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Workflow Modifications and Addition of MALDI-TOF Technology Significantly Improved Turn-Around-Time to Identification of Common Urine Pathogens

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Workflow Modifications and Addition of MALDI-TOF Technology Significantly Improved Turn-Around-Time to Identification of Common Urine Pathogens

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Abstract

Background:

In order to improve the identification of common aerobic urine cultures as well as antimicrobial susceptibility testing (AST) setup at an Academic Medical Center, work-flow modifications and MALDI-TOF technology were incorporated. Previously, the majority of species identification was achieved with conventional identification/antimicrobial susceptibility combo panels. All urine cultures, regardless of laboratory receipt time, were previously read once per day on 1st shift.

Methods:

The initial workflow modification involved addition of a 2nd shift urine culture reading. Urine specimens received from 8:00 AM to 4:00 PM were read on 1st shift, while urine specimens received from 4:00 PM to 8:00 AM were read on 2nd shift.

Additionally, urine cultures were sorted into categories: no growth (NG) at 24 hours, no growth at <24 hours, single colonies of growth, multiple colonies of growth, and potential contaminants. No growth cultures were signed out at 24 hours. No growth cultures at < 24 hours were reincubated to be read on subsequent shift. Cultures with growth were set aside as either single colony types or multiple colony types. Cultures of probable contaminants were signed out.

Once cultures were sorted, the isolated colonies underwent MALDI-TOF analysis (Bruker) and antimicrobial susceptibility testing (AST) as appropriate. Individual technologists setup the MALDI-TOF target plate map and spotted the associated target plate. AST was setup at the same time. The MALDI-TOF was then operated by a central technologist and results reported by the original technologist reading the culture.

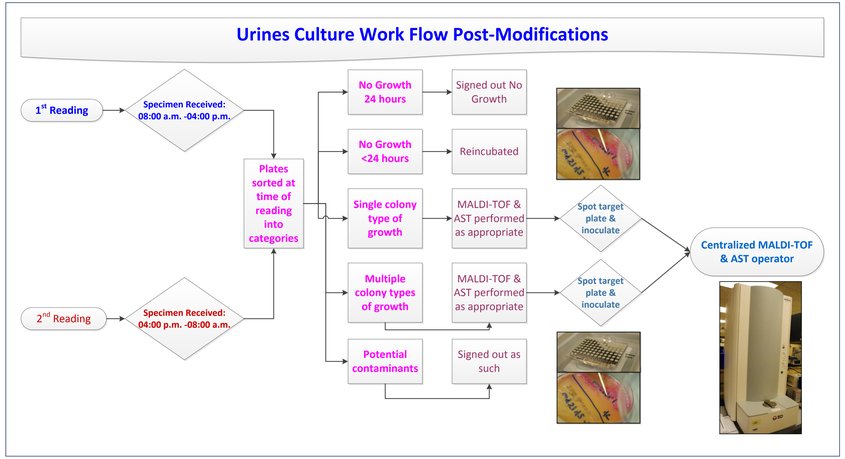
Results:

Retrospective pre-workflow (September-November 2013) and post-workflow (May, June, October 2014) modification turn-around-times were compared for 16 commonly isolated pathogens. These pathogens consisted of common urine pathogens as noted in Table 1. *Staphylococcus aureus* was previously identified in our laboratory by a positive coagulase test and not included in this analysis. The average turn-around-times, standard deviations and the p-values for each organism are indicated in Table 1.

Conclusion:

Converting from conventional identification methods to MALDI-TOF, in conjunction with workflow modifications such as a 2nd culture reading, notably improved urine culture turn-around-time for identification and AST.

Laboratory Process



Motivation for implementation:

- Surgical and Oncology Clinicians were dissatisfied with the urine culture turn-around-time, especially in cases of 24 hour negative cultures as this impacted discharge for high risk patients
  - The solution from the lab perspective was to incorporate an afternoon reading for specimens received later on the prior day, allowing 24 hour negative cultures to be signed out before accrual of an additional inpatient day
- Further improvements were sought through incorporation of MALDI-TOF technology to allow faster identification times.
  - This also allowed clinicians to apply more effective empiric antimicrobial therapy based on organism identification.

Table 1. The average turn-around-times for common urine pathogens

	Pre-Workflow Modifications (Sept., Oct., Nov., 2013)		Post-Workflow Modifications (May, June, Oct. 2014)		
Organism	**Average hrs (N)**	**STDev (±)**	**Average hrs (N)**	**STDev (±)**	**P-value (<0.05 significant)**
Acinetobacter baumannii/ calcoaceticus complex	62.42 (12)	24.36	54.65 (11)	18.56	0.398
Citrobacter freundii complex	73.93 (22)	22.36	39.24 (30)	48.52	5.792×10^{-07}
Citrobacter koserii	62.81 (26)	21.70	29.46 (27)	45.52	2.559×10^{-08}
Enterobacter aerogenes	62.73 (32)	17.14	27.87 (21)	8.49	2.194×10^{-10}
***Enterobacter cloacae* complex**	62.9 (45)	23.80	40.36 (41)	22.65	2.128×10^{-05}
Enterococcus faecalis	67.12 (246)	23.28	38.85 (164)	19.63	2.01×10^{-29}
Enterococcus faecium	91.39 (19)	25.75	57.06 (67)	29.83	2.163×10^{-05}
Escherichia coli	52.83 (1041)	15.22	30.50 (929)	12.92	4.29×10^{-63}
Klebsiella oxytoca	53.31 (28)	15.39	33.59 (15)	16.56	0.001
Klebsiella pneumoniae	55.93 (291)	18.02	38.52 (255)	22.43	3.50×10^{-21}
Morganella morganii	66.83 (21)	19.96	36.94 (14)	14.00	1.016×10^{-05}
Proteus mirabilis	58.74 (143)	21.19	31.05 (109)	11.54	4.01×10^{-30}
Pseudomonas aeruginosa	66.82 (155)	20.47	40.54 (88)	21.28	3.42×10^{-17}
Serratia marcescens	62.37 (11)	23.85	29.95 (16)	24.15	0.001
Staphylococcus saprophyticus	69.50 (21)	16.40	55.72 (19)	23.31	0.040
Stenotrophomonas maltophilia	85.71 (10)	20.49	58.18 (8)	46.95	0.018

Future Considerations:

- Evaluate clinical history for urines collected on inpatients to determine rate of urosepsis
  - Evaluate the difference between Length of Stay (LOS) in the pre-modification verses post-modification group
  - Trend in decreased length of stay noted, but further analysis to needed to determine root cause.
- Future algorithm, in conjunction with Infection Control, will be incorporation of a positive Urinalysis with reflex to Urine Culture and a negative Urinalysis with cancellation of Urine Culture