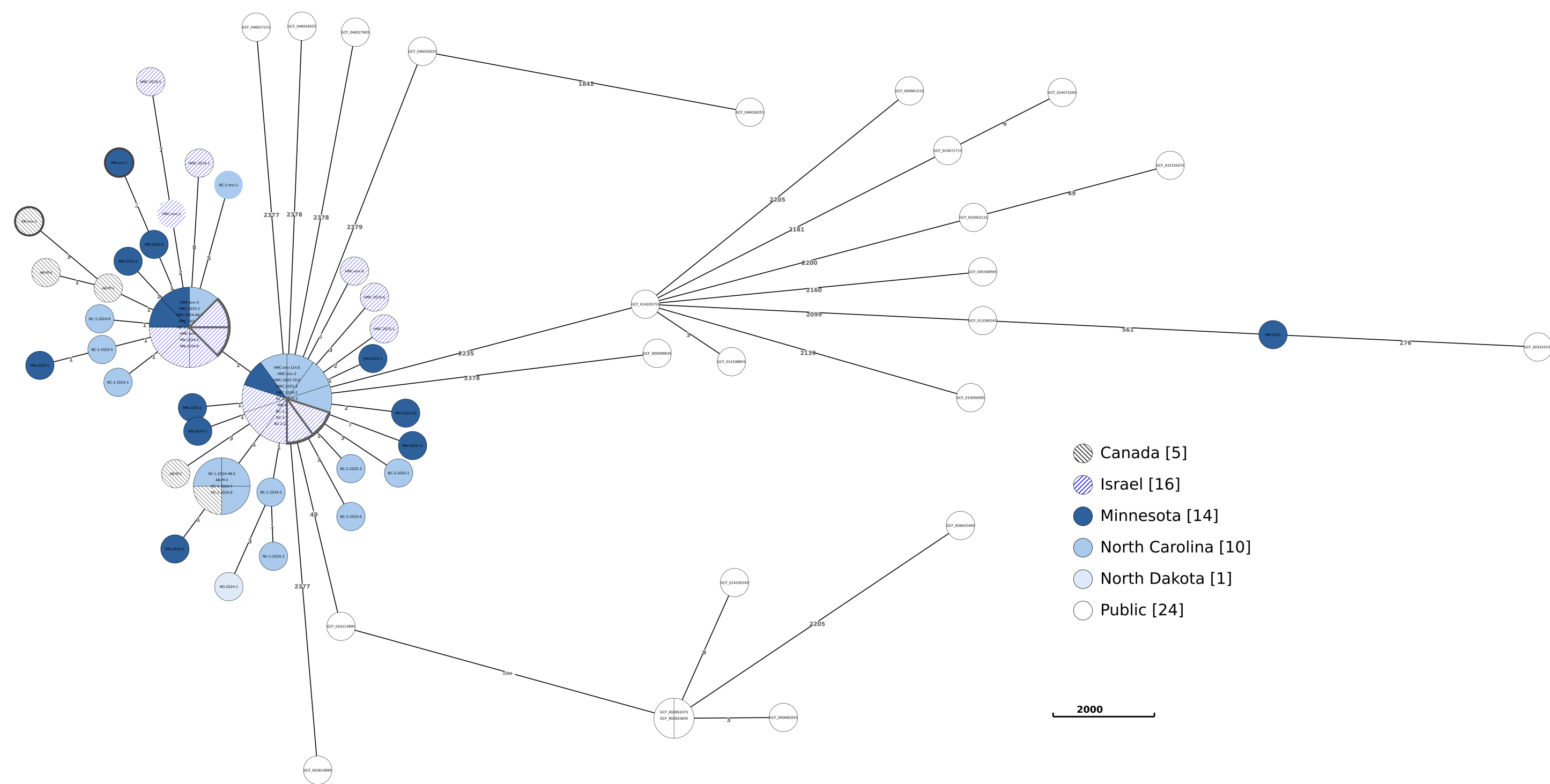


**SUPPLEMENTAL FIGURE 2. Core genome multilocus sequence typing (cgMLST) of *P. fungorum* cluster isolates\*,<sup>†</sup> compared to publicly available genomes: Minnesota, North Carolina, North Dakota, Canada and Israel, May 2023-April 2025.**



\*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).  
<sup>†</sup>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). 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>