

Poster Abstract Session:

51. *C. difficile* Diagnostics

Thursday: 12:30 p.m. - 2:00 p.m.

Room:

Presenters:

- 320** **Increased *Clostridium difficile* (CD) Detection and Decreased Empiric Treatment/Ancillary Testing after switch from Toxin A/B Immunoassay to PCR for Diagnosis of CD Infection**
LAURIE LABUSZEWSKI, PHARMD¹, URVASHI THAKKAR, PHARMD², STUART JOHNSON, MD, FIDSA³, PAUL SCHRECKENBERGER, PHD¹ and JORGE PARADA, MD, MPH¹; ¹Loyola University Medical Center, Maywood, IL, ²Western University College of Pharmacy, Pomona, CA, ³Edward Hines Jr. VA Hospital, Hines, IL
- 321** **Utility of Perirectal Swab Specimens for Diagnosis of *Clostridium difficile* Infection**
SIRISHA KUNDRAPU, M.D.¹, VENKATA SUNKESULA, M.D, M.S², LUCY JURY, N.P.², AJAY K. SETHI, PHD³ and CURTIS J. DONSKEY, MD²; ¹Case Western Reserve University, Cleveland, OH, ²Louis Stokes Cleveland Veterans Affairs Medical Center, Cleveland, OH, ³University of Wisconsin-Madison, Madison, WI
- 322** **Commercial *Clostridium difficile* Toxin PCR Assay of Stools from Pediatric Inpatients with Diarrhea with Cytotoxicity Confirmation of Positives**
JILL LEIBOWITZ, MD; Steven and Alexandra Cohen Children's Medical Center of New York of the North Shore-LIJ Health System, New Hyde Park, NY, VIJAYA SOMA, MD; Seattle Children's Research Institute, Seattle, WA and LORRY RUBIN, MD; Hofstra North Shore-LIJ School of Medicine, New Hyde Park, NY
- 323** **Stools from Asymptomatic Pediatric Inpatients at Risk for *Clostridium difficile*-Associated Diarrhea Frequently Test Positive Using a Commercial PCR Assay**
JILL LEIBOWITZ, MD; Steven and Alexandra Cohen Children's Medical Center of New York of the North Shore-LIJ Health System, New Hyde Park, NY, VIJAYA SOMA, MD; Hofstra North Shore-LIJ School of Medicine, New Hyde Park, NY and LORRY RUBIN, MD; Hofstra North Shore-LIJ School of Medicine, New Hyde Park, NY
- 324** **Regional Differences in *Vancomycin-resistant enterococcus* and *C difficile* Colonization Rates in Critically Ill Veterans**
LINDA MCKINLEY, RN, BSN, MPH, CIC; Madison VA Medical Center, Madison, WI, MARY HAGLE, RN, PHD; Milwaukee VA Medical Center, Milwaukee, WI, HELENE MORIARTY, RN, PHD; Philadelphia VA Medical Center, Philadelphia, PA, TOM SHORT, PHD; John Carroll University, University Heights, OH and NASIA SAFDAR, MD, PHD; University of Wisconsin School of Medicine and Public Health, Madison, WI
- 325** **Changes in *Clostridium difficile* Testing Practices and their Impact on Stool Rejection Policies across Multiple U.S. Laboratories**
JESSICA COHEN, MPH¹, DUNCAN MACCANNELL, PHD¹, LEIGH ANN CLARK, MPH², WENDY BAMBERG, MD³, REBECCA PERLMUTTER, MPH⁴, JOHN DUNN, DVM, PHD⁵, JOELLE NADLE, MPH⁶, STACY HOLZBAUER, DVM⁷, CAROL LYONS, MPH⁸, ERIN PHIPPS, DVM⁹, GHINWA DUMYATI, MD, FSHEA¹⁰, ZINTARS G. BELDAVS, MS¹¹ and FERNANDA LESSA, MD¹; ¹Division of Healthcare Quality Promotion, Centers for Disease Control and Prevention, Atlanta, GA, ²Georgia Emerging Infections Program, Decatur, GA, ³Colorado Dept. of Public Health and Environment, Denver, CO, ⁴Maryland Dept. of Health and Mental Hygiene, Baltimore, MD, ⁵Tennessee Department of Health, Nashville, TN, ⁶California

Emerging Infections Program, Oakland, CA, ⁷CDC CEFO assigned to the MN Dept. of Hlth, St. Paul, MN, ⁸Connecticut Emerging Infections Program, New Haven, CT, ⁹New Mexico Emerging Infections Program, Albuquerque, NM, ¹⁰University of Rochester, Rochester, NY, ¹¹Oregon Health Authority, Portland, OR

- 326** **The Nose Knows Not: Poor Predictive Value of Stool Sample Odor for Detection of *Clostridium difficile***
KRISHNA RAO, MD¹, DANIEL BERLAND, MD¹, CAROL YOUNG, MT(ASCP)², SETH WALK, MS, PHD³ and DUANE NEWTON, PHD³; ¹University of Michigan Health Systems, Ann Arbor, MI, ²University of Michigan Health System, Ann Arbor, MI, ³University of Michigan, Ann Arbor, MI
- 327** **Evaluation of a Commercial PCR Assay for Detection of Environmental Contamination with *Clostridium difficile***
ABHISHEK DESHPANDE, M.D., PH.D.¹, JENNIFER CADNUM, B.S.², BRETT SITZLAR, B.S.², SIRISHA KUNDRAPU, M.D.² and CURTIS J. DONSKEY, MD²; ¹Case Western Reserve University, Cleveland, OH, ²Louis Stokes Cleveland Veterans Affairs Medical Center, Cleveland, OH
- 328** **Severe *Clostridium difficile* Infection in Patients with Negative Results for *tcdB* by the Xpert® *C. difficile* assay**
JEROME LEIS, MD¹, WAYNE GOLD, MD, FRCPC¹, JOHN NG, PHD¹, ZAHIR HIRJI¹, DYLAN PILLAI, MD, PHD², GEORGE BROUKHANSKI, PHD¹, PAUL RAGGIUNTI¹, SUSY HOTA, MD¹, ALLISON MCGEER, MD, FSHEA¹ and SUSAN POUTANEN, MD, MPH¹; ¹University of Toronto, Toronto, ON, Canada, ²University of Calgary, Calgary, AB, Canada
- 329** **Does Empirical *Clostridium difficile* Infection (CDI) Therapy Result in False-Negative CDI Diagnostic Test Results?**
VENKATA SUNKESULA, M.D, M.S.¹, SIRISHA KUNDRAPU, M.D.² and CURTIS J. DONSKEY, MD¹; ¹Louis Stokes Cleveland Veterans Affairs Medical Center, Cleveland, OH, ²Case Western Reserve University, Cleveland, OH
- 330** **Prospective Evaluation of the Epidemiology of *Clostridium difficile* Colonization and Infection among Hematopoietic Stem Cell Transplant Recipients**
VARINIA URDAY-CORNEJO, MD¹, CHRISTOPHER CROSWELL¹, TEENA CHOPRA, MD, MPH², ALYSSA LIUBAKKA¹, JESSICA CUTRIGHT, BS¹, HOSSEIN SALIMNIA, PHD³, PAUL LEPHART, PHD³, SANJAY REVANKAR, MD¹, PRANATHARTHI CHANDRASEKAR, MD¹ and GEORGE ALANGADEN, MD⁴; ¹Wayne State University, Detroit, MI, ²Detroit Medical Center/ Wayne State University, Detroit, MI, ³Detroit Medical Center University Laboratories, Detroit, MI, ⁴Henry Ford Health System, Detroit, MI
- 331** **Multilocus sequence typing analysis of 85 *C. difficile* strains isolated from a teaching hospital in Houston Texas, September through December 2011**
ZHI-DONG JIANG; The University of Texas, School of Public Health, Houston, TX, RAVI PANCHUMARTHI; UNIVERSITY OF TEXAS SCHOOL OF PUBLIC HEALTH, HOUSTON, TX, KEVIN W. GAREY, PHARM.D, M.S.; University of Houston College of Pharmacy, Houston, TX, TODD M. LASCO, PHD; Saint Lukes Episcopal Hospital, Houston, TX, JANE CHEN; UNIVERSITY OF TEXAS SCHOOL OF PUBLIC HEALTH, HOUSTON, TX and HERBERT DUPONT, MD, FIDSA; St. Luke's Episcopal Hospital and Kelsey Research Foundation and Kelsey-Seybold Clinic, Houston, TX
- 332** ***Clostridium difficile* Whole Genome Sequencing Suggests Limited Transmission Arising From Mixed Infection**
DAVID EYRE, BM, BCH¹, MADELEINE CULE, PHD², DAVID GRIFFITHS, BSC³, TIM PETO, MB BS, DPHIL⁴, A. SARAH WALKER, PHD² and DANIEL WILSON, DPHIL²; ¹Nihr Oxford

Biomedical Research Centre, Oxford, United Kingdom, ²NIHR Oxford Biomedical Research Centre, Oxford, United Kingdom, ³National Institute for Health Research Oxford Biomedical Research Centre, Oxford, United Kingdom, ⁴University of Oxford, Oxford, United Kingdom

- 333** **Title: Safety of Clostridium Difficile Testing Algorithm using Glutamate Dehydrogenase Antigen and Toxin Enzyme Immunoassay with Reflex PCR for Discordant Test**
CECILIA BIG, MD, DAVID SENGSTOCK, MD, MS, NATASHA BAGDASARIAN, MD, MPH, VIJAYALAKSHMI NAGAPPAN, MD, PADMAJA VEMURI, MD, DAVID WEIDENDORF, MD and **RAMA THYAGARAJAN, MD**; Oakwood Hospital and Medical Center, Dearborn, MI
- 334** **Prevalence and Molecular Epidemiology of Clostridium difficile (CD) in Food and Companion Animals, Retail Meats, and Humans in Minnesota**
MEGAN K. SHAUGHNESSY, MD¹, TIM SNIDER, DVM², ROCIO SEPULVEDA², DAVID BOXRUD, MS³, ELIZABETH CEBELINSKI, BS³, STACY HOLZBAUER, DVM⁴, KIRK SMITH, DVM, PHD³, JEFF BENDER, DVM MS DACVPM⁵, FRANCISCO DIEZ-GONZALEZ, PHD⁵ and JAMES R. JOHNSON, MD¹; ¹University of Minnesota, Minneapolis, MN, ²University of Minnesota, St Paul, MN, ³Minnesota Department of Health, St. Paul, MN, ⁴CDC CEFO assigned to the Minnesota Department of Health, St. Paul, MN, ⁵University of Minnesota, St. Paul, MN
- 335** **Screening for Vancomycin Resistant Enterococcus (VRE) Colonization During Clostridium difficile Testing is Not Cost Effective at a Canadian Teaching Hospital**
SUNIL VARGHESE, MD, MA¹, KATHRYN SUH, MD, MSC, FRCPC¹, NATALIE BRUCE, RN, BSCN, CIC¹, KARAM RAMOTAR, PHD¹ and VIRGINIA ROTH, MD²; ¹The Ottawa Hospital, Ottawa, ON, Canada, ²The Ottawa Hosp, Ottawa, ON, Canada
- 336** **Toxin A/B EIA Compared to Molecular Amplification Testing for Clostridium Difficile: Cost and Resource Utilization Analyses**
REDA A. AWALI, MD¹, BRINDHA GOPALA KRISHNAN, MD¹, HARLEEN KAUR, MD¹, INDU K. CHALANA, MD², PAULA ROBINSON, RN¹, SANJAY REVANKAR, MD³, JUDY MOSHOS, BS, MT⁴, PAUL LEPHART, PHD⁵, RICHARD FACKLER, BBA¹, KEITH KAYE, MD, MPH, FIDSA, FSHEA⁶ and TEENA CHOPRA, MD, MPH⁷; ¹Detroit Medical Center, Wayne State University, Detroit, MI, ²Wayne State University / Detroit Medical Center, Detroit, MI, Detroit, MI, ³Wayne State University, Detroit, MI, ⁴Sinai-Grace Hospital, Detroit Medical Center, Detroit, MI, ⁵DMC University Laboratories, Detroit, MI, ⁶Detroit Medical Center (DMC) / Wayne State University, Detroit, MI, ⁷Detroit Medical Center/ Wayne State University, Detroit, MI
- 337** **Comparative Analysis of Two Culture Media and PCR for the Detection of Toxigenic and Non-Toxigenic C. difficile**
CHRISTOPHER CROSWELL¹, VARINIA URDAY-CORNEJO, MD¹, ALYSSA LIUBAKKA¹, JESSICA CUTRIGHT, BS¹, HOSSEIN SALIMNIA, PHD², PAUL LEPHART, PHD³, TEENA CHOPRA, MD, MPH⁴, PRANATHARTHI CHANDRASEKAR, MD¹ and GEORGE ALANGADEN, MD⁵; ¹Wayne State University, Detroit, MI, ²Detroit Medical Center/Wayne State University, Detroit, MI, ³Detroit Medical Center University Laboratories, Detroit, MI, ⁴Detroit Medical Center/ Wayne State University, Detroit, MI, ⁵Henry Ford Health System, Detroit, MI

Session #51 Presentations:

320. Increased Clostridium difficile (CD) Detection and Decreased Empiric Treatment/Ancillary Testing after switch from Toxin A/B Immunoassay to PCR for Diagnosis of CD Infection

Part of Session: 51. *C. difficile* Diagnostics

LAURIE LABUSZEWSKI, PHARMD¹, URVASHI THAKKAR, PHARMD², STUART JOHNSON, MD, FIDSA³, PAUL SCHRECKENBERGER, PHD¹ and JORGE PARADA, MD, MPH¹; ¹Loyola University Medical Center, Maywood, IL, ²Western University College of Pharmacy, Pomona, CA, ³Edward Hines Jr. VA Hospital, Hines, IL

Background: Polymerase chain reaction (PCR) assays have superior sensitivity compared to toxin A/B Enzyme Immunoassay (EIA) testing for the detection of *C. difficile* (CD). Low sensitivity testing methods may lead to diagnostic uncertainty and impact use of ancillary services, specialty consultations and antibiotics (ABX). We assessed how switching from EIA to PCR testing affected ABX prescribing practices and other aspects of patient management at our institution.

Methods: We conducted a retrospective chart review of adult inpatients tested for CD between 7/1/09-12/31/09 (EIA group) and 07/01/11-12/31/11 (PCR group) and treated with oral/IV metronidazole (metro) or oral vancomycin (vanc). We excluded patients receiving metro for non-CD indications or receiving oral vanc tapers for previous CD. Use of ABXs, diagnostic testing and specialty consultations were examined for CD-negative patients in both groups.

Results: Overall, 1,003 CD tests were performed on 664 patients in the EIA group, and 12.6% (n=97) were positive, while 955 tests were performed on 668 patients in the PCR group and 25% (n=167) were positive (p<0.001). The PCR group had fewer repeat CD tests (p<0.001). After exclusions there were 246 patients in the EIA group and 237 patients in PCR group. 1418 vs 636 doses of metro were administered to CD-negative patients in the EIA vs PCR groups (p=0.23). 388 vs 43 doses of oral vanc were administered to CD-negative patients in the EIA vs PCR groups (p=0.007). Compared to the EIA group, the PCR group had significantly decreased ABX treatment days (p=0.004), abdominal radiologic imaging studies (abdominal x-ray p=0.013, abdominal/pelvic CT scan p=0.002), sigmoidoscopy/colonoscopy (p=0.006), and infectious disease consults (p=0.033).

Conclusion: With PCR testing significantly more CD was detected. There was a marked decrease in total ABX treatment days, overall oral vanc use, use of radiologic testing, sigmoidoscopy/colonoscopy, and infectious diseases consultations amongst patients who tested CD-negative by PCR vs EIA. We postulate that lack of confidence in a negative result by the lower sensitivity EIA drove physicians to continue CD treatment and obtain more ancillary tests and services in order to obtain an accurate CD diagnosis.

Findings in the abstracts are embargoed until 12:01 a.m. PST, Oct. 17th with the exception of research findings presented at the IDWeek press conferences.

321. Utility of Perirectal Swab Specimens for Diagnosis of *Clostridium difficile* Infection

Part of Session: 51. *C. difficile* Diagnostics

SIRISHA KUNDRAPU, M.D.¹, VENKATA SUNKESULA, M.D, M.S², LUCY JURY, N.P.², AJAY K. SETHI, PHD³ and CURTIS J. DONSKEY, MD²; ¹Case Western Reserve University, Cleveland, OH, ²Louis Stokes Cleveland Veterans Affairs Medical Center, Cleveland, OH, ³University of Wisconsin-Madison, Madison, WI

Background: Nearly all testing for *Clostridium difficile* infection (CDI) is accomplished through collection of stool specimens. However, patients with severe disease complicated by ileus may be unable to produce stool specimens and a variety of factors may result in delays in specimen collection. We hypothesized that collection of perirectal swabs might provide an accurate and efficient testing strategy for CDI.

Methods: We conducted a 4-month prospective study of inpatients being tested for CDI. Perirectal swabs collected by research staff and stool specimens collected by clinical nurses were tested by polymerase chain reaction (Xpert *C. difficile*, Cepheid) and by culture for toxigenic *C. difficile*. The sensitivity, specificity, positive predictive value (PPV), negative predictive value (NPV), and time to diagnosis of CDI (i.e., from order placement to completion of lab result) were determined for perirectal swabs in comparison to standard testing of stool specimens.

Results: Of 139 patients with stool specimens tested, 23 (17%) were diagnosed with CDI. The sensitivity, specificity, PPV, and NPV of perirectal swabs for diagnosis of CDI were 95.7%, 100%, 100%, and 99.1%, respectively. The median time from CDI test order to test result was 0.5 days (interquartile range; 0, 1 days) for perirectal swab specimens versus 1.2 days (interquartile range, 1.2, 2.1) for stool specimens (P <0.0001). The one patient with positive stool test results but negative results of perirectal PCR testing also had negative culture results from the perirectal swab.

Conclusion: Testing of perirectal swabs by PCR is an accurate and efficient method to diagnose CDI. This testing method will be useful in settings where it is impossible or impractical to collect stool specimens and when rapid diagnosis is required to expedite infection control and management decision-making.

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322. Commercial *Clostridium difficile* Toxin PCR Assay of Stools from Pediatric Inpatients with Diarrhea with Cytotoxicity Confirmation of Positives

Part of Session: 51. *C. difficile* Diagnostics

JILL LEIBOWITZ, MD; Steven and Alexandra Cohen Children's Medical Center of New York of the North Shore-LIJ Health System, New Hyde Park, NY, VIJAYA SOMA, MD; Seattle Children's Research Institute, Seattle, WA and LORRY RUBIN, MD; Hofstra North Shore-LIJ School of Medicine, New Hyde Park, NY

Background: Commercial PCR-based assays for *C. difficile* have been studied in adults, but experience in pediatric patients is limited. Pediatric patients may have a higher rate of asymptomatic carriage than adults. We determined the frequency of positive stool PCR assays for *C. difficile* toxin DNA among tested pediatric inpatients with diarrhea & describe their epidemiologic features.

Methods: The study population was inpatients 1-18 years of age with diarrhea who had stool specimens submitted for testing over a 5 month period. Stools were tested using a *C. difficile* toxin DNA PCR assay (Xpert *C. difficile*, Cepheid, Sunnydale, CA). A cytotoxicity assay (Cytotoxicity Assay for *Clostridium difficile* Toxin, Bartels, Carlsbad, CA) was performed on PCR-positive samples. Demographic and clinical data were abstracted. Proportions were compared using Fisher's Exact test. Medians were compared using the Mann-Whitney test.

Results: Of 121 stools, PCR was positive in 25 (21%). Samples were positive in 27%, 16%, & 21% of patients ages 1-3y, 4-11y & 12-18y, respectively; differences were not significant. Of the 25 PCR-positive specimens, 17 (68%) were classified as nosocomial. The PCR-positive & -negative groups did not differ significantly with respect to median age (10y vs. 11y, $p=0.44$), median hospital days prior to stool collection (5 vs. 2.5, $p=0.33$), receipt of antimicrobials in the preceding 30 d (84% vs. 69%; $p=0.21$), or median antibiotic days in the preceding 30 d (10 vs. 5, $p=0.30$). Of the 23 PCR-positive stools tested, 14 (61%) demonstrated cytotoxin activity. The cytotoxicity-positive and negative groups did not differ significantly with respect to median age (8.5y vs. 7y, $p=0.75$), median hospital days prior to stool collection (5.5 vs. 2, $p=0.19$), receipt of antimicrobials in the preceding 30 d (79% vs. 89%, $p=1.0$), or median antibiotic days in the preceding 30 d (10 vs. 10, $p=0.57$). Of the PCR-positive, cytotoxicity-positive specimens, 11 of 14 were classified as nosocomial compared to 4 of 9 of the PCR-positive, cytotoxicity-negative specimens ($p=0.18$).

Conclusion: Stool *C. difficile* PCR assays are frequently positive in hospitalized children with diarrhea, but specimens are frequently negative by cytotoxicity testing. Further studies are needed to determine the significance of this testing discrepancy.

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323. Stools from Asymptomatic Pediatric Inpatients at Risk for *Clostridium difficile*-Associated Diarrhea Frequently Test Positive Using a Commercial PCR Assay

Part of Session: 51. *C. difficile* Diagnostics

JILL LEIBOWITZ, MD; Steven and Alexandra Cohen Children's Medical Center of New York of the North Shore-LIJ Health System, New Hyde Park, NY, VIJAYA SOMA, MD; Hofstra North Shore-LIJ School of Medicine, New Hyde Park, NY and LORRY RUBIN, MD; Hofstra North Shore-LIJ School of Medicine, New Hyde Park, NY

Background: Many laboratories use polymerase chain reaction (PCR)-based stool assays to detect *Clostridium difficile* toxin DNA, but experience in pediatric patients is limited. We compared the detection rate of *C. difficile* by PCR in high-risk pediatric patients without diarrhea to those with diarrhea who were tested for *C. difficile*.

Methods: Stool specimens from inpatients ages 1-18y with diarrhea and from consented inpatients without diarrhea were tested for *C. difficile* toxin DNA using a commercial PCR assay (Xpert *C. difficile*/Epi, Cepheid, Sunnydale, CA). A cytotoxicity assay was performed on positive samples. Demographic, clinical & laboratory data were abstracted. Proportions were compared using Fisher's Exact test. Medians were compared using Mann-Whitney test.

Results: Of 53 pediatric inpatients without diarrhea, a stool sample tested positive for *C. difficile* toxin DNA in 13 (25%). Included were patients in the pediatric ICU, 7 (29%) positive of 24; oncology unit, 1 (11%) positive of 9; other units, 5 (25%) positive of 20. Among the age groups, 1-3y, 4-11y, 12-18y, the percent positive did not differ significantly. Of the 13 PCR-positive stools, 1 (9%) demonstrated cytotoxin activity. The PCR-positive and negative groups did not differ significantly with respect to median age (7y vs. 6.5y, $p=0.71$), hospital days prior to stool collection (5 vs. 4, $p=0.6$), receipt of antimicrobials in the preceding 30 days (77% vs. 78%; $p=1.0$), or antibiotic days in the preceding 30 days (4 vs. 3.5,

p=0.87). From pediatric inpatients with diarrhea tested by PCR, 25 (21%) of 121 stool samples were positive; of 23 PCR-positive specimens tested, 14 (61%) demonstrated cytotoxin activity. The proportion of PCR-positives between symptomatic & asymptomatic patients did not differ significantly (p=0.56). Of the PCR-positive specimens, the proportion that exhibited cytotoxicity was significantly higher in the group with diarrhea (p=0.0039).

Conclusion: *C. difficile* PCR assays are frequently positive in hospitalized children both with & without diarrhea. Stools positive by PCR are frequently negative by cytotoxicity testing. Our findings suggest that a positive *C. difficile* PCR test result in a hospitalized child with diarrhea should be interpreted with caution.

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324. Regional Differences in *Vancomycin-resistant enterococcus* and *C difficile* co-Colonization Rates in Critically Ill Veterans

Part of Session: 51. *C. difficile* Diagnostics

LINDA MCKINLEY, RN, BSN, MPH, CIC; Madison VA Medical Center, Madison, WI, **MARY HAGLE, RN, PHD**; Milwaukee VA Medical Center, Milwaukee, WI, **HELENE MORIARTY, RN, PHD**; Philadelphia VA Medical Center, Philadelphia, PA, **TOM SHORT, PHD**; John Carroll University, University Heights, OH and **NASIA SAFDAR, MD, PHD**; University of Wisconsin School of Medicine and Public Health, Madison, WI

Background: In 2007, the Department of Veterans Affairs (VA) implemented a nationwide *Methicillin-resistant Staphylococcus aureus* (MRSA) initiative that included active screening for MRSA colonization on all patient admissions. Identification and subsequent isolation of these patients have led to a reduction in overall MRSA infections. Screening and isolation for other multi-drug resistant organisms (e.g., *Vancomycin-resistant enterococcus*, VRE) has not been implemented.

Methods: A prospective study was conducted to identify the admission prevalence rate of VRE in patients admitted to the intensive care unit (ICU) in two VA facilities in Milwaukee and Madison, WI. VRE colonization was identified from perirectal swabs using rapid PCR assay.

Results: Over a period of three months, we found 15 of 61 subjects (26%) colonized with VRE upon ICU admission at the Madison VA Medical Center and 7 of 94 subjects (7%) at the Milwaukee VA Medical Center. We found 5 of 17 (29%) VRE positive subjects co-colonized with CDI during ICU admission at the Madison VA Medical Center and 0 of 5 subjects (0%) at the Milwaukee VA Medical Center; total of 5 of 22 (23%). Patients at both facilities were comparable regarding average severity of illness and demographics. During the same time period, MRSA prevalence rates upon ICU admission at Madison and Milwaukee VA were comparably lower at 10% and 13% respectively. The rate of VRE infections was 1.0 per 1000 patient days at Madison and 0.5 per 1000 patient days at Milwaukee.

Conclusion: Patients at the Madison VA ICU have a greater prevalence of VRE on admission compared with a similar facility in Milwaukee. VRE colonization will be missed in two-thirds of this population when relying on screening in CDI patients alone. Further studies are needed to account for regional differences in VRE admission prevalence and their relationship to targeted infection control interventions.

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325. Changes in *Clostridium difficile* Testing Practices and their Impact on Stool Rejection Policies across Multiple U.S. Laboratories

Part of Session: 51. *C. difficile* Diagnostics

JESSICA COHEN, MPH¹, **DUNCAN MACCANNELL, PHD¹**, **LEIGH ANN CLARK, MPH²**, **WENDY BAMBERG, MD³**, **REBECCA PERLMUTTER, MPH⁴**, **JOHN DUNN, DVM, PHD⁵**, **JOELLE NADLE, MPH⁶**, **STACY HOLZBAUER, DVM⁷**, **CAROL LYONS, MPH⁸**, **ERIN PHIPPS, DVM⁹**, **GHINWA DUMYATI, MD, FSHEA¹⁰**, **ZINTARS G. BELDAVS, MS¹¹** and **FERNANDA LESSA, MD¹**; ¹Division of Healthcare Quality Promotion, Centers for Disease Control and Prevention, Atlanta, GA, ²Georgia Emerging Infections Program, Decatur, GA, ³Colorado Dept. of Public Health and Environment, Denver, CO, ⁴Maryland Dept. of Health and Mental Hygiene, Baltimore, MD, ⁵Tennessee Department of Health, Nashville, TN, ⁶California Emerging Infections Program, Oakland, CA, ⁷CDC CEFO assigned to the MN Dept. of Health, St. Paul, MN, ⁸Connecticut Emerging Infections Program, New Haven, CT, ⁹New Mexico Emerging Infections Program, Albuquerque, NM, ¹⁰University of Rochester, Rochester, NY,

Background:

At least five nucleic acid amplification assays (NAAT), with higher sensitivity than traditional enzyme immunoassays (EIA), have been approved for *Clostridium difficile* testing. Laboratory practice guidelines discourage *C. difficile* testing of formed stools and repeat testing regardless of assay type. We surveyed laboratories participating in the *C. difficile* infection population-based surveillance serving a population of 11.2 million in 10 US sites to assess differences in stool rejection policies based on NAAT adoption.

Methods:

Laboratories were surveyed in December 2011. Data collection included current testing practices, changes to testing algorithms and stool rejection policies in the past year, and number of stool specimens tested and number of stools positive for *C. difficile* in the 3 months pre- and post- NAAT implementation. Chi-square and Wilcoxon rank sum tests were used to evaluate differences in categorical and continuous variables, respectively.

Results:

Surveys were completed by 107 (91%) of the 118 labs surveyed; representing 79 inpatient and 28 outpatient labs. A total of 47 (44%) labs were using NAAT, of these 23 (50%) switched to NAAT as either first line (n=17) or second line (n=6) in 2011. EIA was used by 22 (96%) labs while EIA/GDH was used by 1 lab prior to the switch. Labs using NAAT were more likely to reject formed stools than labs that do not (89% vs. 52%, $P < .001$). More stringent policies were implemented by 20 labs after the switch; 11 of the 12 labs that did not reject formed stools previously began rejecting formed stools after adoption of NAAT and 12 restricted testing of multiple specimens within 48 hours. Data from 16 labs show the median number of specimens tested decreased from 345 to 247 ($P < .001$) and percent of positive specimens increased from 10% to 20% ($P < .001$) in the 3 months after NAAT implementation.

Conclusion:

Rejection policies varied significantly depending on test used. Labs using NAAT reported rejecting formed stools more commonly than labs using toxin assays, and a higher *C. difficile* positivity rate. The implementation of NAAT will likely improve compliance with recommended stool rejection policies, improve detection and, depending on relative cost compared to EIA, reduce costs by performing fewer tests.

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326. The Nose Knows Not: Poor Predictive Value of Stool Sample Odor for Detection of *Clostridium difficile*

Part of Session: 51. *C. difficile* Diagnostics

KRISHNA RAO, MD¹, DANIEL BERLAND, MD¹, CAROL YOUNG, MT(ASCP)², SETH WALK, MS, PHD³ and DUANE NEWTON, PHD³;
¹University of Michigan Health Systems, Ann Arbor, MI, ²University of Michigan Health System, Ann Arbor, MI, ³University of Michigan, Ann Arbor, MI

Background:

C. difficile is a major cause of nosocomial infection and poses a challenge to infection control procedures. A nurse-driven protocol may result in earlier isolation and decreased transmission. Gas chromatography has shown that unique volatile compounds differentiate *C. difficile* positive and negative stool samples and other studies have shown that nurses in the clinical setting may be able to identify *C. difficile* positive stool samples by odor. Our study examined this hypothesis in a controlled laboratory setting.

Methods:

Nurses were recruited from inpatient wards at our hospital. Our microbiology lab randomly set aside 5 positive and 5 negative stool samples based on results from 2-step testing (GDH/toxin EIA followed by PCR for EIA discordants) for *Clostridium difficile* toxin (CDTOX) from patients with liquid stool. We surveyed nurses on age, work experience, and if they felt they could detect *C. difficile* by odor. They were instructed to sniff each sample, 10 total samples per nurse, and record their opinion if CDTOX positive stool was present. Fisher's exact and Mann-Whitney tests were used to assess statistical significance.

Results:

18 nurses participated. Experience ranged from 1 to 30 yrs (8 had > 10 yrs of experience). 11 felt confident they could tell if CDI was present by odor (61%). The median percent correct per individual was 45%. However, the median percent of correct answers for CDTOX positive samples was 31% vs. 74% for CDTOX negative samples ($p=0.0119$). By Fisher's exact tests, no single individual's sniffing ability was better than that predicted by chance (mean sensitivity / specificity = 0.26/0.69). Those with confidence in sniffing ability did not perform better than others based on median percent correct (40% vs. 50%; $p=0.2471$) and more experienced nurses were no different than less experienced nurses in identifying

CDTOX status based on median percent correct (both 45%; $p = 0.8887$).

Conclusion:

In the controlled laboratory setting of our study, nurses were unable to identify *C. difficile* positive stool samples by odor, but CDTOX negative samples elicited more correct answers than CDTOX positive samples. More experience and confidence in the ability to diagnose CDI by odor do not improve performance.

Findings in the abstracts are embargoed until 12:01 a.m. PST, Oct. 17th with the exception of research findings presented at the IDWeek press conferences.

327. Evaluation of a Commercial PCR Assay for Detection of Environmental Contamination with *Clostridium difficile*

Part of Session: 51. *C. difficile* Diagnostics

ABHISHEK DESHPANDE, M.D., PH.D.¹, JENNIFER CADNUM, B.S.², BRETT SITZLAR, B.S.², SIRISHA KUNDRAPU, M.D.² and CURTIS J. DONSKEY, MD²; ¹Case Western Reserve University, Cleveland, OH, ²Louis Stokes Cleveland Veterans Affairs Medical Center, Cleveland, OH

Background: Contaminated environmental surfaces are an important source for transmission of *Clostridium difficile*. However, there are currently no efficient and easy to use methods to assess the effectiveness of environmental disinfection.

Methods: We tested the hypothesis that a commercial real-time polymerase chain reaction (PCR) for the toxin B gene *tcdB* (Xpert[®] *C. difficile*, Cepheid) would provide a sensitive and efficient method to detect toxigenic *C. difficile* in the environment. Pre-moistened swabs and gauze pads were used to culture high-touch surfaces (toilet seat/hand rail, table/bed rail, phone/call button) in *C. difficile* infection (CDI) rooms before and after post-discharge cleaning by housekeeping. The sensitivity, specificity, positive predictive value (PPV), and negative predictive value (NPV) of PCR from swabs was compared to toxigenic culture by direct plating of swabs.

Results: Of 22 CDI rooms, 9 were sampled before and 13 were sampled after post-discharge cleaning. One or more *C. difficile* swab cultures were positive for 6 of 9 active CDI rooms and 6 of 13 (46%) cleaned rooms. PCR testing of swabs was specific but had low sensitivity in comparison to culture (Table). Lowering the PCR cycle threshold (Ct) value to 45 increased sensitivity without decreasing specificity. PCR positivity correlated with greater levels of contamination (5/5 sites positive when ≥ 10 colonies (range: 11-215) present versus 0/6 when < 10 colonies recovered ($P < 0.001$). In comparison to swabs, gauze cultures had 50% higher site positivity in both active CDI and cleaned rooms.

Conclusion: In comparison to culture, we found that a commercial PCR assay had good sensitivity for detection of heavy environmental contamination, but poor sensitivity for detection of low levels of contamination that were typically present after rooms were cleaned. Modifications of the assay such as lowering the PCR Ct or increasing the surface area sampled may result in improved sensitivity.

Table. Diagnostic accuracy of PCR for detection of environmental *C. difficile*

	No. PCR +/No. culture +	Sensitivity (%)	Specificity (%)	PPV (%)	NPV (%)
Active CDI patient in room	2/6	33.33	100	100	42.86
After terminal cleaning	1/6	16.67	100	100	58.33
Active CDI patient in room (Ct < 45)	5/6	83.33	100	100	75
After terminal cleaning (Ct < 45)	2/6	33.33	100	100	63.64

Findings in the abstracts are embargoed until 12:01 a.m. PST, Oct. 17th with the exception of research findings presented at the IDWeek press conferences.

328. Severe *Clostridium difficile* Infection in Patients with Negative Results for *tcdB* by the Xpert® *C. difficile* assay

Part of Session: 51. *C. difficile* Diagnostics

JEROME LEIS, MD¹, WAYNE GOLD, MD, FRCPC¹, JOHN NG, PHD¹, ZAHIR HIRJI¹, DYLAN PILLAI, MD, PHD², GEORGE BROUKHANSKI, PHD¹, PAUL RAGGIUNTI¹, SUSY HOTA, MD¹, ALLISON MCGEER, MD, FSHEA¹ and SUSAN POUTANEN, MD, MPH¹; ¹University of Toronto, Toronto, ON, Canada, ²University of Calgary, Calgary, AB, Canada

Background:

C. difficile (CD) real-time polymerase chain reaction (PCR) for *tcdB* is more sensitive and reduces turnaround time when compared to toxin immunoassay. We noted typical amplification curves with high cycle thresholds (Ct) and low endpoints (Ept) that are labeled negative by the Xpert® assay (Cepheid) and undertook this project to determine their significance.

Methods:

An indeterminate (IND) Xpert® CD assay result was defined as detection of a typical PCR amplification curve with a non-zero numeric Ct and Ept >10, and interpreted as negative by the Xpert® assay. For 5 months after implementation of Xpert® in our laboratory, non-duplicate stools with an IND result were retested by Xpert®, cultured for toxigenic CD, and isolates were subjected to PCR ribotyping, toxin genotyping and multilocus variable-number tandem repeat analysis (MLVA) typing. Chart reviews were completed to assess if patients met the SHEA/IDSA CD infection (CDI) case definition and illness severity was compared with Ct and culture results.

Results:

During the first year after implementation of the Xpert® assay, 14% (1151/8413) of specimens were positive and 1% (97/8413) were IND. IND results were not associated with one user or one machine module, and the percentage was stable over time. Of the 48 patients with IND results in the first 5 months, 39 (81%) met the CDI case definition, and 7 (18%) met criteria for severe CDI. Toxigenic stool cultures were positive for 86% (6/7) of patients with severe CDI, 19% (6/32) of patients with non-severe CDI, and 44% (4/9) of patients who did not meet CDI case definition ($p=0.002$). Lower Ct and higher Ept were associated with greater likelihood of toxigenic culture positivity ($p=0.03$) and more severe symptoms ($p=0.06$). Typing of CD isolates confirmed that IND results were not associated with a particular strain.

Conclusion:

One-third of results that have typical amplification curves, but are interpreted as negative by Xpert®, are positive by toxigenic culture and most meet the case definition of CDI. The mechanism of these false-negative results is not technique-related, equipment-related, or due to particular CD strains. IND results should be reported to clinicians as they may impact patient care decisions.

Findings in the abstracts are embargoed until 12:01 a.m. PST, Oct. 17th with the exception of research findings presented at the IDWeek press conferences.

329. Does Empirical *Clostridium difficile* Infection (CDI) Therapy Result in False-Negative CDI Diagnostic Test Results?

Part of Session: 51. *C. difficile* Diagnostics

VENKATA SUNKESULA, M.D, M.S¹, SIRISHA KUNDRAPU, M.D.² and CURTIS J. DONSKEY, MD¹; ¹Louis Stokes Cleveland Veterans Affairs Medical Center, Cleveland, OH, ²Case Western Reserve University, Cleveland, OH

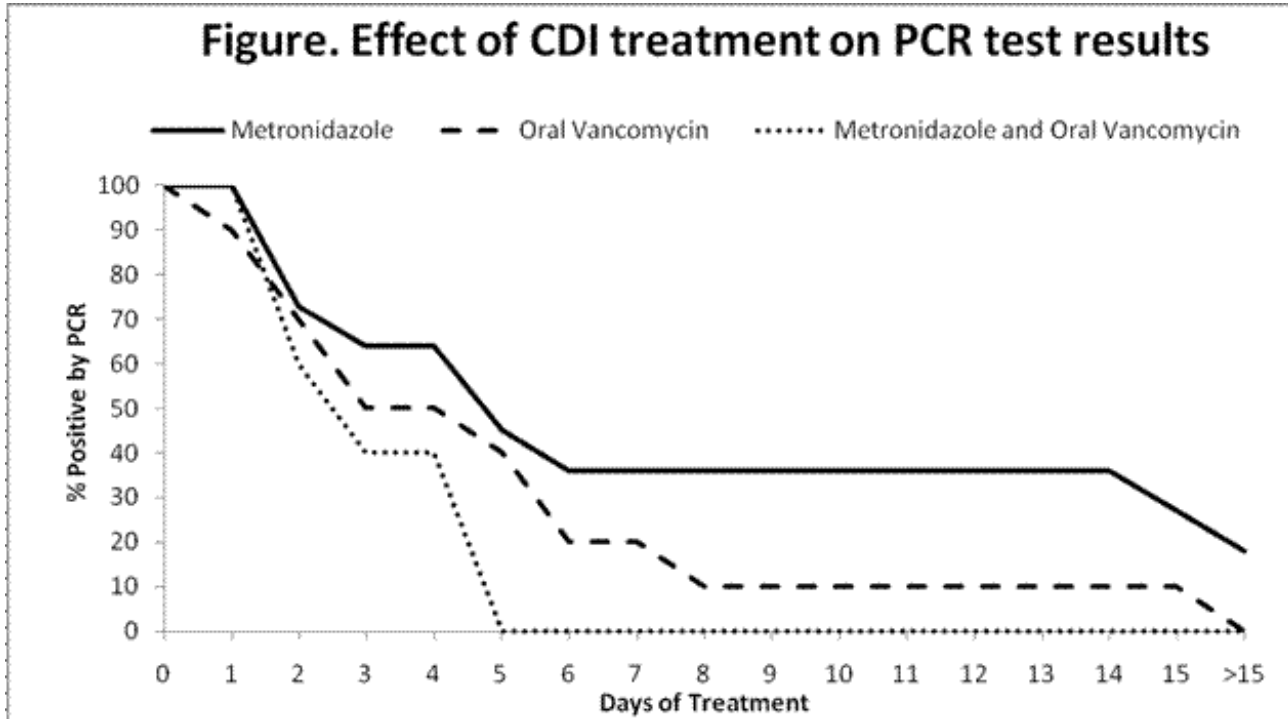
Background: Patients with suspected *Clostridium difficile* infection (CDI) often receive empirical CDI therapy while awaiting diagnostic test results. Because CDI treatment suppresses *C. difficile* in the colon, we hypothesized that empirical therapy might result in false-negative CDI diagnostic test results.

Methods: We conducted a 6-month prospective study of inpatients being tested for CDI. We determined the frequency of empirical therapy for CDI and calculated the time on empirical therapy prior to collection of a stool sample for testing. For a cohort of CDI patients, we tested multiple stool samples during therapy to determine the impact of CDI therapy on results of polymerase chain reaction (PCR) for toxin B genes.

Results: Of 151 patients being tested for CDI, 29 (19%) patients were empirically treated, of whom 27 tested negative. The median duration of empirical CDI therapy prior to collection of a stool sample was 24 hours (range, 6 hours to 9 days). For 26 CDI patients with serial testing, PCR results converted to negative within 7 days in 7 of 11 (64%) metronidazole-treated patients and 14 of 15 (93%) vancomycin or vancomycin plus metronidazole-treated patients ($P=0.11$) (Figure). There were no differences between patients who did or did not convert to negative PCR with regard to age, ATLAS score, age adjusted Charlson comorbidity index, infection with the NAP1 epidemic strain, or clinical treatment response. Within 1 and 2 days of treatment, 1 (4%) and 7 (27%) of 26 CDI patients had converted to negative PCR results,

respectively.

Conclusion: Empirical treatment of patients with suspected CDI resulted in negative stool PCR results in only 4% of patients after 1 day of therapy, but negative results occurred in 27% or more of infected patients when stool collection was delayed ≥ 2 days. Positive PCR results often persisted for several days after start of CDI therapy.



Findings in the abstracts are embargoed until 12:01 a.m. PST, Oct. 17th with the exception of research findings presented at the IDWeek press conferences.

330. Prospective Evaluation of the Epidemiology of *Clostridium difficile* Colonization and Infection among Hematopoietic Stem Cell Transplant Recipients

Part of Session: 51. *C. difficile* Diagnostics

VARINIA URDAY-CORNEJO, MD¹, CHRISTOPHER CROSWELL¹, TEENA CHOPRA, MD, MPH², ALYSSA LIUBAKKA¹, JESSICA CUTRIGHT, BS¹, HOSSEIN SALIMNIA, PHD³, PAUL LEPHART, PHD³, SANJAY REVANKAR, MD¹, PRANATHARTHI CHANDRASEKAR, MD¹ and GEORGE ALANGADEN, MD⁴; ¹Wayne State University, Detroit, MI, ²Detroit Medical Center/ Wayne State University, Detroit, MI, ³Detroit Medical Center University Laboratories, Detroit, MI, ⁴Henry Ford Health System, Detroit, MI

Background:

Clostridium difficile infection (CDI) occurs in 4-20% of Hematopoietic Stem Cell Transplant (HSCT) recipients. Asymptomatic carriage of *Clostridium difficile* (*C. diff*) is believed to occur in about 7% of healthy adults and 11-25% of hospitalized patients (pts).

We performed a prospective study to examine the rates of asymptomatic carriage of *C. diff* and symptomatic CDI in the HSCT recipients to better understand the epidemiology of CDI in this population.

Methods:

This study began in December 2010 and was performed at the Karmanos Cancer Center, a 100 bed tertiary care hospital in Detroit, Michigan. Informed consent was obtained from all pts admitted to the HSCT unit before study enrollment. Stool samples were collected within 72 hours of hospital admission and weekly thereafter until hospital discharge. Samples were anaerobically cultured for *C. diff* using two different culture media: CCFA-VA and CCFA-HB media. All culture positive stool samples were tested by PCR for confirmation of toxigenic *C. diff*. Medical data on pt demographics and clinical outcomes was collected.

Results:

Data on the first 50 pts (planned study enrollment of 200 pts) is presented. The median follow up was 284 days (range =

196-372 d). The overall study population had a mean age of 50 yr, 48% were women, 92% were allogeneic HSCT recipients, 52% had been hospitalized within the last 30 d. Of the 50 pts, 21 (42%) were colonized with *C. diff* at hospital admission of which 7 (33%) were colonized with a toxigenic strain. All 7 (100%) pts colonized with a toxigenic strain developed CDI during the hospital stay compared to 1/14 (7%) colonized with a non-toxigenic strain at admission. Of the 29 pts not colonized at admission 6 (29%) subsequently became colonized with *C. diff*; 3 toxigenic and 3 non-toxigenic strains. Overall 14/50 pts developed CDI during the period of follow-up, of these 36 % had a recurrent episode of CDI.

Conclusion:

CDI occurs frequently in the HSCT population at our institution and recurrent CDI occurs in a third of pts with CDI. Asymptomatic colonization with *C. diff* at time of hospitalization is common. Colonization with a toxigenic strain at admission is predictive of CDI. Additional studies are needed to elucidate the clinical and infection control implications of these findings.

Findings in the abstracts are embargoed until 12:01 a.m. PST, Oct. 17th with the exception of research findings presented at the IDWeek press conferences.

331. Multilocus sequence typing analysis of 85 *C. difficile* strains isolated from a teaching hospital in Houston Texas, September through December 2011

Part of Session: 51. *C. difficile* Diagnostics

ZHI-DONG JIANG; The University of Texas, School of Public Health, Houston, TX, RAVI PANCHUMARTHI; UNIVERSITY OF TEXAS SCHOOL OF PUBLIC HEALTH, HOUSTON, TX, KEVIN W. GAREY, PHARM.D, M.S.; University of Houston College of Pharmacy, Houston, TX, TODD M. LASCO, PHD; Saint Lukes Episcopal Hospital, Houston, TX, JANE CHEN; UNIVERSITY OF TEXAS SCHOOL OF PUBLIC HEALTH, HOUSTON, TX and HERBERT DUPONT, MD, FIDSA; St. Luke's Episcopal Hospital and Kelsey Research Foundation and Kelsey-Seybold Clinic, Houston, TX

Background: In epidemiological research, genotyping of strains plays an important role in tracing potential source(s), identifying infection clusters, and defining mode(s) of transmission. Multilocus sequence typing (MLST) facilitates the separation of isolates by indexing variation in intragenic sequences of a set (generally, 5 to 7) of housekeeping genes.

Methods: A total of 85 *C. difficile* (CD) clinical isolates collected between September and December of 2011 from a large teaching hospital in Houston, Texas were analyzed by MLST analysis of six housekeeping genes (*aroE*, *dutA*, *tpi*, *recA*, *gmk*, and *sodA*).

Results: The number of alleles ranged from 7 (*recA* and *gmk*) to eleven (*sodA*). Allelic profiles revealed 20 different sequence types (STs). All STs lacked correlation with geographic source, but correlated to CD toxigenic type. The dendrogram generated from a matrix of pairwise genetic distances showed no hypervirulent lineage within the population of toxigenic human isolates. However, A- B+ variant isolates shared the same STs that appeared as a divergent lineage in the population studied, indicating a single evolutionary origin.

Conclusion: This study focused on human clinical isolates collected from a single geographic location. It sets a baseline of MLST data for epidemiologic studies underway designed to identify clustering and hospital transmission of strains of CD, and the relationship between genotype pattern and disease severity using clinical severity data from infected patients.

Findings in the abstracts are embargoed until 12:01 a.m. PST, Oct. 17th with the exception of research findings presented at the IDWeek press conferences.

332. *Clostridium difficile* Whole Genome Sequencing Suggests Limited Transmission Arising From Mixed Infection

Part of Session: 51. *C. difficile* Diagnostics

DAVID EYRE, BM, BCH¹, MADELEINE CULE, PHD², DAVID GRIFFITHS, BSC³, TIM PETO, MB BS, DPHIL⁴, A. SARAH WALKER, PHD² and DANIEL WILSON, DPHIL²; ¹Nihr Oxford Biomedical Research Centre, Oxford, United Kingdom, ²NIHR Oxford Biomedical Research Centre, Oxford, United Kingdom, ³National Institute for Health Research Oxford Biomedical Research Centre, Oxford, United Kingdom, ⁴University of Oxford, Oxford, United Kingdom

Background: Whole genome sequencing (WGS) offers the prospect of high precision outbreak investigation using genetic data. However, potentially undetected mixed infection impairs exclusion of transmission with certainty. *Clostridium*

difficile (CD) mixed infection rates of ~7% are described, but their significance in transmission is unclear.

Methods: Hospital admission / ward movement data on 1276 CD cases in Oxfordshire, UK (Sep07 – Mar10) were analysed in a stochastic compartmental transmission model. Independently, isolates were multi-locus sequence typed (MLST). 15 high probability transmissions ($p > 0.45$) had putative donors and recipients with discordant sequence types (STs). WGS of primary stool cultures from each putative donor and recipient was undertaken using Illumina HiSeq. Reads were mapped to the CD630 reference. Assuming each culture contained a mix of 1 or 2 STs, a maximum likelihood estimate of the identity, and relative proportions, of each ST present was obtained using Illumina base counts at the MLST loci. Estimator performance was assessed using 100 sequences from sub-culture of a single colony, and 10000 simulated mixes of these sequences.

Results: Sequences were obtained from 13 putative donors and 15 putative recipients (2 donors had 2 putative recipients). In 27/28 samples the estimated dominant ST matched the original ST from MLST PCR. The remaining sample was significantly contaminated with another *Clostridium* species. Only 1/28, a recipient, had a minor ST recovered (8.4% of the sample) that created a new donor-recipient ST match. The minor ST was that predicted by the transmission model.

In 100 sequences each derived from a single colony, thus expected not to be mixed, the known ST was recovered on all occasions and accounted for median 99.9% (IQR 99.0-100%) of the sample. In 10000 simulated mixed ST infections the mixture proportion was estimated with a root mean square error of 0.068, and the correct STs were obtained on 9706/10000 occasions.

Conclusion: WGS can detect mixed ST infection without labor-intensive multiple colony typing. In this sample of cases significantly enriched for the possibility of mixed infection only 1/15 putative donor-recipient pairs showed evidence of a mixed infection that might have been missed on initial typing and supported transmission.

Findings in the abstracts are embargoed until 12:01 a.m. PST, Oct. 17th with the exception of research findings presented at the IDWeek press conferences.

333. Title: Safety of Clostridium Difficile Testing Algorithm using Glutamate Dehydrogenase Antigen and Toxin Enzyme Immunoassay with Reflex PCR for Discordant Test

Part of Session: 51. *C. difficile* Diagnostics

CECILIA BIG, MD, DAVID SENGSTOCK, MD, MS, NATASHA BAGDASARIAN, MD, MPH, VIJAYALAKSHMI NAGAPPAN, MD, PADMAJA VEMURI, MD, DAVID WEIDENDORF, MD and **RAMA THYAGARAJAN, MD**; Oakwood Hospital and Medical Center, Dearborn, MI

Background:

Introduction & background: Clostridium difficile infections (CDI) are a significant cause of hospital-associated morbidity and mortality. PCR tests for CDI are sensitive but expensive. At a community hospital system comprised of four teaching centers, stools from symptomatic patients are tested with a combined Glutamate Dehydrogenase Antigen (GDH) and Clostridium Difficile Toxin Enzyme Immunoassay (toxin EIA); subsequently, PCR is done when GDH is positive but toxin EIA is negative. The combination GDH/toxin EIA has a reported 90.5% sensitivity with a negative predictive value of 97.6%. The current study aimed to determine whether patients with negative testing for CDI by GDH/toxin EIA suffered adverse clinical consequences due to undiagnosed CDI, as measured by death or readmission for CDI within 7 days.

Methods:

Methods: We queried the hospital microbiology database for all first-time stool tests during hospitalization for CDI in adult inpatients during the month of September 2011. All initial positive GDH/toxin EIA tests were excluded. Charts from the first 100 patients with initial negative tests were examined for repeat CDI testing, death, or re-admission within 7 days.

Results:

Results: 18 of the first 100 patients with initial negative tests had one or more repeat tests; only one of the repeat test was positive (1% false negative rate). That positive repeat test was ordered the following day and the patient was successfully treated. Three patients expired due to unrelated causes; 18 were discharged without any further medical care at our facility; laboratory data confirmed that the remaining 79 patients were alive after 7 days. No patient with a negative test was re-admitted or died within 7 days due to CDI.

Conclusion:

Conclusion: Preliminary results suggest that after a negative GDH/toxin EIA, poor outcome as a result of undiagnosed CDI is rare. The GDH/toxin EIA combination is a safe and effective method to rule out clinically significant CDI.

Findings in the abstracts are embargoed until 12:01 a.m. PST, Oct. 17th with the exception of research

334. Prevalence and Molecular Epidemiology of *Clostridium difficile* (CD) in Food and Companion Animals, Retail Meats, and Humans in Minnesota

Part of Session: 51. *C. difficile* Diagnostics

MEGAN K. SHAUGHNESSY, MD¹, TIM SNIDER, DVM², ROCIO SEPULVEDA², DAVID BOXRUD, MS³, ELIZABETH CEBELINSKI, BS³, STACY HOLZBAUER, DVM⁴, KIRK SMITH, DVM, PHD³, JEFF BENDER, DVM MS DACVPM⁵, FRANCISCO DIEZ-GONZALEZ, PHD⁵ and JAMES R. JOHNSON, MD¹; ¹University of Minnesota, Minneapolis, MN, ²University of Minnesota, St Paul, MN, ³Minnesota Department of Health, St. Paul, MN, ⁴CDC CEFO assigned to the Minnesota Department of Health, St. Paul, MN, ⁵University of Minnesota, St. Paul, MN

Background: Community associated *Clostridium difficile* infection (CA-CDI), i.e., CDI in patients who lack classic CDI risk factors (recent hospitalization or antibiotic use), is increasing and accounts for approximately 50% of CDI cases in central Minnesota. Some have speculated that animals and food may serve as CA-CDI sources. We collected samples from humans, animals, and meat products to explore this hypothesis.

Methods: Since 2007, the Minnesota Department of Health (MDH) has collected and genotyped CD isolates from central Minnesota as part of human CDI surveillance. In November 2011, we began collecting food and companion animal fecal samples (goal n = 600) and retail meat products (goal n = 300) from the same geographic region. Sample characteristics for fecal samples (geographic region, animal diarrhea status, age, antibiotic use) and retail meats (geographic region, antibiotic-free labeling) are recorded. Animal fecal and retail meat samples are cultured using a single alcohol shock method. CD-like colonies are confirmed as CD using egg yolk agar, blood agar, PRO disk, and Gram stain. Confirmed CD isolates undergo binary toxin PCR, toxinotyping, and *tcdC* gene sequencing.

Results: Sample collection is ongoing. Of 164 animal fecal samples tested to date, 17 (10%) yielded CD; the majority porcine (n = 10) and bovine (n = 4). Preliminary results showed a higher trend in the CD positivity rate among diarrhetic (26%) versus healthy animals (5%), (P = .15). To date, of 129 retail meat samples tested, none were CD-positive. Molecular analysis shows that most CD isolates are binary toxin positive (81%), toxinotype V (75%), with a 39 base pair deletion in *tcdC* (81%). In parallel, MDH's human CDI surveillance project has yielded 138 human CD isolates during the same time frame.

Conclusion: CD has been recovered from food animals in Minnesota, but not from retail meats. Future plans include (i) completing collection and CD testing of animal fecal and retail meat samples, (ii) comparative molecular analysis of CD isolates from animals, meats, and humans including pulsed field gel electrophoresis, (iii) and statistical analysis of CD prevalence in relation to sample characteristics. Preliminary data from retail meat currently does not support the hypothesis that meat products are a key source of CA-CDI.

Findings in the abstracts are embargoed until 12:01 a.m. PST, Oct. 17th with the exception of research findings presented at the IDWeek press conferences.

335. Screening for Vancomycin Resistant Enterococcus (VRE) Colonization During *Clostridium difficile* Testing is Not Cost Effective at a Canadian Teaching Hospital

Part of Session: 51. *C. difficile* Diagnostics

SUNIL VARGHESE, MD, MA¹, KATHRYN SUH, MD, MSC, FRCPC¹, NATALIE BRUCE, RN, BSCN, CIC¹, KARAM RAMOTAR, PHD¹ and VIRGINIA ROTH, MD²; ¹The Ottawa Hospital, Ottawa, ON, Canada, ²The Ottawa Hosp, Ottawa, ON, Canada

Background: From January-December 2010, The Ottawa Hospital (TOH) was screening all patients on admission for VRE colonization. As part of outbreak management, screening roommates of patients with VRE (contact tracing), point prevalence surveys, and discharge/transfer screening were routinely performed. VRE screening was also simultaneously performed on all stool samples submitted for *C. difficile* testing. This retrospective review assessed the costs and incremental yield of VRE detection from stool samples submitted for *C. difficile* testing.

Methods: Data from January - December 2010 were collected retrospectively. Information was obtained from surveillance data available through the Departments of Microbiology, Clinical Quality and Performance Measurement, and Infection Control.

Results: 44616 VRE screening tests were performed during the study period. 403 separate patients were identified with VRE. From 7071 stool specimens submitted for *C. difficile* testing, 41 separate patients were identified with VRE. Of these 41 patients, 24 (59%) would have been subsequently identified by VRE screening that was performed for other infection control indications. Time from initial positivity (at the time of *C. difficile* testing) to subsequent positive test was 0-281 days

(mean 22.5 days, median 5.5 days, mode 4 days). VRE testing of *C. difficile* specimens identified only 17 patients (4.2% of all patients with VRE) who would not otherwise have been detected. The total cost for VRE screening with *C. difficile* testing was approximately \$35,000 CDN.

Conclusion: The overall yield of VRE testing on samples sent for *C. difficile* testing is low at TOH. Only 4.2% of patients with VRE were identified solely through screening of stool specimens submitted for *C. difficile* testing. Given the low morbidity associated with VRE colonization, this calls into question the cost effectiveness of routinely testing *C. difficile* stool specimens for VRE.

Findings in the abstracts are embargoed until 12:01 a.m. PST, Oct. 17th with the exception of research findings presented at the IDWeek press conferences.

336. Toxin A/B EIA Compared to Molecular Amplification Testing for *Clostridium Difficile*: Cost and Resource Utilization Analyses

Part of Session: 51. *C. difficile* Diagnostics

REDA A. AWALI, MD¹, BRINDHA GOPALA KRISHNAN, MD¹, HARLEEN KAUR, MD¹, INDU K. CHALANA, MD², PAULA ROBINSON, RN¹, SANJAY REVANKAR, MD³, JUDY MOSHOS, BS, MT⁴, PAUL LEPHART, PHD⁵, RICHARD FACKLER, BBA¹, KEITH KAYE, MD, MPH, FIDSA, FSHEA⁶ and TEENA CHOPRA, MD, MPH⁷; ¹Detroit Medical Center, Wayne State University, Detroit, MI, ²Wayne State University / Detroit Medical Center, Detroit, MI, ³Wayne State University, Detroit, MI, ⁴Sinai-Grace Hospital, Detroit Medical Center, Detroit, MI, ⁵DMC University Laboratories, Detroit, MI, ⁶Detroit Medical Center (DMC) / Wayne State University, Detroit, MI, ⁷Detroit Medical Center/ Wayne State University, Detroit, MI

Background: Since molecular amplification testing has only recently been adopted for CDI diagnosis, its cost-effectiveness in detecting CD in a hospital setting is still unclear. We did this study to evaluate the cost-effectiveness of diagnosis of CDI by molecular amplification (MA) as compared with Toxin A/B EIA.

Methods: Data on 229 CDI positive patients (tested by either EIA or Illumigene assay) were obtained from the microbiology laboratory at one of the Detroit Medical Center hospitals between July 2009 and December 2011. Additional data on isolation days and costs of contact isolation were acquired from the infection control department of the participating hospital. Outcome measures were number and type of CD tests ordered per patient and duration of contact isolation and associated costs. Costs were calculated from the private payer perspective and analyzed using Wilcoxon rank-sum test. Statistical analysis was done using IBM SPSS Statistics 20.0.

Results: Fifty-three CDI patients were admitted to the hospital during the first 15 months of the study and were tested using the EIA. The 176 patients admitted during the second 15 months of the study were diagnosed by MA. The mean age of EIA patients was higher than that of MA patients (67 ± 15 vs 60.4 ± 20 ; $p=0.016$). There was a female predominance in both groups (53% in EIA group and 59% in PCR group).

The median number of tests ordered per patient was much higher in the EIA group than the MA group (2, IQR [1-3] vs 1, IQR [1-1]; $p<0.0001$). Also, the median number of isolation days per patient was greater in the EIA group than in MA group (8, IQR [5-10] vs. 7, IQR [4-9]; $p=0.082$). Although not statistically significant, the estimated median of costs attributable to contact isolation of CDI patients (i.e. private room, gowns, gloves) was higher in EIA group than in MA group (\$8539, IQR [5355-10710] vs \$7497, IQR [4284-9639]; $p=0.082$)

Conclusion: Patients in the MA group were younger than those in the EIA group, possibly due to the increased sensitivity of the MA test. Use of MA was associated with decreased number of CDI tests performed, shorter durations of contact isolation for patients with CDI and fewer costs related to contact isolation.

Findings in the abstracts are embargoed until 12:01 a.m. PST, Oct. 17th with the exception of research findings presented at the IDWeek press conferences.

337. Comparative Analysis of Two Culture Media and PCR for the Detection of Toxigenic and Non-Toxigenic *C. difficile*

Part of Session: 51. *C. difficile* Diagnostics

CHRISTOPHER CROSWELL¹, VARINIA URDAY-CORNEJO, MD¹, ALYSSA LIUBAKKA¹, JESSICA CUTRIGHT, BS¹, HOSSEIN SALIMNIA, PHD², PAUL LEPHART, PHD³, TEENA CHOPRA, MD, MPH⁴, PRANATHARTHI CHANDRASEKAR, MD¹ and GEORGE ALANGADEN, MD⁵; ¹Wayne State University, Detroit, MI, ²Detroit Medical Center/Wayne State University, Detroit, MI, ³Detroit Medical Center University Laboratories, Detroit, MI, ⁴Detroit Medical Center/ Wayne State University, Detroit, MI, ⁵Henry Ford

Background:

Clostridium difficile (*C. diff*) is an anaerobic gram positive bacillus that causes *C. diff* infection (CDI). Epidemiological studies utilize special culture media to isolate *C. diff*, in order to determine rates of asymptomatic carriage of *C. diff* or to evaluate environmental contamination with *C. diff*. The goal of this study was to compare the effectiveness of two different culture media used to isolate toxigenic and non-toxigenic *C. diff*. The two media tested were a new modified cycloserine-cefoxitin, fructose agar enriched with horse blood (CCFA-HB) and the commonly used pre-reduced cycloserine-cefoxitin agar with vancomycin (CCFA-VA). Culture results were confirmed by *C. diff* real-time PCR (TIB, MolBiol) for the identification of toxigenic *C. diff*.

Methods:

Prospective stool samples from 50 asymptomatic hematopoietic stem-cell transplant recipients from an ongoing study of CDI were cultured on both CCFA-HB and CCFA-VA media, followed by incubation in an anaerobic chamber. The *C. diff* real-time PCR assay was performed on all samples to identify toxigenic *C. diff* and to confirm culture results. Sensitivity, specificity, negative predictive values, and positive predictive values were calculated.

Results:

C. diff was isolated from 21 of the 50 samples using CCFA-HB, and 7 of these tested positive by PCR for toxigenic *C. diff*. In contrast, *C. diff* was isolated from 6 of the 50 samples using CCFA-VA media, and 4 of these tested positive by PCR. The sensitivity, specificity, negative predictive value and positive predictive value for CCFA-HB compared to PCR were 100%, 67%, 100%, and 33%. The sensitivity, specificity, negative predictive value, and positive predictive value for CCFA-VA were 57%, 95%, 93%, and 67%.

Conclusion:

CCFA-HB media supports the growth of both toxigenic and non-toxigenic *C. diff* strains, and is considerably more sensitive than the CCFA-VA media. Conversely, the CCFA-VA media offers more specificity for the isolation of toxigenic *C. diff*. Based upon this study, CCFA-HB is the preferred media for population studies evaluating asymptomatic carriage rates of toxigenic and non-toxigenic *C. diff*. The use of the current standard media, CCFA-VA, for this purpose may result in an underestimation.

Findings in the abstracts are embargoed until 12:01 a.m. PST, Oct. 17th with the exception of research findings presented at the IDWeek press conferences.