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 cost 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, (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 adult outpatients with diarrhea. A pathogen was detected in 88/452 (19.5%). 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 clearly indicated for 19/452 subjects (4.2%). Limiting testing to patients with an additional enteric symptom (abdominal pain, nausea, vomiting, fecal urgency, tenesmus, or flatulence), a travel history, or an immunocompromising condition would reduce testing by 25.9%, with a treatable pathogen identified in 18/331 (5.4%) (sensitivity 94.7%, specificity 27.7%). Further modifying testing criteria to exclude subjects with vomiting, 18/288 (6.3%) had a treatable pathogen (sensitivity 94.7%, specificity 37.3%), and a pathogen which could change management was detected in 28/288 (9.7%) (sensitivity 96.6%, specificity 38.5%). Excluding immunocompromised subjects or those with a travel history, American College of Gastroenterology guidelines for testing were met by 293/348 (84.2%) with a documented duration of diarrhea, and a treatable pathogen was detected in 8/293 (2.7%) vs. 3/55 (5.5%) who did not meet testing guidelines.

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.

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, 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, neutropenia, or requiring emergent care, we attempted to collect rectal swabs and stool from all participants. Specimens were subjected to testing with the Luminex 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% (871/1,147) and 67.6% (1,024/1,514); $P < 0.0001$. 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 (i.e., higher viral loads; $P < 0·0001$) in SSs 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.

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

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 comprehensive knowledge of resistance 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 baumanii* treated with ciprofloxacin, 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 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 (KPC-2, KPC-3, NDM-1, OXA-48, and CTX-M15).

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 result

		Susc	Intd	Res
Actual (MIC)	Susc	79		1
	Intd	1	1	3
	Res	1		87

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 (demonstrated for carbapenemases) in a single assay, strains with unexplained resistance can be prioritized for further study.

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

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.

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 bla_{KPC} gene was confirmed by PCR. When environmental CPO isolates were detected, EVS procedures and practices were reviewed.

Results. In June 2016, bla_{KPC}+ *Leclercia adecarboxylata* was isolated from an EVS closet floor drain, and in August 2016, from drains in four additional closets. In the previous 10 years, *Leclercia* sp. was isolated just once from a clinical culture. In September 2016, routine surveillance revealed new-onset bla_{KPC}+ *L. adecarboxylata* colonization in a stem cell transplant recipient. Investigation included 33 cultures collected from sink and floor drains, EVS equipment, and other items. EVS equipment, 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 bla_{KPC}+ *L. adecarboxylata*. Whole genome sequencing demonstrated genetic relatedness of the *Leclercia* isolates. Floor cleaner was changed to a disinfectant solution. Extensive decontamination of 67 EVS closets and equipment was performed urgently. No further patient or environmental cultures have grown bla_{KPC}+ *L. adecarboxylata*.

Conclusion. The recovery of a highly unusual organism, rarely found in clinical specimens, that was also carrying a bla_{KPC}+ plasmid, allowed us to detect environmental spread of this organism in the hospital. The ability to track this organism using genome 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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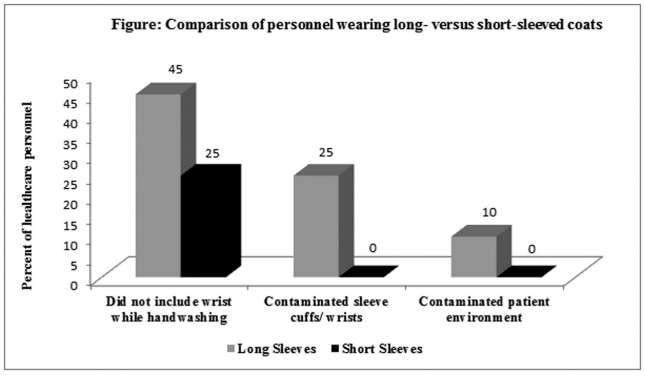
Background. Physician's white coats are frequently contaminated, but seldom cleaned. Therefore, in the UK, a "bare below the elbows" dress code policy includes a recommendation that personnel wear short sleeves. However, it has not been demonstrated that wearing short sleeves reduces the likelihood of pathogen transmission.

Methods. We conducted a randomized, cross-over 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 while examining a mannequin contaminated with cauliflower mosaic virus DNA followed by examination of an uncontaminated mannequin. We compared the frequency of transfer of the DNA marker with the sleeves and/or wrists and with the uncontaminated mannequin. During work rounds, physicians were observed to determine how often the sleeves of white coats contacted patients or the environment.

Results. During work rounds and simulated examinations, the sleeve cuff of long-sleeved coats frequently contacted the patient/mannequin or environment. Contamination with the DNA marker was detected significantly more often on the sleeves and/or wrists when personnel wore long- vs short-sleeved coats (5 of 20, 25% vs 0 of 20, 0%; P = 0.02). In one of five (20%) instances of sleeve and/or wrist contamination, the DNA marker was transferred to the second mannequin. It was also observed that healthcare personnel were less likely to include their wrist in handwashing between simulations if they were wearing long-sleeved coats.

Conclusion. During simulations of patient care, the sleeve cuff of long-sleeved white coats frequently became contaminated with a viral DNA marker that could be transferred. These results provide support for the recommendation that healthcare personnel wear short sleeves to reduce the risk for pathogen 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 tracheostomy), 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 pasturei*, 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 measurements were not collected for continuous procedures (mechanical ventilation and noninvasive ventilation).

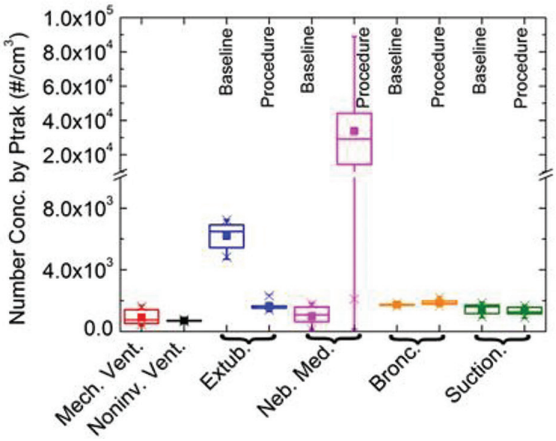

Figure 2: Particle size distribution measurements for nebulized medication samples versus all other procedure samples, combined.