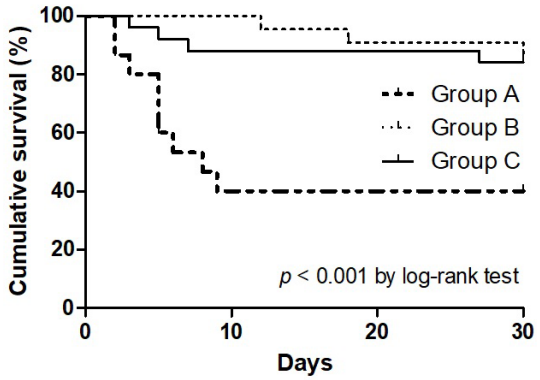
bacteremia was identified in 22 patients (35.5%) and was significantly more common in group A (60.0% [9/15]) than groups B (43.5% [10/23]) or C (12.5% [3/24]) (P = 0.01). Thirty-day mortality rates were also significantly higher in group A than groups B or C (60.0% [9/15] vs. 13.0% [3/23] and 16.7% [4/24], 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.



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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.

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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.

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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

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

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