

Supplementary Information

Systematic characterization of the peroxidase gene family provides new insights into fungal pathogenicity in *Magnaporthe oryzae*

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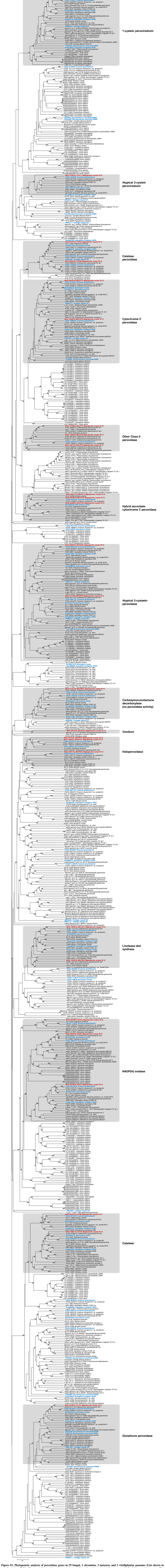


Figure S1. Phylogenetic analysis of genes in 29 fungal, 1 chromista, 3 metazoa, and 2 viridiplantae genomes (List shown in supplementary Table S1). A neighbor-joining tree was constructed based on the amino acid sequences of all of the peroxidase genes. The numbers at the nodes indicate bootstrap values (%) in 10,000 bootstrap replicates; only nodes supported by 50 bootstraps or more are shown. Gray boxes are the phylogenetic positions of 2% *Magnaporthe oryzae* peroxidase genes. Red and blue letters denote *M. oryzae* and five selected fungal species, respectively.

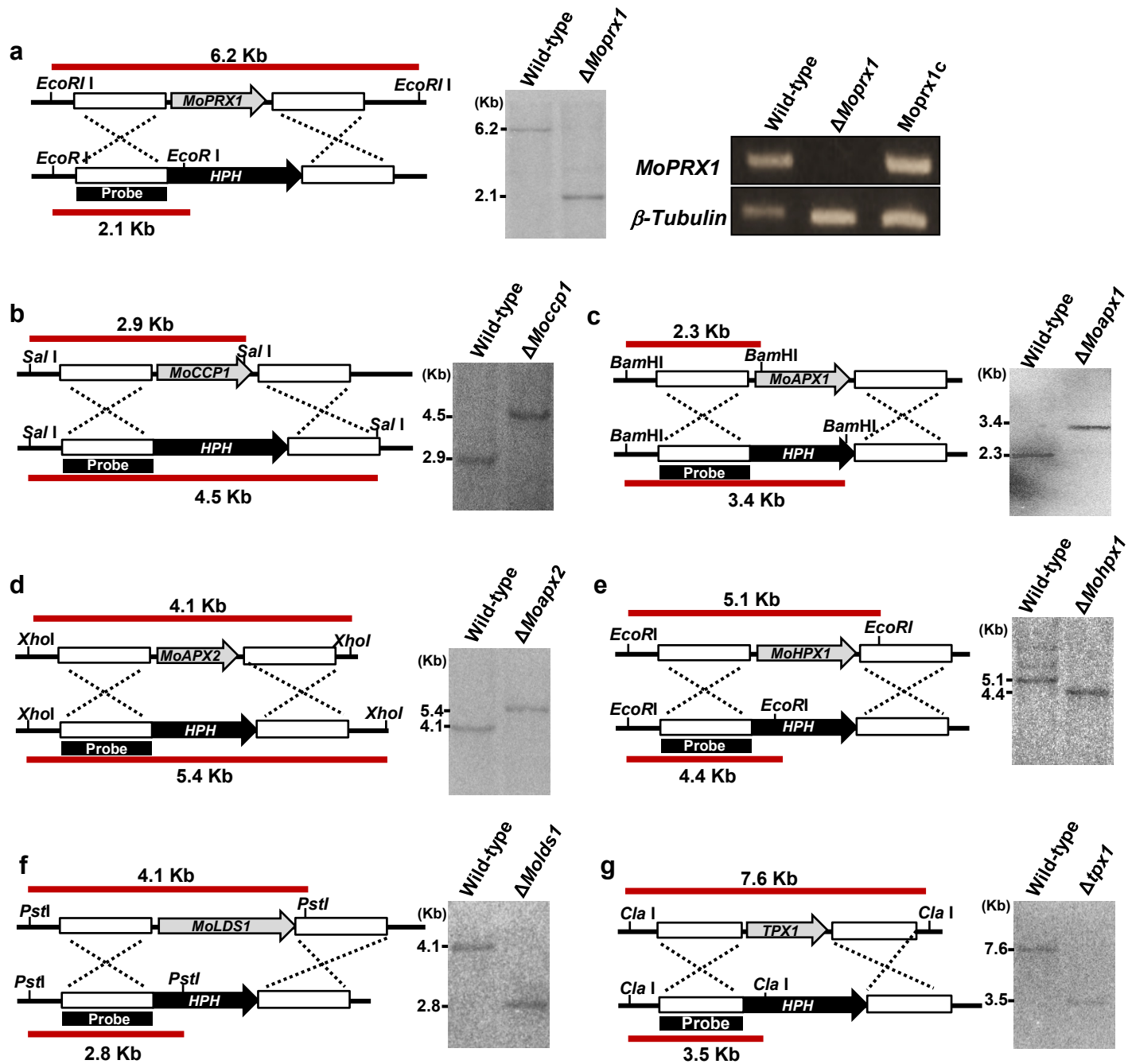


Figure S2. Generation of deletion mutants for selected *M. oryzae* peroxidase genes. A total of seven knockout vectors were constructed by PCR amplification. Approximately 1.2~1.5-kb upstream and downstream flanking sequences were amplified using UF/UR and DF/DR, respectively (primer list in Supplementary Table S6), and ligated with the 1.4-kb or 2.1-kb *HPH* cassette. Southern blots analysis of appropriate enzyme-digested genomic DNAs from the wild-type strain and putative gene deletion mutants. The blots were hybridized with each probe shown in Supplementary Fig. S2 (a-g). For the complementation of Δ Moprpx1, putative complemented transformants were generated and tested for transcriptional expression of *MoPRX1* gene by RT-PCR (a).

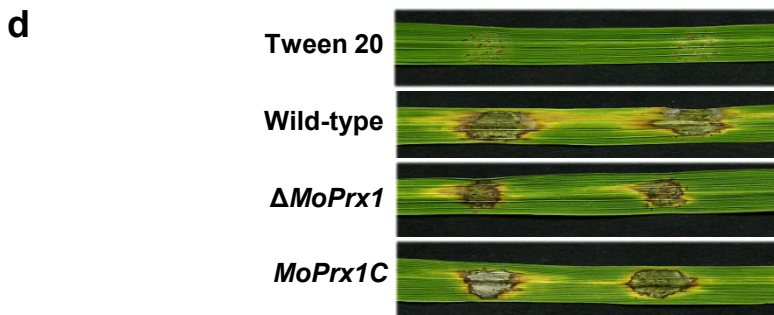
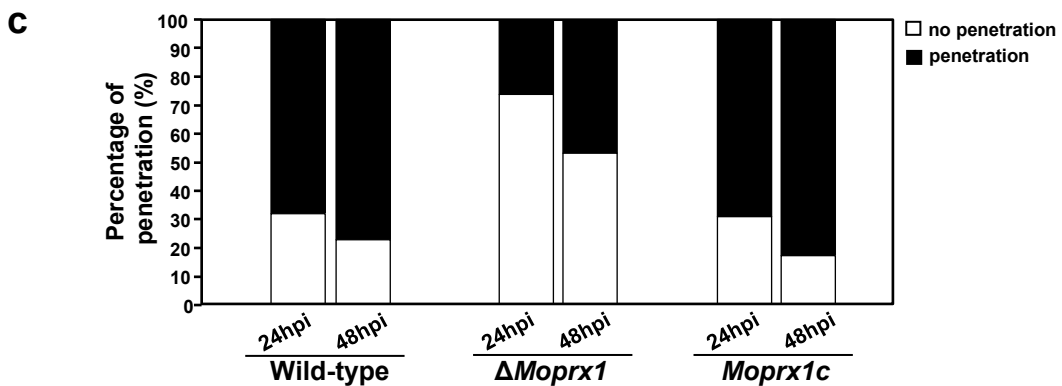
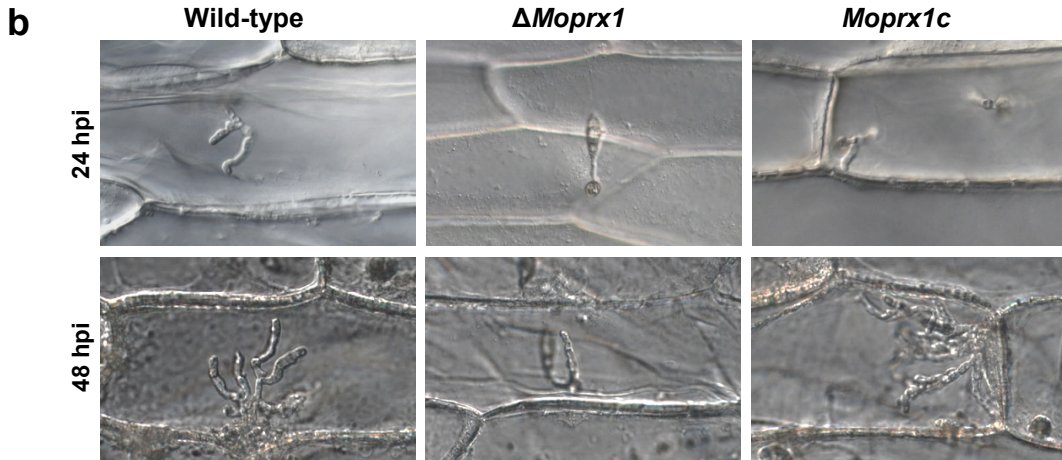
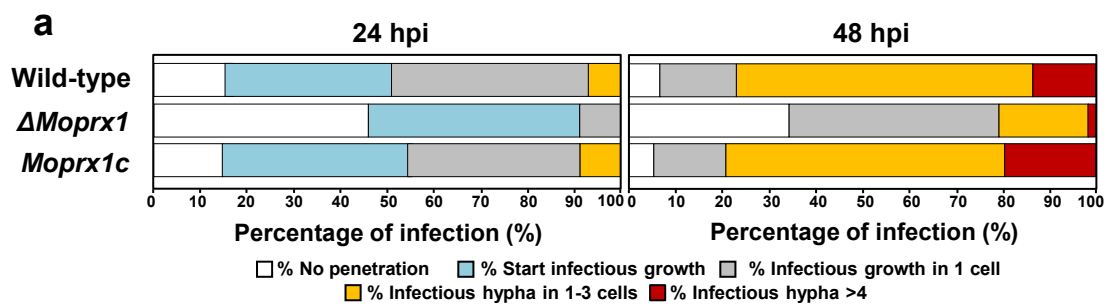


Figure S3. Penetration percentage and pathogenicity of $\Delta Mopr1$ on rice sheaths and leaves, and onion epidermal cells. (a) Quantitative measurement of rice sheath assay by $\Delta Mopr1$. Frequency was measured by counting three replicates of 75-100 appressoria. (b) Appressorial penetration assay on onion epidermal cell by drop inoculation with 2×10^4 conidia/ml and observed at 24 and 48 hpi. Images were captured using a 20-ms exposure to transmitted light with a DIC filter. (c) Percentage of appressorial penetration of onion epidermal cells. Data were obtained by counting three replicates of >100 appressoria. (d) Infiltration experiment on rice leaves. The conidial suspension (5×10^4 conidia/ml) was used as an inoculum. Photograph was taken at 5 dpi.

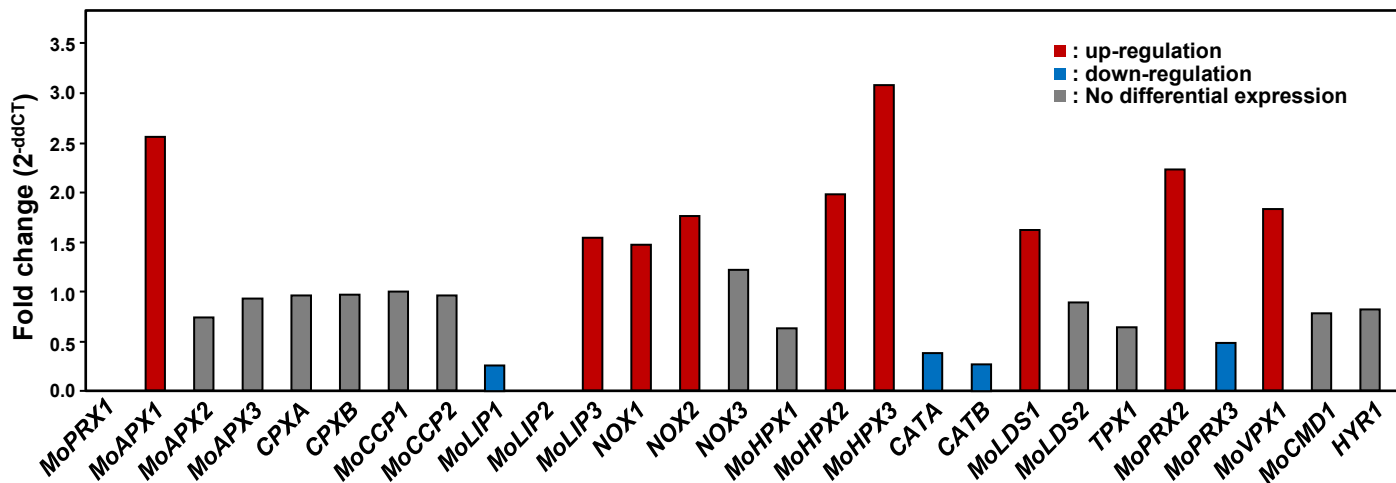


Figure S4. Expression profiles of 27 *M. oryzae* peroxidase genes in $\Delta MoprX1$. Upregulated genes (more than 1.5-fold) are indicated by red bars, and downregulated genes (less than 0.5-fold) are denoted by blue bars. The genes not showing differential expression are marked in gray.

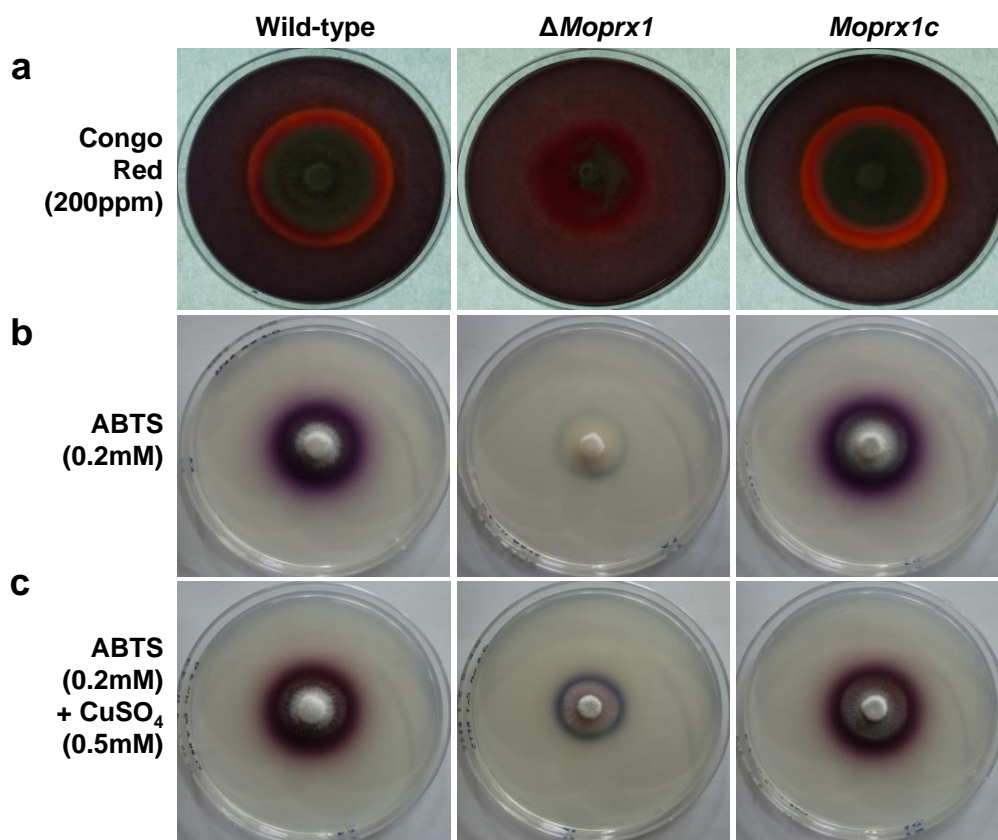


Figure S5. Extracellular enzyme activity in $\Delta Mopr1$. The wild-type, $\Delta Mopr1$, and *Mopr1c* strains were inoculated on complete media (CM) containing (a) 200 ppm Congo Red, and (b) 0.2 mM ABTS, and (c) 0.2 mM ABTS with 0.5 mM CuSO₄. The 5-mm-diameter mycelial blocks were inoculated onto media, and incubated at 25°C. ABTS discoloration was observed at 4 dpi and Congo Red discoloration at 9 dpi.

Table S1. Peroxidase genes from 29 fungal, three metazoan, two viridiplantae and one chromistal genomes

Kingdom	Phylum/		No. of	Haem peroxidase						Non-haem peroxidase				
	Subphylum	Species name		Peroxidases	Animal peroxidase-Cy clooxygene superfamily	Catalase superfamily	Class I	ClassII	DyP-type peroxidase	NAD(P)H oxidase superfamily	Alkylhydroperoxidase D-like superfamily	Glutathione peroxidase	Haloperoxidase	Peroxi-redoxin
Chromista	Oomycota	<i>Phytophthora infestans</i>	31	0	2	4	0	7	4	0	7	0	7	
		<i>Aspergillus fumigatus</i> Af293	25	3	4	3	0	4	1	2	1	0	7	
Fungi	Ascomycota	<i>Aspergillus nidulans</i>	25	3	4	3	0	5	1	2	1	0	6	
		<i>Blumeria graminis</i> f.sp. <i>hordei</i>	14	2	2	3	0	0	2	0	1	0	4	
		<i>Botrytis cinerea</i>	30	2	6	4	0	9	1	1	1	0	6	
		<i>Candida albicans</i> SC5314	14	0	1	2	0	0	0	0	4	0	7	
		<i>Coccidioides immitis</i> RS	15	3	2	3	0	0	2	1	1	0	3	
		<i>Colletotrichum graminicola</i> M1.001	34	4	4	4	7	5	3	1	1	0	5	
		<i>Fusarium graminearum</i>	31	4	5	5	1	5	3	2	1	0	5	
		<i>Fusarium oxysporum</i>	45	7	6	8	1	10	3	3	1	0	6	
		<i>Histoplasma capsulatum</i> H88	18	3	3	2	0	2	2	1	1	0	4	
		<i>Magnaporthe oryzae</i> 70-15	27	2	2	7	3	3	3	1	1	1	4	
		<i>Mycosphaerella graminicola</i>	42	4	3	2	2	18	2	2	1	1	7	
		<i>Neurospora crassa</i>	20	3	3	4	0	2	2	1	1	0	4	
		<i>Podospora anserina</i>	23	2	4	3	1	5	3	1	1	0	3	
		<i>Saccharomyces cerevisiae</i> S288C	11	0	2	1	0	0	0	0	3	0	5	
		<i>Schizosaccharomyces pombe</i> 132	5	0	1	0	0	0	0	0	1	0	3	
	Basidiomycota	<i>Cryptococcus neoformans</i> var. <i>grubii</i> H99	14	0	4	2	0	0	0	0	3	0	5	
		<i>Heterobasidion irregulare</i> TC 32-1	32	2	3	5	7	6	2	2	0	0	5	
		<i>Laccaria bicolor</i>	23	2	1	2	1	7	2	1	1	0	6	
		<i>Melampsora larici-populina</i> 98AG31	39	3	6	2	0	18	5	1	1	0	3	
		<i>Phanerochaete chrysosporium</i>	39	3	5	1	16	3	2	1	1	0	7	
		<i>Puccinia graminis</i> f. sp. <i>tritici</i>	24	0	4	2	0	12	2	0	1	0	3	
		<i>Serpula lacrymans</i> S7.3	19	2	4	1	0	3	2	0	1	0	6	
		<i>Ustilago maydis</i> 521	14	1	0	3	0	3	0	1	1	0	5	
		Blastocladiomycota	<i>Allomyces macrogynus</i>	21	0	0	4	0	0	7	0	4	0	6
		Chytridiomycota	<i>Batrachomyces dendrobatidis</i> JAM81	11	0	3	2	0	0	1	0	1	0	4
Microsporidia	<i>Encephalitozoon cuniculi</i>	2	0	0	0	0	0	0	0	1	0	1		
Zygomycota	<i>Phycomyces blakesleeanus</i>	14	0	2	2	0	0	0	0	2	0	8		
	<i>Rhizopus oryzae</i>	19	0	4	3	0	2	0	0	3	0	7		
Metazoa	Arthropoda	<i>Drosophila melanogaster</i>	20	0	2	0	0	0	2	0	4	0	12	
	Chordata	<i>Homo sapiens</i>	53	0	1	0	0	0	19	0	13	0	20	
	Nematoda	<i>Caenorhabditis elegans</i>	16	0	3	0	0	0	2	0	7	0	4	
Viridiplantae	Streptophyta	<i>Arabidopsis thaliana</i>	63	3	7	18	0	0	14	0	9	0	12	
		<i>Oryza sativa</i> (japonica cultivar-group)	63	4	6	18	0	0	17	0	7	0	11	
Total			896	62	109	123	39	129	109	24	88	2	211	

Table S2. Predicted peroxidase genes in *M. oryzae*

Class	Type	Locus	Protein Length	Signal peptide	Annotation		
Haem	Class I peroxidase	Hybrid Ascorbate-Cytochrome C peroxidase	MGG_00461	476		hypothetical protein, <i>MoAPX1</i>	
			MGG_08200	804	V	hypothetical protein, <i>MoAPX2</i>	
			MGG_09398	548	V	hypothetical protein, <i>MoAPX3</i>	
	Catalase peroxidase		MGG_04337	750		catalase-peroxidase 1, <i>CPXA</i>	
			MGG_09834	786	V	catalase-peroxidase 2, <i>CPXB</i>	
	Cytochrome C peroxidase		MGG_04545	362		cytochrome c peroxidase, <i>MoCCP1</i>	
			MGG_10368	300		cytochrome c peroxidase, <i>MoCCP2</i>	
	Class II peroxidase	Other class II peroxidase		MGG_07790	474	V	ligninase H2, <i>MoLIP1</i>
				MGG_10877	264	V	hypothetical protein, <i>MoLIP2</i>
				MGG_14940	428		ligninase C, <i>MoLIP3</i>
NAD(P)H oxidase superfamily	NADP(H) oxidase		MGG_00750	553		cytochrome b-245 heavychain subunit beta, <i>NOX1</i>	
			MGG_06559	582		cytochrome b-245 heavychain subunit beta, <i>NOX2</i>	
DyP-type peroxidase	Haloperoxidase (haem)		MGG_16840	242	V	hypothetical protein, <i>MoHPX1</i>	
			MGG_07574	257	V	hypothetical protein, <i>MoHPX2</i>	
			MGG_07871	241	V	hypothetical protein, <i>MoHPX3</i>	
Catalase superfamily	Catalase		MGG_10061	743		catalase-1, <i>CATA</i>	
			MGG_06442	715	V	catalase-3, <i>CATB</i>	
Animal peroxidase	Linoleate diol synthase (PGHS like)		MGG_10859	1153		heme peroxidase, <i>MoLDS1</i>	
			MGG_13239	1171		linoleate diol synthase, <i>MoLDS2</i>	
Non haem	Peroxiredoxin	1-Cysteine peroxiredoxin	MGG_08256	224		mitochondrial peroxiredoxin PRX1, <i>MoPRX1</i>	
		Atypical 2-Cysteine peroxiredoxin (type Q, BCP)	MGG_07503	314		thioredoxin peroxidase, <i>TPX1</i>	
		Atypical 2-Cysteine peroxiredoxin (type II &V)	MGG_00860	184		AphC/TSA family protein, <i>MoPRX2</i>	
	Haloperoxidase	Vanadium chloroperoxidase	MGG_02210	595		vanadium chloroperoxidase, <i>MoVPX1</i>	
	Alkyhydroperoxidase D-like superfamily	Carboxymuconolactone decarboxylase (no peroxidase activity)	MGG_01347	243		4-carboxymuconolactone decarboxylase, <i>MoCMD1</i>	
	Glutathione peroxidase	Fungi-Bacteria glutathione peroxidase	MGG_07460	172		peroxiredoxin HYR1, <i>HYR1</i>	

Table S4. Characterization of transformants including deletion mutants for seven peroxidase genes in *M. oryzae* pathogenicity-related phenotypes

Strain	Conidiation (10 ⁵ / ml) ^a	Conidial germination (%) ^b	Appressorium formation (%) ^c
Wild-type	55.7±1.5 ^{E d}	97.7±1.5 ^B	97.3±1.5 ^{BC}
<i>ΔMopr1</i>	42.7±7.5 ^B	96.7±1.2 ^{AB}	93.0±3.6 ^A
<i>Mopr1c</i>	56.3±1.5 ^E	94.3±1.5 ^A	96.0±1.0 ^{ABC}
<i>ΔMocp1</i>	49.0±1.0 ^{CD}	96.3±0.6 ^{AB}	95.0±2.6 ^{ABC}
<i>ΔMoap1</i>	57.3±1.2 ^E	95.7±0.6 ^{AB}	94.7±2.1 ^{AB}
<i>ΔMoap2</i>	44.7±2.3 ^{BC}	94.7±1.5 ^A	97.7±0.6 ^{BC}
<i>ΔMohp1</i>	50.3±1.5 ^D	97.7±0.6 ^B	98.3±0.6 ^C
<i>ΔMold1</i>	47.0±1.0 ^{BCD}	95.7±1.5 ^{AB}	95.0±1.0 ^{ABC}
<i>Δtp1</i>	10.7±2.1 ^A	96.7±1.5 ^{AB}	96.0±1.0 ^{ABC}

^a Conidiation was measured by counting the number of conidia collected with 5 ml of sterilized distilled water from 7-day-old V8 juice agar plate; ^b Percentage of conidial germination on hydrophobic surfaces was measured under a light microscope with three replicates; ^c Percentage of appressorium formation on hydrophobic surfaces was measured using germinated conidia with three replicates; ^d Duncan's test was used to determine significance at the 95% probability level. The same letters in a column showed no significant difference.

Table S5. Total RNA was extracted from five conditions including infection-related developments (conidia, germinated conidia, appressoria, and infectious growth) and oxidative stress treatment

Categories	Conditions	Conc.	Treated time	Basal medium for treatment
Infection-related developments	Conidia Germinated conidia Appressoria 78 hpi on rice			
Oxidative stress	H ₂ O ₂	2.5 mM	4 h	CM

Note: Germinated conidia and appressoria were harvested after 4 h and 16 h, respectively, on hydrophobic surface for RNA extraction.

Table S6. List of primers used in this study

Primer name	Sequence (5' → 3')
Knock-out constructs	
<i>MoPRX1</i>	
<i>MoPRX1</i> _UF	TTC CAG GGG TAC TAT GGC AAC AA
<i>MoPRX1</i> _UR	CCT CCA CTA GCT CCA GCC AAG CC AAT CCG GGC CCA GTT TAG GTT TAT
<i>MoPRX1</i> _DF	GTT GGT GTC GAT GTC AGC TCC GGA G TCA ATA TGG CGC CGC AGC AGT AAT
<i>MoPRX1</i> _DR	GTACTCGCCTGCCCTGCCTATCTT
<i>MoPRX1</i> _UNF	GCTGCTAAAGGGATTGGCTACTCA
<i>MoPRX1</i> _DNR	ATGGTCGCCGCTATTTGCTTATG
<i>MoPRX1</i> _UF_F	ATAAACCTAAACTGGGCCCGGATT
<i>MoPRX1</i> _DF_R	ATTACTGCTGCGGCGCCATATTGA
<i>MoCCPI</i>	
<i>MoCCPI</i> _UF	TCT CGT TCC TGC AGA TGC CGT C
<i>MoCCPI</i> _UR	CCT CCA CTA GCT CCA GCC AAG CC TGA GGT CTC TGA CTT CAG TGG TAG GT
<i>MoCCPI</i> _DF	GTT GGT GTC GAT GTC AGC TCC GGA G TTG GGG AGG ACT TGA TGG TTA GAC TTG
<i>MoCCPI</i> _DR	CAG CCT GGA CTC GAG CAA CAC
<i>MoCCPI</i> _UNF	GCC GGA ACT TCC AGT TTG AAG ACA ACT ACC TA
<i>MoCCPI</i> _DNR	AAA CTG AGC GAG GAC TAC GAC GCC
<i>MoCCPI</i> _UR_F	ACC TAC CAC TGA AGT CAG AGA CCT CA
<i>MoCCPI</i> _DF_R	CAA GTC TAA CCA TCA AGT CCT CCC CAA
<i>MoAPX1</i>	
<i>MoAPX1</i> _UF	CAG TGG AGG AAT CAG CAA CTC TCA GC
<i>MoAPX1</i> _UR	CCT CCA CTA GCT CCA GCC AAG CC CCA TTG CCT TTA TGC GGA AGT TCT TGT
<i>MoAPX1</i> _DF	GTT GGT GTC GAT GTC AGC TCC GGA G CAT GAG CGC GTT TCA CAG GAC TC
<i>MoAPX1</i> _DR	TGA CAC GCC AAG ACC TAC CAC AGA G
<i>MoAPX1</i> _UNF	AAG GGG AAA CAT TGC GCA GAC ATC ACA
<i>MoAPX1</i> _DNR	CTT GCC AGC CTA TCT TGT CCA GTA GTG G
<i>MoAPX1</i> _UR_F	ACA AGA ACT TCC GCA TAA AGG CAA TGG
<i>MoAPX1</i> _DF_R	GAG TCC TGT GAA ACG CGC TCA TG
<i>MoAPX2</i>	
<i>MoAPX2</i> _UF	GCG GCT ATA GAA AGA TCC GGC ATG AAT
<i>MoAPX2</i> _UR	CCT CCA CTA GCT CCA GCC AAG CC ACA GCA GAT TGT GTG GTG ATG CAC
<i>MoAPX2</i> _DF	GTT GGT GTC GAT GTC AGC TCC GGA G GGA TGA GAA TGA GCC AAG CAG GGA ATT
<i>MoAPX2</i> _DR	TCG GAG ACG CCT AGC CTT CCC TA
<i>MoAPX2</i> _UNF	AAG GTC TCT TAA GGC ACA TTT CGT GCG G
<i>MoAPX2</i> _DNR	TGC CCC TAG AAC TCG TTA GTC AGT CTA GTT CG
<i>MoAPX2</i> _UR_F	GTG CAT CAC CAC ACA ATC TGC TGT
<i>MoAPX2</i> _DF_R	AAT TCC CTG CTT GGC TCA TTC TCA TCC
<i>MoHPX1</i>	
<i>MoHPX1</i> _UF	TCGTGAGAGGTGAGGACAATAAAC
<i>MoHPX1</i> _UR	CCT CCA CTA GCT CCA GCC AAG CC CTG CCA AAG GAC GAA GGA TTG AAA
<i>MoHPX1</i> _DF	GTT GGT GTC GAT GTC AGC TCC GGA G ACT GCT GTT TGA GAT GTC CA
<i>MoHPX1</i> _DR	CAA CAC GCA TGA CTC CAC CTA CAA
<i>MoHPX1</i> _UNF	TGG CTA GAC ATC TGA GGT TAT
<i>MoHPX1</i> _DNR	CTG GTT CGA GGA TGT TTA GTT
<i>MoHPX1</i> _UR_F	TTT CAA TCC TTC GTC CTT TGG CAG
<i>MoHPX1</i> _DF_R	TGG ACA TCT CAA ACA GCA GT
<i>MoLDS1</i>	
<i>MoLDS1</i> _UF	GGT AAG TAA CAT GCT AGG CAT TTG GAG TCT CG
<i>MoLDS1</i> _UR	CCT CCA CTA GCT CCA GCC AAG CC GCA ATG GGA ACG CCA TCG TGT ATT
<i>MoLDS1</i> _DF	GTT GGT GTC GAT GTC AGC TCC GGA G TGA CTG TTG GTG GGA TAA GAC TGA ATG AA

<i>MoLDS1_DR</i>	GAC TGG AAA GTG CCA AGT ATC CTG CTA
<i>MoLDS1_UNF</i>	GCG GTC TGA TAG ACC AAT TAA TAG CGA GGC TAA C
<i>MoLDS1_DNR</i>	ACA TTC AGG GAC AAT GAA TAC GTC CCT GCA G

TPXI

<i>TPXI_UF</i>	GCG GTT GAA TCT CGG ACA TA
<i>TPXI_UR</i>	CCT CCA CTA GCT CCA GCC AAG CC AGG GTA TGG CTC ACG AAA CTA AG
<i>TPXI_DF</i>	GTT GGT GTC GAT GTC AGC TCC GGA G TGT AGG ATG AGC GAC GAT AGT
<i>TPXI_DR</i>	AAG TTC GTC GAG GTT TCG GA
<i>TPXI_UNF</i>	CGA ATT GAA GCA CGC TGA GAG GTT
<i>TPXI_DNR</i>	TTG ACC TGT TCT CGC GCT TCT TTG
<i>TPXI_UR_F</i>	CTT AGT TTC GTG AGC CAT ACC CT
<i>TPXI_DF_R</i>	ACT ATC GTC GCT CAT CCT ACA

Hygromycin phosphotransferase

<i>HPH_F</i> (1.4 Kb)	GGCTTGGCTGGAGCTAGTGGAGG
<i>HPH_R</i> (1.4Kb)	GTTGGTGTTCGATGTCAGCTCCGGAG
<i>HPH_F</i> (2.1 Kb)	AGAAGATGATATTGAAAGG
<i>HPH_R</i> (2.1Kb)	GCACAGGTACACTTGTTTAGAG
<i>SYP_HPH_R</i>	ATGCCTGAACTCACGCGACGTCTGTGCG

GFP tagging

<i>MoPRX1_ORF_R_eGFP</i>	TCGCCCTTGCTCACCATCTCCT TGGGCAG
<i>eGFP_F</i>	ATGGTGAGCAAGGGCGAGGAG
<i>NcTerm_R</i>	ATCATCATGCAACATGCA
<i>NcTerm_R_nested</i>	GATGTATTAAGAGTATAGGGGTC
<i>MoPRX1_ORF_F_HindIII</i>	AAGCTTATGGCCGAAGAGCAGCGT
<i>MoPRX1_ORF_R_Xbal</i>	TCTAGACTACTCCTTGGGCAGCGGCGTA

qRT-PCR

β -Tubulin	
<i>TubF</i>	CTCCAGGGTTTCCAGATCAC
<i>TubR</i>	CCTCACCAGTGTACCAATGC
<i>MoAPX1_qRT_F</i>	CTTTCAGCCATGGTGTCTCTG
<i>MoAPX1_qRT_R</i>	ATGCTTCCAGCTCATCGT
<i>MoAPX2_qRT_F</i>	CAGGACTTGAAGACACTTGGG
<i>MoAPX2_qRT_R</i>	GTAACAGTGAAGGACGAGATACC
<i>MoAPX3_qRT_F</i>	ACGCCAGCATCTTTTACGAG
<i>MoAPX3_qRT_R</i>	CAAGGTCTCAAACGTCGAG
<i>CPXA_qRT_F</i>	TGTTCCCGTTCCATTCACCT
<i>CPXA_qRT_R</i>	GATCTGTTCCGTGGTAACTCG
<i>CPXB_qRT_F</i>	TGACCTGATTGACGATGCC
<i>CPXB_qRT_R</i>	CTTGTCAGAGTTGCGGTAGG
<i>MoCCP1_qRT_F</i>	GATGGTCCTAAGCAGTACGTC
<i>MoCCP1_qRT_R</i>	CGGCAGAGAAGTCCTTGAAG
<i>MoCCP2_qRT_F</i>	ACGGGTCTGAAGCAGTTTG
<i>MoCCP2_qRT_R</i>	GAAATCCGCAAAGAACAGGTC
<i>MoLIP1_qRT_F</i>	GCGTCCCACACTTCTCAC
<i>MoLIP1_qRT_R</i>	GCTTGTGCGTGAAGTTTTCG
<i>MoLIP2_qRT_F</i>	CGTCAATGGTAACAACTCTGC
<i>MoLIP2_qRT_R</i>	AGGAAAGCAGTCATGGAAGG

<i>MoLIP3_qRT_F</i>	CTTCACCTCTTGACTCAACCG
<i>MoLIP3_qRT_R</i>	ATGGAGGGATAAATGTCGGTG
<i>NOX3_qRT_F</i>	ATCAACACCCAGAGAAACCC
<i>NOX3_qRT_R</i>	GTACTACTACATTCGGGTCATCG
<i>NOX2_qRT_F</i>	GAGAGGCAGAAGGAACTTACG
<i>NOX2_qRT_R</i>	TCCTTGACAGCATAGTTGACG
<i>NOX1_qRT_F</i>	ATTGATGGTCCCTATGGTGC
<i>NOX1_qRT_R</i>	ACCAATACCAGTTCCAATGAGG
<i>MoHPX1_qRT_F</i>	GGAAGGACTGGGTCAAGATTC
<i>MoHPX1_qRT_R</i>	TTTCTGGGCTGTGATCTTG
<i>MoHPX2_qRT_F</i>	TTCACCTTTATCGAGTCGGC
<i>MoHPX2_qRT_R</i>	TGCTCGAAAGGAAGACGTTG
<i>MoHPX3_qRT_F</i>	CGGGAGTGGTTGAAGGTTAAT
<i>MoHPX3_qRT_R</i>	CCTGCTCAAACCTTGTGGAAAC
<i>CATA_qRT_F</i>	ACTTTAGCAACATCACCTCGG
<i>CATA_qRT_R</i>	GTCGGTATAGAATCTCGTGGC
<i>CATB_qRT_F</i>	CTTTCCTCTCACTTCCTCTTCC
<i>CATB_qRT_R</i>	AGTCAACTAACCCTTGGTGTG
<i>MoLDS1_qRT_F</i>	CTACAACCATCCCTTCAACCC
<i>MoLDS1_qRT_R</i>	GAGTCAAAGATCAGCCCAGG
<i>MoLDS2_qRT_F</i>	CTTCCCTAACCCTACTACGCC
<i>MoLDS2_qRT_R</i>	GACCCAGACTCTCCATAATCTTC
<i>MoPRX1_qRT_F</i>	TGGATCAAGGACATCAACGAC
<i>MoPRX1_qRT_R</i>	GCGGATGGTAAAGGCAATTC
<i>TPX1_qRT_F</i>	CCCGTGGAGTGTTTCGTTATTG
<i>TPX2_qRT_R</i>	CCTTAGCCTCTTCAACCTTGG
<i>MoPRX2_qRT_F</i>	AGCCACATCCCTTCATACATG
<i>MoPRX2_qRT_R</i>	GCCCAAGCCTTCATAACAAAG
<i>MoPRX3_qRT_F</i>	TTGTCATCGTCAGTGTTCCG
<i>MoPRX3_qRT_R</i>	CTTCTCGACGTAGCTCTTGAG
<i>MoVPX1_qRT_F</i>	TCACTCCATACCTCCCTGAG
<i>MoVPX1_qRT_R</i>	GTTTTCCTGGCGATGCTTG
<i>MoCMD1_qRT_F</i>	CTCTCGGATAAGCAGTGGG
<i>MoCMD1_qRT_R</i>	GTGATCTCGACAACCTCACG
<i>HYR1_qRT_F</i>	GACTACAAGGGCAAGGTCCG
<i>HYR1_qRT_R</i>	GAAGCCGAGGATGGTAAAGTC
