# Comparison of a molecular multiplex lower respiratory tract (pneumonia) panel to conventional culture: potential enhancement of antimicrobial management in hospitalized patients

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## Background/Introduction

Rapid and accurate identification of pathogens causing lower respiratory tract infections is crucial for patient management. Identification using traditional diagnostic methods typically takes 2-3 days or longer and clinicians must rely on the clinical diagnosis to guide initial antimicrobial therapy which is often broad spectrum. The BioFire FilmArray Pneumonia Panel (Investigational Use Only) is a multiplexed nucleic acid amplification test that provides results in one hour. The assay identifies 33 bacterial and viral targets, including antimicrobial resistance genes from sputum or bronchioalveolar lavage (BAL) specimens. We evaluated the pneumonia panel using these specimens in addition to bronchial wash (BW) specimens. We compared these results to conventional culture to assess the potential for earlier initiation of more pathogen-specific therapy.

## Methods

The study was a non-randomized evaluation of the pneumonia panel conducted at three laboratories within the Sanford Health System. A total of 144 lower respiratory tract specimens including sputa, BAL and BW were tested using both the pneumonia panel and routine Gram stain and culture. Patient management was assessed by reviewing the medical record. Based on this review, we identified potential antimicrobial therapy interventions including escalation, de-escalation or no change.

## Results

Of the 144 specimens tested, a change in management was likely in 103 (71.5%) of cases. Management would have remained the same in 41 (28.5%) cases (Fig. 1). Of those where a change in management was likely, escalation of antimicrobial therapy would have occurred in 33 (22.9%) of cases (Fig. 1). De-escalation would have occurred in 70 (48.6%) of cases (Fig. 1). The pneumonia panel was also compared with culture for concordance (Fig. 2). The pneumonia panel identification matched the culture identification in 71 specimens (47%) (Fig. 2). The pneumonia panel detected additional pathogens in 57 specimens (37.5 %) (Fig. 2). Twelve (7.9%) specimens grew organisms that were not included in the panel (Fig. 2).

In addition, the pneumonia panel identification was compared to the potential patient management decision (Fig. 3). An identification of one of the Gram-negative enteric organisms was most likely to be associated with potentially no change in empiric therapy, while an identification of *Pseudomonas aeruginosa* was most likely to require potential escalation of therapy (Fig. 3). An identification of a respiratory virus was most likely to be associated with potentially de-escalating therapy (Fig. 3).

One complication of predicting patient management is that the panel identified more than one potential pathogen approximately 38% of the time (Fig. 4). For 19% of specimens, the panel identified at least 3 potential pathogens.

Figure 1. Patient Management (n=144)

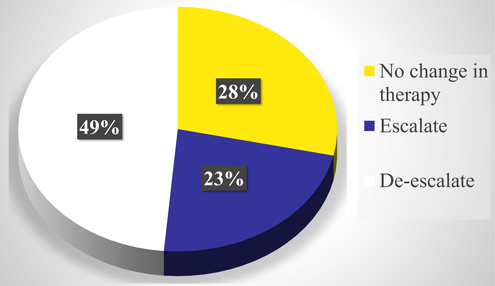



Figure 2. Panel correlation to culture

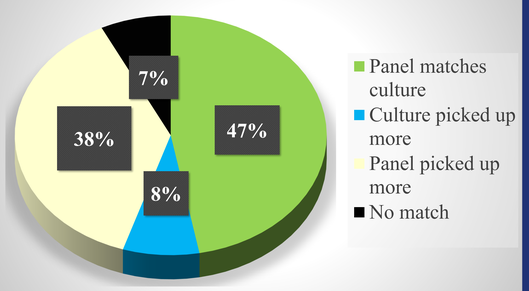
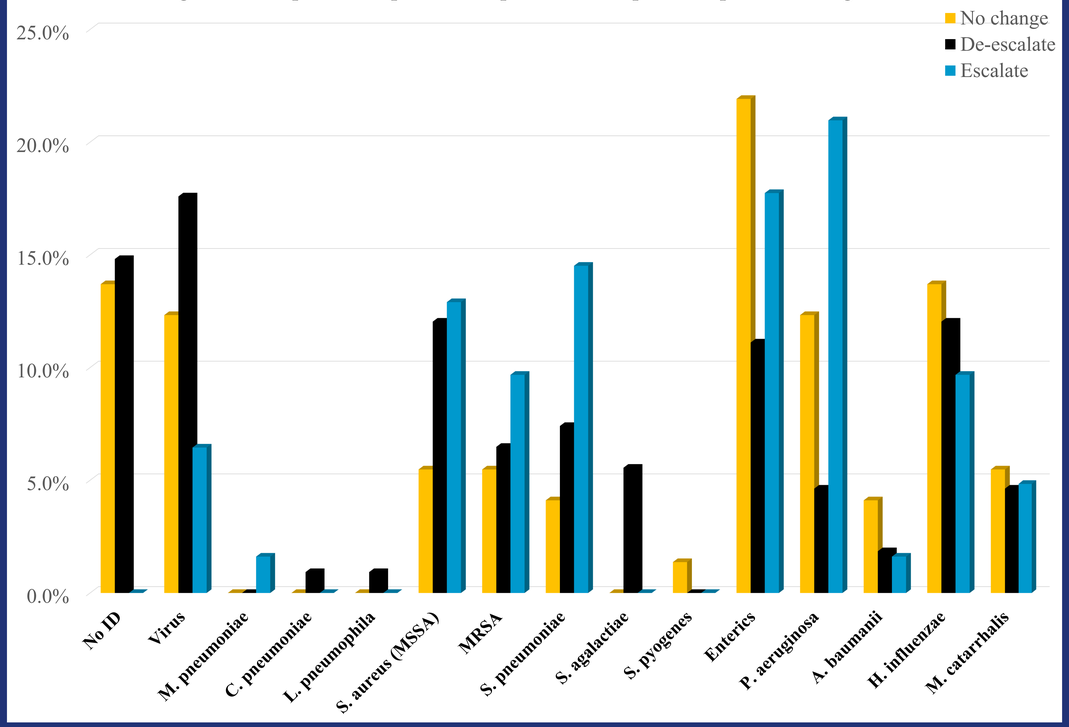



Figure 3. Comparison of pneumonia panel ID with potential patient management

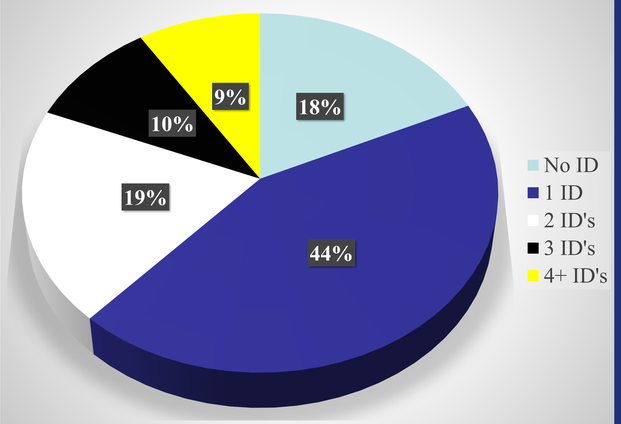



## Conclusions/Discussion

Implementation of a rapid multiplexed molecular pneumonia panel can provide clinically actionable results that may offer the potential for earlier targeted therapy and improved usage of antibiotics in hospitalized patients. The pneumonia panel detected more pathogens than culture, however, the clinical significance of the presence of these organisms is unclear and additional work is needed to further define interpretive criteria.

The laboratory must work closely with Pharmacy, Infectious Disease, and providers to ensure proper use of the pneumonia panel and for proper antibiotic stewardship.

Figure 4. Number of ID's per panel

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