

Supplementary Figures

Genome-based taxonomy of the *Pseudomonas syringae* and *Pseudomonas lutea* phylogenetic groups of species and proposal of *Pseudomonas maioricensis* sp. nov., isolated from agricultural soil

Magdalena Mulet, Margarita Gomila, Antonio Busquets, David Sánchez, Jorge Lalucat^{1*} and Elena García-Valdés^{1*}

*Corresponding authors

Figure S1. Phylogenomic analyses of 44 selected strains in the *P. avellanae* GTDB species cluster. **(A)** core genome phylogeny based on the concatenated sequences of 1,902 orthologous genes (1,572,618 nt); **(B)** aggregated ANI values, **(C)** GGDC values. Red line indicates the species thresholds. DC3000 and BPIC 631T groups are indicated in different colors. Strain name and genome assembly number is indicated for each genome.

Figure S2. Phylogenomic analysis of selected strains in the *P. tremae* GTDB species cluster. autoMLST phylogenetic tree based on 85 housekeeping gene sequences. Bar indicates phylogenetic distance.

Figure S3. Transmission electron microscopy of a flagellated cell of *P. maioricensis* S25^T

Figure S4. Pathogenicity test of *P. maioricensis* S25^T on citrus leaves. *P. caspiana* FBF102^T is the positive control.

Figure S5. Dendrogram of the main protein profiles of whole cells obtained by MALDI-TOF MS

(A)

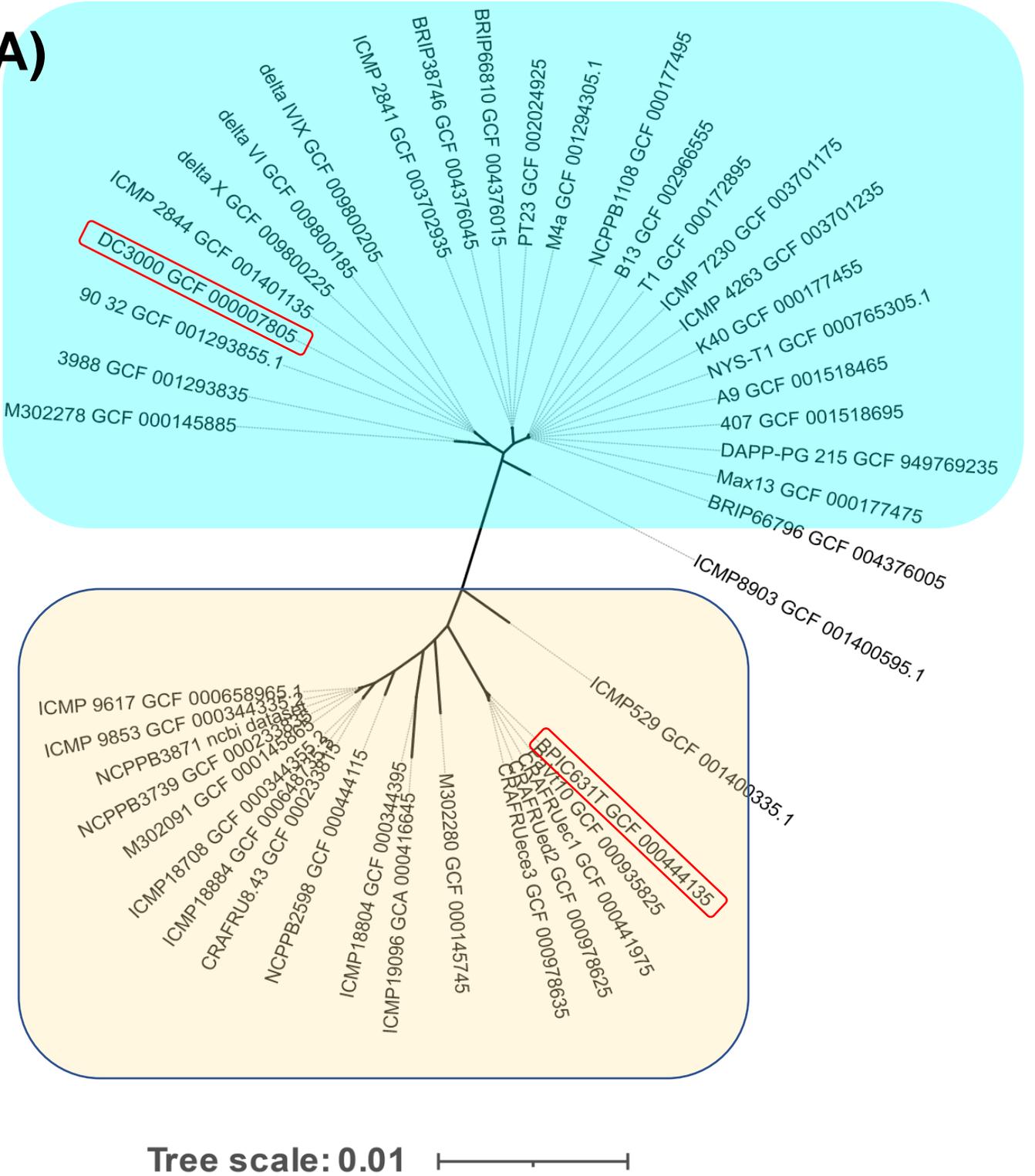


Figure S1. Phylogenomic analyses of 44 selected strains in the *P. avellanae* GTDB species cluster. **(A)** core genome phylogeny based on the concatenated sequences of 1,902 orthologous genes (1,572,618 nt); **(B)** aggregated ANI values, **(C)** GGDC values. Red line indicates the species thresholds. DC3000 and BPIC 631T groups are indicated in different colors. Strain name and genome assembly number is indicated for each genome.

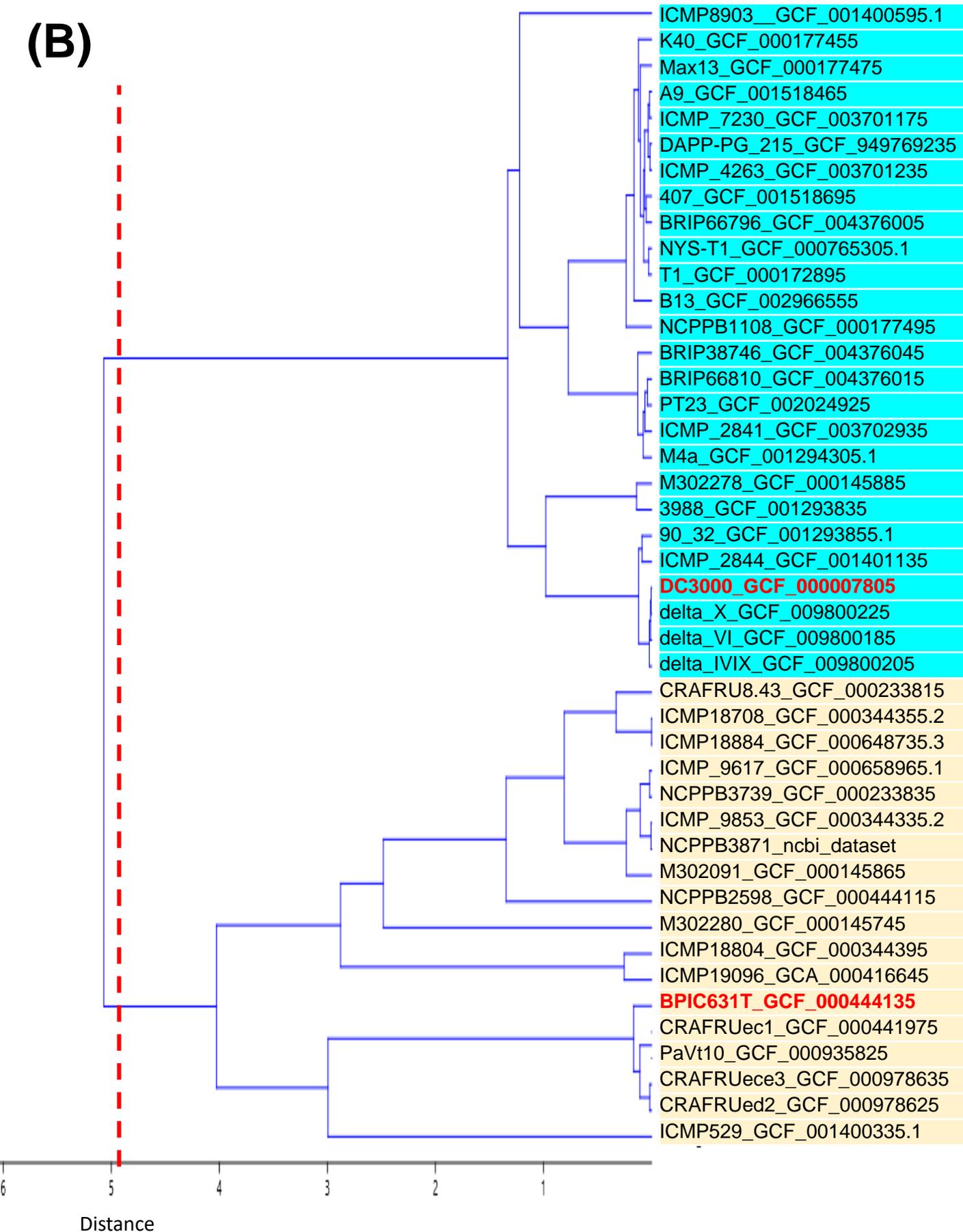
(B)

Figure S1. Phylogenomic analyses of 44 selected strains in the *P. avellanae* GTDB species cluster. (A) core genome phylogeny based on the concatenated sequences of 1,902 orthologous genes (1,572,618 nt); **(B)** aggregated ANI values, (C) GGDC values. DC3000 and BPIC 631T groups are indicated in different colors. Red line indicates the species thresholds.

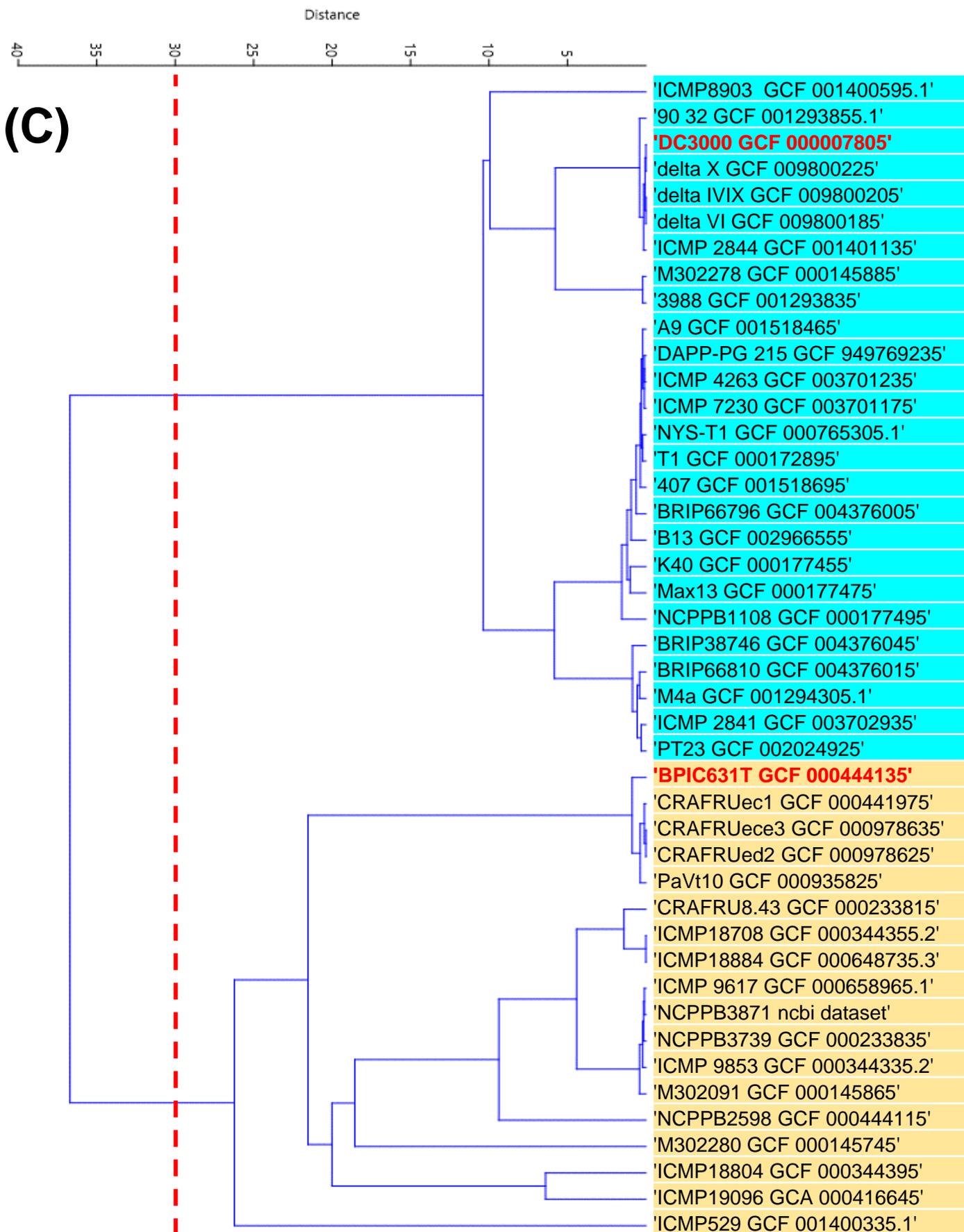


Figure S1. Phylogenomic analyses of 44 selected strains in the *P. avellanae* GTDB species cluster. (A) core genome phylogeny based on the concatenated sequences of 1,902 orthologous genes (1,572,618 nt); (B) aggregated ANI values, (C) GGDC values. DC3000 and BPIC 631T groups are indicated in different colors. Red line indicates the species thresholds.

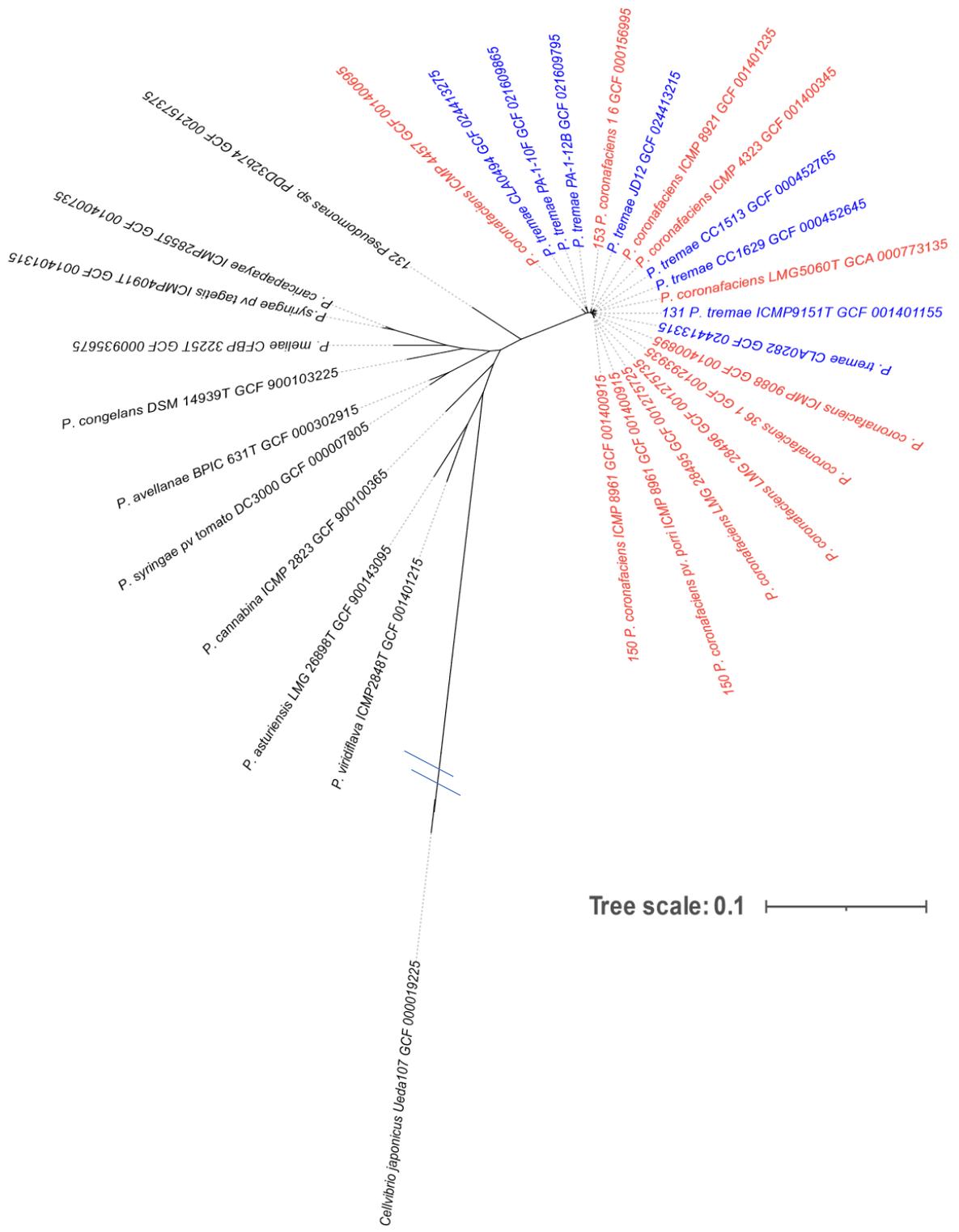


Figure S2. Phylogenomic analysis of selected strains in the *P. tremae* GTDB species cluster. autoMLST phylogenetic tree based on 85 housekeeping gene sequences. Bar indicates phylogenetic distance.

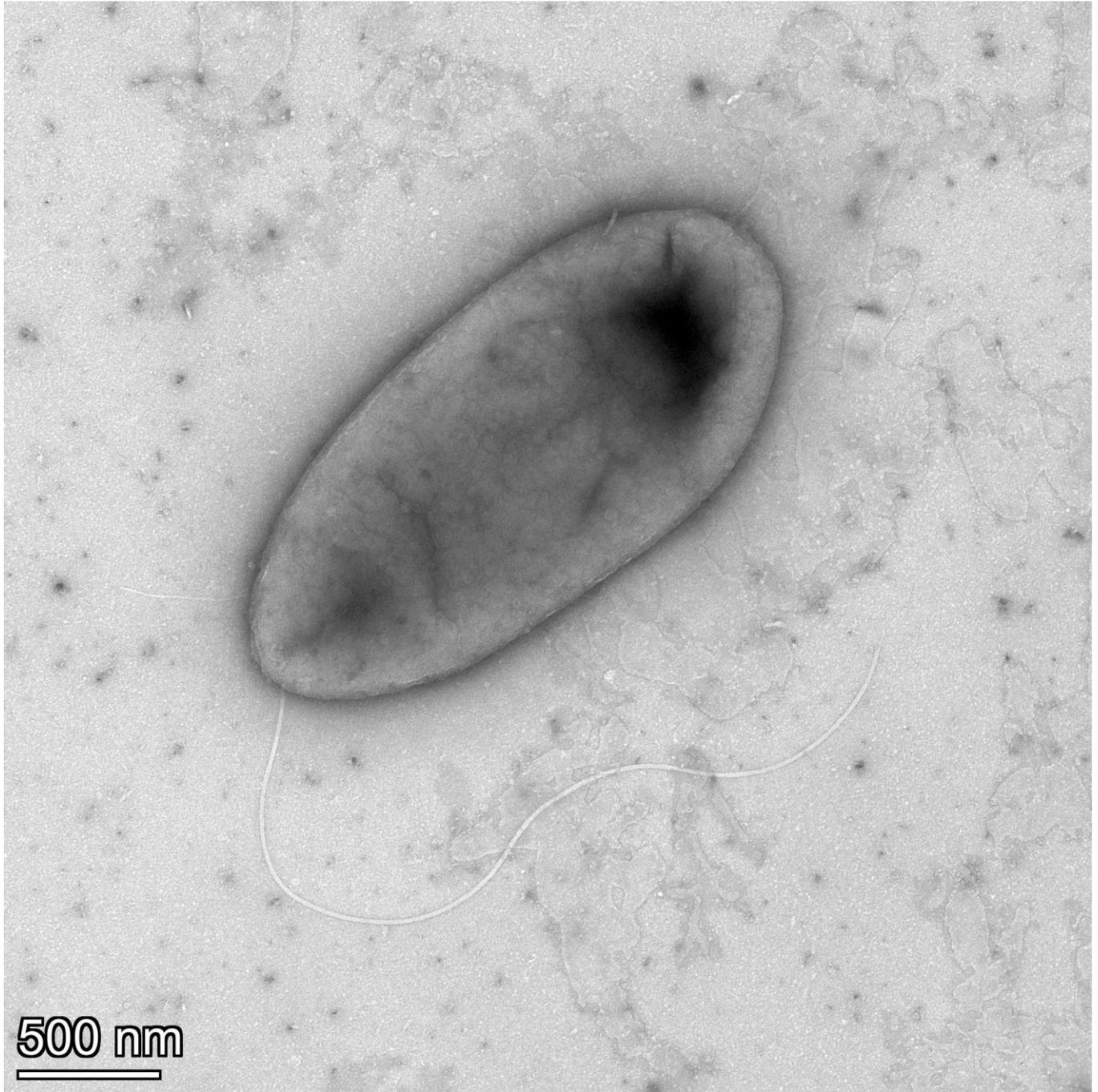


Figure S3. Transmission electron microscopy of a flagellated cell of *P. maioricensis* S25T.



FBF102^T (Day 4)



FBF102^T (Day 8)



S25 (Day 7)

Figure S4. Pathogenicity test of *P. maioricensis* S25^T on citrus leaves. *P. caspiana* FBF102^T is the positive control.

MSP Dendrogram

P. aeruginosa ATCC 10145^T
P. cichrorii ATCC 10857^T
P. tremae LMG 22121^T
P. congelans LMG 21466^T
P. savastanoi LMG 2209^T
P. caricapapayae LMG 2152^T
P. viridiflava ATCC 13223^T
P. syringae ATCC 19310^T
P. cannabina LMG 5096^T
P. avellanae CIP 105176^T
P. caspiana CECT 9164^T
***P. maioricensis* S25^T**
P. quasicaspiana LMG 32434^T
P. folii LMG 32142^T

Distance Level

1000 900 800 700 600 500 400 300 200 100 0

Figure S5. Dendrogram of the main protein profiles of whole cells obtained by MALDI-TOF MS.