**Supplementary Material**

Transmission of *Clostridioides difficile* infection (CDI) from patients < 3 years of age in a pediatric oncology setting

**Authors:**

Elizabeth Robilotti, MD MPH1, 2

Weihua Huang, PhD3

N. Esther Babady, PhD1, 4

Donald Chen, MD5, 6

Mini Kamboj, MD1, 2

(1) Infectious Diseases, Department of Medicine, Memorial Sloan Kettering Cancer Center (MSKCC), New York, NY, USA.

(2) Infection Control, Department of Medicine, Memorial Sloan Kettering Cancer Center (MSKCC), New York, NY, USA.

(3) Department of Pathology, New York Medical College, Valhalla, NY, USA.

(4) Clinical Microbiology Service, Department of Laboratory Medicine, Memorial Sloan Kettering Cancer Center (MSKCC), New York, NY, USA.

(5) Infection Prevention and Control Department, Westchester Medical Center, Valhalla, NY, USA

(6) Infectious Diseases, Department of Medicine, New York Medical College, Valhalla, NY, USA

**Corresponding Author:**

Elizabeth Robilotti MD MPH

1275 York Avenue Box 9 New York, NY 10065

ph: 212.639.6156 fax: 212.717.3021

**Supplementary Figure 1: The most frequent *C. difficile* MLST sequence types in Pediatric and Adult CDI cases at study institution (2014-2017)**

**Supplementary Table 1: Donor Demographics/Total days admitted**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Donor Cluster** | **Age (yrs)** | **ST** | **Underlying diagnosis** | **Chemo in 30*d*** | **Abx in 30*d*** | **Diarrheal stools documented** | **LOS of index CDI hospitalization (days)****(median = 7*d*; average = 37*d*)** |
| **1** | **2** | **2** | **Retinoblastoma** | **Yes** | **Yes** | **No** |

|  |
| --- |
| **7** |

 |
| **2** | **1** | **2** | **Neuroblastoma** | **Yes** | **Yes** | **Yes** | **5** |
| **3** | **2** | **42** | **ALL** | **Yes** | **Yes** | **No**  | **84** |
| **4** | **1** | **110** | **Neuroblastoma** | **Yes** | **Yes** | **No**  | **5** |
| **5** | **2** | **3** | **Primary immunodeficiency (DOCK 8)** | **No** | **Yes** | **Yes** | **127** |
| **6** | **1** | **8** | **Retinoblastoma** | **No** | **Yes** | **No** | **3** |
| **7** | **2** | **37** | **Primary immunodeficiency/DLBCL** | **No** | **Yes** | **Yes** | **28** |

ALL = acute lymphoblastic leukemia; Chemo = chemotherapy; *d* = days; DLBCL = diffuse large B-cell lymphoma; DOCK8 = Dedicator of Cytokinesis 8; LOS = length of stay; ST = sequence type

**Supplementary Table 2:** Stool Consistency and symptoms for included patients as extracted from electronic health record.

|  |  |  |  |
| --- | --- | --- | --- |
| Stool Constancy | Liquid n=8 | Semiformed n=28 | Formed n= 3 |
| Diarrhea | Yes = 24 | No=15 |  |
| Laxative use within 48hrs hours | Yes= 6 | No=33 |  |

**Supplementary Methods:**

**MLST banking and CD culture**: Stools were thawed, and ethanol shocked with a 1:4 dilution in 100% ethanol for at least 1 hour. After incubation and centrifugation, samples were inoculated on selective media for the detection of *C. difficile* and incubated anaerobically. Growth confirmation of a single colony by PRO disk was performed with the remaining portion of the colony subbed to a blood agar plate for isolation. After a 48-hour anaerobic incubation, samples were submitted for whole genome sequencing.1

**WGS**: Genomic DNA was extracted from each isolate using the QIAamp Genomic DNA kit (Qiagen). WGS was performed using the Nextera XT Sample Prep Kit and paired-end sequencing (150 bp ×2) on the NextSeq 550 platform (Illumina). Multi-locus sequence typing (MLST) was identified by MLST algorithm (https://github.com/tseemann) after *de novo* sequence assembly using SPAdes (v3.9.0). SNPs were identified using Snippy (v3.2, https://github.com/tseemann) with alignment and mapping to R0104 (ST1) complete genome (NCBI accession number: CP025044) as reference. Phylogenetic tree and pair-wise distance matrix were generated from CoreSNP analysis of Snippy.

**1.** Sim JH, Anikst V, Lohith A, Pourmand N, Banaei N. Optimized Protocol for Simple Extraction of High-Quality Genomic DNA from Clostridium difficile for Whole-Genome Sequencing. *J Clin Microbiol* 2015;53:2329-2331.