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Turn-Around-Time Improvements for Positive Blood Cultures from Incorporation of Workflow Modifications

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#1501

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Abstract

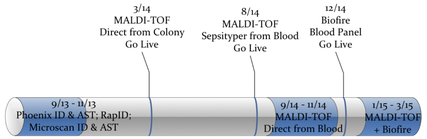
Background:
Emergence of direct from positive blood culture bottle identification (ID) methods reveal opportunities for improving bacterial ID and select resistance marker detection turn-around-times. Each system has various advantages and disadvantages; each institution must select the method/s that best fit the laboratory and patient needs. Here we elucidate improvements in 24 hour workflow through incorporating multiple rapid technologies for positive blood culture ID into a 24 hour algorithm.

Methods:
MALDI-TOF (Bruker) analysis with sepsityper extraction (aerobic Gram-positive and anaerobic bacteria); MALDI-TOF analysis with serum separator tube concentration (Gram-negative bacteria); and a FilmArray Blood Culture Panel (Biofire) were utilized. MALDI was utilized on 1st shift for single bacterium positives. FilmArray was performed on 2nd and 3rd shift for aerobic bottles and on 1st shift for gram-positive cocci in clusters and *Candida*. We examined all events during our pre-modification (September-November 2013) and post-modification (late-December 2014-March 2015) time periods and defined an event as the first positive blood culture for a patient within the examined data period. The Antimicrobial Stewardship Pharmacist (ASP) was notified with identifications and also *KPC* carbapenemase positives, to implement a carbapenem-resistant Enterobacteriaceae (CRE) empiric treatment algorithm. For KPC positives (CRE) a custom minimum inhibitory concentration (MIC) panel was utilized, replacing a standard susceptibility panel and Etests. Finally, 2nd shift began susceptibility setup on subcultured bloods that had turned positive from 11 p.m.-6 a.m.

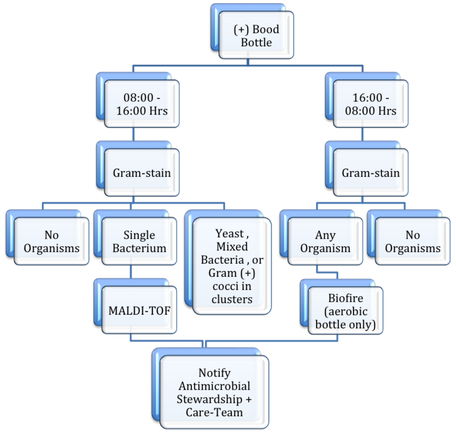
Results:
Pre- and post- workflow modification average turn-around times (TAT) and p-values are shown in the Table. Detection of either the KPC or the mecA marker significantly improved the TAT needed for phenotypic detection of carbapenem or methicillin resistance. KPC was detected in 3 *Enterobactericeae*.

Conclusions:
Improvements to patient care are to be determined, but strong collaboration with ASP is anticipated to make a significant impact on patient outcomes. Of note, while having a universal *Staphylococcus* species target is useful, it can lead to complications with multi-species positive bottles. With the universal *Staphylococcus* species target, it is not possible to differentiate between a mixed coagulase negative *Staphylococcus* species (CNSS) versus *Staphylococcus aureus* when both are present as the CNSS may harbor the *mec*A target, preventing adequate treatment. Furthermore, a *Staphylococcus lugdunensis* specific marker would be clinically useful.

Time-line of Workflow



MALDI-TOF plus Biofire Blood Culture Algorithm



Data Communication

- Email of all positive blood culture identifications generated and sent to Antimicrobial Stewardship Pharmacists at least twice daily
- Clinician (Care-team) directly notified with identification at time determined
- Direct 24/7 phone call for KPC positive Enterobacteriaceae to a Antimicrobial Stewardship Pharmacist

Table 1: Turn-around-time Improvements Noted Over Time

Organism	Pre-Workflow Modifications (Biochemical & Enzymatic Identification)		Post-Workflow Modifications (MALDI-TOF Only)		Post-Workflow Modifications (MALDI-TOF + Biofire)		p-value (<0.05)
	Average TAT, hours (N)	Standard deviation (±)	Average TAT, hours (N)	Standard deviation (±)	Average TAT, hours (N)	Standard deviation (±)	
Methicillin susceptible *Staphylococcus aureus* (MSSA)	**44.7 (56)**	**17.8**	**30.2(47)**	**14.6**	**34.5 (47)**	**23.7**	**0.177**
Methicillin resistant *Staphylococcus aureus* (MRSA)	**43.3 (18)**	**10.2**	**64.0(15)**	**21.5**	**21.3 (25)**	**13.1**	**$2.519x10^{-07}$**
Escherichia coli	**62.1 (62)**	**10.4**	**27.1(69)**	**12.2**	**22.7 (73)**	**13.3**	**$2.616x10^{-40}$**
Pseudomonas aeruginosa	**69.7 (18)**	**18.3**	**42.1(12)**	**20.1**	**34.1 (10)**	**11.8**	**$1.599x10^{-06}$**
Streptococcus pneumoniae	**35 (5)**	**9.30**	**20.1(2)**	**0.02**	**11.7 (8)**	**4.6**	**0.003**
***Beta-hemolytic Streptococcus* (GRP A)**	**37.2 (1)**	**-**	**26.1(3)**	**14.3**	**13.5 (4)**	**5.2**	**-**
***Beta-hemolytic Streptococcus* (GRP B)**	**43.7 (6)**	**16.2**	**28.5(7)**	**19.5**	**38.2 (6)**	**20.6**	**0.619**
Candida glabrata	**84.3 (6)**	**30.9**	**74.5 (7)**	**14.6**	**69.3 (6)**	**19.8**	**0.344**
Candida albicans/dubliniensis	**76.4 (6)**	**18.4**	**76.2 (6)**	**18.31**	**76.4 (7)**	**27.3**	**0.0002**
Enterobacter cloacae complex/ E. aerogenes	**63.1 (5)**	**12.7**	**34.0(17)**	**31.8**	**19.95 (8)**	**9.46**	**0.0004**
Proteus mirabilis	**82.4 (7)**	**29.5**	**35.5(5)**	**18.2**	**43.2 (4)**	**22.4**	**0.038**
Klebsiella pneumoniae	**62.5 (29)**	**11.0**	**25.3(29)**	**12.9**	**27.98(27)**	**21.4**	**$5.029x10^{-09}$**
***Klebsiella pneumonia* + KPC**	**NA**	**NA**	**NA**	**NA**	**14.8 (5)**	**2.3**	**-**
***Enterococcus* species**	**NA**	**NA**	**NA**	**NA**	**20.3 (6)**	**6.7**	**-**
***Enterococcus faecalis/faecium* VRE**	**68.3 (6)**	**13.3**	**60.2 (4)**	**19.2**	**22.7 (8)**	**8.3**	**$7.033x10^{-05}$**
Enterococcus faecalis/faecium	**70.3 (27)**	**17.2**	**35.0 (14)**	**10.3**	**38.1 (18)**	**25.6**	**0.0005**
Universal *Staphylococcus species*	**NA**	**NA**	**NA**	**NA**	**33.97 (74)**	**21.1**	**$6.140x10^{-31}$**
Coagulase negative *Staphylococcus*, including *Staph. lugdunensis*	**78.1 (159)**	**19.1**	**50.9(185)**	**19.7**	**54.4 (86)**	**20.73**	**$2.297x10^{-15}$**

Future Considerations

- Determine if patient outcomes were impacted by improvement in time-to-identification of organisms
- Evaluation of Antimicrobial Stewardship Pharmacist recommendations and patient Care-Team actions
  - Types of intervention performed
- Assess time to appropriate antimicrobial therapy and Length of Stay (LOS) impact
- Determine if unnecessary antibiotic exposure was minimized through differentiation of coagulase negative *Staphylococcus* (potential contaminants) from *Staphylococcus aureus* as well as through educational initiatives

Select References

- Doern, C. D., et al. 2013. Charting Uncharted Territory: a Review of the Verification and Implementation Process for Matrix-Assisted Laser Desorption Ionization-Time of Flight Mass Spectrometry (MALDI-TOF MS) for Organism Identification. Clinical Microbiology Newsletter. 35 (9):69-78
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