An Ecological Snapshot of *Clostridioides difficile*: Characterizing Genetic Diversity of *C. difficile* within Banner - University Medical Center Phoenix

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**Introduction**

*Clostridioides difficile* is the most common etiologic agent of antibiotic-associated diarrhea and is responsible for over 400,000 cases of nosocomial infections in the USA annually. *C. difficile* infection (CDI) also accounts for an estimated financial burden greater than $5 billion nationally each year.

Appreciating local *C. difficile* genetic diversity is an important step in understanding the role that CDI plays in healthcare delivery on the systems level, and in designing and implementing effective infection control practices on the hospital level. There has not been a comprehensive investigation on *C. difficile* genetic diversity within an Arizona hospital since 1991 or within Banner-University Medical Center Phoenix (BUMCP) since its opening.

**Materials and Methods**

A laboratory-based surveillance study design was selected to characterize *C. difficile* ecology. All unique clinical stool specimens from the BUMCP clinical microbiology lab consistent with the diagnosis of CDI per standard screening protocol were eligible for inclusion, deidentified and banked. Collection took place from March 2017–October 2018.

All clinical specimens underwent selection with TCCFA and anaerobic culturing. Colonies were isolated and identified. Total genomic DNA was isolated and purified for phylogenetic typing (ribotyping). DNA was prepared for fully-automated capillary electrophoresis-based PCR to analyze 16S-23S intergenic spacer regions: resulting electropherograms were cross-referenced with an in-house reference tool and an international master database.

**Results**

267 clinical stool samples were determined to be eligible for inclusion in this study. *C. difficile* could not be isolated from 19 samples. Another 19 samples failed the capillary PCR process. 4 samples could not be reliably classified during analysis. 225 samples (84.3% overall) were successfully genetically typed and include for analysis (Figure 1).

83 ribotypes were identified and sorted into bins based on incidence of disease per specific ribotype (Figure 2). CDI burden is not evenly distributed among strains: 43 ribotypes (51.8%) accounted for 19.1% of CDI, while 17 ribotypes (20.5%) accounted for 60.4% of disease.

A visual model of ribotype distribution was constructed for demonstrative purposes (Figure 3).

**Conclusion**

There is an uneven distribution of disease burden relative to ribotype. This finding is consistent with similar investigations in other geographies. The highest burdens of disease are attributable to ribotypes 027, 106 and 176—all well-documented hypervirulent outbreak associated strains.

**Summary**

- 83 distinct genetic types of *C. difficile* were identified in BUMCP over the study period.
- 43 strains (51.8%) were each represented by only one case (15.1% of typable cases) and another 23 strains (27.7%) were represented by two cases (20.4% of typable cases).
- 3 historically outbreak-associated strains—RT027, RT106 and RT176—were implicated in 30.2% of all typable cases of CDI.

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