1113. Real-Time Evolution of Extensively Drug-Resistant Vibrio cholerae
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Background. Bay of Bengal is known as the epicenter of a number of distinct waves of global transmission of cholera. Vibrio cholerae, the etiological agent of acute diarrheal disease cholera, has extraordinary competency to acquire exogenous DNA by horizontal gene transfer (HGT) and acclimatize them into their genome for structuring metabolic process, developing drug resistance and disease. Antimicrobial resistance (AMR) in V. cholerae is a global concern. However, little is known about the identity, source, acquisition process, and stability of the resistance traits in the genome of cholera pathogen.

Methods. Antibiotic susceptibility testing of V. cholerae isolated from different parts of India during 2001–2017 was performed using Discs and E-strips. Whole-genome sequencing of resistant (R), multidrug resistant (MDR), extensively drug resistant (XDR), and pandrug (PDR) resistant V. cholerae was done by next-generation DNA sequencing. Mobile genetic elements (MGEs) linked with AMR genes were tagged by allelic exchange methods. Whole-cell proteome analysis was done by iTRAQ analysis.

Results. Almost 99% of V. cholerae isolates (n = 438) are resistant against ≥2 antibiotics (≥2 RA; n = 76) are resistant against ≥10 antibiotics; and 7.5% isolates (n = 33) are resistant against ≥24 antibiotics. Highest resistance was detected against sulfamethaxazole (99.8%, n = 442). In addition, resistance to nalidixic acid (n = 428), trimethoprim (n = 421), and streptomycin (n = 409) are also very high. All the sequenced resistant isolates carries multiple resistance genes and are linked with MGEs like integrating conjugative elements, transposons etc. Most of the resistance traits are functional and expressed even in the absence of antibiotics.

Conclusion. Our comprehensive analysis of 443 clinical V. cholerae isolates show that the cholera pathogen is continuously evolving to counterbalance the antimicrobial effects of antibiotics. Several MGEs linked with AMR genes and other fitness factors potentially propagate to other bacterial species through HGTs. Knowledge of the present study would be useful to understand the evolution of cholera pathogen and management of cholera by helping selection of specific drug regimen against the pathogens.

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1114. Utility of a Bedside Diagnostic Testing Algorithm to Screen for Hospital-Onset C. difficile infection
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Background. Molecular assays have improved C. difficile detection in hospitalized patients. However, asymptomatic carriers have been missclassified as hospital onset C. difficile infection (HO-CiD), which has implications for management and infection prevention programs. At our facility, we implemented robust antibiotic stewardship policies in 2016 and had an SIR for HO-CiD of 0.73 for the year. In Q1 2017, this increased to 1.88. These cases revealed that nearly all tests, found positive for C. diffi-
cile in the field met a standard definition of clinically significant diarrhea (CSD). Moreover, many patients did not have a clinical change in condition that supported a diagnosis of C. difficile. We reasoned that an algorithm for appropriate testing for C. difficile would significantly reduce our perceived rates of HO-CiD. We also reasoned that this tool could efficiently be used at the bedside during a clinical assessment.

Methods. To determine which patients had CSD, we designed, educated on and implemented an algorithm to screen for appropriate testing. It required three major elements: three or more loose stools in 24 hours, no gastric motility agents 48 hours prior, and a clinical change in condition (e.g., leukocytosis, fever, abdominal cramp-
ing). The completed algorithm accompanied the stool specimen and was required for testing. We evaluated each submitted algorithm for method validation. From this, we determined testing appropriateness and algorithm tool selectivity.

Results. One year post-algorithm implementation (PR-A and PO-A, respectively) were defined. Following its introduction, we noted a 57% decline in rates of HO-CiD (23 cases PR-A vs. 10 cases PO-A), and a 44% reduction in tests sent for C. difficile (average of 41 tests/month PR-A vs. 23 tests/month PO-A). We only used NAA testing. We also noted a marked rule-in adherence to the algorithm as time elapsed. The PDSA tool was used to refine the algorithm, with improved utilization by providers.

Conclusion. A simple bedside algorithm leads to more appropriate testing of patients for C. difficile infection. A significant decline in reported rates of HO-CiD was noted. This was an additional benefit of diagnostic stewardship, as fewer tests are sent. This tool can be used immediately and independent of an electronic health record, is very cost effective, and is applicable to hospitals with low rates of HO-CiD.

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1115. Use of a Fluoroquinolone (FQ) vs. a Non-Fluoroquinolone (Non-FQ)-Based Antibiotic Regimen in the Treatment of Acute, Uncomplicated Diverticulitis
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Background. The management of acute, uncomplicated diverticulitis (DVT) remains based on expert consensus rather than on evidence from randomized clinical trials. The most common antibiotic (AB) regimen used in this patient population is metronidazole plus a fluoroquinolone (FQ). Non-FQ options, including B-lactam and macrolide regimens are available. Since there is a lack of clinical data comparing outcomes between these regimens, it remains uncertain whether patients presenting with acute, uncomplicated DVT require a FQ-based regimen. Increasing rates of FQ resistance and awareness of collateral damage have raised concern about whether this class should remain a first-line option.

Methods. This retrospective cohort study was conducted utilizing electronic health records to identify patients 18 years of age or older with acute, uncomplicated DVT, defined by ICD 10 codes. Patients included had CT confirmed DVT and were started on a guideline recommended AB regimen. Data points collected included length of stay, 30-day readmission due to DVT, time to conversion from IV to PO AB, progression to surgery, and discharge AB regimen. The primary objective is to evaluate differences in length of stay and 30 day re-admission rates. The secondary objectives are to evaluate time from intravenous (IV) to oral (PO) AB, progression to surgery, and discharge AB between the two groups.

Results. 136 patients were evaluated, 71 FQ and 65 non-FQ. Length of stay was 4 days (1–18) in the FQ group vs. 5 days (1–19) in the non-FQ group (P = 0.236). 11% of patients in the FQ group vs. 9% of patients in the non-FQ group had a DVT related mortality (P = 0.451). 108% of patients in the FQ group vs. 23% of patients in the non-FQ group progressed to GI surgery during the admission. Time from IV to PO conversion of AB was 34.2 hours (0–63) in the FQ group vs. 48.4 hours (8–81) hours in the non-FQ group. Lastly, 63 of the 71 patients who were started on a FQ were discharged on an oral FQ. Forty five of the 65 patients started on a non-FQ were discharged on an oral FQ.

Conclusion. In the treatment of acute, uncomplicated DVT outcomes including length of stay, 30-day readmission, time from IV to PO AB, and progression to surgery were comparable in patients receiving treatment with a FQ based AB regimen vs. a non-FQ based regimen.

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1116. Comparison of Short-Course vs. Prolonged-Course Antimicrobial Therapy in the Management of Intra-Abdominal Infections
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Background. When managing complicated intra-abdominal infections (IAIs), the current Infectious Diseases Society of America (IDSA) guidelines recommend an antimicrobial treatment duration of 4–7 days. Although recent evidence supports this shorter course of therapy, antimicrobials are still often administered for 10–14 days due to concern for subsequent complications. The purpose of this study was to compare clinical outcomes of short-course (SC) vs. prolonged-course (PC) antimicrobial therapy in the management of IAI at our institution.

Methods. IRB-approved, single-center, retrospective cohort including all patients at the University of Toledo Medical Center who were admitted between January 1, 2016–June 30, 2017 with an IAI received antimicrobials for ≥24 hours, and had at least one sign of IAI. Patients with concomitant infections at sites other than the abdomen, primary peritonitis or pancreatitis, immunocompromising conditions, or bacteremia were excluded. Primary outcome of clinical cure was compared between SC (≤7 days of antimicrobial treatment) and PC (>7 days) groups. Secondary outcomes included hospital length of stay (LOS), ICU LOS, 28-day all-cause mortality, and 30-day read-

results. Multivariable logistic regression was performed to assess factors associ-
ed with clinical cure.

Results. One hundred seventy-five patients were included, 73 SC and 102 PC. Baseline characteristics were similar between groups. Rate of clinical cure for SC vs. PC was 74.0% vs. 67.6% (P = 0.367). Secondary outcomes including hospital LOS (5.5 days vs. 5.8 days, P = 0.372), ICU LOS (3.0 days vs. 5.0 days, P = 0.117), 28-day all-cause mortality (66.1% vs. 20.6%, P = 0.063), and 30-day readmission (19.2% vs. 20.6%, P = 0.818) were also not significantly different. After multivariable logistic regression, the only variable independently associated with clinical cure was diverticulitis (adjusted odds ratio 0.337, 95% CI 0.133 – 0.853).

Conclusion. In patients with IAI, there was no significant difference observed in rates of clinical cure between SC and PC antimicrobial therapy. These results further support the IDSA recommendations for a shorter duration of therapy for patients with IAI.

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1117. Avascular Necrosis of the Femoral Head as a Sequela of Shiga Toxin-producing Escherichia coli (STEC) Infection
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Background. Shiga toxin-producing Escherichia coli (STEC) infection may be com-
pli
cated by the hemolytic-uremic syndrome (HUS). Long-term sequelae of HUS are most
often related to renovascular disease. Os
teocartilaparccal complications are rare. Avascular
necrosis (AVN) has not been previously reported as a complication of STEC infection.

Methods. We report two cases of United States Marine Corps (USMC) recruits who
developed AVN of the femoral head following STEC infection during a large outbreak.

Results. Between October and November 2017, an STEC outbreak occurred at
Marine Corps Recruit Depot San Diego (MCRR-SD) affecting over 250 USMCR recruits.
Case 1: A 19-year-old recruit developed nine days of non-bloody diarrhea. Stool culture,
Escherichia coli O157. Complete blood count (CBC) was normal 5 days after symptom
resolution. One month after resolution of his infection, he developed right hip pain.
Magnetic resonance imaging (MRI) revealed right femoral head AVN (Image 1). He was
treated conservatively with nonsteroidal anti-inflammatory drug (NSAID) and physical
therapy. Case 2: A 19-year-old recruit developed seven days of dysentery. Stool culture,
producing Shiga toxin enzyme immunoassay (EIA), and polymerase chain reaction (PCR) demon-
strated E. coli O157. Complete blood count (CBC) was normal 5 days after symptom
resolution. One month after resolution of his infection, he developed right hip pain.
Magnetic resonance imaging (MRI) revealed right femoral head AVN (Image 1). He was
treated conservatively with nonsteroidal anti-inflammatory drug (NSAID) and physical
therapy prior to his left hip core decompression and sub-chondroplasy.

Conclusion. AVN of the hip is rare among healthy young adults and is not commonly
observed in military recruits. We hypothesize that STEC-associated subclinical intravas-
tular coagulopathy may cause microscopic occlusive disease. AVN should be considered
in patients with new non-traumatic hip pain after known or suspected STEC infection.

1 Image 1: Hypointense T1 signal sclerosis and collapse of the bone fragment with a peripheral
rim of hypointense signal on MRI.

1 Image 2: Hypointense T1 signal in superior left femoral head with sub
tal subchondral colla-
pase on MRI.

1118. Viral Species Richness and Composition in Young Children With Loose or Watery
Stool in Ethiopia
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Background. Stool consistency is an important diagnostic criterion in both
research and clinical medicine and is often used to define diarrhea disease.

Methods. We examine the pediatric enteric virome across stool consistency to
evaluate differences in richness and community composition using fecal samples col-
lected from children participating in a clinical trial in the Amhara region of Ethiopia.
The consistency of each sample was graded according to the modified Bristol Stool
Form Scale for children (mBSFS-C) before a portion of stool was preserved for viral
metagenomic analysis. Stool samples were grouped into 29 pools according to stool
consistency type. Differential abundance was determined using negative-biomial
modeling.

Results. Of 446 censused children who were eligible to participate, 317 pre-

ced for the study visit examination and 269 provided stool samples. The mean age
of children with stool samples was 2.7 years old. Species richness was high-
est in watery-consistency stool and decreased as stool consistency became firmer
(Spearman’s r = -0.45, P = 0.013). The greatest differential abundance comparing loose or watery to formed stool was for norovirus GII (7.64, 95% CI 5.8, 9.5) fol-
lowed by astrovirus A (5.93, 95% CI 4.0, 7.89) and adenovirus subtypes 2 (5.81,
95% CI 3.9, 7.7).

Conclusion. We documented a difference in pediatric enteric viromes according
to mBSFS-C stool consistency category, both in species richness and composition. Our
results suggest that loose or watery stool, as measured by the mBSFS-C, may signal
enteric viral infection in young children. Additional studies are warranted to confirm
these findings.

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1119. Risk Factors for Clostridium difficile Infection and Persistence among
Guatemalan Children
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Background. Little is known about the epidemiology and risk factors for
Clostridium difficile infection (CDI) among children in low and middle-income coun-
tries (LMICs). We sought to characterize the clinical, demographic, and environmental
factors associated with C. difficile acquisition and persistence over time, and assess the
relationship between CDI and additional diarrheal pathogens among rural and urban
Guatemalan children.

Methods. Children 6–35 months old with acute nonbloody diarrhea (<72 hours)
were enrolled in an acute diarrhea clinical trial between March 2015 and January 2016
at two sites (one rural and one urban) in Guatemala. Stool samples collected at base-
line and 30 days later were analyzed by multiplex PCR (FilmArray™ GI-Panel, BioFire,
USA) that identifies 22 viral, parasitic and bacterial diarrheal pathogens includ-
ing C. difficile. Subjects were characterized by combination of baseline and 30-day
C.difficile sample results: –/+ (new acquisition), +/- (clearance), and +/+ (persis-
tence). Associations between these categorizations and demographic, epidemiologic,
and co-infesting pathogenic organisms were assessed using multivariable generalized
linear models.

Results. CDI was present in 26 of 298 subjects at baseline; 13 (50%) had persist-
tence at 30 days and 13 (50%) cleared. New acquisition at day 30 occurred in 23 sub-
jects. In a multivariable analysis adjusted for age, recent hospitalization was marginally
significantly associated with C. difficile presence in stool at baseline (prevalence ratio
[PR] 2.65, P = 0.07). In subjects with either new C. difficile acquisition or persistence
between baseline and day 30, residence in the rural site (PR 0.33, P = 0.003) and
presence of E. coli pathotypes: enteropathogenic (EPEC), enteraggeregative (EAEC),
and enterotoxigetic (ETEC) (PR 0.43, P = 0.011) were associated with reduced risk of
CDI.

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