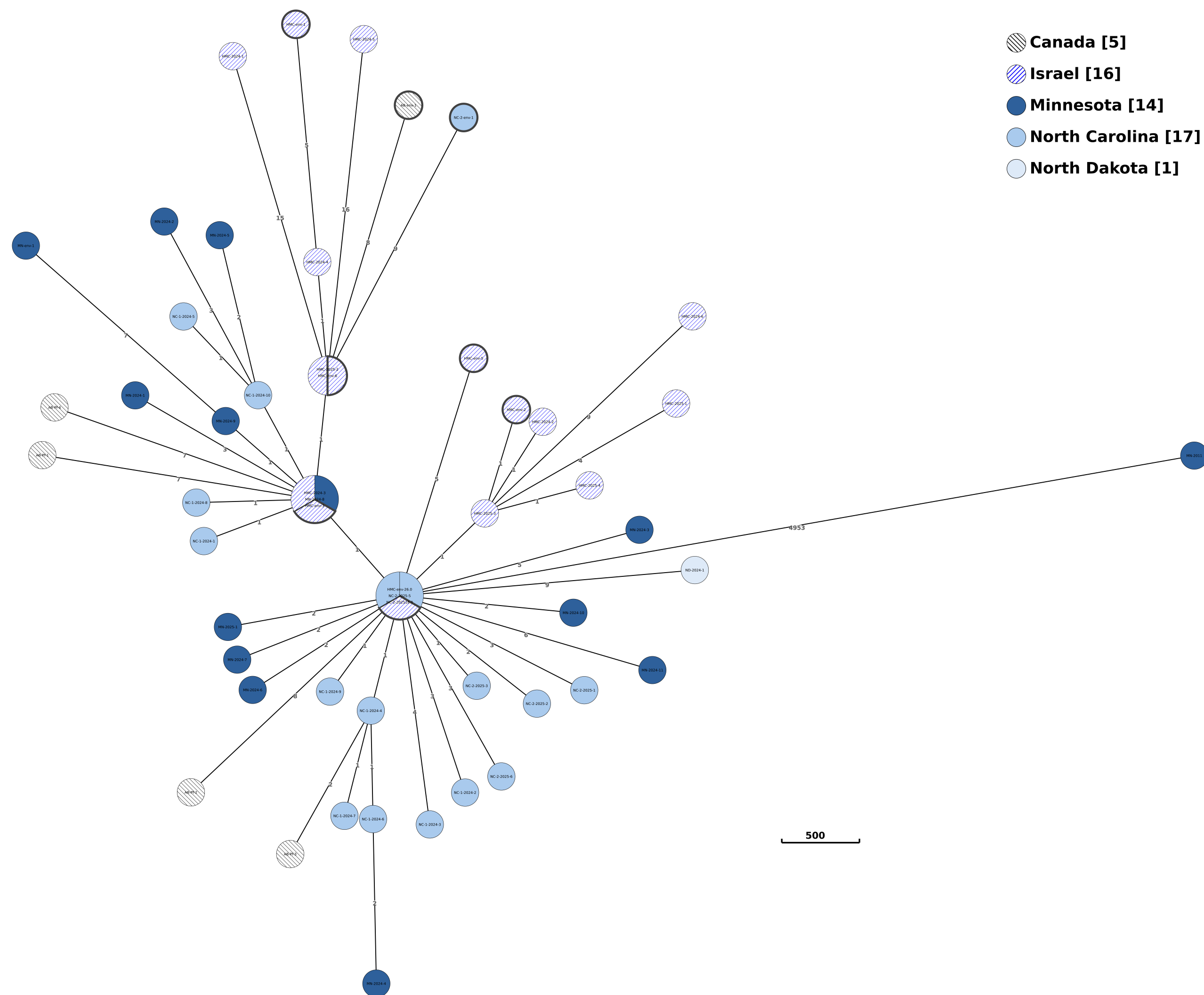**SUPPLEMENTARY FIGURE 1. Core genome multilocus sequence typing (cgMLST) of _P. fungorum_ cluster isolates\*,[†]**
**- Minnesota, North Carolina, North Dakota, Canada, and Israel, May 2023-April 2025.**



\* All 52 _P. fungorum_ isolates from this cluster (43 clinical isolates [including 2 isolates from one patient] and 9 ultrasound gel isolates (outlined in black)) were analyzed.
The analysis was carried using cgMLST alongside one historical clinical isolate from 2011 (outlier, far right).
[†]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 5,219 loci (at 100% genome presence threshold).
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

**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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