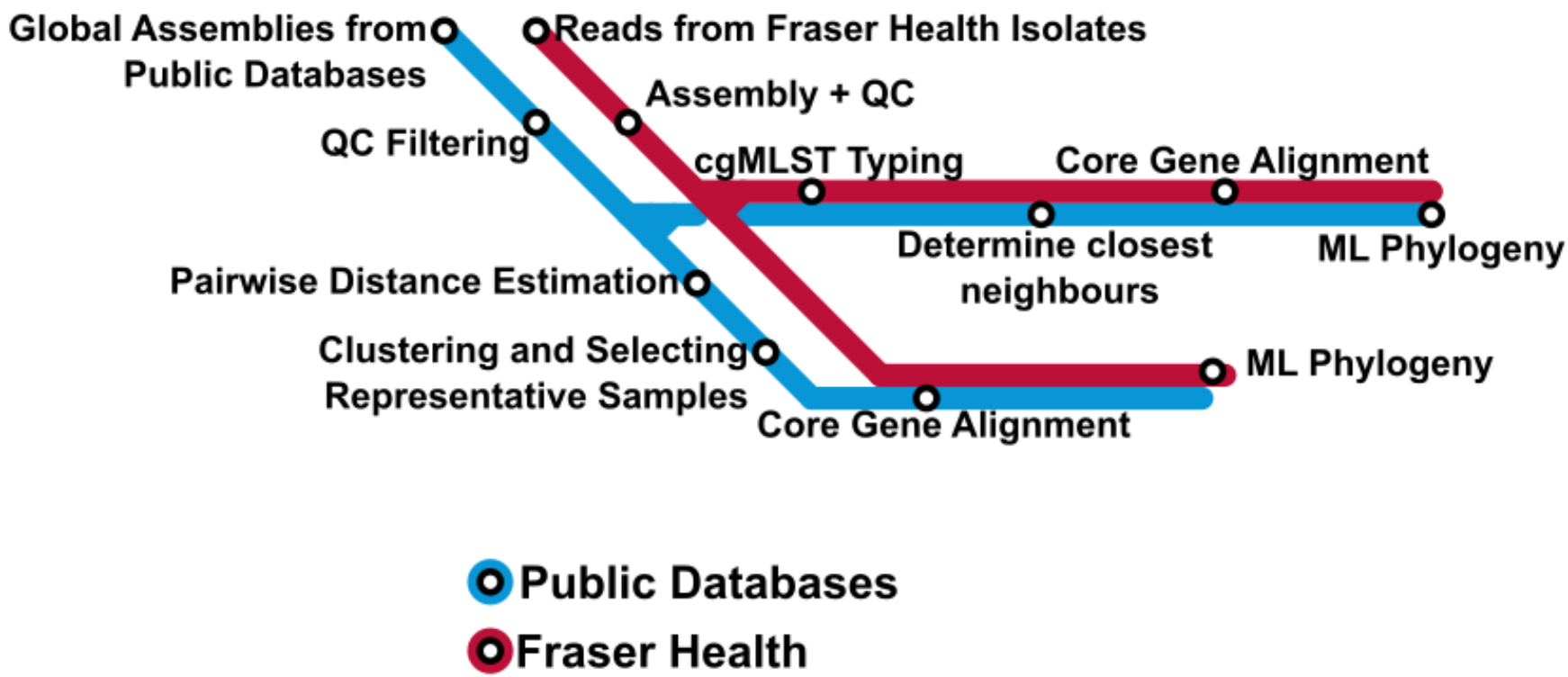


Characterization of *C. difficile* clinical isolates and comparisons to local and global isolates with WGS

PRESENTER:
Ashaan Brooks

BACKGROUND: *Clostridioides difficile* infection (CDI) is a frequently healthcare-associated disease. Commonly used diagnostic assays offer limited resolution in determining the relatedness of strains from different patients. By comparing clinical isolates from patients at Abbotsford General Hospital and throughout Fraser Health with publicly available sequences, we sought to identify potential transmission events and situate Fraser Health strains within a broader global context.

METHODS



RESULTS

- Fraser Health isolates were found primarily in clades 1 and 2, with one isolate from clade 5. This matches the general distribution of *C. difficile* in North America (Zhao et al., 2021).
- Fraser Health isolates tended to be more closely related (by cgMLST distance) to strains from public databases than other Fraser Health isolates.

C. difficile clinical isolates from Fraser Health hospitals are phylogenetically diverse, and do not form a distinct regional cluster when compared to global sequences

Figure 1: Fraser Health isolates and representative sequences from clades 1-5

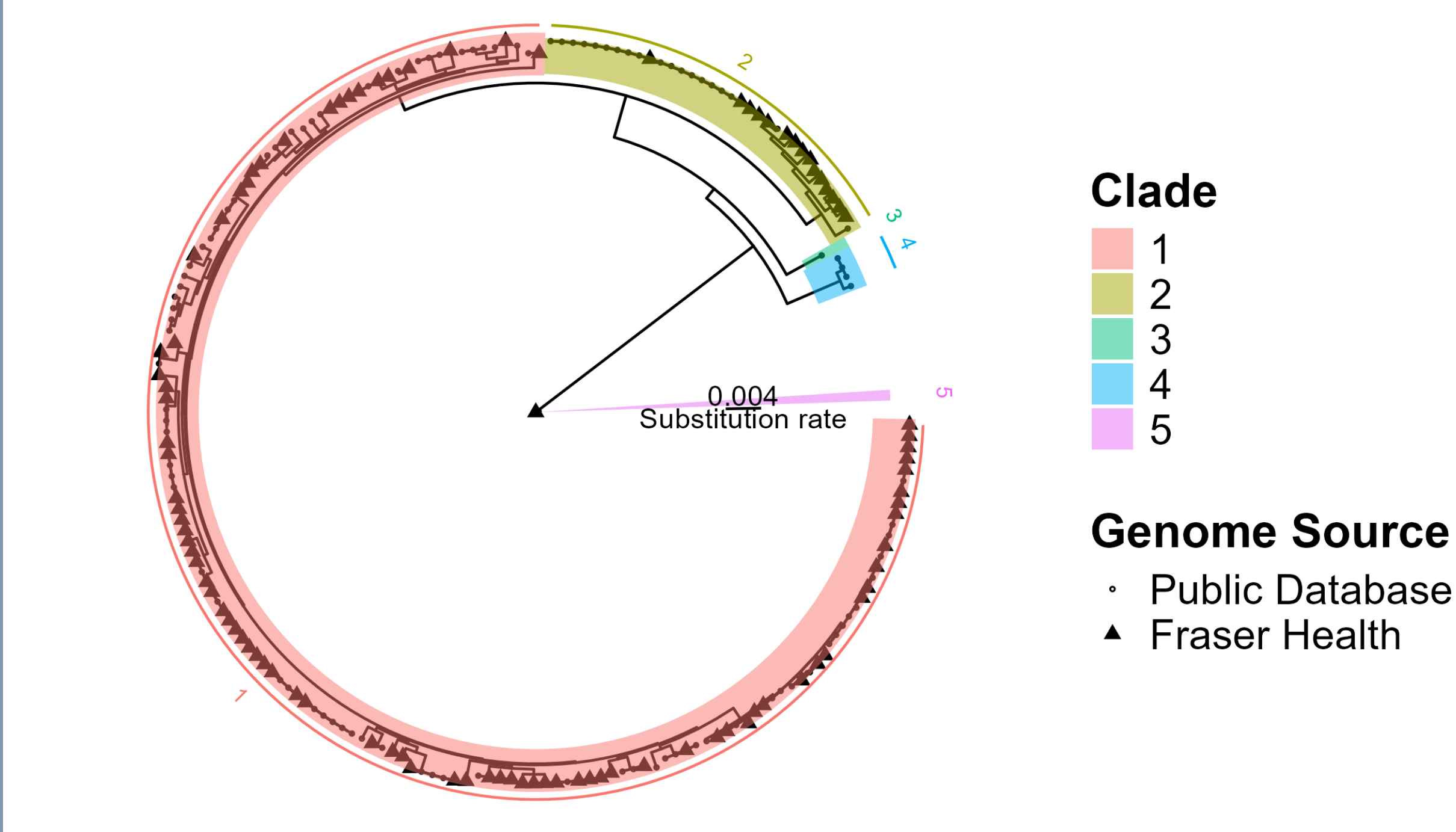


Figure 1: Fraser Health isolates are found throughout the species tree of *C. difficile*. Representative genomes from public databases were selected by k-means clustering based on pairwise distances, with one sequence from each cluster used to represent the species tree.

Figure 2: Fraser Health isolates and closest sequences from public databases

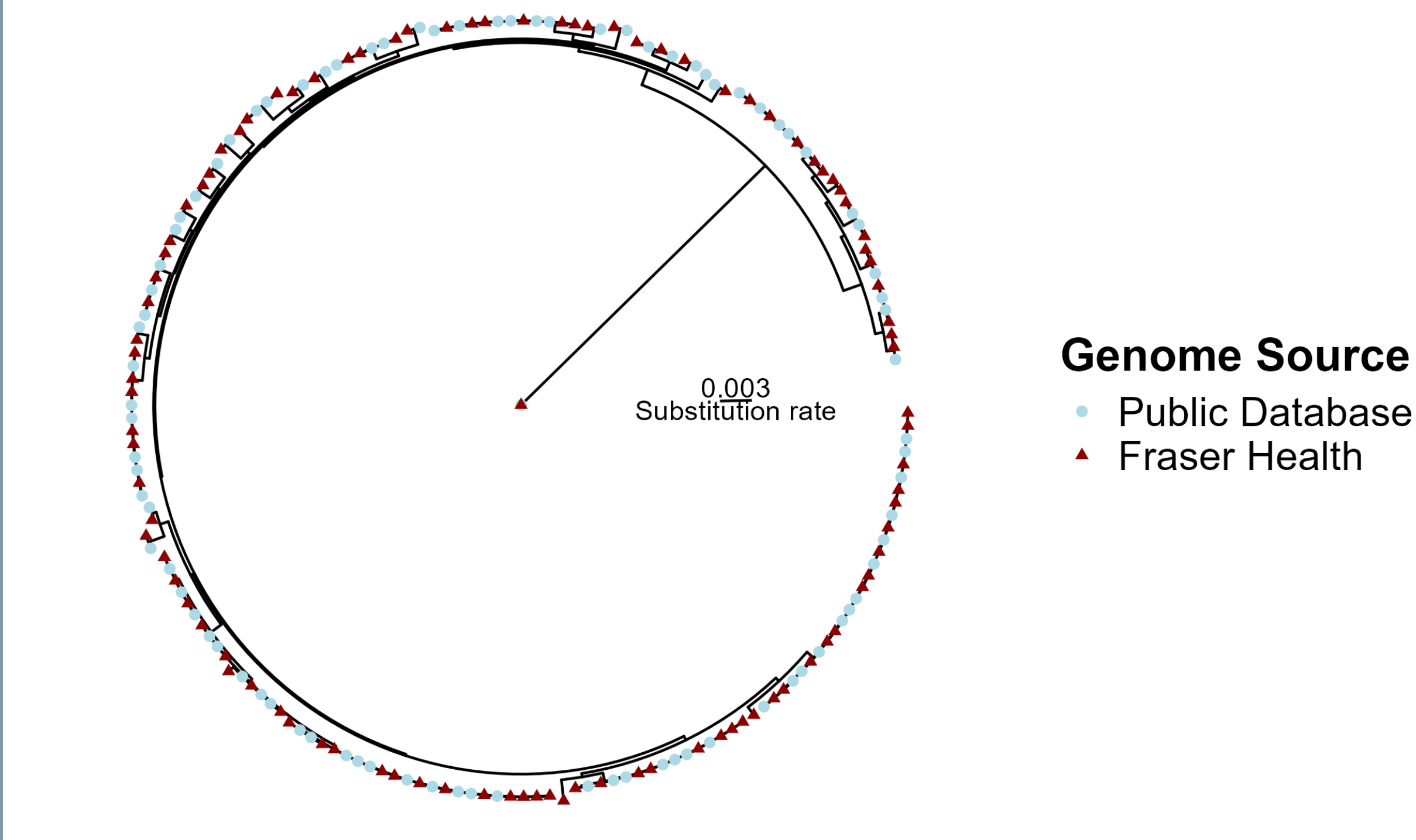


Figure 2: Fraser Health isolates tend to be more closely related to closest sequences from public databases than other Fraser Health isolates, based on cgMLST allelic differences. Only one pair of Fraser Health isolates had less distance to each other than to a sequence in the public database.

Figure 3: Geographic distribution of the closest sequence to each Fraser Health isolate

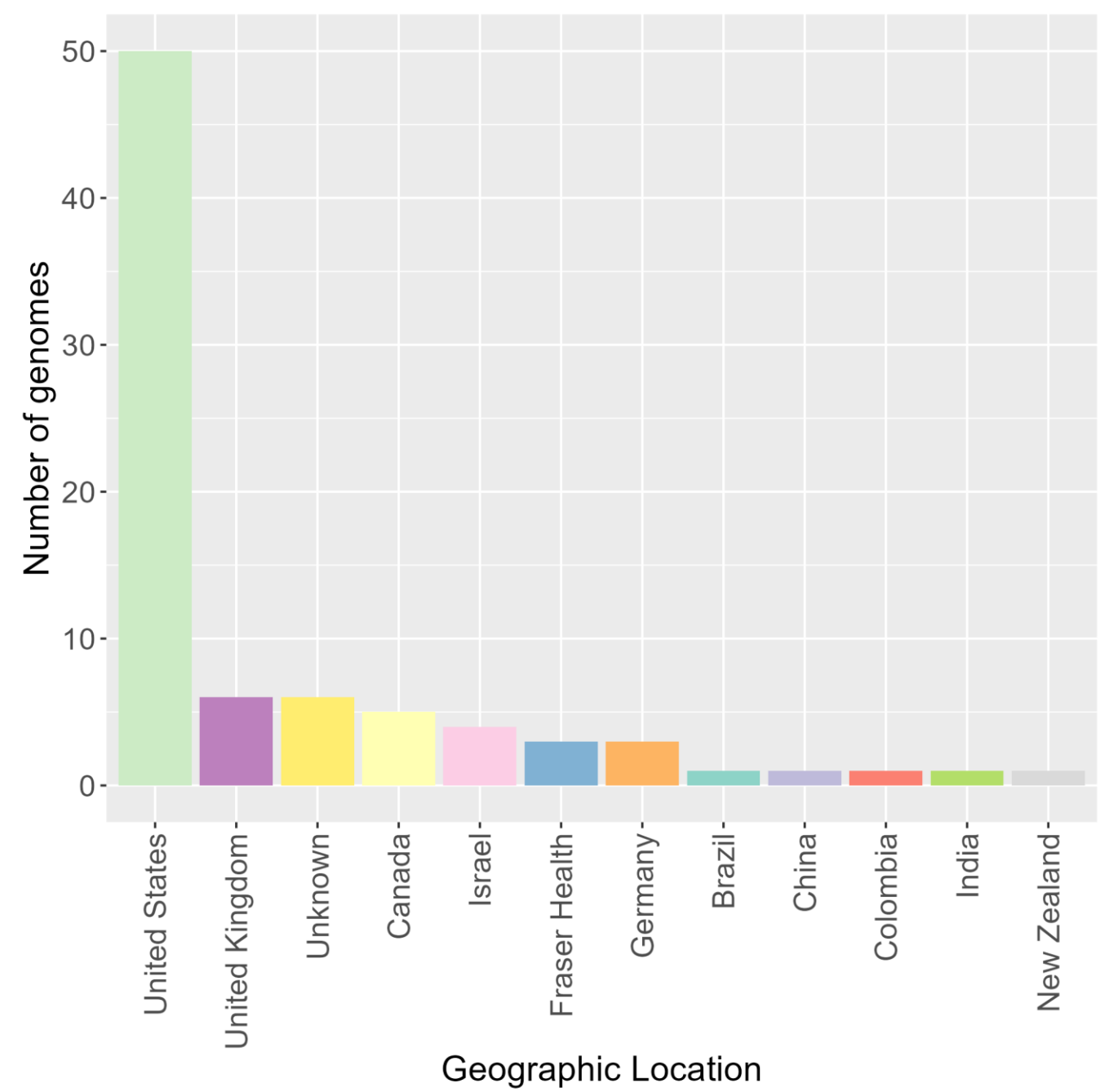


Figure 3: Closest sequences to Fraser Health isolates come primarily from the USA, as well as other countries across the globe.

DISCUSSION

- The lack of closely related isolates within Fraser Health is reflective of sparse sampling, where most strains causing cases of CDI are not isolated and sequenced.

REFERENCES

Zhao, H., Nickle, D. C., Zeng, Z., Law, P. Y., Wilcox, M. H., Chen, L., Peng, Y., Meng, J., Deng, Z., Albright, A., Zhong, H., Xu, X., Zhu, S., Shen, J., Blanchard, R. L., Dorr, M. B., Shaw, P. M., & Li, J. (2021). Global landscape of *Clostridioides difficile* phylogeography, antibiotic susceptibility, and toxin polymorphisms by post-hoc whole-genome sequencing from the modify I/II studies. *Infectious Diseases and Therapy*, 10(2), 853–870. <https://doi.org/10.1007/s40121-021-00426-6>

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Ashaan Brooks,
ashaan_brooks@sfu.ca