Conclusion. In CDI cancer patients, co-infection with other enteropathogens is common. Patients with CDIB were less likely to have a recent admission to a health care facility. The use of GABA-like drugs was associated with a higher risk of bacterial co-infection.

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1186. Clinical Characteristics of Diarrheal Illness with Enteropathogenic *E. coli* (EPEC) Diagnosed with FilmArray (BioFire Diagnostics, Salt Lake City, UT) Multiplex PCR (MPCR) Testing. Maria Georgen BS, Paul Schreckenberger, PhD, Paul O'Keefe MD. Loyola University Medical Center, Maywood, Illinois, USA

Maria Georgen, BS; Loyola University Chicago Stritch School of Medicine, Chicago, Illinois

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Background. EPEC is a known cause of diarrhea, predominately in children, which has not been identified with conventional stool culture in most medical centers. MPCR testing assesses stool samples in which DNA targets for 20 or more pathogens are tested with rapid turnaround. This method has become the standard for diagnostic testing in many clinical laboratories. MPCR testing has identified EPEC as among the most frequent pathogens in published studies.

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 diarrhea-causing *E. coli* (ETEC, EAEC and EIEC but none with STEC) in 17, *C. difficile* in 7, viruses (astrovirus 3, sapovirus 2, norovirus 2, rotavirus 2), *Campylobacter* 3, *Giardia* 2, *Salmonella* 2, *Pleisiomonas* 1 and *Yersinia* 1.

Patients ages ranged from <1 to 100 with 37 over age 19. Half were female. 7/46 had received antibiotic prior to sample collection. 10 reported recent travel. 51/52 presented to the emergency department, urgent care centers or ambulatory clinics. Symptoms included fever in 15/54, nausea 16/54, vomiting 14/54 and abdominal pain in 17/56. Diarrhea was described as watery in 23/32 and bloody in only 3. Antibiotic treatment was prescribed for 6/24 with EPEC only and for 22/31 with coinfection. A follow-up encounter was documented for 24 patients with EPEC only: 13 resolved, 3 remained ill and 8 could not be assessed.

Conclusion. EPEC is frequently found in stools from 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 necessary.

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

Otto G. Vanderkooi, MD[1]; Jianling Xie, MD, MPH[2]; Bonita Lee, MD MSc FRCPC[3]; Samina Ali, MDCM[3]; Xiao-Li Pang, PhD[3]; Linda Chui, PhD[4]; Daniel C. Payne, PhD, MSPH[5]; Phillip Tarr, MD, FIDSA[6]; Ran Zhuo, PhD[3]; Brendon Parsons, PhD[4]; Lara Osterreicher, RN[7]; Kelly Kim, BSc[8] and Stephen Freedman, MDCM[8]; [1]The University of Calgary, Calgary, AB, Canada, [2]Alberta Children's Hospital, Calgary, AB, Canada, [3]University of Alberta, Edmonton, AB, Canada, [4]Laboratory Medicine and Pathology, University of Alberta, Edmonton, AB, Canada, [5]Division of Viral Diseases, Centers for Disease Control and Prevention, Atlanta, Georgia, [6]Pediatric Gastroenterology, Washington University, St. Louis, Missouri, [7]Alberta Health Services, Calgary, AB, Canada, [8]University of Calgary, Calgary, AB, Canada

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Background. While nearly 2 million children are brought to emergency department (ED) annually due to vomiting and/or diarrhea from acute gastroenteritis (AGE), it is estimated that 90% of AGE cases do not seek medical care. We sought to determine whether the disease severity and enteropathogen burden of disease of children with AGE brought for ED care is different from those cared for at home.

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 score we excluded the index ED visit and intervention from all calculations. Secondary objectives included the enteropathogen burden of disease. Two rectal swabs and stool were collected and tested for enteropathogens by enteric bacterial culture, Luminex xTAG GPP, and a 5-virus in-house RT-qPCR panel.

Results. Between December 9, 2014 and December 31, 2016, 1,623 participants were enrolled with 81.5% from the EDs. Median age was 20.1 months. Children who went to ED were less likely to have a family physician (62 vs. 82%, $P < 0.001$), more likely to have clinical dehydration (Clinical Dehydration Scale score 3 vs 1, $P < 0.001$) and vomiting (91 vs. 85%, $P = 0.004$), previously received IV fluids (4.1 vs. 0.7%, $P = 0.001$) or been admitted (5.4 vs. 1.3%, $P = 0.002$). The MVS score was similar between groups when the contribution of the index 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 for 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

Heather Selheimer, BSc[1]; Rebekah Mosci, MS[2]; James Rudrik, PhD[3] and Shannon Manning, PhD[4]; [1]Microbiology and Molecular Genetics, Michigan State University, East Lansing, Michigan, [2]Michigan State University, East Lansing, Michigan, [3]Michigan Department of Community Health, Lansing, Michigan, [4]Pediatrics and Human Development, Michigan State University, East Lansing, Michigan

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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 exists 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 genes for O-antigen (serotype), multilocus sequence typing (MLST) and virulence factors were extracted. CRISPRFinder and Geneious were used for CRISPR loci.

Results. A phylogenetic tree based on MLST found no geographic clustering of the strains. Similarly, no difference was observed for *stx1* (MI: 89.6%, CT: 83.5%), *stx2* (MI: 6.9%, CT: 7.1%), *stx1/stx2* (MI: 3.4%, CT: 9.4%), *ehxA* (MI: 80.0%, CT: 81.2%) and *eae* (MI: 86.7%, CT: 94.1%) frequencies across geographical locations. Although the CRISPR loci were similar within related STs, which was independent of serotype, some variation was detected between locations.

Conclusion. These data highlight the circulation of common non-O157 STEC lineages capable of causing disease in different populations. 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 frequencies 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

Ibrahim Abdel-Messih Khalil, M.D, MPH; Institute for Health Metrics and Evaluation, University of Washington, Seattle, Washington

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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-factual approach by modeling the proportion of diarrheal cases that are positive for 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 29.5% 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 24.2% (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 evidence-based Public Health policy, to reduce the global 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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