

Supplemental tables and figures belonging to

Comparative genomics and pathogenicity potential of members of the *Pseudomonas syringae* species complex on *Prunus* spp.

Michela Ruinelli, Jochen Blom, Theo H.M. Smits and Joël F. Pothier

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16 **Table S1** List of phytotoxins and phytohormons encoding genes screened in this study.

Product	Gene nomenclature	Reference Genome	NCBI locus tags	Reference
Coronatine	<i>corR, corS, corP, cmaA-E, cmaT, cmaU, cfa1-9, cfl</i>	AE016853.1	PSPTO_4680 to PSPTO_4690 and PSPTO_4704 to PSPTO_4712	[1-3]
Cytokinin	<i>ptz</i>	N.A.	CAA27315.1	[4]
IAA conjugation	<i>iaaL</i>	AE016853.1	PSPTO_0371	[1, 5, 6]
IAA synthesis	<i>iaaM/iaaH</i>	CP000075.1	Psyr_1536/Psyr_1537	[7, 8]
Mangotoxin	<i>mboA-F</i>	CP005970.1	PSYRMG_10110 to PSYRMG_10135	[9, 10]
Phaseolotoxin	N.D.	CP000058.1	PSPPH_4298 to PSPPH_4320	[11, 12]
Syringolin	<i>sylA-E</i>	CP000075.1	Psyr_1706 to Psyr_1702	[8, 13]
Syringomycin	<i>syrB1, syrB2, syrC, syrE, syrD, syrP, syrF, syrG, salA</i>	CP000075.1	Psyr_2613 to Psyr_2607 and Psyr_2602 to Psyr_2601	[8, 14-17]
Syringopeptin	<i>sypA-C</i>	CP000075.1	Psyr_2615 to Psyr_2614	[8, 18-20]
Tabtoxin	N.D.	AEAP01	PSYTB_28452 to PSYTB_28507	[21-23] [24]
Type III secretion system	<i>hrp/hrc</i>	CP000058.1	PSPPH_1295 to PSPPH_1270	[25-27]
Type III secretion system 2	N.D.	CP000058.1	PSPPH_2515 to PSPPH_545	[28]

N.D.: not determined.

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Table S2 List of type III effectors (T3E) screened in this study and their respective locus tags in reference genomes.

T3E	Locus tag on EDGAR	Reference genome	Reference
AvrA1	pv_aesculi_2250_3486	ACXT01	[29]
AvrB2	PSPPH_A0120	CP000058-CP000060	[27]
AvrB4	IYO_003600	CP011972-CP011973	[30]
AvrD1	IYO_003570	CP011972-CP011973	[30]
AvrE1	IYO_006770	CP011972-CP011973	[30]
AvrPto1	PSPTO_4001	AE016853.1-AE016855.1	[1]
AvrRpm1	IYO_008065	CP011972-CP011973	[30]
AvrRpm2	IYO_024217	CP011972-CP011973	[30]
AvrRps4	PSPPH_A0087	CP000058-CP000060	[27]
AvrRpt2	PTOT1_2469	ABSM01	[31]
HopA1	PSPTO_5354	AE016853.1-AE016855.1	[1]
HopAA1-1	PSPTO_1372	AE016853.1-AE016855.1	[1]
HopAA1-2	PSPTO_4718	AE016853.1-AE016855.1	[1]
HopAB1	PSPPH_A0127	CP000058-CP000060	[27]
HopAD1	PSPTO_4691	AE016853.1-AE016855.1	[1]
HopAE1	PSPPH_4326	CP000058-CP000060	[27]
HopAF1	PSPTO_1568	AE016853.1-AE016855.1	[1]
HopAG1	CFBP2118_04399	LT962481	this study
HopAH1	PSPTO_0905	AE016853.1-AE016855.1	[1]
HopAI1	PSPTO_0906	AE016853.1-AE016855.1	[1]
HopAJ1	PSPTO_0852	AE016853.1-AE016855.1	[1]
HopAK	PSPTO_4101	AE016853.1-AE016855.1	[1]
HopAL1	CFBP4215_01700	LT962480	this study
HopAM1-1	PSPTO_1022	AE016853.1-AE016855.1	[1]
HopAM1-2	PSPTO_A0005	AE016853.1-AE016855.1	[1]
HopAO1	PSPTO_4722	AE016853.1-AE016855.1	[1]
HopAO2	IYO_003720	CP011972-CP011973	[30]
HopAQ1	PSPTO_4703	AE016853.1-AE016855.1	[1]
HopAR1	CFBP2118_04979	LT962481	this study
HopAS1	PSPPH_4736	CP000058-CP000060	[27]
HopAT1	PSPPH_5225	CP000058-CP000060	[27]
HopAU1	PSPPH_A0031	CP000058-CP000060	[27]
HopAV1	PSPPH_A0056	CP000058-CP000060	[27]
HopAW1	IYO_003657	CP011972-CP011973	[30]
HopAY1	PSPPH_A0129	CP000058-CP000060	[27]
HopAZ1	IYO_018555	CP011972-CP011973	[30]
HopB1	PSPTO_1406	AE016853.1-AE016855.1	[1]
HopBB1-1	IYO_003727	CP011972-CP011973	[30]
HopBB1-2	IYO_003675	CP011972-CP011973	[30]
HopBC1	PSYAR_24412	AEAO01	[32]
HopBD1	PLA106_27566	AEAM01	[32]
HopBD2	NCPPB2254_03267	ODAM01000001-ODAM01000246	this study
HopBE1	PSYAR_10899	AEAO01	[32]
HopBF1	CFBP3840_p400101	LT963409-LT963413	this study

HopBG1	PMA4326_30242	AEAK01	[32]
HopBI1	PL963_p300075	LT963395-LT963401	this study
HopBJ1	N018_19725	CP007014-CP007015	N.A.
HopBK1	PSYRMG_01235	CP005970	[9]
HopBL1	CFBP3840_p100112	LT963409-LT963413	this study
HopBL2	CFBP3840_00659	LT963409-LT963413	this study
HopBM1	PSPTO_5633	AE016853.1-AE016855.1	[1]
HopBN1	IYO_013150	CP011972-CP011973	[30]
HopC1	PSPTO_0589	AE016853.1-AE016855.1	[1]
HopD1	PSPTO_0876	AE016853.1-AE016855.1	[1]
HopE1	PSPTO_4331	AE016853.1-AE016855.1	[1]
HopF3	PSPPH_3498	CP000058-CP000060	[27]
HopG1	PSPTO_4727	AE016853.1-AE016855.1	[1]
HopH1	PSPTO_0588	AE016853.1-AE016855.1	[1]
HopI1	IYO_005160	CP011972-CP011973	[30]
HopK1	PSPTO_0044	AE016853.1-AE016855.1	[1]
HopM1	PSPTO_1375	AE016853.1-AE016855.1	[1]
HopN1	IYO_006735	CP011972-CP011973	[30]
HopO1-1	PSPTO_A0018	AE016853.1-AE016855.1	[1]
HopO1-2	PSPTO_4594	AE016853.1-AE016855.1	[1]
HopP1	PSPTO_2678	AE016853.1-AE016855.1	[1]
HopQ1-1	PSPTO_0877	AE016853.1-AE016855.1	[1]
HopQ1-2	PSPTO_4732	AE016853.1-AE016855.1	[1]
HopR1	PSPTO_0883	AE016853.1-AE016855.1	[1]
HopS1	PLA106_22893	AEAM01	[32]
HopS2	IYO_004052	CP011972-CP011973	[30]
hopT1-1	PSPTO_A0019	AE016853.1-AE016855.1	[1]
hopT1-2	PSPTO_4593	AE016853.1-AE016855.1	[1]
HopU1	PSPTO_0501	AE016853.1-AE016855.1	[1]
HopV1	PSPTO_4720	AE016853.1-AE016855.1	[1]
hopX1	PSPTO_A0012	AE016853.1-AE016855.1	[1]
HopX2	A250_06861	CM002753-CM002754	[33]
HopY1	PSPTO_0061	AE016853.1-AE016855.1	[1]
HopZ3	IYO_029045	CP011972-CP011973	[30]
HopZ4	PLA107_32571	AEAF01	[32]
HopZ5	IYO_008282	CP011972-CP011973	[30]

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23 **Table S3** Metrics of the PacBio RSII sequencing results.

Strain ^a	Pcerasi PL963	Pavii CFBP 3846	Pscer CFBP 6110	Pscer CFBP 6109	Pmp1 CFBP 3840	Pmp1 CFBP 2116	Pmp2 CFBP 3800	Pmp2 CFBP 6411	Psy CFBP 2118	Psy CFBP 4215
Number of SMRTcells	6	6	5	6	5	6	6	5	5	6
Total number of reads	351,993	438,533	366,949	433,733	116,470	482,110	464,181	114,712	104,850	142,016
Total number of bases	2,040,283,420	2,364,983,321	2,903,342,251	1,846,300,534	899,391,466	2,500,388,640	2,748,099,409	635,868,141	706,366,439	802,154,567
Mean read length (bp)	5,796	5,392	7,912	4,256	7,636	5,186	5,920	5,543	6,736	5,648
N ₅₀ read length (bp)	9,563	9,716	11,239	7,583	11,001	8,825	9,738	8,429	10,106	8,373
Number of mapped reads	315,221	360,451	337,334	338,842	110,755	409,023	409,513	105,062	96,950	131,578
Mean coverage (×)	252.75	298.33	344.84	244.23	124.36	324.87	328.24	88.04	103.54	114.59
Total number of contigs	1Chr+6PP	1Chr+5PP	1Chr ^b +3PP	1Chr+3PP	1Chr ^b +4PP	1Chr+4PP	1Chr ^b +2PP	1Chr	1Chr	1Chr
Size of Chr (bp)	5,889,419	6,120,158	5,907,507	6,015,874	6,013,125	6,034,464	6,450,957	6,363,674	6,031,285	6,035,297
G+C content (%) of Chr	59.02	58.74	58.25	58.2	58.16	58.15	58.47	58.55	59.26	59.31
CDS of Chr	5,278	5,517	5,441	5,577	5,434	5,464	5,728	5,693	5,118	5,129
Size of PP1 (bp)	127,474	43,975 ^{c,d}	127,142 ^c	118,774 ^{c,d}	110,420 ^d	19,743 ^c	83,341 ^d			
G+C content (%) of PP1	54.82	56.04	55.32	55.48	54.65	53.35	56.28			
CDS PP1	140	57	143	149	137	30	87			
Size of PP2 (bp)	144,075 ^d	109,843 ^d	94,021 ^d	86,328 ^d	90,464	61,361 ^{c,d}	67,760 ^{c,d}			
G+C content (%) of PP2	55.58	55.74	55.96	56.26	55.04	55.18	55.31			
CDS PP2	155	125	110	95	115	67	96			
Size of PP3 (bp)	81,323 ^d	108,842 ^d	103,529 ^d	111,777 ^d	86,369 ^d	83,816				
G+C content (%) of PP3	55.11	55.79	56.51	56.6	58.26	54.81				
CDS PP3	94	128	108	114	84	104				
Size of PP4 (bp)	70,589 ^d	77,492 ^d			78,348	82,845 ^d				
G+C content (%) of PP4	55.2	55.94			55.2	55.87				
CDS PP4	81	100			104	103				
Size of PP5 (bp)	48,121 ^d	41,285 ^d								
G+C content (%) of PP5	55.02	54.5								
CDS PP5	67	68								
Size of PP6 (bp)	18,360 ^d									
G+C content (%) of PP6	55.34									
CDS PP6	29									
Total genome size (bp)	6,379,361	6,501,595	6,232,199	6,332,753	6,378,726	6,282,229	6,602,058	6,363,674	6,031,285	6,035,297
Total number of CDS	5,844	5,995	5,802	5,935	5,874	5,768	5,911	5,693	5,118	5,129
NCBI accession numbers	LT963395- LT963401	LT963402- LT963407	OLMP01000001- OLMP01000002 LT985210- LT985212	LT963391- LT963394	LT963409- LT963413	LT985192-LT985195 OLMD01000001- OLMD01000002	OLMQ01000001- OLMQ01000003 LT985190- LT98519	LT963408	LT962481	LT962480

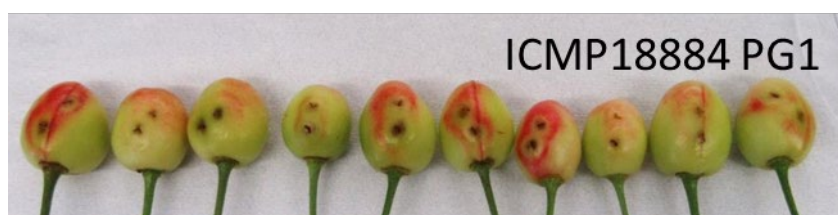
^a Strains abbreviation code: see Table 2.1; ^bChromosome (Chr) is circularized based on other genomes; ^c Putative plasmid (PP) is not circularized; ^d PP possessed a plasmid replication protein encoding gene *repA*.

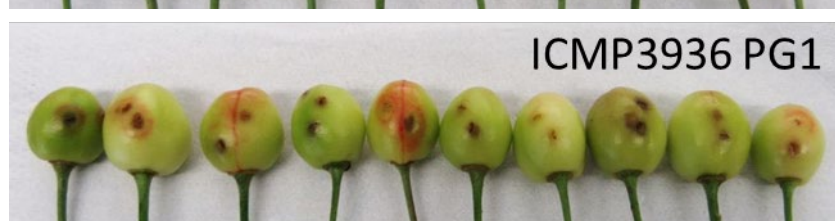
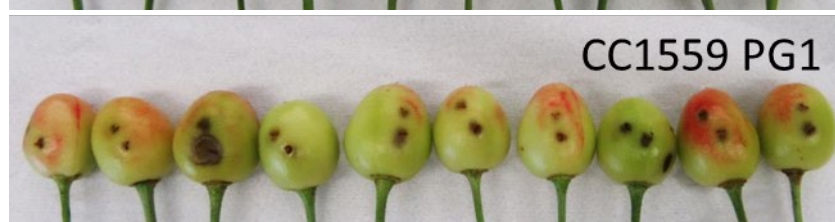
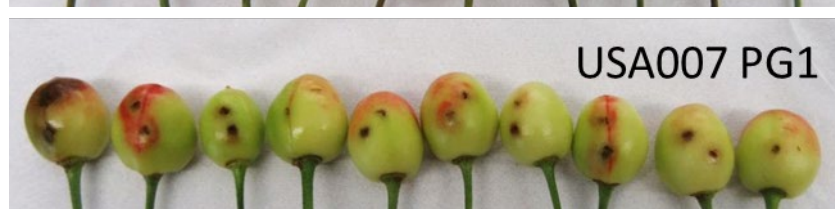
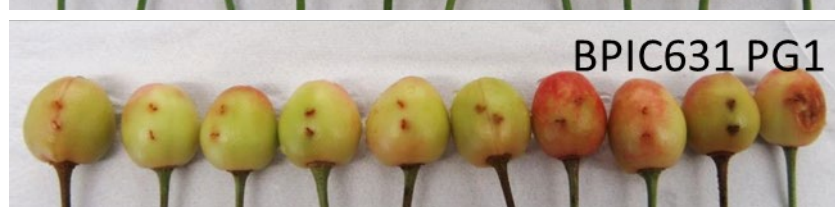
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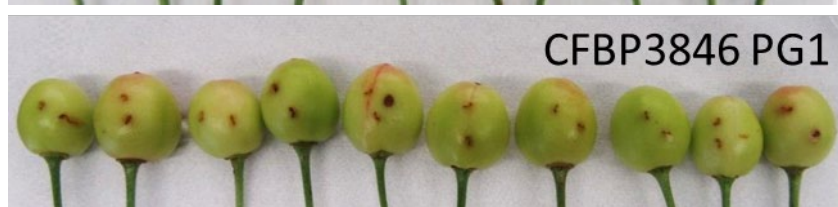
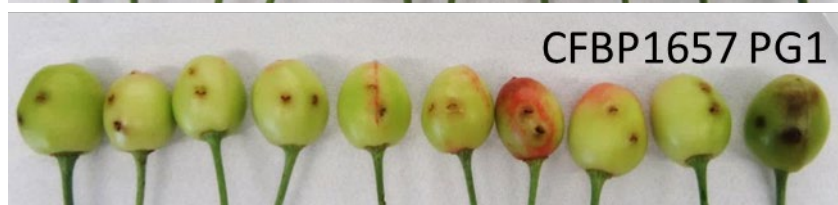
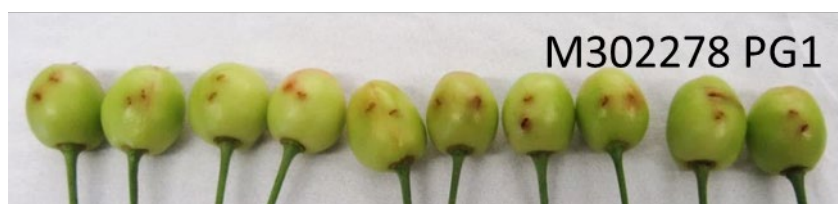
Table S4 Metrics of the Illumina MiSeq sequencing results for the two *Pseudomonas syringae* pv. persicae (Ppe) strains.

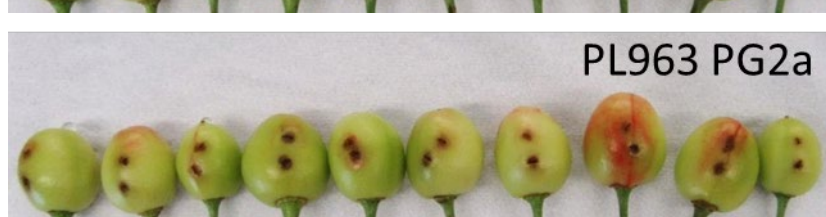
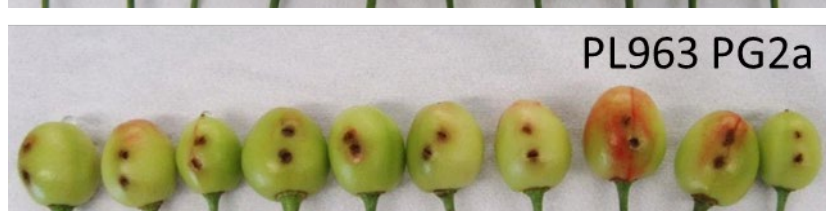
	Ppe CFBP 1573	Ppe NCPPB 2254
Total number of reads	1,948,134	935,008
Total number of contigs	214	246
Max. contig length (bp)	206,399	210,561
Min. contig length (bp)	549	536
Mean contig length (bp)	30,187	26,114
N₅₀ read length(bp)	67,876	64,693
Mean coverage (×)	61	43
Genome size (bp)	6,460,112	6,423,988
G+C content (%)	58.5	58.8
# CDS	6,079	5,990
NCBI accession numbers	ODAL01000001- ODAL01000214	ODAM01000001- ODAM01000246

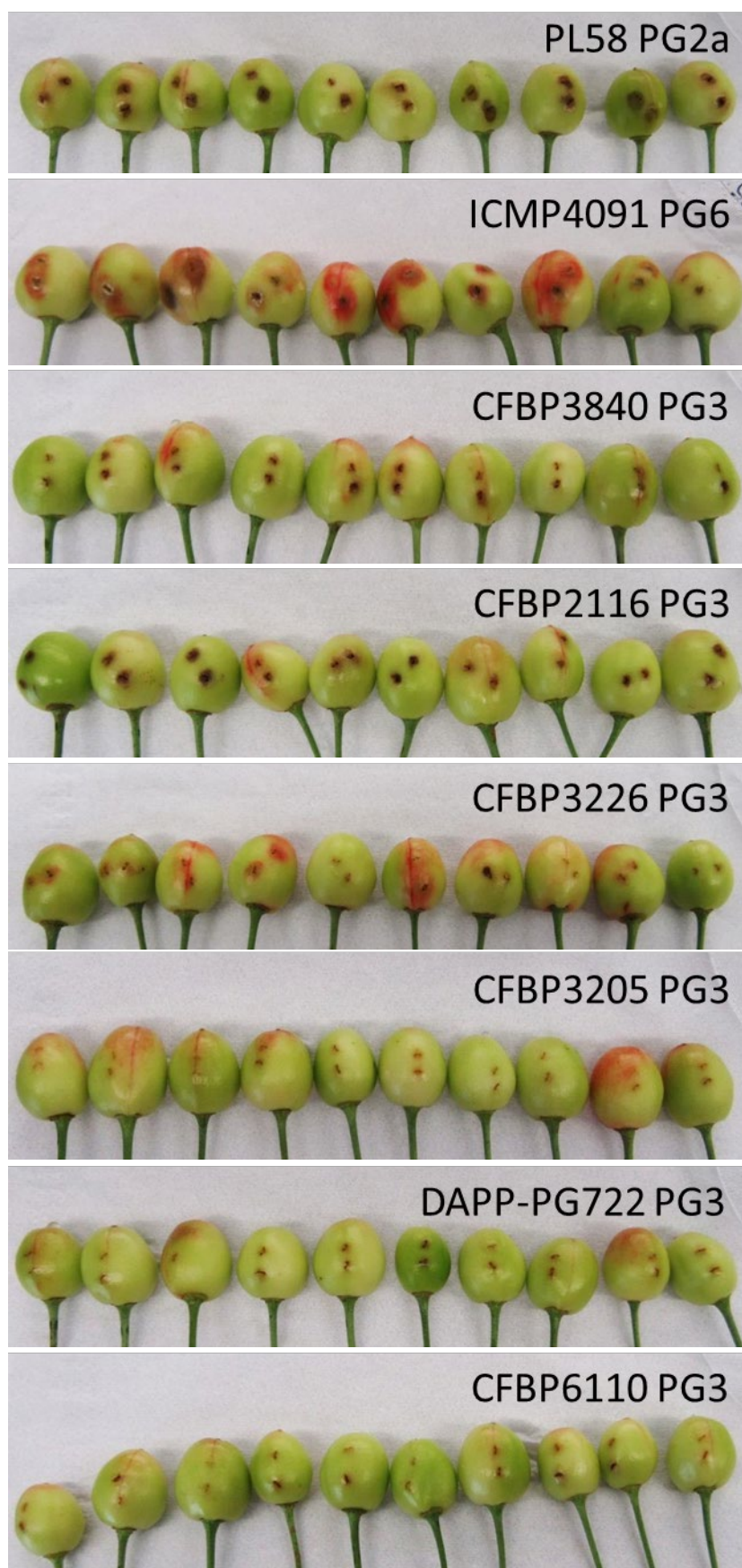
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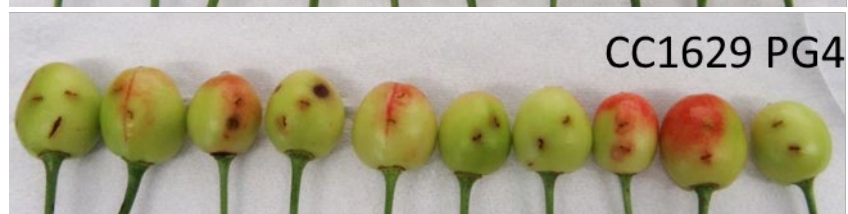
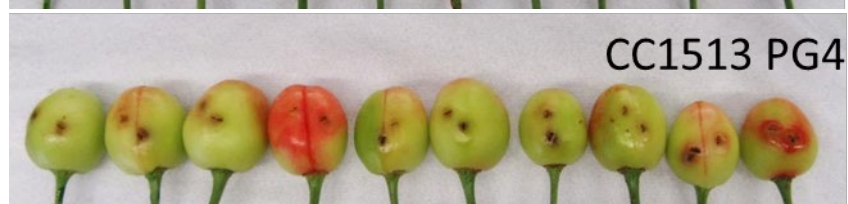
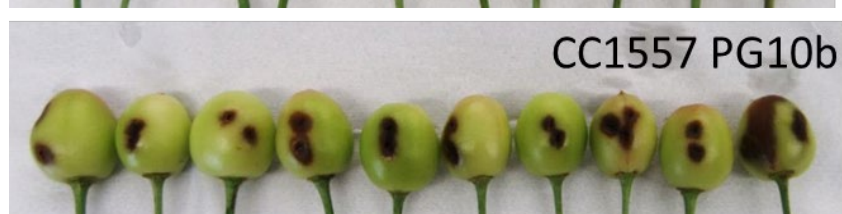
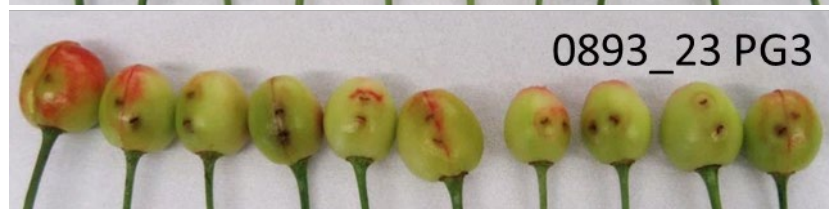












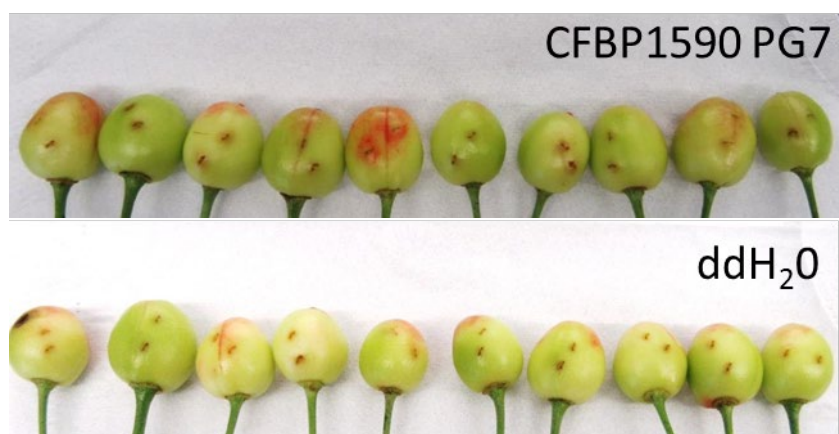


Figure S2 Pathogenicity test results performed on cherry immature fruitlets.

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