



S1 Figure. Phylogenetic analysis of 270 *X. euvesicatoria* pv. *perforans* strains. (A) Maximum likelihood phylogenetic tree of *Xanthomonas euvesicatoria* pv. *perforans* strains based on aligned nucleotide sequences of 887 core genes. The tree was inferred using RAxML using a GTRGAMMAI substitution model. The tree was rooted using the 11 genetically diverged strains that make up core gene cluster 10. (B) Neighbor-net network inferred using SNPs from aligned whole genome sequences, including *X. euvesicatoria* pv. *euvesicatoria* strain 85-10 (bolded) as an outgroup. Core gene cluster 10 strains are highlighted. Reticulations in the network indicate conflicting phylogenetic relationships.