

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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1 Supplementary Figures and Tables

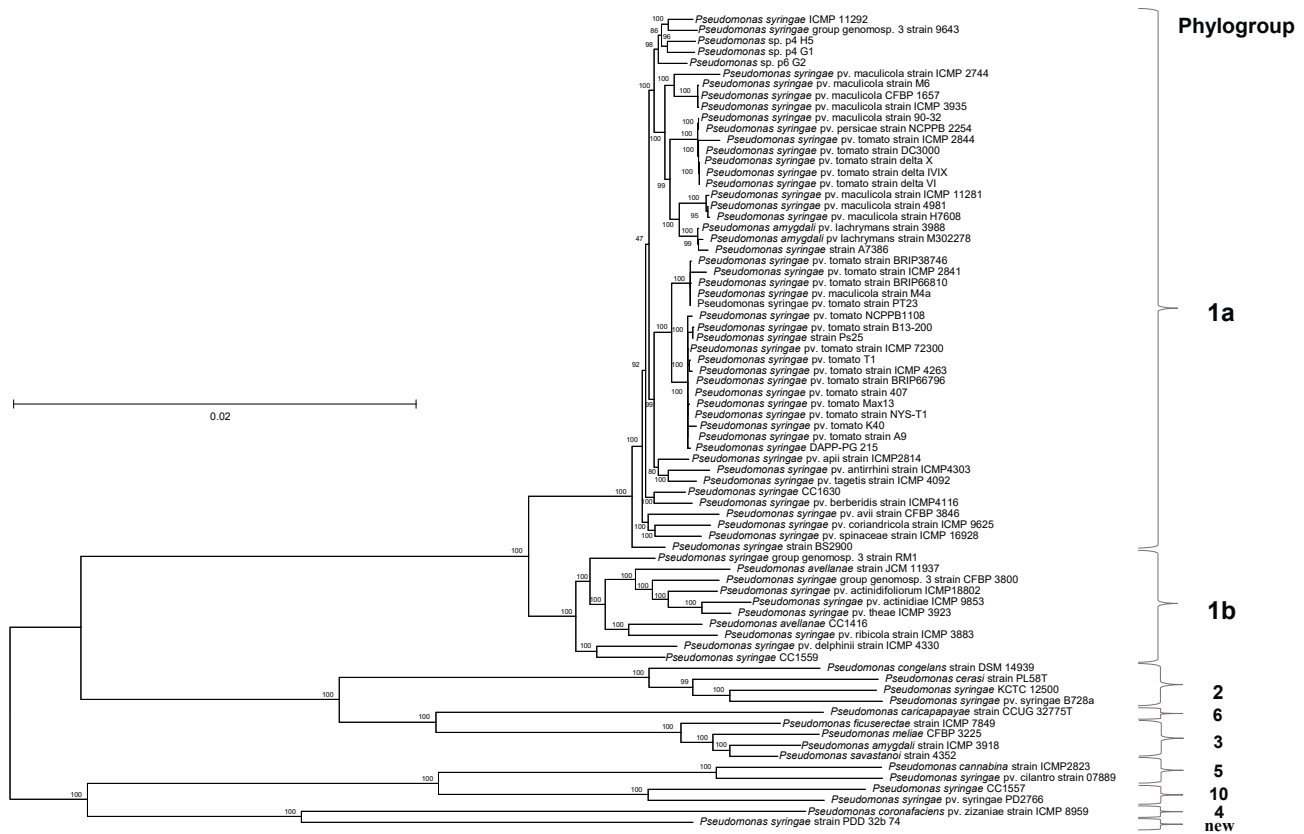


Figure S1. Core genome phylogenetic tree of 73 genomes taken from the *Pseudomonas syringae* species complex and representative of 10 out of 13 phylogroups according to Berge *et al.* (2014), plus the newly sequenced *P. syringae* pv. tomato DAPP-PG 215. To build the tree, the core genes of the selected 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.

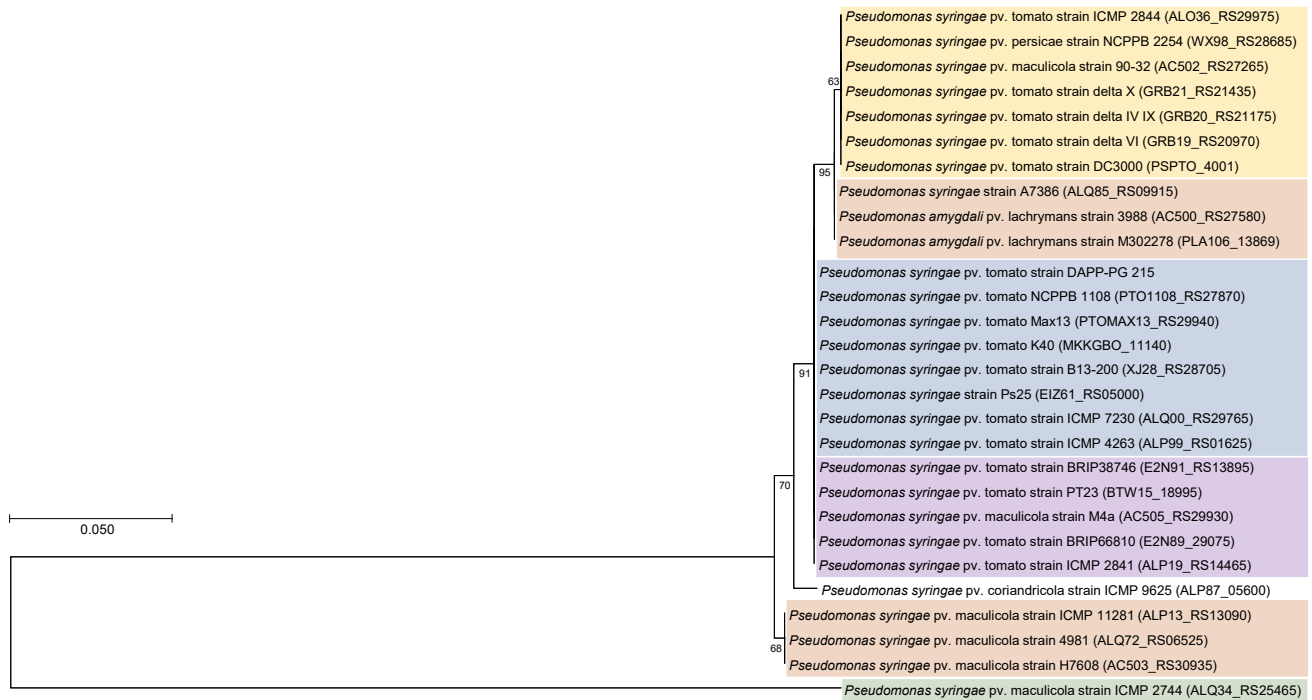


Figure S2. Dendrogram based on the presence of *avrPtoI* in the *Pseudomonas syringae* phylogroup PG01a. Avirulence gene *avrPtoI* was identified in 28 genomes out of 49. Dendrogram was constructed with MEGA 11 (Tamura et al., 2021) according to neighbor-joining clustering method (Saitou and Nei, 1987) with gamma distribution ($\alpha = 5$) 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.

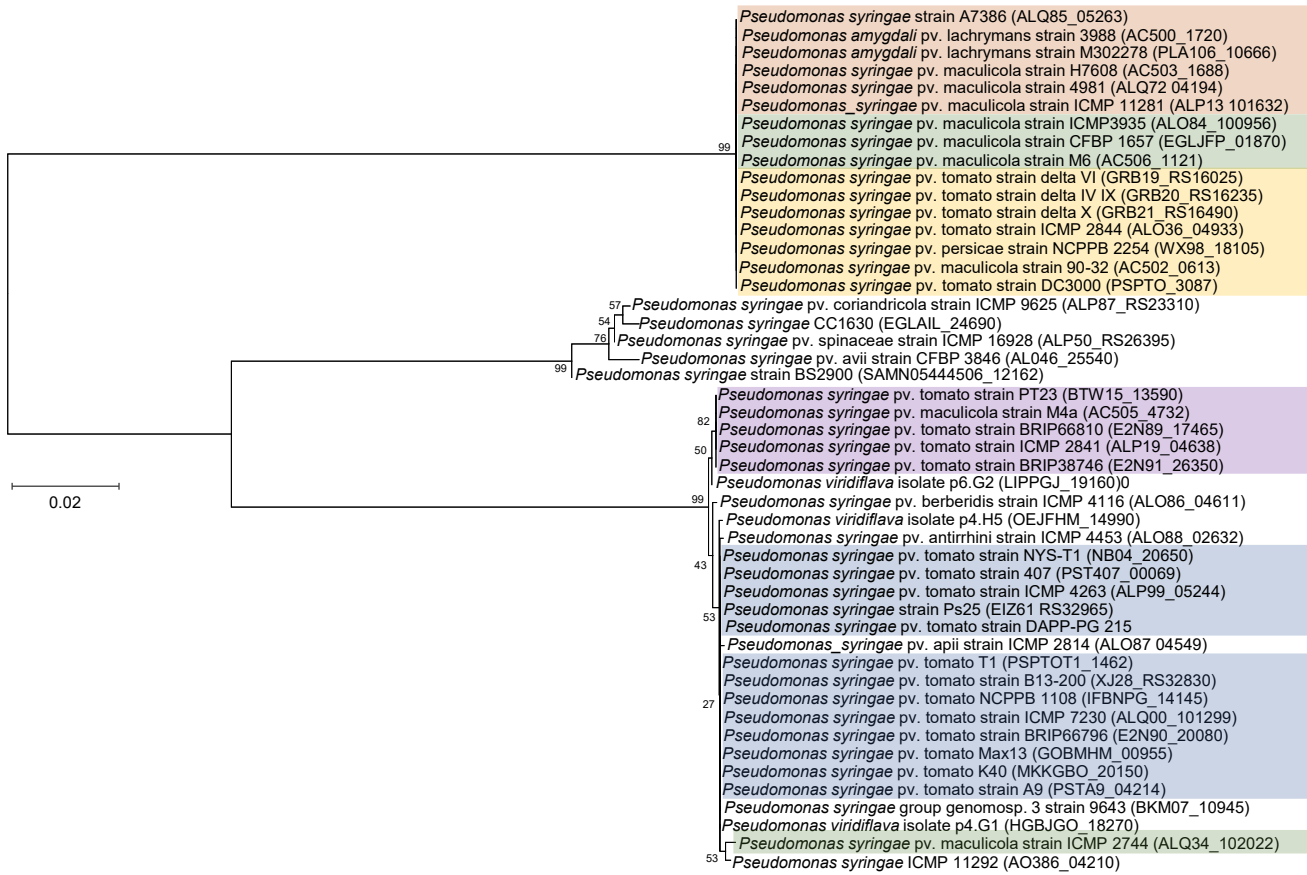


Figure S3. Dendrogram based on the presence of *avrPtoB* in the *Pseudomonas syringae* phylogroup PG01a. Avirulence gene *avrPtoB* was identified in 46 genomes out of 49. Dendrogram was built with MEGA 11 (Tamura et al., 2021) according to neighbor-joining clustering method (Saitou and Nei, 1987) with gamma distribution ($\alpha = 5$) 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.

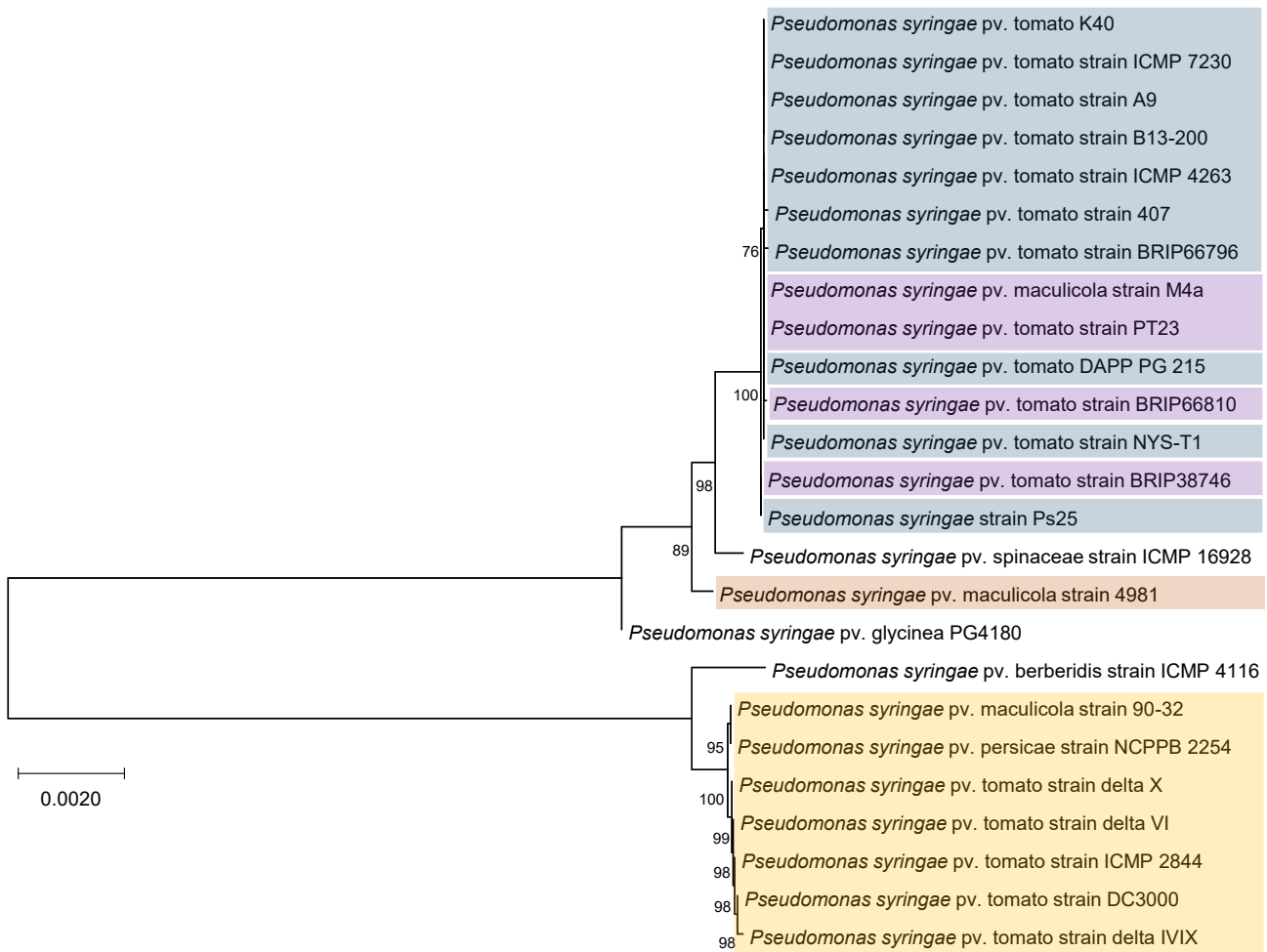


Figure S4. Concatenated neighbor-joining tree based on *corP*, *corS*, *corR*, and *cfa* (*cfa1*, *cfa2*, *cfa3*, *cfa4*, *cfa5*, *cfa6*, *cfa7*, *cfa8*, *cfa9* and *cfl*) and *cma* (*cmaA*, *cmaB*, *cmaC*, *cmaD*, *cmaE*, *cmaT*, *cmaU*) cluster gene sequences for all the *Pseudomonas syringae* phylogroup 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 ($\alpha = 5$) 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
<i>P. cerasi</i> PL58 ^T	PL, 2007	<i>Prunus cerasus</i>	LT222313-LT222319	Kalužna <i>et al.</i> , 2016
<i>P. syringae</i> CC1557	FR, 2006	Snow	CP007014-CP007015	N.A.
<i>P. syringae</i> pv. tomato DAPP-PG 215	IT, 1995	<i>Solanum lycopersicum</i>	GCA_949769235	Buonaurio <i>et al.</i> , 1996
<i>P. syringae</i> pv. actinidiae ICMP 9853	JAP, 1984	<i>Actinidia deliciosa</i>	CP018202-CP018204	N.A.
<i>P. syringae</i> pv. tomato DC3000	UK, 1960	<i>Solanum lycopersicum</i>	AE016853-AE016855	Buell <i>et al.</i> , 2003
<i>P. syringae</i> pv. tomato B13-200	CA, 2016	<i>Solanum lycopersicum</i>	CP019871-CP19874	N.A.
<i>P. syringae</i> Ps25		<i>Solanum lycopersicum</i>	CP034558	Mazo-Molina <i>et al.</i> , 2019
<i>P. amygdali</i> pv. lachrymans M302278	US, 1935	<i>Cucumis sativus</i>	AEAM000000000	Baltrus <i>et al.</i> , 2011
<i>P. amygdali</i> pv. lachrymans 3988	US, 1935	<i>Cucumis sativus</i>	LGLJ000000000	N.A.
<i>P. amygdali</i> ICMP 3918			LKBW000000000	N.A.
<i>P. avellanae</i> CC1416	US, 2004	Epilithon	AVEP000000000	Baltrus <i>et al.</i> , 2014
<i>P. avellanae</i> JCM 11937	GRC, 2003	<i>Corylus avellana</i>	BMNO000000000	N.A.
<i>P. cannabina</i> ICMP 2823	HU, 1957	<i>Cannabis sativa</i>	LJPX000000000	Thakur <i>et al.</i> , 2016
<i>P. caricapapayae</i> CCUG 32775 ^T	BR	<i>Carica papaya</i>	VXJY000000000	N.A.
<i>P. congelans</i> DSM 14939			FNJH000000000	N.A.
<i>P. coronafaciens</i> pv. zizaniae ICMP 8959			RBPM000000000	N.A.
<i>P. ficuserectae</i> ICMP 7849	JP	<i>Ficus erecta</i>	RBSO000000000	Dillon <i>et al.</i> , 2019
<i>P. meliae</i> CFBP 3225	JP, 1974	<i>Melia azedarach</i>	JYHE000000000	Bartoli <i>et al.</i> , 2015
<i>P. savastanoi</i> 4352		<i>Olea europaea</i>	LGKR000000000	N.A.
<i>Pseudomonas</i> sp. p4 G1			UUPT01000001-UUPT01000064	N.A.
<i>Pseudomonas</i> sp. p4 H5			UVTG01000001-UVTG01000101	N.A.
<i>Pseudomonas</i> sp. p6 G2			UVYY01000001-UVYY01000240	N.A.
<i>P. syringae</i> CC1559	FR, 2006	Snow	AVEG000000000	Baltrus <i>et al.</i> , 2014
<i>P. syringae</i> CC1630	US, 2007	<i>Onobrychis</i> sp.	AVED000000000	Baltrus <i>et al.</i> , 2014
<i>P. syringae</i> ICMP 11292	NZ, 1991	<i>Actinidia deliciosa</i>	LKGU000000000	N.A.
<i>P. syringae</i> KCTC 12500			AYTM000000000	N.A.
<i>P. syringae</i> group genomosp. 3 strain 9643	UK, 2012	<i>Prunus domestica</i>	MLET000000000	N.A.
<i>P. syringae</i> group genomosp. 3 strain CFBP 3800			OLMQ000000000	N.A.
<i>P. syringae</i> group genomosp. 3 strain RM1	UK, 2013	<i>Aquilegia vulgaris</i>	MLEU000000000	N.A.
<i>P. syringae</i> pv. actinidiflorum ICMP18802	NZ	<i>Actinidia chinensis</i>	MUKM000000000	N.A.
<i>P. syringae</i> pv. antirrhini ICMP4303			LJPT000000000	N.A.
<i>P. syringae</i> pv. apii ICMP2814	US	<i>Apium graveolens</i> L. var. dulce	LJPR000000000	Thakur <i>et al.</i> , 2016
<i>P. syringae</i> pv. avii CFBP 3846	FR, 1991	<i>Prunus avium</i>	LT963402-LT963407	Ruinelli <i>et al.</i> , 2019
<i>P. syringae</i> pv. berberidis ICMP4116	NZ		LJPU000000000	Thakur <i>et al.</i> , 2016
<i>P. syringae</i> pv. cilantro 0788 9	US, 1988	<i>Coriandrum sativum</i>	LGLN000000000	Mott <i>et al.</i> , 2016
<i>P. syringae</i> pv. coriandricola ICMP 9625	NZ	<i>Coriandrum sativum</i>	RBRV000000000	Dillon <i>et al.</i> , 2019
<i>P. syringae</i> pv. delphinii ICMP 4330	UK	<i>Delphinium</i> sp.	RBQG000000000	Dillon <i>et al.</i> , 2019
<i>P. syringae</i> pv. maculicola CFBP 1657	NZ, 1965	<i>Brassica oleracea</i>	JYHH000000000	Bartoli <i>et al.</i> , 2015
<i>P. syringae</i> pv. maculicola M6	UK, 1965	<i>Brassica oleracea</i>	LGLC000000000	N.A.
<i>P. syringae</i> pv. maculicola 4981	ZW	<i>Brassica oleracea</i> var. botrytis	RBO000000000	Dillon <i>et al.</i> , 2019

<i>P. syringae</i> pv. <i>maculicola</i> 90 32	US, 1990	<i>Brassica oleracea</i>	LGLH00000000	N.A.
<i>P. syringae</i> pv. <i>maculicola</i> H7608		<i>Brassica rapa</i> subsp. <i>oleifera</i>	LGLG00000000	N.A.
<i>P. syringae</i> pv. <i>maculicola</i> ICMP 11281	CN	<i>Brassica rapa</i>	RBQU00000000	Dillon <i>et al.</i> , 2019
<i>P. syringae</i> pv. <i>maculicola</i> ICMP 2744	UK	<i>Brassica nigra</i>	RBQA00000000	Dillon <i>et al.</i> , 2019
<i>P. syringae</i> pv. <i>maculicola</i> ICMP 3935	NZ	<i>Brassica oleracea</i> var. <i>botrytis</i>	LJQR00000000	Thakur <i>et al.</i> , 2016
<i>P. syringae</i> pv. <i>maculicola</i> M4a	US, 1965	<i>Raphanus sativus</i>	LGLE00000000	N.A.
<i>P. syringae</i> pv. <i>persicae</i> NCPPB 2254	FR, 1969	<i>Prunus persica</i>	ODAM00000000	Ruinelli <i>et al.</i> , 2019
<i>P. syringae</i> pv. <i>ribicola</i> ICMP 3883		<i>Ribes aureum</i>	RBNR00000000	Dillon <i>et al.</i> , 2019
<i>P. syringae</i> pv. <i>spinacea</i> ICMP 16928	JP	<i>Spinacia oleracea</i>	RBTF00000000	Dillon <i>et al.</i> , 2019
<i>P. syringae</i> pv. <i>syringae</i> B728a	US, 1987	<i>Phaseolus vulgaris</i>	CP000075	Feil <i>et al.</i> , 2005
<i>P. syringae</i> pv. <i>syringae</i> PD2766	US	<i>Actinidia deliciosa</i>	LKEM00000000	N.A.
<i>P. syringae</i> pv. <i>tagetis</i> ICMP 4092	UK	<i>Tagetes erecta</i>	RBQC00000000	Dillon <i>et al.</i> , 2019
<i>P. syringae</i> pv. <i>theae</i> ICMP 3923	JP, 1970	<i>Camellia sinensis</i>	LJRU00000000	Thakur <i>et al.</i> , 2016
<i>P. syringae</i> pv. <i>tomato</i> K40	USA, 2005	<i>Solanum lycopersicum</i>	SAMN00000000	N.A.
<i>P. syringae</i> pv. <i>tomato</i> Max13	FR	<i>Solanum lycopersicum</i>	ADFZ00000000	N.A.
<i>P. syringae</i> pv. <i>tomato</i> NCPB1108	UK, 1961	<i>Solanum lycopersicum</i>	ADGA00000000	N.A.
<i>P. syringae</i> pv. <i>tomato</i> T1	1986	<i>Solanum lycopersicum</i>	ABSM00000000	Almeida <i>et al.</i> , 2009
<i>P. syringae</i> pv. <i>tomato</i> 407	US, 2004	<i>Solanum lycopersicum</i>	LNKZ00000000	Thapa and Coaker, 2016
<i>P. syringae</i> pv. <i>tomato</i> A9	US, 2005	<i>Solanum lycopersicum</i>	LNKY00000000	Thapa and Coaker, 2016
<i>P. syringae</i> pv. <i>tomato</i> BRIP38746	AU, 1973	<i>Solanum lycopersicum</i>	SNVG00000000	Griffin <i>et al.</i> , 2019
<i>P. syringae</i> pv. <i>tomato</i> BRIP66796	AU, 2015	<i>Solanum lycopersicum</i>	SNVF00000000	Griffin <i>et al.</i> , 2020
<i>P. syringae</i> pv. <i>tomato</i> BRIP66810	AU, 2015	<i>Solanum lycopersicum</i>	SNVE00000000	Griffin <i>et al.</i> , 2021
<i>P. syringae</i> pv. <i>tomato</i> ICMP 2841	DK	<i>Solanum lycopersicum</i>	RBUK00000000	Dillon <i>et al.</i> , 2019
<i>P. syringae</i> pv. <i>tomato</i> ICMP 2844	UK, 1960	<i>Solanum lycopersicum</i>	LJRN00000000	Thakur <i>et al.</i> , 2016
<i>P. syringae</i> pv. <i>tomato</i> ICMP 4263	NZ	<i>Solanum lycopersicum</i>	RBRJ00000000	N.A.
<i>P. syringae</i> pv. <i>tomato</i> ICMP 7230	NZ	<i>Solanum lycopersicum</i>	RBRI00000000	N.A.
<i>P. syringae</i> pv. <i>tomato</i> NYS-T1	US, 2009	<i>Solanum lycopersicum</i>	JRRA00000000	Jones <i>et al.</i> , 2015
<i>P. syringae</i> pv. <i>tomato</i> PT23		<i>Solanum lycopersicum</i>	MSDS00000000	Meaden and Koskella, 2017
<i>P. syringae</i> pv. <i>tomato</i> delta IVIX		<i>Solanum lycopersicum</i>	CP047072	N.A.
<i>P. syringae</i> pv. <i>tomato</i> delta VI		<i>Solanum lycopersicum</i>	CP047071	N.A.
<i>P. syringae</i> pv. <i>tomato</i> delta X		<i>Solanum lycopersicum</i>	CP047073	N.A.
<i>P. syringae</i> A7386		<i>Cucumis sativus</i>	RBOB00000000	Dillon <i>et al.</i> , 2019
<i>P. syringae</i> BS2900			FNPP00000000	N.A.
<i>P. syringae</i> PDD 32b 74	FR, 2005	air	MTSA00000000	Besaury <i>et al.</i> , 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	<i>eriC, crcB</i>
GI-5	Chromosome	267958	270788	2830	52.98	5	
GI-6	Chromosome	275358	279146	3788	55.1	5	<i>arsC, arsNI</i>
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	<i>hopD1, hopQ1-1</i>
GI-11	Chromosome	864351	867627	3276	47.27	3	<i>avrA</i>
GI-12	Chromosome	882720	894919	12199	53.8	16	
GI-13	Chromosome	899039	906516	7477	50.37	10	<i>hop-T1</i>
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	<i>hopF2</i>
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	<i>hopC1</i>
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	<i>hopAFI</i>
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	<i>hopT1-2, hopS</i>
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	<i>avrD, hopD1, hopQ1-1</i>
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, <i>avrPtoI</i>
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

2 References

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