SUPPLEMENTARY INFORMATION

Pathogen profile

Pseudomonas savastanoi pv. savastanoi: Some like it knot

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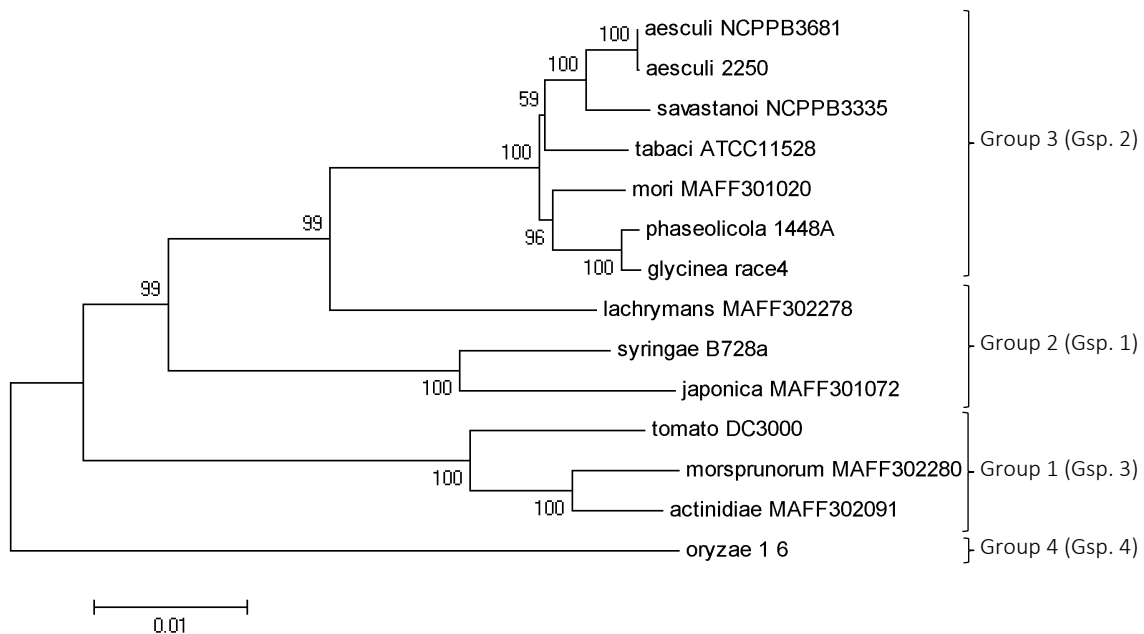http://onlinelibrary.wiley.com/wol1/doi/10.1111/j.1364-3703.2012.00816.x/suppinfo

Fig. S1 Evolutionary relationships of *P. savastanoi* pv. savastanoi and selected *P. syringae* pathovars. Tree was constructed by multilocus sequence analysis using a concatenated data set (exactly 12000 nt) of *acnB, fruK, gapA, gltA, gyrB, pgi, recA* and *rpoD* genes. Phylogenetic groups 1, 2, 3 and 4 (Sarkar & Guttman, 2004, Studholme, 2011) correspond to genomospecies (Gsp) 3, 1, 2 and 4 (Gardan et al., 1999), respectively. Sequence alignment using Muscle, determination of the optimal nucleotide substitution model and phylogenetic tree construction were done using MEGA5 (Tamura *et al.*, 2011); all positions containing gaps and missing data were eliminated using the option of complete deletion. Bootstrap values (1,000 repetitions) are shown on branches. Similar or identical topologies were obtained by maximum likelihood. The scale bar represents nucleotide substitutions per site.

Table S1 Primers used for the detection of *Pseudomonas savastanoi* pv. savastanoi.

Table S2 Comparison of the deduced products of *iaaM*-1 (PSA3335_1475) and *iaaH*-1 (PSA3335_1476), from *Pseudomonas savastanoi* pv. savastanoi NCPPB 3335, with their homologues in selected organisms.

Table S3 Accession numbers and coordinates of the nucleotide sequences used for the construction of the neighbour-joining tree shown in Fig. 2.

Fig. S1 Evolutionary relationships of *P. savastanoi* pv. savastanoi and selected *P. syringae* pathovars. Tree was constructed by multilocus sequence analysis using a concatenated data set (exactly 12000 nt) of *acnB, fruK, gapA, gltA, gyrB, pgi, recA* and *rpoD* genes. Phylogenetic groups 1, 2, 3 and 4 (Sarkar & Guttman, 2004, Studholme, 2011) correspond to genomospecies (Gsp) 3, 1, 2 and 4 (Gardan et al., 1999), respectively. Sequence alignment using Muscle, determination of the optimal nucleotide substitution model and phylogenetic tree construction were done using MEGA5 (Tamura *et al.*, 2011); all positions containing gaps and missing data were eliminated using the option of complete deletion. Bootstrap values (1,000 repetitions) are shown on branches. Similar or identical topologies were obtained by maximum likelihood. The scale bar represents nucleotide substitutions per site.

Table S1 Primers used for the detection of *P. savastanoi* pv. savastanoi

Reference	Type of PCR	Target	Primer pair	Sequence (5' → 3')	Amplicon size (nt)	Observations
(Penyalver *et al.,* 2000, *Appl. Environ. Microbiol.* 66, 2673-2677)	Conventional	*iaaL* gene	IAALF IAALR	GGCACCAGCGGCAACATCAA CGCCCTCGGAACTGCCATAC	454	

(Bertolini *et al.,* 2003, *Phytopathology*, 93, 286-292)	Nested	*iaaL* gene	External pair
			  IAALF-IAALR
			Internal pair
			  IAALN1
			  IAALN2
				See above
				
				CTC CCT CTC CAA CGT CTT C
				GCC TGA TGA TTT TCT TCT G
					338	Nested PCR in a single closed tube; sensitivity is highly increased by a dot blot hybridization step.

(Tegli *et al.,* 2010, *BMC Microbiol.* 10: 156-169)	Conventional	Chromosomal DNA; possible intergenic region	PsvF PsvR	GGCGATGTTCTCAGCGGATTTG GATCAAGTGTCCAAGGAAGTGAAGG	388	Authors designed primer pairs for the differential identification of pathovars fraxini, nerii and savastanoi.
	Real time		PsvRT-F PsvRT-R PsvRT-P	CGGATTTGGTTTGCGGGGTA AATGGGGTGACACTAAAAATTGTGAA (HEX)CTCGTGCGATCTAAACAGCCGT AGC(BHQ-1)	298	

Table S2 Comparison of the deduced products of *iaaM-1* (PSA3335_1475) and *iaaH-1* (PSA3335_1476), from *Pseudomonas savastanoi* pv. savastanoi NCPPB 3335, with their homologs in selected organisms[a]

Strain	iaaM-1			iaaH-1		
	Prot. Acc. number	Id.	Similarity	Prot. Acc. number	Id.	Similarity
P. savastanoi pv. nerii EW2009	AAA25852	100.0	100.0	AAA25853	97.6	97.6
P. syringae pv. syringae B728a	AAY36585	94.4	97.7	AAY36586	92.6	95.5
P. savastanoi pv. savastanoi NCPPB 3335 (*iaaM-2* and *iaaH-2*)	(-) [b]			EFI00888	92.4	95.3
P. syringae pv. aceris MAFF302273	EGH68944	94.4	97.7	EGH68943	92.2	95.5
P. syringae pv. glycinea race 4	AEGH01000077 (1829-3502) [c]	91.9	95.0	EFW83486	91.9	94.6
P. syringae pv. glycinea B076	AEGG01000022 (403-2076) [c]	91.9	95.0	EFW81447	91.9	94.6
Dickeya dadantii 3937	ADM96599	66.2	77.4	ADM96600	58.1	73.1
Burkholderia phymatum STM815	ACC76653	69.0	79.2	ACC76652	55.6	72.6
Pantoea agglomerans pv. gypsophilae PD713	AAC17187	69.1	80.1	AAC17186	55.2	68.7
P. chlororaphis subsp. chlororaphis GP72	AHAY01000223 (4470-6176) [c]	55.8	72.5	AHAY01000223 (4430-3102) [c]	42.7	57.6
Agrobacterium tumefaciens C58	AAD30489	36.8	50.9	AAD30488	30.1	45.3

[a] Global alignments were done using the EMBOSS Needle Protein Sequence Alignment interface (http://www.ebi.ac.uk/Tools/psa/emboss_needle/); figures represent percentage of amino acid identity (Id.) and similarity.
[b] *iaaM-2* (PSA3335_1017) is a pseudogene.
[c] In these cases, proteins were deduced from the corresponding nucleotide contig sequences, with figures in parenthesis indicating the CDS coordinates.

Table S3 Accession numbers and coordinates of the nucleotide sequences used for the construction of the NJ tree shown in Figure 2

Strain	Gsp.[a]	Accession number	Coordinates[b]
P. cannabina pv.			
alisalensis ES4326 [c]	9	AEAK01000502	41622-42809
P. syringae pv.			
actinidiae CRA-FRU 8.43	8	AFTG01000160	3312-4499
actinidiae MAFF302091	8	AEAL01000291	3491-4678
actinidiae NCPPB 3739	8	AFTH01000772	5774-6961
actinidiae NCPPB 3871	8	AFTF01000420	5775-6962
aesculi 2250	2	ACXT01000531	14852-16039
aesculi NCPPB 3681 (0893_23) [d]	2	ACXS01000384	3051-4238
glycinea B076	2	AEGG01000003	5442-6577
glycinea race 4	2	ADWY01001392	1-1133
lachrymans MAFF302278	3	AEAM01000068	15292-16479
mori MAFF301020	2	AEAG01001010	58-1245
morsprunorum MAFF302280	uncertain	AEAE01000140	20038-21225
oryzae 1_6	4	ABZR01000421	2353-3540
tabaci ATCC 11528	2	ACHU02000160	9306-10493
theae NCPPB 2598	8	AGNN01000139	1477-2664
tomato DC3000	3	NC_004578	406323-407510
tomato K40	3	ADFY01000268	14995-16182
tomato Max13	3	ADFZ01000040	39074-40261
tomato NCPPB 1108	3	ADGA01000161	20655-21842
tomato T1	3	ABSM01000063	2149-3318
P. savastanoi pv.			
nerii EW2009	2	M35373	1100-2287
savastanoi NCPPB 3335 iaaL1	2	GG774623	112-1286
savastanoi NCPPB 3335 iaaL2	2	NZ_GG774681	14330-13137

[a] Gsp, genomospecies; data taken from Gardan et al. (1999 Int. J. Syst. Bacteriol. 49,469-478) and Parkinson et al. (2011 Plant Pathol. 60,338-344).
[b] Position of the *iaaL* CDS within the sequence.
[c] *P. cannabina* pv. alisalensis ES4326 was previously designated *P. syringae* pv. maculicola ES4326 (Bull et al. 2011 Phytopathology 101,847-858).
[d] These names were reported as synonymous (Green et al. 2010 PLoS ONE 5(4):e10224)