within 2 weeks were included only once. Patients with recurrent BSI after more than 2 weeks of negative blood cultures were considered distinct cases and included more than once. Carbapenem resistance was defined as an imipenem minimum inhibitory concentration of ≥2 µg/ml. Extensive EMR data for each patient were compiled into a relational database using SQLLite. Possible risk factors for carbapenem resistance were queried from the database and analyzed via univariate methods. Significant factors were then entered into a multiple logistic regression model in a forward stepwise approach using SPSS.

**Results.** A total of 613 cases of *K. pneumoniae* BSI were identified in 540 unique patients. The overall incidence of imipenem resistance was 10% (61 cases). Significant markers of resistance included in the final model were (1) prior colonization with imipenem-resistant *Klebsiella pneumoniae*; (2) hospital unit (defined as high-risk unit, low-risk unit, and emergency department); (3) total inpatient days in the previous 5 years; (4) total days of oral or parenteral antibiotics in the past 2 years; and (5) age >60 years old (Figure 1). The model generated a receiver operating characteristic curve with an area under the curve of 0.75 (Figure 2). At a cut point of 0.083, the model correctly predicted 72% of imipenem-resistant cases while incorrectly labeling 32% of susceptible cases as resistant (Sn = 72%, Sp = 63%, Figure 3).

**Conclusion.** A multiple logistic regression model using EMR data can generate immediate, clinically useful predictions of carbapenem resistance in patients with *K. pneumoniae* BSI. Larger data sets are needed to improve and validate these findings.

**Figure 1. Algorithm variables**

**Figure 2. Receiver operating characteristic curve**

**Figure 3. Classification table**

**Disclosures.** All authors: No reported disclosures.

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**989. Direct Detection and Identification of Prosthetic Joint Pathogens in Synovial Fluid by Metagenomic Shotgun Sequencing**

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**Background.** Detection and identification of microorganism(s) involved in peri-prosthetic joint infection (PJI) can inform surgical management and directed antibiotic therapy. Metagenomic shotgun sequencing is a powerful tool with the potential to change how many PJI are diagnosed as it allows direct detection and identification of pathogens in clinical specimens. In the largest series to date, we utilized a metagenomics-based approach applied to SF to define potential microbial etiologies of failed total knee arthroplasties (TKAs).

**Methods.** Synovial fluid was collected from 112 failed TKAs (74 PJI and 38 aseptic implant failure [AF]) via preoperative arthrocentesis. Cell count and differential, standardized culture and DNA-based metagenomic shotgun sequencing were performed. Human DNA was depleted using the MoYsis basic kit prior to DNA extraction, whole genome amplification, and sequencing. Taxonomic assignment of reads and pathogen identification was achieved using a pipeline incorporating k-mer- and marker gene-based classification software. A scheme for analysis and filtration of false-positives was created and applied, incorporating cut-offs for the number of reads, quality scores, and coverage across a reference genome. Patients were classified as having PJI using the IDSA criteria and expert review. Analyses were recorded as percent agreement, with 95% confidence intervals (CI) of metagenomics to SF culture.

**Results.** Metagenomic analysis identified the known pathogen in 54 (90%) (CI, 79.5%–96.2%) of the 60 culture-positive PJI analyzed and one (2%) (CI, 0.0%–8.9%) potential polymicrobial infection not detected by culture. For the 14 culture-negative PJI enrolled, metagenomic analysis showed a sensitivity of 79% (CI, 49.2%–92.4%) while BioFire™ respiratory panel (RP) sensitivity was <20% (CI, 7.9%–31.7%). For potential findings; potential pathogens were identified in three (2%) (CI, 4.7%–50.8%) culture-negative PJI cases, with one potential microbial. Of the 37 culture-negative AF cases, metagenomics showed 97% (CI, 85.8%–99.9%) agreement with negative culture and identified one (3%) (CI, 0.0%–14.2%) potential pathogen. For the one culture-positive AF case, metagenomic results were negative, suggesting possible culture contamination.

**Conclusion.** Metagenomic shotgun sequencing performed on SF can be used to diagnose PJI and may be particularly useful for culture-negative PJI.

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**990. Clinical Impact of Two Different Multiplex Respiratory Panel Assays on Management of Hospitalized Children Aged ≤24 months**

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**Background.** Highly multiplexed molecular assays are popular in clinical laboratories due to their high sensitivity, specificity and relatively rapid turn-around time (TAT) for results. Luminex® respiratory viral panel (RVP) detects 12 respiratory viruses, while BioFire™ respiratory panel (RP) detects 20 respiratory pathogens (17 viruses, 3 bacteria). The aim of the current study was to compare the impact of RVP and RP assay on management of hospitalized children aged ≤24 months.

**Methods.** Retrospective data were collected to compare the clinical impact from two multiplex molecular assays (RVP, December 2008–May 2012; RP August 2012–June 2015) on management and outcomes of hospitalized patients. Patients aged ≤24 months and positive for at least one respiratory virus were included. Patients who were (1) receiving immune suppressive therapy, (2) neonates requiring intensive care, (3) receiving immune suppressive therapy and had evidence of contamination.

**Results.** A total of 810 patients in RVP and 2,095 patients in RP group were included. The median TAT for RVP and RP assay were 29 hours (IQR 26–58 hours) and 4 hours (IQR 2–8 hours), respectively (P < 0.001). Following PCR test reporting, the rate of antibiotic discontinuation was significantly higher in RVP group (28%, 595/2095) compared with RP group (22%, 135/595) vs. RVP group (135/595) vs. RVP group (135/595) vs. RVP group (P < 0.001). Antibiotics were discontinued more often in older children aged 6–24 months (23%, 113/492) compared with children aged < 60 days (11%, 34/297) (P < 0.001). Following positive influenza test results, more children received timely oseltamivir in the RP group (85%, 48/56) compared with the RVP group (17%, 74/415) (P < 0.001). The median length

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of hospitalization (LOH) was shorter in the RP group (48 hours, IQR 32–76 hours) than in the RVP group (54 hours, IQR 39–89 hours) (P < 0.001).

Conclusion. Rapid availability of test results from RP assay was associated with reduced antibiotic use, timely antiviral therapy and decreased LOH. The implementation of a more comprehensive respiratory multiplex molecular assay with rapid reporting of test results has the potential to improve management of hospitalized children, decrease unnecessary antibiotic therapy and reduce overall costs.

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991. Clinical Yield of Routine Use of Molecular Testing for Adult Outpatients with Diarrhea

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Background. Molecular diagnostics for enteropathogens increase yield while reducing turnaround time. However, many pathogens do not require specific therapy, and the expense is substantial.

Methods. We reviewed the use of the FilmArray GI Panel (BioFire Diagnostics, Salt Lake City, Utah) in adult outpatients at the University of Virginia and identified clinical features that could limit testing without reducing yield. We defined yield as (a) detection of a pathogen with knowledge of drug susceptibility, (b) detection of a pathogen for which antimicrobial therapy is indicated, or (c) detection of a pathogen that can change management, which additionally included viral pathogens in immunocompromised patients.

Results. Between March 23, 2015 and February 25, 2016, we reviewed 452 tests from 311 adult outpatients with diarrhea. A pathogen was detected in 202/452 (44.7%) tests. The most common pathogens were: enteropathogenic E. coli (36; 8.0%), norovirus (17; 3.8%), Campylobacter (7; 1.5%), enteroaggregative E. coli (6; 1.3%), Giardia (6; 1.3%), and sapovirus (5; 1.1%). Based on clinical guidelines, antimicrobial treatment was clinically indicated for 19/202 subjects (4.2%). Limiting testing to patients with an additional enteric symptom or flatulence, a travel history, or an immunocompromising condition did not improve testing efficiency. The overall positive predictive value was 21.6% (95% CI: 15.7%, 28.2%). Other changes did not improve testing efficiency.

Conclusion. Testing could be reduced by 36.3% without decreasing clinical yield by limiting testing to patients with diarrhea with an additional enteric symptom and no history of vomiting, a travel history, or an immunocompromising condition. ACG guidelines did not improve testing efficiency.

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992. Enteropathogen Detection in Children with Diarrhea and/or Vomiting: A Cohort Study Comparing Rectal Flocked Swabs and Stool Specimens

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Background. Diarrheal stool samples are currently preferred for enteropathogen detection, but they are inconvenient to collect if they are not immediately available, leading to suboptimal return rates and delayed or missed diagnostic opportunities. We sought to compare the enteropathogen yields of rectal swabs and stool specimens in an outpatient cohort of children with diarrhea and/or vomiting.

Methods. Eligible children were < 18 years of age, with ≥3 episodes of vomiting or diarrhea in 24 hours and <7 days of symptoms. After excluding those enrolled within the prior fortnight, unable to follow-up, having psychiatric illness, neuromotor, or requiring parenteral fluid replacement, we attempted to collect a rectal flocked swab and stool sample from participants. Specimens were subjected to testing with the Lumixen xTAG Gastrointestinal Pathogen Panel, an in-house 5-virus panel and bacterial culture. Primary outcomes were comparative (submitted paired specimens only) and overall (all specimens, unsubmitted specimens analyzed as negative) yields. We used McNemar’s test to conduct pathogen-specific analyses, and generalized estimating equations to perform global (i.e., any) pathogen analyses with adjustments made for the presence of diarrhea, location, and their interactions with specimen type.

Results. Of the 1,519 subjects enrolled, 1,147 (75.5%) and 1,514 (99.7%) provided stool and swab specimens, respectively. The proportions of specimens positive for any pathogen were 75.9% (87/114) and 67.6% (102/151) (P = 0.0001). Comparative yield adjusted OR in stool relative to swabs were 1.24 (95% CI: 1.11, 1.38) and 1.76 (95% CI: 1.47, 2.11) in children with and without diarrhea at presentation, respectively. Overall concordance analysis yielded a kappa of 0.76 (95% CI: 0.71, 0.80). Paired positive viral specimens had lower median cycle threshold values (8 higher viral loads; P < 0.0001) in SsSs compared with swabs for all viruses. In overall yield analysis, the proportions positive for a pathogen were 57.3% and 67.4% for stool and rectal swabs, respectively; unadjusted OR: 0.65 (95% CI: 0.59, 0.72) for stool relative to swab.

Conclusion. Rectal swabs should be performed when enteropathogen identification, and/or rapid detection, is needed, molecular diagnostic technology available, and stool not immediately available.

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993. Rapid Phenotypic Antibiotic Susceptibility Testing Through RNA Detection

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Background. Culture-based antibiotic susceptibility testing, the gold standard, is too slow to guide early antibiotic selection, while newer genotypic methods require cumbersome mechanisms to predict phenotype. Quantitative measurement of key antibiotic-responsive transcripts offers a rapid, phenotypic assay for assessing antibiotic susceptibility, agnostic to the genetic basis for resistance.

Methods. We performed RNA-Seq on Klebsiella pneumoniae and Acinetobacter baumannii treated with cefepimox, gentamicin, or meropenem for 0, 10, 30, and 60 minutes. For each, we identified 50 responsive transcripts whose expression levels differ most between susceptible and resistant organisms upon antibiotic exposure. We measured their expression using a multiplexed fluorescent RNA hybridization assay (NanoString) in 69 clinical isolates, including a “test of set” of multidrug-resistant strains from the CDC, in an 8-hour assay. Gene expression data from test strains were compared against known susceptible and resistant isolates to generate a transcriptional susceptibility metric. We also designed NanoString probes to detect 5 carbapenemase genes (CarbMapenemase Detection Assay, CDC). Each gene fragment was 400–500 bp, including the open reading frame, 5’ UTR, and 3’ UTR.

Results. Across all bacteria-antibiotic pairs tested, a susceptibility metric derived from these transcriptional assays correctly grouped isolates in 167 of 173 tests (Table 1), with 1 of 88 resistant isolates classified as susceptible. Five of six incorrectly grouped isolates were within one dilution of the breakpoint MIC, including the misclassified resistant isolate.

Table 1. RNA signature results

| Susc | Intd | Res |
|------|------|-----|
| Actual (MIC) | 79 | 3 | 1 |
| | 1 | 3 | 1 |
| | 1 | 3 | 1 |

We also detected all five targeted carbMapenemase genes.

Conclusion. We demonstrate phenotypic antibiotic resistance detection based on fluorescent RNA detection in an 8-hour assay. We have previously published proof-of-concept studies that this assay may be run on a positive blood culture bottle with minimal sample processing. By coupling this phenotypic assay with detection of genetic resistance determinants (determined for carbapenemases) in a single assay, strains with unexplained resistance can be prioritized for further study.

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995. Tracking an Unusual Carbapenemase-producing Organism from Drains to Patient Using Whole Genome Sequencing

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Session: 134. Where Did That Come From? Transmission Risks in Healthcare
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Background. The NIH Clinical Center conducts patient and environmental surveillance for carbapenemase-producing organisms (CPO). Previous investigation revealed that sink drains can become colonized with CPO. Subsequent surveillance targets included potential aqueous reservoirs, such as floor drains of environmental services (EVS) closets.

Disclosures. All authors: No reported disclosures.