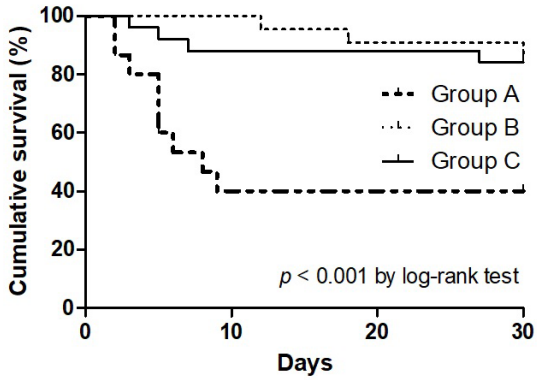
bacteremia was identified in 22 patients (35.5%) and was significantly more common in group A (60.0% [9/15]) than groups B (43.5% [10/23]) or C (12.5% [3/24]) ($P$ = 0.01). Thirty-day mortality rates were also significantly higher in group A than groups B or C (60.0% [9/15] vs. 13.0% [3/23] and 16.7% [4/24], respectively; $P$ < 0.001) (Figure 1). *C. difficile* bacteremia ($P$ = 0.16), polymicrobial infection ($P$ = 0.91), and antimicrobial therapy for *C. difficile* ($P$ = 0.48) were not significantly associated with 30-day mortality. In a multivariate analysis, group A was an independent risk factor for 30-day mortality. (adjusted odds ratio; 7.29 [95% confidence interval; 1.68–31.68], $P$ = 0.01).

***Conclusion.*** Extraintestinal *C. difficile* infection was not commonly associated with *C. difficile* enterocolitis. Extraintestinal *C. difficile* infection accompanied by GI disruption with malignancy was associated with significantly poorer outcomes.

**Figure 1.** Kaplan-Meier survival curve of patients up to 30 days after culture, stratified for groups A, B, and C.




***Disclosures.*** **All authors:** No reported disclosures.

**2406. Trends of Clostridioides difficile-Associated Diarrhea at a Tertiary Care Center in India**

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***Background.*** *Clostridioides difficile* has been recognized as a significant cause of morbidity and mortality globally. Its infection can range from asymptomatic carriage to antibiotic-associated diarrhea and colitis. Reports of outbreak with the hypervirulent strain (N1/NAP1 Ribotype 027) has raised the concern on the magnitude and severity of *C. difficile* infections. This study aimed to determine the prevalence of *C. difficile*-associated diarrhea (CDAD) among the patients at a tertiary care hospital in India.

***Methods.*** A retrospective analysis from January 2015-December 2018 was done to determine the trends of *C. difficile* infection. ELISA for detection of toxins A and B was performed on stool samples. A diagnosis of CDAD was made in all patients with stool samples positive for toxins A and B.

***Results.*** Samples from 1311 patients were received from January 2015-December 2018 from patients with suspected nosocomial diarrhea. 9/1311 were culture positive for *C. difficile*, 7/9 were both culture and ELISA positive. A total of 74 patients were positive for ELISA for detection of toxins A and B. The prevalence of CDAD in the years 2015–2018 were as follows: 4.01% (10/249) in 2015, 10.03% (26/259) in 2016, 4.7% (21/446) in 2017 and 5.32% (19/357) in 2018, respectively. Malignancy was found to be the most common underlying pathological condition 15/69. Most common group of antibiotics used in these patients of CDAD were carbapenems 20/64. Amongst 82.6% (57/69) of the patients were hospitalized. Diarrhea was associated with fever in 40.5% (28/69) of the patients.

***Conclusion.*** Our results show over all variable prevalence of CDAD over the years and was higher in the year 2016. Timely appropriate diagnosis, high index of suspicion in high-risk patients and proper implementation of antimicrobial stewardship programs may help in reducing morbidity and mortality in patients of CDAD.

***Disclosures.*** **All authors:** No reported disclosures.

**2407. Overexpression of Virulence Factors in Biofilm from Recurrent *Clostridium (Clostridioides) difficile* Infection Isolates.**

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***Background.*** Recurrent *Clostridium* (*Clostridioides*) *difficile* infection (R-CDI) remains a significant healthcare problem. Our aim was to analyze virulence/colonization determinants including spore formation, and expression of quorum sensing factors and adhesion capability in *C. difficile* biofilms, which serve as a potential reservoir for *C. difficile* in R-CDI.

***Methods.*** Isolates obtained from patients with R-CDI ($n$ = 39) and non-recurrent CDI (NR-CDI) ($n$ = 93) were analyzed. Isolates were identified by PCR and MALDI-TOF MS and ribotyped by 16S-RNA amplification and capillary electrophoresis.

***Biofilm production in a*** *C. difficile* and in a *C. difficile*-microbiota (*Enterococcus* and *Lactobacillus* species) model was assessed by the crystal violet method. Spore counts were determined both in planktonic and biofilm growth.

***RNA was extracted from a selection of strains from R-CDI ($n$ = 10) and NR-CDI ($n$ = 10) isolate biofilms and relative expression levels of:*** *spo0A, sigH, slpA, cwp84, agrD1* ***and*** *luxS* ***were determined.***

***Results.*** All NR-CDI and R-CDI isolates were biofilm producers and most were strongly adherent (90.90%) and 027 ribotype (81.37%).

***In the*** *C. difficile* biofilm model, spore formation was higher in R-CDI than in the NR-CDI isolates ($P$ = 0.015). In the biofilm of *C. difficile*-microbiota, no difference was detected in spore formation between the R-CDI and NR-CDI isolates ($P$ = 0.677).

***Expression of*** *sigH* ***(p = 0.***007), *spo0A* (p = 0.003), *cwp84* (p = 0.001) and *agrD1* (p = 0.001) was higher in R-CDI than NR-CDI isolates. No difference was shown in *slpA* (p = 0.066) and *luxS* (p = 0.400) expression between groups.

***Conclusion.*** Our data suggest that expression of sporulating pathway genes, *sigH*, *spo0A*, the quorum sensing gene, *agrD1*; and adhesion-associated gene, *cwp84* is higher in R-CDI isolates, in addition to elevated spore formation, which may have an impact on the recurrence of the infection.

***Disclosures.*** **All authors:** No reported disclosures.

**2408. Genotypic Corroboration of Epidemiologically Linked Clusters to Detect Outbreaks of *C. difficile* at a Tertiary Care Hospital**

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***Background.*** The Society for Healthcare Epidemiology of America (SHEA) recommends that surveillance for healthcare facility-onset *C. difficile* infections (HO CDI) be conducted to detect elevated rates or outbreaks of CDI and stratify data by hospital unit when possible to facilitate detection of clusters. At Memorical Sloan Kettering Cancer Center, strain typing of isolates using multi-locus sequence typing (MLST) is performed routinely and in real time to inform control efforts. Genotyping can conclusively establish or debunk transmission events based on routine surveillance. Management of *C. difficile* outbreaks is time and resource intensive.

***Methods.*** A retrospective analysis was conducted to identify all nosocomial *C. difficile* cases between July 2013 and July 2018. Based on Memorial Sloan Kettering's baseline surveillance data, a cluster of *C. difficile* was defined as three or more hospital-acquired cases (as defined by NHSN) on the same inpatient unit within a 7-day period. Data were analyzed to quantify the number of clusters observed and determine genetic relatedness among cases to detect an outbreak.

***Results.*** A total of 1,116 HO CDI cases occurred during the 5-year time period. Annual nosocomial rates of CDI remained stable ($P$ = 0.052). Eighty clusters were identified; 63 clusters had 3 cases within each cluster, 16 were each made up of 4 cases, and 1 cluster consisted of 5 cases. Two clusters had strain typing concordance amongst all 3 cases; strain type 42 and strain type 1. Among all the epidemiologically linked clusters over the 5-year period, only 2.5% were genetically linked suggestive of true outbreaks.

***Conclusion.*** The majority of HO-CDI clusters detected on clinical surveillance are non-clonal. Genotyping should be routinely used to corroborate clusters identified on microbiological surveillance before costly outbreak control interventions are deployed.

**Table 1.** Number and percentage of genetically concordant and discordant C. difficile clusters identified in a tertiary-care cancer center between July 2013 and July 2018.

| Genetic Relatedness | Number of Clusters (n=80) | Percentage |
|---|---|---|
| Number of concordant clusters | 2* | 2.5% |
| Number of discordant clusters | 78 | 97.5% |

*Strain type 42 and 1

***Disclosures.*** **All authors:** No reported disclosures.

**2409. External Validation and Comparison of Clostridioides difficile Severity Scoring Systems**

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***Background.*** Annually in the US alone, *Clostridioides difficile* infection (CDI) afflicts nearly 500,000 patients causing 29,000 deaths. Since early and aggressive interventions could save lives but are not optimally deployed in all patients, numerous studies have published predictive models for adverse outcomes. These models are usually developed at a single institution, and largely are not externally validated. This aim of this study was to validate the predictability for severe CDI with previously published risk scores in a multicenter cohort of patients with CDI.

***Methods.*** We conducted a retrospective study on four separate inpatient cohorts with CDI from three distinct sites: the Universities of Michigan (2010–2012 and 2016), Chicago (2012), and Wisconsin (2012). The primary composite outcome was admission to an intensive care unit, colectomy, and/or death attributed to CDI within 30 days of positive test. Structured query and manual chart review abstracted data from the medical record at each site. Published CDI severity scores were assessed and compared with each other and the IDSA guideline definition of severe CDI. Sensitivity, specificity, area under the receiver operator characteristic curve (AuROC), precision-recall curves, and net reclassification index (NRI) were calculated to compare models.

***Results.*** We included 3,775 patients from the four cohorts (Table 1) and evaluated eight severity scores (Table 2). The IDSA (baseline comparator) model showed poor performance across cohorts(Table 3). Of the binary classification models, including those that were most predictive of the primary composite outcome, Jardin, performed poorly with minimal to no NRI improvement compared with IDSA. The continuous score models, Toro and ATLAS, performed better, but the AuROC varied by site by up to 17% (Table 3). The Gujja model varied the most: from most predictive in the University of Michigan 2010–2012 cohort to having no predictive value in the 2016 cohort (Table 3).

***Conclusion.*** No published CDI severity score showed stable, acceptable predictive ability across multiple cohorts/institutions. To maximize performance and clinical utility, future efforts should focus on a multicenter-derived and validated scoring system, and/or incorporate novel biomarkers.

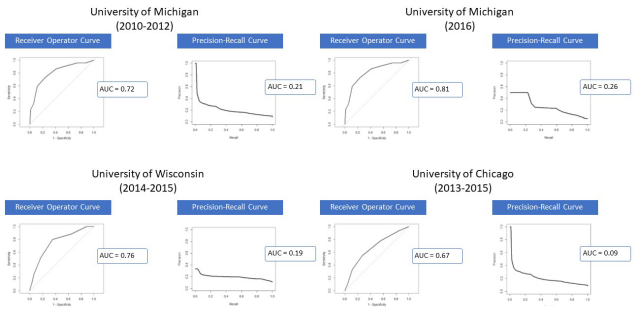

Figure 1: Area Under the Receiver Operator Curves and Precision Recall Curves for ATLAS Model

Table 1. Characteristics of the study population.

| | University of Michigan (2010-2012) | University of Michigan (2016) | University of Wisconsin (2014-2015) | University of Chicago (2013-2015) |
|---|---|---|---|---|
| **Total Patients** | 1144 | 646 | 515 | 1343 |
| **Age (years) [mean± SD]** | 57.3±18.0 | 57.7±18.2 | 59.3±16.1 | 58.7 ±18.5 |
| **Severe C Diff [n (%)]** | 90(7.9%) | 29 (4.5%) | 35 (6.8%) | 64 (5.8%) |
| **Male [n (%)]** | 519 (45.3%) | 330 (47.6%) | 251(48.7%) | 639 (47.8%) |
| **WBC (x10$^3$cells/μL) [mean ± SD]** | 13.4± 12.4 | 12.2±15.5 | 12.7±19.5 | 11.2 ±11.9 |
| **Baseline Creatinine (mg/dL) [mean± SD]** | 1.4± 1.7 | 1.2±1.3 | N/A | 1.6 ±2.2 |
| **Peak Creatinine (mg/dL) [mean± SD]** | 1.6±1.8 | 1.3±1.8 | 2.0±2.4 | 2.1±2.4 |
| **Outcomes** | | | | |
| **30 Day Mortality [n (%)]** | 89 (7.8%) | 41 (6.3%) | 45 (8.7%) | 117(8.7%) |
| **ICU Transfer [n (%)]** | 114 (10.0%) | 11 (1.7%) | 61 (11.8%) | 84(6.3%) |
| **Colectomy [n (%)]** | 6 (0.5%) | 3 (0.5%) | 6 (1.2%) | 21(1.6%) |
| **Attributable Outcomes** | | | | |
| **30 Day Mortality [n (%)]** | 49 (4.3%) | 23 (3.6%) | 17 (3.3%) | 39(2.9%) |
| **ICU Transfer [n (%)]** | 49 (4.3%) | 5 (0.8%) | 26 (5.0%) | 18(1.3%) |
| **Colectomy [n (%)]** | 4 (0.3%) | 1 (0.2%) | 5(1%) | 16(1.2%) |

Table 2. Published severe CDI scoring systems assessed in this study.

| Name | Description |
|---|---|
| **IDSA** | Binary: WBC >15000 cells/μL and/or 1.5-fold increase of serum creatinine from baseline |
| **Zar** | Binary: 2 or more points: Age >60 years, temperature >38.3°C, albumin level <2.5mg/dL, or peripheral WBC >15,000 cells/μL are worth 1 point. Admission to the ICU or pseudomembranes on endoscopy are each worth 2 points. |
| **Gujja** | Binary: An elevation of the WBC > 30,000 cells/μL and 1.5-fold increase of serum creatinine from baseline |
| **Belmares** | Binary: 1 point for each of the following: Temperature ≥ 38°C, Ileus, SBP<100mmHg. Point scale for WBC: <15,000cells/μL (0), ≥15,000cells/μL - <30,000cells/μL (1)≥30,000cells/μL. Point scale for CT findings: No findings (0), 1 Finding (1),≥2 Findings (20 |
| **Na** | Binary:2 or more: Age>65years, Peak serum creatinine >2mg/dL, or WBC>20,000 cells/μL |
| **Jardin** | Binary: Any two of the following: intensive care unit admission, Age >60 years, Temperature >38.3°C, Albumin <2.5 mg/dL, WBC >15,000 cells/μL |
| **Toro** | Continuous: 1 point for each of the following: Altered mental status, abdominal pain or distention, WBC >20,000 cells/μL or <1500 cells/μL, Albumin <2.5 mg/dL, ascites or colitis on imaging, MAP<65mmHg, Temperature ≥ 101°F, Tachycardia >110bpm, Admission or ICU transfer |
| **ATLAS** | Continuous: Point scale: Age: < 60 years (0), 60 -79 years (1), >=80 years (2),Treatment with systemic antibiotics during CDI therapy (>1 day) No (0), Yes (1),Temperature: ≤37.5°C (0), 37.6°C - 38.5°C (1), ≥ 38.6°C (2), WBC: < 16,000cells/μL (0), 16,000 cells/μL-25,000 cells/μL (1), ≥ 25,000 cells/μL (2), Serum Albumin: > 35 g/L (0), 26 - 35 g/L (1), ≤25 g/L (2), Serum creatinine: ≤ 120 μmol/L (0), 121 - 179 μmol/L (1), ≥180 μmol/L (2) |

Table 3. Performance measures of the CDI severity scoring systems across cohorts vs. the primary composite outcome (attributable 30-day ICU admission, colectomy, and/or death)

| | University of Michigan (2010-2012) | | | | University of Michigan (2016) | | | | University of Wisconsin (2014-2015) | | | | University of Chicago (2013-2015) | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Sen | Spec | AUC | NRI‡ | Sen | Spec | AUC | NRI‡ | Sen | Spec | AUC | NRI‡ | Sen | Spec | AUC | NRI‡ |
| IDSA | 0.59 | 0.70 | 0.63 | * | 0.72 | 0.67 | 0.70 | * | 0.80 | 0.53 | 0.67 | * | 0.53 | 0.62 | 0.58 | * |
| Zar | 0.52 | 0.74 | 0.62 | -0.01 | 0.68 | 0.73 | 0.62 | 0.03 | 0.77 | 0.72 | 0.75 | 0.16 | 0.42 | 0.81 | 0.62 | 0.07 |
| Gujja | 0.12 | 0.98 | 0.37 | -0.01 | 0.00 | 1.00 | - | -0.38 | 0.14 | 0.99 | 0.70 | -0.20 | 0.03 | 0.99 | 0.50 | -0.15 |
| Belmares† | 0.51 | 0.74 | 0.62 | -0.03 | 0.5 | 0.88 | 0.69 | 0.02 | 0.34 | 0.93 | 0.64 | -0.06 | 0.11 | 0.96 | 0.53 | -0.10 |
| Na | 0.41 | 0.87 | 0.64 | 0.02 | 0.41 | 0.91 | 0.74 | 0.11 | 0.34 | 0.86 | 0.60 | -0.13 | 0.34 | 0.81 | 0.57 | -0.02 |
| Jardin | 0.52 | 0.71 | 0.67 | -0.03 | 0.68 | 0.73 | 0.70 | 0.03 | 0.77 | 0.72 | 0.74 | -0.27 | 0.42 | 0.82 | 0.62 | 0.07 |
| Toro | 0.23 | 0.94 | 0.66 | 0.01 | 0.21 | 0.97 | 0.83 | 0.07 | 0.21 | 0.97 | 0.81 | 0.20 | 0.07 | 0.98 | 0.69 | 0.13 |
| ATLAS | 0.16 | 0.95 | 0.72 | 0.07 | 0.15 | 0.98 | 0.81 | 0.17 | 0.14 | 0.98 | 0.76 | -0.03 | 0.09 | 0.97 | 0.67 | 0.11 |

* Comparison model
ǂ NRI range from -2 to +2
‡ Score modified for Universities of Wisconsin and Chicago

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## 2410. Molecular Characteristics of Environmental Clostridioides difficile From a Large Texas Hospital

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***Background.*** *Clostridioides difficile* is an anaerobic spore-forming, toxin-producing Gram-positive bacillus listed by the CDC as an "urgent threat" pathogen. Epidemiologic studies using whole-genome sequencing (WGS) have found that genetically distinct lineages infections occur in hospitalized patients, in addition to the fact that *C. difficile* spores persist on hospital surfaces after disinfection. The purposes of this study were to isolate and characterize *C. difficile* from the environment of a large Texas hospital.

***Methods.*** We collected 330 swab samples of hospital environmental surfaces using sterile cotton gauze. The samples were then anaerobically enriched in brain heart infusion broth for 48–72 hours and plated onto cycloserine–cefoxitin fructose agar (CCFA). Suspected colonies were then genetically characterized using PCR (for *tcdA, tcdB, cdtA, cdtB* and *tpi* genes) and genotyped using fluorescent PCR ribotyping techniques.

***Results.*** A total of 90/330 (27.3%) environmental samples were culture positive for *C. difficile*, of which 75/90 (82.1%) tested were toxigenic *C. difficile* by the presence of *tcdA, tcdB, cdtA* or *cdtB.* A total of 16 distinct ribotypes were identified from 41 *C. difficile* isolates tested using a fluorescent-ribotyping method. The predominant ribotypes isolated were F078–126 (8/41), F002 (5/41), F106 (4/41), F255 (4/41), and F014-020 (3/41).

***Conclusion.*** We found a diversity of *C. difficile* strain types in various hospital high-touch surface environment in addition to ribotype F027 and F078, suggesting the hospital environment a reservoir and significant source *C. difficile* infections.

***Disclosures.*** **All authors:** No reported disclosures.

## 2411. One Dose Vancomycin Prophylaxis for In-Hospital Clostridioides difficile - Associated Disease

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***Background.*** *Clostridioides difficile* - associated disease (CDAD) is the most common cause of healthcare-associated diarrhea with increasing prevalence and mortality rates. Recent reports suggest that prophylactic administration of vancomycin or fidaxomicin might reduce in-hospital CDAD incidence. The aims of this study were to