

**1638. *Clostridium difficile* Strains Colonizing Long-Term Care Facility (LTCF) Residents are Similar to Strains Causing Infection in both LTCF and Hospital Patients Suggesting a Shared Continuum of Transmission**

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**Background.** *Clostridium difficile* infection (CDI) is endemic in long-term care facilities (LTCFs). Asymptomatic residents colonized with toxigenic strains are a potential reservoir for transmission both in LTCFs and affiliated hospitals. We used restriction endonuclease analysis (REA) to type and compare *C. difficile* isolates colonizing LTCF residents and infecting both LTCF and hospital patients.

**Methods.** Asymptomatic residents were enrolled from the LTCF associated with either Cleveland VA Hospital (n = 200) or Hines VA Hospital (n = 200) from February 2012 through August 2012. Cultures for asymptomatic colonization with *C. difficile* were obtained from the perirectal area on admission and at 2-week intervals during LTCF stay. All colonizing isolates underwent REA typing. In addition, available isolates causing CDI with onset in either the LTCF or affiliated VA hospital were typed for comparison.

**Results.** Four percent of enrolled Hines LTCF residents were colonized with a toxigenic *C. difficile* strain during the study, most commonly BI 6/8/17, L group, or BM group (Table). For hospital- and LTCF-onset Hines CDI isolates, BI 6/8/17 was also the most common group isolated accounting for 33% of cases. Group AL was found only at Hines. In comparison, 19% of Cleveland LTCF residents were colonized; the

predominant groups were BI 6/8/17, BI non-6/8/17, and DQ, a binary toxin positive group not found at Hines (Table). In Cleveland, the three most common REA groups isolated from both hospital- and LTCF-onset CDI were also the same as those found in colonized LTCF patients (table).

| REA Group     | Hines                |                     | Cleveland            |                     |
|---------------|----------------------|---------------------|----------------------|---------------------|
|               | Colonizing, N=10 No. | Infecting, N=30 No. | Colonizing, N=41 No. | Infecting, N=42 No. |
| BI 6/8/17     | 2                    | 10                  | 8                    | 9                   |
| BI non-6/8/17 | 1                    | 3                   | 8                    | 8                   |
| BM            | 2                    | 1                   | 2                    | 0                   |
| L             | 2                    | 0                   | 1                    | 0                   |
| DH            | 1                    | 1                   | 3                    | 1                   |
| AL            | 1                    | 4                   | 0                    | 0                   |
| DQ            | 0                    | 0                   | 7                    | 9                   |
| G             | 0                    | 3                   | 1                    | 2                   |
| Y             | 0                    | 1                   | 3                    | 2                   |
| Other groups  | 0                    | 5                   | 5                    | 4                   |
| Non-specific  | 1                    | 2                   | 3                    | 7                   |

**Conclusion.** The BI group and specifically BI 6/8/17 remains endemic at both sites. Although the prevalence of toxigenic *C. difficile* colonization varied significantly between the two LTCFs, in both sites the predominant colonizing strain(s) were the most common infecting strains in both the LTCF and hospital. This suggests a shared continuum of transmission between asymptomatic, colonized LTCF residents and both affiliated hospital and LTCF CDI cases.

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