or more enteric symptom (nausea, vomiting, abdominal pain/cramps, tenesmus, fecal urgency, moderate to severe flatulence), and one of the following: grossly bloody diarrhea, persistent diarrhea (14 – 30 days), worsening or relapsing diarrhea, fever ≥ 101 F°, severe diarrhea > 10 bouts in 24hrs, immunosuppression, pregnancy, food handler, infant < 1 year and their care takers, age ≥ 65 years old, concern for disseminated Gi infection with no previous Gi testing in the past 30 days.

**Results.** Overall appropriateness of GI panel testing based on our generated criteria was 36% (n = 144/400). This included all tests ordered in the outpatient clinic, emergency department, inpatient medical/surgical wards, and intensive care units. Considering that there is no well-established standard criteria for ordering the GI panel for investigating suspected infectious diarrhea. After implementation at our academic tertiary-care medical center the GI panel was used inappropriately in most cases without a criteria for ordering in place to aid clinicians. Educating healthcare providers about appropriate testing indications is being performed. Further studies are needed to assess if our generated criteria will lead to decreased costs and unnecessary testing.

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1183. Clinical Predictors of Shigellosa and Campylobacter Infection in Children in the United States

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**Session:** 146. Enteric Infections and Diagnostics

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**Background.** Infectious gastroenteritis is a major cause of morbidity and mortality among children worldwide. While most episodes are self-limiting, for select pathogens such as Shigella and Campylobacter, etiological diagnosis may allow effective antimicrobial therapy and aid public health interventions. Unfortunately, clinical predictors of such pathogens are not well established and are based on small studies using bacterial culture for identification.

**Methods.** We used prospectively collected data from a multi-center study of pediatric gastroenteritis employing multi-pathogen molecular diagnostic testing to determine clinical predictors associated with 1) Shigella and 2) Shigella or Campylobacter infection. We used machine learning algorithms for clinical predictor identification, then performed logistic regression on features extracted plus pre-selected variables of interest.

**Results.** Of acute diarrhea, we detected Shigella spp. in 56 (5.6%) and Campylobacter spp. in 24 (2.4%). Compared with children who had neither pathogen detected (of whom, >70% had ≥1 potential pathogen identified), bloody diarrhea (odds ratio 4.0), headache (OR 2.2), fever (OR 7.1), summer (OR 3.3), and sick contact with Gi illness (OR 2.2), were positively associated with Shigella, and out-of-state travel (OR 0.3) and vomiting and/or nausea (OR 0.4) were negatively associated (Table). For Shigella or Campylobacter, predictors were similar but season was no longer significantly associated with infection.

**Conclusion.** These results can create prediction models and assist clinicians with identifying patients who would benefit from diagnostic testing and earlier antibiotic treatment. This may curtail unnecessary antibiotic use, and help to direct and target appropriate use of stool diagnostics.

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1184. High Genetic Variability of Norovirus Leads to Diagnostic Test Challenges

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**Background.** It is important to understand the diagnostic accuracy of syndromic multiplex panels such as the Lumine xtAG Gastrointestinal Pathogen Panel (GPP) as they are increasingly employed as routine diagnostic tests in laboratories worldwide. Recent evaluations in our laboratory identified lower detection rates of norovirus genogroup II (NoV GII) using the GPP as compared with our lab-developed RT-qPCR Gastroenteritis Virus Panel (GVP). This study is to characterize the NoV strains in samples with discordant NoV GII test results between GPP and GVP and determine the genotypes of the two assay panels.

**Methods.** We genotyped all NoV GII strains with discordant test result in stool samples or rectal swabs collected prospectively from a cohort of children with acute gastroenteritis between December 2014 and July 2016. The sensitivity of GVP and GPP for NoV GII were compared by analyzing GVP threshold cycle (Ct) and using ten-fold serial dilutions of positive samples of various NoV GII genotypes.

**Results.** All discordant samples (11%; 63/607) tested positive for NoV GII by GVP but negative by GPP. Thirty-five percent (22/63) were successfully genotyped; 44% (9/22) of those were NoV GII genotype 2 (GI2). The median Ct value of discordant positive was lower than those with discordant results (19.8 vs. 33.7 respectively; P < 0.0001). GVP was 10-fold and at least 10,000-fold more sensitive than GVP in detecting NoV GI3 and GI2, respectively, but has similar sensitivity for NoV GI1. All GI2 variants with discordant test results differed genetically from the common GI2 variants.

**Conclusion.** GPP has Suboptimal sensitivity to detect NoV GI2 and its use may lead to an underestimation of NoV disease burden with some cases not being detected.

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1185. Risk Factors and Clinical Outcomes of Cancer Patients with Clostridium difficile Associated Diarrhea Co-infected with a Second Enteropathogen

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**Session:** 146. Enteric Infections and Diagnostics

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**Background.** Cancer patients are at an increased risk for C. difficile infection (CDI), which is often identified along with other enteropathogens. The impact of co-infections on outcomes has not been established in this population. We compared the risk factors and clinical characteristics of patients with CDI monoinfection (CDIM) and patients coinfected with bacterial (CDIB) or viral (CDIV) enteropathogens.

**Methods.** Adult patients presenting with primary or recurrent CDI (n = 88) identified on a two-step GI multiplex assay (Biofire) followed by toxin A/B EIA, were classified into CDIM (n = 66), CDIB (n = 12), and CDIV (n = 10) groups. Demographic and clinical data were collected and risk factors and outcomes compared by Fisher’s exact test, ANOVA, and the Kruskal–Wallis test. CDI severity was determined using Zar’s criteria, presence of bacteremia, and ICU stay.

**Results.** During the study period, 2017 diarrheal samples were submitted to the microbiology laboratory. An enteric pathogen was identified in 311 (15%) patients. CDI was identified in 18 cases of which 12 (25%) cases had a second pathogen. CDIM was found in 66 (21%), CDIB in 12 (4%), and CDIV in 10 (3%) subgroups. The most common co-pathogens identified were diarrheagenic E. coli in the CDIB group (9/12, 75%) and norovirus in the CDIV group (8/10, 80%). Groups were similar in terms of demographics, number of recurrences, health care acquisition, comorbidities, disease severity, serum creatine at presentation, presence of toxin by EIA, and mortality. Patients with CDIM were more likely to have a recent hospitalization than the CDIB group (44/66 67% vs. 3/12 25%, P = 0.01). Clinical symptoms at presentation were similar for the three groups except for nausea which was more common in the CDIB group when compared with CDI (8/10, 80% vs. 25/66, 38%; P = 0.02). The use of proton pump inhibitors was similar in the three groups. There was however, a higher proportion of patients taking GABA-like drugs within 90 days among the CDIB patients (10/12, 83%) than the group with CDIM (25/66, 38%; P = 0.01).

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1186. Clinical Characteristics of Diarrheal Illness with Enteropathogenic E. coli (EPEC) Diagnosed by FilmArray BacT (BioFire Diagnostics, Salt Lake City, UT). Multiplex PCR (MPCR) Testing. Mary George BS, Paul Schreckenberger, PhD, Paul O’Keefe MD. Loyola University Medical Center, Mayo’s, Illinois, USA

Methods. We have completed a retrospective review of medical records of patients who tested positive for EPEC in our medical center.

Results. EPEC was found in 56 of 332 MPCR samples analyzed between February 1, 2016, and July 31, 2016. EPEC was the only pathogen in 25 while co-infecting pathogens were found in 31. Co-infections included other diarrheal-causing E. coli (EPEC, EAEC and EIEC) but none with STEC in 17. C. difficile in 7, viruses (astrovirus 3, sapovirus 2, norovirus 2, rotavirus 2). Campylobacter 3, Guarda 2, Salmonella 2, Plesiomonas 1, and 9 cases were unclassified.

Conclusion. EPEC is frequently found in stools in persons with diarrhea when MPCR is employed. Symptoms cannot be attributed to EPEC alone when other pathogens are found, but our analysis does suggest that EPEC is a common cause of diarrheal illness in adults as well as children. Prospective studies on natural history and treatment are needed.

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1187. Gastroenteritis Severity: A Prospective Cohort Comparison of Children in Emergency Department and Home Settings

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Methods. Subjects were prospectively recruited by the APPETITE team in pediatric EDs in 2 urban centers and via HealthLink, a province-wide nurse telephone advice line. Eligibility criteria included: <18 years old, AGE defined by ≥ 3 episodes of vomiting or diarrhea in the preceding 24 hours, and < 7 days of symptoms. The primary outcome was index encounter disease severity quantified using the modified Vesikari Scale (MVS) score. To eliminate the impact of the index encounter on the data visit to the score was excluded (8.1 vs. 7.8, P = 0.15). Participants recruited in the ED were not significantly more likely to have bacterial pathogens (8.0 vs. 3.7%, P = 0.09) but were less likely to have viral pathogens identified (64.1 vs. 80.7, P = 0.001).

Conclusion. Children presenting to ED care had disease severity scores that were similar to children managed at home when the contribution of the index ED visit was accounted for. Viral pathogens were more common in AGE receiving care at home while those presenting to the ED and potentially have a clinically greater likelihood of having a bacterial enteropathogen.

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1188. Genetic Variation in Shiga Toxin-producing Escherichia coli Recovered from Patients in Michigan and Connecticut

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Background. Shiga toxin-producing Escherichia coli (STEC) is a gram-negative foodborne pathogen that causes approximately 265,000 illnesses in the US annually. STEC O157 and six non-O157 STEC serotypes are most commonly associated with illness, though variation in the ability of different STEC types to cause disease. Consequently, we sought to examine genetic variation in virulence genes and clustered regularly interspaced repeat (CRISPR) loci among clinical strains of diverse lineages from different geographic locations.

Methods. Isolates were collected from a sentinel surveillance in 2000–2006 by the Michigan Department of Health and Human Services (n = 44) and Connecticut Department of Public Health (n = 115). Whole genome sequencing was performed and reference genomes were identified using whole genome sequencing of a reference strain of the different lineages. Strains had similar virulence gene profiles, though the diversity of the CRISPR loci varied across strains. The latter could be impacted by varying selective pressures that could affect disease frequency and symptom severity. Continued surveillance of non-O157 STEC is needed to elucidate the genetic characteristics that are most important for disease severity.

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1189. The Global Burden of Rotavirus Diarrheal Diseases: Results from the Global Burden of Diseases Study 2016

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Background. More than 1,300,000 deaths were attributable to diarrhea in 2015, with more than 400,000 of these deaths from children under 5 years of age. The Global Burden of Disease Study 2016 (GBD2016), an ongoing effort to measure global epidemiological trends, estimates diarrhea disease burden and the burden attributable to rotavirus and other enteric pathogens.

Methods. Diarrhea deaths are estimated using a suite of prediction models for all ages, both sexes, and for all countries and some subnational geographic areas from 1980 to 2016 using an ensemble modeling tool called CODEm. To estimate the burden of rotavirus, we calculated a population attributable fraction using a counter-factorial approach. We used a modification of the Vesikari and Manuguerra index encounter disease severity scale as the index encounter for calculating the number of deaths caused by rotavirus and applying odds ratios describing the odds of diarrhea given rotavirus detection.

Results. In 2016, rotavirus was the leading cause of diarrhea mortality in children under 5 years old, responsible for 25.9% of diarrhea deaths in this age group (149,200 deaths, 95% Uncertainty Interval (UI): 119,200–189,400), and responsible for 15.3% of diarrhea deaths among all ages (202,300 deaths, 95% UI: 165,800–246,400). The population attributable fraction of diarrhea mortality due to rotavirus is generally stable across geographic regions. The global attributable fraction of rotavirus decreased by 2% (95% UI: 16.7–31.6%) between 2005 and 2016.

Conclusion. The global deaths attributable to rotavirus in children under 5 is substantial and the burden in older children and adults may be unrecognized. GBD 2016 estimates describe epidemiological trends for rotavirus diarrhea and will inform global planning to reduce the burden of rotavirus. Our findings call for acceleration of delivery existing rotavirus vaccines and development of more affordable options for Low and Middle Income countries.

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