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

Stephen Clark, MD[1]; Michael Sidlak, MS[2]; Amy Mathers, MD[3]; Melinda Poulter, PhD[2]; James Platts-Mills, MD[4]; [1]Department of Medicine, University of Virginia, Charlottesville, Virginia; [2]Clinical Microbiology, University of Virginia, Charlottesville, Virginia; [3]University of Virginia Health System, Charlottesville, Virginia; [4]Division of Infectious Disease and International Health, University of Virginia, Charlottesville, Virginia

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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.

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

Stephen Freedman, MDCM, MSc[1]; Alberto Nettel-Aguirre, PhD[2]; Jianling Xie, MD, MPH[3]; Bonita Lee, MD MSc FRCPC[4]; Linda Chui, PhD[5]; Xiao-Li Pang, PhD[4]; Ran Zhuo, PhD[4]; Brendon Parsons, PhD[5]; James Dickinson, MBBS[2]; Otto G. Vanderkooi, MD[6]; Samina Ali, MDCM[4]; Lara Osterreicher, RN[7]; Karen Lowerison, AHT[2]; Phillip Tarr, MD, FIDSA[8]; Alberta Pediatric EnTeric Infection TEam (APPETITE); [1]Pediatrics, University of Calgary, Calgary, AB, Canada; [2]University of Calgary, Calgary, AB, Canada; [3]Alberta Children's Hospital, Calgary, AB, Canada; [4]University of Alberta, Edmonton, AB, Canada; [5]Laboratory Medicine and Pathology, University of Alberta, Edmonton, AB, Canada; [6]The University of Calgary, Calgary, AB, Canada; [7]Alberta Health Services, Calgary, AB, Canada; [8]Washington University School of Medicine, St. Louis, Missouri

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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; $P < 0{\cdot}0001$) 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.

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993. Rapid Phenotypic Antibiotic Susceptibility Testing Through RNA Detection

Roby Bhattacharyya, MD PhD[1,2]; Jamin Liu, BS[2]; Peijun Ma, PhD[2]; Nirmalya Bandyopadhyay, PhD[2]; Jonathan Livny, PhD[2]; Deborah Hung, MD PhD[2]; [1]Department of Medicine, Division of Infectious Diseases, Massachusetts General Hospital, Boston, Massachusetts; [2]Broad Institute, Cambridge, Massachusetts

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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

Amanda M. Ramsburg, BSN[1]; Rebecca A. Weingarten, PhD[2]; Sean P. Conlan, PhD[3]; John P. Dekker, MD, PhD[4]; Angela V. Michelin, MPH[1]; Robin T. Odom, MS[1]; MaryAnn Bordner, RN[1]; Caroline J. Zellmer, BS[1]; David K. Henderson, MD[1]; Julia A. Segre, PhD[3]; Karen M. Frank, MD, PhD[2]; Tara N. Palmore, MD[1]; [1]Hospital Epidemiology Service, NIH Clinical Center, NIH, Bethesda, Maryland; [2]Department of Laboratory Medicine, NIH Clinical Center, NIH, Bethesda, Maryland; [3]National Human Genome Research Institute, NIH, Bethesda, Maryland; [4]Department of Laboratory Medicine, National Institutes of Health Clinical Center, Bethesda, Maryland

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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.