

Supplemental Table S2: Information of *X. fastidiosa* isolates and strains for phylogeny.

Strain	Host plant	Place of isolation	Reference	GenBank Accession
<i>Xylella fastidiosa</i> subsp. <i>fastidiosa</i>				
ATCC 35879	Grape	USA (FL)	[1]	JQAP000000.1
CCPM1	Grape	USA (GA)	[2]	PUJB000000.1
CFBP7969	Grape	USA(NC)	[3]	PHFQ000000.1
CFBP7970	Grape	USA (FL)	[3]	PHFR000000.1
CFBP8071	Almond	USA (CA)	[3]	PHFP000000.1
CFBP8073	Coffee	France	[4]	LKES000000.1
CFBP8082	Annual ragweed	USA (FL)	[3]	PHFT000000.1
CFBP8351	Grape	USA (CA)	[3]	PHFU000000.1
DSM 10026	Grape	USA (FL)	(Varghese JN, unpublished)	FQWN000000.1
EB92-1	Elderberry	USA (FL)	[5]	AFDJ000000.1
GB514	Grape	USA (TX)	[6]	CP002165.1
gfpWM1-1 Rec1	Recombinants of WM1-1 with KLN59.3 donor	In vitro	[7]	PUJD000000.1
gfpWM1-1 Rec2	Recombinants of WM1-1 with KLN59.3 donor	In vitro	[7]	PUJE000000.1
IVIA5235	Cherry	Spain	[8]	CP047171.1
M23	Almond	USA (CA)	[9]	CP001011.1
NS1-CmR	Mutant of TemeculaL	In vitro	[10]	PUJF000000.1
NS1pglA Rec	Recombinant of NS1-CmR and pglA-KmR	In vitro	[11]	PUJG000000.1
pglA-KmR	Grape	USA (CA)	[12]	PUJH000000.1
Stag's Leap	Grape	USA (CA)	[13]	LSMJ000000.1
Temecula1	Grape	USA (CA)	[14]	PUJI000000.00
Temecula1gfp	Mutant of Temecula1	In vitro	[15]	PUJC000000.1
p TemeculaL	Grape	USA (CA)	[16]	PUJJ000000.00.1
TemeculaLAlmaRec1	Recombinant of TemeculaL with AlmaEM3 donor	In vitro	[16]	PUIW000000.1
TemeculaLAlmaRec2	Recombinant of TemeculaL with AlmaEM3 donor	In vitro	[16]	PUIX000000.1

TemeculaStar	Grape	USA (GA)	[16]	PUJI000000 00.1
TPD3	Grape	Taiwan	[17]	VJWG0000 0000.1
TPD4	Grape	Taiwan	[17]	VJWH0000 0000.1
WM1-1	Grape	USA (GA)	[2]	PUJK00000 000.1
XYL1732	Grape	Spain	[18]	QTJT00000 000.1
XYL2055	Grape	Spain	[18]	QTJS00000 000.1
<i>Xylella fastidiosa subsp. morus</i>				
MUL0034	Mulberry	USA (CA)	[19]	CP006740.1
Mul-MD	Mulberry	USA (MD)	[20]	AXDP0000 0000.1
<i>Xylella fastidiosa subsp. sandyi</i>				
CFBP8356	Coffee	Costa Rica	[3]	PHFV00000 000.1
Ann-1	Oleander	USA (CA)	[19]	AAAM0000 0000.4
CO33	Coffee	Italy	[21]	LJZW00000 000.1
<i>Xylella fastidiosa subsp. multiplex</i>				
AlmaEM3	Blueberry (Emerald)	USA (GA)	[22]	PUIY00000 000.1
BB01	Blueberry	USA (GA)	[23]	MPAZ0000 0000.1
BB08-1	Blueberry	USA (FL)	[22]	PUIZ00000 000
CFBP8078	Periwinkle	USA (FL)	[3]	PHFS00000 000.1
CFBP8417	Spanish Broom	France	[3]	LUYB0000 0000.1
CFBP8418	Spanish Broom	France	[3]	LUYA0000 0000.1
Dixon	Almond	USA (CA)	[24]	AAAL0000 0000.2
ESVL	Almond	Spain	[25]	QPQV0000 0000.1
IVIA5901	Almond	Spain	[8]	CP047134.1
M12	Almond	USA (CA)	[9]	CP000941
sycamore Sy-VA	Sycamore	USA (VA)	[20]	JMHP00000 000.1
TOS14	Spanish Broom	Italy	[26]	SMTJ00000 000.1

TOS4	Almond	Italy	[26]	SMTH0000 0000.1
TOS5	Myrtle-leaf milkwort	Italy	[26]	SMTI00000 000.1
ATCC 35871	Hybrid Plum	USA (GA)	(Kyrpides et al, unpublished)	AUAJ00000 000.1
Griffin-1	Oak	USA (GA)	[27]	AVGA0000 0000.1
<i>Xylella fastidiosa</i> subsp. <i>pauca</i>				
3124	Coffee	Brazil (São Paulo)	[28]	CP009829.1
CFBP8072	Coffee	France	[4]	LKDK0000 0000.1
CoDiRO	Olive	Italy (Apulia)	[29]	JUJW00000 000.1
De Donno	Olive	Italy (Apulia)	[30]	CP020870.1
PD7202	Coffee	Netherlands	[31]	RRUA0000 0000.1
PD7211	Coffee	Netherlands	[31]	RRTZ00000 000.1
32	Coffee	Brazil (São Paulo)	[32]	AWYH000 00000.1
11399	Orange	Brazil	[33]	JNBT00000 000.1
6c	Coffee	Brazil (São Paulo)	[32]	AXBS0000 0000.2
9a5c	Sweet orange	Brazil (São Paulo)	[34]	AE003849. 1
COF0324	Coffee	Brazil	(Knight et al, 2017, unpublished)	LRVG0000 0000.1
COF0407	Coffee	Costa Rica	(Knight et al, 2017, unpublished)	LRVJ00000 000.1
CVC0251	Sweet orange	Brazil	(Knight et al, 2017, unpublished)	LRVE0000 0000.1
CVC0256	Sweet orange	Brazil	(Knight et al, 2017, unpublished)	LRVF00000 000.1
Fb7	Sweet orange	Argentina (Corrientes)	[35]	CP010051.2
Hib4	Hibiscus	Brazil (São Paulo)	(Pierry and da Silva, 2017, unpublished)	CP009885.1
J1a12	Sweet orange	Brazil (São Paulo)	(Pierry and da Silva, 2017, unpublished)	CP009823.1
OLS0478	Oleander	Costa Rica	(Knight et al, 2017, unpublished)	LRVI00000 000.1
OLS0479	Oleander	Costa Rica	(Knight et al, 2017, unpublished)	LRVH0000 0000.1
Pr8x	Plum	Brazil (São Paulo)	(Pierry and da Silva 2015, unpublished)	CP009826.1

Salento-1	Olive	Italy (Apulia)	[36]	CP016608.1
Salento-2	Olive	Italy (Apulia)	[37]	CP016610.1
U24D	Sweet orange	Brazil (São Paulo)	(Da Silva, 2017 unpublished)	CP009790.1

Reference:

1. Chen, J.; O’Leary, M.; Burbank, L.; Zheng, Z.; Deng, X. Whole Genome Sequence of *Xylella fastidiosa* ATCC 35879 T and Detection of Genome Rearrangements Within Subsp. *fastidiosa*. *Curr. Microbiol.* **2020**, *77*, 1858–1863.
2. Denancé, N.; Briand, M.; Gaborieau, R.; Gaillard, S.; Jacques, M.-A. Identification of genetic relationships and subspecies signatures in *Xylella fastidiosa*. *BMC Genom.* **2019**, *20*, 239.
3. Jacques, M.-A.; Denancé, N.; Legendre, B.; Morel, E.; Briand, M.; Mississippi, S.; Durand, K.; Olivier, V.; Portier, P.; Poliakoff, F. New coffee plant-infecting *Xylella fastidiosa* variants derived via homologous recombination. *Appl. Environ. Microbiol.* **2016**, *82*, 1556–1568.
4. Zhang, S.; Flores-Cruz, Z.; Kumar, D.; Chakrabarty, P.; Hopkins, D.L.; Gabriel, D.W. The *Xylella fastidiosa* biocontrol strain EB92-1 genome is very similar and syntenic to Pierce’s disease strains. *J. Bacteriol.* **2011**, *193*, 5576–5577.
5. Schreiber, H.; Koirala, M.; Lara, A.; Ojeda, M.; Dowd, S.; Bextine, B.; Morano, L. Unraveling the first *Xylella fastidiosa* subsp. *fastidiosa* genome from Texas. *Southwest. Entomol.* **2010**, *35*, 479–483.
6. Kandel, P.P.; Almeida, R.P.; Cobine, P.A.; De La Fuente, L. Natural competence rates are variable among *Xylella fastidiosa* strains and homologous recombination occurs in vitro between subspecies *fastidiosa* and *multiplex*. *Mol. Plant Microbe Interact.* **2017**, *30*, 589–600.
7. Landa, B.B.; Velasco-Amo, M.P.; Marco-Noales, E.; Olmo, D.; López, M.M.; Navarro, I.; Monterde, A.; Barbé, S.; Montes-Borrego, M.; Román-Écija, M. Draft genome sequence of *Xylella fastidiosa* subsp. *fastidiosa* strain IVIA5235, isolated from *Prunus avium* in Mallorca Island, Spain. *Microbiol. Resour. Announc.* **2018**, *7*, e01222-18.
8. Chen, J.; Xie, G.; Han, S.; Chertkov, O.; Sims, D.; Civerolo, E. Whole genome sequences of two *Xylella fastidiosa* strains (M12 and M23) causing almond leaf scorch disease in California. *J. Bacteriol.* **2010**, *192*, 4534–4534.
9. Matsumoto, A.; Young, G.M.; Igo, M.M. Chromosome-based genetic complementation system for *Xylella fastidiosa*. *Appl. Environ. Microbiol.* **2009**, *75*, 1679–1687.
10. Kandel, P.P.; Lopez, S.M.; Almeida, R.P.; De La Fuente, L. Natural Competence of *Xylella fastidiosa* Occurs at a High Frequency Inside Microfluidic Chambers Mimicking the Bacterium’s Natural Habitats. *Appl. Environ. Microbiol.* **2016**, *82*, 5269–5277, doi:10.1128/AEM.01412-16.
11. Roper, M.C.; Greve, L.C.; Warren, J.G.; Labavitch, J.M.; Kirkpatrick, B.C. *Xylella fastidiosa* requires polygalacturonase for colonization and pathogenicity in *Vitis vinifera* grapevines. *Mol. Plant Microbe Interact.* **2007**, *20*, 411–419.
12. Chen, J.; Wu, F.; Zheng, Z.; Deng, X.; Burbank, L.; Stenger, D. Draft genome sequence of *Xylella fastidiosa* subsp. *fastidiosa* strain Stag’s leap. *Genome Announc.* **2016**, *4*, doi:10.1128/genomeA.00240-16
13. Van Sluys, M.; De Oliveira, M.; Monteiro-Vitorello, C.; Miyaki, C.; Furlan, L.; Camargo, L.; Da Silva, A.; Moon, D.; Takita, M.; Lemos, E. Comparative analyses of the complete genome sequences of Pierce’s disease and citrus variegated chlorosis strains of *Xylella fastidiosa*. *J. Bacteriol.* **2003**, *185*, 1018–1026.

14. Newman, K.L.; Almeida, R.P.P.; Purcell, A.H.; Lindow, S.E. Use of a green fluorescent strain for analysis of *Xylella fastidiosa* colonization of *Vitis vinifera*. *Appl. Environ. Microbiol.* **2003**, *69*, 7319–7327.
15. Potnis, N.; Kandel, P.P.; Merfa, M.V.; Retchless, A.C.; Parker, J.K.; Stenger, D.C.; Almeida, R.P.; Bergsma-Vlami, M.; Westenberg, M.; Cobine, P.A. Patterns of inter-and intrasubspecific homologous recombination inform eco-evolutionary dynamics of *Xylella fastidiosa*. *ISME J.* **2019**, *13*, 2319–2333.
16. Castillo, A.I.; Tuan, S.-J.; Retchless, A.C.; Hu, F.-T.; Chang, H.-Y.; Almeida, R.P. Draft Whole-Genome Sequences of *Xylella fastidiosa* subsp. *fastidiosa* Strains TPD3 and TPD4, Isolated from Grapevines in Hou-li, Taiwan. *Microbiol. Resour. Announc.* **2019**, *8*, doi:10.1128/MRA.00835-19.
17. Gomila, M.; Moralejo, E.; Busquets, A.; Seguí, G.; Olmo, D.; Nieto, A.; Juan, A.; Lalucat, J. Draft genome resources of two strains of *Xylella fastidiosa* XYL1732/17 and XYL2055/17 isolated from Mallorca vineyards. *Phytopathology* **2019**, *109*, 222–224.
18. Schuenzel, E.L.; Scally, M.; Stouthamer, R.; Nunney, L. A multigene phylogenetic study of clonal diversity and divergence in North American strains of the plant pathogen *Xylella fastidiosa*. *Appl. Environ. Microbiol.* **2005**, *71*, 3832–3839.
19. Guan, W.; Shao, J.; Davis, R.E.; Zhao, T.; Huang, Q. Genome sequence of a *Xylella fastidiosa* strain causing sycamore leaf scorch disease in Virginia. *Genome Announc.* **2014**, *2*, doi:10.1128/genomea.00773-14.
20. Giampetruzzi, A.; Loconsole, G.; Boscia, D.; Calzolari, A.; Chiumenti, M.; Martelli, G.P.; Saldarelli, P.; Almeida, R.P.; Saponari, M. Draft genome sequence of CO33, a coffee-infecting isolate of *Xylella fastidiosa*. *Genome Announc.* **2015**, *3*, doi:10.1128/genomea.01472-15.
21. Oliver, J.E.; Sefick, S.A.; Parker, J.K.; Arnold, T.; Cobine, P.A.; De La Fuente, L. Ionome changes in *Xylella fastidiosa*-infected *Nicotiana tabacum* correlate with virulence and discriminate between subspecies of bacterial Isolates. *Mol. Plant Microbe Interact.* **2014**, *27*, 1048–1058, doi:10.1094/MPMI-05-14-0151-R.
22. Van Horn, C.; Chang, C.-J.; Chen, J. De novo whole-genome sequence of *Xylella fastidiosa* subsp. *multiplex* strain BB01 isolated from a blueberry in Georgia, USA. *Genome Announc.* **2017**, *5*, doi:10.1128/genomea.01598-16.
23. Bhattacharyya, A.; Stilwagen, S.; Reznik, G.; Feil, H.; Feil, W.S.; Anderson, I.; Bernal, A.; D'Souza, M.; Ivanova, N.; Kapatral, V. Draft sequencing and comparative genomics of *Xylella fastidiosa* strains reveal novel biological insights. *Genome Res.* **2002**, *12*, 1556–1563.
24. Giampetruzzi, A.; Velasco-Amo, M.P.; Marco-Noales, E.; Montes-Borrego, M.; Roman-Ecija, M.; Navarro, I.; Monterde, A.; Barbé, S.; Almeida, R.P.; Saldarelli, P. Draft genome resources of two strains (“ESVL” and “IVIA5901”) of *Xylella fastidiosa* associated with almond leaf scorch disease in Alicante, Spain. *Phytopathology* **2019**, *109*, 219–221.
25. Giampetruzzi, A.; D’Attoma, G.; Zicca, S.; Abou Kubaa, R.; Rizzo, D.; Boscia, D.; Saldarelli, P.; Saponari, M. Draft genome sequence resources of three strains (TOS4, TOS5, and TOS14) of *Xylella fastidiosa* infecting different host plants in the newly discovered outbreak in Tuscany, Italy. *Phytopathology* **2019**, *109*, 1516–1518.
26. Chen, J.; Huang, H.; Chang, C.-J.; Stenger, D.C. Draft genome sequence of *Xylella fastidiosa* subsp. *multiplex* strain Griffin-1 from *Quercus rubra* in Georgia. *Genome Announc.* **2013**, *1*, doi:10.1128/genomea.00756-13.
27. Li, W.-B.; Pria Jr, W.; Teixeira, D.; Miranda, V.; Ayres, A.; Franco, C.; Costa, M.; He, C.-X.; Costa, P.; Hartung, J. Coffee leaf scorch caused by a strain of *Xylella fastidiosa* from citrus. *Plant Dis.* **2001**, *85*, 501–505.

28. Giampetruzzi, A.; Chiumenti, M.; Saponari, M.; Donvito, G.; Italiano, A.; Loconsole, G.; Boscia, D.; Cariddi, C.; Martelli, G.P.; Saldarelli, P. Draft genome sequence of the *Xylella fastidiosa* CoDiRO strain. *Genome Announc.* **2015**, *3*, doi:10.1128/genomea.01538-14.
29. Giampetruzzi, A.; Saponari, M.; Almeida, R.P.; Essakhi, S.; Boscia, D.; Loconsole, G.; Saldarelli, P. Complete genome sequence of the olive-infecting strain *Xylella fastidiosa* subsp. *pauca* De Donno. *Genome Announc.* **2017**, *5*, doi:10.1128/genomea.00569-17.
30. Bergsma-Vlami, M.; van de Bilt, J.; Tjou-Tam-Sin, N.; Helderma, C.; Gorkink-Smits, P.; Landman, N.; van Nieuwburg, J.; van Veen, E.; Westenber, M. Assessment of the genetic diversity of *Xylella fastidiosa* in imported ornamental *Coffea arabica* plants. *Plant Pathol.* **2017**, *66*, 1065–1074.
31. Grisard, E.C.; Teixeira, S.M.R.; de Almeida, L.G.P.; Stoco, P.H.; Gerber, A.L.; Talavera-López, C.; Lima, O.C.; Andersson, B.; de Vasconcelos, A.T.R. Trypanosoma cruzi clone Dm28c draft genome sequence. *Genome Announc.* **2014**, *2*, doi:10.1128/genomea.01114-13.
32. Niza, B.; Merfa, M.V.; Alencar, V.C.; Menegidio, F.B.; Nunes, L.R.; Machado, M.A.; Takita, M.A.; de Souza, A.A. Draft genome sequence of 11399, a transformable citrus-pathogenic strain of *Xylella fastidiosa*. *Genome Announc.* **2016**, *4*, doi:10.1128/genomea.01124-16.
33. Simpson, A.J.G.; Reinach, F.d.C.; Arruda, P.; Abreu, F.A.d.; Acencio, M.; Alvarenga, R.; Alves, L.C.; Araya, J.E.; Baia, G.S.; Baptista, C. The genome sequence of the plant pathogen *Xylella fastidiosa*. *Nature* **2000**, *406*, 151–157.
34. da Silva, V.S.; Shida, C.S.; Rodrigues, F.B.; Ribeiro, D.C.; de Souza, A.A.; Coletta-Filho, H.D.; Machado, M.A.; Nunes, L.R.; de Oliveira, R.C. Comparative genomic characterization of citrus-associated *Xylella fastidiosa* strains. *BMC Genom.* **2007**, *8*, 474.
35. Bleve, G.; Marchi, G.; Ranaldi, F.; Gallo, A.; Cimaglia, F.; FRANCESCO LOGRIECO, A.; Mita, G.; Ristori, J.; Surico, G. Molecular characteristics of a strain (Salento-1) of *Xylella fastidiosa* isolated in Apulia (Italy) from an olive plant with the quick decline syndrome. *Phytopathol. Mediterr.* **2016**, *55*, 139–146.
36. Ramazzotti, M.; Cimaglia, F.; Gallo, A.; Ranaldi, F.; Surico, G.; Giovanni, M.; Bleve, G.; Marchi, G. Insights on a founder effect: The case of *Xylella fastidiosa* in the Salento area of Apulia, Italy. *Phytopathol. Mediterr.* **2018**, *57*, 8–25.