Background. The incidence of Clostridioides difficile infection (CDI) has been rising among children, both in the community and hospital setting. The genomic variability and molecular epidemiology of CDI in children, especially with cancer are poorly understood. We aim to evaluate the molecular epidemiology and relatedness of C. difficile isolates among inpatient and outpatient pediatric oncology and stem cell transplant patients (POTP) using whole-genome sequencing (WGS). Results. Among 141 CDI episodes in 89 patients; 103 stool samples were cultured, and 101 (98%) isolates were sequenced identifying 23 different strain types in 81 (80%) isolates. 34 (38%) patients had multiple episodes of CDI. 16 clusters of related isolates were identified (figure), 10 (62%) of which involved only multiple specimens from the same patient. For the 6 clusters involving multiple patients, epidemiologic investigation revealed only 2 (33%) potential transmission events. Conclusion. WGS identified a highly diverse group of C. difficile isolates among POTP with CDI. Although WGS identified clusters of closely related isolates in multiple patients, epidemiologic investigation of shared inpatient exposures identified potential transmission in only two clusters. C. difficile transmission was uncommon.

Disclosures. All authors: No reported disclosures.