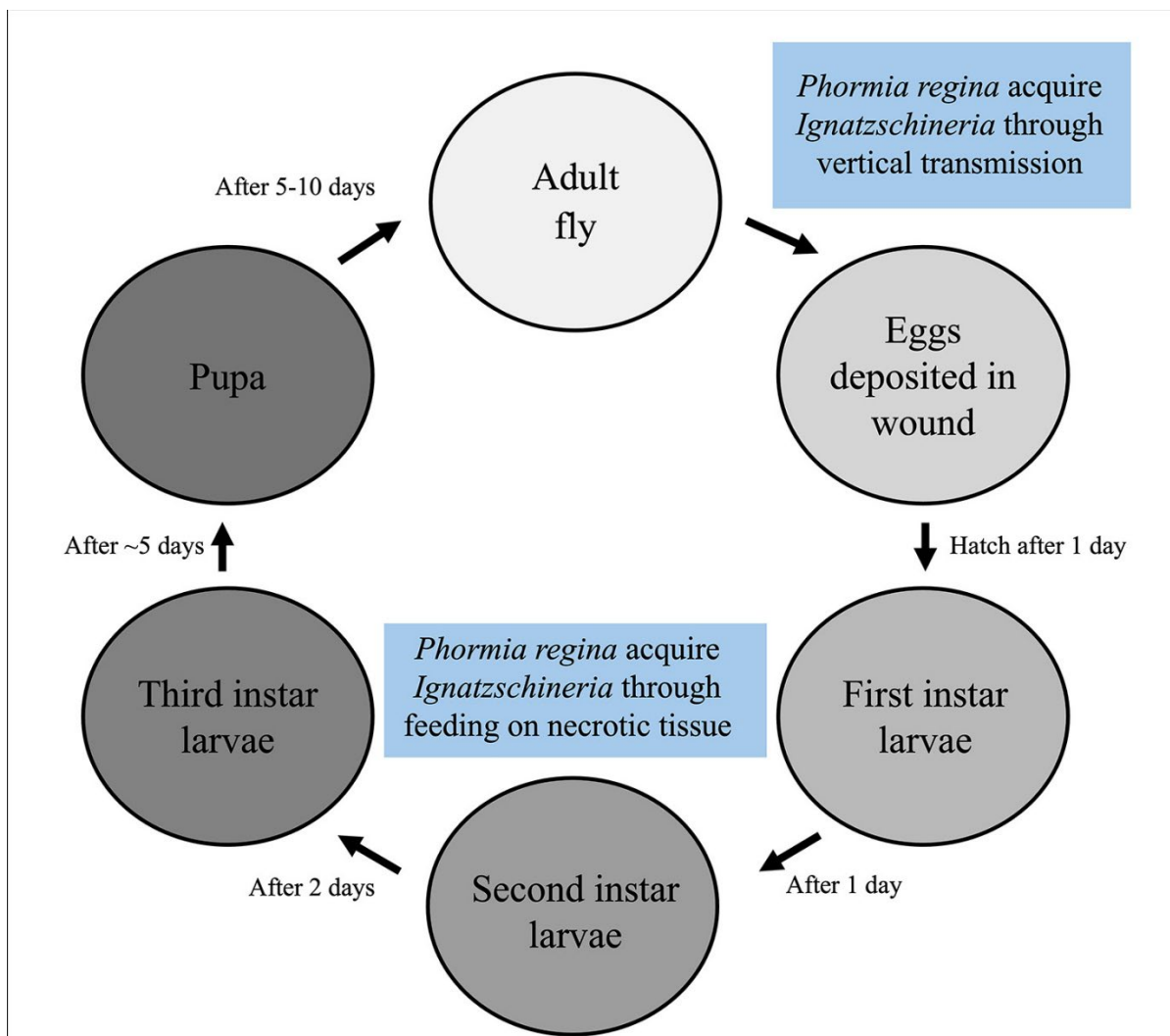
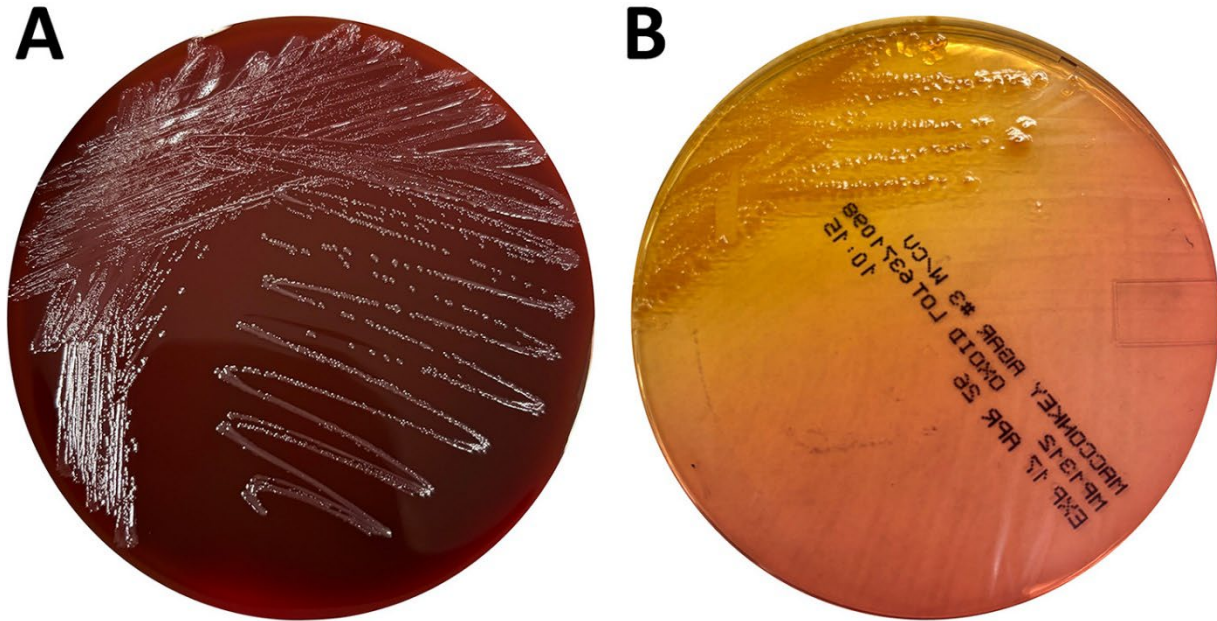


# *Phormia regina* as Vector for *Ignatzschineria* spp. Bacteremia in Persons Experiencing Homelessness, Canada, 2025

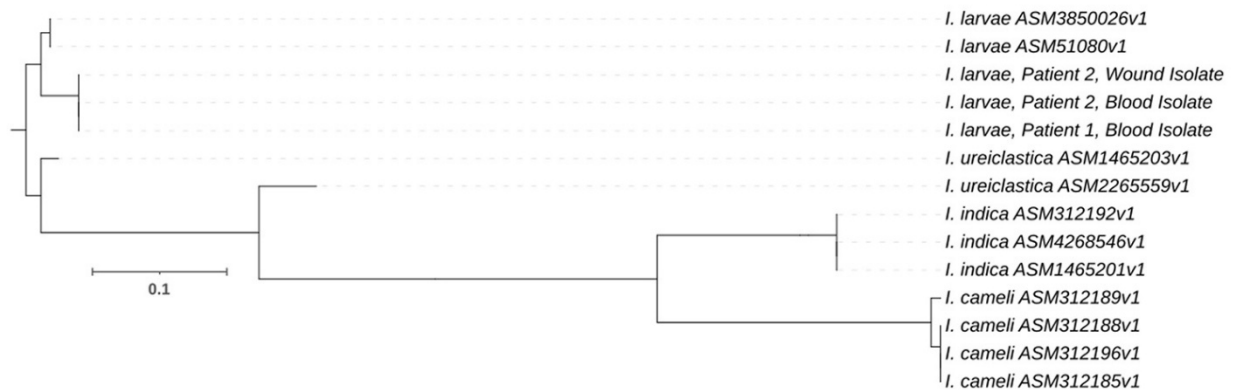
## Appendix



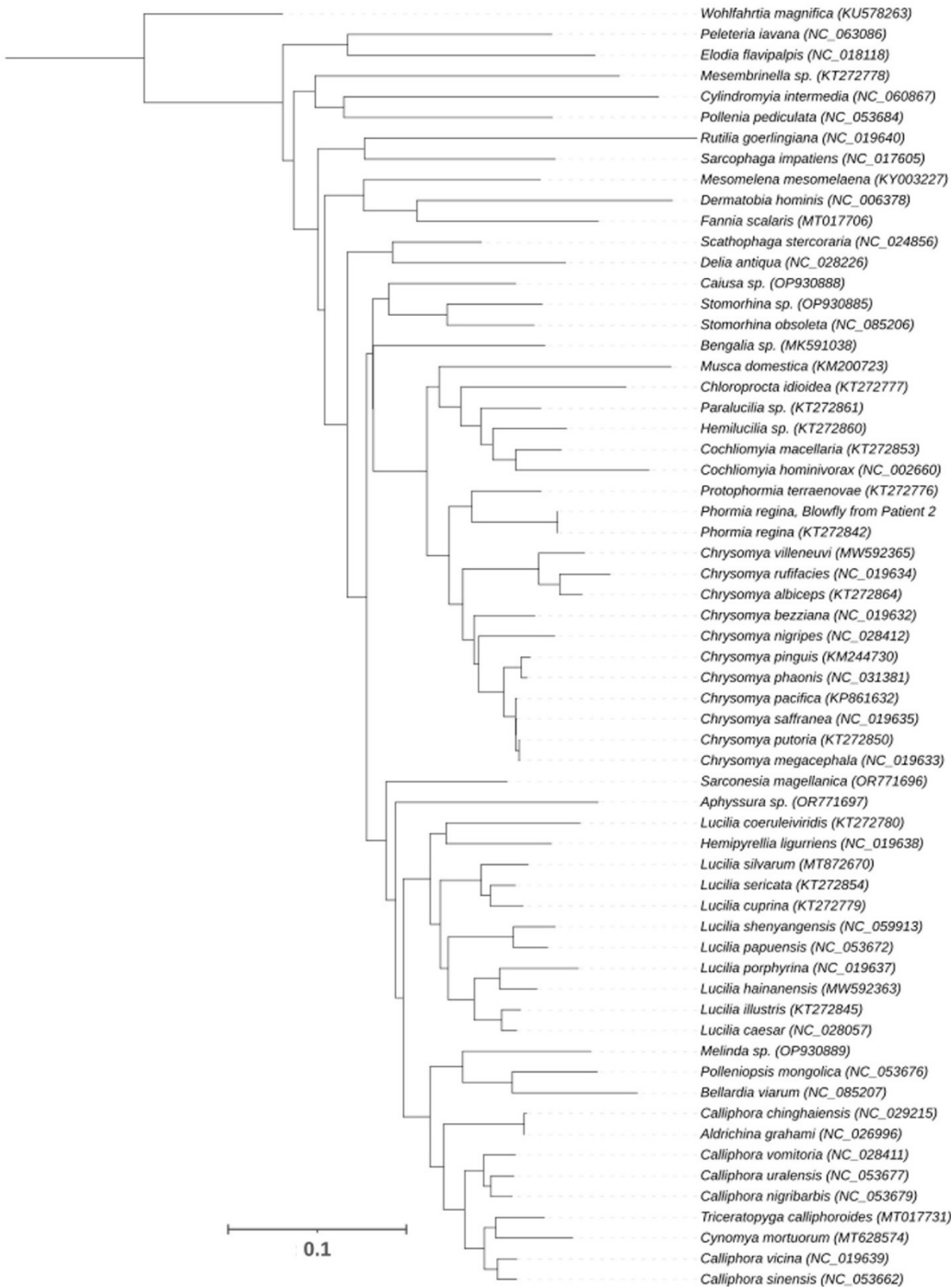
**Appendix Figure 1.** Life cycle of *Phormia regina* and proposed transmission points of *Ignatzschineria* larvae in wound myiasis. There are two main ways for *P. regina* to acquire *Ignatzschineria*: through vertical transmission and through feeding on necrotic and decaying tissue.



**Appendix Figure 2.** Growth of pure *Ignatzschineria larvae* on sheep blood agar (A) and MacConkey agar (B) after 24 hours at 37°C under aerobic conditions.



**Appendix Figure 3.** Whole-genome core phylogenetic analysis of *Ignatzshineria* clinical isolates. This core-genome phylogenetic tree, derived from multi-sequence alignment of single-copy orthologs, illustrates the evolutionary relationships of the *I. larvae* isolates (from Patient 1 and Patient 2) in the context of publicly available *Ignatzshineria* reference genomes. The tree was constructed using Buscogeny (Webster & Chapman, 2024) based on core single-copy orthologs identified by BUSCO. Tree scale bar represents 0.1 substitutions per site.



**Appendix Figure 4.** Phylogenetic analysis of COX1 amino acid sequence. This maximum-likelihood phylogenetic tree illustrates the relationship of the blow fly isolate recovered from case-patient 2 among 63 representative species within the family Calliphoridae and related calypterate flies. Identification was based on the cytochrome c oxidase subunit I (COX-1) gene. Sequences were aligned using MAFFT version 7 (with --auto parameter), and the tree was reconstructed using IQ-TREE 2. The tree scale bar indicates 0.1 substitutions per site.