CLOSTRIDIUM DIFFICILE INFECTION SURVEILLANCE IN A HEALTHCARE SETTING: STRAIN DIVERSITY AND IDENTIFICATION OF NOVEL MOLECULAR TYPES (RIBOTYPES)

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Clostridium difficile infection (CDI) is typically precipitated by antibiotic-mediated clearance of gut microbiota. While community-associated CDIs have been reported, few studies have parsed between hospital-acquired and hospital-precipitated CDI. Currently, there are no clear molecular ‘signatures’ that distinguish hospital-acquired from community-associated strains. **Objective:** To monitor Clostridium difficile (CD) frequency, and compare isolates from patients. **Methods:** CD prevalence was monitored in a 487-bed hospital beginning in 2015. Patient CD specimens were cultured from diarrheic stool, and further characterized via ribotype analysis. Unique isolates were also assessed for toxin production. Comparative proteomics was performed on a subset of patient isolates using fully-quantitative mass spectrometry. **Results:** A total of 188 specimens of unique CD isolates, were obtained from patients, and belonged to a wide range of ribotypes (>40). This study revealed an increase in the “outbreak-associated” RT027 ribotype compared to our previous surveillances. In addition, we found 19 CDI cases caused by isolates belonging to a previously uncharacterized RT500, which represent 11% of our collection. CD isolates – even those of identical ribotype - expressed a wide range of toxin levels, suggesting that they were not clonal. Proteomic analyses suggested broad differences even within strains belonging to the same ribotype, and a possible community-associated ‘signature’ was not readily identifiable. **Conclusions:** The distribution of CD ribotypes in patient isolates suggests that patients may acquire CD in the community, but that CDI itself is likely hospital-precipitated. Ongoing studies are focused on genome sequencing and further in-vitro and in-vivo characterization of select isolates.