two cases, while Haemophilus influenzae was detected once. One positive result included co-detection of Streptococcus pneumoniae and Haemophilus influenzae; this result was interpreted cautiously because bacterial co-detection in CSF may suggest contamination in some circumstances.

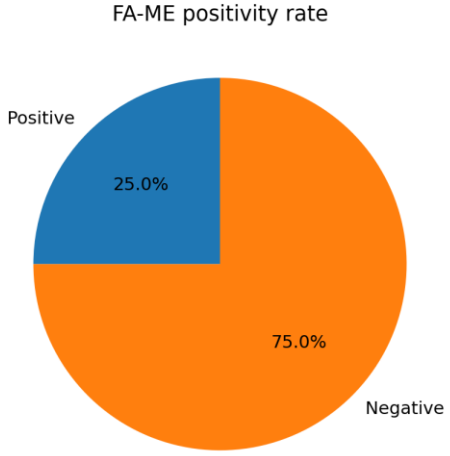

Figure 10: Positivity rate of the FilmArray Meningitis/Encephalitis Panel (FA-ME).

Table 12: Pathogens detected by FA-ME.

Pathogen	n
HSV-1	**3**
HHV-6	**1**
Enterovirus	**1**
Varicella-zoster virus	**1**
Listeria monocytogenes	**2**
Streptococcus pneumoniae	**2**
Haemophilus influenzae	**1**

The availability of biological parameters varied across patients, resulting in different sample sizes for each analysis (Table 13). Cytological examination results were available for 36 patients, including 9 with a positive FA-ME result and 27 with a negative result. Protein concentration measurements were available for 32 patients (7 FA-ME positive and 25 FA-ME negative), whereas serum CRP values were available for 35 patients (9 FA-ME positive and 26 FA-ME negative).

Patients with a positive FA-ME result exhibited significantly higher CSF cellularity than those with a negative molecular panel. The mean leukocyte count reached 273.6 cells/mm³ in the positive group compared with 115.6 cells/mm³ in the negative group (p = 0.004). Median values showed a similar trend, suggesting a stronger inflammatory response among patients with documented pathogens.

Likewise, cerebrospinal fluid protein concentrations were significantly higher in FA-ME-positive patients. The mean protein level was 2.99 g/L compared with 0.63 g/L in patients with negative molecular results (p = 0.008). These findings are consistent with the presence of blood–brain barrier disruption and meningeal inflammation in patients with microbiologically confirmed central nervous system infection.

In contrast, no significant difference was observed for serum CRP concentrations between positive and negative FA-ME groups (p = 0.569). Although CRP values displayed substantial variability, systemic inflammatory response did not appear to be associated with molecular pathogen detection in cerebrospinal fluid.

Overall, positive FA-ME results were associated with significantly increased CSF cellularity and protein concentrations, whereas CRP levels did not differ significantly between the two groups.

Table 13: Inflammatory and biochemical parameters according to FA-ME result.

Parameter	Results FA/ME	n	Mean	Median	Standard deviation	p-value
Cytology elements/mm3	positive	9	273.56	180.00	301.40	0.004
	Negative	27	115.630	0.000	441.266	
Proteinorrachia (g/L)	positive	7	2.99	1.46	4.09	0,008
	Negative	25	0.626	0.480	0.544	
CRP (mg/L)	positive	9	36.11	11.90	47.46	0,569
	Negative	26	85.581	12.700	137.492	

Direct examination and culture were positive in two positive FA-ME specimens, both corresponding to Listeria monocytogenes. Gram stain showed Gram-positive bacilli, concordant with molecular detection, which strengthened the clinical significance of these results. Pneumococcal detections were more difficult to interpret because Gram stain and culture were not contributory in the available data. This point is important because false-positive pneumococcal FA-ME results have been reported, particularly in relation to pre-analytical contamination. Clinicobiological correlation therefore remains essential for bacterial FA-ME detections.

Table 14: Clinical and biological correlation of the positive FA-ME results.

Pathogen detected	CSF cytology	Glycorrhachia	Proteinorachia	CRP	Gram stain	Culture	PCT	Infection type	Imaging
Listeria monocytogenes	520 (80% lymphocytes, 20% PMN)	0.37	1.46	1.1	Gram-positive bacilli	+	NA	Co-infection	Normal
Listeria monocytogenes	266 (78% lymphocytes, 15% monocytes, 7% PMN)	0.18	1.39	311	Gram-positive bacilli	+	2.05	Mono-infection	Normal
HHV-6	109 (90% lymphocytes, 10% PMN)	0.15	2.56	23	0	0	<0.5	Mono-infection	Suggestive
HSV-1	190 (35% lymphocytes,	0.63	0.59	11.9	0	0	<0.5	Mono-infection	NA

	65% PMN)								
HSV-1	18 (75% lymphocytes, 25% PMN)	0.65	3	125	0	0	<0.5	Mono-infection	Suggestive
HSV-1	180 (90% lymphocytes, 10% PMN)	0.61	0.67	80	0	0	<0.5	Mono-infection	Suggestive
Enterovirus	600 (80% lymphocytes, 20% PMN)	0.75	0.68	28	0	0	<0.5	Mono-infection	NA
VZV	520 (80% lymphocytes, 20% PMN)	0.37	1.46	1.1	Gram-positive bacilli	+	NA	Co-infection	Normal
Streptococcus pneumoniae	830 (80% PMN, 20% lymphocytes)	0.63	12	84	0	0	<0.5	Mono-infection	Suggestive
Streptococcus pneumoniae + H. influenzae	NA	NA	NA	NA	NA	NA	NA	Co-infection	NA

DISCUSSION

This study provides an overview of BioFire FilmArray syndromic testing in a Moroccan tertiary care center, covering upper respiratory tract infections, lower respiratory tract infections and suspected meningoencephalitis. The contribution of the platform was not limited to pathogen identification. It also documented co-infections, seasonal viral circulation, semi-quantitative bacterial load and selected resistance determinants. At the same time, the study highlights a central limitation of syndromic molecular diagnostics: a positive result is not equivalent to a clinical diagnosis and must be interpreted according to specimen type, clinical presentation, radiology, cytology and conventional microbiological findings.

For upper respiratory tract infections, FA-RP had its highest yield in pediatric patients, particularly in children younger than two years. This age gradient is clinically plausible because young children are exposed frequently to respiratory viruses and have immature or still-developing immune responses. HREV was the dominant respiratory pathogen across age groups and was also present in all co-infections, supporting its central role in acute respiratory tract infections and in exacerbations of lower airway disease. RSV detections were mainly pediatric and showed winter peaks, consistent with established RSV epidemiology. SARS-CoV-2 detections reflected the pandemic context of the study period and the overlap between routine respiratory viral testing and COVID-era screening.

The strong representation of pediatric departments among positive FA-RP requests is important for interpretation. It suggests that the panel was mainly used for acute respiratory presentations in children rather than for nosocomial outbreak investigations. This recruitment pattern likely contributed to the high proportion of viral detections, the predominance of HREV and the frequency of co-infections. The presence of abnormal imaging or inflammatory markers in many positive cases also shows that viral detection does not necessarily correspond to mild disease. Viral respiratory infections may be associated with radiological pneumonia, bacterial superinfection or decompensation of underlying cardiopulmonary disease, particularly in children with complex hospital backgrounds.

For lower respiratory tract infections, FA-PN yielded positive results in a clinically relevant proportion of specimens, with bacterial targets predominating over viral detections. The bacterial spectrum was led by Staphylococcus aureus, Klebsiella pneumoniae, Haemophilus influenzae and Serratia marcescens, with additional detections of Acinetobacter baumannii complex, Escherichia coli and Pseudomonas aeruginosa. This profile differs from the cohort of Yoo et al., in which Acinetobacter calcoaceticus-baumannii complex, Pseudomonas aeruginosa and Staphylococcus aureus were the most frequent concordant pathogens.[1] It also differs from ICU-focused cohorts, where Pseudomonas aeruginosa often predominates.[2] These differences probably reflect local epidemiology, specimen type, case mix and the inclusion of both ICU and non-ICU patients in the present series.

The semi-quantitative bacterial load provided by FA-PN was one of the most informative elements of the pneumonia-panel analysis. In this cohort, culture positivity was concentrated among detections with higher molecular loads, whereas lower loads were less consistently associated with bacterial growth. This gradient is consistent with Yoo et al., who reported that most bacteria detected at >=10^6 copies/mL also yielded significant growth in culture.[1] Caméléna et al. further emphasized that clinically meaningful interpretation of bacterial quantification depends on specimen type, with different thresholds for sputum, blind bronchoalveolar lavage and protected specimen brush samples.[2] In routine practice, bacterial load should therefore guide

interpretation but should not be used as an isolated diagnostic threshold.

Discordance between molecular detection and culture was expected in some cases. Culture may be negative after antimicrobial exposure, when bacterial burden is low, or when organisms are fastidious or non-viable. Molecular assays may therefore identify pathogens missed by culture. Conversely, PCR may detect colonization or residual nucleic acid without proving active infection. This issue is particularly important for polymicrobial lower respiratory specimens, which were frequent in the present series. Culture and AST remain essential complements to FA-PN, especially when antimicrobial therapy is being escalated, narrowed or discontinued.

Resistance gene detection was clinically relevant. CTX-M predominated and was mainly associated with Klebsiella pneumoniae; available culture and AST confirmed ESBL-producing K. pneumoniae in corresponding cases. NDM, OXA-48-like and mecA were also detected. These results are important in a tertiary-care setting where multidrug-resistant organisms may rapidly compromise empirical therapy. However, resistance-marker interpretation has limits. As reported by Yoo et al., a resistance gene detected in a polymicrobial sample cannot always be assigned with certainty to a specific organism.[1] Caméléna et al. also emphasized that the absence of a detected resistance gene does not guarantee susceptibility, because mechanisms outside the panel may be present.[2] Molecular resistance results should therefore accelerate early decision-making but not replace phenotypic AST.

The FA-ME results provide an additional illustration of the value of syndromic molecular testing in urgent infectious syndromes. The positivity rate among CSF specimens reflected a selected population with suspected central nervous system infection. HSV-1 was the most frequent viral pathogen, and several HSV-1 detections were supported by CSF pleocytosis, elevated proteinorachia and imaging findings suggestive of encephalitis. Rapid identification is clinically important because delayed acyclovir treatment in herpes simplex encephalitis is associated with poor neurological outcome. Enterovirus and VZV detections also support the role of FA-ME in viral CNS infections, where conventional culture is generally not useful.

Bacterial FA-ME detections required closer clinicobiological interpretation. The two Listeria monocytogenes detections were strongly supported by conventional microbiology, as both had positive culture and Gram-positive bacilli on direct examination. Pneumococcal detections were less straightforward. One case showed marked neutrophilic pleocytosis and very high proteinorachia compatible with bacterial meningitis, despite negative culture. Another pneumococcal detection occurred with Haemophilus influenzae and lacked sufficient supporting data, raising the possibility of contamination or a control-sample issue. This reinforces the need to interpret FA-ME results with CSF cytology, biochemistry, Gram stain, culture and clinical context.

This study has several strengths. It describes the implementation of multiple FilmArray syndromic panels in a Moroccan tertiary-care context and provides local epidemiological data across respiratory and neurological syndromes. It also links molecular findings with available culture, inflammatory markers, cytology and imaging, which is essential for interpreting positive PCR results. The main limitations are the retrospective design, incomplete clinical data in some cases and the limited number of positive results for individual pathogens, particularly for FA-PN and FA-ME. For this reason, robust per-pathogen diagnostic performance could not be calculated. The study also did not assess clinical impact on antimicrobial escalation or de-escalation, length of stay or outcomes.

Overall, the data support FilmArray as a rapid and clinically useful adjunct to conventional microbiology. Its greatest value lies in early broad-spectrum pathogen detection, rapid recognition of selected resistance markers and improved etiological orientation in syndromes where empirical therapy is common. Its limitations are equally important: cost, restricted target range, possible over-detection, difficulty distinguishing colonization from infection in respiratory samples and the continued need for culture and AST. Rational prescription and multidisciplinary interpretation are therefore necessary to maximize clinical benefit.

CONCLUSION

In this retrospective Moroccan tertiary-care experience, BioFire FilmArray syndromic panels contributed to the etiological diagnosis of respiratory tract infections and suspected meningoencephalitis. FA-RP mainly documented pediatric viral respiratory infections, with HREV as the predominant pathogen and frequent co-infections in younger children. FA-PN provided rapid detection of lower respiratory bacterial and viral pathogens, semi-quantitative bacterial load information and early resistance-marker identification. FA-ME enabled rapid diagnosis of viral and bacterial CNS infections, particularly HSV-1 and Listeria monocytogenes, but required careful clinicobiological correlation. FilmArray should be considered a complementary tool that accelerates microbiological orientation and supports antimicrobial stewardship, while conventional culture, AST and clinical interpretation remain indispensable.

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CONFLICTS OF INTEREST
The author declares no conflict of interest.

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