

S. Campigli, S. Luti, T. Martellini, D. Rizzo, L. Bartolini, C. Carrai, J. Baskarathevan, L. Ghelardini, F. Peduto Hand, G. Marchi (2023). TaqMan qPCR assays improve *Pseudomonas syringae* pv. *actinidiae* biovar 3 and *P. viridiflava* (PG07) detection within the *Pseudomonas* sp. community of kiwifruit. *Phytopathologia Mediterranea* 62(1): 95-114. doi: 10.36253/phyto-14400

Supplementary Table S1. Geographic origin, orchard, plant tissue, symptom type, and year of isolation of bacteria recovered on KBCA during this study from *Actinidia chinensis* var. *deliciosa* cv. Hayward in Tuscany (Italy). The classification of isolates within or outside the Pssc was obtained by means of neighbour joining analysis using the sequence of a fragment of the *cts* gene (409bp) according to Berge *et al.*, 2014. For strains that can be ascribed to the Pssc, the phylogroup (01-13) or the subclade (a to d) of appurtenance is given. For each *cts* sequence that differed from the rest by one or more nucleotides a different allele number was assigned.

Isolate	Phylogroup/subclade (Berge <i>et al.</i> , 2014)	<i>cts</i> Allele	Year	Tissue	Symptom ^a	Orchard/ Nursery ^b	Geographic origin
KL337	PG01/b	1	2018	leaf	gs	O-1	Lutirano
KL362	PG01/b	1	2018	leaf	ts	O-1	Lutirano
KL309	PG01/b	1	2018	leaf	ts	O-1	Lutirano
KL310	PG01/b	1	2018	leaf	ts	O-1	Lutirano
KL328	PG01/b	1	2018	leaf	ts	O-1	Lutirano
KL303	PG01/b	1	2018	leaf	ts	O-1	Lutirano
KL86	PG01/b	1	2015	leaf	gs	O-2	Lutirano
KL103	PG01/b	1	2015	leaf	gs	O-2	Lutirano
KL11	PG01/b	1	2014	cane	gs	O-2	Lutirano
KL16	PG01/b	1	2014	leaf	gs	O-2	Lutirano
KL354	PG01/b	1	2018	leaf	ts	O-3	Lutirano
KL380	PG01/b	1	2018	cane	bc	O-3	Lutirano
KL15	PG01/b	1	2014	leaf	gs	O-3	Lutirano
KL342	PG01/b	1	2018	leaf	ts	O-4	Lutirano
KL343	PG01/b	1	2018	leaf	ts	O-4	Lutirano
KL318	PG01/b	1	2018	leaf	ts	O-4	Lutirano
KL331	PG01/b	1	2018	leaf	ts	O-5	Lutirano
KL334	PG01/b	1	2018	leaf	ts	O-5	Lutirano
KL344	PG01/b	1	2018	leaf	ts	O-5	Lutirano
KL356	PG01/b	1	2018	leaf	ts	O-5	Lutirano
KL357	PG01/b	1	2018	leaf	ts	O-5	Lutirano
KL358	PG01/b	1	2018	leaf	ts	O-5	Lutirano
KL359	PG01/b	1	2018	leaf	ts	O-5	Lutirano
KL320	PG01/b	1	2018	leaf	ts	O-5	Lutirano
KL34	PG01/b	2	2014	leaf	gs	O-3	Lutirano
KL46	PG01/b	3	2014	leaf	gs	O-3	Lutirano
KL51	PG01/b	3	2014	leaf	gs	O-3	Lutirano
KL78	PG01/b	3	2014	leaf	gs	O-3	Lutirano
KL17	PG02/b	4	2014	leaf	gs	O-2	Lutirano
KL66	PG02/b	4	2014	leaf	gs	O-2	Lutirano
KL71	PG02/b	4	2014	leaf	gs	O-2	Lutirano
KL72	PG02/b	4	2014	leaf	gs	O-2	Lutirano
KL93	PG02/b	4	2015	leaf	gs	O-2	Lutirano
KL94	PG02/b	4	2015	leaf	gs	O-2	Lutirano
KL106	PG02/b	4	2015	leaf	gs	O-2	Lutirano
KL107	PG02/b	4	2015	leaf	gs	O-2	Lutirano
KL111	PG02/b	4	2015	leaf	gs	O-2	Lutirano

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Supplementary Table S1. (Continued).

Isolate	Phylogroup/subclade (Berge <i>et al.</i> , 2014)	cts Allele	Year	Tissue	Symptom ^a	Orchard/ Nursery ^b	Geographic origin
KL338	PG02/b	4	2018	leaf	gs	O-2	Lutirano
KL341	PG02/b	4	2018	leaf	gs	O-2	Lutirano
KL20	PG02/b	4	2014	leaf	gs	O-3	Lutirano
KL28	PG02/b	4	2014	leaf	gs	O-3	Lutirano
KL1	PG02/b	5	2014	leaf	gs	O-1	Lutirano
KL3	PG02/b	5	2014	leaf	gs	O-1	Lutirano
KL47	PG02/b	6	2014	leaf	gs	O-3	Lutirano
KL308	PG02/b	7	2018	leaf	ts	O-1	Lutirano
KL108	PG02/b	7	2015	leaf	gs	O-3	Lutirano
KL109	PG02/b	7	2015	leaf	gs	O-3	Lutirano
KL58	PG02/b	8	2014	leaf	gs	O-2	Lutirano
KL82	PG02/b	8	2014	leaf	gs	O-2	Lutirano
KL388	PG02/b	9	2018	cane	bc	O-3	Lutirano
KL306	PG02/b	10	2018	leaf	ts	O-1	Lutirano
KL307	PG02/b	10	2018	leaf	ts	O-1	Lutirano
KL88	PG02/b	10	2015	leaf	gs	O-2	Lutirano
KL95	PG02/b	10	2015	leaf	gs	O-2	Lutirano
KL96	PG02/b	10	2015	leaf	gs	O-2	Lutirano
KL97	PG02/b	10	2015	leaf	gs	O-2	Lutirano
KL98	PG02/b	10	2015	leaf	gs	O-2	Lutirano
KL327	PG02/b	10	2018	leaf	gs	O-2	Lutirano
KL339	PG02/b	10	2018	leaf	gs	O-2	Lutirano
KL340	PG02/b	10	2018	leaf	gs	O-2	Lutirano
KL7	PG02/b	11	2014	leaf	gs	O-1	Lutirano
KL8	PG02/b	11	2014	leaf	gs	O-1	Lutirano
KFi11	PG02/b	12	2020	leaf	- ^c	N-2	Florence
KFi12	PG02/b	12	2020	leaf	-	N-2	Florence
KLU 3B	PG02/a	13	2016	leaf	gs	O-7	Lucca
KVPT7RA	PG02/a	13	2016	leaf	gs	N-1	Pistoia
KVPT7RC	PG02/a	13	2016	leaf	gs	N-1	Pistoia
KFi8	PG02/d	14	2020	leaf	-	N-2	Florence
KFi9	PG02/d	14	2020	leaf	-	N-2	Florence
KL52	PG02/d	15	2014	leaf	gs	O-3	Lutirano
KL27	PG02/d	16	2014	leaf	gs	O-2	Lutirano
KL22	PG02/d	16	2014	leaf	gs	O-2	Lutirano
KL391	PG02/d	16	2018	cane	bc	O-3	Lutirano
KL349	PG02/c	17	2018	leaf	gs	O-2	Lutirano
KLU7A	PG02	18	2016	leaf	gs	O-7	Lucca
KLU7B	PG02	18	2016	leaf	gs	O-7	Lucca
KLU7C	PG02	18	2016	leaf	gs	O-7	Lucca
KLU8A	PG02	19	2016	leaf	gs	O-7	Lucca
KVPT4A	unknown ^d	20	2016	leaf	ts	N-1	Pistoia
KVPT4B	unknown	20	2016	leaf	ts	N-1	Pistoia
KVPT4C	unknown	20	2016	leaf	ts	N-1	Pistoia
KL332	PG07/a	21	2018	leaf	ts	O-5	Lutirano
KL345	PG07/a	22	2018	leaf	gs	O-5	Lutirano
KL5	PG07/a	23	2014	leaf	gs	O-1	Lutirano
KL6	PG07/a	23	2014	leaf	gs	O-1	Lutirano

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Supplementary Table S1. (Continued).

Isolate	Phylogroup/subclade (Berge <i>et al.</i> , 2014)	cts Allele	Year	Tissue	Symptom ^a	Orchard/ Nursery ^b	Geographic origin
KL24	PG07/a	24	2014	leaf	gs	O-2	Lutirano
KL48	PG07/a	24	2014	leaf	gs	O-3	Lutirano
KL396	PG07/a	24	2018	cane	bc	O-3	Lutirano
KL397	PG07/a	24	2018	cane	bc	O-3	Lutirano
KL317	PG07/a	24	2018	leaf	ts	O-4	Lutirano
KL212	PG12/b	25	2017	sap	-	O-1	Lutirano
KL381	PG12/b	25	2018	cane	bc	O-3	Lutirano
KL383	PG12/b	25	2018	cane	bc	O-3	Lutirano
KL389	PG12/b	25	2018	cane	bc	O-3	Lutirano
KL395	PG12/b	25	2018	cane	bc	O-3	Lutirano
KL398	PG12/b	25	2018	cane	bc	O-3	Lutirano
KL399	PG12/b	25	2018	cane	bc	O-3	Lutirano
KL414	PG12/b	25	2018	cane	bc	O-3	Lutirano
KL417	PG12/b	25	2018	cane	bc	O-3	Lutirano
KL421	PG12/b	25	2018	cane	bc	O-3	Lutirano
KL422	PG12/b	25	2018	cane	bc	O-3	Lutirano
KL423	PG12/b	25	2018	cane	bc	O-3	Lutirano
KL425	PG12/b	25	2018	cane	bc	O-3	Lutirano
KL431	PG12/b	25	2018	cane	bc	O-3	Lutirano
KL432	PG12/b	25	2018	cane	bc	O-3	Lutirano
KL433	PG12/b	25	2018	cane	bc	O-3	Lutirano
KL438	PG12/b	25	2018	cane	bc	O-3	Lutirano
KL445	PG12/b	25	2018	cane	bc	O-3	Lutirano
KL419	PG12/b	26	2018	cane	bc	O-3	Lutirano
KL211	unknown	27	2017	sap	-	O-1	Lutirano
KL224	unknown	28	2017	sap	-	O-3	Lutirano
KL420	unknown	29	2018	cane	bc	O-3	Lutirano
KL402	unknown	30	2018	cane	bc	O-3	Lutirano
KL415	unknown	31	2018	cane	bc	O-3	Lutirano
KL213	PG13/a	32	2017	sap	-	O-1	Lutirano
KL350	PG13/a	32	2018	leaf	gs	O-2	Lutirano
KL384	PG13/a	32	2018	cane	bc	O-3	Lutirano
KL448	PG13/a	32	2018	cane	bc	O-3	Lutirano
KL315	PG13/a	33	2018	leaf	ts	O-4	Lutirano
KL316	PG13/a	33	2018	leaf	ts	O-4	Lutirano
KL222	PG13/a	34	2017	sap	-	O-3	Lutirano
KL393	PG13/a	35	2018	cane	bc	O-3	Lutirano
KL57	PG13/a	36	2014	leaf	gs	O-2	Lutirano
KL351	PG13/a	36	2018	leaf	gs	O-3	Lutirano
KL416	PG13/a	36	2018	cane	bc	O-3	Lutirano
KL429	PG13/a	36	2018	cane	bc	O-3	Lutirano
KL447	PG13/a	36	2018	cane	bc	O-3	Lutirano
KL50	PG13/a	37	2014	leaf	gs	O-3	Lutirano
KL73	PG13/a	37	2014	leaf	gs	O-3	Lutirano
KL104	PG13/a	37	2015	leaf	gs	O-3	Lutirano
KL302	PG13/a	37	2018	leaf	ts	O-1	Lutirano
KL330	PG13/a	37	2018	leaf	ts	O-1	Lutirano
KL319	PG13/a	37	2018	leaf	ts	O-5	Lutirano

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Supplementary Table S1. (Continued).

Isolate	Phylogroup/subclade (Berge <i>et al.</i> , 2014)	cts Allele	Year	Tissue	Symptom ^a	Orchard/ Nursery ^b	Geographic origin
KL321	PG13/a	37	2018	leaf	ts	O-5	Lutirano
KL322	PG13/a	37	2018	leaf	ts	O-5	Lutirano
KL323	PG13/a	37	2018	leaf	ts	O-5	Lutirano
KL355	PG13/a	37	2018	leaf	ts	O-5	Lutirano
KL375	PG13/a	37	2018	leaf	gs	O-5	Lutirano
KL377	PG13/a	37	2018	leaf	gs	O-5	Lutirano
KL378	PG13/a	37	2018	leaf	gs	O-5	Lutirano
KL390	PG13/a	37	2018	cane	bc	O-3	Lutirano
KL392	PG13/a	37	2018	cane	bc	O-3	Lutirano
KL403	PG13/a	37	2018	cane	bc	O-3	Lutirano
KL407	PG13/a	37	2018	cane	bc	O-3	Lutirano
KL411	PG13/a	37	2018	cane	bc	O-3	Lutirano
KL412	PG13/a	37	2018	cane	bc	O-3	Lutirano
KL413	PG13/a	37	2018	cane	bc	O-3	Lutirano
KL426	PG13/a	37	2018	cane	bc	O-3	Lutirano
KL439	PG13/a	37	2018	cane	bc	O-3	Lutirano
KL430	PG13/a	38	2018	cane	bc	O-3	Lutirano
KL434	PG13/a	38	2018	cane	bc	O-3	Lutirano
KL435	PG13/a	38	2018	cane	bc	O-3	Lutirano
KL436	PG13/a	38	2018	cane	bc	O-3	Lutirano
KL437	PG13/a	38	2018	cane	bc	O-3	Lutirano
KL304	unknown	39	2018	leaf	ts	O-1	Lutirano
KL305	unknown	39	2018	leaf	ts	O-1	Lutirano
KL89	unknown	40	2015	leaf	gs	O-2	Lutirano
KL90	unknown	40	2015	leaf	gs	O-2	Lutirano
KL385	unknown	41	2018	cane	bc	O-3	Lutirano
KL386	unknown	41	2018	cane	bc	O-3	Lutirano
KL387	unknown	41	2018	cane	bc	O-3	Lutirano
KL408	unknown	41	2018	cane	bc	O-3	Lutirano
KL409	unknown	41	2018	cane	bc	O-3	Lutirano
KL32	unknown	42	2014	leaf	gs	O-3	Lutirano
KL418	unknown	42	2018	cane	bc	O-3	Lutirano
KL382	unknown	43	2018	cane	bc	O-3	Lutirano
KL80	unknown	44	2015	leaf	gs	O-3	Lutirano
KL105	unknown	44	2015	leaf	gs	O-3	Lutirano
KL313	unknown	45	2018	leaf	ts	O-3	Lutirano
KL210	<i>Pseudomonas</i> sp.	46	2017	sap	-	O-2	Lutirano
KLU4A	<i>Pseudomonas</i> sp.	47	2016	leaf	gs	O-7	Lucca
KLU6A	<i>Pseudomonas</i> sp.	48	2016	leaf	gs	O-7	Lucca
KL300	<i>Pseudomonas</i> sp.	49	2018	leaf	ts	O-1	Lutirano
KL301	<i>Pseudomonas</i> sp.	49	2018	leaf	ts	O-1	Lutirano
KL329	<i>Pseudomonas</i> sp.	49	2018	leaf	ts	O-1	Lutirano
KL115	<i>Pseudomonas</i> sp.	49	2015	leaf	gs	O-3	Lutirano
KL116	<i>Pseudomonas</i> sp.	49	2015	leaf	gs	O-3	Lutirano
KL444	<i>Pseudomonas</i> sp.	49	2018	cane	bc	O-3	Lutirano
KL446	<i>Pseudomonas</i> sp.	49	2018	cane	bc	O-3	Lutirano
KL346	<i>Pseudomonas</i> sp.	50	2018	leaf	ts	O-1	Lutirano
KL65	<i>Pseudomonas</i> sp.	50	2014	leaf	gs	O-2	Lutirano

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Supplementary Table S1. (Continued).

Isolate	Phylogroup/subclade (Berge <i>et al.</i> , 2014)	cts Allele	Year	Tissue	Symptom ^a	Orchard/ Nursery ^b	Geographic origin
KL101	<i>Pseudomonas</i> sp.	50	2015	leaf	gs	O-2	Lutirano
KL102	<i>Pseudomonas</i> sp.	50	2015	leaf	gs	O-2	Lutirano
KL311	<i>Pseudomonas</i> sp.	50	2018	leaf	gs	O-2	Lutirano
KL84	<i>Pseudomonas</i> sp.	50	2015	leaf	gs	O-3	Lutirano
KL85	<i>Pseudomonas</i> sp.	50	2015	leaf	gs	O-3	Lutirano
KL112	<i>Pseudomonas</i> sp.	50	2015	leaf	gs	O-3	Lutirano
KL113	<i>Pseudomonas</i> sp.	50	2015	leaf	gs	O-3	Lutirano
KL312	<i>Pseudomonas</i> sp.	50	2018	leaf	ts	O-3	Lutirano
KL314	<i>Pseudomonas</i> sp.	50	2018	leaf	ts	O-3	Lutirano
KL333	<i>Pseudomonas</i> sp.	50	2018	leaf	ts	O-4	Lutirano
KL335	<i>Pseudomonas</i> sp.	50	2018	leaf	ts	O-4	Lutirano
KL336	<i>Pseudomonas</i> sp.	50	2018	leaf	ts	O-4	Lutirano
KL91	Undetermined ^c	51	2015	leaf	gs	O-3	Lutirano
KL372	Undetermined	51	2018	leaf	gs	O-3	Lutirano
KL373	Undetermined	51	2018	leaf	gs	O-3	Lutirano
KL92	Undetermined	52	2015	leaf	gs	O-3	Lutirano
KL118	Undetermined	52	2015	leaf	gs	O-3	Lutirano
KL394	Undetermined	53	2018	cane	bc	O-3	Lutirano
KL217	<i>Pseudomonas</i> sp.	54	2017	sap	-	O-3	Lutirano
KL219	<i>Pseudomonas</i> sp.	54	2017	sap	-	O-3	Lutirano
KL221	<i>Pseudomonas</i> sp.	54	2017	sap	-	O-3	Lutirano
KL204	<i>Pseudomonas</i> sp.	55	2017	sap	-	O-2	Lutirano
KL207	<i>Pseudomonas</i> sp.	55	2017	sap	-	O-2	Lutirano
KL401	<i>Pseudomonas</i> sp.	56	2018	cane	bc	O-3	Lutirano
KL220	<i>Pseudomonas</i> sp.	57	2017	sap	-	O-3	Lutirano
KL206	<i>Pseudomonas</i> sp.	58	2017	sap	-	O-2	Lutirano
KL208	<i>Pseudomonas</i> sp.	59	2017	sap	-	O-2	Lutirano
KL405	<i>Pseudomonas</i> sp.	60	2018	cane	bc	O-3	Lutirano
KL427	<i>Pseudomonas</i> sp.	61	2018	cane	bc	O-3	Lutirano
KL406	<i>Pseudomonas</i> sp.	61	2018	cane	bc	O-3	Lutirano
KL404	<i>Pseudomonas</i> sp.	61	2018	cane	bc	O-3	Lutirano
KL400	<i>Pseudomonas</i> sp.	62	2018	cane	bc	O-3	Lutirano
KL410	<i>Pseudomonas</i> sp.	63	2018	cane	bc	O-3	Lutirano
KL201	<i>Pseudomonas</i> sp.	64	2017	sap	-	O-2	Lutirano
KL216	<i>Pseudomonas</i> sp.	65	2017	sap	-	O-1	Lutirano
KL200	<i>Pseudomonas</i> sp.	65	2017	sap	-	O-2	Lutirano
KL202	<i>Pseudomonas</i> sp.	65	2017	sap	-	O-2	Lutirano
KL203	<i>Pseudomonas</i> sp.	65	2017	sap	-	O-2	Lutirano
KL205	<i>Pseudomonas</i> sp.	65	2017	sap	-	O-2	Lutirano
KL209	<i>Pseudomonas</i> sp.	65	2017	sap	-	O-2	Lutirano
KL218	<i>Pseudomonas</i> sp.	65	2017	sap	-	O-3	Lutirano
KL223	<i>Pseudomonas</i> sp.	65	2017	sap	-	O-3	Lutirano
KL347	<i>Pseudomonas</i> sp.	66	2018	leaf	gs	O-2	Lutirano
KL428	<i>Pseudomonas</i> sp.	67	2018	cane	bc	O-3	Lutirano
KL99	<i>Pseudomonas</i> sp.	68	2015	cane	bc	O-2	Lutirano
KL100	<i>Pseudomonas</i> sp.	68	2015	cane	bc	O-2	Lutirano
KL114	<i>Pseudomonas</i> sp.	68	2015	cane	bc	O-3	Lutirano
KL424	<i>Pseudomonas</i> sp.	68	2018	cane	bc	O-3	Lutirano

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Supplementary Table S1. (Continued).

Isolate	Phylogroup/subclade (Berge <i>et al.</i> , 2014)	<i>cts</i> Allele	Year	Tissue	Symptom ^a	Orchard/ Nursery ^b	Geographic origin
KL440	<i>Pseudomonas</i> sp.	68	2018	cane	bc	O-3	Lutirano
KL441	<i>Pseudomonas</i> sp.	68	2018	cane	bc	O-3	Lutirano
KL442	<i>Pseudomonas</i> sp.	68	2018	cane	bc	O-3	Lutirano
KL443	<i>Pseudomonas</i> sp.	68	2018	cane	bc	O-3	Lutirano
KL449	<i>Pseudomonas</i> sp.	68	2018	cane	bc	O-3	Lutirano
KCU2 1-B	Undetermined	69	2016	leaf	gs	O-8	Pistoia
KFi2	Undetermined	70	2020	leaf	-	N-2	Florence
KL325	Undetermined	71	2018	leaf	-	O-3	Lutirano
KL326	Undetermined	71	2018	leaf	-	O-3	Lutirano
KCU3 3-B	Undetermined	72	2016	leaf	gs	O-8	Pistoia
KL360	Undetermined	73	2018	leaf	gs	O-3	Lutirano

^a ts, typical bacterial canker leaf spot; gs, generic bacterial canker leaf spot; bc, bacterial canker; See material and methods for description.

^b Orchards: Lutirano from O-1 to O-5; Lucca, O-7; Pistoia, O-8; Nursery: Pistoia, N-1; Florence, N-2;

^c (-) asymptomatic.

^d Unknown, the allele could be ascribed to the Pssc following the procedure described by Berge *et al.*, 2014 but it could not be allocated into canonical PGs by Neighbour Joining analysis.

^e Undetermined, the allele could not be ascribed to the Pssc and it appears to be only distantly related to the *Pseudomonas* spp. references included in the Neighbour Joining analysis.

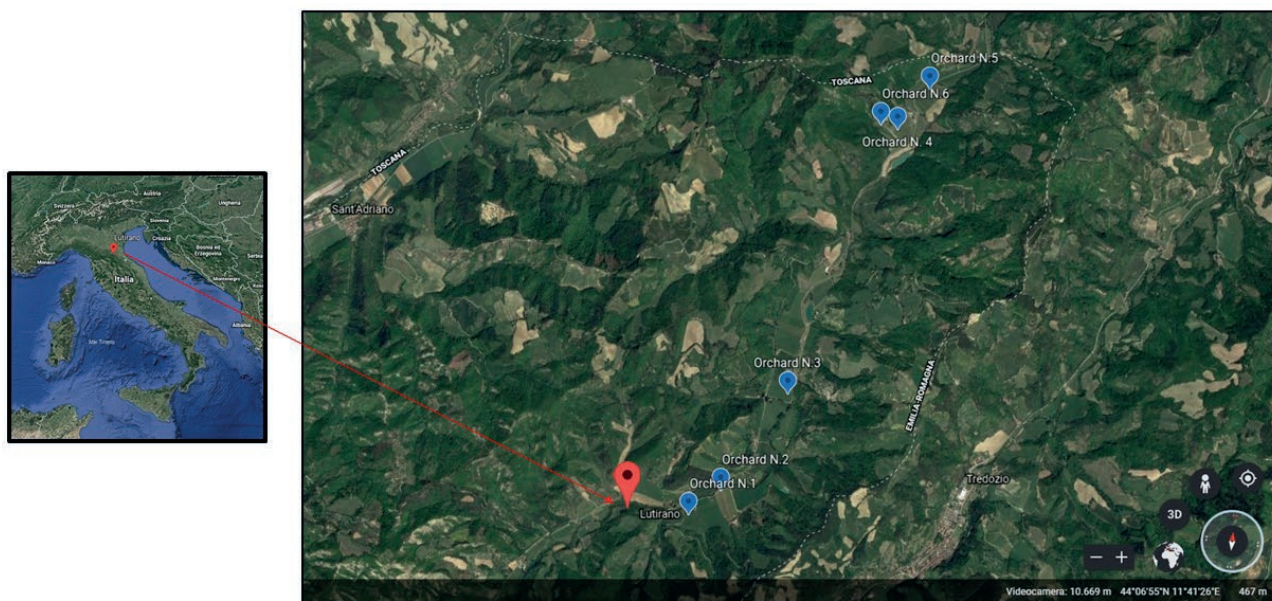
Supplementary Table S2. Results of *Actinidia chinensis* var. *deliciosa* cv. Hayward leaf indexing by means of dilution plating of leaf macerates on KBCA followed by isolate characterization, or by amplification of the total nucleic acids extracted from the same leaf using the qPCR_{Psa3} and qPCR_{Pv7} assays.

Sampling date	Leaf (orchard/ plant)	Symptom scoring	KBCA Psa3	qPCR _{Psa3}	KBCA Pv	qPCR _{Pv7}
05/07/2018	1/1	al ^a	-	-	-	+
05/07/2018	2/2	al	-	-	-	-
05/07/2018	3/2	al	-	-	-	+
05/07/2018	5/4	al	-	-	-	+
05/07/2018	6/2	al	-	-	-	-
05/07/2018	7/5	al	-	-	-	-
06/11/2018	1/1	ts	+	+	-	+
06/11/2018	2/1	ts	-	-	-	-
06/11/2018	3/2	gs	-	+	-	-
06/11/2018	5/2	ts	+	+	+	+
06/11/2018	6/2	ts	+	+	-	-
06/11/2018	7/4	al	-	-	-	-
07/16/2018	1/1	ts	+	+	-	+
07/16/2018	2/4	gs	-	-	-	-
07/16/2018	3/7	al	-	-	-	-
07/16/2018	5/7	ts	+	+	-	-
07/16/2018	6/7	gs	-	-	+	+
07/16/2018	7/7	gs	-	-	-	-
09/24/2018	1/2	gs	+	+	-	-
09/24/2018	2/2	gs	-	-	-	-
09/24/2018	3/2	gs	-	-	-	-
09/24/2018	5/2	gs	-	-	-	-
09/24/2018	6/6	ts	+	-	-	-
09/24/2018	7/3	gs	-	-	-	-
10/22/2018	1/4	gs	-	-	-	-
10/22/2018	2/5	gs	-	-	-	-
10/22/2018	3/5	gs	-	-	-	-
10/22/2018	5/1	gs	-	-	-	-
10/22/2018	6/2	gs	-	-	-	-
10/22/2018	7/3	gs	-	-	-	-

^a al, asymptomatic; ts, typical bacterial canker spots ; gs, generic bacterial canker spots. See material and methods for description.

Supplementary Table S3. Evaluation of the specificity of qPCR_{Pv7} and qPCR_{Psa3} assays according to Sanger sequencing of their relative amplicons. Leaves of *Actinidia chinensis* var. *deliciosa* cv. Hayward were infected with Pv7aKL317 or Psa3KL318 and indexed with the two protocols 4, 11, 18 and 42 days after inoculation (DAI). Identity of qPCR amplicon sequences was evaluated by comparison to the homologous sequences of the two strains.

Leaf	DAI	Inoculum type	Cq qPCR _{Pv7} (% identity to KL317)	Cq qPCR _{Psa3} (% identity to KL318)
1	4	KL317	29.77 (100)	>40
2	4	KL317	34.80 (100)	>40
3	4	KL317	33.76 (100)	>40
4	4	KL318	>40	33.42 (100)
5	4	KL318	>40	36.57 (100)
6	4	KL318	>40	36.29 (100)
7	4	KL318	>40	34.42 (100)
8	11	KL317	30.82 (100)	>40
9	11	KL317	32.76 (100)	>40
10	11	KL318	>40	34.81 (100)
11	18	KL317	35.84 (100)	>40
12	18	KL317	36.51 (100)	>40
13	18	KL318	>40	34.73 (100)
14	18	KL318	>40	36.63 (100)
15	42	KL317	33.83 (100)	>40
16	42	KL318	>40	36.01 (100)

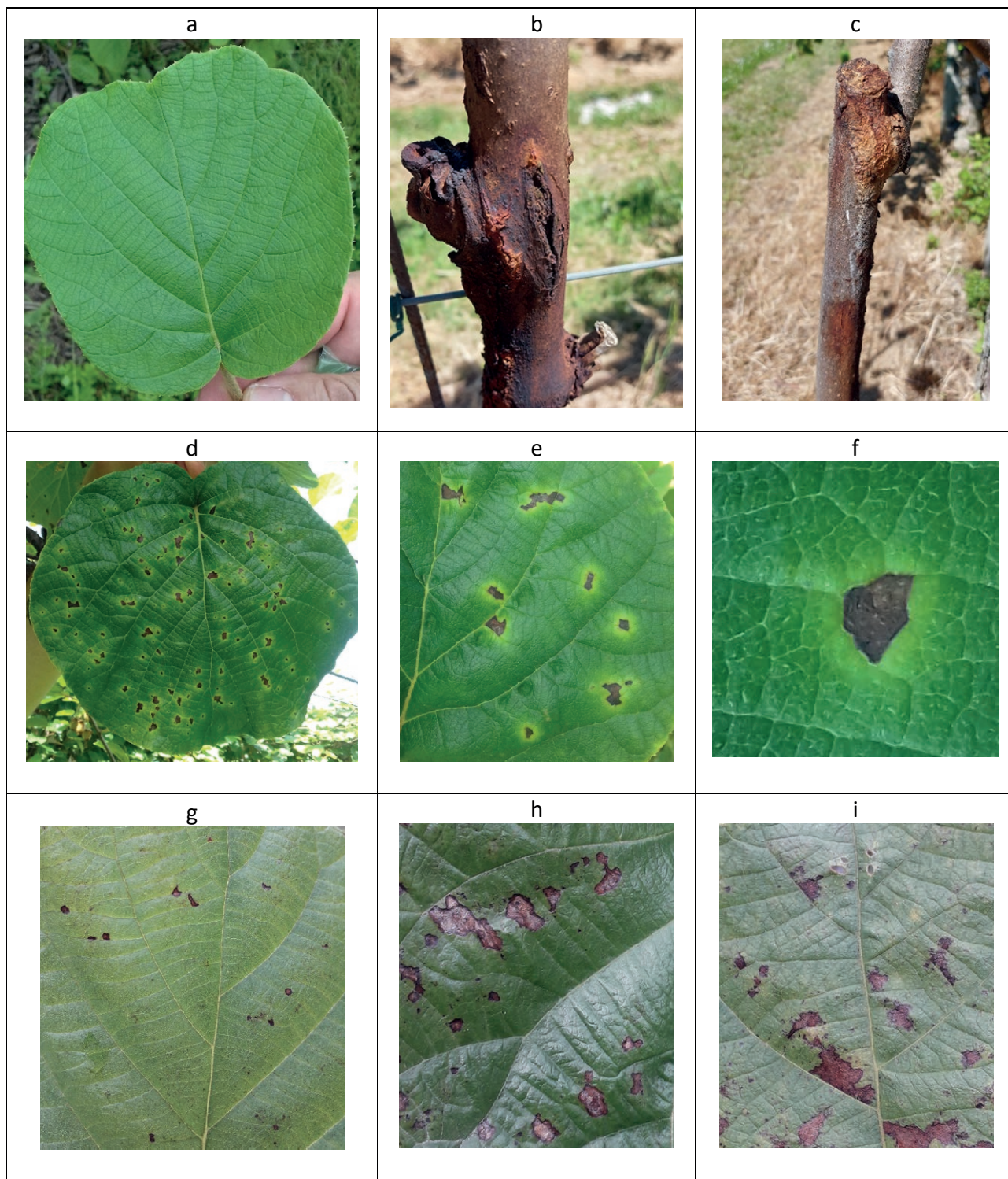


Supplementary Figure S1. Geographic location of the six *Actinidia chinensis* var. *deliciosa* cv. Hayward orchards at Lutrano (Tuscany, Italy) that were sampled during the 2018 vegetative season to test the specificity and sensitivity *in vivo* of qPCRs and BIO-PCRs assays developed in this study. Most of the bacterial isolates used in this work were obtained between 2014 and 2018 from these orchards.

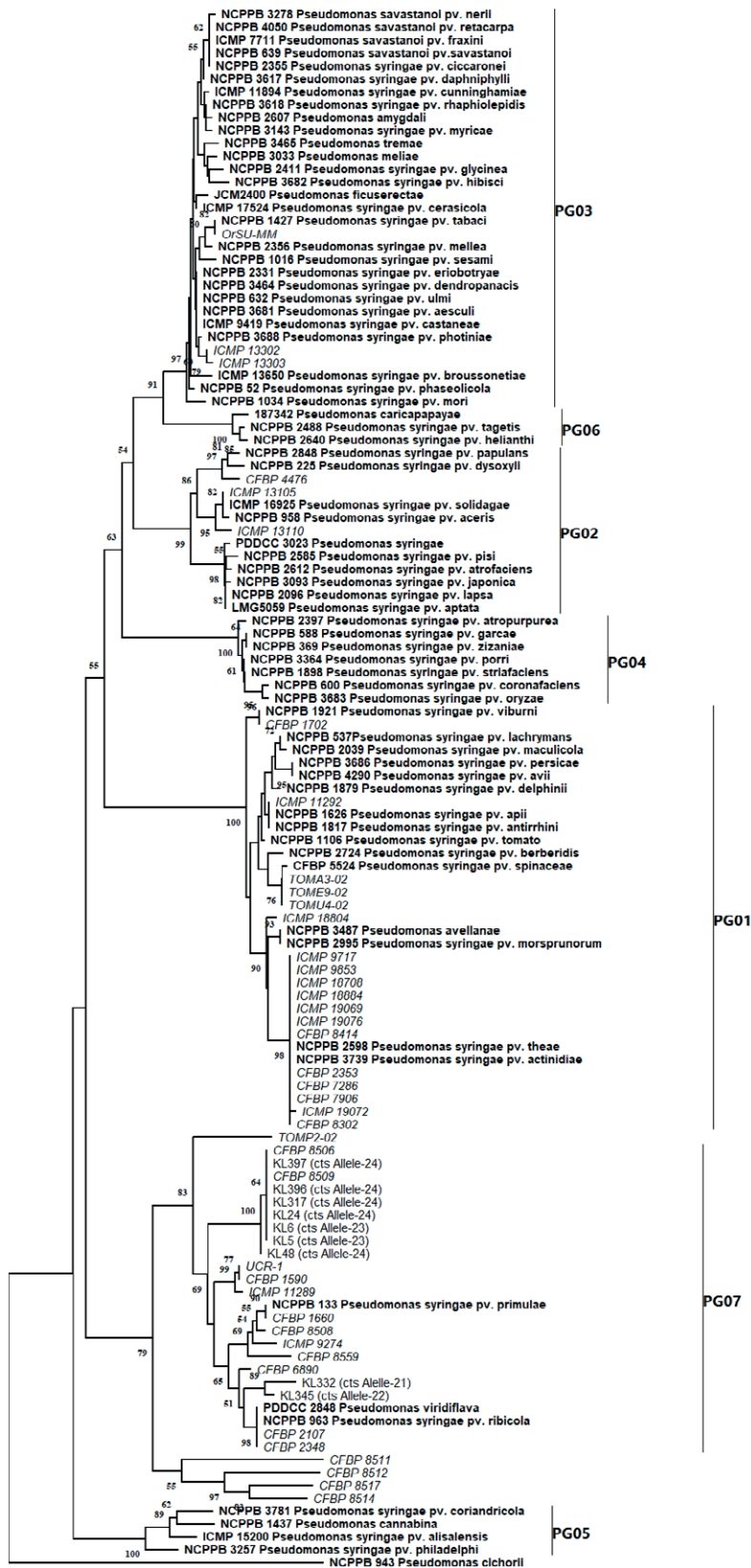
a

KL103_ <i>lscy</i>	1	ATGATTGCAGGTCGGCGCCATTTTCGATTGCAGGCCGCTACATC---TAGCAGGTAACATC
NZ708_RS29580	1	ATGATTGCAGGTCGGCGCCATTTTCGATTGCAGGCCGCTACATC---TAGCAGGTAACATC
KL103_ <i>lscβ</i>	1	ATGTCCACTAGCAGCTCTGCTTTAAGCCAGCTCAAAAATAGTCCTCTAGCAGGTAACATC
NZ708_RS29190	1	ATGTCCACTAGCAGCTCTGCTTTAAGCCAGCTCAAAAATAGTCCTCTAGCAGGTAACATC
JN853_RS31240	1	ATGTCCACTAGCAGCTCTGCTTTAAGCCAGCTCAAAAATAGTCCTCTAGCAGGTAACATC
JN853_RS30430	1	ATGTCCACTAGCAGCTCTGCTTTAAGCCAGCTCAAAAATAGTCCTCTAGCAGGTAACATC
CT122_RS00110	1	ATGTCCACTAGCAGCTCTGCTTTAAGCCAGCTCAAAAATAGTCCTCTAGCAGGTAACATC
KL103_ <i>lscα</i>	1	ATG-----AGTAACGTC
NZ708_RS18335	1	ATG-----AGTAACGTC
JN853_RS21105	1	ATG-----AGTAACGTC
CT122_RS12590	1	ATG-----AGTAACGTC
consensus	1	***.....*...*
KL103_ <i>lscy</i>	58	AACTACGAACCTACTGTCTGGTCCCGCGCCGATGCGCTGAAGGTCAATGAAAATGACCCG
NZ708_RS29580	58	AACTACGAACCTACTGTCTGGTCCCGCGCCGATGCGCTGAAGGTCAATGAAAATGACCCG
KL103_ <i>lscβ</i>	61	AACTACGAACCTACTGTCTGGTCCCGCGCCGATGCGCTGAAGGTCAATGAAAATGACCCG
NZ708_RS29190	61	AACTACGAACCTACTGTCTGGTCCCGCGCCGATGCGCTGAAGGTCAATGAAAATGACCCG
JN853_RS31240	61	AACTACGAACCTACTGTCTGGTCCCGCGCCGATGCGCTGAAGGTCAATGAAAATGACCCG
JN853_RS30430	61	AACTACGAACCTACTGTCTGGTCCCGCGCCGATGCGCTGAAGGTCAATGAAAATGACCCG
CT122_RS00110	61	AACTACGAACCTACTGTCTGGTCCCGCGCCGATGCGCTGAAGGTCAATGAAAATGACCCG
KL103_ <i>lscα</i>	13	AACTACGCACCTACTGTCTGGTCCCGTGCAGGATGCACTGAAGGTCAATGAAAATGACCCG
NZ708_RS18335	13	AACTACGCACCTACTGTCTGGTCCCGTGCAGGATGCACTGAAGGTCAATGAAAATGACCCG
JN853_RS21105	13	AACTACGCACCTACTGTCTGGTCCCGTGCAGGATGCACTGAAGGTCAATGAAAATGACCCG
CT122_RS12590	13	AACTACGCACCTACTGTCTGGTCCCGTGCAGGATGCACTGAAGGTCAATGAAAATGACCCG
consensus	61	**.....*...*...*...*...*...*...*...*...*...*...*...*...*
KL103_ <i>lscy</i>	118	ACCACCACGCAGCCACTGGTCAGTGCAGGACTTTCGGTCATGAGTGATACGGTATTTCATC
NZ708_RS29580	118	ACCACCACGCAGCCACTGGTCAGTGCAGGACTTTCGGTCATGAGTGATACGGTATTTCATC
KL103_ <i>lscβ</i>	121	ACCACCACGCAGCCACTGGTCAGTGCAGGACTTTCGGTCATGAGTGATACGGTATTTCATC
NZ708_RS29190	121	ACCACCACGCAGCCACTGGTCAGTGCAGGACTTTCGGTCATGAGTGATACGGTATTTCATC
JN853_RS31240	121	ACCACCACGCAGCCACTGGTCAGTGCAGGACTTTCGGTCATGAGTGATACGGTATTTCATC
JN853_RS30430	121	ACCACCACGCAGCCACTGGTCAGTGCAGGACTTTCGGTCATGAGTGATACGGTATTTCATC
CT122_RS00110	121	ACCACCACGCAGCCACTGGTCAGTGCAGGACTTTCGGTCATGAGTGATACGGTATTTCATC
KL103_ <i>lscα</i>	73	ACCACCACGCAGCCACTGGTCAGCCCGGACTTTCGGTCATGAGTGATACGGTATTTCATC
NZ708_RS18335	73	ACCACCACGCAGCCACTGGTCAGCCCGGACTTTCGGTCATGAGTGATACGGTATTTCATC
JN853_RS21105	73	ACCACCACGCAGCCACTGGTCAGCCCGGACTTTCGGTCATGAGTGATACGGTATTTCATC
CT122_RS12590	73	ACCACCACGCAGCCACTGGTCAGCCCGGACTTTCGGTCATGAGTGATACGGTATTTCATC
consensus	121	**.....*...*...*...*...*...*...*...*...*...*...*...*...*
KL103_ <i>lscy</i>	178	TGGGATACCATGCCGCTGCGCGAGCTGGATGGCAGCGTGTTTCGGTCAACCGCTGGTCCG
NZ708_RS29580	178	TGGGATACCATGCCGCTGCGCGAGCTGGATGGCAGCGTGTTTCGGTCAACCGCTGGTCCG
KL103_ <i>lscβ</i>	181	TGGGATACCATGCCGCTGCGCGAGCTGGATGGCAGCGTGTTTCGGTCAACCGCTGGTCCG
NZ708_RS29190	181	TGGGATACCATGCCGCTGCGCGAGCTGGATGGCAGCGTGTTTCGGTCAACCGCTGGTCCG
JN853_RS31240	181	TGGGATACCATGCCGCTGCGCGAGCTGGATGGCAGCGTGTTTCGGTCAACCGCTGGTCCG
JN853_RS30430	181	TGGGATACCATGCCGCTGCGCGAGCTGGATGGCAGCGTGTTTCGGTCAACCGCTGGTCCG
CT122_RS00110	181	TGGGATACCATGCCGCTGCGCGAGCTGGATGGCAGCGTGTTTCGGTCAACCGCTGGTCCG
KL103_ <i>lscα</i>	133	TGGGATACCATGCCGCTGCGCACAGCTCGACGGCACCAATTGTCCTCGGTCAACCGCTGATCG
NZ708_RS18335	133	TGGGATACCATGCCGCTGCGCACAGCTCGACGGCACCAATTGTCCTCGGTCAACCGCTGATCG
JN853_RS21105	133	TGGGATACCATGCCGCTGCGCACAGCTCGACGGCACCAATTGTCCTCGGTCAACCGCTGATCG
CT122_RS12590	133	TGGGATACCATGCCGCTGCGCACAGCTCGACGGCACCAATTGTCCTCGGTCAACCGCTGATCG
consensus	181	*****.....*...*...*...*...*...*...*...*...*...*...*...*...*
KL103_ <i>lscy</i>	238	GTTAT
NZ708_RS29580	238	GTTAT
KL103_ <i>lscβ</i>	241	GTTAT
NZ708_RS29190	241	GTTAT
JN853_RS31240	241	GTTAT
JN853_RS30430	241	GTTAT
CT122_RS00110	241	GTTAT
KL103_ <i>lscα</i>	193	GTGAT
NZ708_RS18335	193	GTGAT
JN853_RS21105	193	GTGAT
CT122_RS12590	193	GTGAT
consensus	241	**..**

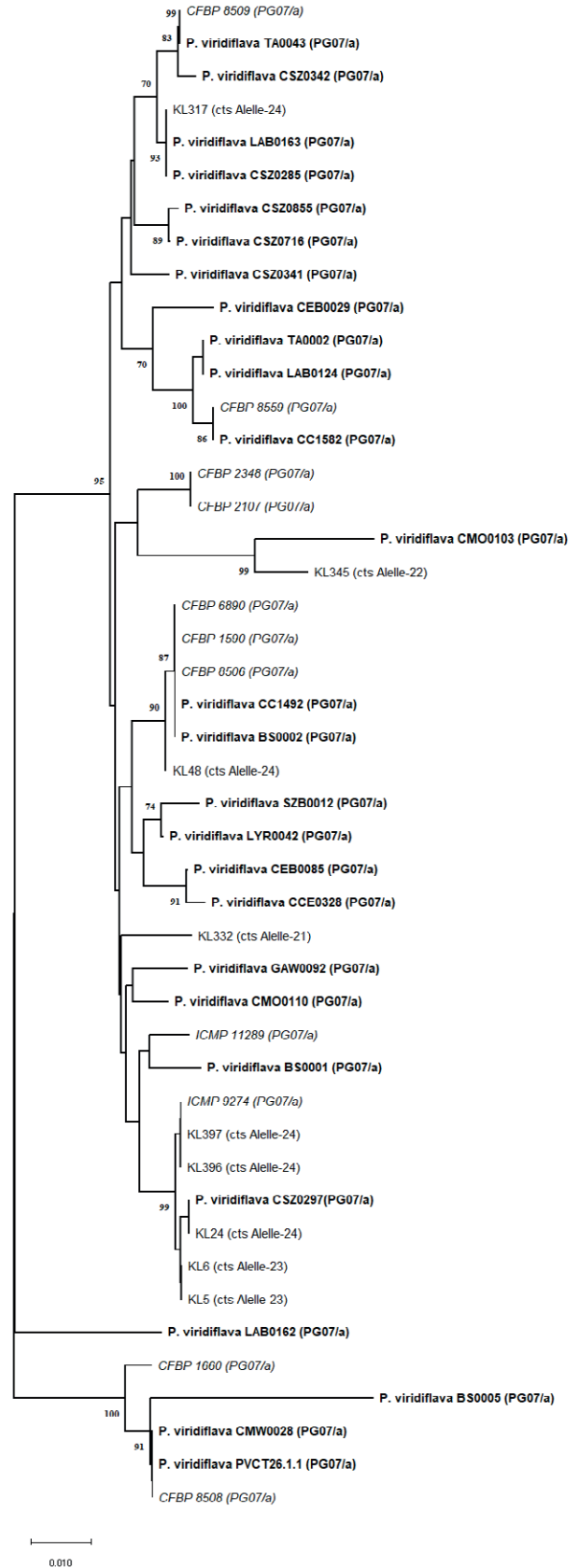
Supplementary Figures S2a and S2b. 2a) Primers and probe placement for qPCR $Psa3$ assay, located on the functional levansucrase coding gene (*lscy*) of *Psa3* (KL103). The other two levansucrase coding genes *lscβ* and *lscα* harbored by KL103 (Luti *et al.*, 2021), as well as the homologous sequences found in the complete genomes of ICMP 18708 (*Psa3*), ICMP 9853 (*Psa1*) and MAFF 212063 (*Psa5*), were also aligned for comparative purposes. Forward primer sequence (Plasm L1), 5'- 3'orientation, position 12-29; reverse primer sequence (Plasm R1), reverse-complement 3'- 5'orientation, position 226-238; probe sequence (Plasm P1), 5'- 3'orientation, position 32- 52, are highlighted in blue, green, and red, respectively. Polymorphic nucleotides are shown in white (.), while identical nucleotides are highlighted in black (*). Whilst (-) indicates a gap in the sequence. *Psa3* ICMP 18708 (accession numbers NZ_CP012179.1 and NZ_CP012180.1): NZ708_RS29190, NZ708_RS18335, and NZ708_RS29580 genes; *Psa1* ICMP9853 (accession numbers NZ_CP018202.1 and NZ_CP018203.1): JN853_RS30430, JN853_RS21105 and JN853_RS31240 genes; *Psa5* MAFF212063 (NZ_CP024712.1): CT122_RS00110 and CT122_RS12590 genes.



Supplementary Figure S3. Examples of symptom types observed on leaves and canes of *Actinidia chinensis* var. *deliciosa* cv. Hayward during orchard monitoring in the 2018 growing season. a) asymptomatic leaf (al); (b and c) bacterial canker (bc): canker with traces of bacterial exudates/plant sap; (d to f) typical bacterial canker spots (ts): brown angular lesions surrounded by a distinct yellow halo that becomes narrow and indistinct on aged leaves; (g to i) generic bacterial canker spots (gs): necrotic spots brown to dark brown in color, size varying from pin point to large, and elliptical, angular or irregular shape without a yellow halo.



Supplementary Figure S4. Neighbor joining maximum composite likelihood unrooted cladogram showing the phylogenetic relatedness among 9 bacterial isolates from *Actinidia chinensis* var. *deliciosa* cv. Hayward in Tuscany (Italy), based on a 584 bp fragment of the *rpdD* gene. Isolates were classified as PG07/a according to *cts* analysis. The homologous sequences of Pssc reference strains from national and international collections (in italic) were also included for comparative purposes. The sequences of 70 *P. syringae* pathotype strains and related pathogen species (in bold) were used according to Parkinson et al. (2011) to fix the boundaries of the 7 phylogroups (PG) in which the Pssc has been partitioned. The sequence of *Pseudomonas cichorii* NCPBB 943 was also included to delimit the Pssc. Bootstrap support (≥ 70) is indicated above or below tree nodes as the percentage of replicate cladograms in which the associated taxa clustered together (1000 replications). The scale bar represents the number of substitutions per nucleotide. The *cts* allele number for each strain is given in parentheses. The proposed PGs within the Pssc are also included.



Supplementary Figure S5. Neighbor joining maximum composite likelihood unrooted cladogram showing the relatedness among 9 bacterial isolates from *Actinidia chinensis* var. *deliciosa* cv. Hayward growing at Lutirano, Tuscany (Italy) sampled in different years and identified as members of the PG07 (*P. viridiflava*) based on *cts* gene sequence analysis according to Berge et al. 2014 (*cts* allele number is given in parentheses). The cladogram was built using a 616 bp fragment of a pathogenicity island (T-PAI) that was amplified according to Bartoli et al. (2014). The homologous sequences of *P. viridiflava* strains ICMP 9274, ICMP 11289, CFBP 8506, CFBP 1590, CFBP 2107, CFBP 6890, CFBP 8508, CFBP 8509, CFBP 8559, *P. syringae* strains CFBP 1660 and CFBP 2348 (in italic), and of 25 *P. viridiflava* reference strains (Plant Associated and Environmental Microbes Database, in bold) were included as reference in the analysis. Bootstrap support (≥ 70) is indicated above or below tree nodes as the percentage of replicate cladograms in which the associated taxa clustered together (1000 replications). The scale bar represents the number of substitutions per nucleotide.