Update on Diagnostic Assays for Rapid Detection of Bacteremia

Karen C Carroll, M.D.
Professor of Pathology
Director, Division of Medical Microbiology
The Johns Hopkins University School of Medicine

Disclosures

Research Funding from:
- Abbott Molecular Diagnostics, Inc.
- Curetis, Inc.
- Accelerate, Inc.
- BD Diagnostics, Inc.

Learning Objectives

At the end of this presentation, the attendee will:
- Learn about the importance of bloodstream infections
- Understand the currently available assays for identification of organisms from positive blood cultures
- Appreciate the difficulty of direct from whole blood testing
Bloodstream Infections (BSI): Clinical Importance

- BSI rank among the most serious clinical problems worldwide
- Estimated 750,000 cases of BSI per year in the USA; 250,000 are nosocomial
- Sepsis and its complications cost $23.7 billion/yr. in the USA
- Attributable mortality ranges from 12%-55%
- Standard culture methods are slow

Pathogen ID
Blood culture
12-72 hrs 5 min 24-72 hrs.

Diverse Multi-Pathogen Broad-Based Technologies

- Verigene BC assays (Nanosphere, Inc.)
- FilmArray BCID (BioFire, Inc.)
- MALDI-TOF MS (Bruker Daltonics, Inc.; bioMerieux, Inc.)
- Accelerate Pheno (Accelerate, Inc.)

Direct from Whole Blood Assays

- T2 CANDIDA (T2 Biosystems, Inc.)
- IRIDICA BAC BSI (Abbott Molecular) [RUO]
The Verigene System
How It Works

Nucleic Acid Detection with the Verigene System
- Extraction of nucleic acids directly from BC media
- Hybridization onto a microarray
- Results analysis

Sample
Well
Extraction Tray Test
Cartridge ReaderUtility
Tray
Processor
SP
Setup
Pellet
Sample In
Nucleic Acid Extraction
Hybridization
Analysis on Reader

Magnetic bead
technology

Two types of
hybridization


The Verigene System
Hybridization Technology Overview

Verigene® Blood Culture Panels

<table>
<thead>
<tr>
<th>Gram positive BC Panel</th>
<th>Gram negative BC Panel</th>
</tr>
</thead>
<tbody>
<tr>
<td>Species/Genus</td>
<td>Resistance</td>
</tr>
<tr>
<td>Staphylococcus</td>
<td></td>
</tr>
<tr>
<td>S. aureus</td>
<td>mecA</td>
</tr>
<tr>
<td>S. epidermidis</td>
<td>mecA</td>
</tr>
<tr>
<td>S. lugdunensis</td>
<td></td>
</tr>
<tr>
<td>Streptococcus spp.</td>
<td></td>
</tr>
<tr>
<td>S. pneumoniae</td>
<td></td>
</tr>
<tr>
<td>S. anginosus</td>
<td></td>
</tr>
<tr>
<td>S. agalactiae</td>
<td></td>
</tr>
<tr>
<td>S. pyogenes</td>
<td></td>
</tr>
<tr>
<td>Enterococcus faecalis</td>
<td>vanA, vanB</td>
</tr>
<tr>
<td>Enterococcus faecium</td>
<td>vanA, vanB</td>
</tr>
<tr>
<td>Listeria spp.</td>
<td></td>
</tr>
</tbody>
</table>

Overall Performance Verigene BC-GP

- More than 25 publications
- Overall 87.6%-99.2% agreement between Verigene assay and conventional results
  - Agreement is better with monomicrobial blood cultures vs. polymicrobial blood cultures (62.5%-74.3%)
  - Misidentifies S. mitis as S. pneumoniae
- Overall agreement for resistance marker detection (meA, vanA, vanB) — 97-100%
- Invalid rates 1.9-6.1%

Verigene BC-GP Impact Studies

- No prospective, randomized trials
- Mean time to identification/resistance detection reduced by 30.1 h- 42 h vs. conventional methods
- In association with active stewardship
  - Time to de-escalation decreased by 29 h
  - Mean-time to optimal therapy decreased by 13-24 h
  - Shortened duration of antibiotic Rx for contaminants by 37 h
  - LOS decreased by 1.5 d
  - Reduced costs

JHH Recommended Antibiotics Based on Verigene BC-GP Results

<table>
<thead>
<tr>
<th>Organism</th>
<th>MSSA</th>
<th>MRSA</th>
<th>CoNS</th>
<th>Staph. lugdunensis</th>
<th>Enterococcus faecalis</th>
<th>VRE (E. faecium)</th>
<th>E. faecium not VRE</th>
<th>Group A streptococcus</th>
<th>Group B streptococcus</th>
<th>Strep pneumoniae</th>
<th>Strep pneumoniae (CNS)</th>
<th>Strep anginosus</th>
<th>Other streptococci</th>
<th>Listeria spp.</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Oxacillin (100%)</td>
<td>Vancomycin (100%)</td>
<td>Cefazolin/Vancomycin</td>
<td>Vancomycin (100%)</td>
<td>Ampicillin (99%)</td>
<td>Vancomycin (89%)</td>
<td>Vancomycin (99%)</td>
<td>Penicillin G (100%)</td>
<td>Penicillin G (100%)</td>
<td>Ceftriaxone (94%)</td>
<td>Ceftriaxone + Vanco</td>
<td>Penicillin G (100%)</td>
<td>Ceftriaxone/Vancomycin</td>
<td>Ampicillin (100%)</td>
</tr>
</tbody>
</table>
Case Presentation

- 17 y.o. previously healthy male was transferred to JHH on 2/11 for MSSA pelvic osteomyelitis and bacteremia.
- Extensive debridement: 2/14, 2/28; received IV oxacillin.
- On 3/3 he spiked a temp.; BC were obtained.
- On 3/4, a single BC grew gpccl
- The ortho team scheduled the patient for surgery
- 2.5 h later the Verigene BC-GP test identified the organism as Staphylococcus species, coagulase negative.
- Surgery, additional ordered tests, and added gentamicin were cancelled.

Verigene BC-GN Test Published Performance

<table>
<thead>
<tr>
<th>Reference</th>
<th>#</th>
<th>ΔTTD* (h)</th>
<th>ID accuracy**</th>
<th>Resistance Markers</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mancini JCM 2014; 52:1242</td>
<td>102</td>
<td>14</td>
<td>97.9%</td>
<td>Enterics PPV, 95.8%; NPV 100%; Pseud, PPV 100%; NPV 78.8%; Acinet 100% both</td>
</tr>
<tr>
<td>Top: Plus ONE 2014; e404064</td>
<td>295</td>
<td>102</td>
<td>N/A</td>
<td>96.9% 94.5% 100% concordance with PCR/sequencing</td>
</tr>
<tr>
<td>Dedemont JCM 2014; 52:3065</td>
<td>125</td>
<td>11.5</td>
<td>97.4%</td>
<td>92.3% concordance with PCR/sequencing</td>
</tr>
<tr>
<td>Ledeboer NA JCM 2015; 53:2460 multicanter</td>
<td>1847</td>
<td>N/A</td>
<td>97.9%</td>
<td>percent agreement for resistance determinants ranged from 94.3% for blaOXA to 100% for blaVIM, blaIMP, blaKPC</td>
</tr>
<tr>
<td>Walker JCM 2016; 54:1789</td>
<td>98 pre</td>
<td>27</td>
<td>99.0%</td>
<td>100% concordance for 11 CTX-M 2 CRE P. aeruginosa neg. by panel</td>
</tr>
</tbody>
</table>

* Decrease in TTD means; ** Only considering organisms in the panel; # Seeded. 729 prospective fresh, 781 prospective or retrospective frozen, 337 simulated. All of the studies report failure to detect K. pneumoniae and problems with polymicrobial cultures.

Mean time to effective Rx for ESBL cases decreased by 34 h, P=.04
The FilmArray BCID panel is designed to identify ~90% of the microorganisms that are typically found in positive blood cultures.

### Gram Positive Bacteria
- Genus N=8:
  - Enterococcus
  - Staphylococcus
  - Streptococcus
- Species:
  - Listeria monocytogenes
  - Staphylococcus aureus
  - Streptococcus agalactiae
  - Streptococcus pyogenes
  - Streptococcus pneumoniae

### Gram Negative Bacteria
- Family N=11:
  - Enterobacteriaceae
- Genus:
  - Proteus
- Species:
  - Acinetobacter baumannii
  - Escherichia coli
  - Enterobacter cloacae complex
  - Haemophilus influenzae
  - Klebsiella oxytoca
  - Klebsiella pneumoniae
  - Neisseria meningitidis
  - Pseudomonas aeruginosa
  - Serratia marcescens

### Fungi N=5
- Candida albicans
- Candida glabrata
- Candida krusei
- Candida parapsilosis
- Candida tropicalis

### Antibiotic Resistance Genes
- KPC
- mecA
- vanA / vanB

*Tests are for the indicated genes, not the functional translation of such resistance. Reporting as the presence of either gene(s).

### FilmArray® BC-ID Assay Performance Characteristics
- TAT: 1 h
- Overall accuracy for isolates in the panel compared to conventional methods: 94-99%
- Resistance marker detection: 98-100% accuracy
- Identified 81-92% of all pathogens routinely recovered in positive blood cultures
- Reduction in time to identification > 29 h*
- Issues with polymicrobial cultures

### Impact of FilmArray® BC-ID Assay

<table>
<thead>
<tr>
<th>Outcome</th>
<th>Standard of care n=207</th>
<th>FilmArray/Template n=198</th>
<th>FilmArray/Stewardship n=212</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Time to org ID</td>
<td>22 h</td>
<td>1.3 h</td>
<td>1.3 h</td>
<td>&lt;.001</td>
</tr>
<tr>
<td>Median duration vancomycin</td>
<td>8.2 h</td>
<td>0</td>
<td>0</td>
<td>.03</td>
</tr>
<tr>
<td>Duration narrow spectrum ß-lactams</td>
<td>42 h</td>
<td>71 h</td>
<td>85 h</td>
<td>.04</td>
</tr>
<tr>
<td>Time to de-escalation</td>
<td>34 h</td>
<td>38 h</td>
<td>21 h</td>
<td>&lt;.001</td>
</tr>
<tr>
<td>Time to escalation</td>
<td>24 h</td>
<td>--</td>
<td>5 h</td>
<td>.04</td>
</tr>
<tr>
<td>% of contaminants not treated</td>
<td>75</td>
<td>89</td>
<td>92</td>
<td>.015</td>
</tr>
</tbody>
</table>

No statistically significant decrease in LOS, mortality, overall hospital costs or antimicrobial costs.
**Rapid Phenotypic Methods**

**MALDI-TOF Mass Spectrometry**
Matrix Assisted Laser Desorption Ionization -Time of Flight

- Pick 1-2 colonies
- Smear colonies on target; apply matrix
- Insert target into MS
- Analyze spectra

**MALDI-TOF MS Systems**
- Two FDA approved systems in the USA
- 192-200 bacteria and yeasts in the approved databases
- Thousands of entries in the "research use only" libraries
- Instrument costs: $180,000 on average
- Identification only—no AST results!
MALDI-TOF MS
Direct from Positive Blood Cultures

<table>
<thead>
<tr>
<th>Method</th>
<th>Steps</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bruker Sepsityper Method</td>
<td>1 mL of pos. blood culture broth, 200 µL lysis buffer centrifuge, wash, re-centrifuge, Ethanol- formic acid extraction, Apply 1 µL of pellet to target plate, proceed with standard MALDI-TOF MS procedure, Specialized software for interpretation</td>
</tr>
<tr>
<td>Lysis Filtration Method</td>
<td>2 mL of pos blood culture broth, 1.0 mL lysis buffer, incubate, add to filter membrane, Wash x 3 with buffer, x 3 with water, Remove organisms with microswab applicator, Transfer to target plate, proceed with standard VMS ID procedure</td>
</tr>
</tbody>
</table>

**Species level ID cut-off is 1.8**
**Genus level ID cut-off is 1.6**

Fothergill A, et. al. JCM 2013; 51: 805

Sepsityper and Lysis Filtration MALDI TOF MS

Multiple publications on Sepsityper (Bruker) using both BacT/Alert non-charcoal bottles and BACTEC media

- General observations
  - Better for GNRs than GPC, especially S. mitis group
  - Problems with poly
  - Overall 15% failure
  - Fothergill study used
    - Correct identification
    - Incorrect identification
    - No identification--19.7%
    - Problems with poly

Alternative extraction methods
- Centrifugation + distilled water + lysis solution
- SDS lysis + centrifugation, DI wash + centrifugation
- 5% saponin lysis solution + centrifugation, wash pellet with DI, centrifuge
- Vacutainer SST (Gram negative pathogens only)


Abbreviated Incubation Using MALDI-TOF MS

- Protocols have examined brief incubation on solid media
- Various lengths of incubation have been evaluated
  - Gram positive pathogens require longer incubation: mean 6 h, optimally 8 h or longer (> 90% accuracy)
  - Gram negative pathogens can incubate as short as 2 h, optimally 4 h or longer (> 90% accuracy)

Combining Rapid Identification and AST Using MALDI-TOF MS

Experience at Houston Methodist Medical

- 50 simulated, 60 clinical BACTEC BC bottles containing GNRs
- 6 mL post. blood culture broth added to vacutainer SST plus tube, centrifuged at 2,000 rpm for 15 min
- Supernatant removed; pellet spotted with swab onto target; aliquot of pellet added to Phoenix ID broth for AST
- Results
  - 98% concordance for ID
  - 1,882 organism-antibiotic tests
  - 5 VM errors (0.26%); 6 M errors (0.32%); 26 minor errors (1.37%)
  - ID results 6.5-24 h earlier; AST results 24 h earlier
- Combined with ASP: decreased LOS, reduction in costs--$3411/pt., decreased mortality


Impact of RDT on Clinical Outcomes in Bloodstream Infections

- A systematic review and meta-analysis
- 31 studies with 5,920 patients
  - Pre- and post-intervention quasi-experimental studies at RDT initiation (83.9%); academic medical centers (93.5%); adult patients (95.2%); presence of stewardship (65%)
- Results: RDT vs conventional methods
  - Decreased time to effective therapy by mean of 5.03 h
  - Decreased LOS by mean of 2.48 d
  - Mortality risk was lower with RDT combined with ASP, but not in non-ASP studies


Impact of RDT with ASP on Mortality

Accelerate Pheno System
ID and AST Direct from Positive Blood Cultures

Recent FDA Approval
Time to Identification: 1½ h
Time to Antibiotic susceptibilities: ~ 7h

Rapid Antimicrobial Susceptibilities
• MICs to enable optimized dosing
• CLSI or EUCAST S, I, R interpretations

Slides and data are courtesy of Malcolm Boswell, Accelerate Diagnostics

Accelerate Pheno™ System

System
• 1-4 module(s)
• Control & Analysis PCs
• Touchscreen monitor

Module
• Automated pipetting robot
• Digital camera
• Custom microscope

Kit
• 48-flow channel cassette
• Reagent cartridge
• Sample seal

Identification Channels  Antibiotics Available

Positive Blood Culture Panel

Identification Channels
Gram- Positive  Gram- Negative
S. aureus  E. faecalis
S. lugdunensis  E. faecium
CoNS spp.  Streptococcus spp.

Gram- Positive
Ampicillin  Ceftaroline
Doxycycline  Erythromycin
TMP-SMX  Daptomycin
Linezolid  Vancomycin

Gram- Negative
E. coli  Klebsiella spp.
K. pneumoniae  Enterobacter spp.
P. aeruginosa  A. baumannii
S. marcescens

Resistance
MRSA (Cefoxitin)  MLSb (Ery-Clind)

Identification  MIC

Fungi
C. albicans  C. glabrata

Antibiotics Available

Positive  Negative
Ampicillin  Ceftazidime
Cefepime  Carbenicillin
Colistin  Gentamicin
Marbofloxacin  Ticarcillin-
Clopamine

Dynamic Dilution
Calculates inoculum concentration for AST
Antibiotic Susceptibilities by Time-Lapse Image Microscopy

- Time lapse images of live immobilized bacterial cells via dark field microscopy
- Reports susceptibilities & MICs to multiple antibiotics within 7 hours

Example A
E. coli vs. 4 μg/mL Pip/Tazo MIC=8 (S)

Example B
E. coli vs. 4 μg/mL Pip/Tazo MIC=128 (R)

• Time lapse images of live immobilized bacterial cells via dark field microscopy
• Reports susceptibilities & MICs to multiple antibiotics within 7 hours

ID Performance Clinical Trial
N=1800 specimens

<table>
<thead>
<tr>
<th>Gram-Positive</th>
<th>Spns.</th>
<th>Spec.</th>
</tr>
</thead>
<tbody>
<tr>
<td>E. coli</td>
<td>91.0</td>
<td>99.5</td>
</tr>
<tr>
<td>S. aureus</td>
<td>97.9</td>
<td>98.5</td>
</tr>
<tr>
<td>Coag-negative Staph spp.</td>
<td>95.3</td>
<td>98.2</td>
</tr>
<tr>
<td>S. lugdunensis</td>
<td>97.5</td>
<td>99.9</td>
</tr>
<tr>
<td>E. faecium</td>
<td>98.0</td>
<td>99.1</td>
</tr>
<tr>
<td>E. faecalis</td>
<td>97.0</td>
<td>99.9</td>
</tr>
<tr>
<td>Streptococcus spp.</td>
<td>97.2</td>
<td>97.6</td>
</tr>
</tbody>
</table>

| Gram-Positive Total | 97.0  | 98.9  |

<table>
<thead>
<tr>
<th>Gram-Negative</th>
<th>Spns.</th>
<th>Spec.</th>
</tr>
</thead>
<tbody>
<tr>
<td>E. coli</td>
<td>97.3</td>
<td>99.7</td>
</tr>
<tr>
<td>K. spp.</td>
<td>96.1</td>
<td>99.6</td>
</tr>
<tr>
<td>C. spp.</td>
<td>96.8</td>
<td>99.3</td>
</tr>
<tr>
<td>E. spp.</td>
<td>97.3</td>
<td>99.5</td>
</tr>
<tr>
<td>P. spp.</td>
<td>97.7</td>
<td>99.6</td>
</tr>
<tr>
<td>S. marcescens</td>
<td>100</td>
<td>99.9</td>
</tr>
<tr>
<td>P. aeruginosa</td>
<td>100</td>
<td>99.4</td>
</tr>
<tr>
<td>A. baumannii</td>
<td>98.6</td>
<td>99.7</td>
</tr>
</tbody>
</table>

| Gram-Negative Total | 97.6  | 99.6  |

<table>
<thead>
<tr>
<th>Yeast</th>
<th>Spns.</th>
<th>Spec.</th>
</tr>
</thead>
<tbody>
<tr>
<td>C. albicans</td>
<td>100</td>
<td>99.6</td>
</tr>
<tr>
<td>C. glabrata</td>
<td>100</td>
<td>98.4</td>
</tr>
</tbody>
</table>

| Yeast Total | 100   | 99.0  |

| All Identified Organisms | 97.4  | 99.3  |

Data from 2016 FDA clinical trial

Antibiotic Susceptibility Performance

<table>
<thead>
<tr>
<th>Gram-Positive Antibiotic</th>
<th>EA%</th>
<th>CA%</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cephalosporin Ceftaroline</td>
<td>94.9</td>
<td>99.5</td>
</tr>
<tr>
<td>Cyclic Lipopeptide Daptomycin</td>
<td>98.1</td>
<td>99.6</td>
</tr>
<tr>
<td>Glycopeptide Vancomycin</td>
<td>97.2</td>
<td>97.9</td>
</tr>
<tr>
<td>Macrolide Erythromycin</td>
<td>98.3</td>
<td>96.6</td>
</tr>
<tr>
<td>Oxazolidinone Linezolid</td>
<td>98.9</td>
<td>99.6</td>
</tr>
<tr>
<td>Penicillin Ampicillin</td>
<td>100.0</td>
<td>100.0</td>
</tr>
<tr>
<td>Sulfonamide TMP-SMX</td>
<td>96.0</td>
<td>96.0</td>
</tr>
<tr>
<td>Tetracycline Doxycycline</td>
<td>94.4</td>
<td>95.8</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Gram-Negative Antibiotic</th>
<th>EA%</th>
<th>CA%</th>
</tr>
</thead>
<tbody>
<tr>
<td>Aminoglycosides Amikacin</td>
<td>93.8</td>
<td>93.8</td>
</tr>
<tr>
<td>Gentamicin</td>
<td>99.5</td>
<td>98.7</td>
</tr>
<tr>
<td>Tobramycin</td>
<td>96.3</td>
<td>96.0</td>
</tr>
<tr>
<td>Carapenem Ertapenem</td>
<td>98.8</td>
<td>98.5</td>
</tr>
<tr>
<td>Meropenem</td>
<td>96.7</td>
<td>96.9</td>
</tr>
<tr>
<td>Cephalosporins Cefazolin</td>
<td>95.7</td>
<td>85.6</td>
</tr>
<tr>
<td>Cefepime</td>
<td>96.2</td>
<td>95.5</td>
</tr>
<tr>
<td>Ceftazidime</td>
<td>92.4</td>
<td>92.1</td>
</tr>
<tr>
<td>Ceftriaxone</td>
<td>94.7</td>
<td>96.4</td>
</tr>
<tr>
<td>Fluorquinolones Cipro</td>
<td>98.4</td>
<td>98.4</td>
</tr>
<tr>
<td>Monobactams Aztreonam</td>
<td>96.4</td>
<td>97.6</td>
</tr>
<tr>
<td>Penicillin-Inhibitors Amp-Sulb</td>
<td>91.0</td>
<td>82.7</td>
</tr>
<tr>
<td>Pip-Tazo</td>
<td>91.0</td>
<td>90.8</td>
</tr>
<tr>
<td>Polymyxins Colistin</td>
<td>94.9</td>
<td>97.6</td>
</tr>
</tbody>
</table>

EA = Essential Agreement (+/- one MIC dilution)
CA = Categorical Agreement (Correct S,I,R category)

Data from FDA clinical trial - 2016 Software
Accelerate Pheno Implementation Challenges

• DOES NOT replace current methods – requires additional tech time & costs
• Costs – capital equipment, panels
• Storage requirements and waste
• Disclaimers for certain bug-drug combinations
• How to work it into current workflow
• Notification of results – how are the AST results notified? Another phone call to the physician? EMR prompts? Education?
• Impact on clinical management needs to be assessed

Challenges with Direct Detection from Whole Blood

• Often < 1 cfu/mL of pathogen in blood
• Contaminant vs. true pathogen
• Detection of dead organisms
• Random nucleic acid in blood
• Reagent contamination with nucleic acid
• What is the true gold standard?

T2Candida Magnetic Resonance Assay

• T2 Biosystems, Lexington MA
• Principle: PCR, hybridization to probe-decorated nanoparticles; analysis by T2MR
• Uses FDA approved T2Dx fully automated instrument
• Detects 5 yeasts, reports 3 results: C. albicans/ C. tropicalis, C. glabrata/C. krusei, C. parapsilosis
• Clinical trial—12 centers
  • 250 contrived samples; 50 negative samples
  • Overall sensitivity 91.1% per assay; specificity 99.4%
  • 1501 prospective patient samples
  • Mean time to negative result 4.2 h vs > 120 h for conventional blood cultures
  • 4 patients positive by both T2 and standard blood cultures
  • 31 discordant cases: 2 positive BC missed by T2MR; 5 of 29 T2MR pos, culture neg had evidence of fungal infections elsewhere

Predictive Value of T2Candida Based on Disease Prevalence

Rubach MP, Hanson KE. Open Forum Infect Dis 2015.

IRIDICA BAC-BSI IUO Assay

- Manufactured by Abbott Molecular, Inc.
- Principle: Broad range PCR/ESI MS directly from 5 mL of whole blood
- 5 instruments—8 h TAT
- Detects 48 bacterial pathogens; 5 yeasts; 4 resistance markers
- Preliminary study by Bacconi et al. JCM 2014;52:3164
  - 331 patient samples: BAC-BSI detected 35 positives compared to 18 by standard methods
  - 83% sensitive, 94% specific
- RADICAL Study (Vincent JL, et al Crit Care Med 2015; 43:2283-91)
  - 9 ICUs in 6 European countries
  - 616 whole blood samples from 529 patients
  - PCR-ESI MS detected a pathogen in 228 cases (37%) compared to 68 (11%) using culture and missed 13 cases positive by culture
  - Clinical analysis performed by independent investigators suggested altered treatment may have occurred in 57% of patients

Summary

- Various platforms exist that identify organisms directly from positive blood culture bottles
- These assays perform better in monomicrobial cultures than polymicrobial specimens
- All demonstrate significant reductions in time to identification and resistance marker detection
- Outcomes studies are available that demonstrate clinical utility when combined with stewardship
- Assays to detect organisms directly from whole blood are available (T2 Candida assay); others are in clinical trials