A secreted protein of 15 kDa plays an important role in *Phytophthora palmivora* development and pathogenicity

Sittiporn Pettongkhao^{1,2,3}, Natasha Navet², Sebastian Schornack⁴, Miaoying Tian^{2,*}, Nunta Churngchow^{1,*}

¹Department of Biochemistry, Faculty of Science, Prince of Songkla University, Hat-Yai, Songkhla 90112, Thailand; ²Department of Plant and Environmental Protection Sciences, University of Hawaii at Manoa, Honolulu, HI 96822, USA; ³East-West Center, Honolulu, Hawaii, USA; ⁴Sainsbury Laboratory Cambridge University (SLCU), Cambridge, UK

*Corresponding author

E-mail address:	Miaoying Tian	Tel: 1-808-956-5305	Email: mtian@hawaii.edu

Nunta Churngchow Tel: + 66 74 288261 Email: nunta.c@psu.ac.th

Supplementary figures

Figure S1. Amino acid sequence alignment of Ppal15kDa and its homologs in *Phytophthora* spp.

P. sojae P. cinnamomi P. palmivora P. capsici P. cinnamomi P. megakarya P. cactorum P. pamivora P. parasitica P. parasitica P. cactorum	XP 009519869.1 PHYCI 93984T0 POM75182.1 PHYCA 14775T0 PHYCI 81820T0 OWZ12090.1 XP 008909746.1 RAW38577.1 Ppal15kDaA OWZ12091.1 XP 008909747.1 RAW38578.1	1 1 1 1 1 1 1 1 1 1	MSRTLQVLLVVMVALLASCNA-DIATKNOFTIATTNAAATKALQKFFAEDSKQNKKNGY MMRMLQVLLVIMVALLASCDAADTPTKNHLTISTTNAGATAKALQKFFADDAKQNKNNGY -MRMJEVLFVFLVASFASCHGAVAPTKNQLTISTKDSTATAKALQKFFADDAKQNKNNAG MIHLLRVLLVALLSLWACEAAATKNQLVISTTNGIATAKALQKFFTDDAKQNKSNGM MFEVPLVFLVVLVTLLANCEGTGTATKSQLTIATTNADATAKALQKFFTDDAKQNKSNGM MFEVPLVFLVVLVTLLANCEGTGTATKSQLTIATTNADATAKALQKFFTDDAKQNKSNGM MIHLLRVLLVVLVTLLANCEGTGTATKSQLTISTRNSTATAKALQKFFTDDAKQNKSNGM MRVLFQALLVLVALLVSCHGATATFTNQLTISTRNSTATAKALQKFFTDDAKQNKDSGF MRVLFQULVLVLVALLVSCHGATTTTNKQLTISTTNATAKALQKFFTDDAKQNNSNGF -MRMIQVVFMLLTALFASCHEAANPTKNQLVVSTTNSTATAKALQKFFTEDAKQNNNGF -MRIIQVVFMLLTALFASCHEAANPTKNQLTISTINASATAKALEKFFTEDAKQNNNGF -MHIIQVVFVFLVLFTSCEEATATTPTKHQLTISTINASATAKALEKFFTEDAKQNNNGF -MLIQVLVFLVALFVSCEAAA-TQNQLTIATTNSTATAKALQKFFNEDSKQNQNNGF -MRMSQVLVFLVLVLVSCEAAA-TQNQLTIATTNSTATAKALQKFFNEDSKQNQNNGF
D aging			
P. sojae P. sinnomomi	XP_009519869.1	60	L <u>MVLSGSAAADEERVSA – GAIAAAEGARAGAGTTVVSSTSGTTKTVTTIYNNNGLWOR</u>
P. cilinamonii P. nalmivora	PHICI 93984T0	60	
P cansici	PUM/5102.1	60	
P. cinnamomi	PHYCI 81820T0	61	LKMNNUSSA - DGERGA GALASGOGPBUGAGTTVVSDGTGSSOTVTVTIVNNGLWOP
P. megakarva	OWZ12090.1	58	
P. parasitica	XP 008909746.1	61	LKVVTISSS-NEERASAGAITSGOGPRAGAGTTVVANDASSGETVTVTVVNNNGLWOR
P. cactorum	RAW38577.1	61	LKVVTISSI-NEERASA-GAMTSGOGPRAGAGTTVVANDAPSGETVTVTHVNNNGLWOR
P. pamivora	Ppal15kDaA	60	LKVVTPASS-DEERASTSVAAAGEGARAGUGTTUVSSGWASGEMVTVTVYNDNGLWOR
P. megakarya	OWZ12091.1	60	LKVVTPESS-GEERASTSAITAGEGARAGTGATVVSSDEPSGEMVTVTVYNNNGLWOR
P. parasitica	XP 008909747.1	58	LKVVT <mark>IP</mark> SS <mark>-E</mark> EERAS <mark>T-SGAIT</mark> AGEGARAAGTTVVSSD <mark>HT</mark> SGETVTVTVINNNGLWOR
P. cactorum	RAW38578.1	58	LKVVT <mark>L</mark> SSS-EEERAS <mark>TSTGAIT</mark> AGEGARVAAGTTVVANDEPLGETVTVTVYNNNGLWQR
P. sojae	XP_009519869.1	118	FQRWWNSLFARRRLRHASN
P. cinnamomi	PHYCI_93984T0	119	FORWWNRLFRNDSTRRLRVAASGANN
P. palmivora	POM75182.1	102	FORWWNRLLNGSTRRLRHPITGEQ
P. capsici	PHYCA_14775T0		
P. cinnamomi	PHYCI_81820T0	118	FQRWWNRLFHRSSSARRI-R
P. megakarya	OWZ12090.1	111	F <u>Q</u> RWWNRLFNR
P. parasitica	XP_008909746.1	118	FLRWWNRLFTGSAANSTRTLRTDN
P. cactorum	RAW38577.1	118	FORWWNRLFKGSSANSTRRLRTDN
P. pannvora	PPaliskDaA	117	
P. negatarya	VP 009000717 1	116	
P. cactorum	AF_000909747.1	117	
r. cactorum	RAW50576.1	11/	

Figure S2. Phylogenetic analyses of Ppal15kDa and its homologs in *Phytophthora* spp. Construction of the phylogenetic tree was performed with the amino acid sequences using the neighbor-joining (NJ) method built in MEGA version 6.0. Bootstrap values were obtained with 1000 replicates and values higher than 50% are shown. The scale bar represents 0.05 amino acid substitutions per site.



Figure S3. The full-length picture of Western blot analysis of total proteins extracted from infiltrated *N. benthamiana* leaves and subjected to SDS-PAGE followed by Western blot with HRP conjugated anti-His monoclonal antibody. Lane M represents the protein standard and lane GFP represents *N. benthamiana* leaves infiltrated with *A. tumefaciens* GV3101 carrying pJL-TRBO-G. Lane A and B represent *N. benthamiana* leaves infiltrated with *A. tumefaciens* GV3101 carrying pJL-TRBO-G. Lane A and B represent *N. benthamiana* leaves infiltrated with *A. tumefaciens* GV3101 carrying pJL-TRBO-F. Lane A and B represent *N. benthamiana* leaves infiltrated with *A. tumefaciens* GV3101 carrying pJL-TRBO-F. Lane A and B represent *N. benthamiana* leaves infiltrated with *A. tumefaciens* GV3101 carrying pJL-TRBO-F. Lane A and B represent *N. benthamiana* leaves infiltrated with *A. tumefaciens* GV3101 carrying pJL-TRBO-F. Lane A and B represent *N. benthamiana* leaves infiltrated with *A. tumefaciens* GV3101 carrying pJL-TRBO-F. Lane A and B represent *N. benthamiana* leaves infiltrated with *A. tumefaciens* GV3101 carrying pJL-TRBO-F. Description of Ppal15kDaA and pJL-TRBO-F. Description of Ppal15kDa.



Figure S4. Chromatograms of the partial sequences of *Ppal15kDa* gene in mutants generated using CRISPR/Cas9 gene editing. The mutant lines exhibited mix peaks. The putative Cas9 cleavage site is shown by an arrow.



Figure S5. Infection assays of *Nicotiana benthamiana* leaves with *P. palmivora* wild-type (WT) strain and four representative lines that went through transformation but did not have mutations resulted from gene editing.



WT T1-4





WT T14-2

WT T20-1

Figure S6. Mycelium growth of WT and mutants. WT and mutants were cultured on 10% unclarified V8 agar. The colony diameters were measured after 5 days.



Figure S7. Zoospore germination assay of *P. palmivora* wild-type (WT) strain and *Ppal15kDa* mutants. Zoospores were cultured on Plich agar for 4 hours and photographed under light microscope. Scale bars = $250 \mu m$.

