

Supplementary Figure 1. Pipeline for identifying and clustering *Phytophthora* effector families with homology to reference avirulence effectors



Supplementary Figure 2. Multiple effector families defined by orthogroup clustering are conserved within *Phytophthora* species. For each reference avirulence effector, an orthogroup with an effector with coverage above 80% is marked as the corresponding effector group. Light gray indicates absence of homologous effector. Abbreviations of species names are described in Supplementary Table 2.



Phylogenetic distance

Supplementary Figure 3. *Avr1*, *Avr3a*, *Avr8*, *Avramr1*, and *Avramr3* are conserved within *Phytophthora* species. The phylogenetic (patristic) distance between reference avirulence effector in *P. infestans* and the closest homolog in the other *Phytophthora* species were calculated from the phylogenetic tree in Fig. 1c, as previously described in Harant et al. (2022).



Supplementary Figure 4. Evaluation of structural predictions of effector domain regions. The numbers at the top of the figure show the number of predicted structures for each avirulence effector. The red horizontal line represents the pIDDT score cutoff for the effector structure to be used for downstream analysis.



Supplementary Figure 5. Structure-based clustering of avirulence effector homologs. The numbers at the top of the figure represent the cluster number. The reference avirulence effector included in each cluster is indicated at the bottom of the figure.



Supplementary Figure 6. Conservation ratio of protein sequence and structure for each effector homologs. The red line and R^2 value represent the Pearson correlation coefficient between normalized bit-score and normalized pTM score.



Supplementary Figure 7. Solanum NLRs recognizing PiAVR effectors also recognize P. parasitica homologs

(a) Representative images of lesion of *P. parasitica* (40402 strain) inoculated on *Solanum* NLR-expressed half compared to the *GFP*-expressed area of *N. benthamiana* leaves (ns: not significant). Expression of *Rpi-vnt1* induced weak cell death phenotype at 2 dpi on the infiltrated region of leaves (black spots). (b) Eight *Solanum* NLRs (*R1, R3a,* and *Rpi-blb2* are not presented cause they cannot induced cell death against *PpAVR* candidates) were co-expressed with their putative corresponding effectors of *P. parasitica* in *N. benthamiana* leaves. Representative image of positive cases are presented. (c) Average lesion size are presented with box plot. Total 8 *Solanum* NLRs were tested for resistance assay against *P. parasitica*. Expression of *Rpi-amr1* significantly reduced lesion size compared to GFP-expressed region of *N. benthamiana* leaves. Statistically significances were analyzed with unpaired *t*-test (**P<0.01).



Supplementary Figure 8. P. parasitica strains exhibited different phenotypes against Rpi-amr1 expression

(a) Representative images of lesion of *P. parasitica* (40164, 40402, and 40906 strains) inoculated on *Rpi-amr1*-expressed half compared to the *GFP*-expressed area of *N. benthamiana* leaves. (b) Average lesion size of *P. parasitica* inoculated on *GFP*-expressed left and right half of *N. benthamiana* leaves were statistically similar (ns: not significant). This result indicate that our inoculation method and environment conditions were even for each cases. (c) Average lesion size are presented with box plot. Total 8 *Solanum* NLRs were tested for resistance assay against *P. parasitica*. Expression of *Rpi-amr1* significantly reduced lesion size of *P. parasitica* 40164 and 40402 strains compared to GFP-expressed region of *N. benthamiana* leaves, but it was not working against 40906 strain. Statistically significances were analyzed with unpaired *t*-test (*P<0.05; ****P<0.0001).



Supplementary Figure 9. Solanum NLRs recognizing PiAVR effectors also recognize P. cactorum homologs

(a) Representative images of lesion of *P. cactorum* (40166 strain) inoculated on *Solanum* NLR-expressed half compared to the *GFP*-expressed area of *N. benthamiana* leaves (ns: not significant; nd: non-determined). Expression of *Rpi-vnt1* induced intensive cell death phenotype at 2.5 dpi on the infiltrated region of leaves (left half of leaf in the picture). (b) Five *Solanum* NLRs were co-expressed with their putative corresponding effectors of *P. cactorum* in *N. benthamiana* leaves. Representative image of positive cases are presented. (c) Average lesion size are presented with box plot. Total 5 *Solanum* NLRs (*Rpi-vnt1* was excluded due to auto-active cell death phenotype started from 2 dpi) were tested for resistance assay against *P. cactorum*. Expression of R8 and *Rpi-amr1* significantly reduced lesion size compared to GFP-expressed region of *N. benthamiana* leaves. Statistically significances were analyzed with unpaired *t*-test (***P<0.001; ****P<0.0001; nd: non-determined).



Supplementary Figure 10. Solanum NLRs recognizing PiAVR effectors also recognize P. palmivora homologs

(a) Representative images of lesion of *P. palmivora* (40410 strain) inoculated on *Solanum* NLR-expressed half compared to the *GFP*-expressed area of *N. benthamiana* leaves (ns: not significant). (b) Four *Solanum* NLRs (*R8* is not presented cause it cannot induced cell death against *PpalAVR* candidates) were co-expressed with their putative corresponding effectors of *P. palmivora* in *N. benthamiana* leaves. Representative image of positive cases are presented. (c) Average lesion size are presented with box plot. Total 4 *Solanum* NLRs were tested for resistance assay against *P. palmivora*. Expression of *R1* and *Rpi-amr1* significantly reduced lesion size compared to GFP-expressed region of *N. benthamiana* leaves. Statistically significances were analyzed with unpaired *t*-test (*P<0.05; **P<0.001; ****P<0.0001; nd: non-determined).



Supplementary Figure 11. *P. cactorum* and *P. palmivora* strains exhibited different phenotypes against expression of *R1*, *R8* or *Rpi-amr1*.

Average lesion size are presented with 10-90 percentile box plot. Total 4 and 5 *Solanum* NLRs were tested for resistance assay against *P. cactorum* and *P. palmivora*, respectively. Although expression of *R8* significantly reduced lesion size of *P. cactorum* 40166 strain, it was not working against 40183 strain. Similarly, while expression of *R1* significantly reduced lesion size of *P. palmivora* 40410 strain, it was not replicated against 40409 strain. Statistically significances were analyzed with unpaired *t*-test (**P<0.01; **P<0.01; ****P<0.0001; ns: not significant; nd: non-determined).



Supplementary Figure 12. Solanum NLRs recognizing PiAVR effectors also recognize P. capsici homologs

(a) Representative images of lesion of *P. capsici* (40476 strain) inoculated on *Solanum* NLR-expressed half compared to the *GFP*-expressed area of *N. benthamiana* leaves (ns: not significant). (b) Five *Solanum* NLRs (*R2* is not presented cause it cannot induced cell death against *PcAvr2* candidates) were co-expressed with their putative corresponding effectors of *P. capsici* in *N. benthamiana* leaves. Representative image of positive cases are presented. (c) Average lesion size are presented with 10-90 percentile box plot. Total 8 *Solanum* NLRs were tested for resistance assay against *P. capsici*. Expression of R1 and *R8* significantly reduced lesion size compared to GFP-expressed region of *N. benthamiana* leaves. Statistically significances were analyzed with unpaired *t*-test (****P<0.0001).



Supplementary Figure 13. HR phenotype screening of T₀ transgenic *N. benthamiana*

(a) Representative images of positive and negative case of HR screening test. Expression of *Avr8* with *GFP* (left, marked with green arrow in picture) through the agroinfiltration triggered clear cell death response in T_0 plant line #4, but not in line #10. *Avr8/R8* were co-expressed as a positive control. (b) Among the 30, 15, and 21 T_0 plant thought to express *R1*, *R8*, and *Rpi-amr1*, respectively, 10, 9, and 7 lines remain after the HR screening step. T_1 seeds were harvested from 6~9 months old *N. benthamiana*. (c) Cell death intensity against corresponding avirulence effector of *P. infestans* in candidate plants thought as expressing *R1*, *R8*, or *Rpi-amr1* is presented as dot blot.



Supplementary Figure 14. T₁ plants expressing *R1* or *R8* were resistant against root infection of *P. capsici* (1st trial).

(a) Picture of root inoculated plants (wild type, *R1*, *R8*, and *Rpi-amr1* transgenic *N*. benthamiana, 35 days old) at 7 days post inoculation. Each plant is inoculated with zoospores of *P. capsici*. *R1* (#3 and #6) and *R8* (#4) plants exhibited resistance phenotypes while WT and *Rpi-amr1* transgenic plants were completely wilt and shrivel. The number of wilt/total plants is presented as fraction above each plant line. (b) The number of healthy, wilt, and dead plants are presented as bar graph. Approximately 30% of *R1* (#3 and #6) and *R8* (#4) plants were also exhibited wilt phenotypes due to heterogeneity of T₁ plants. (c) The ratio of healthy/total plants of each line is presented as line graph. Approximately 30% of *R1* (#3 and #6) and *R8* (#4) plants were also exhibited wilt phenotypes due to heterogeneity of T₁ plants.



Supplementary Figure 15. T₁ plants expressing *R1* or *R8* were resistant against root infection of *P. capsici* (2nd trial).

(a) Picture of root inoculated plants (wild type, *R1*, *R8*, and *Rpi-amr1* transgenic *N. benthamiana*, 29 days old) at 4 days post inoculation. Each plant is inoculated with zoospores of *P. capsici. R1* (#3 and #6) and *R8* (#4 and #11) plants exhibited resistance phenotypes while WT and *Rpi-amr1* transgenic plants were completely wilt and shrivel. The number of wilt/total plants is presented as fraction above each plant line. (b) The ratio of healthy/total plants of each line is presented as line graph. Approximately 30% of *R1* (#3 and #6) and 50% *R8* (#4 and #11) plants were also exhibited wilt phenotypes.



Supplementary Figure 16. T₁ plants expressing *R1* or *R8* were resistant against root infection of *P. capsici* (3rd trial).

(a) Picture of root inoculated plants (wild type, *R1*, *R8*, and *Rpi-amr1* transgenic *N. benthamiana*, 30 days old) at 6 days post inoculation. Each plant is inoculated with zoospores of *P. capsici. R1* (#3 and #6) and *R8* (#11 and #13) plants exhibited resistance phenotypes (*R8* exhibited relatively less intensive resistance) while WT and *Rpi-amr1* transgenic plants were completely wilt and shrivel. The number of wilt/total plants is presented as fraction above each plant line. (b) The ratio of healthy/total plants of each line is presented as line graph. Approximately 30% of *R1* (#3 and #6) and 70% *R8* (#11 and #13) plants were also exhibited wilt phenotypes.



Supplementary Figure 17. Conservation ratio of protein sequence and structure for each cloned effector homologs. Red and blue dots represent HR-positive and HR-negative, respectively.



Supplementary Figure 18. Comparison of protein structures of HR-positive and HR-negative effectors. HR-positive (a, c, e) and HR-negative (b, d, f) effectors are compared against the reference avirulence effectors PiAvr1 (a-b), PiAvr8 (c-d), and PiAvramr1 (e-f), respectively. Effector homologs of one species are shown in the same color.

(a)

PiAvr1.PITG_16663 PcacAvr1a.KAG2773429.1 PpalAvr1a.POM66420 PpalAvr1b.POM58004 PcAvr1a.PHYCA_113929 PcAvr1b_1.PHYCA_567591 PcAvr1b_2.PHYCA_567591 PcAvr1c.PHYCA_129759 PpAvr1a.PPTG_12206 PpAvr1b.PPTG_20226 PcacAvr1b.KAG2771952.1

PiAvr1.PITG 16663 PcacAvr1a.KAG2773429.1 PpalAvr1a.POM66420 PpalAvr1b.POM58004 PcAvr1a.PHYCA_113929 PcAvr1b_1.PHYCA_567591 PcAvr1b_2.PHYCA_567591 PcAvr1c.PHYCA_129759 PpAvr1a.PPTG_12206 PpAvr1b.PPTG_20226 PcacAvr1b.KAG2771952.1

1 MVSKLPSFIESFVKNRK IESWIQNKVTDDFVLSELKLVRLPGTSLADDPNFKLFQKFKIGGWLEEKATTTKAWENL	GLDSLPFDQVSKID	90
1 MGQLMPSFIKSRLTNWRINSWIONNRPDDYVLRKLKLTGLAEKTLTENPNYKIFOKFKVNGWLKERATTTKAWGDL	GL TR FSMY DV H <mark>K</mark> AD	90
1 MG - LQ <mark>S F</mark> ISSLLSTRQ INSWIKAGKTDD FVMNTLGLTGLTGEKLKNNPN FKK FQE FQVGRWLKENTPTSSVLENLK	KLNELDYAAL I TAD	88
1 MG LL <mark>S</mark> F L <mark>PS</mark> NWQ IKFWIKTG <mark>KTDDFVM</mark> NTLGIAGLTGEKLKNNPNFKKFQQFQVGRWL <mark>K</mark> EKTPTSLVLEKL	KLNELDYAAL I KAD	85
1 MGG-FTTYVKDSLTKWRINSKIKSWKNKKTDEYVLKKLGLSTLTGKDLVNAPKYSQFQDFKVGMVLKEATPTTTVFNTL	GLNKVE - GAVENAD	92
1 MGG - FTSYLMDSFTKWRINSKINSWNKQKTDEYVLAKLGLSTLTGKELVKAAKYPQFQDFKVGVWLKEATPTTSVFSTL	GLDKVE - GAVE <mark>K</mark> AD	92
1 MGG - FPSYLMDSFTKWR INSKI NSWNKQK TDEYVLAKLGLSTLTGKELVKAAKYPQFQDFKVGVWLKEATPTTSVFSTL	GLDKVE - GAVEKAD	92
1 MGG-FPSYLKDSFTKWFINSKIKSWKKOKTDEYVLSKLGLSTLTGKDLVNAPKYSOFODFKVGMVLKEATPTTTVFNTL	GLNKVE - GAVE <mark>K</mark> AD	92
1 MGVLIPOLKMMBVTSWIKNGKSDDYVMDKLKLTGLIGRALTEDPNFKYFOKFKVDGWLKKGASTTTAWDDLC	GLNS IALGEVTKVD	85
1 MGVL IPGLKNWRVTSWIKNGKSEDYVLNKLHLTNL IGRAL IDDPN FKY FOK FKYDGWLKOKAST TAAWDOLO	GLSTLSVNEITKVD	85
1 MSLPVPSHIKSRVTNWRINSWIKNRYSDDYVLVNLRLIGLAGKILIKHINFKIFOKFKIDGWLKESAIIIKAWDHU	<u>GLKGLNVAQLKELT</u>	90
91 EFKTYTQYYTVLNKKASKLDIDQWHGLLS <mark>GGS</mark> PEELMAKAMILRTLG <mark>R</mark> -DVLERRVMLGGHVVVP	F	155
91 EFKTYTQYVTVLNKKASKLD I DQWHGLLS <mark>GGSPEE</mark> LMAKAM I LRTLGR - DVLERRVMLGGHVVVP 91 <mark>GFNTYTHYV I ALFKK</mark> AKKAD <mark>SE</mark> EWSRLLRER <mark>SVTE</mark> LVTKTM I L <mark>R</mark> GFA <mark>R</mark> - DDQRLR <mark>SMLG</mark>	F	155 149
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91 EFKTYTQYVTVLNKKASKLDIDQWHGLLSGGSPEELMAKAMILRTLGR - DVLERRVMLGGHVVVP - 91 GENTYTHYVIALEKKAKKADSEWSRLLRERSVTELVTKTMILRGFAB - DDQRLRSMLG - 89 GYNTYVVVFDLGKRANKYNIEDWPTLFGTGTIEQLKHRAGLLRWWNN - EDLDMFMASTIRSQQV - 86 GYNTYVNYVFDLGKRANQYDIEDWPKLFGTGTIEQLQHRAGLLRWWNN - DNLDMFMASTIRSQQV - 93 DFGTYVKYVILGEKADNYPLSQWPRLFGGGSLEQLELKRKILBLQKR - NVLEINFMLG - 93 DFGTYVKYVMALGEKADDYPITRWRELFGGGSPEQLKLKRQLLFLARR - DEFDIRIMLG -	F L L	155 149 153 150 150 150 150
91 EFK TYTQYVTVLNK KASKLD I DQWHGLLSGGSPEELMA KAMI LRTLGR - DVLERRVMLGGHVVVP 91 GFN TYTHYV I A LFK KAKK ADSEEWSRLLRERSVTELVTK TMI LRGFAB - DDORLRSNLG 89 GYN TYVKYVFDLGK RANK YN I EDWPTLFGTGT I EQLCHRAGLLRWMNN - EDLDMFMAS TIRSQV 86 GYN TYVNYVFDLGK RANK YN I EDWPKLFGTGT I EQLCHRAGLLRWMNN - DNLDMFMAS AIRSQV 93 DFGTYVKYV I TLGEKADNYPLSQWPRLFGGGSLEQLELKRK I LBLQKR - NVLE INFMLG 93 DFGTYVKYVMALGEKADDYP I TRWRELFGGGSPEQLKLK RQLLFLARR - DEFD I RIMLG 93 DFGTYVKYVMALGEKADDYP I TRWRELFGGGSPEQLKLK RQLLFLARR - DEFD I RIMLG 94 DFGTYVKYVMALGEKADDYP I TRWRELFGGGSPEQLKLK RQLLFLARR - DEFD I RIMLG 95 DFGTYVKYVMALGEKADDYP I TRWRELFGGGSPEQLKLK RQLLFLARR - DEFD I RIMLG 96 TFRIYQY I TELNKKARNI FMDRWSNLFGGGSETELAIKYSILAKLGR TDSIDLQLMVESRGMI AFLKAVKKHGKILDERV		155 149 153 150 150 150 150 150 178
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(b)

PiAvr8.PITG_07558 PpAvr8a.PPTG_08692 PpAvr8b.PPTG_18711 PcAvr8a.PHYCA_97196 PcAvr8b.PHYCA_133657 PsAvr8a.PHYSO_286355 PsAvr8b.PHYSO_288926 PcacAvr8b.KAG2786055.1 PpalAvr8a.POM63697.1 . PpalAvr8b.POM74542.1 PpalAvr8c_1.POM58761.1 PpalAvr8c_2.POM58761.1 PcAvr8c.PHYCA_101579 PsAvr8c_1.PHYSO_286372 PsAvr8c_2.PHYSO_286372

PiAvr8.PITG_07558 PpAvr8a.PPTG_08692 PpAvr8b.PPTG_18711 PcAvr8a.PHYCA_97196 PcAvr8b.PHYCA_133657 PsAvr8a.PHYSO_286355 PsAvr8b.PHYSO_288926 PcacAvr8b.KAG2786055.1 PpalAvr8a.POM63697.1 PpalAvr8b.POM74542.1 PpalAvr8c_1.POM58761.1 PpalAvr8c_2.POM58761.1 PcAvr8c.PHYCA_101579 PsAvr8c_1.PHYSO_286372 PsAvr8c_2.PHYSO_286372

PiAvr8.PITG_07558 PpAvr8a.PPTG_08692 PpAvr8b.PPTG_18711 PcAvr8a.PHYCA_97196 PcAvr8b.PHYCA_133657 PsAvr8a.PHYSO_286355 PsAvr8b.PHYSO_288926 PcacAvr8b.KAG2786055.1 PpalAvr8a.POM63697.1 PpalAvr8b.POM74542.1 PpalAvr8c_1.POM58761.1 PpalAvr8c_2.POM58761.1 PcAvr8c.PHYCA_101579 PsAvr8c_1.PHYSO_286372 PsAvr8c_2.PHYSO_286372 1

1

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1

1

1	MTDTTLDSEDNNEDSGERSWKHVKVRWKLE-TEKSDDFVRKALKLNGLDDTAMKAHKNYKYYAYFAKKAEDYLFNKWLRNH	VPT	84
1	MASTARKVEGINE	ITT.	84
1		1.1	70
1	MGNMFK IWWKYVKVQLWLE- IKM5KEYVKTALKLDGLDDADTK IHKNYKYYSYFADKSEEYRLTGWLQKD	Y 1 1	12
1	MGSLITK	VPT	76
1	MG	ATT	69
4	NOT THAT A CARDEN A		03
1	NGD TDVPV THINKDGNVKQRTGGSSLLTKNANAQVTWWLE-AGASDDTVKGALALKGLKGDALKPHNNKYYAHPVKASEEYQLNKWLTKN		93
1	MS	VST	69
1	M	FTT	64
1		TTT	67
3	M		0/
1	M	YTT	67
1	MGFIKYLKVQWVLE-TGKSDDHVRKALKLNGLDDATMKTRPNYKYYKYFARKLVDYKLAKWLQKKI	FTT	67
1		ETT	67
1		1.1	
1	MGITIPTKVKLFWWLEFKNKPNSYVKTKLGLDKLDDVALKNHKNYPLYLKYKDKREEYQLWELAGRS	YST	70
1	MEN	VST	72
1	MEN	VST	72
			12
		-	
85	FEAW-KSLNLG-KITKADQLKEIANTKNFISYSRFVKQYDDNVVSTLNAGYNPPVVAVARGASEAEITARTMIMASARRDDI	DVA 1	166
85	EDAW-KNIKID-RIT	KVA 1	166
70			154
13	DAWHRELNEN-RTICANELINKVEATDARWIKHTVNMHDTLTVRQMITGNAPE-VVVDRGATAREMTARTTTMAKARRSD	KAA	154
77	YSAW-VKL <mark>GLG-SID</mark>	AYA 1	153
70	YSVW-KILKLE-NVSSKOLKSSPAYRTYVDYVNOFDDLSQRKWGAYKLPEMVGSSKTEMMAKSSIWGEAKRSE/	AYV 1	143
1			175
54			110
70	EQAW-KNLGLH-KLD	DYV 1	44
65	FQVW-KTLKLD-KITKYQQLDDILDTDAFRLYMRYVKHFNRGVVSKLKNGYKPDGVMVERGASDAEMWVRALIMAQAGMKDE	EYA 1	146
68	ETWW-KELGES-HITTVNOLDDIMDIPNEHIN TRYVNDEDTNVERTIVAGYNPPAVMIDPWASEAEMVMPTTIMAOAGPDD		140
			1.40
58	FNTW-TENGEH-DVVLKISDDLVKLMSTANGYTMKDYVNKADFYADASLKAGYKPP-TSMDSYATEREKTARTTTMANAHTKD	AVA 1	150
68	FNVW-TKLGFQ-DVTLKTSDDLLKLLNTANGKIYKRYVNGVDYRARKSLYAGYKPS-ISIDSYATEAEMIARTTIMANAEKNE/	AVA 1	150
68	ENVW-TKLGEQ-DVTLKTSDDLLKLLNTANGKIMKEVVNGVDYRARKSLYAGYKES-IS DSYATEAEMIARTTIMANAEKNE/	AVA 1	150
71	Y EW KNECLD, KILLTI BROMTYDDIAAE I KKI EOTEREDWK RYAKEEDOURI ANECSOVYDDTYE IDENASTI (EKYVRAHJAAADAK IDKE		160
~	TREW-RIEGED-RITTERROWTODTRAETREEGTEFFRUTRETAREFDURREAMPOSOTTEDTFFDENASTVERTWAARVWADARTDE		102
73	YDAW-VKLIGLE-DVP	DYV 1	148
73	YDAW-VKLGLE-DVP		148
1122			
-			
5/		2	205
67	KVLLGMTV - PGH PTIPLRGNDLMK VDYKFFTLFLEKKAK	2	210
55		2	208
= 4			202
54		4	202
44	MALDMEG	1	153
76	KLALGMTE GYN-RMKVLKOAALEGDKDFNYFLLFVREREPAMRDELARLE - KLAKLSKRORKAOREMLDDLKLIEKYRO RNGG AG	2	258
15		1	178
47			170
47	QVLLGLIII-PDR-VNKLLKGDALKAHPDYKYFKLFLAKAETRRDAEINKIR-MRANA	2	202
50	KVLLGNTV - PGK PREVLQCDALKE GA I PY FQMFQKLKKELSV	1	196
51			217
		2	/
51		2	213
51	KALLGLIV - PGK PLTTLKNDALQKHRGYTYFEYYQGLRGLKVNDK ENFEKLFQTLK TRN - AAT TA	2	213
33		1	193
10			104
+9			191
49	KAALGILGKSGEALTTHAGYKYYKQYLGHLEEAAA	1	191



Supplementary Figure 19. Sequence alignments of cloned effector domain for HR-positive and HR-negative effectors in a) Avr1 b) Avr8 c) Avramr1. The top and bottom of the thick solid lines represent HR-positive and HR-negative effectors, respectively. Sequences are colored according to amino acid properties defined in the Clustal X color scheme implemented in Jalview. Red, blue, and yellow boxes indicate each WY domain region, and black boxes indicate sequences that differently conserved between HR positive and negative.

Name	PITG locus_tag	UniprotID (Swiss-Prot)
Avr1	PITG_16663	sp_D0NVB5_AVR1_PHYIT
Avr2	PITG_22870	
Avr3aEM	PITG_14371	sp_D0NPN8_A3AEM_PHYIT
Avr3aKI	PITG_14371	sp_E2DWQ7_A3AKI_PHYIN
Avr3b	PITG_18215	sp_D0NXM3_SFI7_PHYIT
Avr4	PITG_07387	sp_B1NNT7_AVR4_PHYIT
Avr8	PITG_07558	
Avr10	PITG_11484	sp_D0NIW0_AVR10_PHYIT
Avramr1	PITG_07569	
Avramr3	PITG_21190	
Avrblb1	PITG_21388	sp_D0P3S7_ABLB1_PHYIT
Avrblb2	PITG_04085	
Avrblb2	PITG_04086	
Avrblb2	PITG_04090	
Avrblb2	PITG_18683	sp_D0NZB7_BLB2B_PHYIT
Avrblb2	PITG_20300	sp_D0P1A8_ABLB2_PHYIT
Avrblb2	PITG_20301	
Avrblb2	PITG_20303	sp_D0P1B2_SFI8_PHYIT
Avrvnt1	PITG_16294	sp_D0NTY1_AVNT1_PHYIT

Supplementary Table 1. List of avirulence effectors used in this study

Species	Prefix	Reported host plants	Homolgous RXLR effectors	Database	e Download URL
Phytophthora infestans	PHIF	Potato, tomato	124	OGOB	https://ogob.ie/v1/gob/data.html
Phytophthora parasitica	PHPA	Potato, egg plant, pepper, tobacco	70	OGOB	https://ogob.ie/v1/gob/data.html
Phytophthora cactorum	PHCR	Strawberry	35	NCBI	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_016864655.1/
Phytophthora megakarya	PHMG	Cocoa	208	NCBI	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_002215365.1/
Phytophthora palmivora	PHPV	Phalaenopsis	72	NCBI	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_002911725.1/
Phytophthora capsici	PHCA	Pepper, pumpkin, cucumber	32	OGOB	https://ogob.ie/v1/gob/data.html
Phytophthora sojae	PHSO	Soybean	74	OGOB	https://ogob.ie/v1/gob/data.html
Phytophthora ramorum	PHRA	Oak tree	27	OGOB	https://ogob.ie/v1/gob/data.html
Hyaloperonospora arabidopsidis	HYAP	Arabidopsis	2	OGOB	https://ogob.ie/v1/gob/data.html
Phytophthora kernoviae	PHKE	Beech tree, Azalea	3	OGOB	https://ogob.ie/v1/gob/data.html
Phytopythium vexans	PPVX	Citrus	0	OGOB	https://ogob.ie/v1/gob/data.html
Pythium ultimum	PYUU	Corn, potato	0	OGOB	https://ogob.ie/v1/gob/data.html

Supplementary Table 2. The number of homologous effectors in selected species

Supplementary Table 3. *Phytophthora* strains used in the study

Species	Strain number	Host plant species	Reference ^a
Phytophthora infestans	T30-4	Potato	(Haas et al., Nature 2009)
Phytophthora parasitica	40164	Potato	KACC
Phytophthora parasitica	40402	Egg plant	КАСС
Phytophthora parasitica	40906	Tobacco	KACC
Phytophthora cactorum	40166	Apple tree	КАСС
Phytophthora cactorum	40183	Strawberry	KACC
Phytophthora palmivora	40409	Cymbidium	КАСС
Phytophthora palmivora	40410	Fig tree	KACC
Phytophthora capsici	40476	Chili pepper	KACC
Phytophthora sojae	40412	Soy bean	KACC
Phytophthora sojae	40468	Soy bean	KACC
Phytophthora sojae	48989	Soy bean	KACC

a) KACC: Korean Agricultural Culture Collection, https://genebank.rda.go.kr/eng/uat/uia/actionMain.do

Supplementary Table 4. Solanum NLRs used for the functional validations

Gene	Promoter/terminator	Reference*	Solanum species
R1	p35s / tNOS	35	S. demissum
R2	p35s / tNOS	36	S. demissum
R3a	Native elements	37	S. demissum
R8	Native elements	38	S. demissum
Rpi-amr1	p35s / tNOS	39	S. americanum
Rpi-blb1	p35s / tNOS	40	S. bulbocastanum
Rpi-blb2	Native elements	41	S. bulbocastanum
Rpi-vnt1	p35s / tNOS	42	S. venturii
			*reference in manuscript