can drastically reduce treatment options and rapidly disseminate. Since broad applications of phenotypic (mCIM/eCIM) and PCR-based detection can be labor intensive and costly, we developed an MIC derived algorithm to streamline use of these definitive carbapenemase detection methodologies.

Methods: To develop the testing criteria, a challenge set of PA (n=92), NDM, IMP, VIM, KPC, SPM, GES, cephalosporinase or efflux/porin mutation and wild-type isolates were utilized. Broth microdilution MICs were determined for: ceftazidime (CAZ), cefepime (FEP), piperacillin/tazobactam (TZP), meropenem (MEM), imipenem (IPM), ceftolozane/tazobactam (C/T), and ceftazidime/avibactam (CZA). To assess the utility of CAZ, FEP, TZP, and C/T screening criteria from the challenge set, 1,209 clinical PA isolates from a US surveillance program were tested. Confirmatory genotypic and phenotypic testing for evidence of carbapenemases was conducted on all criteria-derived isolates using the Xpert Carba-R assay and the modified carbapenem inactivation method (mCIM)/EDTA-modified carbapenem inactivation method (eCIM), respectively.

Results: Test performance and characteristics of the challenge set are displayed in **Table 1.** Of the 1,209 clinical isolates, 230 (19%) were IPM and MEM resistant. 116 isolates met the defined criteria (using most common anti-pseudomonal β-lactams) of: IPM and MEM resistance; non-susceptibility to CAZ, FEP, and TZP. Carba-R identified 5 carbapenemase-producing isolates (all bla_{VIM}-positive), while the mCIM/eCIM detected 7 carbapenemase-producing isolates (including the 5 bla_{VIM}-positive isolates).

Table 1. Characteristics of the Challenge Set of 92 P. aeruginosa isolates utilized in algorithm development.

Susceptibility	Carbapenemase Producers, n=57	Non-Carbapenemase Producers,		Test Performance	
		Cephalosporinase or efflux/porin mutation, n=20	Wild Type, n=15	Sensitivity, % (95% CI)	Specificity, % (95% CI)
IPM + MEM- Resistant	57 (100%)	15 (75%)	1 (7%)	100% (94-100%)	54% (37-71%)
IPM + MEM- Resistant AND FEP + CAZ + TZP- Non-Susceptible	57 (100%)	12 (60%)	0 (0%)	100% (94-100%)	66% (48-81%)
IPM + MEM- Resistant AND FEP + CAZ + TZP- Resistant	47 (82%)	6 (30%)	0 (0%)	83% (70-91%)	83% (66-93%)
IPM + MEM- Resistant AND FEP + CAZ + TZP- Non-Susceptible + CZA- Resistant	49 (86%)	8 (40%)	0 (0%)	86% (74-94%)	77% (60-90%)
IPM + MEM- Resistant AND FEP + CAZ + TZP- Non-Susceptible + C/T- Resistant	57 (100%)	4 (20%)	0 (0%)	100% (94-100%)	89% (73-97%)
IPM + MEM- Resistant AND FEP + CAZ + TZP- Non-Susceptible + C/T- Resistant + CZA- Resistant	49 (86%)	3 (15%)	0 (0%)	86% (74-94%)	91% (77-98%)

Conclusion: In the presence of carbapenem resistance, non-susceptibility to FEP, CAZ, and TZP (or C/T when available) is a useful starting point to delineate CP-PA versus non-CP-PA. This MIC criterion combined with either mCIM/eCIM or PCR-based testing is a pragmatic and streamlined approach to identify CP-PA, while providing vital information to guide therapeutic and infection control measures.

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657. Diagnostic Utility of Dedicated Fungal Blood Cultures for Diagnosis of Candidemia

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Session: P-25. Diagnostics: Bacteriology/mycobacteriology

Background: Blood culture techniques have improved to the point where they are considered sensitive enough for detection of *Candida*. Expert guidelines clarifying the utility of use of dedicated fungal isolator cultures are lacking, and we wondered what utility, if any, they add for the diagnosis of candidemia.

Methods: All patients with cultures between March 2016-February 2020 positive for Candida were examined via manual chart review, noting time to positivity and time of initiation of antifungal therapy.

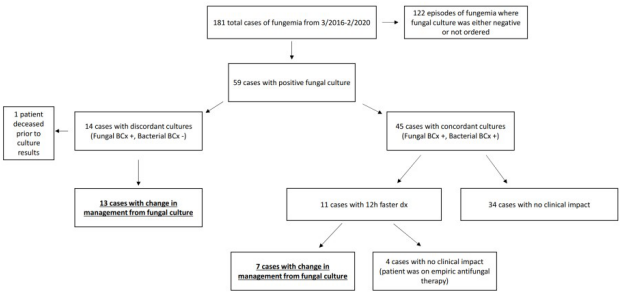
Results: We focused on cases of candidemia where a fungal culture was ordered and turned positive (59 out of the total 181 cases of candidemia). We eliminated an additional 10 cases where fungal cultures were sent while already on antifungal therapy or in patients already known to be fungemic, given our interest in *de novo* diagnoses. Another case was removed due to lack of clinical details, as the patient was discharged prior to culture results and managed at a different medical facility.

There were 14 cases with discordant growth (fungal culture positive, bacterial culture negative). One patient passed away prior to culture results, but in the remaining 13 cases, the fungal culture changed clinical management, in most cases by prompting initiation of antifungal therapy.

The remaining 36 cases involved with concordant growth between bacterial and fungal cultures. In 11 of those cases, the fungal culture isolated yeast 12 or more hours faster than its paired bacterial culture (average 40.7 +/- 26.6 hours). In 7 of these cases, the fungal culture changed management – in the remaining cases, the patient was already on empiric therapy.

Among all cultures sent in patients not receiving antifungals that isolated *Candida,* the overall time to positivity for fungal cultures was 37.2 +/- 13 hours, while bacterial cultures took 54 +/- 26.4 hours.

Fungal Culture Results



Conclusion: Fungal cultures changed management in 20/59 cases of candidemia (34%) either by making the diagnosis faster than a bacterial culture or making it outright. Given the morbidity and mortality associated with candidemia, rapid diagnosis is critically important. More specific guidelines optimizing how to best utilize fungal cultures to help standardize practice among clinicians will be critical going forward.

Disclosures: **Omai Garner, PhD, D(ABMM)**, **Beckman Coulter** (Scientific Research Study Investigator)

658. Effect of HIV Status on Tuberculosis Load as Detected by Xpert MTB/RIF in Sputum vs. Saliva Samples

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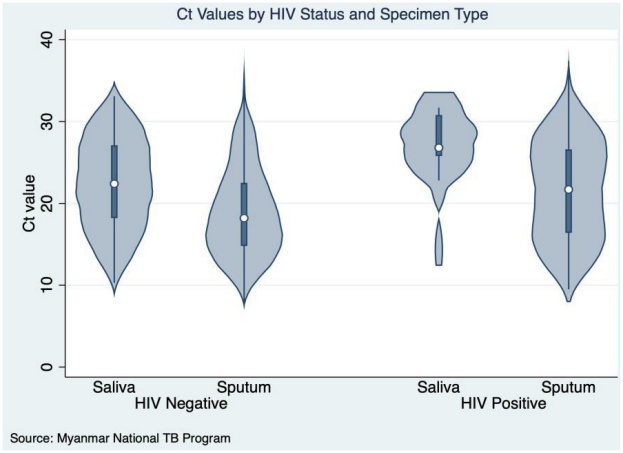
Session: P-25. Diagnostics: Bacteriology/mycobacteriology

Background: Tuberculosis (TB) is the most common co-infection among people living with HIV, but HIV positivity is associated with a lower *Mycobacterium tuberculosis* (MTB) bacillary load in sputum, making TB often difficult to diagnose with current diagnostic solutions. GeneXpert MTB/RIF (Cepheid, USA), a rapid, molecular diagnostic assay, has transformed the TB diagnostic landscape and can be used to diagnose TB and limited drug resistance in HIV patients from direct clinical samples in < 2 hours, but results can be significantly affected by sample bacterial load, which is quantified by the GeneXpert MTB/RIF (Xpert) instrument using Ct values. Our primary objective was to assess how a patient's HIV status affected their MTB bacterial load in sputum vs. saliva samples submitted for Xpert diagnosis of TB.

Methods: We completed a retrospective analysis of >4,000 patient records from the Myanmar National TB Program captured as part of a nation-wide electronic reporting system developed with the assistance of FIND (Geneva). De-identified records included HIV status, Xpert testing results, and for a subset of patients, specimen type. With this diagnostic information, we compared the distribution of MTB load (quantified by Xpert Ct values) in sputum and saliva in HIV positive vs. HIV negative patients using STATA.

Results: Based on mean Ct value comparison independent of HIV status, saliva samples (mean Ct = 22.7) contained a significantly lower bacterial load of MTB as compared to sputum samples (mean Ct=19.2, p < .001).Within saliva samples, a lower bacterial load was also detected in HIV positive patients (mean Ct = 26.9) compared to HIV negative patients (mean Ct = 22.3, p< .05). Similarly, in sputum samples, a lower bacterial load was detected in HIV positive patients (mean Ct = 21.6) compared to HIV negative patients (mean Ct = 19.0, p < .001) (Figure 1).

Figure 1. Ct Values by HIV Status and Specimen Type



Conclusion: Sputum samples have a significantly higher bacterial load on average compared to saliva samples independent of HIV status. Additionally, when looking at both saliva and sputum as sample types, HIV positive patients have significantly lower bacterial load than individuals who are HIV negative. Based on these results, sputum is the optimal sample type for Xpert TB detection, especially in people living with HIV.

Disclosures: **All Authors**: No reported disclosures

659. Evaluation of Four Chromogenic Agars for Urine Culture Including Time and Cost Savings Analysis

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Session: P-25. Diagnostics: Bacteriology/mycobacteriology

Background: With a volume of approximately 5000 urine culture specimens per month in our tertiary-care university center hospital's microbiology laboratory, we wanted to evaluate methods aiming to improve workflow and performance while reducing turnaround time and potentially overall cost.

Methods: 310 urine culture specimens as well as selected less frequent pathogens (*A. urinae* - 26 strains, *C. urealyticum* - 4 strains) were plated on four chromogenic agars in parallel with standard protocol MacConkey (MAC) and blood agar (BA). Chromogenic agars evaluated were: Uri*Select*™ 4 (Bio-Rad), CHROMID® CPS® Elite (bioMérieux), *Brillance*™ UTI *Clarity*™ agar Biplate (Oxoid) and BD™ CHROMagar™ Orientation (BD). Primary outcome was overall growth performance for frequent pathogens and for gram positives, where chromogenic agars were previously reported to underperform.The number of additional tests needed and the appreciation of different media by laboratory personnel were also assessed. A sub-analysis measured the total time required to plate and to read 50 consecutive specimens comparatively for the 4 chromogenic agars and for MAC/BA.

Results: Global performance was 90% for Uriselect, 88% for ChromID, 89% for Chromagar and 81% for Brillance compared to 84% for standard method. ChromID and Brillance supported the growth of more *A. urinae* and *C. urealyticum* than the other 2 chromogenic agars. All monoplate chromogenic agars were appreciated equally by technologists. In addition, for all chromogenic agars, working time was reduced by half as compared to MAC/BA. We estimated a time economy of approximately 80 hours per month in our laboratory, translating in a net annual economy.

Conclusion: All 4 chromogenic medias evaluated in our study had an acceptable performance, with specific strengths and weaknesses for each one. The choice of ChromID CPS Elite (bioMérieux) for our center was based on pre-established criteria including performance for more fastidious gram positives, best time and cost economy, and compatibility with current identification method and susceptibility testing platform. However, since the 4 chromogenic agars have been adequately verified in our laboratory, we consider that they could be interchangeable if needed.

Disclosures: **All Authors**: No reported disclosures

660. Evaluation of Qvella's FAST-Prep™ Liquid Colony™ for Early Antimicrobial Sensitivity Testing of Positive Blood Culture by Disk Diffusion Method

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Session: P-25. Diagnostics: Bacteriology/mycobacteriology

Background: Conventional antimicrobial susceptibility testing (AST) of microorganisms from positive blood cultures (PBC) can take ≥ 2 days. In order to improve the turnaround time for AST on a PBC, CLSI and EUCAST have made efforts to standardize procedures for disk diffusion (DD) direct from a PBC. Qvella Corporation (Richmond Hill, ON, Canada) has recently developed FAST-Prep, an automated centrifugal sample preparation system that rapidly delivers a Liquid Colony consisting of a purified, concentrated, viable cell suspension directly from a PBC. This study was performed to investigate the feasibility of DD AST off of a PBC using a FAST-Prep Liquid Colony.

Methods: Contrived PBC samples were prepared by spiking 6 species of Gram-positive and 4 species of Gram-negative bacteria (3-5 strains per species) into FA® Plus bottles and incubating in the BACT/ALERT® VIRTUO® System (bioMerieux, Durham, NC). After positivity, 3 mL of PBC was added to the FAST-Prep cartridge. After 20 minutes of processing in the FAST-Prep instrument, the Liquid Colony was removed from the cartridge and a 0.5 McFarland sample was prepared for DD AST. In parallel, the DD AST from a PBC was performed using 4 drops of PBC (CLSI direct method). Both methods were compared to conventional colony-based DD AST. After 16-18 hours of incubation zone diameters and S/I/R interpretations were determined. Categorical agreement (CA) and errors for both DD AST methods were calculated. In addition, colony plate counting was performed on 0.5 McFarland suspensions of Liquid Colony and the plate colony to determine biomass recovery and sample purity.

Results: CA for a FAST-Prep DD AST for Gram-positive and Gram-negative bacteria was 95.6% and 98.6%, respectively, compared to CA for CLSI DD AST of 77.2% and 81.9%, respectively. Biomass in the Liquid Colony was $7.2x10^8$ and $1.2x10^9$ CFU for Gram-positive and Gram-negative bacteria, respectively. Cell concentration in the 0.5 McFarland suspension of the Liquid Colony was $3.7x10^7$ and $5.9x10^7$ CFU/mL for Gram-positive and Gram-negative bacteria, respectively, which was similar to the concentration for the reference colony suspension.

Conclusion: The results support the potential role of FAST-Prep in providing a Liquid Colony for use in rapid AST.

Disclosures: Susan M. Novak-Weekley, PhD, D(ABMM), Qvella (Employee, Shareholder) Aye Aye Khine, PhD, Qvella (Employee, Shareholder) Tino Alavie, PhD, Qvella (Employee) Namidha Fernandez, MS, Qvella (Employee) Laxman Pandey, MS, Qvella (Employee) Abdossamad Talebpour, PhD, Qvella (Employee, Shareholder)

661. Futility of Bacterial Bone Marrow Cultures: Experience over a 19 Year Period

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Session: P-25. Diagnostics: Bacteriology/mycobacteriology

Background: Bone marrow biopsies are often performed on patients with unclear diagnoses and cultures may be ordered for both routine bacterial, mycobacterial and fungal pathogens. They are performed in semi-sterile conditions and involve needle penetration through the skin, posing an increased risk of skin contamination. These cultures also require a substantial amount of laboratory personnel time.

Methods: Cultures collected from 2001-2020 were surveyed in the lab electronic record. We assessed the culture type (fungal, bacterial, mycobacterial), and the presence of pathogens and contaminants. An organism was deemed a contaminant if it was consistent with skin flora or listed as a contaminant in the report given to the physician. Organisms for which the role in bone marrow disease is unclear were included as possible pathogens. For questionable non-contaminant organisms, clinical significance was determined based on if patient was treated for the organism. For all bone marrow cultures, growth of the same organism within 1 month of the bone marrow specimen was surveyed to determine whether the organism would have been found by alternative methods.

Results: Of 483 bacterial bone marrow cultures, there were 110 (23%) positives, of which 76 (69%) were deemed contaminants. Twenty (18%) of the 76 contaminants grew in the routine bacterial culture. However, 49 (65%) contaminants grew in the AFB culture, of which 10 also grew in the bacterial culture. For the 34 non-contaminant organisms, 26 were determined to be clinically significant. Nineteen of the 26 had a matching culture (usually blood) growing the organism within 1 month. The majority of pathogens were mycobacteria (18 of the 34). Fungal organisms represented 5 cultures and 11 were bacterial. Of the 11 bacterial organisms, 1 was a *Helicobacter* species (grown in special media), and 4 had a matching positive blood culture. Only 4 (1% of 483) bacterial non-contaminants grew in the routine bacterial culture. Given an unknown number of true negatives, we can only conclude a positive predictive value (PPV) of 0.16 for routine bacterial cultures. Including AFB and fungal cultures, the PPV increased to 0.30.

Conclusion: Our findings indicate that routine bacterial bone marrow culture is unlikely to yield a novel result and is likely a poor use of lab resources.

Disclosures: **All Authors**: No reported disclosures

662. Identification of Clinically Relevant Microbes with the MasSpec Pen

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Session: P-25. Diagnostics: Bacteriology/mycobacteriology

Background: In the age of antimicrobial resistance, rapid identification of infectious agents is critical for antimicrobial stewardship and effective therapy. To this end, ambient ionization mass spectrometry techniques have been applied for rapid identification of microbes directly from culture isolates. We have developed a handheld, mass spectrometry-based device, the MasSpec Pen, that permits direct molecular analysis of