New Phytologist Supporting Information

Xylella fastidiosa's relationships: the bacterium, the host plants and the plant microbiome

Blanca B. Landa, Maria Saponari, Oseias R. Feitosa-Junior, Annalisa Giampetruzzi, Filipe J. D. Vieira, Eliana Mor, and Silke Robatzek

Acceptance date: 5 January 2022

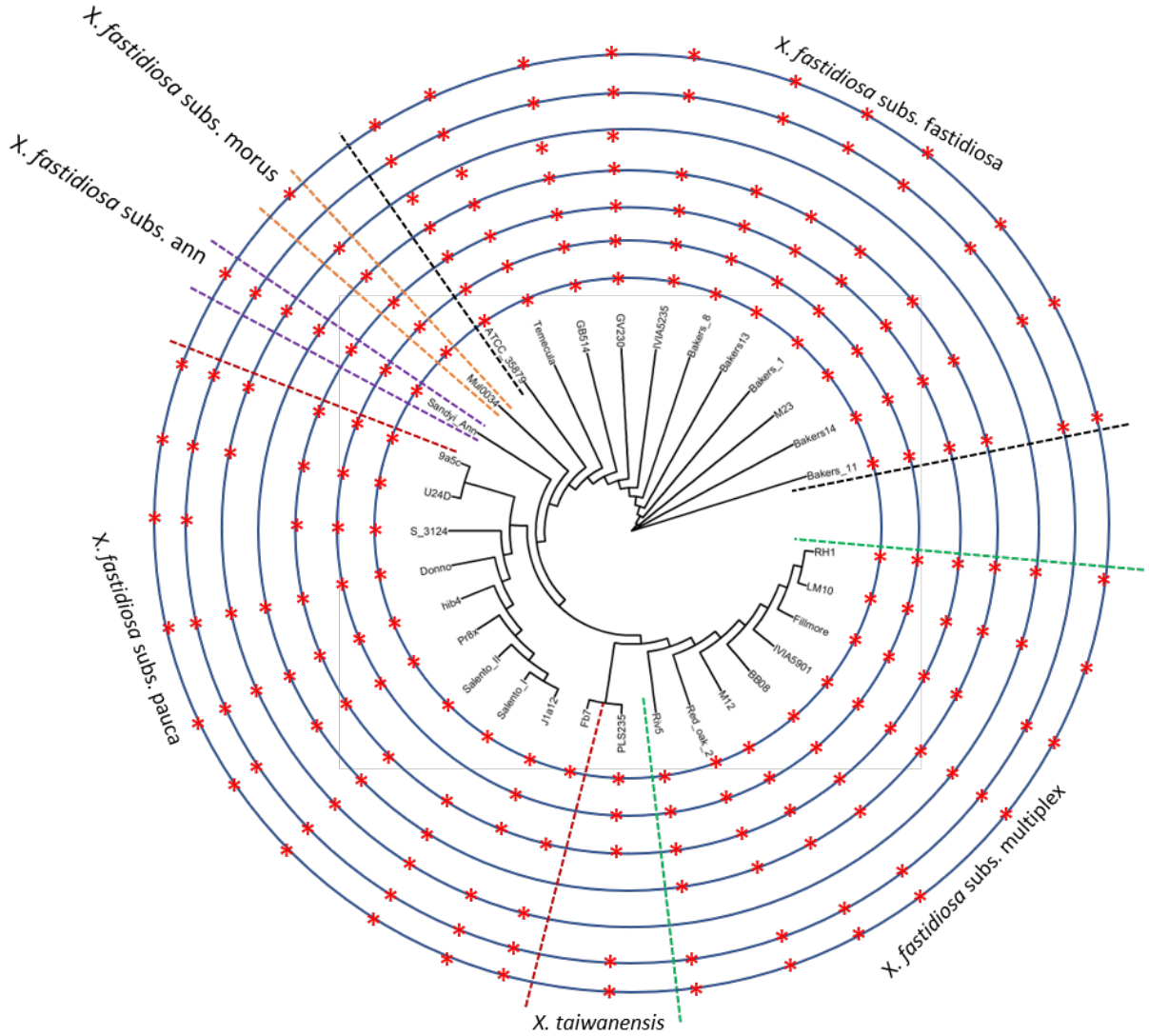

Figure S1. Presence/absence of genes coding for potential PAMPs and CWDE across well-annotated genomes of *Xylella* species. The circles from in to out represent elf18, csp20, chiA, pglA, prtA, lesA and wzy. GBK and fasta files of both the amino acid and nucleotide sequences of the represented genomes were downloaded from the NCBI database. Blast searches were performed using the sequence of *X. fastidiosa* subsp. *fastidiosa* Temecula as a template. Blasts using Koala were performed to check for presence absence of the LPS, EPS, and PGN biosynthesis pathway, as well as secretion systems.

Table S1. Gene expression to microbial stimuli in xylem tissues. For creating this list, two published datasets were crossed: Wendrich *et al.*, 2020 (https://bioit3.irc.ugent.be/plant-sc-atlas/) and Fröscher *et al.,* 2020

(https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE158567), focusing on xylem cell files. For consistency, we applied rather stringent criteria that at least one cell from a given row needed to have a p-value under 0,05. Since *NLR* genes were mostly low expressed, this might have excluded NLRs from our analysis.

Table S2. Potential *PRRs* and *NLRs* in genomes of plants susceptible to *X. fastidiosa* based on annotation searches. GBK files from each of the host plants' genomes were downloaded from the NCBI database. Then, for retrieving the number of potential *PRR* and *NLR* genes we have searched for known protein keywords related to these two families of genes using python custom scripts to parse the GBK files using the Biopython library and specifically SeqIO function. Based on gene name or TAIR locustag (in the case of *A. thaliana*) we dropped the duplicate genes (splicing products).