Molecular and Clinical Epidemiology of *Clostridium difficile* Infection in Three Diverse Medical Centers in New York

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BACKGROUND

*Clostridium difficile* (CD) isolates from patients with hospital acquired CD infection (CDI) can be genetically very diverse. The purpose of this study is to determine the epidemiology and genetic diversity of all CD isolates from 3 medical centers in the greater New York area.

METHODS

During 6 consecutive months, Westchester Medical Center (WMC) a tertiary care hospital, Orange Regional Medical Center (ORMC), a large community hospital that refers patients to WMC, and Memorial Sloan Kettering Cancer Center (MSKCC) a specialty cancer hospital, collected data for all hospitalized CDI patients, identified by a stool PCR for toxigenic B gene (*Xpert C. difficile*, Cepheid Inc.). Multilocus sequence typing (MLST) was performed; pubmlst was used for strain type identification. Miles between sites: WMC-ORMC: 50, WMC-MSKCC: 27, ORMC-MSKCC: 76.

RESULTS

515 patients had 573 CDI episodes. 371 (65%) CD isolates were typed. Distinct MLST sequence types (ST) were: 34 ST for 124 WMC isolates, 27 ST for 55 ORMC isolates, and 40 ST for 192 MSKCC isolates. The predominant ST were similar at WMC and ORMC; MSKCC differed with fewer ST 1 (9% vs 26% p<0.001).

CONCLUSIONS

- *C. difficile* ST were diverse at each hospital.
- ST distribution was similar for WMC and ORMC, 2 hospitals that transfer patients between them.
- MSKCC ST differed from WMC / ORMC; there were significantly fewer NAP-1 ST, and CDI complications were less frequent.
- These results will be used to further understand CDI transmission and the correlation between ST and epidemiologic definitions, and CDI outcome.

REFERENCES


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