revealing symptoms among FMO and BMO, respectively, with no significant difference. Tenderness to palpation of the mastoid bone (64.3% vs 38.9%; p=0.02) and stenosis of the external auditory canal (92.9% vs 72.2%; p=0.02) were significantly more frequent among FMO cases. Complications were significantly more frequent among FMO cases (42.9% vs 9.3%; p< 0.001). Treatment duration was significantly longer among FMO cases (70[40-90] days vs 45[34-75] days; p=0.03).

Conclusion: Our study showed that FMO affected more frequently the elderly and diabetic patients, when compared with BMO. Regardless of the causative agent, the clinical presentation was similar. However, the outcome was poor among FMO cases with the occurrence of complications, requiring a longer duration of treatment.

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652. Comparison of fosfomycin (FOF) activity and prevalence of subpopulations between Escherichia coli (EC) and Klebsiella pneumoniae (KP) during susceptibility testing

Jadyn C. Anderson[1]; Amanda R. Krueger, BS[1]; Elizabeth C. Smith, BS[1]; Morgan L. Bixby, BS[1]; Hunter V. Brigman, BS[1]; Elizabeth B. Hirsch, PharmD[2]; [1]University of Minnesota College of Pharmacy, Minneapolis, MN; [2]University of Minnesota, Minneapolis, MN

Session: P-25. Diagnostics: Bacteriology/mycobacteriology

Background: In the United States, interpretive criteria for FOF are established only for EC, yet those criteria are often extrapolated to KP. Recent studies have highlighted both inferior clinical outcomes after FOF treatment and difficulties in interpretation of inner colony subpopulations, the presence of which may affect clinical efficacy. We sought to compare FOF activity against EC and KP and to determine the prevalence of inner colony subpopulations following disk diffusion (DD) testing of the two species.

Methods: A convenience collection of 73 KP and 42 EC isolates from 3 U.S. institutions were included. Minimal inhibitory concentration (MIC) testing was performed in duplicate on separate days using agar dilution (AD) and DD as recommended by the Clinical and Laboratory Standards Institute guidelines, with application of EC susceptibility (≤ 64mg/L) breakpoints. The frequency and counts of inner colonies observed during DD testing was calculated, and colonies were subcultured for use in future studies.

Results: $MIC_{50/90}$ values were 1/16 mg/L and 32/256 mg/L for EC and KP respectively. All EC isolates were considered susceptible and therefore categorical agreement was 100%. The majority of KP isolates were considered susceptible (83.6% with AD and 86.3% with DD) and categorical agreement between the methods was 84.9%. Inner colonies were observed during DD testing in 88.1% of EC isolates and 80.8% of KP isolates during at least one replicate, with 47.6% of EC isolates and 39.7% of KP isolates showing inner colony growth during both DD test replicates. More than 10 inner colonies were observed in 50% of EC isolates compared to 12.3% of KP isolates.

Conclusion: KP isolates demonstrated considerably higher FOF MIC values compared to EC, as evidenced by $MIC_{50/90}$ values 4-5 dilutions higher than those for EC. The categorical agreement rate was higher among EC than KP, highlighting concerns regarding the practice of extrapolating FOF susceptibility breakpoints for EC to KP. The high frequency of inner colonies observed in DD for both species necessitates further studies to determine best practices for interpreting their relevance, fitness, and resistance in order to identify potential impacts to clinical efficacy of FOF.

Disclosures: **Elizabeth B. Hirsch, PharmD**, **Merck** (Grant/Research Support)**Nabriva Therapeutics** (Advisor or Review Panel member)

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653. Comparison of Yeasts identification by Biofire, Culture and ePlex for Quality Assurance purpose

jeffrey lin, DO[1]; Thein Myint, MBBS[1]; Vaneet Arora, MD, MPH[1]; Julie A. Ribes, MD, PhD[1]; [1]University of Kentucky, lexington, Kentucky

Session: P-25. Diagnostics: Bacteriology/mycobacteriology

Background: At the University of Kentucky Medical center (UKMC), positive fungal blood cultures are concurrently run through the Biofire Blood Culture Identification (BCID) panel which detects 5 *Candida* species. The newer platform, the GenMarkDx ePlex BCID-FP (fungal panel) is designed to detect 16 fungal targets. Our study compares the performance of the Biofire BCID panel's with culture as the gold standard method. We examine the percentage of agreement by both testing methods and predict the performance of the GenMarkDx ePlex BCID-FP panel based on culture results. We also look at the number of other yeasts not included in Biofire BCID panel that could be picked up by the GenMarkDx ePlex BCID-FP panel.

Methods: Positive fungal blood cultures from July 1, 2018 to June 30, 2019 were run through the Biofire BCID panel. Culture results were used to extrapolate whether the GenMarkDx ePlex FP would provide any additional diagnostic benefit. Results were categorized as true or false positives and negatives as compared to culture as the gold standard.

Results: A total of 141 blood cultures were tested via the Biofire BCID panel for the identification of yeasts. Of these, 123 (87%) yielded Biofire results in concordance with culture results. We would expect these also to be positive on the GenMarkDx ePlex BCID-FP panel. In addition, 18 specimens (13%) would have tested positive on the GenMarkDx ePlex BCID-FP panel and not the Biofire BCID panel. These organisms were noted to be *Candida lusitaniae* (n=6), *Cryptococcus neoformans* (n=3), *Candida dublinensis* (n=2), and *Candida keyfr* (n=1). Organisms that were found on culture that were not detected by both GenMarkDx ePlex BCID-FP panel and Biofire

BCID panel were *Candida nivariensis* (n=2), *Pichia ohmeri* (n=1), *Trichospon* species (n=2).

Conclusion: Based on these data, we expect that the ePlex would have correctly identified 95.9% of the yeasts in this patient population. This represents an additional 18 (13%) of specimens that could be detected rapidly from the positive blood culture if the GenMarkDx ePlex BCID-FP panel were used instead of the Biofire BCID panel. Early identification can influence the choice of antifungal agent. Less than 5 % of the yeasts would have remained unidentified by ePLex compared to 13% for Biofire.

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654. Core Antibiotic-Induced Transcriptional Signatures Reflect Susceptibility to All Members of an Antibiotic Class

Melanie A. Martinsen, BS[1]; Roby P. Bhattacharyya, MD, PhD[2]; [1]Broad Institute, Boston, Massachusetts; [2]Massachusetts General Hospital, Boston, Massachusetts

Session: P-25. Diagnostics: Bacteriology/mycobacteriology

Background: Current growth-based antibiotic susceptibility testing (AST) is too slow to guide key clinical decisions. We previously demonstrated a combined **Gen**otypic and **Phe**notypic **AST** assay using **R**NA detection (GoPhAST-R) that can provide AST in < 4h directly from blood culture, 24-36h faster than standard growth-based methods. GoPhAST-R quantifies specific mRNA expression signatures using the multiplexed hybridization RNA-detection platform, NanoString. After brief antibiotic exposure, susceptible cells become stressed, eliciting transcriptional changes that distinguish them from unharmed resistant cells. Here, we assess the generalizability of transcriptional signatures of susceptibility within an antibiotic class.

Methods: For *Escherichia coli* and *Klebsiella pneumoniae*, we assessed the ability of the top ten antibiotic-responsive genes previously identified for ciprofloxacin, gentamicin, and meropenem to predict susceptibility to two other fluoroquinolones (FQ), two other aminoglycosides (AG), and six other beta-lactams (BL), respectively, across 6-8 clinical isolates for each drug for a total of 184 pathogen-drug pairs. After standardized antibiotic exposure (60m for FQs and AGs, 120m for BLs, each at its CLSI breakpoint MIC), samples were mechanically lysed and used as input for NanoString assays as previously described (Bhattacharyya, Nat Med 2019).

Results: In both species, the top ten genes identified for AST of ciprofloxacin, gentamicin, and meropenem showed similar normalized fold-induction upon treatment with three FQs, three AGs, and seven BLs, respectively, allowing robust distinction of susceptible and resistant isolates (Fig 1).
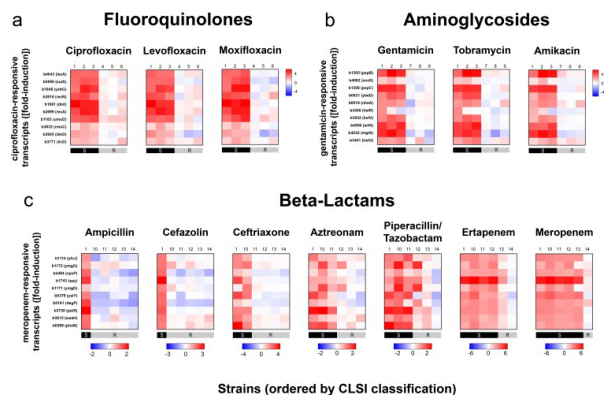
Figure 1

Figure 1. Heatmaps of normalized, log-transformed fold-induction of the top ten antibiotic-responsive transcripts from *E. coli* for ciprofloxacin (a), gentamicin (b), and meropenem (c) upon exposure to other fluoroquinolone (a), aminoglycoside (b), and beta-lactam (c) antibiotics. Strains, denoted by numbers over the heatmap columns, were treated at CLSI breakpoint concentrations for each respective drug. Gene identifiers for antibiotic-responsive transcripts are listed with gene names at the left of each antibiotic class panel. CLSI classifications of each strain based on broth microdilution are shown below (S, susceptible; R, resistant).

Conclusion: We show that a shared set of genes optimized for AST of one antibiotic can predict susceptibility to all members of that drug class, consistent with a conserved core transcriptional response related to mechanism of action. We demonstrate this phenomenon for two common pathogens with propensity for multidrug resistance treated with multiple members of three major antibiotic classes in common clinical use. This unified set of genes for susceptibility prediction would streamline GoPhAST-R implementation, in turn facilitating efficient deployment of antibiotics and reducing unnecessary broad-spectrum use.

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656. Development and Application of a Pragmatic Algorithm for the Detection of Carbapenemase-Producing Pseudomonas aeruginosa (CP-PA)

Christian M. Gill, PharmD[1]; Tomefa E. Asempa, PharmD[2]; David P. Nicolau, PharmD[2]; [1]Center for Anti-Infective Research & Development, Hartford Hospital, Hartford, Connecticut; [2]Hartford Hospital, Hartford, CT

Session: P-25. Diagnostics: Bacteriology/mycobacteriology

Background: Historically, carbapenem-resistance in *P. aeruginosa* (PA) has been mediated by inducible AmpC, drug efflux, and porin loss; however, carbapenemase production is an increasingly recognized entity. Of these mechanisms, carbapenemases