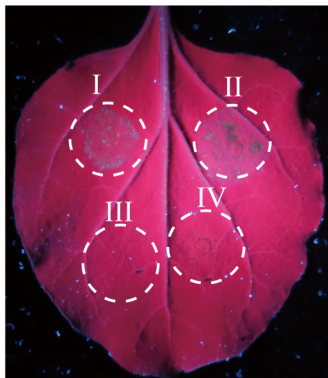
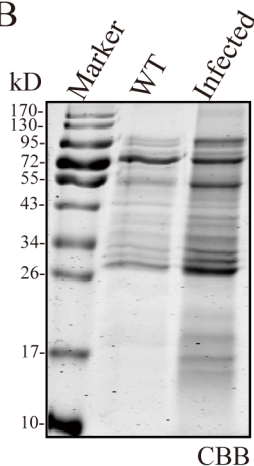


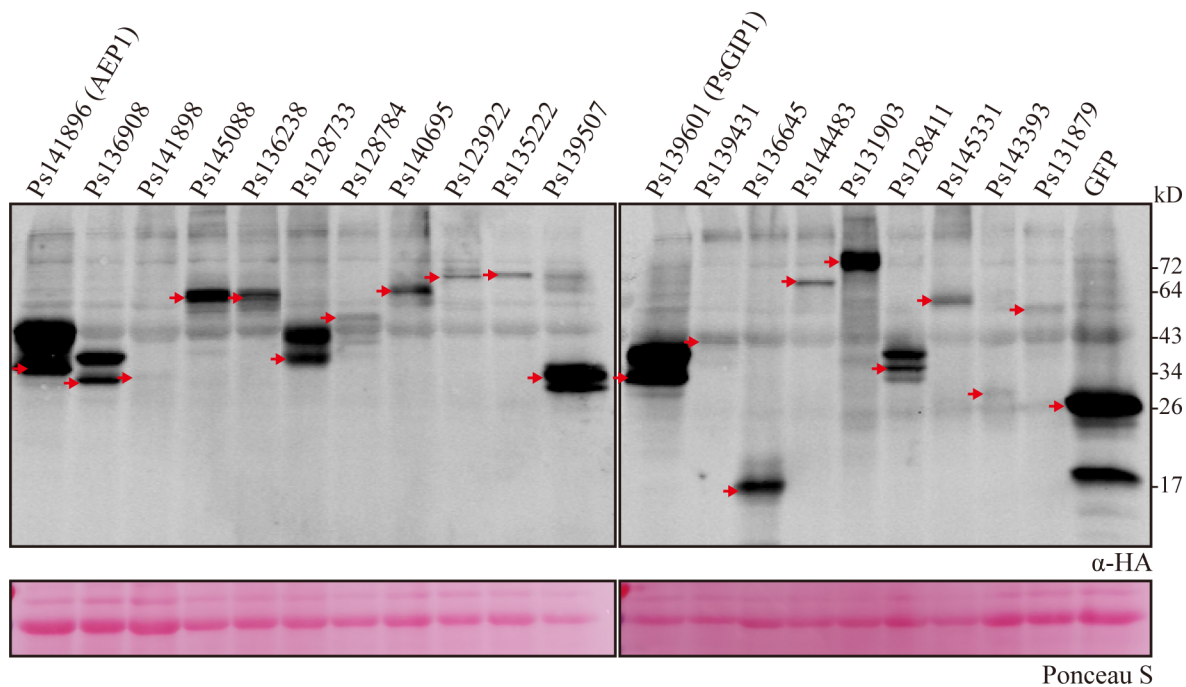
A



B



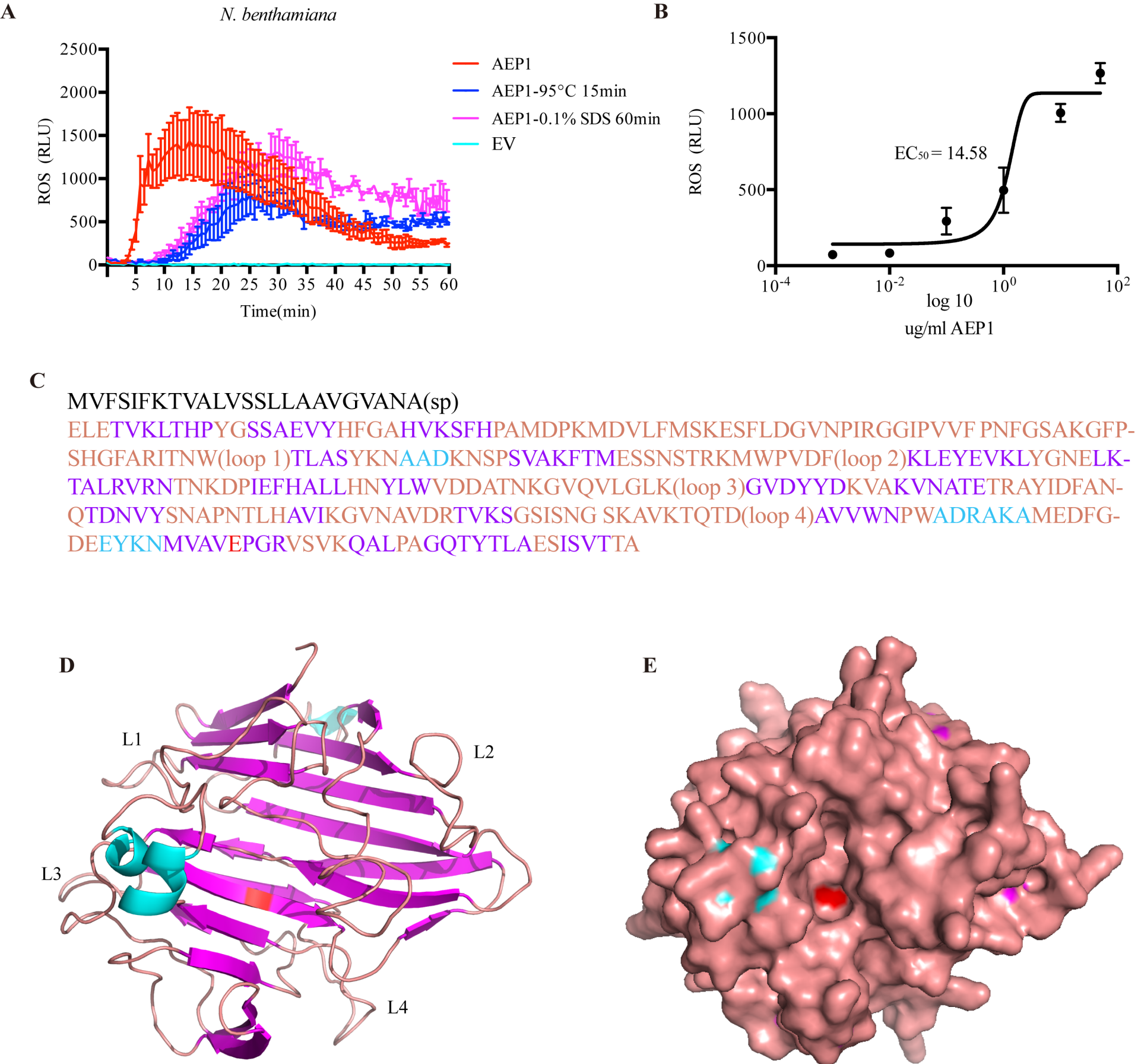
Supplemental Figure S1. Apoplastic fluid from *P. sojae* infected soybean leaves triggers cell death in *N. benthamiana*. A, Infected apoplastic fluid (I, II), protease K treated-infected apoplastic fluid (III), uninfected apoplastic fluid (IV). Cell death was photographed 4 days after infiltration. B, Uninfected (WT) or infected apoplastic fluid was run in SDS-PAGE and stained with Coomassie brilliant blue (CBB).



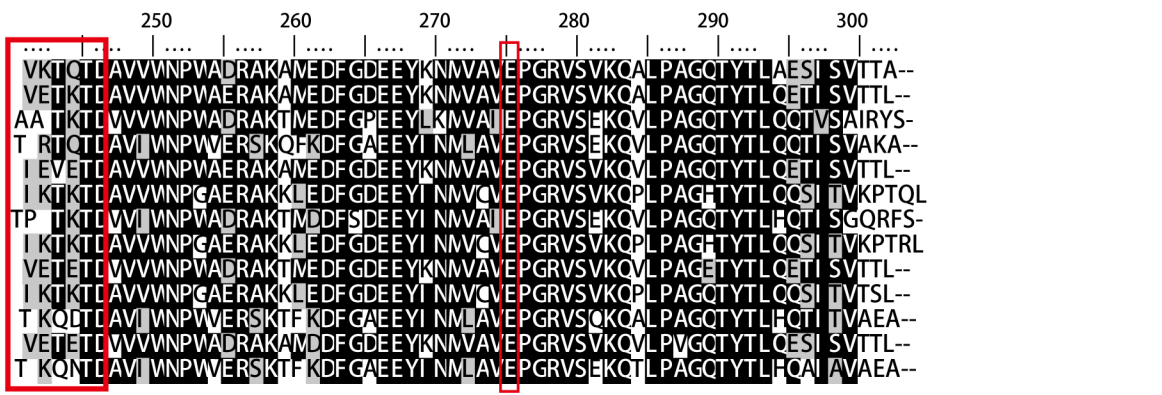
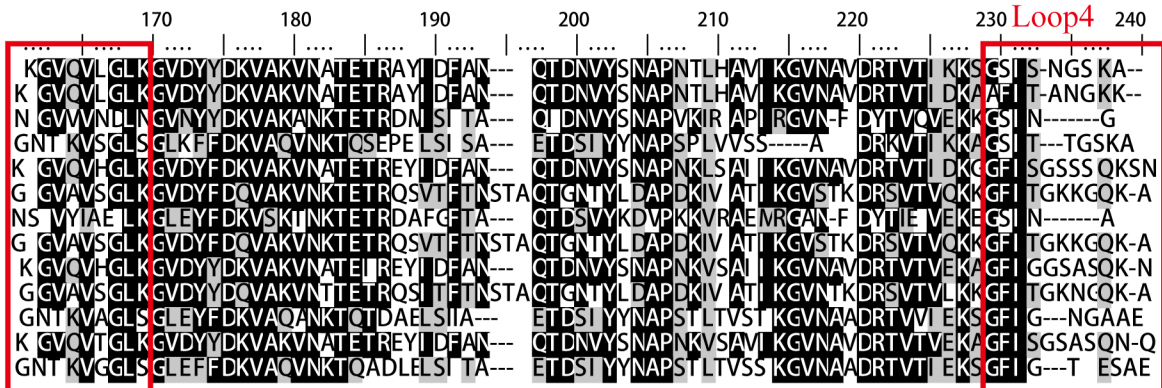
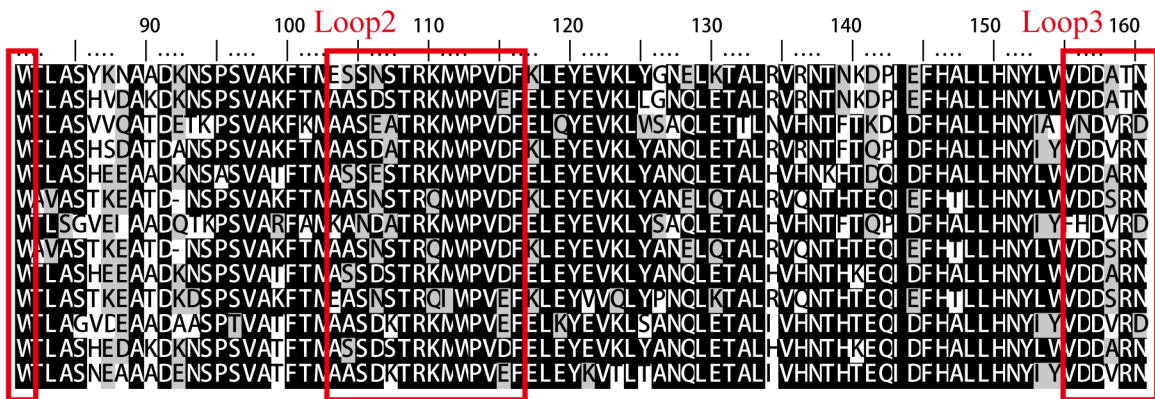
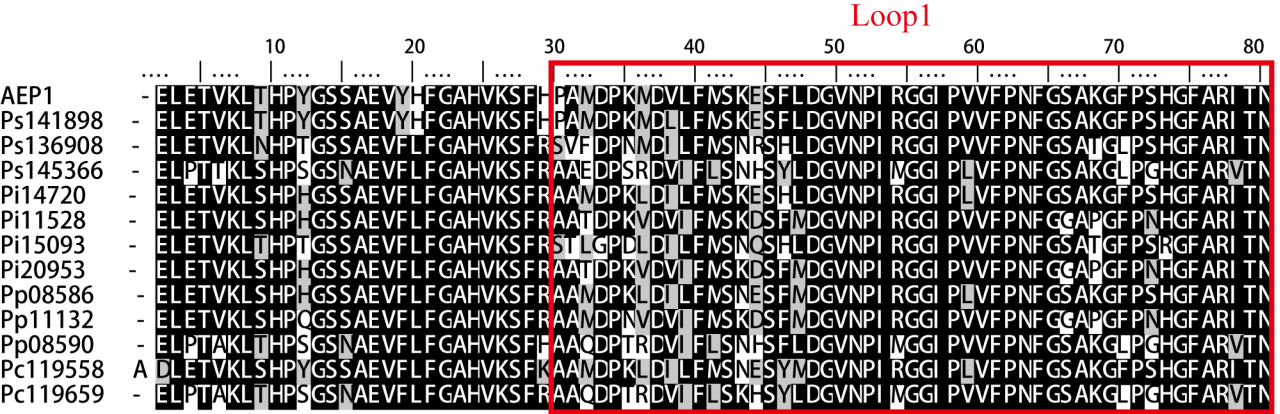
Supplemental Figure S2. Detection of transiently expressed proteins by western blot. Expected protein bands were indicated by red arrowheads. Ponceau staining was used to indicate equal loading in each sample.

JGI ID (<i>Phytophthora sojae</i> v1.1)	No. of Peptide	Peptide Sequence	Hits in soybean	Protein Function prediction
141896	5	AMEDFGDEEYKNMVAVEPG R	14/20	Aldose 1 -epimerase
		ESFLDGVNPIR	0/11	
		LTHPYGSSAEVYHFGAHVK	14/19	
		MDVLFMSK	0/8	
		NTNKDPIEFHALLHNYLWVD DATNK	0/25	

Supplemental Figure S3. Unique peptides matching AEP1 identified in the apoplast fluid.

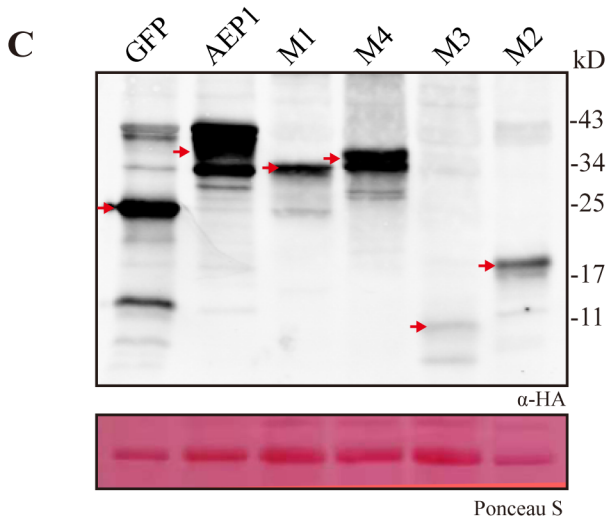
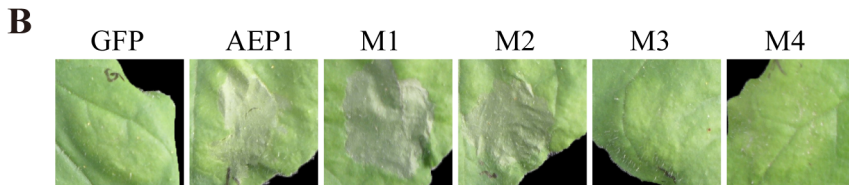
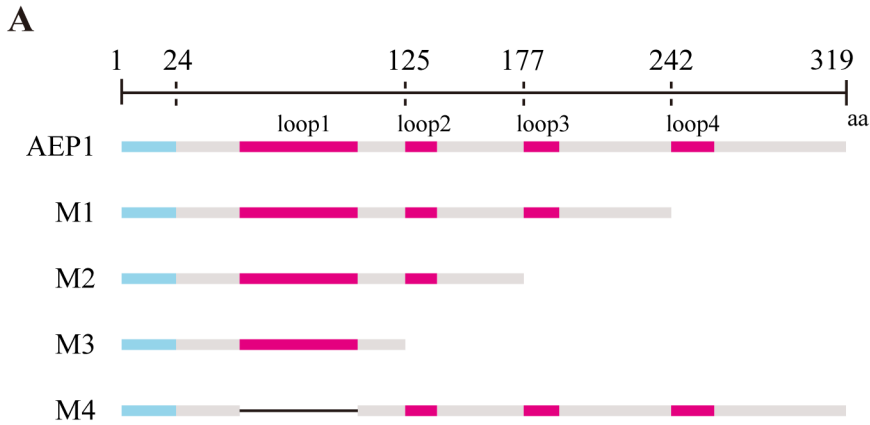


Supplemental Figure S4. Physico-chemical properties of AEP1 protein. A, Production of reactive oxygen species (ROS) in *N. benthamiana* leaves treated by 1 μ M AEP1, heat-treated 1 μ M AEP1 or SDS treated 1 μ M AEP1. EV was used as a negative control. Mean values \pm SE of three replicates are shown. B, Dose-response relationship for AEP1-induced ROS in *N. benthamiana* leaves. A concentration gradient of AEP1 protein (0.001 μ g/ml, 0.01 μ g/ml, 0.1 μ g/ml, 1 μ g/ml, 10 μ g/ml and 50 μ g/ml) was tested. The maximums of ROS burst in 1 hour were calculated. Mean values \pm SE of three replicates is shown. C, The predicted secondary structure of AEP1. Helix, sheet and loop are marked as cyan, magenta and lightpink. D, AEP1 protein structural model is built. 2ciq (a hexose-6phosphate mutarotase, yeast ymr099c) was designed as template (32.15% identity with AEP1). Loops containing more than 10 amino acids are signed as loop1, loop2, loop3 and loop4. E, The surface of AEP1 protein structure. The catalytic amino acid E292 is marked as red.



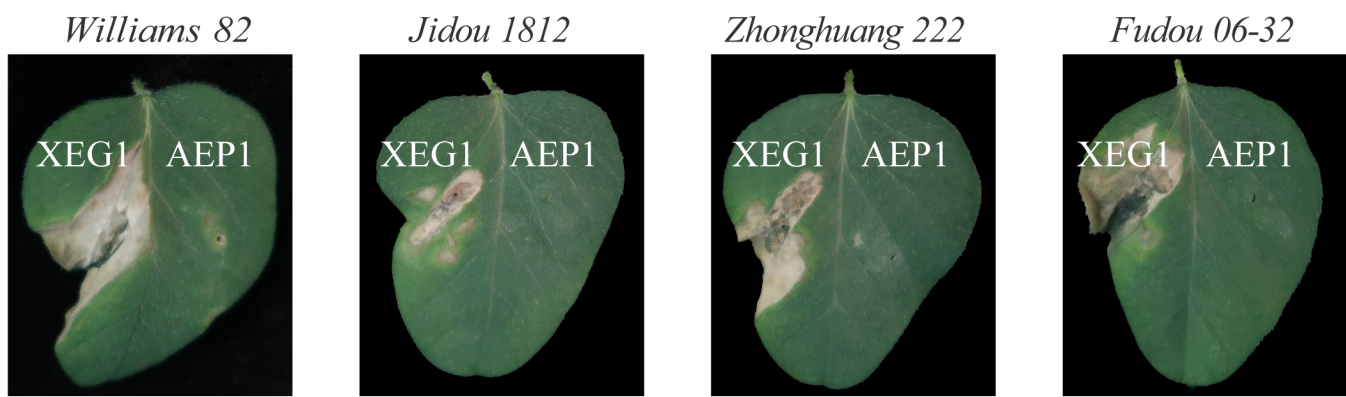
catalytic site

Supplemental Figure S5. Sequence (without signal peptide) alignment of secreted aldose 1-epimerase in different *Phytophthora* spp. 4 loops and catalytic amino acid is framed by red boxes.

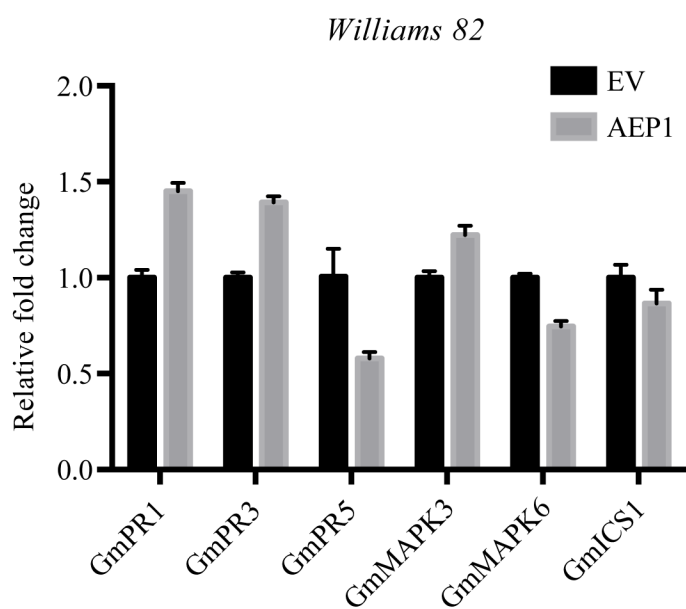


Supplemental Figure S6. The N-terminal region is required for AEP1 triggered cell death. **A**, The schematic of AEP1 and deletion mutants. **B**, Cell death triggered by AEP1 or deletion mutants. AEP1 and mutants were transiently expressed in *N. benthamiana* leaves. Cell death was photographed at 4 dpi. The background of photo was deducted for a better display. GFP was used as a negative control. **C**, Expression of AEP1 and mutants detected by western blot using anti-HA. Ponceau staining was used to indicate the amount of loading in each sample.

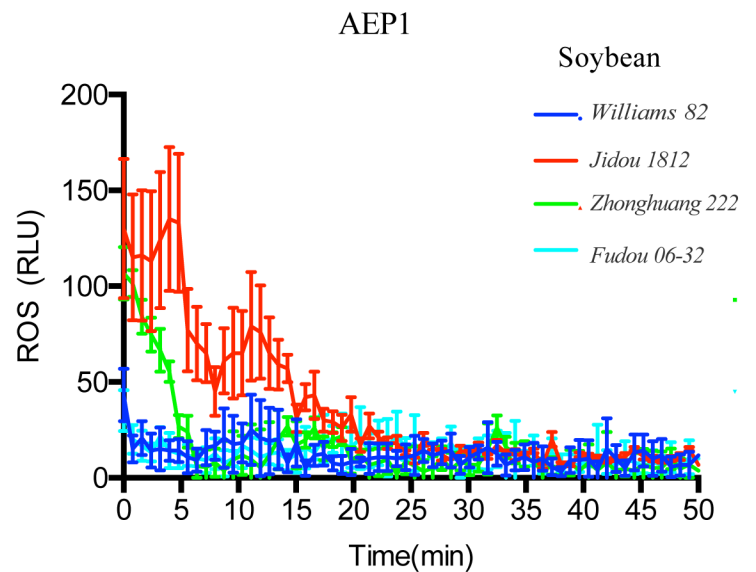
A



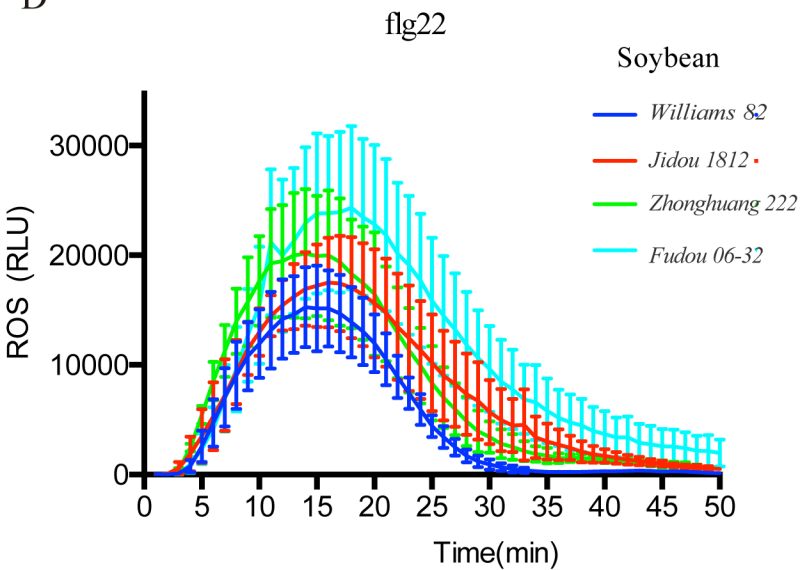
B



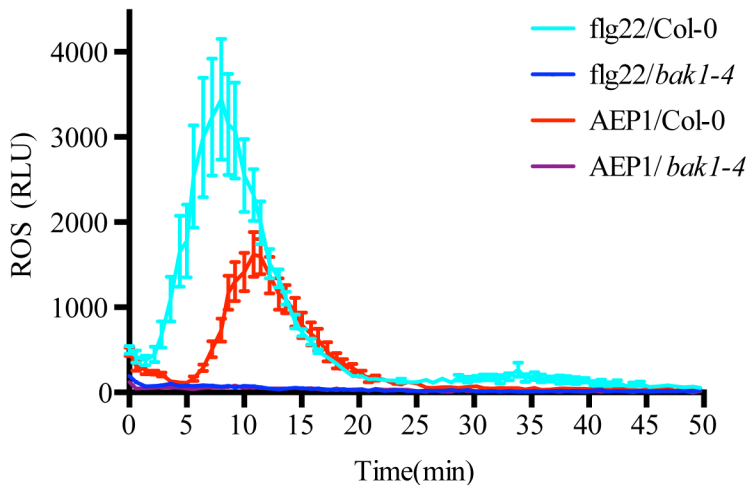
C



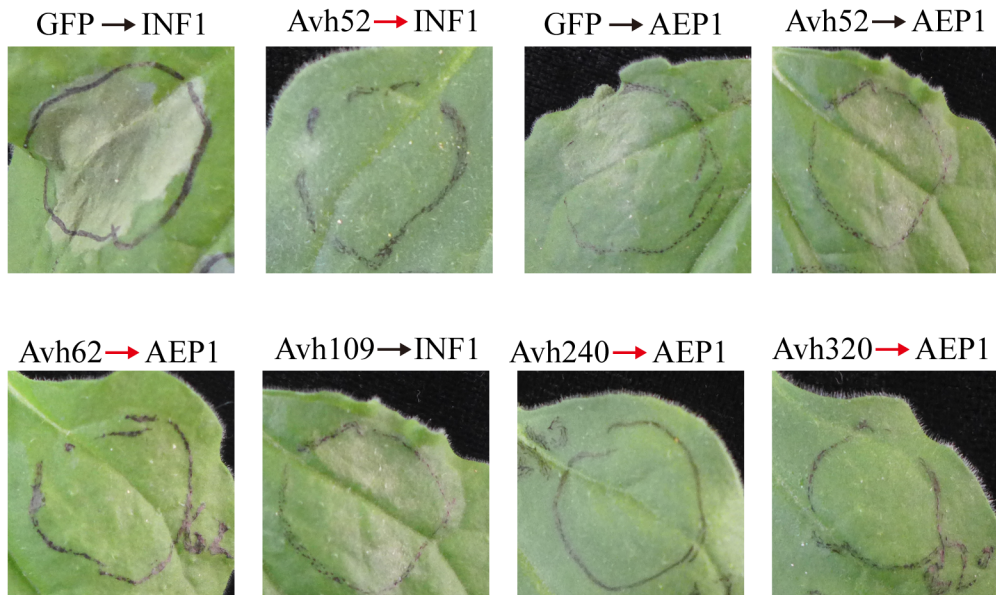
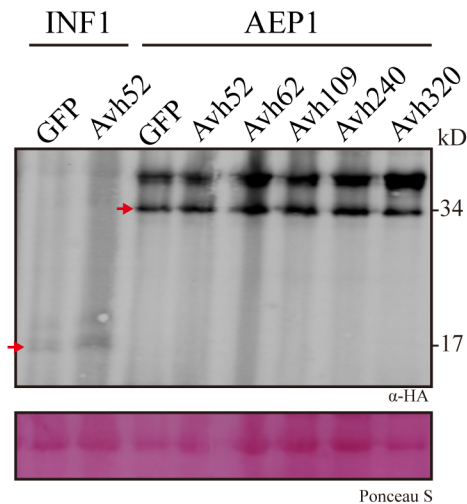
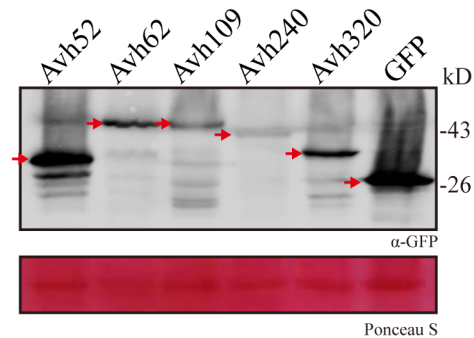
D



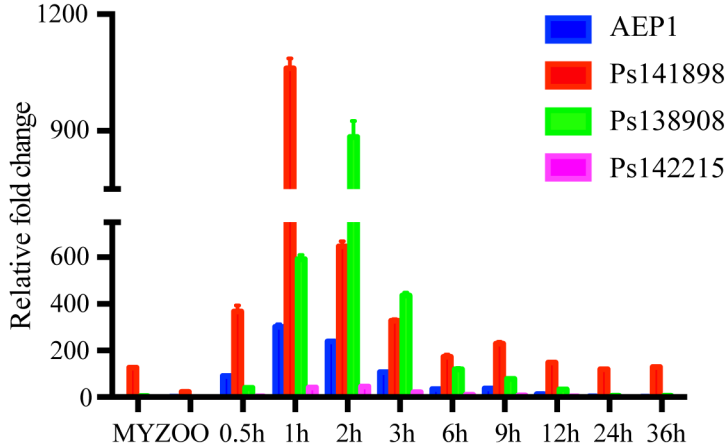
Supplemental Figure S7. AEP1 could not trigger cell death or immune responses in soybean. A, Cell death triggered by the purified AEP1 and XEG1 protein. Purified AEP1 protein was infiltrated into soybean leaves (20 μ M). XEG1 was used as a positive control. Cell death was photographed 7 days after infiltration of indicated proteins. The background of photo was deducted for a better display. Experiment was repeated with similar result. B, Relative expression of defense-related marker genes in soybean roots triggered by AEP1 (1 μ M). Transcript levels were normalized to soybean *GmCYP2*. Bars represent the mean fold changes of AEP1-treated soybean roots relative to EV-treated soybean roots. The value of EV treated roots was set as 1. All the experiments repeated three times with similar results. C, D, Production of reactive oxygen species (ROS) in soybean leaves treated by 1 μ M AEP1 or flg22 (200 nM). flg22 was used as a positive control. Mean values \pm SE of three replicates are shown.



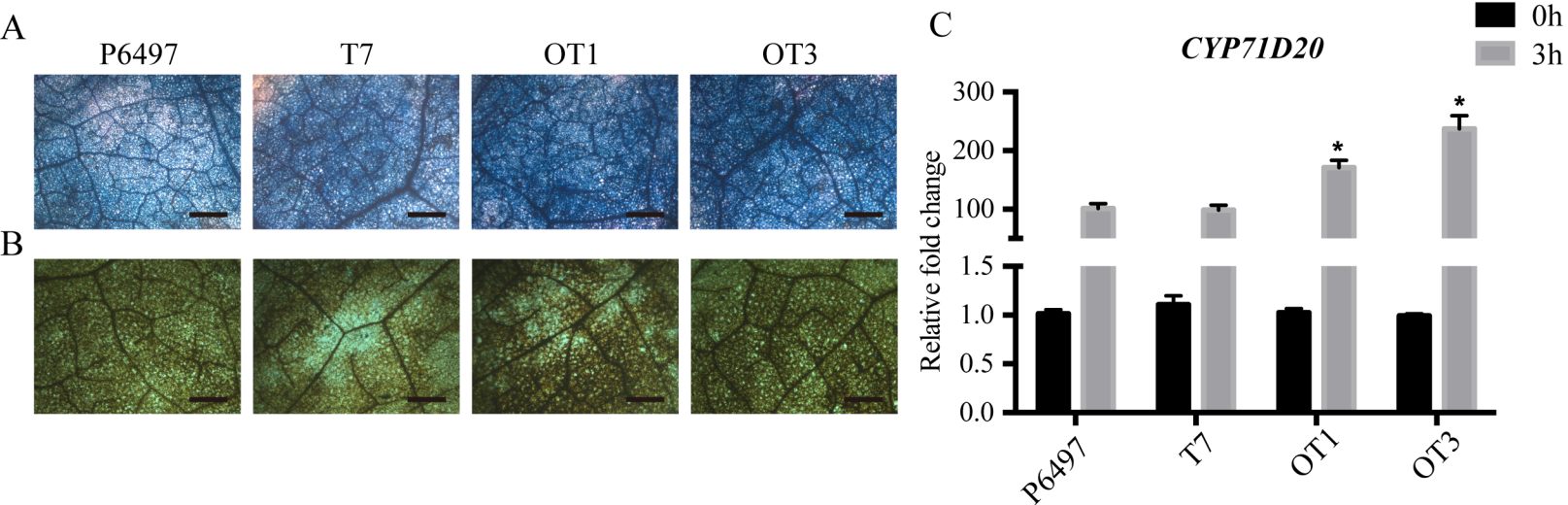
Supplemental Figure S8. AEP1 could trigger ROS burst in *Arabidopsis*. Production of reactive oxygen species (ROS) in *Arabidopsis* Col-0 and *bak1-4* leaves treated by 1 μ M AEP1 or flg22 (200 nM). flg22 was used as a positive control. Mean values \pm SE of three replicates are shown.

A**B****C**

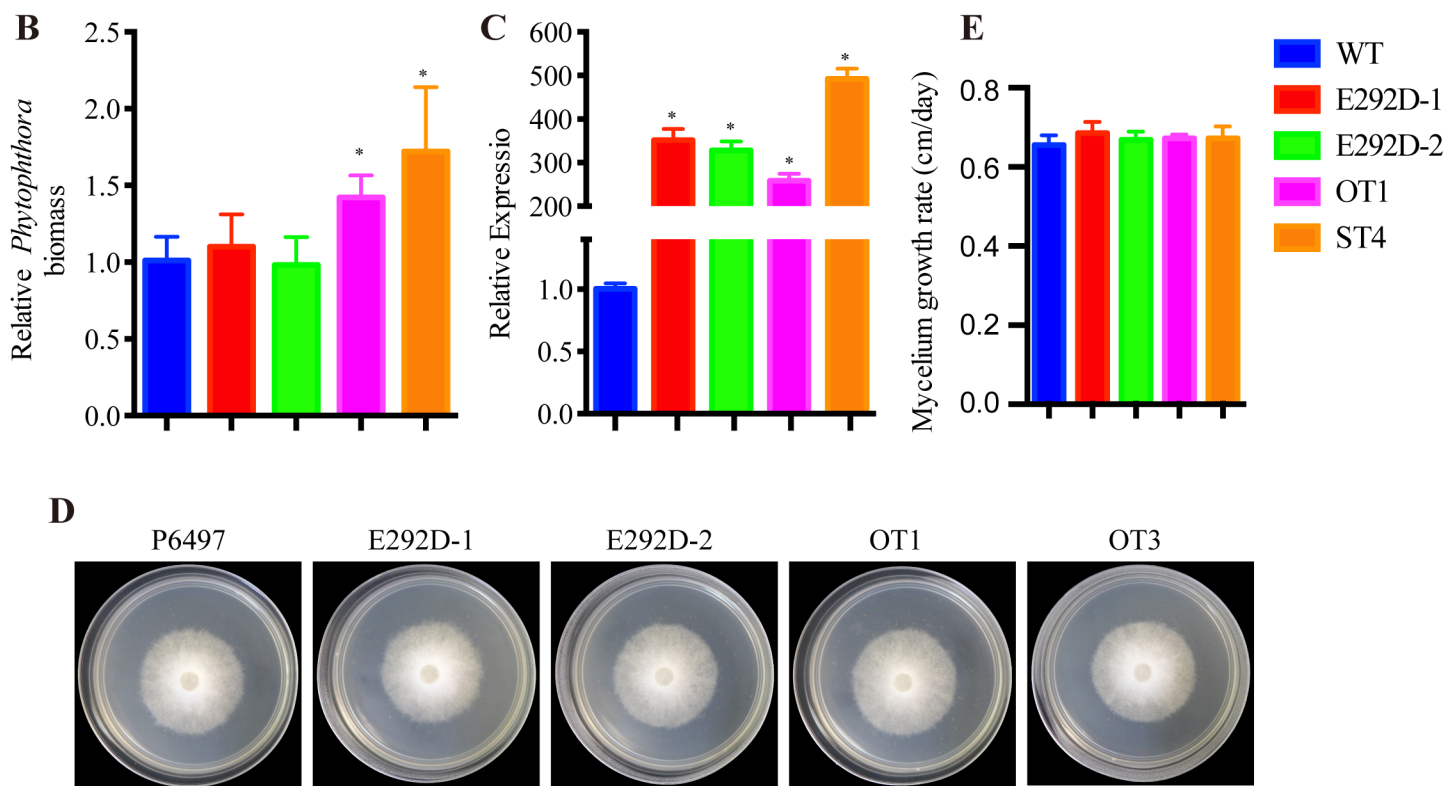
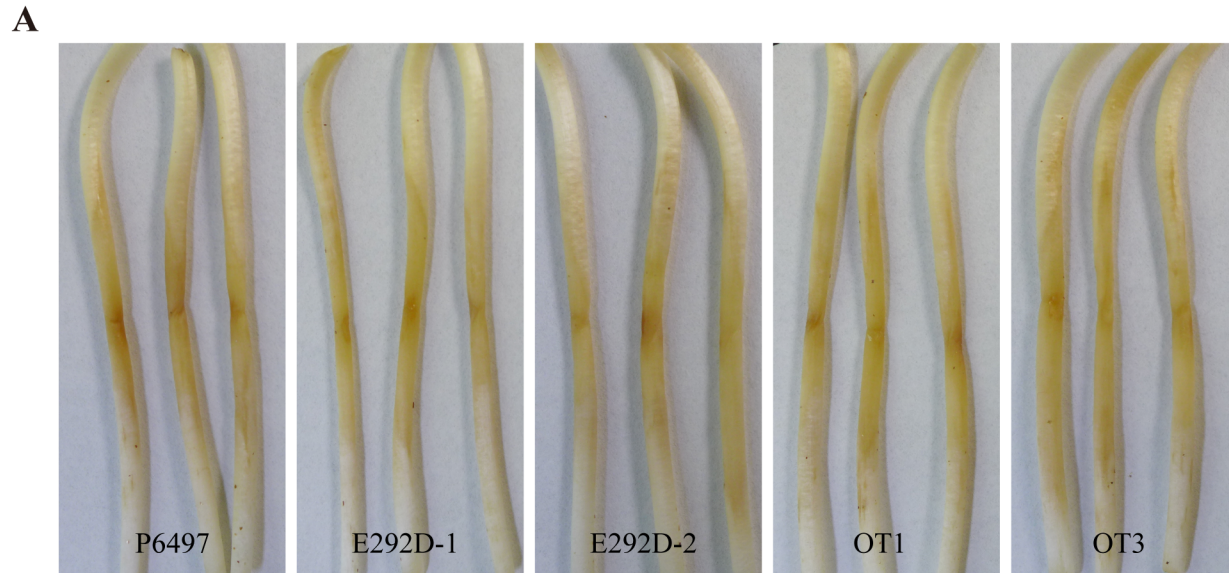
Supplemental Figure S9. *Phytophthora sojae* effectors could suppress AEP1 triggered cell death. A, AEP1 or INF1 was agro-infiltrated in *N. benthamiana* 12 h post agro-infiltrated with *P. sojae* RxLR effectors. GFP was used as a negative control. The arrowhead is red when cell death is suppressed. Cell death was photographed 3 days after infiltration with AEP1 and INF1. This experiment was repeated 3 times with similar results. B, Western-blot of INF1 or AEP1 when co-expressed with effectors. C, Western-blot of expressed effectors. Ponceau staining was used to indicate the amount of loading in each sample in each sample.



Supplemental Figure S10. Aldose 1-epimerases are highly expressed during infection. Relative expression of *P. sojae* aldose 1-epimerases at MY-mycelium, ZOO-zoospores and infection stages. Transcript levels were normalized to *P. sojae* actin. AEP1 expression fold in the mycelium stage was set as 1.

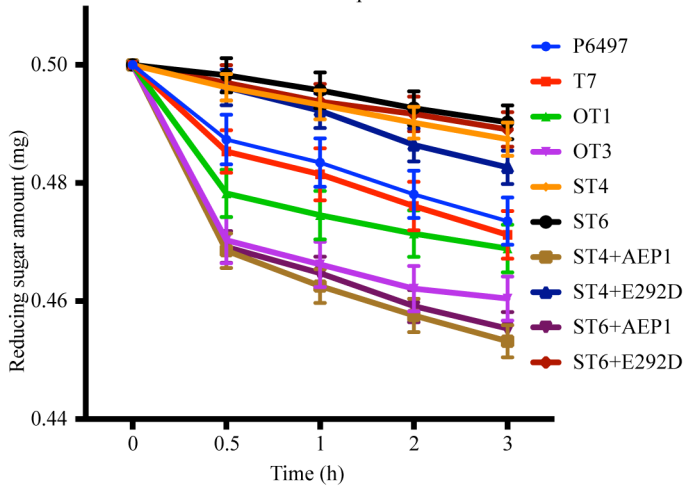


Supplemental Figure S11. *Phytophthora sojae* AEP1-overexpression lines triggered stronger immune responses on *N. benthamiana*. A-B, Cell death or H₂O₂ accumulation induced by infection of *P. sojae* in leaves of *N. benthamiana*. *N. benthamiana* leaves were inoculated by *P. sojae* zoospores and were collected 2 days post inoculation. Cell death was photographed under a microscope after trypan blue or DAB staining. Bars=500 μ m. C, Relative expression of *CYP71D20* in *N. benthamiana* leaves triggered by zoospores of *P. sojae*. Samples were collected 0 and 3 hours after soak-inoculated with zoospores (100/10 μ l). Leaf samples were assayed by RT-qPCR. Transcript levels were normalized to *EF-1 α* . Bars represent the mean fold changes of the 3 hours inoculation samples relative to 0 hours inoculation samples, which was set as 1. Error bars represent the standard deviation of three biological repeats. *, significant differences ($P < 0.05$, t-test).



Supplemental Figure S12. *AEP1* contributes to *P. sojae* virulence by its enzyme activity. A, Disease symptoms of the etiolated soybean seedlings inoculated with *P. sojae* strains. Disease symptoms were photographed 2 days post inoculation (dpi). *Phytophthora* infection assay was repeated three times with similar results. B, Relative biomass of *P. sojae* strains detected in the inoculated etiolated soybean seedlings. Inoculated samples were collected 2 dpi and were used to isolate gDNA for quantitative PCR. The values were calculated by normalizing *P. sojae* actin to soybean *GmCYP2* and the value detected in P6497-inoculated sample was set as 1. Error bars represent the standard deviation of three biological repeats. *, significant differences ($P < 0.05$, t-test). C, Transcript levels of *AEP1* in mycelium of *P. sojae* transformants assayed by RT-qPCR. *P. sojae* actin was used as an internal reference. *AEP1* expression levels were normalized to that detected in P6497. *, significant differences ($P < 0.05$, t-test). D, E, *P. sojae* strains were cultured on V8 medium. Colonies were photographed and their growth was measured. Error bars represent the standard deviation of three biological repeats.

Glucose uptake



Supplemental Figure S13. Time points of the amount of extracellular D-glucose uptaken by *Phytophthora* strains. Error bars represent the standard deviation of three biological repeats.

Supplementary table 1

PrimersSequencesUsed for

pGR107(C)3HA-AEP1-F: CAGCACCAGCTAGCATCGATGGTGTCTCCATC cloning full length AEP1 in *P. sojae*
pGR107(C)3HA-AEP1-R: AATCTCTAGAGGATCCCCGGCCGTGGTGACCGA
pGR107(C)3HA-Ps141898-F: CAGCACCAGCTAGCATCGATGGTGTCCCCATC cloning full length Ps141898 in *P. sojae*
pGR107(C)3HA-Ps141898-R: AATCTCTAGAGGATCCCCAGAGTGGTGACCGA
pGR107(C)3HA-Ps138908-F: CAGCACCAGCTAGCATCGATGGTGTGCTCCTTCcloning full length Ps138908 in *P. sojae*
pGR107(C)3HA-Ps138908-R: AATCTCTAGAGGATCCCCGAGTATCGGATGGC
pGR107(C)3HA-Ps139507-F: CAGCACCAGCTAGCATCGATGGCGCGTCTATCTcloning full length Ps139507 in *P. sojae*
pGR107(C)3HA-Ps139507-R: AATCTCTAGAGGATCCCCGCTTCTTGAGCTAGAAT
pGR107(C)3HA-AEP1nosp-F: GATAGCCGGTACCCCCATGGAGCTCGAGACCGTcloning AEP1 without signal peptide in *P. sojae*
pGR107(C)3HA-Ps142215-F: CAGCACCAGCTAGCATCGATGTTGGCCTTCAAGcloning full length Ps142215 in *P. sojae*
pGR107(C)3HA-Ps142215-R: AATCTCTAGAGGATCCCCGGCCTTGGCGACCT
pGR107(C)3HA-PPTG08586-F: CAGCACCAGCTAGCATCGATGGTTAACGCTTTCATCTCAAGcloning full length PPTG08586 in *P. parasitica*
pGR107(C)3HA-PPTG08586-R: AATCTCTAGAGGATCCCCAGCGTGGTGACCGAGATG
pGR107(C)3HA-PPTG11132-F: CAGCACCAGCTAGCATCGATGGTTACCTCGTTCGTGTCCcloning full length PPTG11132 in *P. parasitica*
pGR107(C)3HA-PPTG11132-R: AATCTCTAGAGGATCCCCGAGCGAGGTGACCGTGACTC
pGR107(C)3HA-PPTG08590-F: CAGCACCAGCTAGCATCGATGCCGCCCTCCAGTCTcloning full length PPTG08590 in *P. parasitica*
pGR107(C)3HA-PPTG08590-R: AATCTCTAGAGGATCCCCAGCTCCCGCCACAGTGATC
pGR107(C)3HA-PPTG15370-F: CAGCACCAGCTAGCATCGATGGTATACTCCTTCCGTTCAGTTCGcloning full length PPTG15370 in *P. parasitica*
pGR107(C)3HA-PPTG15370-R: AATCTCTAGAGGATCCCCGTTAGTGATGCGGGCAAAGC
pGR107(C)3HA-PITG_14720-F: CAGCACCAGCTAGCATCGATGGTTAACGCATTCATCTCAAGcloning full length PITG_14720 in *P. infestans*
pGR107(C)3HA-PITG_14720-R: AATCTCTAGAGGATCCCCAAAGTGGTGACCGAGATGGTC
pGR107(C)3HA-PITG_11528-F: CAGCACCAGCTAGCATCGATGGTCAAGTTCATGTCCcloning full length PITG_11528 in *P. infestans*
pGR107(C)3HA-PITG_11528-R: AATCTCTAGAGGATCCCCAGTTCGTGGGCTTGACCG
pGR107(C)3HA-PITG_15093-F: CAGCACCAGCTAGCATCGATGGTGTACTCCTTCTGTTCAGGACcloning full length PITG_15093 in *P. infestans*
pGR107(C)3HA-PITG_15093-R: AATCTCTAGAGGATCCCCAGAGAAGCGCTGACCCGAA
pGR107(C)3HA-PITG_20953-F: CAGCACCAGCTAGCATCGATGGTCAGCTCGTTCATGTCCcloning full length PITG_20953 in *P. infestans*
pGR107(C)3HA-PITG_20953-R: AATCTCTAGAGGATCCCCAGTCTGTGGCTTGACCG
pGR107(C)3HA-Pc_119558-F: CAGCACCAGCTAGCATCGATGGTCAACGCTTTCATTTTCcloning full length Pc_119558 in *P. capsici*
pGR107(C)3HA-Pc_119558-R: AATCTCTAGAGGATCCCCAGCGTGGTGACCGAGATG
pGR107(C)3HA-Pc_119659-F: CAGCACCAGCTAGCATCGATGCCATCCTTCCAGTCTATCcloning full length Pc_119659 in *P. capsici*
pGR107(C)3HA-Pc_119659-R: AATCTCTAGAGGATCCCCAGCTTCCGCTACAGCGATGG
pPIC9K-nospAEP1-6*his-F: GAAGCTTACGTAGAAGAGCTCGAGACCGTcloning AEP1 without signal peptide
pPIC9K-nospAEP1-6*his-R: GAATTAATTCGCGGCTCAGTGGTGGTGGTGGTGGGCCGTGGTGACCGA
AEP1(E292D)-1R: GTCGACGGCGACCATGTTCTsite mutant of AEP1
AEP1(E292D)-2R: CATGGTCGCGTCGACCCCGCCGCTGA
pTOR(C)GFP-AEP1-F: CTCGAGGTCGACGGTATCATGGTGTCTCCATCcloning full length AEP1
pTOR(C)GFP-AEP1-R: GGTGAATTCGATATCATCGGCCGTGGTGACCGA
PsActin-F: ACTGCACCTTCCAGACCATC *P. sojae* biomass analysis
PsActin-R: CCACCACCTTGATCTTCATG
NbEF1a-RT-F: GTATGCCTGGGTGCTTGACAntje Heese et al., 2007
NbEF1a-RT-R: ACAGGGACAGTTCCAATACCA
qPCR-GmCYP2-F: CGGGACCAGTGTGCTTCTTCAsoybean biomass analysis
qPCR-GmCYP2-R: CCCCTCCACTACAAAGGCTCG
RT-NbCyp71D20-F: GTTGACGCCATTGTTGAG Antje Heese et al., 2007
RT-NbCyp71D20-R: ATCTTCGCCTCCTAATGC
RT_Pi5_F: CCTCCAAGTTTGAGCTCGGATAGT inducing expression analysis in *N. benthamiana*
RT_Pi5_R: CCAAGAAATTCTCCATGCACCTGTGC
RT_Acre31_F: AATTCCGCCATCGTGTCTTGGTC inducing expression analysis in *N. benthamiana*
RT_Acre31_R: GAGAAACTGGGATTGCCTGAAGGA
RT_NbWRKY7_F: CACAAGGGTACAAACAACACAG inducing expression analysis in *N. benthamiana*
RT_NbWRKY7_R: GGTTCATTTGGTTTCATGTAAG
RT_NbWRKY8_F: AACAAATGGTCCAATAATGC inducing expression analysis in *N. benthamiana*
RT_NbWRKY8_R: TGCATATCCTGAGAAACCATT
RT-AEP1-F: CGATGCCGTCGTCTGGAA silencing efficiency analysis
RT-AEP1-R: GCCGTGGTGACCGAAATG
RT-Ps141898-F: ATTGAGTTCCACGCTCTGCT silencing efficiency analysis
RT-Ps141898-R: ACACGTTGTCCGTCTGGTTAG
RT-Ps138908-F: CCACCGATGAGACCAAGC silencing efficiency analysis
RT-Ps138908-R: TCGTTCACGCGCATGTAG
RT-Ps139507-F: CCACCGATGAGACCAAGC silencing efficiency analysis
RT-Ps139507-R: TCGTTCACGCGCATGTAG
pGR107(C)3HA-Ps145088-F: CAGCACCAGCTAGCATCGATGGTTACGATCTCCGG cloning full length Ps145088 in *P. sojae*
pGR107(C)3HA-Ps145088-R: AATCTCTAGAGGATCCCCAGCCAGAGCAGGGAT
pGR107(C)3HA-Ps136238-F: CAGCACCAGCTAGCATCGATGGTGTTCCTCGTC cloning full length Ps136238 in *P. sojae*
pGR107(C)3HA-Ps136238-R: AATCTCTAGAGGATCCCCAGCCAGAGCGGGAT
pGR107(C)3HA-Ps128784-F: CAGCACCAGCTAGCATCGATGCAGATCATCGCC cloning full length Ps128784 in *P. sojae*
pGR107(C)3HA-Ps128784-R: AATCTCTAGAGGATCCCCAGACAGGTATGTGGTGT
pGR107(C)3HA-Ps128733-F: CAGCACCAGCTAGCATCGATGCAGATCTCGCT cloning full length Ps128733 in *P. sojae*
pGR107(C)3HA-Ps128733-R: AATCTCTAGAGGATCCCCAGGTACGAGGTGTGCT
pGR107(C)3HA-Ps123922-F: CAGCACCAGCTAGCATCGATGAACGTCCTCTC cloning full length Ps123922 in *P. sojae*
pGR107(C)3HA-Ps123922-R: AATCTCTAGAGGATCCCCGTAGCTGTCCACCTTG

pGR107(C)3HA-Ps131879-F: CAGCACCAGCTAGCATCGATGTTCTCAAGACGG cloning full length Ps131879 in P. sojae
pGR107(C)3HA-Ps131879-R: CAGCACCAGCTAGCATCGATGTTCTCAAGACGG
pGR107(C)3HA-Ps135222-F: CAGCACCAGCTAGCATCGATGCGAGCGCTGGCA cloning full length Ps135222 in P. sojae
pGR107(C)3HA-Ps135222-R: CAGCACCAGCTAGCATCGATGCGAGCGCTGGCA
pGR107(C)3HA-Ps139507-F: TCAGCACCAGCTAGCATATGGCGCGCTCATCTC cloning full length Ps139507 in P. sojae
pGR107(C)3HA-Ps139507-R: TAGAGGATCCCCGGGAATGCTTCTTGAGCTAGAATTGCC
pGR107(C)3HA-Ps139431-F: CAGCACCAGCTAGCATCGATGCTGAGCCCCAAG cloning full length Ps139431 in P. sojae
pGR107(C)3HA-Ps139431-R: TAGAGGATCCCCGGGAATACAGGCCTTGCCTTC
pGR107(C)3HA-Ps143393-F: CAGCACCAGCTAGCATCGATGAAGATCTTCGCCG cloning full length Ps143393 in P. sojae
pGR107(C)3HA-Ps143393-R: TAGAGGATCCCCGGGAATCAGCAACGCCGTCAC
pGR107(C)3HA-Ps140695-F: CAGCACCAGCTAGCATCGATGGTGAACGCCAAG cloning full length Ps140695 in P. sojae
pGR107(C)3HA-Ps140695-R: AATCTCTAGAGGATCCCCAGGTTGGGGAACGT
pGR107(C)3HA-Ps136645-F: CAGCACCAGCTAGCATCGATGAACATCAAGGGACT cloning full length Ps136645 in P. sojae
pGR107(C)3HA-Ps136645-R: AATCTCTAGAGGATCCCCGCGCAGGACTCGCC
pGR107(C)3HA-Ps144483-F: CAGCACCAGCTAGCATCGATGAAGTCTTCAGTGT cloning full length Ps144483 in P. sojae
pGR107(C)3HA-Ps144483-R: TAGAGGATCCCCGGGAATGACCACAATGATCTTCGC
pGR107(C)3HA-Ps131903-F: TCAGCACCAGCTAGCATATGCTCATGTCGTGG cloning full length Ps131903 in P. sojae
pGR107(C)3HA-Ps131903-R: TAGAGGATCCCCGGGAATCTCGAACGATCCGTAC
pGR107(C)3HA-Ps128411-F: CAGCACCAGCTAGCATCGATGCGTCTTCCTAGC cloning full length Ps128411 in P. sojae
pGR107(C)3HA-Ps128411-R: AATCTCTAGAGGATCCCCATACTCCGCAACGTAAA
pGR107(C)3HA-Ps145311-F: CAGCACCAGCTAGCATCGATGTGGGCTCTCAAG cloning full length Ps145311 in P. sojae
pGR107(C)3HA-Ps145311-R: TAGAGGATCCCCGGGAATCAACAGACTCGAAC
pGR107(C)3HA-M1-R: TAGAGGATCCCCGGGAATCCGTACGGTCCACGGCGTT constructin AEP1 deletion mutant
pGR107(C)3HA-M2-R: TAGAGGATCCCCGGGAATCCCACAGGTAGTTGTGCAG constructin AEP1 deletion mutant
pGR107(C)3HA-M3-R: TAGAGGATCCCCGGGAATCCATGGTGAACCTTGCCAC constructin AEP1 deletion mutant
pGR107(C)3HA-M4-1R: TGTAGCTGGCCAGCGTGTGGAACGACTTGACGTG constructin AEP1 deletion mutant
pGR107(C)3HA-M4-1F: AAGTCGTTCCACACGCTGGCCAGCTACAAGAA constructin AEP1 deletion mutant

Supplemental Table S2

AEP1 sgRNAs

sgRNA1	GTCCATCTTTGGGTCCATAGCGG
sgRNA2	GTCAGCAGCATTCTTGTAGCTGG
sgRNA3	TCCATCTTTGGGTCCATAGCGGG
sgRNA4	CCCCGCTATGGACCCAAAGATGG
sgRNA5	CAAGTCGTTCCACCCCGCTATGG
sgRNA6	GGAGAGCATTTCGGTCACCACGG