2427. A Laboratory Simulation and Field Study of Simplified Qualitative and Quantitative Environmental Cultures for Clostridioides difficile

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Background. Reliable, simple methods to assess environmental contamination with *Clostridioides difficile* are needed for studies of terminal disinfection effectiveness and transmission of *C. difficile* from fomites. We compared two novel sampling methods for assessment of *C. difficile* contamination: (1) isopropanol wipe sampling with broth enrichment (IW), where alcohol wipes are used to sample surfaces followed by immersion in CDBB-TC broth and (2) ethanol-shock hand imprint sampling (HI), where surfaces are sampled by gloved hands moistened with ethanol hand sanitizer followed by imprinting hands on selective agar (CDBA-TC). Both methods allow for sampling of complex surfaces common in hospital environments.

Methods. We performed a laboratory simulation study using six 10-fold dilutions (10^1–10^6) of *C. difficile* spores from two strains sampled from fiberglass surfaces by IW and HI. We then performed a field study of 10 sites in 11 hospital rooms of patients with *C. difficile* infection (CDI) diagnosed < 48 hours prior to sampling. Results for the HI and IW method were quantitative and qualitative, respectively. We compared room contamination prevalence (total CFU per room by HI and sites positive/total sites per room) to the cycle crossing threshold (C_T) from the diagnostic *C. difficile* PCR test (Cepheid) from the room occupant.

Results. The IW laboratory limit of detection was 10^1 spores compared with 10^4 spores for HI. In the field study, IW and HI detected *C. difficile* contamination in 9/11 (82%) rooms at 22/110 (20%) sites and 5/11 (45%) rooms at 22/110 (20%) sites, respectively (Table 1). Six rooms with no detection by the HI method had a lower median number of sites positive per room compared with the 5 rooms with ≥1 cfu (1 vs 6, $P < 0.05$) (Table 1). The most commonly contaminated sites were linens (53%), call bells (43%), toilets (40%), blood pressure cuffs (40%), over-bed tables (38%), and bedrails (30%) (Table 2). Higher *tcdB* C_T was associated with a lower total room contamination prevalence (Figures 1 and 2).

Conclusion. Our data suggest that the IW method is more sensitive for detection of *C. difficile* in the hospital environment, but the HI method offers quantitation. The prevalence of hospital room contamination for CDI patients appears to correspond with their toxin burden as estimated by PCR.

Table 1. Field study of two methods for *C. difficile* recovery from 11 rooms occupied by recently-diagnosed patients with *C. difficile* infection. For each room, 10 sites per room were cultured.

Room	Unit type	Hours from diagnosis to sampling	*tcdB* - Ct	sites positive by HI	sites positive by IW	Total positive sites	Total CFU	Sites positive by HI	Sites positive by IW
1	ICU	26	29.6	0	1	1	0	-	P
2	ICU	23	26.6	1	1	2	1	A	S
3	ICU	24	20.6	5	4	6	70	CRTSA	CPST
4	ICU	25	32.8	0	1	1	0	-	X
5	floor	5	23.3	7	7	9	38	CSTRPOX	CSPRBDX
6	ICU	31	34.2	0	0	0	0	-	-
7	floor	13	23.5	7	4	7	177	RBPSTOC	RBPS
8	floor	16	29.4	2	0	2	4	OV	-
9	floor	29	36.3	0	1	1	0	-	V
10	floor	28	35.2	0	1	1	0	-	T
11	floor	23	29.0	0	2	2	0	-	PS

ICU= intensive care unit, *tcdB*-C_T= cycle crossing threshold for tcdB target on *C. difficile* PCR from the stool sample from the recently-diagnosed room occupant, HI=hand imprint method, IW= isopropanol wipe method, CFU=colony forming units, P=pillowcases, S=sheets, C= call bell, T=toilet, B=blood pressure cuff, X=sequential compression device, R=bed rail, A=patient abdomen, O=over-bed table, D= portable electronic vital signs monitor, V=visitor chairs

Table 2. Field study of two methods for *C. difficile* recovery from 112 sites in 11 rooms occupied by recently-diagnosed patients with *C. difficile* infection stratified by site sampled in descending frequency of sampling.

Item/Site sampled	Positive/Total (%)	Positive by IW	Positive by HI	HI CFU range**
Sink*	0/12 (0%)	0	0	-
Toilet	4/11 (36%)	2	3	9-138
Bed rail	3/10 (30%)	2	3	3-14
Over-bed table	3/10 (30%)	0	3	1-6
Pillowcases	5/10 (50%)	5	2	2-5
Call bell	3/9 (33%)	2	3	1
Sheets	5/9 (56%)	5	3	1-4
Computer keyboard	0/8 (0%)	0	0	-
Doorknobs	0/6 (0%)	0	0	-
Visitor chairs	2/6 (33%)	1	1	2
Blood pressure cuff	2/5 (40%)	2	1	9
Sequential compression device	2/4 (50%)	2	1	20
Monitor lead wires	0/3 (0%)	0	0	-
Patient abdomen	2/3 (66%)	0	2	1-21
Fecal management system	0/1 (0%)	0	0	-
Portable electronic vitals unit	1/1 (100%)	1	0	-
Room telephone	0/1(0%)	0	0	-
Portable thermometer probe	0/1 (0%)	0	0	-
Ventilator	0/1 (0%)	0	0	-
Totals	32/111 (29%)	22	22	

IW = isopropanol wipe broth enrichment technique, HI= hand imprint ethanol shock technique, *1 additional portable hallway sink was sampled outside the 11th room sampled
**where only 1 site was positive the CFU at the site is listed

Figure 1. Total hand imprint CFU per room vs PCR crossing threshold

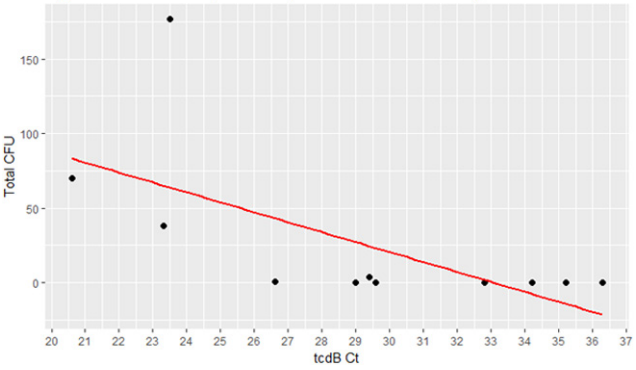
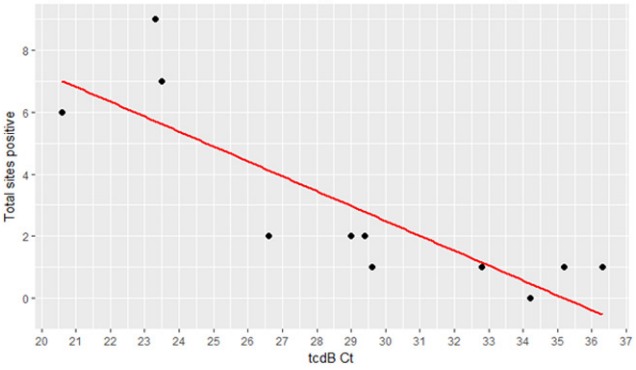


Figure 2. Total number of sites positive per room vs PCR crossing threshold



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2428. Whole-genome Sequencing to Determine *Clostridium difficile* Transmission

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Background. *Clostridium difficile* is a major problem in healthcare institutions due to its substantial attributable morbidity, mortality and costs. Although traditionally recognized as a nosocomial infection, there is increasing evidence that hospital-based transmission may not be as common as previously thought. Whole-genome sequencing (WGS) has superior discriminatory ability than other previously used techniques for *C. difficile* typing. This study aimed to investigate whether WGS could help to elucidate *C. difficile* transmission patterns at The Royal Melbourne Hospital (RMH).

Methods. All *C. difficile* isolates (N = 138) identified in patients admitted to RMH from November 1, 2015 to October 31, 2016 had molecular typing performed by WGS, multilocus sequence typing (MLST) and PCR ribotyping. Clinical epidemiological data were collected for each episode so that patient locations could be examined together with molecular typing information to determine putative transmissions in the hospital.

Results. After combining molecular and clinical epidemiology, a picture of diverse *C. difficile* emerged. Only 7 (6%) of isolates appeared to have been transmitted from other hospital patients, according to combined WGS and patient location data. However, both PCR ribotyping (33%) and MLST (44%) had significantly higher proportions of putative transmissions in this cohort.

Conclusion. This finding has significant implications for the Infection Prevention team as efforts toward prevention of *C. difficile* infection may need to be redirected away from the current focus on prevention of nosocomial transmission. Future studies are needed to broaden understanding of *C. difficile* transmission dynamics so that other sources can be identified and targeted for intervention.

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2429. Whole-genome Sequencing of Healthcare-Onset *C. difficile* Infection (HO-CDI) Cases Shows Widespread Presence of Antimicrobial Resistance Genes

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Background. *Clostridioides difficile* infection (CDI) is the most common pathogen to cause healthcare-associated infections. Unlike some other bacterial pathogens antimicrobial treatment is seldom based on culture with susceptibility testing with infrequent surveillance for antimicrobial resistance. We have evaluated healthcare-onset CDI (HO-CDI) for both transmission and antimicrobial resistance emergence.

Methods. We identified cases of HO-CDI diagnosed by PCR within a 3 month period (October 1/2018–December 31/2018) at University of Virginia Health System with overlapping stays in the same inpatient units with other HO-CDI. Chart review of all cases was performed. *C. difficile* was cultured from stool, then DNA was extracted and underwent sequencing on Illumina Miseq platform. Antimicrobial resistance genes were screened using NCBI's AMRFinder tool from the *de-novo* assembled contigs using SPAdes. All the *C. difficile* isolates underwent antibiotic susceptibility testing.

Results. Eleven patients were identified with overlapping stays from 5 units. Mean age was 64 years and 63.6% were female. 36.3% of cases were severe CDI with one case of fulminant CDI. There was one recurrence within 90 days (9.1%). Patients were treated with PO vancomycin (72.7%) or IV metronidazole and PO vancomycin (27.3%), none were treated with metronidazole alone. None of the hospital strains were genetically related. There were two isolates with binary toxin gene (*cdtB*), one ribotype 027 (CD196) and one ribotype 078 (M120). Ninety-one percent of isolates had *vanG*-like gene cluster and *vanZ1* originally identified in *Enterococcus* sp. *erm*(B), *tet*(M), and *cfr*(C) genes were also detected in several strains. All isolates were susceptible to vancomycin, metronidazole, and tigecycline. There was one strain with moxifloxacin resistance associated with the presence of *erm*(B) gene. None of the isolates were susceptible to clindamycin.

Conclusion. There were no widely circulating clones or direct transmissions found in this small sample of HO-CDI cases at our hospital. Like others have we demonstrate carriage of many *vanG/Z* genes without conferring phenotypic resistance to vancomycin. The origin and function of Van genes in *C. difficile* could be an area of future research.

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2430. Comorbidity and Severity of Illness Risk Adjustment for Hospital-Onset Clostridioides difficile Infection

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Background. Hospital-onset *C. difficile* infection (HO-CDI) rates are publicly reported. However, patient-level risk factors are not included in the current risk adjustment methodology, and the knowledge as to which risk factors to include is incomplete. This study aimed to determine whether electronically-available comorbidities and laboratory indicators of severity of illness are risk factors for HO-CDI.

Methods. We performed a retrospective cohort study of all adult patients admitted to three hospitals (one academic, two community) in Baltimore, Maryland between January 1, 2016 and January 1, 2018. Information extracted from electronic medical records included demographics, ICD-10 codes, laboratory results within 24 hours of admission (i.e., hematocrit, hemoglobin, platelet count, leukocytes, BUN, CO2, creatinine, glucose, sodium, and potassium), medication administration (i.e., antibiotic and antacid use), and *C. difficile* test result. Comorbid conditions were assessed by the Elixhauser Comorbidity Index components. HO-CDI was defined by positive laboratory test > 3 days after admission. Potential risk factors for HO-CDI were assessed using bivariate log binomial regression. Multivariable log binomial regression was conducted using significant ($P < 0.1$) covariates.

Results. At hospital 1 (academic), 314 of the 48,057 (0.65%) eligible patient admissions had HO- CDI; 41 of the 8,791 (0.47%) and 75 of the 29,211 (0.26%) of patient admissions at community hospitals 2 and 3, respectively, had HO-CDI. In multivariable analysis, Elixhauser Score was a significant risk factor for HO-CDI at all hospitals when controlling for antibiotic and antacid use; for every one-point increase in Elixhauser Score, there was an increased risk of HO-CDI of 1.27 (95% CI: 1.21, 1.32) at hospital 1, 1.38 (95% CI: 1.24, 1.54) at hospital 2, and 1.28 (95% CI: 1.10, 1.31) at hospital 3. Table 1 shows significant risk factors for HO-CDI for each hospital. When individual comorbidities were assessed in the regression analysis, fluid and electrolyte disorders were a significant risk factor for HO-CDI for all hospitals.

Conclusion. Laboratory values upon admission and electronically available patient comorbidities are important risk factors for HO-CDI and should be considered for future risk adjustment.

Table 1. Multivariable log binomial regression models for risk adjustment of HO-CDI for individual hospitals stepwise regression **(Model 1)**

Hospital 1				Hospital 2				Hospital 3			
Characteristics	Risk Ratio	95% Confidence Interval	p value	Characteristics	Risk Ratio	95% Confidence Interval	p value	Characteristics	Risk Ratio	95% Confidence Interval	p value
Antibiotic Use	3.15	(2.20, 4.50)	< 0.001	Antibiotic Use	4.37	(1.76, 10.86)	0.002	Gender (female)	0.64	(0.40, 1.04)	0.07
H2 Blocker Use	1.52	(1.20, 1.91)	< 0.001	Elixhauser Score	1.38	(1.24, 1.54)	< 0.001	Antibiotic use	4.86	(2.27, 10.39)	<.001
PPI Use	1.55	(1.21, 1.97)	< 0.001	Abnormal Leukocytes	2.78	(1.47, 5.24)	0.002	H2 receptor blocker use	2.56	(1.56,4.20)	< 0.001
Elixhauser Score	1.27	(1.21, 1.32)	< 0.001					PPI use	1.61	(1.00, 2.61)	0.051
Abnormal Leukocytes	1.37	(1.09, 1.73)	0.008					Total Elixhauser	1.28	(1.17, 1.39)	<.001
								Abnormal Creatinine	2.08	(1.24, 3.47)	0.005

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2431. When More is Less – Recognizing More Community-onset *Clostridium difficile* Infections Helps to Dramatically Lower C diff Standardized Infection Ratio (SIR)

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Background. It is essential to recognize the true burden of community-onset (CO) *Clostridium difficile* infection (CDI) in hospital, not only because it prevents late recognition of CO CDI as being classified as a hospital-onset (HO) event, but also to assure appropriate contact precautions and therapeutic measures are deployed in a timely fashion. We recognized that our timely diagnosis of CO-CDI was suboptimal and sought to improve early recognition of CO-CDI.

Methods. We developed an automated daily report for all patients during their first 3 days of hospitalization who had loose stools documented in the nursing flow sheets and no stool sample sent to the lab. This report was automatically pushed out to the unit nurse managers, as well as reviewed by the infection preventionists (IP). Nurse managers alerted staff to acquire a stool sample to send to the lab. If stool testing still was not sent at the time of IP review of these symptomatic cases, then the IP called the nurse caring for the patient to encourage that a stool sample be sent ASAP and before the third hospital day was completed.

Results. We increased early appropriate stool testing for patients with documented loose stools during the first 3 days of hospitalization. Improved early diagnosis and better lab stewardship was associated with a marked increase in CO-CDI (15.6/month in 2015 vs 58.7/month in the last year), as well as a decrease in HO-CDI (22.8/month in 2015 vs 7.4/month last year) (Figure 1). In turn, we saw a remarkable drop in our CDI SIR (2 year pre-intervention SIR = 1.49 vs post-intervention SIR for the last 1.5 years = 0.41) (Figure 2).

Conclusion. After several years of our CDI SIR remaining stubbornly around 1.5, we developed a system of enhanced recognition of patients who had loose stools early in their hospitalization. This aided in better recognition of CDI present on admission, substantially increasing our detection of CO-CDI. We also noted decreases in HO-CDI, presumably secondary to no longer diagnosing patients later in their hospitalization as HO-CDI cases who actually had been admitted with CO-CDI. Better early recognition and isolation of patients with CDI also helped to decrease inadvertent *C. difficile* transmission in hospital, contributing to decreases in HO-CDI. In turn, we noted a remarkable decrease in our CDI SIR.

Figure 1

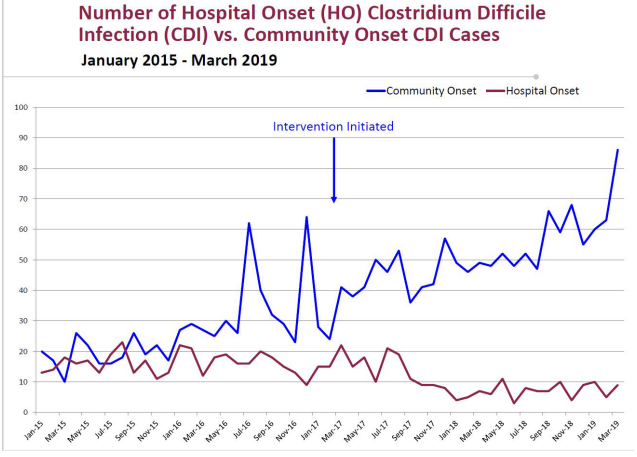
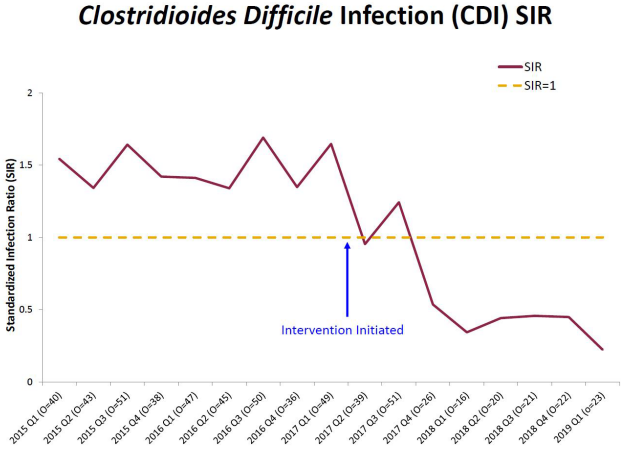


Figure 2



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