IDWeek 2022
Poster #168

Closing Time: A Quasi-experiment Comparing Time to Optimal Therapy using Traditional Identification and Susceptibility Methods, Rapid Identification, or Rapid Identification with Phenotype for Gram-negative Bloodstream Infections

Rachel Perry, PharmD; Nicholas Mercuro, PharmD, BCIDP; Kristina Connolly, PharmD, BCIDP; Eliza Dollard, PharmD, BCIDP; Patricia Stogsdill, MD, FIDSA; Minkey Wungwattana, PharmD, BCIDP
Maine Medical Center, Portland, Maine

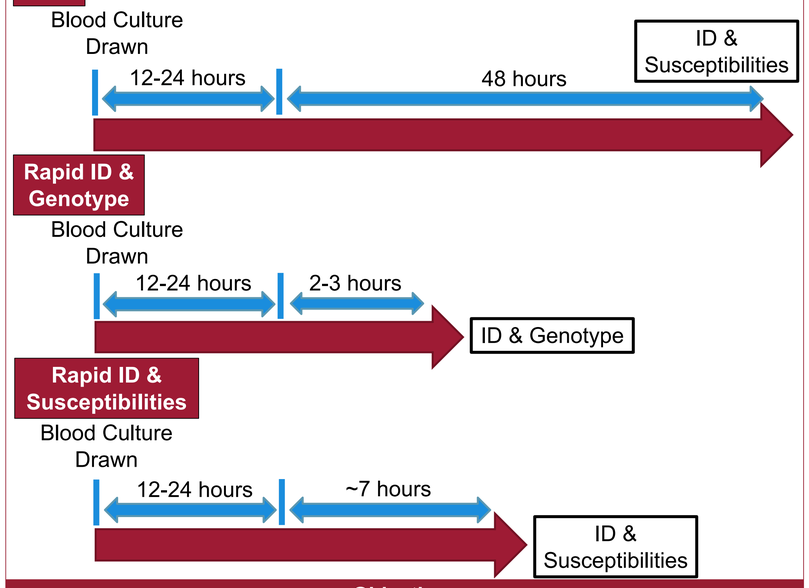
Correspondence:
Minkey Wungwattana
Maine Medical Center
Minkey.Wungwattana@mainehealth.org

Background

- Gram negative (GN) bloodstream infections (BSI) are a common cause of community and hospital acquired sepsis and can be associated with up to 38% mortality in patients that receive inappropriate therapy[1]
- Standard of care (SOC) blood culture (BCx) diagnostics can take up to 72 hours to identify the offending organism and susceptibilities whereas rapid diagnostic testing (RDT) can provide these results 45-60 hours sooner
- RDT has been shown to decrease time to pathogen-directed therapy, length of hospital stay, and mortality when paired with antimicrobial stewardship intervention[2-4]
- Maine Medical Center (MMC) adopted the Verigene rapid nucleic acid identification (ID) in 2016, which provides rapid organism ID and genotype
- MMC transitioned to Accelerate Pheno in 2020, which provides rapid organism ID and susceptibilities

SOC

Figure 1. Processing Time for Diagnostic Testing



Objectives

Evaluate the time to optimal therapy (TTOT) in patients with GN bacteremia across three time periods

- Standard of care (Pre-RDT)
- Rapid ID and genotype (RDT1)
- Rapid ID and susceptibilities (RDT2)

Definitions

- Time to active therapy (TTAT): time (hours) from blood culture positivity to administration of first susceptible antibiotic
- TTOT: time (hours) from blood culture positivity to appropriate antibiotic therapy based on susceptibility results, spectrum of activity, and guideline recommendations

Methods

Quasiexperiment of adult patients at MMC with GN BSI between January 1, 2013, and June 30, 2021

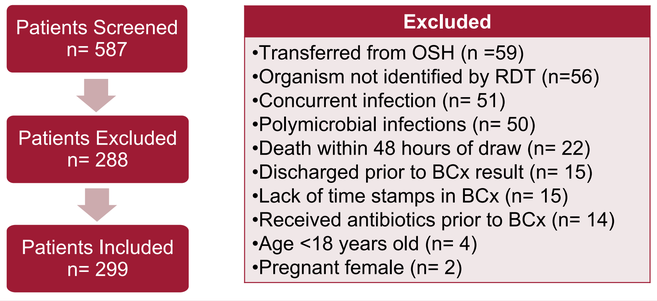
Figure 2. Time Periods

Pre-RDT: Jan. 1, 2013 – Oct. 30, 2016 → RDT1: Dec. 1, 2016 – Dec. 31, 2019 → RDT2: Feb. 20, 2020 – Jun. 33, 2021

Table 1. Inclusion & Exclusion Criteria

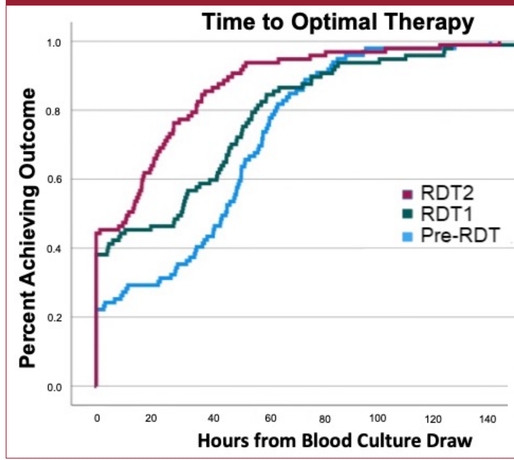
Inclusion Criteria	Exclusion Criteria
Patients admitted to MMC between January 1, 2013, and June 30, 2021, for GN BSI	• <18 years old • Polymicrobial infections • Organisms not identified by the RDT panels • Received effective antibiotics prior to blood culture draw • Transferred from an outside hospital • Discharged prior to blood culture result and followed up outside of MaineHealth • Pregnant female • Expired within 48 hours of blood culture draw • GN BSI with same organism in preceding 7 days

Figure 3. Patient Allocation



Results

Time to Optimal Therapy



Time to Optimal Therapy (Hours)	
Pre-RDT	46 (7-61)
RDT1	30 (0-53)
RDT2	12 (0-28)
p	<0.001

*Data presented as median (IQR) unless otherwise specified

- P < 0.001; Pre-RDT vs RDT2
- P= 0.031; Pre-RDT vs RDT1
- P= 0.021; RDT1 vs RDT2

Table 2. Baseline Characteristics

Characteristic	Pre-RDT n= 100	RDT1 n= 100	RDT2 n= 99	p
Sex- male, n (%)	45 (45)	45 (45)	49 (49.5)	0.764
Age- years	72 (61, 81)	71.5 (66, 81)	73 (62, 80)	0.541
CCI	5 (3, 7)	5 (4, 7)	5 (3, 8)	0.873
Pitt Bacteremia	0.5 (0, 2)	0 (0, 1)	0 (0, 1)	0.076

*Data presented as median (IQR) unless otherwise specified

Figure 4. Source of Infection

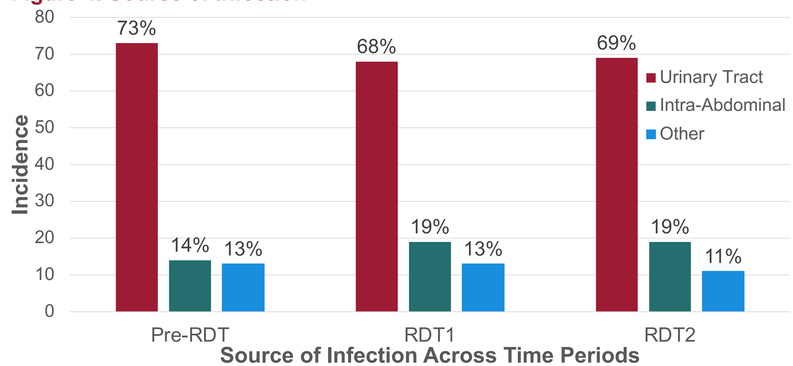


Table 3. Secondary Outcomes

Outcome	Pre-RDT	RDT1	RDT2	p
TTAT- hours	0 (0, 0)	0 (0, 0)	0 (0, 0)	0.28
Anti-MRSA Coverage- hours	9.5 (0, 24)	0 (0, 24)	0 (0, 24)	0.05
Duration of Therapy- days	13 (10, 15)	13 (9, 15)	11 (8.5, 14)	0.02
Length of Hospital Stay- days	4 (3, 6)	5 (3, 7)	5 (3, 8)	0.45
C. difficile Infection, n (%)	3 (3)	0 (0)	3 (3)	0.22
30-Day Inpatient Mortality, n (%)	2 (2)	0 (0)	2 (2)	0.37
Time to Oral Step-Down- hours	60 (48, 83)	59 (48, 94)	62 (38, 84)	0.77

*Data presented as median (IQR) unless otherwise specified

Discussion & Conclusion

- TTOT was significantly shorter when comparing no RDT to either RDT method
- Phenotypic RDT resulted in shortest TTOT
- Time for patients to transition to oral antibiotics did not differ between cohorts
- Significantly shorter duration of therapy was observed in RDT2
- Phenotypic RDT led to the quickest time to optimal antibiotic therapy

Disclosures

Registration & travel to IDWeek 2002 for MW and RP were funded by Accelerate Diagnostics, Inc. Accelerate Diagnostics, Inc. was not involved in the conception, data collection, and data analysis of this study.
Nothing to disclose: NM, KC, ED, PS.

References

1. Kang CI, et al. *AAC*. 2005;49(2):760-766.
2. Banerjee R, et al. *CID*. 2021;73(1):e39-e46.
3. Walsh TL, et al. *Infection*. 2021;49(3):511-519.
4. Timbrook TT, et al. *CID*. 2017;64(1):15-23.
5. Hogan CA, et al. J Clin Micro. 2020;58(9).