Supplementary Material

Race-specific genotypes of *Pseudomonas syringae* pv. tomato are defined by the presence of mobile DNA elements within the genome

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# Supplementary Figures and Tables



**Figure S1.** Core genome phylogenetic tree of 73 genomes taken from the *Pseudomonas syringae* species complex and representative of 10 out of 13 phylogroups according to Berge *et al*. (2014), plus the newly sequenced *P. syringae* pv. tomato DAPP-PG 215. To build the tree, the core genes of the selected genomes are computed. In a following step, alignments of each core gene set are generated using MUSCLE, and the alignments are concatenated to one huge alignment. This alignment of 753,574 AA-residues per genome is then used as input for FastTree software to build the tree. Numbers at the nodes are local support values computed by FastTree using the Shimodaira-Hasegawa test.



**Figure S2.** Dendrogram based on the presence of *avrPto1* in the *Pseudomonas syringae* phylogroup PG01a. Avirulence gene *avrPto1* was identified in 28 genomes out of 49. Dendrogram was constructed with MEGA 11 (Tamura et al., 2021) according to neighbor-joining clustering method (Saitou and Nei, 1987) with gamma distribution (*α* = 5) and 95% cut-off of the site coverage to gaps and missing data partial deletion. Numbers at the nodes are bootstrap values for 1,000 replicates expressed as a percentage value.



**Figure S3.** Dendrogram based on the presence of *avrPtoB* in the *Pseudomonas syringae* phylogroup PG01a. Avirulence gene *avrPtoB* was identified in 46 genomes out of 49. Dendrogram was built with MEGA 11 (Tamura et al., 2021) according to neighbor-joining clustering method (Saitou and Nei, 1987) with gamma distribution (*α* = 5) and 95% cut-off of the site coverage to gaps and missing data partial deletion. Numbers at the nodes are bootstrap values for 1,000 replicates expressed as a percentage value.



**Figure S4.** Concatenated neighbor-joining tree based on *corP*, *corS*, *corR*, and *cfa* (*cfa1*, *cfa2*, *cfa3*, *cfa4*, *cfa5*, *cfa6*, *cfa7*, *cfa8*, *cfa9* and *cfl*) and *cma (cmaA*, *cmaB*, *cmaC*, *cmaD*, *cmaE*, *cmaT*, *cmaU*) cluster gene sequences for all the *Pseudomonas syringae* phylogroup PG01a strains carrying these genes for coronatine synthesis (concatenated alignment length: 90,558 bp). Tree was built with MEGA 11 (Tamura et al., 2021) according to neighbor-joining clustering method (Saitou and Nei, 1987) with gamma distribution (*α* = 5) and 95% cut-off of the site coverage to gaps and missing data partial deletion. Numbers at the nodes are bootstrap values for 1,000 replicates expressed as a percentage value.

**Table S1.** List of genome sequenced *Pseudomonas* strains used in this study.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Strain** | **Origin** | **Host** | **GenBank accession** | **Reference** |
| *P. cerasi* PL58T | PL, 2007 | *Prunus cerasus* | LT222313-LT222319 | Kałużna *et al*., 2016 |
| *P. syringae* CC1557 | FR, 2006 | Snow | CP007014-CP007015 | N.A. |
| *P. syringae* pv. tomato DAPP-PG 215 | IT, 1995 | *Solanum lycopersicum* | GCA\_949769235 | Buonaurio *et al*., 1996 |
| *P. syringae* pv. actinidiae ICMP 9853 | JAP, 1984 | *Actinidia deliciosa* | CP018202-CP018204 | N.A. |
| *P. syringae* pv. tomato DC3000 | UK, 1960 | *Solanum lycopersicum* | AE016853-AE016855 | Buell *et al*., 2003 |
| *P.* syringae pv. tomato B13-200 | CA, 2016 | *Solanum lycopersicum* | CP019871-CP19874 | N.A. |
| *P. syringae* Ps25 |  | *Solanum lycopersicum* | CP034558 | Mazo-Molina *et al*., 2019 |
| *P. amygdali* pv. lachrymans M302278 | US, 1935 | *Cucumis sativus* | AEAM00000000 | Baltrus *et al*., 2011 |
| *P. amygdali* pv. lachrymans 3988 | US, 1935 | *Cucumis sativus* | LGLJ00000000 | N.A. |
| *P. amygdali* ICMP 3918 |  |  | LKBW00000000 | N.A. |
| *P. avellanae* CC1416 | US, 2004 | Epilithon | AVEP00000000 | Baltrus *et al*., 2014 |
| *P. avellanae* JCM 11937 | GRC, 2003 | *Corylus avellana* | BMNO00000000 | N.A. |
| *P. cannabina* ICMP 2823 | HU, 1957 | *Cannabis sativa* | LJPX00000000 | Thakur *et al*., 2016 |
| *P. caricapapayae* CCUG 32775T | BR | *Carica papaya* | VXJY00000000 | N.A. |
| *P. congelans* DSM 14939 |  |  | FNJH00000000 | N.A. |
| *P. coronafaciens* pv. zizaniae ICMP 8959 |  |  | RBPM00000000 | N.A. |
| *P. ficuserectae* ICMP 7849 | JP | *Ficus erecta* | RBSO00000000 | Dillon *et al*., 2019 |
| *P. meliae* CFBP 3225 | JP, 1974 | *Melia azedarach* | JYHE00000000 | Bartoli *et al.*, 2015 |
| *P. savastanoi* 4352 |  | *Olea europaea* | LGKR00000000 | N.A. |
| *Pseudomonas* sp. p4 G1 |  |  | UUPT01000001-UUPT01000064 | N.A. |
| *Pseudomonas* sp. p4 H5 |  |  | UVTG01000001-UVTG01000101 | N.A. |
| *Pseudomonas* sp. p6 G2 |  |  | UVYY01000001-UVYY01000240 | N.A. |
| *P. syringae* CC1559 | FR, 2006 | Snow | AVEG00000000 | Baltrus *et al*., 2014 |
| *P. syringae* CC1630 | US, 2007 | *Onobrychis* sp. | AVED00000000 | Baltrus *et al*., 2014 |
| *P. syringae* ICMP 11292 | NZ, 1991 | *Actinidia deliciosa* | LKGU00000000 | N.A. |
| *P. syringae* KCTC 12500 |  |  | AYTM00000000 | N.A. |
| *P. syringae* group genomosp. 3 strain 9643 | UK, 2012 | *Prunus domestica* | MLET00000000 | N.A. |
| *P. syringae* group genomosp. 3 strain CFBP 3800 |  |  | OLMQ00000000 | N.A. |
| *P. syringae* group genomosp. 3 strain RM1 | UK, 2013 | *Aquilegia vulgaris* | MLEU00000000 | N.A. |
| *P. syringae* pv. actinidifoliorum ICMP18802 | NZ | *Actinidia chinensis* | MUKM00000000 | N.A. |
| *P. syringae* pv. antirrhini ICMP4303 |  |  | LJPT00000000 | N.A. |
| *P. syringae* pv. apii ICMP2814 | US | *Apium graveolens L. var. dulce* | LJPR00000000 | Thakur *et al*., 2016 |
| *P. syringae* pv. avii CFBP 3846 | FR, 1991 | *Prunus avium* | LT963402-LT963407 | Ruinelli *et al.*, 2019 |
| *P. syringae* pv. berberidis ICMP4116 | NZ |  | LJPU00000000 | Thakur *et al*., 2016 |
| *P. syringae* pv. cilantro 0788 9 | US, 1988 | *Coriandrum sativum* | LGLN00000000 | Mott *et al*., 2016 |
| *P. syringae* pv. coriandricola ICMP 9625 | NZ | *Coriandrum sativum* | RBRV00000000 | Dillon *et al*., 2019 |
| *P. syringae* pv. delphinii ICMP 4330 | UK | *Delphinium* sp. | RBQG00000000 | Dillon *et al*., 2019 |
| *P. syringae* pv. maculicola CFBP 1657 | NZ, 1965 | *Brassica oleracea* | JYHH00000000 | Bartoli *et al*., 2015 |
| *P. syringae* pv. maculicola M6 | UK, 1965 | *Brassica oleracea* | LGLC00000000 | N.A. |
| *P. syringae* pv. maculicola 4981 | ZW | *Brassica oleracea* var. *botrytis* | RBOO00000000 | Dillon *et al*., 2019 |
| *P. syringae* pv. maculicola 90 32 | US, 1990 | *Brassica oleracea* | LGLH00000000 | N.A. |
| *P. syringae* pv. maculicola H7608 |  | *Brassica rapa* subsp*. oleifera* | LGLG00000000 | N.A. |
| *P. syringae* pv. maculicola ICMP 11281 | CN | *Brassica rapa* | RBUQ00000000 | Dillon *et al*., 2019 |
| *P. syringae* pv. maculicola ICMP 2744 | UK | *Brassica nigra* | RBQA00000000 | Dillon *et al*., 2019 |
| *P. syringae* pv. maculicola ICMP 3935 | NZ | *Brassica oleracea* var. *botrytis* | LJQR00000000 | Thakur *et al*., 2016 |
| *P. syringae* pv. maculicola M4a | US, 1965 | *Raphanus sativus* | LGLE00000000 | N.A. |
| *P. syringae* pv. persicae NCPPB 2254 | FR, 1969 | *Prunus persica* | ODAM00000000 | Ruinelli *et al*., 2019 |
| *P. syringae* pv. ribicola ICMP 3883 |  | *Ribes aureum* | RBNR00000000 | Dillon *et al*., 2019 |
| *P. syringae* pv. spinaceae ICMP 16928 | JP | *Spinacia oleracea* | RBTF00000000 | Dillon *et al*., 2019 |
| *P. syringae* pv. syringae B728a | US, 1987 | *Phaseolus vulgaris* | CP000075 | Feil *et al*., 2005 |
| *P. syringae* pv. syringae PD2766 | US | *Actinidia deliciosa* | LKEM00000000 | N.A. |
| *P. syringae* pv. tagetis ICMP 4092 | UK | *Tagetes erecta* | RBQC00000000 | Dillon *et al*., 2019 |
| *P. syringae* pv. theae ICMP 3923 | JP, 1970 | *Camellia sinensis* | LJRU00000000 | Thakur *et al*., 2016 |
| *P. syringae* pv. tomato K40 | USA, 2005 | *Solanum lycopersicum* | SAMN0000000 | N.A. |
| *P. syringae* pv. tomato Max13 | FR | *Solanum lycopersicum* | ADFZ00000000 | N.A. |
| *P. syringae* pv. tomato NCPPB1108 | UK, 1961 | *Solanum lycopersicum* | ADGA00000000 | N.A. |
| *P. syringae* pv. tomato T1 | 1986 | *Solanum lycopersicum* | ABSM00000000 | Almeida *et al*., 2009 |
| *P. syringae* pv. tomato 407 | US. 2004 | *Solanum lycopersicum* | LNKZ00000000 | Thapa and Coaker, 2016 |
| *P. syringae* pv. tomato A9 | US. 2005 | *Solanum lycopersicum* | LNKY00000000 | Thapa and Coaker, 2016 |
| *P. syringae* pv. tomato BRIP38746 | AU, 1973 | *Solanum lycopersicum* | SNVG00000000 | Griffin *et al.*, 2019 |
| *P. syringae* pv. tomato BRIP66796 | AU, 2015 | *Solanum lycopersicum* | SNVF00000000 | Griffin *et al.*, 2020 |
| *P. syringae* pv. tomato BRIP66810 | AU, 2015 | *Solanum lycopersicum* | SNVE00000000 | Griffin *et al.*, 2021 |
| *P. syringae* pv. tomato ICMP 2841 | DK | *Solanum lycopersicum* | RBUK00000000 | Dillon *et al*., 2019 |
| *P. syringae* pv. tomato ICMP 2844 | UK, 1960 | *Solanum lycopersicum* | LJRN00000000 | Thakur *et al*., 2016 |
| *P. syringae* pv. tomato ICMP 4263 | NZ | *Solanum lycopersicum* | RBRJ00000000 | N.A. |
| *P. syringae* pv. tomato ICMP 7230 | NZ | *Solanum lycopersicum* | RBRI00000000 | N.A. |
| *P. syringae* pv. tomato NYS-T1 | US, 2009 | *Solanum lycopersicum* | JRRA00000000 | Jones *et al.*, 2015 |
| *P. syringae* pv. tomato PT23 |  | *Solanum lycopersicum* | MSDS00000000 | Meaden and Koskella, 2017 |
| *P. syringae* pv. tomato delta IVIX |  | *Solanum lycopersicum* | CP047072 | N.A. |
| *P. syringae* pv. tomato delta VI |  | *Solanum lycopersicum* | CP047071 | N.A. |
| *P. syringae* pv. tomato delta X |  | *Solanum lycopersicum* | CP047073 | N.A. |
| *P. syringae* A7386 |  | *Cucumis sativus* | RBOB00000000 | Dillon *et al*., 2019 |
| *P. syringae* BS2900 |  |  | FNPP00000000 | N.A. |
| *P. syringae* PDD 32b 74 | FR, 2005 | air | MTSA00000000 | Besaury *et al*., 2017 |

**Table S2.** Genomic islands and prophages identified in *Pseudomonas syringae* pv. tomato DAPP-PG 215. Classification of identified prophages into intact (score > 90), questionable (score 70-90), and incomplete (score < 70) is done by PHASTER based on the presence of phage-like genes, size, and similarity to known phages.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Name** | **Location** | **Start (bp)** | **End (bp)** | **Size (bp)** | **GC %** | **CDS** | **Note** |
| GI-1 | Chromosome | 134144 | 139563 | 5419 | 52.85 | 7 |  |
| GI-2 | Chromosome | 228917 | 233808 | 4891 | 48.04 | 6 |  |
| GI-3 | Chromosome | 237698 | 249518 | 11820 | 54.02 | 16 |  |
| GI-4 | Chromosome | 252270 | 258286 | 6016 | 52.98 | 10 | *eriC, crcB* |
| GI-5 | Chromosome | 267958 | 270788 | 2830 | 52.98 | 5 |  |
| GI-6 | Chromosome | 275358 | 279146 | 3788 | 55.1 | 5 | *arsC, arsN1* |
| GI-7 | Chromosome | 474111 | 481728 | 7617 | 54.27 | 7 |  |
| GI-8 | Chromosome | 803316 | 805525 | 2209 | 53.81 | 4 |  |
| GI-9 | Chromosome | 808252 | 811575 | 3323 | 53.19 | 8 |  |
| GI-10 | Chromosome | 825986 | 829982 | 3996 | 51.96 | 4 | *hopD1, hopQ1-1* |
| GI-11 | Chromosome | 864351 | 867627 | 3276 | 47.27 | 3 | *avrA* |
| GI-12 | Chromosome | 882720 | 894919 | 12199 | 53.8 | 16 |  |
| GI-13 | Chromosome | 899039 | 906516 | 7477 | 50.37 | 10 | *hop-T1* |
| GI-14 | Chromosome | 907473 | 913151 | 5678 | 46.9 | 9 |  |
| GI-15 | Chromosome | 1124514 | 1127439 | 2925 | 47.37 | 3 |  |
| GI-16 | Chromosome | 1464536 | 1472851 | 8315 | 51.81 | 11 | *hopF2* |
| GI-17 | Chromosome | 1506800 | 1511810 | 5010 | 51.15 | 10 |  |
| GI-18 | Chromosome | 1736511 | 1740081 | 3570 | 54.43 | 6 |  |
| GI-19 | Chromosome | 1741976 | 1748489 | 6513 | 53.88 | 8 |  |
| GI-20 | Chromosome | 1771702 | 1778060 | 6358 | 54.53 | 8 |  |
| GI-21 | Chromosome | 1782695 | 1787242 | 4547 | 49.75 | 6 |  |
| GI-22 | Chromosome | 1818355 | 1833738 | 15383 | 48.15 | 5 |  |
| GI-23 | Chromosome | 1818355 | 1833738 | 15383 | 53.9 | 19 | *hopC1* |
| GI-24 | Chromosome | 1960161 | 1963133 | 2972 | 51.57 | 5 |  |
| GI-25 | Chromosome | 1965185 | 1973037 | 7852 | 47.62 | 7 |  |
| GI-26 | Chromosome | 2791500 | 2793770 | 2270 | 52.66 | 8 |  |
| GI-27 | Chromosome | 2866203 | 2870908 | 4705 | 48.13 | 8 |  |
| GI-28 | Chromosome | 2967638 | 2974386 | 6748 | 55.02 | 9 |  |
| GI-29 | Chromosome | 3880645 | 3885730 | 5085 | 46.48 | 5 |  |
| GI-30 | Chromosome | 3973090 | 3976931 | 3841 | 56.43 | 9 |  |
| GI-31 | Chromosome | 4397511 | 4403680 | 6169 | 51.04 | 5 |  |
| GI-32 | Chromosome | 4410176 | 4414526 | 4350 | 49.66 | 9 | *hopAF1* |
| GI-33 | Chromosome | 4495231 | 4499538 | 4307 | 52.84 | 6 |  |
| GI-34 | Chromosome | 4650506 | 4653339 | 2833 | 46.64 | 6 |  |
| GI-35 | Chromosome | 5074853 | 5080257 | 5404 | 53.37 | 8 | *hopT1-2, hopS* |
| GI-36 | Chromosome | 5136274 | 5138958 | 2684 | 52.24 | 5 |  |
| GI-37 | Chromosome | 5150450 | 5153919 | 3469 | 49.9 | 5 |  |
| GI-38 | Chromosome | 5465197 | 5467466 | 2269 | 52.06 | 4 |  |
| GI-39 | Chromosome | 5494967 | 5500153 | 5186 | 47.69 | 7 |  |
| GI-40 | Chromosome | 5504041 | 5509625 | 5584 | 54.02 | 9 |  |
| GI-41 | Chromosome | 5804073 | 5815124 | 11051 | 51.1 | 10 |  |
| GI-42 | Chromosome | 5850075 | 5853387 | 3312 | 46.12 | 6 |  |
| GI-43 | Chromosome | 5890460 | 5897338 | 6878 | 51.17 | 6 |  |
| GI-44 | Chromosome | 5958882 | 5964005 | 5123 | 50.32 | 10 |  |
| GI-45 | Plasmid p107 | 75700 | 70283 | 5417 | 49.26 | 9 |  |
| GI-46 | Plasmid p81 | 9452 | 21061 | 11609 | 51.72 | 11 | *avrD*, *hopD1*, *hopQ1-1* |
| GI-47 | Plasmid p81 | 22086 | 27535 | 5449 | 51.7 | 9 |  |
| PR-1 | Chromosome | 481728 | 489809 | 8081 | 58.24 | 6 | incomplete |
| PR-2 | Chromosome | 525093 | 543650 | 18557 | 59.64 | 23 | intact |
| PR-3 | Chromosome | 1111403 | 1119541 | 8138 | 53.89 | 8 | incomplete |
| PR-4 | Chromosome | 1463760 | 1489507 | 25747 | 55.54 | 13 | incomplete |
| PR-5 | Chromosome | 1480861 | 1505863 | 25002 | 59.74 | 30 | intact |
| PR-6 | Chromosome | 1728315 | 1739514 | 11199 | 56.27 | 10 | incomplete |
| PR-7 | Chromosome | 3563961 | 3622352 | 58391 | 58.58 | 64 | intact |
| PR-8 | Chromosome | 3871504 | 3884578 | 13074 | 51.52 | 14 | incomplete |
| PR-9 | Chromosome | 3912386 | 3977686 | 65300 | 57.74 | 94 | intact, *avrPto1* |
| PR-10 | Chromosome | 4340000 | 4346660 | 6660 | 58.73 | 7 | incomplete |
| PR-11 | Chromosome | 5806461 | 5852818 | 46357 | 56.36 | 49 | intact |
| PR-12 | Chromosome | 5852865 | 5887730 | 34865 | 58.59 | 42 | questionable |
| PR-13 | Plasmid p107 | 15075 | 21697 | 6622 | 54.46 | 7 | questionable |
| PR-14 | Plasmid p107 | 54234 | 65603 | 11369 | 55.07 | 16 | incomplete |

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