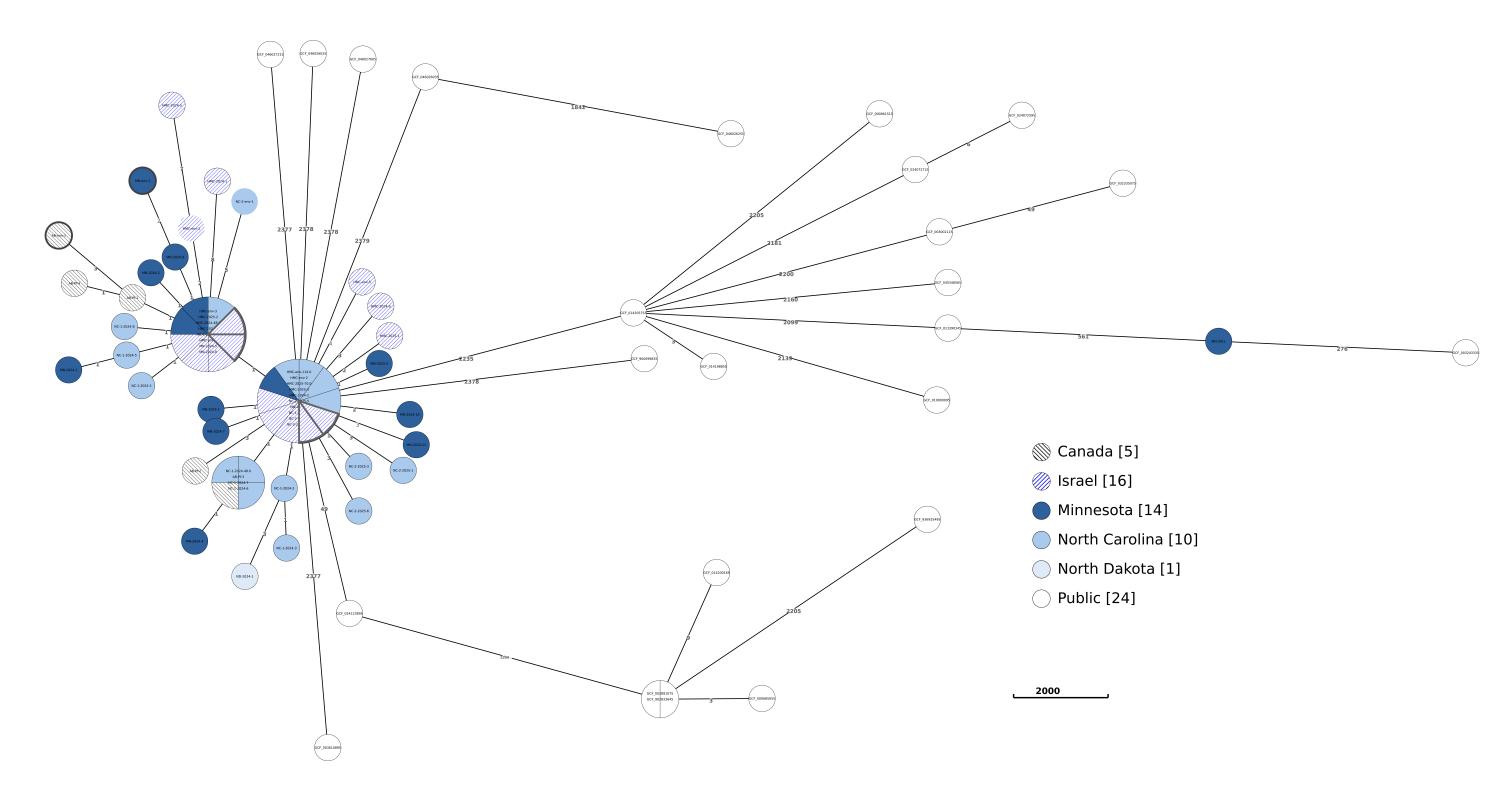
SUPPLEMENTAL FIGURE 2. Core genome multilocus sequence typing (cgMLST) of *P. fungorum* cluster isolates*,[†] compared to publicly available genomes: Minnesota, North Carolina, North Dakota, Canada and Israel, May 2023-April 2025.



*All 52 *P. fungorum* isolates from this cluster (43 clinical isolates and 9 ultrasound gel isolates (outlined in black)) were analyzed using cgMLST alongside one historical clinical isolate from 2011 (dark blue, right) and 24 publicly available *P. fungorum* genomes (white).

Node sizes are proportional to the number of identical genomes represented in a node. Labeled distances indicate the number of differing alleles.

Detailed sequencing and bioinformatics methods are available at https://www.health.state.mn.us/diseases/idlab/mmwr.html

MMWR: Detection of *Paraburkholderia* in Clinical Specimens Associated with Use of Nonsterile Ultrasound Gel for Percutaneous Procedures — United States, Canada, and Israel, May 2023 April 2025

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[†]Genomes were assembled using Shovill with SPAdes and the cgMLST scheme was created using chewBBACA with Prodigal training and visualized using GrapeTree in a minimum-spanning phylogenetic tree. The analysis used an ad hoc scheme of 2,380 loci (at 100% genome presence threshold).