or more enteric symptom (nausea, vomiting, abdominal pain/cramps, tenesmus, fecal urgency, moderate to severe flatulence), and one of the following: grossly bloody diarrhea (dysenteric), 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 panel testing in the past 30 days.

Results. Overall appropriateness of GI panel testing based off our generated criteria was 36% (n = 144/400). This included all tests ordered in the outpatient clinics, emergency department, inpatient medical/surgical wards, and intensive care units.

Conclusion. Currently there is not a 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 *Shigella* and *Campylobacter* Infection in Children in the United States

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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 diagnostics 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 993 children enrolled with 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.

Feature	Shigella or Campylobacter not detected (n=913)	Shigella detected (n=56)		Shigella or Campylobacter detected (n=80)	
	N (%)	N (%)	OR (95% CI)	N (%)	OR (95% CI)
Bloody diarrhea	91(10.0)	15(26.8)	**4.0 (1.9-8.5)**	23(28.8)	**3.8 (2.1-6.9)**
Fever	458(50.1)	47(83.9)	**7.1 (2.8-18.2)**	62(77.5)	**5.1 (2.4-10.5)**
Headache	236(25.9)	24(42.9)	**2.2 (1.2-4.2)**	35(43.8)	**2.4 (1.4-4.0)**
Vomiting/nausea	726(79.5)	34(60.7)	**0.4 (0.2-1.0)**	49(61.3)	**0.5 (0.3-1.1)**
Sick Contact with GI illness	206(22.6)	17(30.4)	**2.2 (1.1-4.3)**	25(31.3)	**2.1 (1.2-3.6)**
Out of state travel	131(14.4)	4(7.1)	**0.3 (0.1-0.95)**	5(6.3)	**0.3 (0.1-0.75)**
Summer season	254(27.8)	34(60.7)	**3.3 (1.7-6.5)**	35(43.8)	**1.6 (0.9-2.7)**

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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 Luminex 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 sensitivity of the two assays for specific NoV GII genotypes.

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; 64% (14/22) of those were NoV GII genotype 2 (GII.2). The median Ct value of concordant 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 GPP in detecting NoV GII.3 and GII.2, respectively, but has similar sensitivity for NoV GII.4. The GII.2 variants with discordant test results differed genetically from the concordant GII.2 variants.

Conclusion. GPP has suboptimal sensitivity to detect NoV GII.2 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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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, 2,017 diarrheal samples were submitted to the microbiology laboratory. An enteric pathogen was identified in 311 (15%) patients. CDI was identified in 88 cases of which 22 (25%) had a second pathogen. CDIM was found in 66 (21%), CDIB in 12 (4%), and CDIV in 10 (3%) subjects. 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, co-morbidities, disease severity, serum creatinine 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 CDIV group when compared with CDIM (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 (26/66, 40%) P = 0.01.