O264
Oral Session
PCR and other molecular tests directly on blood: what is new?

ACCURACY AND POTENTIAL CLINICAL UTILITY OF TWO RAPID MOLECULAR PANELS FOR DETECTION OF BLOOD STREAM INFECTION

C. Ward[1], K. Stocker[2], J. Begum[2], P. Wade[1], U. Ebrahimsa[1], S. Goldenberg[1]

[1]Department of Infectious Diseases, Guy's & St Thomas' NHS Foundation Trust, London, United Kingdom ; [2]Department of Infection, GSTS Pathology, London, United Kingdom

Objectives

Delayed antimicrobial therapy in septic patients is associated w ith excess mortality. Blood cultures can take 48 hours or more to identify the causative pathogen and its resistance profile, during w hich patients are prescribed empirical broad-spectrum antimicrobials. Commercially developed assays are now available that can detect the presence of common pathogens associated w ith blood stream infection from positive blood culture bottles. Some of these panels also have antimicrobial resistance markers. We aimed to assess tw o such assays, their potential to reduce the time taken to identify organisms and to improve antimicrobial stew ardship practice.

Methods

Positive blood cultures (BioMerieux BacTalert) w ere tested using conventional methods (culture and species level identification using MALDI-TOF (Bruker) w ith antimicrobial sensitivity testing using Vitek2. Results and turnaround time w ere compared retrospectively w ith tw o rapid molecular methods; Nanosphere Verigene Blood culture Gram positive and/or Gram negative cartridges (according to preliminary Gram stain results), and the BioFire FilmArray Blood culture Identification Panel. All assays w ere performed according to manufacturers instructions. Antimicrobial prescribing data under conventional testing w ere collected and used to estimate theoretical benefit in antimicrobial stew ardship had the rapid methods been used prospectively.

Results

A total of 173 patient samples w ere tested (first positive bottle per patient only, Gram stains w ith yeasts excluded). The mean time from blood culture positivity alert to species level identification w as 25.68 hours for MALDI-TOF, 2.3 hours for Verigene and 1.07 hours for FilmArray. The mean time from sample collection to positivity alert w as 31.65 hours, w ith a mean of 3.74 hours of sample transportation time.

The most common pathogens identified w ere Coagulase Negative *Staphylococci* (39%), *E. coli* (17%) and *Staphylococcus aureus* (8%).

When culture and phenotypic/MALDI-TOF identification w ere used as the gold standard the overall sensitivity, specificity, positive and negative predictive values w ere 97.4%, 99.8%, 94.4% and 99.8% respectively for Verigene and 98.1%, 98.6%, 85.3% and 99.8% respectively for FilmArray. The FilmArray produced 26 positives for *Pseudomonas aeruginosa* w hich could not be confirmed using culture or the Verigene; these w ere considered to be false positives and resulted in a specificity of 84.8% for this organism. There w as significant theoretical opportunity for earlier intervention had either of the assays been used prospectively. This included opportunities for more directed therapy (including broader and narrow er spectrum of activity) and for discontinuation of antimicrobials at an earlier time.

Conclusion

The diagnostic accuracy of both assays w as very similar, resulting in excellent performance characteristics w ith the exception of several false positives for *Pseudomonas aeruginosa* w ith the FilmArray. Use of these assays could reduce the turnaround time to identification by a minimum of 23 hours and has the potential to improve antimicrobial stew ardship and give important clues as to the source of the blood stream infection.

	Results for Nanosphere Verigene					Results for BioFire FilmArray				
	Sensitivity % (95%CI)	Specificity % (95%CI)	Positive Predictive Value % (95%CI)	Negative Predictive Value % (95%CI)	Kappa (95%CI)	Sensitivity % (95%CI)	Specificity % (95%CI)	Positive Predictive Value % (95%CI)	Negative Predictive Value % (95%CI)	Kappa (95%CI)
Staphylococcus aureus	100 (80.6-100)	100 (97.6-100)	100	100	1.0	100 (80.6-100)	100 (97.6-100)	100	100	1.0
Staphylococcus spp	95.5 (78.2-99.2)	99.3 (96.3-99.9)	95.5 (74.8-99.3)	99.3 (95.7-99.9)	0.95 (0.88-1.0)	98.5 (92.1-99.7)	100 (96.5-100)	100	99.1 (93.8-99.9)	0.99 (0.96-1.0)
Staphylococcus epidermidis	100 (92.3-100)	99.2 (95.7-99.9)	97.9 (86.7-99.7)	100	0.99 (0.96-1.0)					
Micrococcus spp	83.3 (43.6-97.0)	100 (97.8-100)	100	99.4 (96.5-99.9)	0.91 (0.72-1.0)					
Streptococcus pneumoniae	100 (20.7-100)	98.8 (95.9-99.7)	33.3 (11.2-66.5)	100	0.5 (-0.1-1.0)	100 (20.7-100)	100 (97.8-100)	100	100	1.0
Enterococcus spp						100 (67.6-100)	100 (97.7-100)	100	100	1.0
Enterococcus faecalis	50 (9.5-90.5)	100 (97.8-100)	100	99.4 (97.7-99.9)	0.66 (0.05-1.0)					
Enterococcus faecium	100 (56.6-100)	99.4 (96.7-99.9)	83.3 (41.5-97.2)	100	0.91 (0.72-1.0)					
Streptococcus agalactiae	100 (51-100)	100 (97.8-100)	100	100	1.0	100 (51-100)	100 97.8-100)	100	100	1.0
Streptococcus spp	85.7 (48.7-97.4)	100 (97.7-100)	100	99.4 (96.4-99.9)	0.92 (0.96-1.0)	100 (64.6-100)	99.4 (96.7-99.9)	87.5 (49.8-98)	100	0.93 (0.79-1.0)
E. coli	100 (88.3-100)	100 97.4-100)	100	100	1.0	100 (88.3-100)	100 97.4-100)	100	100	1.0
Pseudomonas aeruginosa	100 (34.2-100)	100 (97.8-100)	100	100	1.0	100 (34.2-100)	84.8 (78.7-89.4)	100	7.1 (5.1-9.9)	0.11 (-0.03-0.26)
Klebsiella pneumonia	100 (51-100)	100 (97.8-100)	100	100	1.0	100 (51-100)	100 (97.8-100)	100	100	1.0
Klebsiella oxytoca	100 (34.2-100)	100 (97.8-100)	100	100	1.0	50 (9.5-90.5)	100 (97.8-100)	100	99.4 (97.7-99.9)	0.66 (0.05-1.0)
Citrobacter spp	100 (43.9-100)	100 (97.8-100)	100	100	1.0					
Enterobacter spp	100 (51-100)	100 (97.8-100)	100	100	1.0	100 (51-100)	100 (97.8-100)	100	100	1.0
Enterobacteriacea						66.7 (20.8-93.9)	100 (97.8-100)	100	99.4 (97.2-99.9)	0.80 (0.42-1.0)
Acinetobacter spp	50 (9.5-90.5)	100 (97.8-100)	100	99.4 (97.7-99.9)	0.66 (0.05-1.0)					