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 their yield is multifaceted.

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, (b) detection of a pathogen for whom 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 adult outpatients with diarrhea. A pathogen was detected in 88/452 (19.5%) from adult outpatients with diarrhea. A pathogen was detected in 88/452 (19.5%). The clinical features that could limit testing without reducing yield. We defined yield as (a) detection of a pathogen, (b) detection of a pathogen for whom antimicrobial therapy is indicated, or (c) detection of a pathogen that can change management, which additionally included viral pathogens in immunocompromised patients.

Conclusion. Molecular diagnostics for enteropathogens increase yield while reducing turnaround time. However, many pathogens do not require specific therapy, and their yield is multifaceted.

Disclosures. All authors: No reported disclosures.

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, too slow to guide early antibiotic selection, while newer genotypic methods require unmet clinical need for earlier diagnostic capability. We performed RNA-seq on Klebsiella pneumoniae and Acinetobacter baumannii treated with cefepime, gentamicin, or meropenem for 0, 10, and 60 minutes. For each, we identified 50 responsive transcripts whose expression levels differed 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 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 carbapenem genes (NDM-1, OXA-48, KPC-3, VIM-2, IMP-1) and 67 phenotypes. Quantitative measurement of key bacterial-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 cefepime, gentamicin, or meropenem for 0, 10, and 60 minutes. For each, we identified 50 responsive transcripts whose expression levels differed 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 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 carbapenem genes (NDM-1, OXA-48, KPC-3, VIM-2, IMP-1) and 67 phenotypes. Quantitative measurement of key bacterial-responsive transcripts offers a rapid, phenotypic assay for assessing antibiotic susceptibility, agnostic to the genetic basis for resistance.

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 only 1 of 88 resistant isolates misclassified 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 |
|------|-----|-----|
| 79   | 3   | 1   |
| 1    | 1   | 87  |

We also detected all five targeted carbapenemase 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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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.

We also detected all five targeted carbapenemase 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.

Disclosures. All authors: No reported disclosures.
Methods. Premoistened swabs were used to culture sink drains, floor drains, and equipment for CPO. Perirectal swabs were ordered monthly for all patients in non-behavioral health wards. Specimens were plated to CRE- and ESBL-selective media, and colonies identified by MALDI-TOF. The presence of the blaKPC gene was confirmed by PCR. When environmental CPO isolates were detected, EVS procedures and practices were reviewed.

Results. In June 2016, blaKPC-L. adecarboxylata was isolated from an EVS closet floor drain, and in August 2016, from drains in four additional closets. In the previous 10 years, Ledeceia sp. was isolated just once from a clinical culture. In September 2016, routine surveillance revealed new-onset L. adecarboxylata colonization in a stem cell transplant recipient. Investigation included 33 cultures collected from sink and floor drains, EVS equipment, and other items. Environmental samples, especially mop buckets, were identified as a likely point source due to their use in patient care areas and closets with contaminated floor drains. Among seven mop buckets sampled, one grew L. adecarboxylata. Whole genome sequencing demonstrated genetic relatedness of the Ledeceia isolates. Floor cleaner was changed to a disinfectant solution. Extensive decontamination of 67 ECVs closets and equipment was performed urgently. No further patient or environmental cultures have grown L. adecarboxylata.

Conclusion. The recovery of a highly unusual organism, rarely found in clinical specimens, that was also carrying a KPC plasmid, allowed us to detect environmental spread of this organism in the hospital. The ability to track this organism using genetic sequencing provided strong evidence of the mode of spread, leading to effective remediation. No evidence-based methods exist for remediating drain contamination, which can serve as a potential reservoir for transmission.

Disclosures. All authors: No reported disclosures.

996. Bare Below the Elbows: A Randomized Trial to Determine Whether Wearing Short-Sleeved Coats Reduces the Risk for Pathogen Transmission

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Session: 134. Where Did That Come From? Transmission Risks in Healthcare

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Background. Physicians’ white coats are frequently contaminated, but seldom cleaned. Therefore, in the UK, a “bare below the elbows” dress code policy includes a recommendation that personnel wear short sleeves. However, it has not been demonstrated that wearing short sleeves reduces the likelihood of pathogen transmission.

Methods. We conducted a randomized, crossover trial involving simulated patient care interactions to test the hypothesis that transmission of pathogens occurs less frequently when personnel wear short- vs long-sleeved coats. Healthcare personnel were randomized to wear either long- or short-sleeved white coats during simulated care of a mannequin contaminated with cauliflower mosaic virus DNA followed by examination of the mode of spread, leading to effective remediation. No evidence-based methods exist for remediating drain contamination, which can serve as a potential reservoir for transmission.

Results. During work rounds, physicians were observed to determine how often the sleeves of long-sleeved coats frequently contacted the patient/mannequin or environment. During simulations if they were wearing long-sleeved coats.

Conclusion. The recovery of a highly unusual organism, rarely found in clinical specimens, that was also carrying a KPC plasmid, allowed us to detect environmental spread of this organism in the hospital. The ability to track this organism using genetic sequencing provided strong evidence of the mode of spread, leading to effective remediation. No evidence-based methods exist for remediating drain contamination, which can serve as a potential reservoir for transmission.

Disclosures. All authors: No reported disclosures.

997. Defining Aerosol Generating Procedures and Pathogen Transmission Risks in Healthcare Settings

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Background. Questions remain about the degree to which small particle aerosols are generated during patient care activities and whether such aerosols could transmit viable pathogens to healthcare personnel. This project measured aerosol production during common medical procedures and collected samples for pathogen recovery.

Methods. Six procedures were targeted for aerosol sampling: extubation, bronchoscopy, mechanical ventilation, noninvasive ventilation, suctioning (open or tracheotomy), and nebulized medication administration. Any patient undergoing one of these procedures was eligible for sampling, with a preference for patients with a respiratory viral infection. Baseline samples were collected when possible. Four real-time aerosol characterization instruments were used to detect small particle aerosols generated during procedures. SKC Biosamplers, placed at 3 feet and 6 feet from the patient, were used for pathogen recovery. All samples were subjected to bacterial culture; viral PCR, and viral culture were added depending on the patient’s respiratory disease profile.

Results. Samples were collected during extubation (n = 1), bronchoscopy (n = 3), mechanical ventilation (n = 13), noninvasive ventilation (n = 6), suctioning (n = 6), and nebulized medication administration (n = 9). Only nebulized medication administration exhibited differences in particle mass concentration between baseline and procedure aerosol measurements. None of the Biosampler samples were PCR positive for a respiratory virus and none had a positive influenza culture. Five samples had positive bacterial cultures, mainly with common environmental or skin contaminants such as Micrococcus luteus, Staphylococcus aureus, and Bacillus flexus.

Conclusion. Significant small particle aerosol generation was only seen with nebulized medication administration. No viruses were recovered and minimal viable bacteria were recovered. Additional study is needed to confirm these findings and examine aerosol generation during other procedures commonly considered to be aerosol-generating.

Figure 1: Particle number concentration measurements for baseline and procedure measurements collected for the targeted procedures. Baseline samples were not collected for continuous procedures (mechanical ventilation and noninvasive ventilation).

Figure 2: Particle size distribution measurements for nebulized medication samples versus all other procedure samples, combined.